**Pacific Northwest
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User Instructions for the Systems Assessment Capability, Rev. 0, Computer Codes

Volume 2: Impact Modules

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June 2002

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Contents

Figures

Tables

1.0 Introduction and Background

1.1 The Groundwater/Vadose Zone Project

In late 1997, the U.S. Department of Energy (DOE) established the Groundwater/Vadose Zone Integration Project (Integration Project). One activity of the Integration Project is an assessment of cumulative impacts for Hanford Site wastes on the subsurface environment and the Columbia River. Through the application of a system assessment capability (SAC), decisions for each cleanup and disposal action will be able to take into account the composite effect of other cleanup and disposal actions.

1.2 Hanford Site

The Hanford Site lies within the semi-arid Pasco Basin of the Columbia Plateau, in southeastern Washington State (see Figure 1-1). The site occupies approximately 1,517 km^2 (586 square miles) and is located north of the city of Richland, Washington. About 6% of the land area has been disturbed and is actively used. The site is located upstream of the confluence of the Yakima and Snake Rivers with the Columbia River, approximately 25 miles north and upstream of the Oregon border. A dry area known for its sandy soils, basalt ridges, and shrub-steppe vegetation, the Hanford Site is bordered by the Columbia River on the north and east. The Yakima River flows near a portion of the southern boundary of the site before it joins the Columbia River south of the city of Richland.

1.3 Overview of the SAC Systems Code

The SAC Systems Code is a tool used to simulate the migration of contaminants (analytes) present on the Hanford Site and assess the potential impacts of the analytes, including dose to humans, socio-cultural impacts, economic impacts, and ecological impacts. The system of codes includes existing computer programs, new computer programs, electronic data libraries, and data formatting processors (or data translators). The relationships among code modules that make up the SAC Systems Code are illustrated in Figure 1-2.

Major modules appearing on the left side of the diagram perform inventory and transport calculations providing estimates of the concentrations of analytes in various media. Modules shown on the right perform calculations related to impacts from the contaminated media. Impacts include potential effects on humans, the ecology of the area, the economy of the region, the proximity of contaminants to social and cultural resources.
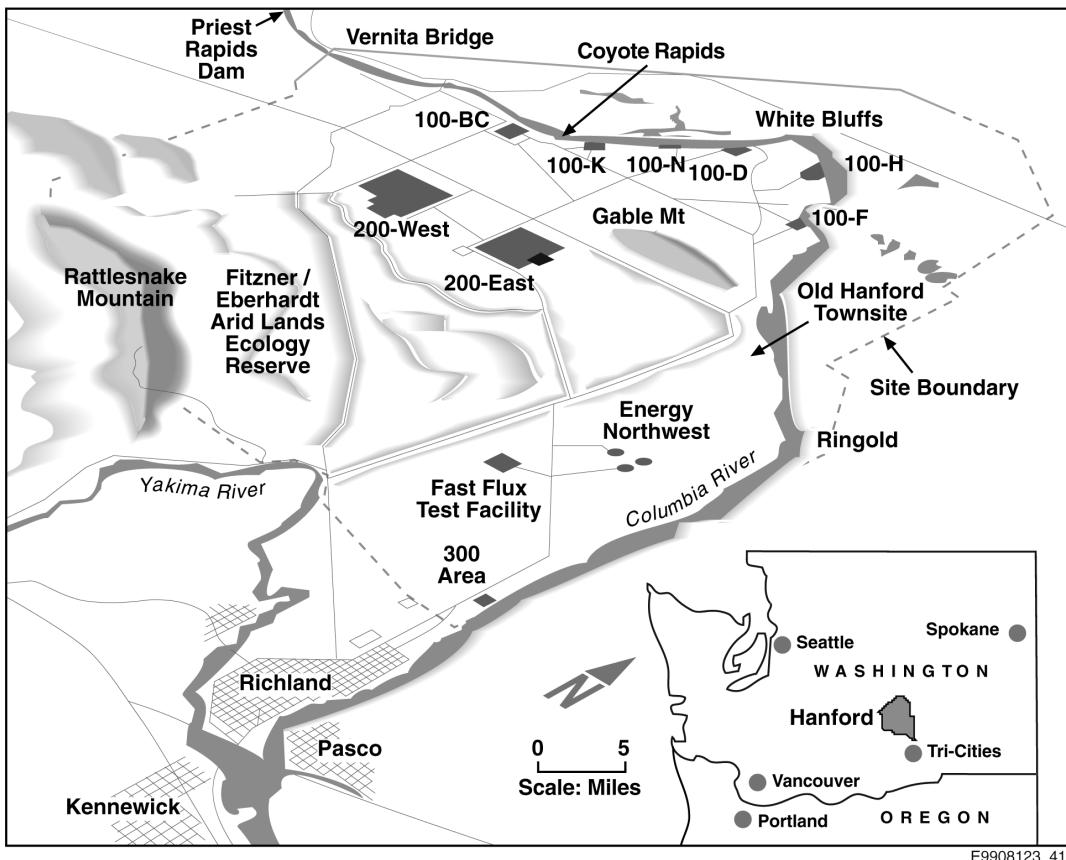
Figure 1-1 Hanford Site Location

The general approach to handling uncertainty in SAC, Rev. 0, is a Monte Carlo approach. Conceptually, one generates a value for every stochastic parameter in the code (the entire sequence of modules from inventory through transport and impacts) and then executes the simulation, obtaining an output value, or result. This process is often called one *realization*. One then repeats the entire process, obtaining another result that is different from the first, but as equally likely to occur as the first result. After repeating this process a number of times, one has a set of equally likely consequences that represent the statistical distribution of all outcomes. Several specialized sampling techniques have been developed to reduce the number of realizations required in a Monte Carlo analysis to obtain a satisfactory description of the output distribution. One of the techniques, called Latin Hypercube Sampling (Iman and Conover 1982), has proven successful for mass transport applications in groundwater systems. The general Monte Carlo approach still applies, and the specific values of the input parameters are chosen from the same statistical distributions, but the sampling scheme spreads the values in such a way as to reduce sampling variability while also supporting a correlation structure between input variables.

1.4 Purpose of This Document

This document contains detailed user instructions for the following four impacts codes developed for Rev. 0 of the SAC:
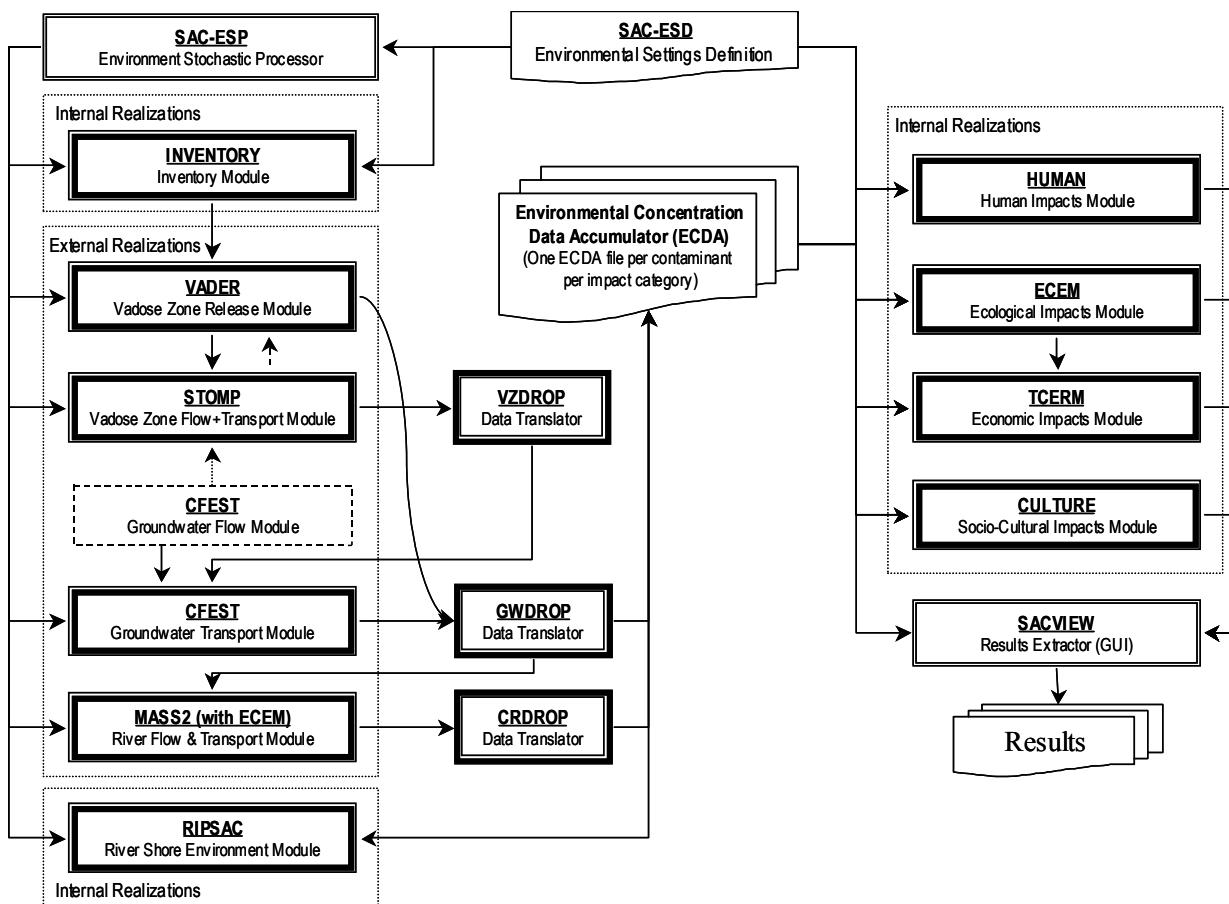
Figure 1-2 Module Information Flow for the SAC Rev. 0 Systems Code

- CULTURE: Socio-cultural impact assessment
- ECEM: Ecological impacts assessment
- HUMAN: Human impacts assessment
- TCERM: Tri-Cities economic impacts assessment.

The suite of computer codes for Rev. 0 of SAC performs many more functions than just impact assessments. They also perform inventory tracking, release of contaminants to the environment, and transport of contaminants through the unsaturated zone, saturated zone, and in the river. User instructions for the other codes are provided in Eslinger et al. (2002).

2.0   Environmental Settings Definition Files

2.1   Overview

As indicated in Figure 1-2, the inventory, release, and transport codes must all be executed to develop a data set of concentration data for use in the impacts codes. Concentration data for every realization are saved only at specified times and locations. Control information for an analysis is provided in one of two general places. In general, if control information is needed by more than one code, it resides in the environmental settings definition (ESD) keyword file. The contents of the ESD keyword file are described in this section. For example, the codes ECDA, HEADER, GWDROP, CRDROP, RIPSAC, and HUMAN all need to know the locations for calculating human impacts, thus the LOCATION keyword is provided in the ESD keyword file (see Section 2.2.7).

The structure of the concentration data files is also described in this section (see Section 2.3) even though the user generally will modify these files directly. The SACView code (see Section 7.0) is provided to allow the user to view the contents of these binary-format data files.

The river transport model can be run with or without background concentrations from upriver sources. A typical method of analyzing a Hanford-related problem is to run the river code with two data sets. First, a transport run is made using background values, but no source term from the Hanford Site is introduced. Then, another transport run is made that is identical to the first run except a Hanford source term is introduced. If the impacts codes are run using these two data sets, their results can be differenced to determine the contribution from Hanford sources. The groundwater model in SAC, Rev. 0 is not set up to model background concentrations; thus, differencing does not currently apply to impacts based on groundwater concentrations. A utility code called ImDiff (see Section 8.0) is provided to facilitate differencing the results from the impacts models.

2.2   ESD Keywords Used by the Impacts Codes

The environmental settings are defined in the ESD keyword file. This file contains information used in more than one module of the suite of codes. A file containing example ESD keywords is provided in Table 2.1. This file is intended to give examples of keywords and does not form a consistent set of keywords that would result in a successful problem execution.

Table 2.1 Example ESD Keywords Used in the Impacts Codes

```
! Purpose:  This file is a nonfunctional example of keywords for the ESD Keyword File

REPORT "ESD_Initial_Mass209.Rpt"          ! Define the ESD report file name
TITLE  "SAC Rev. 0 Initial Assessments"   ! Define the problem title
USER   "Engel & Nichols"                  ! Define the user for the ESD program
REALIZAT 25                               ! Number of realizations to run
PERIOD START=1944 STOP=3050 CLOSURE=2050  ! Time period for the analysis

!************************************** Analytes **************************************
ANALYTE ID="Sr90"  NAME="Strontium 90"  TYPE="NR"    COMPUTE
  MOLWGT   = 89.9077  MOLDIFF  = 5.0E-11      HALFLIFE = 28.78   SPECIFIC = 1.3976E+2
  DFIMM    = 0        DFSED    = 3.72000E-21 GAMMA    = 0        HENRY    = 0
```

```
ANALYTE ID="CCl4"   NAME="Carbon Tetrachloride" TYPE="NS"  COMPUTE
  HENRY  = 2.99E+03 MOLDIFF=5.0E-08   MOLWGT = 153.8  HALFLIFE = 0.0
ANALYTE ID="CrVI" NAME="Hexavalent Chromium"  TYPE="NS"    COMPUTE
  HENRY  = 0        MOLDIFF=1.0E-10   MOLWGT = 100.0  HALFLIFE = 0.0

!*********************** ECDA Concentration Related Files ***********************
! SACVIEW header file for ECDA concentration files
FILE HEADER NAME="G:\Initial\Ecda\Sacview_Initial.Hdr" CREATE
!
! ECDA record number index map files for concentration data by impact type
FILE I_HUMAN  NAME="G:\Initial\Ecda\HUMA_Initial.Map"  CREATE
FILE I_ECOLOG NAME="G:\Initial\Ecda\ECOL_Initial.Map"  CREATE
FILE I_ECONOM NAME="G:\Initial\Ecda\ECON_Initial.Map"  CREATE
FILE I_CULTUR NAME="G:\Initial\Ecda\CULT_Initial.Map"  CREATE
!
! ECDA Concentration data files for each impact type and analyte
FILE C_HUMAN  ANALYTE="Sr90"   NAME="G:\Initial\Ecda\HUMA_Sr90_Initial.Dat"   CREATE
FILE C_ECOLOG ANALYTE="Sr90"   NAME="G:\Initial\Ecda\ECOL_Sr90_Initial.Dat"   CREATE
FILE C_ECONOM ANALYTE="Sr90"   NAME="G:\Initial\Ecda\ECON_Sr90_Initial.Dat"   CREATE
FILE C_CULTUR ANALYTE="Sr90"   NAME="G:\Initial\Ecda\CULT_Sr90_Initial.Dat"   CREATE
!
FILE C_HUMAN  ANALYTE="CrVI"   NAME="G:\Initial\Ecda\HUMA_CrVI_Initial.Dat"   CREATE
FILE C_ECOLOG ANALYTE="CrVI"   NAME="G:\Initial\Ecda\ECOL_CrVI_Initial.Dat"   CREATE
FILE C_ECONOM ANALYTE="CrVI"   NAME="G:\Initial\Ecda\ECON_CrVI_Initial.Dat"   CREATE
FILE C_CULTUR ANALYTE="CrVI"   NAME="G:\Initial\Ecda\CULT_CrVI_Initial.Dat"   CREATE
!
FILE C_HUMAN  ANALYTE="CCl4"   NAME="G:\Initial\Ecda\HUMA_CCl4_Initial.Dat"   CREATE
FILE C_ECOLOG ANALYTE="CCl4"   NAME="G:\Initial\Ecda\ECOL_CCl4_Initial.Dat"   CREATE
FILE C_ECONOM ANALYTE="CCl4"   NAME="G:\Initial\Ecda\ECON_CCl4_Initial.Dat"   CREATE
FILE C_CULTUR ANALYTE="CCl4"   NAME="G:\Initial\Ecda\CULT_CCl4_Initial.Dat"   CREATE

!*********************** Soil-water Partition Coefficients (Kd's) ***********************
ECHO KDSOIL ! Echo soil-water Kd values to the ECDA report file
FILE KDSOIL NAME="G:\Initial\ecda\KDSOIL_Initial.Dat" SEED=232323.0 CREATE
KDSOIL "KDCCl4"  9 -8.5172 0.2243 "Soil-water Kd for carbon tetrachloride (m^3/kg)"
KDSOIL "KDCr"    1  0.00          "Soil-water Kd for chromium (m^3/kg)"
KDSOIL "KDSr"    9 -3.9120 1.4903 "Soil-water Kd for strontium (m^3/kg)"

!***************** ECDA concentration solution times for human impacts **************
TIMES HUMAN
  1980 1982 1984 1986 1988 1990 2000 2010 2020 2030 2040 2050
  2060 2070 2080 2090 3000 3010 3020 3030 3035 3040 3045 3050

!********************** ECDA concentration solution times for cultural impacts ******
TIMES CULTURAL
  1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000
  2010 2050 2090 2140 2220 2720 2800 2840 2880 2900 3000 3050

!********************** ECDA concentration solution times for ecological impacts *****
! Verified on 5/8/2001 by Paul W. Eslinger
TIMES ECOLOGICAL
  1990 1992 1994 1996 1998 2000 2010 2020 2030 2040 2050 2060
  2065 2070 2075 2080 2090 2095 3000 3010 3020 3030 3040 3050

!********************** ECDA concentration solution times for economic impacts ******
! Verified on 5/8/2001 by Paul W. Eslinger
TIMES ECONOMIC
```

```
  2000 2005 2010 2015 2020 2025 2030 2035 2040 2045 2050 2055
  2500 3000 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050


!*************************** Human Locations **************************************
LOCATION HUMAN ID="HL0151" NAME="Human location"
  EASTING =  594737.5  NORTHING=  127827.4  POP=0  GRO_WAT ! Upland
LOCATION HUMAN ID="HL0152" NAME="Human location"
  EASTING =  594792.4  NORTHING=  127831.2  POP=0  SUR_WAT POR_WAT SEDIMENT ! River
LOCATION HUMAN ID="HL0443" NAME="Human location"
  EASTING =  598044.1  NORTHING=  102721.5  POP=0  GRO_WAT SOIL SEE_WAT ! Riparian


!*************************** Ecological Locations ********************************
LOCATION Ecological ID="EL0001" NAME="Ecological location"
  EASTING =  557375.3  NORTHING=  144885.2
  GRO_WAT SOIL SEE_WAT ! Riparian
  APSD    = 4.00E-02  COXYGEN = 1.10E-02  POROSITY= 3.50E-01  FOC  = 1.0E+00
  VEGCOV  = 5.00E-01  NECF    = 1.00E+00  RHOS    = 1.50E+00  SRH  = 1.8E-02
  TEMP    = 2.85E+02  MSWIND  = 3.44E+00  MZWIND  = 3.44E+00  AREA = 2.5E+03
  LENGTH  = 5.00E+01
!
LOCATION Ecological ID="EL0002" NAME="Ecological location"
  EASTING =  557363.4  NORTHING=  144938.9
  SUR_WAT POR_WAT SEDIMENT ! River
  APSD    = 4.00E-02  COXYGEN = 1.10E-02  POROSITY= 3.50E-01  FOC  = 1.0E+00
  VEGCOV  = 5.00E-01  NECF    = 1.00E+00  RHOS    = 1.50E+00  SRH  = 1.8E-02
  TEMP    = 2.85E+02  MSWIND  = 3.44E+00  MZWIND  = 3.44E+00  AREA = 2.5E+03
  LENGTH  = 5.00E+01
!
LOCATION Ecological ID="EL0674" NAME="Ecological location"
  EASTING =  593332.3  NORTHING=   68646.5
  SUR_WAT POR_WAT SEDIMENT ! River
  APSD    = 4.00E-02  COXYGEN = 1.10E-02  POROSITY= 3.50E-01  FOC  = 1.0E+00
  VEGCOV  = 5.00E-01  NECF    = 1.00E+00  RHOS    = 1.50E+00  SRH  = 1.8E-02
  TEMP    = 2.85E+02  MSWIND  = 3.44E+00  MZWIND  = 3.44E+00  AREA = 2.5E+03
  LENGTH  = 5.00E+01


!*************************** Economic Locations
****************************************
LOCATION ECONOMIC ID="EN0011" NAME="ECONOMIC location"
  EASTING =  595445.1  NORTHING=  109753.5  SUR_WAT ! River
LOCATION ECONOMIC ID="EN0021" NAME="ECONOMIC location"
  EASTING =  607747.5  NORTHING=   99528.3  SUR_WAT ! River
LOCATION ECONOMIC ID="EN0014" NAME="ECONOMIC location"
  EASTING =  588021.6  NORTHING=  134116.6  GRO_WAT ! Upland


!*************************** Cultural Locations
****************************************
LOCATION Cultural ID="CL0001" NAME="Cultural location"
  EASTING =  574521.6  NORTHING=  154366.6  AREA= 8.86290E+05
  GRO_WAT ! Upland
LOCATION Cultural ID="CL1683" NAME="Cultural location"
  EASTING =  561735.4  NORTHING=  146626.0  AREA= 3.62779E+04
  SUR_WAT POR_WAT SEDIMENT ! River
LOCATION Cultural ID="CL1684" NAME="Cultural location"
  EASTING =  561740.4  NORTHING=  146672.0  AREA= 1.53460E+04
  SUR_WAT POR_WAT SEDIMENT ! River
```

```
!***************************** Effective Energies
*****************************************
! Used in Ecological models for radioactive analytes
RADIUS ID="Radius"      1.4,           2,          3,          5,          7,
        10,        20,         30
RADIUS ID="Cs137" 2.57E-01, 2.67E-01, 2.84E-01, 3.16E-01, 3.46E-01,
  3.88E-01, 5.00E-01, 5.82E-01
RADIUS ID="Sr90"  1.14E+00, 1.14E+00, 1.14E+00, 1.14E+00, 1.14E+00,
  1.14E+00, 1.14E+00, 1.14E+00


!********************** Plant and Animal Growth and Respiration
GROWTH   DELTA=0.002 BETA=0.25
RESPIRE  GAMMA=0.2   PHI=0.032


!************************* Biotic Species Information
SPECIE ID="AMCOOT" TYPE="TA" NAME="American coot"
  AE      =8.10000E-01 DIFFHT =2.00000E-01  ETWATER=2.00000E+01 FMR    =1.63087E+02
  FWATER  =5.00000E-01 FDW    =1.70000E-01  GE     =1.90000E+03 INHRATE=6.15926E-01
  PCS     =2.50000E-01 PCW    =5.00000E-01  PSI    =1.00000E+00 RADIUS =5.00000E+00
  SA      =7.84063E+02 SADHER =1.45000E+00  SOILING=1.80000E-01 THETA  =1.00000E+00
  WATERING=4.61024E-02 WEIGHT =6.92000E-01
!
SPECIE ID="BEAVER" TYPE="TA" NAME="Beaver"
  AE      =8.10000E-01 DIFFHT =4.00000E-02  ETWATER=2.00000E+01  FMR    =3.76195E+02
  FWATER  =1.00000E+00 FDW    =1.70000E-01  GE     =1.70000E+03  INHRATE=1.17514E+01
  PCS     =2.20000E-01 PCW    =1.00000E+00  PSI    =1.00000E+00  RADIUS =2.00000E+01
  SA      =7.55836E+03 SADHER =1.45000E+00  SOILING=9.00000E-02  THETA  =1.00000E+00
  WATERING=1.43439E+00 WEIGHT =1.95000E+01

END
```

In the following keyword descriptions, some data are optional for a particular problem definition and some are required. Data that are required are enclosed in square brackets. For AB to be required, it would be denoted by [AB]. If only one of the three items AB, BC, CD were required, it would be written as [AB|BC|CD]. The vertical bars indicate to choose one of the items in the list. Optional items are enclosed in normal brackets. For DE to be an optional entry, it would be denoted by {DE}. The {} or [] symbols are indicators of whether the data are required; the symbols do not need to be entered when the keyword is constructed. The keyword name can contain any number of characters; however, only the first eight characters are read (for example, REALIZAT has the same effect as REALIZATION).

In some instances, numerical values or quote strings are associated with a modifier. In this description, the association is indicated by using the equal (=) symbol. The = symbol is not required but may be used when the keyword is constructed. When a numerical value or quote string is associated with a modifier, it must be physically entered on the input line directly after the modifier.

2.2.1   ANALYTE Keyword in the ESD Keyword File

The ANALYTE keyword is used to define the analytes to be used in the simulation. The syntax for this keyword is the following:

```
ANALYTE [ID="quote 1"] [TYPE="quote 2"] [NAME="quote 3"] {COMPUTE}
   {MOLDIFF=N1}  {HENRY=N2}  {DFIMM=N3}  {DFSED=N4}
   {GAMMA=N5} {HALFLIFE=N6} {MOLWGT=N7} {SPECIFIC=N8}
```

A separate ANALYTE keyword must be entered for every analyte to be included in the simulation. The optional modifier COMPUTE can be entered. If COMPUTE is not present, the analyte will not be included in the run although information is included in the environmental settings file.

The modifiers associated with the ANALYTE keyword are given in Table 2.2.

Table 2.2 Modifiers Associated with the ANALYTE Keyword in the ESD File

Modifier	Description
ID	The quote string associated with the ID modifier is an analyte identification string up to six characters in length. The analyte identification string is case sensitive, and spaces or hyphens change the definition. All data in the analyte identification strings must satisfy the following conventions: • Only the first entry in the analyte identification string is capitalized • No embedded spaces or hyphens are used, even for radionuclides • Individual elements are defined using the standard element abbreviation
TYPE	The quote string associated with the TYPE modifier string is a two-character analyte type indicator. The following are valid entries for this string: • NR – if the analyte is a radioactive element or an inorganic compound containing a radionuclide • NS – if the analyte is a stable (nonradioactive) element or inorganic compound • OR – if the analyte is an organic compound containing a radionuclide • OS – if the analyte is an organic compound, containing a stable (nonradioactive) elemental analyte or compound
NAME	The quote string associated with the NAME modifier is an analyte name or description up to 72 characters in length.
MOLDIFF	The numerical entry associated with the MOLDIFF modifier is the molecular diffusivity of the analyte. This value has units of cm^2/sec and is used only in the ecological modules. Entry of this modifier is optional. If it is not present, the value of MOLDIFF defaults to zero.
MOLWGT	The numerical entry associated with the MOLWGT modifier is the molecular weight of the analyte. This value has units of g/mole.
HENRY	The numerical entry associated with the HENRY modifier is the Henry's law coefficient for organic analytes. This value has units of $Pa\text{-}m^3$/mole and is used only in the impacts modules. Entry of this modifier is optional. If it is not present, the value of HENRY defaults to zero.

Modifier	Description
HALFLIFE	The numerical entry associated with the HALFLIFE modifier is the half-life of the analyte. This value has units of years. Entry of this modifier is optional. If it is not present, the value of HALFLIFE defaults to infinity (decay constant value of zero).
SPECIFIC	The numerical entry associated with the SPECIFIC modifier is the specific activity of the analyte. This value has units of curies per gram. Entry of this modifier is required if the analyte is radioactive. It is not used for nonradioactive analytes.
DFIMM	The numerical entry associated with the DFIMM modifier is the immersion external dose factor for radioactive analytes. This value has units of mrad/yr per uCi/m^3 and is used only in the impacts modules. Entry of this modifier is optional. If it is not present, the value of DFIMM defaults to zero.
DFSED	The numerical entry associated with the DFSED modifier is the sediment external dose factor for radioactive analytes. This value has units of Sv-m^3/sec-Bq and is used only in the impacts modules. Entry of this modifier is optional. If it is not present, the value of DFSED defaults to zero.
GAMMA	The numerical entry associated with the GAMMA modifier is the gamma decay energy for radioactive analytes. This value has units of MeV/nt and is used only in the impacts modules. Entry of this modifier is optional. If it is not present, the value of GAMMA defaults to zero.
COMPUTE	The optional modifier COMPUTE can be entered. If COMPUTE is not present, the analyte will not be included in the run although information is included in the environmental settings file.

The following ANALYTE keywords select the analytes carbon tetrachloride and strontium-90 for analysis:

```
ANALYTE ID="CCl4"   NAME="Carbon Tetrachloride" TYPE="NS"  COMPUTE
  HENRY  = 2.99E+03 MOLDIFF=5.0E-08    MOLWGT = 153.8  HALFLIFE = 0.0

ANALYTE ID="Sr90"  NAME="Strontium 90"  TYPE="NR" COMPUTE
  MOLWGT   = 89.9077    MOLDIFF  = 5.0E-11
  HALFLIFE = 28.78      SPECIFIC = 1.3976E+2
  DFIMM    = 0          DFSED    = 3.72000E-21
  GAMMA    = 0          HENRY    = 0
```

2.2.2   END Keyword in the ESD Keyword File

The END keyword signifies the end of all keyword data. It should be the last keyword in the keyword file. Any data in the keyword file after the END keyword will be ignored. The following is the syntax for this keyword record:

```
END
```

There are no modifiers or quote strings associated with the END keyword.

2.2.3   FILE Keyword in the ESD Keyword File

The FILE keyword is used to enter the names of many of the files used in a simulation run. The following is the syntax for the FILE keyword record:

```
FILE [NAME="quote 1"] {ANALYTE="quote 2"} {HEADER|KDSOIL|DILUTE}
   { C_HUMAN | C_ECONOM | C_CULTUR | C_ECOLOG |   C_HUMAN |
     C_ECONOM | C_CULTUR | C_ECOLOG } {CREATE} {SEED=N1}
```

The file names are entered in quote strings, which must be enclosed in double quotation marks. Path names up to 72 characters long are supported. At least one FILE keyword is required for every run of the code if concentrations are to be generated. Every file definition requires the entry of a separate FILE keyword. File type modifiers associated with the FILE keyword are given in Table 2.3.

Table 2.3 Modifiers Associated with the FILE Keyword in the ESD File

Modifier	Description
C_HUMAN	This modifier indicates that the FILE keyword is defining a concentration file for human impacts. Concentrations for each analyte are contained in separate files. The ANALYTE modifier is used to associate an analyte with this file (see the ANALYTE keyword in Section 2.2.1).
C_CULTUR	This modifier indicates that the FILE keyword is defining a concentration file for cultural impacts. Concentrations for each analyte are contained in separate files. The ANALYTE modifier is used to associate an analyte with this file (see the ANALYTE keyword in Section 2.2.1).
C_ECONOM	This modifier indicates that the FILE keyword is defining a concentration file for economic impacts. Concentrations for each analyte are contained in separate files. The ANALYTE modifier is used to associate an analyte with this file (see the ANALYTE keyword in Section 2.2.1).
C_ECOLOG	This modifier indicates that the FILE keyword is defining a concentration file for ecological impacts. Concentrations for each analyte are contained in separate files. The ANALYTE modifier is used to associate an analyte with this file (see the ANALYTE keyword in Section 2.2.1).
CREATE	When this modifier is present, the file will be created under the control of the ESP. If the CREATE modifier is not present, no ESP-related actions occur for that file.
I_HUMAN	This modifier indicates that the FILE keyword is defining a record index file for mapping into all binary files of concentrations supporting human impacts.
I_CULTUR	This modifier indicates that the FILE keyword is defining a record index file for mapping into all binary files of concentrations supporting cultural impacts.
I_ECONOM	This modifier indicates that the FILE keyword is defining a record index file for mapping into all binary files of concentrations supporting economic impacts.
I_ECOLOG	This modifier indicates that the FILE keyword is defining a record index file for mapping into all binary files of concentrations supporting ecological impacts.

Modifier	Description
KDSOIL	This modifier indicates that the FILE keyword is defining a file to contain stochastic realizations of all of the random variables defined using the KDSOIL keyword.
DILUTE	This modifier indicates that the FILE keyword is defining a file to contain stochastic realizations of all of the random variables defined using the DILUTE keyword.
HEADER	This modifier indicates that the FILE keyword is defining a header file for use by the SACView graphical user interface that allows extraction of human-readable concentration data.
SEED	If the file name is associated with the KDSOIL or DILUTE modifiers, the SEED modifier must also be entered. The numerical value associated with the SEED modifier is the value for the random number generator and must have an entry in the range 1 to 999999.

The following are example entries that define the concentration files for carbon-14 and zinc for the full suite of cultural, ecological, economic, and human impacts:

```
FILE C_HUMAN ANALYTE="C14"  NAME="\Test\Human\C14\Conc.dat"
FILE C_CULTUR ANALYTE="C14"  NAME="\Test\Cultural\C14\Conc.dat"
FILE C_ECONOM ANALYTE="C14"  NAME="\Test\Ecomonics\C14\Conc_ec.dat"
FILE C_ECOLOG ANALYTE="C14"  NAME="\Test\Ecology\C14\Conc_bugs.dat"
FILE C_HUMAN ANALYTE="Zn"  NAME="\Test\Human\Zinc\Conc.dat"
FILE C_CULTUR ANALYTE="Zn"  NAME="\Test\Cultural\Zinc\Conczn.dat"
FILE C_ECONOM ANALYTE="Zn"  NAME="\Test\Ecomonics\Zinc\Conc_ec.dat"
FILE C_ECOLOG ANALYTE="Zn"  NAME="\Test\Ecology\Zinc\Conc_bugs.dat"
```

If present, the CREATE flag causes the following actions by the ECDA or HEADER codes under control of the ESP:

- Deletion of any existing file by that name and creation of a new file.
- If the file is associated with the HEADER, DILUTE, KDSOIL, I_HUMAN, I_ CULTUR, I_ ECONOM, or I_ ECOLOG modifiers, new data are written to the file.
- If the file is associated with the C_HUMAN, C_CULTUR, C_ECONOM, or C_ECOLOG modifiers, the concentration data are initialized to the value –1.0, except for groundwater concentrations, which are initialized to 0.0.

The following are example entries that define the files for soil-water Kd values and the water dilution factors for the river-shore module:

```
FILE KDSOIL NAME="KDSOIL.CSV" SEED=23232.0 CREATE
FILE DILUTE NAME="DILUTE.CSV" SEED=12345.0 CREATE
```

The following are example entries that define the ECDA record number index files for all four impact types:

```
FILE I_HUMAN  "HUMA_MAP.CSV" CREATE
FILE I_ECOLOG "ECOL_MAP.CSV" CREATE
```

```
FILE I_ECONOM "ECON_MAP.CSV" CREATE
FILE I_CULTUR "CULT_MAP.CSV" CREATE
```

2.2.4   FILLECDA Keyword in the ESD Keyword File

The FILLECDA keyword controls filling ECDA files with random concentrations as they are initialized, rather than filling them with negative or zero concentrations. The following is the keyword's syntax:

```
FILLECDA   [N₁]
```

The value N_1 is the seed for the random-number generator. A value between 1 and 999999 must be entered. Every concentration entry in the concentration data files will set to a random value on the (0,1) interval if this keyword is used.

This keyword is useful for generating concentration files for stress testing of the codes. There are no modifiers or quote strings for the FILLECDA keyword. This keyword should not be used during a production run.

2.2.5   GROWTH Keyword in the ESD Keyword File

The GROWTH keyword defines the growth rate equation for water respiring species. These data are used in the biotic transport portion of the MASS2 code as well as the ecological impacts code ECEM. The following is the keyword's syntax:

```
GROWTH   [DELTA=N₁]  [BETA=N₂]
```

Both the delta and beta parameters must be specified. The following is an example of this keyword:

```
GROWTH DELTA=0.002 BETA =0.25
```

A description of the mathematical model for the growth of species is provided in Section 4.1.2. In summary, the growth rate of a given water-respiring species is provided by the regression equation $G = \delta \bullet w^{-\beta}$ (Thomann et al. 1992) where δ and β are regression parameters and w is the body weight of the species (kg@ wet weight).

2.2.6   KDSOIL Keyword in the ESD Keyword File

The KDSOIL keyword is used to enter the definition of a statistical distribution for the solid-aqueous distribution coefficient (K_d) to be used for calculating soil concentrations from groundwater concentrations. The following is the general syntax for the KDSOIL keyword:

```
KDSOIL ["quote₁"] [Dist_Index Parameters] {TRUNCATE U1 U2}  {"quote₂"}
```

The entry for quote₁ must be a unique character string of up to 20 characters that will be used to identify this stochastic variable in subsequent uses. It is case sensitive and embedded spaces are significant. The entry for quote₂ is a description for the stochastic variable that can be up to 64 characters long. An entry

for quote$_2$ is not required, although it is used for labeling purposes if present. Section 10.0 contains information on the statistical distributions available in the simulation.

A K$_d$ that is triangular on the triple (0.2, 0.5, 0.99) could use the following keyword entry:

```
KDSOIL "ID#1"  6  0.2  0.5  0.99 "Example Kd for users guide"
```

2.2.7 LOCATION Keyword in the ESD Keyword File

The LOCATION keyword identifies the locations where concentrations will be generated for use in the impacts modules. The following is the keyword's syntax:

```
LOCATION [ID="quote₁"] [EASTING=N1] [NORTHING=N2] {AREA=N3}
    HUMAN|ECOLOGICAL|ECONOMIC|CULTURAL] {COMPUTE} {POP=N4}
    {GRO_WAT}  {SUR_WAT} {POR_WAT} {SEDIMENT} {SOIL} {SEE_WAT}
    [TITLE= "quote₂"]
```

Table 2.4 contains the modifiers and associated data for the LOCATION keyword.

Table 2.4 Modifiers Associated with the LOCATION Keyword in the ESD File

Modifier	Description
COMPUTE	If the COMPUTE modifier is entered, this location will be included in the simulation. If COMPUTE is not entered, this location will be ignored.
ID	The location identification string is entered using the ID modifier. This string is limited to 15 characters and must be unique. It is used to associate other data with a specific location.
TITLE	A descriptive title for this location is entered using the TITLE modifier. This quote string is limited to 72 characters. It is used only for output labeling purposes.
EASTING	This entry is associated with the easting coordinate (meters, state plane coordinate system) for the location.
NORTHING	This entry is associated with the northing coordinate (meters, state plane coordinate system) for the location.
---	One of the four modifiers HUMAN, ECOLOGICAL, ECONOMIC, or CULTURAL must be entered. This modifier identifies the impacts module for which this location is being defined.
GRO_WAT	Presence of this optional modifier indicates that groundwater concentrations will be computed at this location.
SUR_WAT	Presence of this optional modifier indicates that surface water concentrations will be computed at this location.
POR_WAT	Presence of this optional modifier indicates that river bottom pore water concentrations will be computed at this location.

Modifier	Description
SEE_WAT	Presence of this optional modifier indicates that seep water concentrations (on the land surface) will be computed at this location.
SOIL	Presence of this optional modifier indicates that soil concentrations (on the land surface) will be computed at this location.
SEDIMENT	Presence of this optional modifier indicates that sediment concentrations (on the river bottom) will be computed at this location.
APSD	Aggregate particle size distribution (mm) used in the erosion threshold wind speed calculations (used in the ecological model).
COXYGEN	Oxygen concentration in surface water (mg/L) (used in the ecological model).
FOC	Fraction soil organic carbon content (unitless) (used in the ecological model).
MSWIND	Mean annual wind speed (m/s) (used in the ecological model).
MZWIND	Mixing zone wind speed (m/s) (used in the ecological model).
NECF	Nonerodible elements correction factor (unitless) used in calculating the threshold air friction velocity (used in the ecological model).
POROSITY	Soil porosity at the location (unitless) (used in the ecological model).
RHOS	Soil density at the location (g/cm^3) (used in the ecological model).
SRH	Surface roughness height (m) used in calculating the threshold friction velocity. (used in the ecological model).
TEMP	Temperature (in Kelvins) used in calculating air concentrations of organic analytes (used in the ecological model).
VEGCOV	Fraction of vegetation cover at the location (unitless) (used in the ecological model).

Locations for cultural, ecological, economic, and human analyses may be different. The following example keywords define three locations for human impacts:

```
LOCATION HUMAN ID="HL0151" NAME="Upland human location"
   EASTING =  594737.5  NORTHING=  127827.4 POP=0 GRO_WAT

LOCATION HUMAN ID="HL0417" NAME="Riparian zone human location"
   EASTING =  557375.3  NORTHING=  144885.2 POP=0 GRO_WAT SOIL SEE_WAT

LOCATION HUMAN ID="HL0413" NAME="Richland municipal water intake"
   EASTING =  595445.1  NORTHING=  109753.5 POP=0 SUR_WAT POR_WAT SEDIMENT
```

The following example keywords define a location for economic impacts:

```
LOCATION ID="Loc #04"  EASTING=123402  NORTHING=12424 COMPUTE
   ECONOMIC GRO_WAT SEE_WAT SOIL
   TITLE="Example of a title line for location #04"
```

The following example keywords define four locations for ecological impacts:

```
LOCATION ID="Loc #06"  EASTING=12346  NORTHING=62423 COMPUTE
   ECOLOGICAL TITLE="Example of a title line for location #06" GRO_WAT

LOCATION ID="Loc #07"  EASTING=723402  NORTHING=72424 COMPUTE
   ECOLOGICAL GRO_WAT SEE_WAT SOIL
   TITLE="Example of a title line for location #07"

LOCATION Ecological ID="SHORE"
   NAME="Shore location for ecological analyses"
   EASTING = 557375.3  NORTHING= 144885.2
   GRO_WAT SOIL SEE_WAT ! Riparian
   APSD=4.00E-02 COXYGEN=1.10E-02 POROSITY=3.50E-01 FOC=1.0E+00
   VEGCOV=5.00E-01 NECF=1.00E+00 RHOS=1.50E+00 SRH=1.8E-02
   TEMP=2.85E+02 MSWIND=3.44E+00 MZWIND=3.44E+00
   AREA=2.5E+03 LENGTH=5.00E+01

LOCATION Ecological ID="RIVER"
   NAME="River location for ecological analyses"
   EASTING = 557363.4  NORTHING=144938.9
   SUR_WAT POR_WAT SEDIMENT ! River
   APSD=4.00E-02 COXYGEN= 1.10E-02 POROSITY=3.50E-01 FOC=1.0E+00
   VEGCOV=5.00E-01 NECF=1.00E+00 RHOS=1.50E+00 SRH=1.8E-02
   TEMP=2.85E+02 MSWIND=3.44E+00 MZWIND=3.44E+00
   AREA=2.5E+03 LENGTH=5.00E+01
```

The following example keywords define two locations for cultural impacts:

```
LOCATION Cultural ID="CL0001" NAME="Upland cultural location"
   EASTING = 574521.6 NORTHING=154366.6 AREA= 8.86290E+05 GRO_WAT

LOCATION Cultural ID="CL3981" NAME="Cultural location in the river"
   EASTING =  593572.8  NORTHING=  66654.6  AREA= 7.96586E+03
   SUR_WAT POR_WAT SEDIMENT
```

2.2.8   PERIOD Keyword in the ESD Keyword File

The PERIOD keyword identifies the start and stop times for the entire simulation. The following is the keyword's syntax:

```
PERIOD [START=year₁]  [STOP=year₂]  [CLOSURE=year₃]
```

The modifier START and the value $year_1$ identify the start of the simulation period. The modifier STOP and the value $year_2$ identify the end of the simulation period. Start and stop years should be entered as whole numbers with the stop year no smaller than the start year. The modifier CLOSURE and the value $year_3$ identify the year of site closure. The year of site closure cannot be smaller than the start year. The following is an example PERIOD keyword that simulates from 1944 through 3050 with site closure occurring at 2050:

```
PERIOD START=1944 STOP=3050 CLOSURE 2050
```

2.2.9   REALIZATION Keyword in the ESD Keyword File

The REALIZATION keyword identifies the number of realizations to be simulated. The following is the keyword's syntax:

```
REALIZATIONS N₁
```

The number of realizations is given by the single numerical entry. The valid number of realizations is 1 or larger. Run times and disk storage requirements are directly proportional to the number of realizations. The following is an example REALIZAT keyword requesting 25 realizations:

```
REALIZAT 25
```

2.2.10 RESPIRE Keyword in the ESD Keyword File

The RESPIRE keyword defines the oxygen respiration for animal species. These data are used in the biotic transport portion of the MASS2 code as well as the ecological impacts code ECEM. The syntax of the keyword is the following:

```
RESPIRE [GAMMA=N₁] [PHI=N₂]
```

Both the gamma and phi parameters must be specified. The following is an example of this keyword:

```
RESPIRE GAMMA=0.2 PHI=0.032
```

A description of the mathematical model for oxygen respiration of animal species is provided in Section 4.1.2.1. In summary, the oxygen respiration rate for a given species is calculated from the equation $\rho = \phi \bullet w^{-\gamma}$, where ϕ and γ are regression parameters (Thomann 1989) and w is the body weight of the species (kg wet weight).

2.2.11 SPECIE Keyword in the ESD Keyword File

The SPECIE keyword is used to enter definitions for possible species to be simulated. The ECEM and MASS2 codes can select species from this master list. The following is the keyword's syntax:

```
SPECIE [ID="quote 1"] [TYPE="quote 2"] [NAME="quote 3"]
   {Modifier=N1} … {Modifier=N36} {EMERGENT}
```

A separate SPECIE keyword must be entered for every species being defined. The modifiers associated with the SPECIE keyword are given in Table 2.5.

Table 2.5 Modifiers Associated with the SPECIE Keyword in the ESD File

Modifier	Description
ID	The quote string associated with the ID modifier is a unique species identification string up to six characters long. The analyte identification string is case sensitive, and spaces or hyphens change the definition.

Modifier	Description

TYPE	The quote string associated with the TYPE modifier string is a two-character analyte type indicator. The following are the valid entries for this string:
	     TA – if the species is a terrestrial animal
	     TP – if the species is a terrestrial plant
	     QA – if the species is an aquatic animal
	     QP – if the species is an aquatic plant

NAME	The quote string associated with the NAME modifier is a species name or description up to 72 characters in length.
AE	The numerical entry associated with the AE modifier is the assimilation efficiency of the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of AE defaults to zero.
AWD	The numerical entry associated with the AWD modifier is the wet-to-dry weight ratio of the species. This value has units of g wet/g dry. Entry of this modifier is optional. If it is not present, the value of AWD defaults to zero.
DIFFHT	The numerical entry associated with the DIFFHT modifier is the diffusion height of the species. This value has units of meters. Entry of this modifier is optional. If it is not present, the value of DIFFHT defaults to zero.
EMERGENT	There is no numerical entry associated with the EMERGENT modifier. Use of this modifier indicates that the species is an emergent plant. An emergent plant is one that has roots in water but grows in the air. This type of plant does not have rain splash of contaminated soil onto the leaves of the plant.
ETWATER	The numerical entry associated with the ETWATER modifier is the exposure time to water of the species. This value has units of hr/day. Entry of this modifier is optional. If it is not present, the value of ETWATER defaults to zero.
FLIPID	The numerical entry associated with the FLIPID modifier is the fraction lipid of the species. This value has units of g lipid/g wet. Entry of this modifier is optional. If it is not present, the value of FLIPID defaults to zero.
FMR	The numerical entry associated with the FMR modifier is the metabolic rate of predator species. This value has units of kcal/day. Entry of this modifier is optional. If it is not present, the value of FMR defaults to zero.
FOC	The numerical entry associated with the FOC modifier is the fraction organic carbon of the species. This value has units of g organic carbon/g dry weight. Entry of this modifier is optional. If it is not present, the value of FOC defaults to zero.
FPA	The numerical entry associated with the FPA modifier is the volume fraction of plant tissue that is air for the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of FPA defaults to zero.
FPL	The numerical entry associated with the FPL modifier is the volume fraction of plant tissue that is lipid for the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of FPL defaults to zero.

Modifier	Description
FPW	The numerical entry associated with the FPW modifier is the volume fraction of plant tissue that is water for the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of FPW defaults to zero.
FW	The numerical entry associated with the FW modifier is the water weight fraction of plant tissue for the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of FW defaults to zero.
FWATER	The numerical entry associated with the FWATER modifier is the fraction exposure to water for the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of FWATER defaults to zero.
FDW	The numerical entry associated with the FDW modifier is the conversion from dry weight to wet weight for the species. This value has units of kg dry/kg wet. Entry of this modifier is optional. If it is not present, the value of FDW defaults to zero.
GE	The numerical entry associated with the GE modifier is the gross energy for the species. This value has units of kcal/kg wet weight. Entry of this modifier is optional. If it is not present, the value of GE defaults to zero.
INHRATE	The numerical entry associated with the INHRATE modifier is the resting inhalation rate for the species. This value has units of m^3/day. Entry of this modifier is optional. If it is not present, the value of INHRATE defaults to zero.
OCAR	The numerical entry associated with the OCAR modifier is the organic carbon assimilation rate for the species. This value has units of g organic carbon assimilated/g ingested. Entry of this modifier is optional. If it is not present, the value of OCAR defaults to zero.
PCS	The numerical entry associated with the PCS modifier is the fraction of surface area in contact with soil for the species. This value has units of 1/day. Entry of this modifier is optional. If it is not present, the value of PCS defaults to zero.
PCW	The numerical entry associated with the PCW modifier is the fraction of surface area available to water soil for the species. This value is unit less. Entry of this modifier is optional. If it is not present, the value of PCW defaults to zero.
PSI	The numerical entry associated with the PSI modifier is the seasonality factor for the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of PSI defaults to zero.
RADIUS	The numerical entry associated with the RADIUS modifier is the radius of the species. This value has units of cm. Entry of this modifier is optional. If it is not present, the value of RADIUS defaults to zero.
RHOP	The numerical entry associated with the RHOP modifier is the plant tissue density of the species. This value has units of kg/m^3. Entry of this modifier is optional. If it is not present, the value of RHOP defaults to zero.
SA	The numerical entry associated with the SA modifier is the surface area of the species. This value has units of cm^2. Entry of this modifier is optional. If it is not present, the value of SA defaults to zero.

Modifier	Description
SADHER	The numerical entry associated with the SADHER modifier is the skin adherence factor for the species. This value has units of mg/cm^2. Entry of this modifier is optional. If it is not present, the value of SADHER defaults to zero.
SEDING	The numerical entry associated with the SEDING modifier is the fraction of diet that is sediment for the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of SEDING defaults to zero.
SOILING	The numerical entry associated with the SOILING modifier is the soil ingestion rate for the species. This value has units of kg soil ingested/kg dry weight. Entry of this modifier is optional. If it is not present, the value of SOILING defaults to zero.
THETA	The numerical entry associated with the THETA modifier is the area use factor for the species. This value is unitless. Entry of this modifier is optional. If it is not present, the value of THETA defaults to zero.
WATERING	The numerical entry associated with the WATERING modifier is the water ingestion rate for the species. This value has units of liters/day. Entry of this modifier is optional. If it is not present, the value of WATERING defaults to zero.
WBMASS	The numerical entry associated with the WBMASS modifier is the wet body mass for the species. This value has units of grams. Entry of this modifier is optional. If it is not present, the value of WBMASS defaults to zero.
WEIGHT	The numerical entry associated with the WEIGHT modifier is the wet body weight for the species. This value has units of kg (wet). Entry of this modifier is optional. If it is not present, the value of WEIGHT defaults to zero.

The following SPECIE keywords define the American Coot and Channel Catfish as species available for simulation:

```
SPECIE ID="AMCOOT" TPYE= "TA" NAME="American coot"
   AE=0.81  DIFFHT=0.2  ETWATER=20 FMR=163.0867887 FWATER=0.5 FDW=0.17
   GE=1900  INHRATE=.6159264 PCS=0.25 PCW=0.5 PSI=1 RADIUS=5
   SA=784.0626481 SADHER=1.45   SOILING=0.18 THETA=1
   WATERING=0.046102353 WEIGHT=0.692

SPECIE ID="CHCATF" TPYE= "QA" NAME="Channel catfish"
   AE=0.85  AWD=5 FLIPID=0.178  FOC=0.45  GE=1200  OCAR=0.8  RADIUS=10
   SEDING=0.19 WBMASS=6802.5
```

2.2.12 TIMES Keyword in the ESD Keyword File

The TIMES keyword identifies the times at which concentration data will be generated to support the calculations by each of the impacts codes. The following is the keyword's syntax:

```
TIMES [HUMAN | ECOLOGICAL | ECONOMIC | CULTURAL] [T₁] {T₂} … {Tₙ}
```

The numerical entries T_1, T_2, …, T_n are the times (whole number years) when outputs are desired. Multiple TIMES keywords can be entered. Only one of the modifiers HUMAN, ECOLOGICAL, ECONOMIC, and CULTURAL is allowed on an individual keyword entry.

The following is an example TIMES keyword that requests concentration data for the three years 2020, 2075, and 3014 for the cultural impacts module:

```
TIMES CULTURAL 2020 2075 3014
```

The following are example time definitions for each of the four impacts modules:

```
TIMES CULTURAL 2023 2075 3014
TIMES ECONOMIC 2020 2075
TIMES ECOLOGICAL 2010 2015 2020 2031 2075 3015 3050
TIMES HUMAN 2022 2072 3215 3014
```

2.2.13 TITLE Keyword in the ESD Keyword File

The TITLE keyword is used to define a single-line problem title. The problem title will be written to output files. If the title is not supplied, then the program will error terminate. The following is the syntax for this keyword record:

```
TITLE ["quote"]
```

The title is entered in a quote string, which must be enclosed in double quotation marks. Titles up to 72 characters long are supported. The following example defines a title for a run of the code:

```
TITLE "Example title line for the environmental settings control file."
```

There are no modifiers associated with the TITLE keyword.

2.3 Environmental Concentration Data Accumulator

The purpose of the Environmental Concentration Data Accumulator (ECDA) is to provide centralized storage for all concentration data of analytes at the locations and times needed to perform impacts calculations.

2.3.1 Format of the Concentration Data (ECDA) Files

The general approach and file structure for the ECDA files has the following characteristics:

- Data storage for different analytes and different impacts types are provided in separate files (9 analytes and 4 impacts types would result in 36 concentration files). This design feature allows addition of an additional analyte to a data set without recalculation of the other analytes.
- The files have a binary, fixed record length, direct-access format.

- A mapping scheme is used to store only "actual" data (no placeholders with wasted storage space).

Each data record in a concentration data file contains the following information: Year, Location ID, Media ID, and Concentration data (realizations 1 to the maximum). The following is the order in which media information always appear in the file:

- GW: Concentrations in groundwater (Ci/m^3 or kg/m^3)
- SP: Concentrations in seep water (Ci/m^3 or kg/m^3)
- SO: Concentrations in soil (land surface) (Ci/kg$_{soil}$ or kg$_{analyte}$/kg$_{soil}$)
- SW: Concentrations in surface water (river) (Ci/m^3 or kg/m^3)
- PW: Concentrations in river bottom pore water (Ci/m^3 or kg/m^3)
- SD: Concentrations in river bottom sediment (Ci/kg$_{sediment}$ or kg$_{analyte}$/kg$_{sediment}$).

An overview of the structure of a concentration data file for human impacts assuming 25 realizations were used is provided in Table 2.6. The structure for this file is identical for all impacts types.

Table 2.6 Structure of a Concentration Data File

Analyte ID	**Human**	
Units for the six media as character strings		
Time 1	Location 1	Media L1-1, 25 realizations
		…
		Media L1-L1MAX, 25 realiz.
	…	…
	Max Human Locations	Media LL-1, 25 realizations
		…
		Media LL-LLMAX, 25 realiz.
Time 2	Location 1	Media L1-1, 25 realizations
		…
		Media L1-L1MAX, 25 realiz.
	…	…
	Max Human Locations	Media LL-1, 25 realizations
		…
		Media LL-LLMAX, 25 realiz.
…	…	…

Max Time	Location 1	Media L1-1, 25 realizations
Human		…
		Media L1-L1MAX, 25 realiz.
	…	…
	Max	Media LL-1, 25 realizations
	Human	…
	Locations	Media LL-LLMAX, 25 realiz.

2.3.2   Format of the Record Map File for Concentration Data

The record map file is an ASCII file that provides indexing information for the storage locations in the binary concentration data files. There is one record map file per impact type because the structure for the concentration data for a given impact type (human, ecological, cultural, or economic) is identical for all analytes. This file is generated by the ECDA code. The user should never modify this file.

The record map file has several header lines that are followed by indexing data. All character data are enclosed in double quotation marks, and records that contain more than one value have the data separated by commas. The following is the definition of the header lines:

- Problem title: The title from the ESD keyword file
- Code Name: The name of the code that generated the file
- Code Version: The version number of the code that generated the file
- Code Date: The modification date of the code that generated the file
- User Name: The user name from the ESD keyword file
- Run ID: The run ID from the code run that generated the file
- Record Length: Record length for the binary data file
- Number of times: The number of solution times requested for this impact type
- List of times: A list of solution times for this impact type, with one time per line
- Number of locations: The number of locations requested for this impact type
- List of locations: A list of locations IDs, with one ID per line
- Number of media: The number of media where contaminated data may be saved
- List of media: A list of the media IDs, with one value per line.

The header data are followed by record map index data. There are as many lines of index data as there are locations. The index data for locations come in the same order as the location IDs provided earlier in the file. Each line of index data contains the location ID followed by as many indices as there are media types. The indices give an offset record number. If a particular medium is not saved at a location, the

index value is set to negative 1. An example record map file for a very small problem is provided in
Table 2.7

<div align="center">Table 2.7 Example Record Index Map File</div>

```
"ECOLOGICAL: Hanford Solid Waste EIS - 10,000 Years"
"ECDA"
"1.00.D.3"
" 9 Mar 2001"
"Paul W. Eslinger"
"20020225135708"
18,"Records in a time block"
16,"Record Length"
2,"Number of times"
8000
10000
6,"Number of locations"
"EL0001"
"EL0002"
"EL0003"
"EL0004"
"EL0005"
"EL0006"
6,"Number of media"
"GW"
"SP"
"SO"
"SW"
"PW"
"SD"
"EL0001",8,9,10,-1,-1,-1
"EL0002",-1,-1,-1,11,12,13
"EL0003",14,15,16,-1,-1,-1
"EL0004",-1,-1,-1,17,18,19
"EL0005",20,21,22,-1,-1,-1
"EL0006",-1,-1,-1,23,24,25
```

2.3.3   Format of the KDSOIL Data File

Entry of one or more KDSOIL keywords in the ESD keyword file (see Section 2.2.6) causes the ECDA
code to generate a data file of KDSOIL values for use in other codes. An example of this file for 19
KDSOIL keywords and 2 realizations is provided in Table 2.8. The file is a text file that starts with seven
header lines. The entry on line 8 is the number of KDSOIL definitions – 19 in this example. The next
line contains the number of realizations – 2 in this example. Each succeeding line contains data for a
single KDSOIL definition in the form of index, identification string, and generated values for each
realization. Multiple data on a single line are separated by commas, and all text data are enclosed in
double quotation marks.

Table 2.8 Example KDSOIL File

```
"KDSOIL"
"SAC Rev. 0 Shakedown2 Assessment"
"ECDA"
"1.00.D.3"
" 9 Mar 2001"
"20020314153720"
"Engel, Eslinger,"
19
2
1,"KDH", 0.00000E+00, 0.00000E+00
2,"KDCCl4", 3.63214E-04, 1.64047E-04
3,"KDPu", 4.54387E-01, 1.22489E+00
4,"KDU", 4.67235E-04, 1.05881E-03
5,"KDSr", 1.63468E-02, 2.80513E-02
6,"KDCs", 6.83420E-01, 9.52710E+00
7,"KDI", 1.39666E-03, 5.42975E-04
8,"KDCr", 0.00000E+00, 7.06699E-05
9,"KDTc", 0.00000E+00, 7.03645E-06
10,"KDZero", 1.00000E-10, 1.00000E-10
11,"KDSUSH", 1.00000E-10, 1.00000E-10
12,"KDSUSCr", 4.72011E-04, 2.20753E-04
13,"KDSUSCs", 1.52260E+01, 4.32762E+01
14,"KDSUSI", 8.94922E-03, 1.25821E-03
15,"KDSUSPu", 2.12136E+01, 2.09212E+00
16,"KDSUSSr", 2.41585E-01, 9.20855E-02
17,"KDSUSTc", 1.78929E-04, 5.34989E-05
18,"KDSUSU", 7.56287E-03, 1.50449E-02
19,"KDSUSCCl4", 1.18195E-03, 4.08758E-04
```

3.0   Cultural Impacts Model (CULTURE)

3.1   Mathematical Models for the Cultural Model

The algorithms for the cultural model are provided in the following sections. The culture code provides three types of solutions. The solutions are

- Calculation of the areal extent where concentrations in surface water, river sediments, or in groundwater underlying soil are above user-specified thresholds
- Calculation of the distance from each of a set of user-specified points to the closest location where the groundwater concentration is above a user-specified threshold
- Calculation of the data for a map showing locations where the concentration of any one or more of several user-specified contaminants are above a set of user-specified thresholds.

3.1.1   Area Calculations for the Cultural Model

The cultural code calculates the areal extent where concentrations in surface water, river sediments, or in groundwater underlying soil are above user-specified thresholds. The concentration data are defined at points in the coordinate system, but the concentration at the point is assumed to apply to an area surrounding the point. The area associated with each point is an input to the code. The area algorithm is the sum of the areas associated with points whose concentrations are above the user-specified thresholds.

3.1.2   Site Calculations for the Cultural Code

The cultural code calculates the distance from each of a set of user-specified points to the closest location where the groundwater concentration is above a user-specified threshold. The minimum distance to a point meeting the concentration threshold is provided by the code. If no concentration exceeds the specified thresholds, a huge distance is returned (typically on the order of 10^{39}).

3.1.3   Map Calculations for the Cultural Code

The cultural code calculates data for a map showing locations where the concentration of any one or more of several user-specified contaminants are above a set of user-specified thresholds, allowing for a different threshold for each contaminant. The map data is a value from 0 to 1 at each of the locations in the concentration data grid for the cultural model. The actual value returned at a location is the fraction of realizations where one or more thresholds were exceeded at that location.

3.2   Code Environment

3.2.1   Location in the Processing Sequence

The CULTURE code requires access to a number of data files developed by the SAC inventory, release, and transport codes (Eslinger et al. 2002). In particular, every code on the left side of Figure 1-2 must have been executed to build a suite of concentration data files before the CULTURE code can be used to

calculate impacts. These concentration data files must have been developed under the control of the same ESD keyword file that the CULTURE code reads to determine processing options.

3.2.2   How the Code Is Invoked

CULTURE can run under either the Windows or the Linux operating system. Under the Windows operating system (Releases 98, NT, or 2000), CULTURE executes in a DOS box. A run of CULTURE is initiated by entering the following command line:

```
CULTURE "Keyfilename"
```

Under the Linux operating system, CULTURE is executed through the following Bourne Shell or C Shell command:

```
culture.exe "Keyfilename"
```

For this command, CULTURE or culture.exe is the name of the executable program and "Keyfilename" is the name of a cultural scenario keyword file. Both the name of the executable program and the keyword file may contain path information. If CULTURE is invoked without entering the name of the keyword file, the code will prompt the user for the file name. The keyword file, which should be prepared using an editor that can handle ASCII files without leaving embedded control codes, contains text control information describing the run. If CULTURE cannot open the keyword file, the code will terminate execution after writing an error message to the standard output device.

3.2.3   Memory Requirements

The CULTURE code uses dynamic memory allocation, so the memory requirements depend on the problem being analyzed. A reasonably large example run required about 10 MB of memory (on a Windows 2000 machine). It is expected that most, if not all, of the runs of the CULTURE code will require less than 20 MB of memory.

3.3   Data Files

The CULTURE code reads four or more input files and writes up to seven output files. The number of input files depends on the number of contaminants being analyzed. The number of output files depends on the options selected in the CULTURE code. These files are described in the following sections.

3.3.1   Input Files

The input files for the CULTURE code are keyword files and a suite of concentration-data-related files. One keyword file controls the case that the CULTURE code will execute, and it points to the ESD keyword file. The suite of concentration data files are all identified in the ESD keyword file – the user of the CULTURE code only needs to identify the ESD keyword file. The following are the input files:

- **ESD Keyword File**: The ESD keyword file contains the control information that the inventory and environmental transport codes use to generate concentration data files. Table 2.1 provides

examples of keywords in the ESD file that control the impacts codes, including the CULTURE code. Definitions for these keywords are given in Section 2.2. Typically, the user of the CULTURE code will not modify the ESD keyword file.

- **CULTURE Keyword File**: The CULTURE keyword file controls the scenario to be analyzed by the CULTURE code. The options and data available are constrained by the case defined in the ESD Keyword file. Section 3.4 describes the contents of the CULTURE keyword file. An example keyword file for the CULTURE code is below provided in Table 3.1.
- **ECDA Concentration Files**: The ECDA files contain all the concentration data available for the impacts codes. The concentrations for all analytes are based on the same time and location data. There is a "map" file for the ECEM code containing indexing information for each of the concentration data files. In addition, there is a separate concentration data file for every analyte used in the impacts scenario. For example, when running a scenario with seven analytes, there will be one map file and seven concentration data files. The structure of a concentration data file is described in Section 2.3.1.

3.3.1.1   ESD Keyword File

The CULTURE code also reads keywords from the environmental settings file. These keywords are read from a different file, and can have a different definition, from a keyword defined for internal use in the CULTURE code. The environmental settings keywords are defined in Section 2.2. The following ESD keywords are required by the CULTURE code:

- ANALYTE – definition of analytes in the environmental simulations
- END – end of the environmental settings keywords
- FILE – file names for the concentration file for each analyte
- LOCATION – locations at which concentrations were generated for the cultural impacts
- REALIZAT – number of realizations that were simulated
- TIMES – times at which concentrations were generated for the cultural impacts
- TITLE – environmental simulation title.

3.3.1.2   CULTURE Keyword File

The keyword definition file contains control information for the desired impact simulation. Individual keywords are defined in Section 3.4. Table 3.1 contains an example keyword file for several analytes and three solution options.

Table 3.1 Example Keyword File for the CULTURE Code

```
! Keyword file for the CULTURE program - drinking water standards thresholds
! Developer: Carmen Arimescu
!
REPORT "G:\Initial\Culture\Cul_dws.rpt"
!
USER "Carmen Arimescu"
REALIZATION 11
!
! Overall problem title
```

```
TITLE "SAC Rev. 0 initial runs for the program CULTURE - background+Hanford"
!
FILE ESD "G:\Initial\ESD_Initial.Key"  ! Input Environmental setting file
FILE HEADER "G:\Initial\Culture\Cul_dws.hdr" ! Output header file for SACVIEW
!
! Output area detailed data
DETAILS  AREA
FILE AREA_DAT "G:\Initial\Culture\Cul_dws_area_det.csv"
!
! Output area summary statistics
STATISTICS  AREA
FILE AREA_STA "G:\Initial\Culture\Cul_dws_area_sta.csv"
!
! Output site detailed data
DETAILS   SITE
FILE  SITE_DAT "G:\Initial\Culture\Cul_dws_site_det.csv"
!
! Output site summary statistics
STATISTICS SITE
FILE SITE_STA "G:\Initial\Culture\Cul_dws_site_sta.csv"
!
! Output map data
FILE MAP "G:\Initial\Culture\Cul_dws_map.csv"
!
EXECUTE
!
! Output times for calculations
!
TIMES
 1990 2000 2010
!
! Groundwater concentration thresholds by analyte
THRESHOLD GRO_WAT ANALYTE="CCl4"         5.0      "ug/L"
THRESHOLD GRO_WAT ANALYTE="Cs137"      200.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="CrVI"       100.0      "ug/L"
THRESHOLD GRO_WAT ANALYTE="H3"       20000.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="I129"         1.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="Sr90"         8.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="Tc99"       900.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="U238"        13.4      "pCi/L"
!
! Surface water concentration thresholds by analyte
THRESHOLD SUR_WAT ANALYTE="CCl4"         0.25     "ug/L"
THRESHOLD SUR_WAT ANALYTE="Cs137"      160.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="CrVI"        11.0      "ug/L"
THRESHOLD SUR_WAT ANALYTE="H3"       20000.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="I129"         0.5      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Pu239"       13.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Sr90"         8.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Tc99"       800.0      "pCi/L"
!
```

```
! Define two area calculations
!
AREA ID="Area01" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129" "Sr90" "Tc99"
  "U238" GRO_WAT TITLE "GW threshold exceeded for at least one analyte"
!
AREA ID="Area10" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129" "Pu239" "Sr90"
  "Tc99" "U238" SUR_WAT TITLE "SW threshold exceeded for at least one
analyte"
!
AREA ID="Area11" ANALYTE="CCl4" SUR_WAT
  TITLE "Area where SW threshold exceeded for CCl4"
!
! Define two maps
!
Map ID="Map01" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129" "Sr90" "Tc99" "U238"
  GRO_WAT  TITLE "GW threshold exceeded for at least one analyte"
!
Map ID="Map10" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129" "Pu239" "Sr90"
  "Tc99" "U238" SUR_WAT TITLE "SW threshold exceeded for at least one
analyte"
!
! Define two site calculations
!
SITE ID="Site01" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129" "Sr90" "Tc99"
  "U238" SUR_WAT  TITLE "SW threshold exceeded for at least one analyte"
  EASTING=5.932908E+05 NORTHING=6.746470E+04
!
SITE ID="Site02" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129" "Sr90" "Tc99"
  "U238" GRO_WAT TITLE "GW threshold exceeded for at least one analyte"
  EASTING=5.647716E+05 NORTHING=1.446166E+05
!
! Locations for the upland maps
LOCATION LIST
  "CL0001"  "CL0002"  "CL0003"  "CL0004"  "CL0005"
  "CL0006"  "CL0007"  "CL0008"  "CL0009"  "CL0010"
  "CL0011"  "CL0012"  "CL0013"  "CL0014"  "CL0015"
  "CL0016"  "CL0017"  "CL0018"  "CL0019"  "CL0020"
END
```

3.3.1.3 ECDA Concentration Files

The ECDA provides a central storage location for concentration data for all analytes at the environmental locations and times needed to perform social-cultural analyses. The ECDA files are described in Section 2.3.1.

3.3.2 Output Files

Up to seven output files can result from a run of the CULTURE code.

3.3.2.1   CULTURE Report File

Excerpted records for an example report file for the CULTURE code are provided in Table 4.2. The omitted records provided solution times and location IDs. This example file is about 30 KB in size and is the typical size for the report file if no debug options are selected. The size of this file grows rapidly when debug options are selected. A run using all debug options having a large number of locations, analytes, solution times, and realizations could easily generate a report file larger than the 2.1-GB file size limit under the Windows operating system.

Table 3.2 Excerpted Records from a Report File Written by the CULTURE Code

```
     CCCCC  U     U L       TTTTTTT U     U RRRRRR  EEEEEEE
    C     C U     U L          T    U     U R     R E
    C       U     U L          T    U     U R     R E
    C       U     U L          T    U     U RRRRRR  EEEE
    C       U     U L          T    U     U R   R   E
    C     C U    UU L          T    U    UU R    R  E
     CCCCC   UUUU U LLLLLLL    T     UUUU U R     R  EEEEEEE


                    Culture      Version 1.00.D.0
                    Last Modified on  7 Sep 2001
                 ---------------------------------------------
                   SAC Rev. 0 Socio-Cultural Impacts Model
                 ---------------------------------------------
                   Developed By Battelle Memorial Institute
                    Pacific Northwest National Laboratories
                             Richland, Washington

         Current Run ID = 200110191010   User Name = Carmen Arimescur
             System Date = 10-19-2001   System Time = 10:10:52


         The software used to generate this output is experimental
            and has not been formally tested or peer reviewed.



                           Review Signatures

Input Prepared By: _____        Date: _____

Input Reviewed By: _____        Date: _____


======================= Echo of the Problem Definition =======================

Title: SAC Rev. 0 initial runs for the program CULTURE - background+Hanford
User:  Carmen Arimescur
  25 Realizations in the ESD keyword file
  11 Realizations utilized in this run

File Name for this Report File
File: G:\Initial\Culture\Cul_dws.rpt
```

```
File Name for CULTURE Input Keyword Data
File: cul_dws.key

File Name for ESD Input Keyword Data
File: G:\Initial\ESD_Initial.Key

File Name for the Output SACVIEW Header File
File: G:\Initial\Culture\Cul_dws.hdr

File Name for the Output MAP Data File
File: G:\Initial\Culture\Cul_dws_map.csv

File Name for Concentration Index File
File: G:\Initial\Ecda\CULT_Initial.Map

File Name for Media Concentrations: Analyte ID="CCl4"
File: G:\Initial\Ecda\CULT_CCl4_Initial.Dat

Analyte Information for 10 analytes.
    1 : H3      : ===> Not used
    2 : Sr90    : ===> Not used
    3 : Tc99    : ===> Not used
    4 : I129    : ===> Not used
    5 : Cs137   : ===> Not used
    6 : U238    : ===> Not used
    7 : Pu239   : ===> Not used
    8 : U       : ===> Not used
    9 : CCl4    : Carbon Tetrachloride
   10 : CrVI    : ===> Not used

Number of times requested is 60
Index  Year
----- -----
   10  1990
   12  2000
...
   69  3040
   70  3050

Number of locations requested is 1618
Index  Location
----- --------
    1  CL0001
    2  CL0002
...
 1617  CL1617
 1618  CL1618

  Thresholds by analyte and media
                   GW         SP         SO         SW         PW         SD
                ---------- ---------- ---------- ---------- ---------- ----------
    1 : H3    : 2.000E+04  None       None       2.000E+04  None       None
    2 : Sr90  : 8.000E+00  None       None       8.000E+00  None       None
    3 : Tc99  : 9.000E+02  None       None       8.000E+02  None       None
    4 : I129  : 1.000E+00  None       None       5.000E-01  None       None
    5 : Cs137 : 2.000E+02  None       None       1.600E+02  None       None
    6 : U238  : 1.340E+01  None       None       None       None       None
```

```
    7 : Pu239  :    None        None        None      1.300E+01    None        None
    8 : U      :    None        None        None       None        None        None
    9 : CCl4   : 5.000E+00      None        None      2.500E-01    None        None
   10 : CrVI   : 1.000E+02      None        None      1.100E+01    None        None

 Map calculation definitions
 Index   SiteID   Name
 -----   ------   ----------------------------------------------------
   1  : Map11  : Map where SW threshold exeeded for CCl4

====================== End of the Problem Definition ========================

Header information from the map file for cultural impacts
   ECDA_PTITLE = CULTURAL: SAC Rev. 0 Initial Assessment - Second Pass
   ECDA_PRGNAM = ECDA
   ECDA_PRGVER = 1.00.D.3
   ECDA_PRGDAT =  9 Mar 2001
   ECDA_USRNAM = Engel & Nichols
   ECDA_CRUNID = 20010730152818
   ECDA_BLOCK  = 8707
   ECDA_RECLEN = 112

Concentration data units conversion factors

    9 : CCl4   : NS : Ground water  : 1.00000E+06 : From kg/m^3       to ug/L
    9 : CCl4   : NS : Seep water    : 1.00000E+06 : From kg/m^3       to ug/L
    9 : CCl4   : NS : Soil          : 1.00000E+09 : From kg/kg        to ug/kg
    9 : CCl4   : NS : Surface water : 1.00000E+06 : From kg/m^3       to ug/L
    9 : CCl4   : NS : Sediment      : 1.00000E+09 : From kg/kg        to ug/kg
    9 : CCl4   : NS : Pore water    : 1.00000E+06 : From kg/m^3       to ug/L

Run completed on:
   Date: 10/19/2001
   Time: 10:11:07
```

3.3.2.2   CULTURE Header File for SACView

The SACView header file is an output file containing information used by the interactive SACView program to allow easy extraction of subsets of the results computed by the CULTURE code. This file is required for every run of the CULTURE code. An example of this file is given in Table 3.3. The file contains the following sections of information:

- A header section of basic run information
- Solution times selected
- Locations used
- Site calculations processed
- Area calculations processed
- Map calculations processed
- Output file names.

The user only specifies the name of this file; users should not modify the file after it is generated by the CULTURE code. See the instructions in Section 7.0 regarding the use of the SACView program.

Because this file has at most a few hundred entries, the file size is always much smaller than 1 MB. File names for options not selected are set to null.

Table 3.3 Example Header File from CULTURE for the SACView Program

```
type: "Cultural"
title: "SAC Rev. 0 initial runs for the program CULTURE - background"
user: "Paul W. Eslinger"
name: "Culture"
version: "1.00.C.0"
date: " 2 Feb 2001"
id: "20010615091252"
envfile: "G:\Initial\Bg\ESD_BG_Initial.Key"
realizations:   4
times:  1
 2000
sites:  0
summary: "\Initial\Culture\Cul_dws_sta_sites_dif.csv"
detail: "\Initial\Culture\Cul_dws_det_sites_dif.csv"
areas: 2
"Area01","Area where GW threshold exceeded for at least one analyte"
analyte:    8
"H3     "
"Sr90   "
"Tc99   "
"I129   "
"Cs137  "
"U238   "
"CCl4   "
"CrVI   "
media:    1
"GRO_WAT"
"Area10","Area where SW threshold exceeded for at least one analyte"
analyte:    9
"H3     "
"Sr90   "
"Tc99   "
"I129   "
"Cs137  "
"U238   "
"Pu239  "
"CCl4   "
"CrVI   "
media:    1
"SUR_WAT"
summary: "\Initial\Culture\Cul_dws_sta_area_dif.csv"
detail: "\Initial\Culture\Cul_dws_det_area_dif.csv"
map: 2
"Map01 ","Map where GW threshold exceeded for at least one analyte"
analyte:    8
"H3     "
```

```
"Sr90  "
"Tc99  "
"I129  "
"Cs137 "
"U238  "
"CCl4  "
"CrVI  "
media:    1
"GRO_WAT"
"Map02 ","Map where GW threshold exceeded for CCl4"
analyte:    1
"CCl4  "
media:    1
"GRO_WAT"
summary: "\Initial\Culture\Cul_dws_det_map_dif.csv"
```

3.3.2.3 CULTURE Area Data File

The area data file is an optional output file that contains the detailed values for area calculations in the CULTURE code. The description of the AREA keyword (Section 3.4.2) explains how to define an area calculation. The description of the AREA_DAT modifier on the FILE keyword (Section 3.4.7) explains how to define the file name. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file after the header line consists of three identifiers followed by a value for every generated realization. An example file for two areas, three realizations, and five times is provided in Table 3.4. The following are the three identifiers on each line:

- Time: Year for which the data are valid
- Area ID: The area identifier
- Solution type: A flag for solution type – the contaminated area.

Table 3.4 Example Area Data File for the CULTURE Code

```
"Time", "AREA ID", "Variable", "Values by realization"
2000,"Area02","AREA_CONT", 7.884E+06, 8.438E+06, 6.759E+06
2000,"Area09","AREA_CONT", 3.663E+07, 2.169E+07, 1.693E+07
2050,"Area02","AREA_CONT", 1.181E+07, 1.350E+07, 1.069E+07
2050,"Area09","AREA_CONT", 3.960E+07, 2.305E+07, 1.999E+07
2100,"Area02","AREA_CONT", 1.519E+07, 1.723E+07, 1.350E+07
2100,"Area09","AREA_CONT", 4.469E+07, 2.655E+07, 2.094E+07
2500,"Area02","AREA_CONT", 5.719E+07, 7.021E+07, 4.329E+07
2500,"Area09","AREA_CONT", 5.532E+07, 1.967E+07, 2.229E+07
3050,"Area02","AREA_CONT", 1.297E+08, 1.486E+08, 1.152E+08
3050,"Area09","AREA_CONT", 5.319E+07, 1.756E+07, 2.043E+07
```

3.3.2.4 CULTURE Area Statistics File

This optional file contains summary statistics for area calculations for the CULTURE code. The description of the AREA keyword (Section 3.4.2) explains how to define an area calculation. The description of the AREA_STA modifier on the FILE keyword (Section 3.4.7) explains how to define the

file name. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of two identifiers followed by summary statistics (nine percentiles, mean value, and standard deviation). A subset of the data written to this file for a run is provided in Table 3.5. The following are the two identifiers on each line:

- Time: Year for which the data are valid
- Area ID: The location identifier where the data are valid.

The data for each record in this file are too long to present without line-wrapping in this document. Each record in the file occupies two lines in Table 3.5.

Table 3.5 Example Area Statistics File for the CULTURE Code

```
"Time","AREA ID","Minimum","5th Percentile","10th Percentile","25th Percentile","Median",
"75th Percentile","90th Percentile","95th Percentile","Maximum","Mean","Standard Deviation"
2000,"Area01", 3.289E+01, 3.289E+01, 3.289E+01, 3.289E+01, 5.383E+01, 5.383E+01, 7.538E+01,
7.538E+01, 1.026E+02, 6.136E+01, 2.801E+01
2000,"Area02", 1.282E+02, 1.282E+02, 1.282E+02, 1.282E+02, 3.953E+02, 3.953E+02, 4.848E+03,
4.848E+03, 1.203E+04, 3.526E+03, 5.155E+03
2050,"Area01", 6.067E+03, 6.067E+03, 6.067E+03, 6.067E+03, 2.613E+04, 2.613E+04, 5.127E+04,
5.127E+04, 1.529E+05, 5.001E+04, 5.999E+04
2050,"Area02", 1.162E+03, 1.162E+03, 1.162E+03, 1.162E+03, 1.114E+04, 1.114E+04, 8.869E+04,
8.869E+04, 1.168E+05, 4.461E+04, 5.410E+04
```

3.3.2.5 Map Data File

The map data file is an optional output file that contains the detailed values for map calculations in the CULTURE code. The description of the MAP keyword (Section 3.4.9) explains how to define a map calculation. The description of the MAP modifier on the FILE keyword (Section 3.4.7) explains how to define the file name. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file after the header line consists of two identifiers followed by a value for every location. A record is written for every location defined using the LOCATION keyword (see Section 3.4.8). Excerpted records from a map data file for three solution times are provided in Table 3.6. The following are the two identifiers on each line:

- Time: Year for which the data are valid
- Map ID: The map identifier.

Table 3.6 Excerpted Records from a Map Data File in the CULTURE Code

```
"Time","MAP ID","Easting","Northing","Percent Exceedance"
1990,"Map11 ", 5.745216E+05, 1.543666E+05, 0.920E+00
1990,"Map11 ", 5.765372E+05, 1.541413E+05, 0.010E+00
...
1990,"Map11 ", 5.940311E+05, 1.027057E+05, 0.000E+00
1990,"Map11 ", 5.947682E+05, 1.026592E+05, 0.007E+00
2000,"Map11 ", 5.745216E+05, 1.543666E+05, 0.022E+00
2000,"Map11 ", 5.765372E+05, 1.541413E+05, 0.000E+00
...
```

```
2000,"Map11 ", 5.940311E+05, 1.027057E+05, 0.310E+00
2000,"Map11 ", 5.947682E+05, 1.026592E+05, 0.000E+00
2010,"Map11 ", 5.745216E+05, 1.543666E+05, 0.222E+00
2010,"Map11 ", 5.765372E+05, 1.541413E+05, 0.000E+00
...
2010,"Map11 ", 5.940311E+05, 1.027057E+05, 0.000E+00
2010,"Map11 ", 5.947682E+05, 1.026592E+05, 0.989E+00
```

3.3.2.6 Site Distance Data File

The site distance data file is an optional output file that contains the detailed values for site distance calculations in the CULTURE code. The description of the SITE keyword (Section 3.4.11) explains how to define an area calculation. The description of the SITE_DAT modifier on the FILE keyword (Section 3.4.7) explains how to define the file name. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file after the header line consists of three identifiers followed by a value for every generated realization. An example file for two sites, five realizations, and two times is provided in Table 3.7. The following are the three identifiers on each line:

- Time: Year for which the data are valid
- Site ID: The site identifier
- Solution type: A flag for solution type – the distance calculation.

Table 3.7 Example Site Distance Data File for the CULTURE Code

```
"Time","SITE ID","Variable","Distance to the site"
2000,"Site01","DIST", 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00
2000,"Site02","DIST", 1.562E-02, 1.562E-02, 1.562E-02, 7.500E+02, 1.562E-02
2050,"Site01","DIST", 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00
2050,"Site02","DIST", 1.704E+03, 3.092E+03, 2.250E+03, 4.387E+03, 7.500E+02
```

3.3.2.7 Site Distance Statistics File

This optional file contains summary statistics for site distance calculations for the CULTURE code. The description of the SITE keyword (Section 3.4.11) explains how to define an area calculation. The description of the SITE_STA modifier on the FILE keyword (Section 3.4.7) explains how to define the file name. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file after the header line consists of two identifiers followed by summary statistics (nine percentiles, mean value, and standard deviation). A subset of the data written to this file for a run is provided in Table 3.8. The following are the two identifiers on each line:

- Time: Year for which the data are valid
- Site ID: The location identifier where the data are valid.

The data for each record in this file are too long to present without line wrapping in this document. Each record in the file after the single header line occupies two lines in Table 3.8.

Table 3.8 Example Site Distance Statistics File for the CULTURE Code

```
"Time","SITE ID","Minimum","5th Percentile","10th Percentile",
"25th Percentile","Median","75th Percentile","90th Percentile",
"95th Percentile","Maximum","Mean","Standard Deviation"
2000,"Site01", 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00,
0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00
2000,"Site02", 1.562E-02, 1.562E-02, 1.562E-02, 1.562E-02, 1.562E-02,
1.562E-02, 6.302E+02, 7.500E+02, 7.500E+02, 1.937E+02, 3.331E+02
2050,"Site01", 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00,
0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00, 0.000E+00
2050,"Site02", 7.500E+02, 7.500E+02, 7.500E+02, 1.704E+03, 4.387E+03,
4.387E+03, 4.500E+03, 4.500E+03, 4.500E+03, 3.414E+03, 1.340E+03
```

3.4   Keyword Descriptions for the CULTURE Code

In the following keyword descriptions, some data are optional and some are required. Data required are enclosed in square brackets. For AB to be required, it would be denoted by [AB]. If only one of the three items AB, BC, CD were required, it would be written as [AB|BC|CD]. The vertical bars indicate to choose one of the items in the list. Optional items are enclosed in normal brackets. For DE to be an optional entry, it would be denoted by {DE}. The {} or [] symbols are indicators of whether the data are required; the symbols do not need to be entered when the keyword is constructed.

In some instances, numerical values or quote strings are associated with a modifier. In this description, the association is indicated by using the equal (=) symbol. The = symbol is not required but may be used when the keyword is constructed. When a numerical value or quote string is associated with a modifier, it must be physically entered on the input line directly after the modifier.

This section defines keywords needed to control the CULTURE directly. The order in which keywords are entered does not matter for many keywords. However, several keywords have a required order of appearance, including the following requirements:

- The REPORT keyword must be the first keyword in the file
- All ANALYTE keywords must precede any AREA, MAP, or SITE keywords
- The END keyword must be the last keyword in the file.

3.4.1   Keywords Required from the Environmental Settings File for the CULTURE Code

The CULTURE code also reads keywords from the environmental settings file. These keywords are read from a different file and can have a different definition from a keyword defined for internal use in the CULTURAL code. The environmental settings keywords are defined in Section 2.0. The following keywords are required:

- ANALYTE – Definition of analytes in the environmental simulations
- END – End of the environmental settings keywords
- FILE – File names for the concentration file for each analyte
- LOCATION – Locations at which concentrations were generated for the cultural impacts

- REALIZAT – Number of realizations that were simulated
- TIMES – Times at which concentrations were generated for the cultural impacts
- TITLE – Environmental simulation title.

3.4.2   AREA Keyword for the CULTURE Code

The AREA keyword controls calculation of the area where concentrations exceed user-supplied thresholds (see the THRESHOLD keyword description in Section 3.4.12). Multiple AREA keywords can be entered. Each entry of the AREA card will cause the specific calculation to be performed for all times steps requested (see the TIMES keyword in Section 3.4.13). The area calculations can be done for groundwater or for contaminated soil. Each AREA keyword defines a different area calculation. The following is the keyword's syntax:

```
AREA [ID="quote 1"] [ANALYTE="quote 2"] {"quote 3"} … {"quote n"}
   [GRO_WAT | SOIL] [TITLE="quote k"]
```

Each occurrence of the AREA keyword must contain one of the modifiers GRO_WAT or SOIL, but not both. This modifier identifies whether the area calculations are to be performed for groundwater concentrations or for soil concentrations. The area calculation for more than one analyte listed on a single AREA keyword returns the union of the area where each analyte is above its respective threshold.

The AREA keyword uses quote strings to enter the following three items:

- A unique identification string up to six characters long (modifier ID)
- A title up to 72 characters long (modifier TITLE)
- A list of analytes (modifier ANALYTE) that will be included in the calculation.

These three modifiers can be entered in any order, together with their associated data, but the group of analyte names (see the ANALYTE keyword description) must be entered as a block.

The following AREA keyword calculates the area underlain by groundwater above the threshold concentration for zinc:

```
AREA ID= "Area #1" ANALYTE="Zn" GRO_WAT TITLE="Area #1 title"
```

The following AREA keyword calculates the area where the concentration of zinc exceeds the threshold for zinc in soil:

```
AREA ID= "Area #2" ANALYTE= "Zn" SOIL TITLE="Area #2 title"
```

Suppose that the three analytes copper, lead, and zinc were being evaluated in a run of the CULTURE code. If the analyst desired area calculations for each analyte individually and for the combined set in both the groundwater and soil, then the following set of eight keywords would be used:

```
AREA ID= "Area #3" ANALYTE= "Cu" GRO_WAT TITLE="Area #3 title"
AREA ID= "Area #4" ANALYTE= "Lead" GRO_WAT TITLE="Area #4 title"
AREA ID= "Area #5" ANALYTE= "Zn" GRO_WAT TITLE="Area #5 title"
```

```
AREA ID= "Area #6" ANALYTE= "Cu" "Zn" "Lead" GRO_WAT TITLE="Area #6 title"
AREA ID= "Area #7" ANALYTE= "Cu" SOIL TITLE="Area #7 title"
AREA SOIL ID= "Area #8" ANALYTE= "Zn" TITLE="Area #8 title"
AREA ID= "Area #9" ANALYTE= "Lead" SOIL TITLE="Area #9 title"
AREA TITLE="LastArea title"  ANALYTE= "Zn" "Lead" "Cu" SOIL ID="LastArea"
```

3.4.3   DEBUG Keyword for the CULTURE Code

The DEBUG keyword is used to activate dumping of intermediate calculations to the report file. It should be used sparingly and with only one or two realizations; otherwise, the volume of output could fill the user's hard drive. The following is this keyword record's syntax:

```
DEBUG [modifier 1] {modifier 2}…{modifier k}
```

Multiple DEBUG cards can be entered with combinations of modifiers, or a single card can be entered containing all of the modifiers. The modifiers can be entered in any order. Table 3.9 describes the modifiers associated with the DEBUG keyword.

Table 3.9 Modifiers Associated with the DEBUG Keyword in the CULTURE Code

Modifier	Description
AREA	Intermediate outputs on calculations for area calculations.
CONCEN	Intermediate results for input concentration data.
SITE	Intermediate outputs on calculations for distance calculations on specific sites.
MAP	Intermediate outputs on calculations for generating map data.
LOGIC	Intermediate outputs tracking program execution flow logic.

The following entries provide examples of the use of the DEBUG keyword:

```
DEBUG SITE
DEBUG MAP
DEBUG MAP SITE AREA
```

There are no quote strings associated with the DEBUG keyword.

3.4.4   DETAILS Keyword for the CULTURE Code

The DETAILS keyword is used to activate reporting of calculations of AREA or SITE calculations by realization to output files. The following is this keyword record's syntax:

```
DETAILS {AREA} {SITE}
```

Multiple DETAILS keywords can be entered with combinations of modifiers, or a single card can be can be entered. The following is an example that turns on reporting for detailed data for both area and site calculations:

```
   DETAILS  SITE  AREA
```

3.4.5 END Keyword for the CULTURE Code

The END keyword signifies the end of all keyword data. It should be the last keyword in the keyword file. All data in the keyword file after the END keyword will be ignored. The following is this keyword record's syntax:

```
   END
```

There are no modifiers or quote strings associated with the END keyword.

3.4.6 EXECUTE Keyword for the CULTURE Code

The EXECUTE keyword signifies that the user wishes to perform problem execution. If this keyword is not entered, then the inputs are checked for consistency, but the problem will not be executed. This is useful if the run being set up is expected to take a significant amount of computation time. The following is this keyword record's syntax:

```
   EXECUTE
```

There are no modifiers or quote strings associated with the EXECUTE keyword.

3.4.7 FILE Keyword for the CULTURE Code

The FILE keyword is used to enter the names of input and output files except for the report file. The names of the files providing concentration data are contained in the environmental scenario file rather than in the keyword file. The following is the syntax for the FILE keyword record:

```
   FILE [modifier1 "quote1"] {modifier2 "quote2"} ... {modifier5 "quote5"}
```

The file names are entered in quote strings, which must be enclosed in double quotation marks. Path names up to 72 characters long are supported. The file name associated with a modifier must be entered before the next modifier is entered. At least one FILE keyword is required for every run of the code. Table 3.10 describes the modifiers associated with the FILE keyword.

Table 3.10 Modifiers Associated with the FILE Keyword in the CULTURE Code

Modifier	Description
AREA_DAT	Output file containing the calculated data, by realization, for each of the area calculations. This file is required only if the AREA modifier is used on the DETAILS keyword.
AREA_STA	Output file containing summary statistics for each of the area calculations. This file is required if any AREA calculations are being performed.
ENVIRON	Input environmental scenario file that contains the definition of the environmental runs from which impacts are to be calculated.

Modifier	Description
HEADER	Output file containing header type information associated with all of the other output files identified in this table.
MAP	Output file containing the calculated map data for each requested map.
SITE_DAT	Output file containing the calculated distance, for each realization, to concentrations that are above a threshold for every requested site. This file is required only if the SITE modifier is used on the DETAILS keyword.
SITE_STA	Output file containing summary statistics for the distance to concentrations that are above a threshold for every requested site. This file is required if any SITE calculations are being performed.

The following is an example entry:

```
FILE  HEADER "TestCase.hdr"  MAP "TestCase.map"
```

The following set of two entries has the same effect as the single entry above:

```
FILE  MAP "TestCase.map"
FILE  HEADER "TestCase.hdr"
```

3.4.8   LOCATION Keyword for the CULTURE Code

The LOCATION keyword identifies the locations that will be used in the impact calculations. At least one LOCATION keyword is required. Multiple LOCATION keywords are allowed. The locations must be a subset of the locations at which environmental data were computed and stored by the inventory, release, and transport modules. The list of desired locations builds sequentially with each LOCATION keyword. Upon program entry, no locations are active. The set of active locations applies to all area, site, or map calculations.

The following is the LOCATION keyword's syntax:

```
LOCATION [ALL | LIST "quote 1" … "quote n"]
```

One of the modifiers ALL or LIST must be entered. If the modifier ALL is entered, then all locations are activated. If the modifier LIST is entered, then it must be followed by one or more location IDs entered as quote strings.

The following two examples illustrate the use of the LOCATION keyword. The first example activates all possible culture locations. The second example activates 32 specific locations.

```
LOCATION ALL

LOCATION LIST
    "CL1619"  "CL1627"  "CL1916"  "CL1924"  "CL2231"  "CL2239"
    "CL2600"  "CL2608"  "CL2960"  "CL2968"  "CL3293"  "CL3301"
```

```
"CL3671"   "CL3679"   "CL3968"   "CL3976"   "CL0001"   "CL1202"
"CL1303"   "CL1404"   "CL1505"   "CL1606"   "CL1011"   "CL1238"
"CL0021"   "CL1222"   "CL1323"   "CL1424"   "CL1525"   "CL1626"
"CL1211"   "CL1278"
```

3.4.9   MAP Keyword for the CULTURE Code

The MAP keyword is used to define the output maps showing where concentrations exceed user-supplied thresholds (see the THRESHOLD keyword description). The term map in this context means that a set of ordered triples will be generated that can be sent to a plotting or contouring program. The first two entries in the triple give the location (easting, northing). The third entry gives a value at the location. The syntax for this keyword record takes one of the following forms:

```
MAP [ID="quote 1"] [ANALYTE="quote 2"] {"quote 3"} … {"quote n"}
    [TITLE="quote k"]
```

The MAP keyword uses quote strings to enter the following three items:

- a unique identification string up to six characters long (modifier ID)
- a title up to 72 characters long (modifier TITLE)
- a list of analytes (modifier ANALYTE) that will be included in the calculation.

These three modifiers can be entered in any order, together with their associated data, but the group of analyte names must be entered as a block.

Multiple MAP keywords can be entered. Each entry of the MAP keyword will cause the specific calculation to be performed for all times steps requested (see the TIMES keyword in Section 3.4.13). The map calculations will be done for all media concentrations at each location. A media can be excluded by setting its respective threshold to a large number. The value reported in the map calculation at a location will be the average number of realizations where one or more analytes exceed their respective thresholds in one or more media concentrations. This number could be interpreted loosely as the probability of contamination being above thresholds at the location.

The following two examples illustrate the use of the MAP keyword:

```
MAP ID="Map #1" TITLE "Example map for radioactive analytes"
    ANALYTE="C14" "Tc99"

MAP ID="Map #2" ANALYTE "Zn" "Cu"
    TITLE "Example map for nonradioactive analytes"
```

3.4.10 REPORT Keyword for the CULTURE Code

The REPORT keyword is used to define the name of the output report (log) file. It must be the first keyword entered in the keyword file. The following is this keyword record's syntax:

```
REPORT ["quote"]
```

The name of the report file is entered in a quote string. File names up to 72 characters long are supported, and path names can be included. The following is an example REPORT keyword record:

```
REPORT "/SAC/SystemCodes/Cultural/Test1.rpt"
```

3.4.11 SITE Keyword for the CULTURE Code

The SITE keyword is used to control calculations of the distance from a specified site to concentrations in groundwater above a specified threshold. The syntax of the SITE keyword is the following:

```
SITE ID="quote 1" NORTHING=N1 EASTING=N2 TITLE="quote 2"
```

Each site is defined by entering a SITE keyword. The quote string associated with the modifier ID contains an identification string for the site and is limited to 6 characters. The quote string associated with the TITLE modifier provides a brief site description and is limited to 72 characters. The values N1 and N2 are the northing and easting location coordinates for the site. The following are two examples for this keyword:

```
SITE ID="Example site 1" NORTHING=23.3445 EASTING=45.665
    TITLE ="Located near the old willow"

SITE TITLE ="Under the old oak tree" EASTING=45.668 NORTHING=23.3456
    ID="Just north of F Slough"
```

The order of entry for the ID and LABEL strings is immaterial. The two location coordinates can be entered in any order.

3.4.12 THRESHOLD Keyword for the CULTURE Code

The AREA, MAP, and SITE keywords all reference thresholds for their calculations. The values of the thresholds are entered using the THRESHOLD keyword. The thresholds apply by analyte and media. The following is the THRESHOLD keyword's syntax:

```
THRESHOLD [Analyte="quote"] [N1]
    [GRO_WAT | SUR_WAT | POR_WAT | SEDIMENT| SOIL | SEE_WAT]
```

The entry for the quote string is the analyte identification string. The media modifiers for the THRESHOLD keyword are given in Table 3.11.

Table 3.11 Modifiers Associated with the THRESHOLD Keyword in the CULTURE Code

Modifier	Description
GRO_WAT	Groundwater concentration.
SEE_WAT	Seep water concentration.
SOIL	Soil concentrations.
SUR_WAT	Surface water (river) concentration.

Modifier	Description
POR_WAT	Pore water (river bottom) concentrations.
SEDIMENT	Sediment concentrations.

The following is an example set of keywords defining some thresholds for several environmental media and several analytes:

```
THRESHOLD GRO_WAT   Analyte="C14"   0.005
THRESHOLD SUR_WAT   Analyte="Tc99" 12.0
THRESHOLD SEE_WAT   Analyte="Zn"    0.0013
THRESHOLD POR_WAT   Analyte="Zn"    0.0014
THRESHOLD SOIL      Analyte="C14"   0.15
THRESHOLD SEDIMENT Analyte="Zn"    85.0
```

The set of example THRESHOLD keywords given above references four analytes. Depending on the desired set of area, site, or map calculations, the user may need to enter six THRESHOLD keyword records for every analyte (one for every possible environmental media identified in Table 3.11).

The following are the data units for the concentrations associated with the THRESHOLD keywords:

- Radioactive analyte, water concentration: pCi/L
- Radioactive analyte, sediment or soil concentration: pCi/kg
- Nonradioactive analyte, water concentration: μg/L
- Nonradioactive analyte, sediment or soil concentration: μg/kg.

3.4.13 TIMES Keyword for the CULTURE Code

The TIMES keyword identifies the times at which the calculations are to be performed. The following is the keyword's syntax:

```
TIMES [T1] {T2} … {Tn}
```

The numerical entries T1, T2, …, Tn are the times (whole number years) when outputs are desired. These times must be a subset of the times at which environmental data were computed and stored by the inventory, release, and transport modules. Only one TIMES card should be entered. The times entered will apply to all AREA, SITE, and MAP calculations. The following is an example TIMES keyword that requests output for the three years 2020, 2075, and 3014:

```
TIMES 2020 2075 3014
```

There are no modifiers or quote strings associated with the TIMES keyword.

3.4.14 TITLE Keyword for the CULTURE Code

The TITLE keyword is used to define a single-line problem title. The problem title will be written to output files. If the title is not supplied, then the program will error terminate. The following is this keyword record's syntax:

```
TITLE ["quote"]
```

The title is entered in a quote string, which must be enclosed in double quotation marks. Titles up to 72 characters long are supported. The following example defines a title for a run of the code:

```
TITLE "Example title line for the cultural impacts code."
```

There are no modifiers associated with the TITLE keyword.

3.4.15 USER Keyword for the CULTURE Code

The USER keyword is used to identify the user of the program. The user name will be written to output files. If the user name is not supplied, then the program will error terminate. The following is this keyword record's syntax:

```
USER ["quote"]
```

The user name is entered in a quote string, which must be enclosed in double quotation marks. User names up to 16 characters long are supported. The following example defines John Q. Public as the user running the code:

```
USER "John Q. Public"
```

There are no modifiers associated with the USER keyword.

3.5 Example Keyword Files

The following three sections provide example keyword files for a data set with nine analytes and 11 realizations. Separate example files are provided for area calculations, map calculations, and site distance calculations. It is possible to calculate any combination of these three types of calculations using a single keyword file.

3.5.1 Example Keyword File for Area Calculations

The following example keyword file (Table 3.12) controls calculations of detailed data and summary statistics for area calculations. The mathematic basis for the detailed data calculations is provided in Section 3.1.1.

Table 3.12 Example Keyword File for Area Calculations in the CULTURE Code

```
!
! Keyword file for the CULTURE code using drinking water thresholds
! This file controls example Area calculations
! Developer: Carmen Arimescu
! Date: 15 Jan 2002
!
REPORT "G:\Initial\Culture\Cul_dws.rpt"
!
! Input Environmental setting file
FILE ESD "G:\Initial\ESD_Initial.Key"
!
! Output header file for GUI data extraction
FILE HEADER "G:\Initial\Culture\Cul_dws.hdr"
!
! Output area detailed data
DETAILS AREA
FILE AREA_DAT "G:\Initial\Culture\Cul_dws_area_det.csv"
!
STATISTICS AREA
FILE AREA_STA "G:\Initial\Culture\Cul_dws_area_sta.csv"
!
! User name
USER "Carmen Arimescur"
!
REALIZATION 11
!
! Overall problem title
TITLE "Example Area Calculations for the CULTURE Code"
!
! Output times for calculations
TIMES 1990 2000 2010
!
! Groundwater concentration thresholds by analyte
THRESHOLD GRO_WAT ANALYTE="CCl4"        5.0      "ug/L"
THRESHOLD GRO_WAT ANALYTE="Cs137"      200.0     "pCi/L"
THRESHOLD GRO_WAT ANALYTE="CrVI"       100.0     "ug/L"
THRESHOLD GRO_WAT ANALYTE="H3"       20000.0     "pCi/L"
THRESHOLD GRO_WAT ANALYTE="I129"         1.0     "pCi/L"
!THRESHOLD GRO_WAT ANALYTE="Pu239"        0.0     "pCi/L - No standard"
THRESHOLD GRO_WAT ANALYTE="Sr90"         8.0     "pCi/L"
THRESHOLD GRO_WAT ANALYTE="Tc99"       900.0     "pCi/L"
THRESHOLD GRO_WAT ANALYTE="U238"        13.4     "pCi/L"
!
! Surface water concentration thresholds by analyte
THRESHOLD SUR_WAT ANALYTE="CCl4"         0.25    "ug/L"
THRESHOLD SUR_WAT ANALYTE="Cs137"      160.0     "pCi/L"
THRESHOLD SUR_WAT ANALYTE="CrVI"        11.0     "ug/L"
THRESHOLD SUR_WAT ANALYTE="H3"       20000.0     "pCi/L"
THRESHOLD SUR_WAT ANALYTE="I129"         0.5     "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Pu239"       13.0     "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Sr90"         8.0     "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Tc99"       800.0     "pCi/L"
THRESHOLD SUR_WAT ANALYTE="U238"        15.0     "pCi/L"
!
! Define area calculations
AREA ID="Area01" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129"
   "Sr90" "Tc99" "U238" GRO_WAT
```

```
   TITLE "Area where GW threshold exceeded for at least one analyte"
!
AREA ID="Area02" ANALYTE="CCl4" GRO_WAT
 TITLE "Area where GW threshold exceeded for CCl4"
!
! Locations for the area calculations
LOCATION LIST
  "CL0001"  "CL0002"  "CL0003"  "CL0004"  "CL0005"
  "CL0006"  "CL0007"  "CL0008"  "CL0009"  "CL0010"
  "CL0011"  "CL0012"  "CL0013"  "CL0014"  "CL0015"
  "CL0016"  "CL0017"  "CL0018"  "CL0019"  "CL0020"
END
```

3.5.2   Example Keyword File for Map Calculations

The following example keyword file (Table 3.13) controls calculations of map data. The mathematic basis for the map data calculations is provided in Section 3.1.2.

Table 3.13 Example Keyword File for Map Calculations in the CULTURE Code

```
!
! Keyword file for the CULTURE code using drinking water thresholds
! This file controls example Map calculations
! Developer: Carmen Arimescu
! Date: 15 Jan 2002
!
REPORT "G:\Initial\Culture\Cul_Map11.rpt"
!
! Input Environmental setting file
FILE ESD "G:\Initial\ESD_Initial.Key"
!
! Output header file for GUI data extraction
FILE HEADER "G:\Initial\Culture\Cul_Map11.hdr"
!
! Output map data
FILE MAP "G:\Initial\Culture\Cul_Map11.csv"
!
EXECUTE
!
! User name
USER "Carmen Arimescu"
!
REALIZATION 11
!
! Overall problem title
TITLE "Example Map Calculations for the CULTURE Code"
!
! Output times for calculations
TIMES 1990 2000 2010 2020
!
! Groundwater concentration thresholds by analyte
THRESHOLD GRO_WAT ANALYTE="CCl4"          5.0      "ug/L"
THRESHOLD GRO_WAT ANALYTE="Cs137"       200.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="CrVI"        100.0      "ug/L"
THRESHOLD GRO_WAT ANALYTE="H3"        20000.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="I129"          1.0      "pCi/L"
!THRESHOLD GRO_WAT ANALYTE="Pu239"         0.0      "pCi/L - No standard"
```

```
THRESHOLD GRO_WAT ANALYTE="Sr90"           8.0        "pCi/L"
THRESHOLD GRO_WAT ANALYTE="Tc99"         900.0        "pCi/L"
THRESHOLD GRO_WAT ANALYTE="U238"          13.4        "pCi/L"
!
! Surface water concentration thresholds by analyte
THRESHOLD SUR_WAT ANALYTE="CCl4"           0.25       "ug/L"
THRESHOLD SUR_WAT ANALYTE="Cs137"        160.0        "pCi/L"
THRESHOLD SUR_WAT ANALYTE="CrVI"          11.0        "ug/L"
THRESHOLD SUR_WAT ANALYTE="H3"         20000.0        "pCi/L"
THRESHOLD SUR_WAT ANALYTE="I129"           0.5        "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Pu239"         13.0        "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Sr90"           8.0        "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Tc99"         800.0        "pCi/L"
THRESHOLD SUR_WAT ANALYTE="U238"          15.0        "pCi/L"
!
! Define the map
Map ID="Map11" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129"
  "Sr90" "Tc99" "U238" SUR_WAT
  TITLE "Map where SW threshold exceeded for any analyte"
!
! Locations for the upland maps
LOCATION LIST
  "CL0001"   "CL0002"   "CL0003"   "CL0004"   "CL0005"
  "CL0006"   "CL0007"   "CL0008"   "CL0009"   "CL0010"
  "CL0011"   "CL0012"   "CL0013"   "CL0014"   "CL0015"
  "CL0016"   "CL0017"   "CL0018"   "CL0019"   "CL0020"
!
END
```

3.5.3   Example Keyword File for Site Calculations

The following example keyword file controls calculations of detailed data and summary statistics for site distance calculations. The mathematic basis for the calculations is provided in Section 3.1.2.

Table 3.14 Example Keyword File for Site Calculations in the CULTURE Code

```
! Keyword file for the CULTURE code using drinking water thresholds
! This file controls example Site calculations
! Developer: Carmen Arimescu
! Date: 15 Jan 2002
!
REPORT "G:\Initial\Culture\Cul_dws.rpt"
!
! Input Environmental setting file
FILE ESD "G:\Initial\ESD_Initial.Key"
!
! Output header file for GUI data extraction
FILE HEADER "G:\Initial\Culture\Cul_dws.hdr"
!
! Output site detailed data
DETAILS SITE
FILE SITE_DAT "G:\Initial\Culture\Cul_dws_site_det.csv"
!
! Output site summary statistics
STATISTICS SITE
FILE SITE_STA "G:\Initial\Culture\Cul_dws_site_sta.csv"
!
```

```
! User name
USER "Carmen Arimescu"
!
REALIZATION 11
!
! Overall problem title
TITLE "Example Site Calculations for the CULTURE Code"
!
! Output times for calculations
TIMES 1990 2000 2010
!
! Groundwater concentration thresholds by analyte
THRESHOLD GRO_WAT ANALYTE="CCl4"          5.0      "ug/L"
THRESHOLD GRO_WAT ANALYTE="Cs137"       200.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="CrVI"        100.0      "ug/L"
THRESHOLD GRO_WAT ANALYTE="H3"        20000.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="I129"          1.0      "pCi/L"
!THRESHOLD GRO_WAT ANALYTE="Pu239"         0.0      "pCi/L - No standard"
THRESHOLD GRO_WAT ANALYTE="Sr90"          8.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="Tc99"        900.0      "pCi/L"
THRESHOLD GRO_WAT ANALYTE="U238"         13.4      "pCi/L"
!
! Surface water concentration thresholds by analyte
THRESHOLD SUR_WAT ANALYTE="CCl4"          0.25     "ug/L"
THRESHOLD SUR_WAT ANALYTE="Cs137"       160.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="CrVI"         11.0      "ug/L"
THRESHOLD SUR_WAT ANALYTE="H3"        20000.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="I129"          0.5      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Pu239"        13.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Sr90"          8.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="Tc99"        800.0      "pCi/L"
THRESHOLD SUR_WAT ANALYTE="U238"         15.0      "pCi/L"
!
!
! Define two site calculations
!
SITE ID="Site01" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129"
  "Sr90" "Tc99" "U238" SUR_WAT
  TITLE "Site using SW threshold exceeded for at least one analyte"
  EASTING=5.932908E+05 NORTHING=6.746470E+04
!
SITE ID="Site02" ANALYTE="CCl4" "Cs137" "CrVI" "H3" "I129"
  "Sr90" "Tc99" "U238" GRO_WAT
  TITLE "Site using GW threshold exceeded for at least one analyte"
  EASTING=5.647716E+05 NORTHING=1.446166E+05
!

! Locations for the upland maps
LOCATION LIST
  "CL0001"  "CL0002"  "CL0003"  "CL0004"  "CL0005"
  "CL0006"  "CL0007"  "CL0008"  "CL0009"  "CL0010"
  "CL0011"  "CL0012"  "CL0013"  "CL0014"  "CL0015"
  "CL0016"  "CL0017"  "CL0018"  "CL0019"  "CL0020"
!
END
```

4.0   Ecological Impacts Model (ECEM)

4.1   Mathematical Formulation for the Ecological Impacts Model

The following sections give the intake and exposure equations for the ecological impacts model. The equations are given for both terrestrial and aquatic species. The concentration equations given in this section are based on equilibrium concepts rather than dynamic formulations.

4.1.1   Terrestrial Species

Terrestrial species are subdivided into plant and animal species. The exposure equations for terrestrial species are given in this section.

4.1.1.1   Terrestrial Plants

The analyte concentrations in terrestrial plants can come from rain splash, root uptake or foliar absorption from vapor, and soil contact. The concentrations also depend on whether the analyte is organic or nonorganic.

4.1.1.1.1   Contaminant Deposition Caused by Rain Splash

The equilibrium concentration in above-ground plant parts from rain splash is calculated using the following equation:

$$C_{par} = EC_{soil} \times K_{ps1}$$

where:
$\quad C_{par}$ =   equilibrium concentration in above-ground plant parts from rain splash (μg/kg or pCi/kg wet plant weight)
$\quad EC_{soil}$ =   concentration in surface soil (top ~1 cm) (μg/kg or pCi/kg dry)
$\quad K_{ps1}$ =   plant-soil partition coefficient for rain splash on fresh-weight basis (kg soil/kg plant wet weight).

If the plant is an emergent plant (rooted in soil but grows in water), then C_{par} is set to zero.

4.1.1.1.2   Root Uptake to Above-Ground Plant Tissue

The equilibrium concentration in above-ground plant parts from root uptake is calculated using the following equations. For organic contaminants, the equation is:

$$C_{pau} = EC_{soil} \times K_{ps2}$$

For inorganic contaminants, the equation is:

$$C_{pau} = EC_{soil} \times B_v \times (1 - f_w)$$

where:

C_{pau}	=	equilibrium concentration in above-ground plant parts from root uptake (μg/kg or pCi/kg wet)
EC_{soil}	=	concentration in surface soil (top ~1 cm) (μg/kg or pCi/kg dry)
K_{ps2}	=	plant-soil partition coefficient for root-zone soil to above-ground plant parts for organic contaminants - fresh weight basis (kg soil/kg plant wet weight)
B_v	=	bioconcentration factor for vegetative plant parts for inorganic contaminants – dry weight basis (kg-soil/kg-dry-plant)
f_w	=	weight fraction of plant tissue that is water (wet to dry conversion).

If the plant is an emergent plant (rooted in soil but grows in water), then the concentration of the analyte in sediment, EC_{sed}, is used in the equation for C_{pau} rather than EC_{soil}.

The plant-soil partition coefficient for root-zone soil to above-ground plant parts for organic contaminants (fresh weight basis) is calculated using the following regression model (McKone 1993):

$$K_{ps2} = 7.7 \times K_{ow}^{-0.58}$$

where K_{ow} is the octanol-water partition coefficient (unitless).

4.1.1.1.3 Foliar Uptake from Soil by Vapor

The equilibrium concentration in above-ground plant parts from vapor uptake is calculated using the following equation (Hope 1995):

$$C_{pav} = EC_{vap} \times K_{pa1}$$

where:

C_{pav}	=	equilibrium concentration in above-ground plant parts from vapor uptake (μg/kg or pCi/kg wet)
K_{pa1}	=	plant-air partition coefficient for air to above-ground plant parts for organic contaminants (m^3/kg wet weight)
EC_{vap}	=	concentration of gas-phase contaminant (μg/m^3 or pCi/m^3).

The plant-air partition coefficient for transfer of analytes in the air to above-ground plant parts for organic contaminants is calculated using the following equation (Reiderer 1990):

$$K_{pa1} = \left[f_{pa} + \left(f_{pw} + [f_{pl} \times K_{ow}] \right) \times \left[\frac{R \times T}{H} \right] \right] \Big/ \rho_p$$

where:

K_{pa1} = plant-air partition coefficient for air to above-ground plant parts for organic contaminants (m^3/kg wet weight)

f_{pa} = volume fraction of plant tissue in air (unitless)

f_{pw} = volume fraction of plant tissue that is water (unitless)

f_{pl} = volume fraction of plant tissue that is lipid (unitless)

K_{ow} = octanol-water partition coefficient (unitless)

R = universal gas constant (Pa-m^3/mol-K)

T = temperature (K)

H = contaminant-specific Henry's law constant (Pa-m^3/mol)

ρ_p = plant tissue density (kg/m^3).

The concentration of gas-phase contaminant is calculated using the following equation (EPA 1991):

$$EC_{vap} = \frac{EC_{soil}}{\left(\dfrac{LS \times V \times Dh}{A}\right) \times \left(\dfrac{[3.14 \times \varsigma \times I]^{0.5}}{2 \times D_{ei} \times E \times K_{as} \times 10^{-3}}\right)}$$

where:

EC_{vap} = concentration of gas-phase contaminant ($\mu g/m^3$ or pCi/m^3)

EC_{soil} = concentration in surface soil (top ~1 cm) ($\mu g/kg$ or pCi/kg dry)

LS = length of side of contaminated area (m)

V = wind speed in mixing zone (m/s)

Dh = diffusion height (m)

A = area of contamination (cm^2)

ς = effective diffusion rate (cm^2/s)

I = exposure interval (s)

D_{ei} = effective diffusivity (cm^2/s)

E = soil porosity (unitless)

K_{as} = soil/air partition coefficient (g soil/cm^3 air)

10^{-3} is a conversion from kg to g.

The effective diffusion rate is calculated from the expression:

$$\varsigma = \frac{D_{ei} \times E}{E + \left(\rho_s \times \left[\dfrac{1 - E}{K_{as}}\right]\right)}$$

where:

ς = effective diffusion rate (cm^2/s)

D_{ei} = effective diffusivity (cm^2/s)

E = soil porosity (unitless)

ρ_s = denotes the soil density (g/cm^3)

K_{as} = soil/air partition coefficient (g soil/cm^3 air).

The soil/air partition coefficient is calculated (EPA 1991) from the expression:

$$K_{as} = \frac{41 \times H}{101,250 \times K_d}$$

where:

    K_{as} = soil/air partition coefficient (g soil/cm³ air)
    H = contaminant-specific Henry's law constant (Pa-m³/mol)
    K_d = soil-water partition coefficient (cm³/g)
    41 = a units conversion factor with units mol/m³-atm
    101,250 a units conversion factor with units Pa/atm.

Furthermore, K_d is calculated (regression model in Nicholls [1991]) using the expression:

$$K_d = 0.62 \times K_{ow} \times f_{oc}$$

where:

    K_d = soil-water partition coefficient (cm³/g)
    K_{ow} = octanol-water partition coefficient (unitless)
    f_{oc} = the soil organic carbon content (unitless)
    0.62 = regression coefficient (cm³/g).

The effective diffusivity is calculated from the expression:

$$D_{ei} = D_i \times E^{0.33}$$

where:

    D_{ei} = effective diffusivity (cm²/s)
    D_i is the molecular diffusivity (cm²/s)
    E = soil porosity (unitless).

4.1.1.1.4 *Foliar Adsorption of Particulates from Soil*

The equilibrium concentration in above-ground plant parts from foliar adsorption of particulates from soil is calculated from the expression:

$$C_{pap} = EC_{par} \times K_{pa2}$$

where:

    C_{pap} = concentration in above-ground plant parts (µg/kg or pCi/kg plant wet)
    EC_{par} = air concentration of particulate-bound contaminant (µg/m³ or pCi/m³)
    K_{pa2} = plant-air partition coefficient for air to above-ground plant parts for particulate-bound contaminants (m³/kg wet weight).

The air concentration of particulate-bound contaminant is calculated (EPA 1991) as:

$$EC_{par} = \frac{EC_{soil}}{PEF}$$

where:

   EC_{par} = air concentration of particulate-bound contaminant ($\mu g/m^3$ or pCi/m^3)
   EC_{soil} = concentration in surface soil (top ~1 cm) ($\mu g/kg$ or pCi/kg dry)
   PEF = the particulate emission factor (m^3/kg).

Furthermore, PEF is calculated from the following expression (EPA 1991):

$$PEF = \frac{LS \times V \times DH \times 3600}{A} \times 1000 \Bigg/ \left[Rf \times (1-G) \times \left(\frac{U_m}{U_t}\right)^3 \times F(x) \right]$$

where:

   LS = length of side of contaminated area (m)
   V = wind speed in mixing zone (m/s)
   A = contaminated area (m2)
   3600 is a conversion with units sec/hr
   1000 is a conversion with units g/kg
   Dh = diffusion height (m)
   PEF = the particulate emission factor (m3/kg)
   Rf = respirable fraction (g/m2-hr)
   G = fraction of vegetative cover (unitless)
   U_m = mean annual wind speed (m/s)
   U_t = erosion threshold wind speed at 10 m (m/s)
   F(x) = Cowherd function (Cowherd et al. 1985) (unitless).

The erosion threshold wind speed is calculated (Cowherd et al. 1985) from:

$$U_t = 2.5 \times TFV \times \ln\left(\frac{10}{SRH}\right)$$

where:

   TFV = the threshold friction velocity (m/s)
   SRH = surface roughness height (m)
   10 is a modeling factor with units of meters.

Furthermore, TFV is calculated from a regression model (Cowherd et al. 1985) using the following equation:

$$TFV = NECF \times \left(\frac{64 + 0.0055 \times APSD \times 1000}{100}\right)$$

where:
   NECF = nonerodible elements correction factor (unitless)
   APSD = the aggregate particle size distribution (mm)
   1000 converts from mm to m.

4.1.1.1.5   Total Plant Burden

The total plant burden can be expressed either as an internal burden or the burden as eaten by herbivores. The internal plant burden (assuming that none of the adsorbed contaminant enters the plant) is calculated from the following expression:

$$C_{pai} = C_{pav} + C_{pau}$$

where:
   C_{pai} = equilibrium tissue concentration of contaminants (µg/kg or pCi/kg tissue)
   C_{pav} = equilibrium concentration in above-ground plant parts from vapor uptake (µg/kg or pCi/kg wet)
   C_{pau} = equilibrium concentration in above-ground plant parts from root uptake (µg/kg or pCi/kg wet).

The total plant burden as eaten by herbivores is calculated from the following expression:

$$C_{pat} = C_{par} + C_{pap} + C_{pai}$$

where:
   C_{pat} = equilibrium concentration of contaminants in and on plant tissue (µg/kg or pCi/kg tissue)
   C_{par} = equilibrium concentration in above-ground plant parts from rain splash (µg/kg or pCi/kg wet)
   C_{pap} = equilibrium concentration in above-ground plant parts from particulate adsorption (µg/kg or pCi/kg wet)
   C_{pai} = equilibrium tissue concentration of contaminants (µg/kg or pCi/kg tissue).

4.1.1.2   Terrestrial Animals

The body burden for terrestrial animals can come from any combination of dermal contact, ingestion, and inhalation. The equations for these exposure routes are provided in this section.

4.1.1.2.1   Dermal Contact with Soil

The equilibrium contaminant body burden in a terrestrial animal species from dermal contact with soil is calculated from the following equation (modified from Hope [1995]):

$$C_{dersi} = D_{dersi} / K_{ei}$$

where:

C_{dersi} =   equilibrium contaminant body burden in species i from dermal contact with soil (µg/kg or pCi/kg body weight)

D_{dersi} =   absorbed daily dose for species i from dermal contact with soil (µg/kg/day or pCi/kg/day)

K_{ei} =   contaminant-specific depuration rate for species i (1/day).

The absorbed daily dose for species i from dermal contact with soil is calculated using the following equation (modified from EPA [1991]):

$$D_{dersi} = EC_{soil} \times SA_i \times P_{csi} \times S_{ai} \times CF \times \alpha_{dci} \times \theta_i \times \psi_i / W_i$$

where:

D_{dersi} =   absorbed daily dose for species i from dermal contact with soil (µg/kg/day or pCi/kg/day)

SA_i =   surface area of species i (cm^2)

P_{csi} =   fraction of surface area of species i in contact with soil per day (1/day)

S_{ai} =   skin adherence factor for species i (mg/cm^2)

EC_{soil} =   concentration in surface soil (top ~1 cm) (µg/kg or pCi/kg dry)

CF   =   Conversion factor (10^{-6} kg/mg)

α_{dci} =   contaminant-specific dermal absorption factor for species i (unitless)

W_i =   body weight of species i (kg wet weight)

θ_i =   area use factor for species i (ratio of contaminant area to home range - unitless)

ψ_i =   seasonality factor for species i (fraction of year spent at the contaminated site – unitless).

The surface area for bird species is calculated from a regression equation (EPA 1993) as:

$$SA_i = 10 \times (1000 \times W_i)^{0.667}$$

where:

SA_i =   surface area of bird species i (cm^2)

W_i =   body weight of species i (kg wet weight).

The surface area for other mammal species is calculated from a regression equation (EPA 1993) as:

$$SA_i = 12.3 \times (1000 \times W_i)^{0.65}$$

where:

SA_i =   surface area of mammal species i (cm2)

W_i =   body weight of species i (kg wet weight).

4.1.1.2.2   Dermal Contact with Water

The equilibrium contaminant body burden in a species from dermal contact with water is calculated from the following equation (Hope 1995):

$$C_{derwi} = D_{derwi} / K_{ei}$$

where:

C_{derwi} = equilibrium contaminant body burden for species i from dermal contact with water (µg/kg or pCi/kg body weight)

D_{derwi} = absorbed daily dose for species i from dermal contact with water (µg/kg/day or pCi/kg/day)

K_{ei} = contaminant-specific depuration rate for species i (1/day).

Furthermore, the value for D_{derwi} is calculated from the following equation (modified from EPA [1991] to include use and seasonality factors):

$$D_{derwi} = EC_{surface} \times SA_i \times P_{cwi} \times ET_{wi} \times CF \times K_{pi} \times \theta_i \times \psi_i / W_i$$

where:

SA_i = surface area of species i (cm^2)

P_{cwi} = fraction of surface area of species i available for contact with water (unitless)

ET_{wi} = average exposure time to water per day for species i (hr/day)

$EC_{surface}$ = concentration in surface water (µg/L or pCi/L)

CF = volumetric conversion factor for water (1 L/1,000 cm^3)

K_{pi} = contaminant-specific dermal absorption factor for species i from water (cm/hr)

W_i = body weight of species i (kg wet weight)

θ_i = area use factor for species i (ratio of contaminant area to home range – unitless)

ψ_i = seasonality factor for species i (fraction of year spent at the contaminated site – unitless).

4.1.1.2.3   Total Dermal Dose

The equilibrium body burden from dermal exposure is calculated from the equation:

$$C_{deri} = C_{dersi} + C_{derwi}$$

where:

C_{deri} = body burden from dermal exposure for species i (µg/kg or pCi/kg body weight)

C_{dersi} = body burden in species i from dermal contact with soil (µg/kg or pCi/kg body weight)

C_{derwi} = body burden for species i from dermal contact with water (µg/kg or pCi/kg body weight).

The total daily dermal absorbed dose is calculated from the equation:

$$D_{derti} = D_{dersi} + D_{derwi}$$

where:

D_{derti} = total daily dermal absorbed dose for species i (µg/kg/day or pCi/kg body weight/day)

D_{dersi} = absorbed daily dose for species i from dermal contact with soil (µg/kg/day or pCi/kg/day)

D_{derwi} = absorbed daily dose for species i from dermal contact with water (µg/kg/day or pCi/kg/day).

4.1.1.2.4   Inhalation of Vapor

The equilibrium contaminant body burden for species i from inhalation of vapor is calculated from the following equation (Hope 1995):

$$C_{ivi} = D_{ivi} \times \left(\frac{\alpha_{vapi}}{K_{ei}} \right)$$

where:

C_{ivi} = body burden for species i from inhalation of vapor (µg/kg or pCi/kg)

D_{ivi} = applied daily dose to species i from vapor inhalation (µg/kg/day or pCi/kg/day)

α_{vapi} = inhalation absorption factor for species i (unitless)

K_{ei} = contaminant-specific depuration rate for species i (1/day).

The applied daily dose to species i from vapor inhalation is calculated from the following equation (modified from Hope [1995] using EPA [1993] calculation for EC_{vap} as above):

$$D_{ivi} = \left[\frac{\left(EC_{vap} \times IR_i \right)}{W_i} \right] \times \theta_i \times \psi_i$$

where:

D_{ivi} = applied daily dose to species i from vapor inhalation (µg/kg/day or pCi/kg/day)

IR_i = resting inhalation rate of species i (m^3/day)

EC_{vap} = concentration of gas-phase contaminant (µg/m^3 or pCi/m^3)

W_i = body weight of species i (kg wet weight)

θ_i = area use factor for species i (ratio of contaminant area to home range – unitless)

ψ_i = seasonality factor for species i (fraction of year spent at the contaminated site – unitless).

4.1.1.2.5   Inhalation of Particulates

The equilibrium contaminant body burden for species i from inhalation of particulates is calculated from the following equation (Hope 1995):

$$C_{ipi} = D_{ipi} \times \left(\frac{\alpha_{pari}}{K_{ei}} \right)$$

where:

C_{ipi} = body burden for species i from inhalation of particulates (µg/kg or pCi/kg)

D_{ipi} = applied daily dose to species i from particulate inhalation (µg/kg/day or pCi/kg/day)

α_{pari} = inhalation particulate absorption factor (unitless)

K_{ei} = contaminant-specific depuration rate for species i (1/day).

The applied daily dose to species i from particulate inhalation is calculated as (modified from Hope [1995] using EPA [1993] calculation for EC_{vap} as above):

$$D_{ipi} = \left[\frac{\left(EC_{par} \times IR_i \right)}{W_i} \right] \times \theta_i \times \psi_i$$

where:

D_{ipi} = applied daily dose to species i from particulate inhalation (µg/kg/day or pCi/kg/day)

IR_i = resting inhalation rate of species i (m³/day)

EC_{par} = air concentration of particulate-bound contaminant (µg/m³ or pCi/m³)

W_i = body weight of species i (kg wet weight)

θ_i = area use factor for species i (ratio of contaminant area to home range – unitless)

ψ_i = seasonality factor for species i (fraction of year spent at the contaminated site – unitless).

4.1.1.2.6   Total Inhalation Dose

The total equilibrium burden from inhalation for species i is calculated as:

$$C_{inhi} = C_{ivi} + C_{ipi}$$

where:

C_{inhi} = body burden from inhalation for species i (µg/kg or pCi/kg body weight)

C_{ivi} = body burden for species i from inhalation of vapor (µg/kg or pCi/kg)

C_{ipi} = body burden for species i from inhalation of particulates (µg/kg or pCi/kg).

The total inhalation applied dose for species i is calculated as:

$$D_{inhi} = D_{ivi} + D_{ipi}$$

where:

D_{inhi} = total inhalation applied dose for species i (µg/kg or pCi/kg body weight/day)

D_{ivi} = applied daily dose to species i from vapor inhalation (µg/kg/day or pCi/kg/day)

D_{ipi} = applied daily dose to species i from particulate inhalation (µg/kg/day or pCi/kg/day).

4.1.1.2.7 *Ingestion of Water*

The equilibrium contaminant body burden for species i from ingestion of water is calculated from the following expression:

$$C_{ingwi} = D_{ingwi} \times \left(\frac{\alpha_{ingi}}{K_{ei}} \right)$$

where:

C_{ingwi} = body burden for species i from ingestion of water (µg/kg or pCi/kg)
D_{ingwi} = applied daily dose to species i from water ingestion (µg/kg/day or pCi/kg/day)
α_{ingi} = ingestion absorption factor for species i (unitless)
K_{ei} = contaminant-specific depuration rate for species i (1/day).

The applied daily dose to species i from water ingestion is calculated from the equation (modified from EPA [1993] to incorporate site use fractions):

$$D_{ingwi} = \left[\frac{(EC_{surface} \times WI_i)}{W_i} \right] \times \theta_i \times \psi_i$$

where:

D_{ingwi} = applied daily dose to species i from water ingestion (µg/kg/day or pCi/kg/day)
WI_i = water ingestion rate of species i (L/day)
$EC_{surface}$ = concentration in surface water (µg/L or pCi/L)
W_i = body weight of species i (kg wet weight)
θ_i = area use factor for species i (ratio of contaminant area to home range – unitless)
ψ_i = seasonality factor for species i (fraction of year spent at the contaminated site – unitless).

4.1.1.2.8 *Ingestion of Soil*

The contaminant body burden to species i from ingestion of soil is calculated from the equation (modified from Hope [1995]):

$$C_{ingsi} = D_{ingsi} \times \left(\frac{\alpha_{ingi}}{K_{ei}} \right)$$

where:

C_{ingsi} = contaminant body burden to species i from ingestion of soil (µg/kg or pCi/kg body weight)
D_{ingsi} = applied daily dose to species i from soil ingestion (µg/kg/day or pCi/kg/day)
K_{ei} = contaminant-specific depuration rate for species i (1/day).

The applied daily dose to species i from soil ingestion is calculated from the equation (modified from EPA [1993] to incorporate site use fractions):

$$D_{ingsi} = EC_{soil} \times SI_i \times NIR_{totali} \times F_{dwi} \times \theta_i \times \psi_i$$

where:

D_{ingsi} = applied daily dose to species i from soil ingestion (µg/kg/day or pCi/kg/day)

SI_i = soil ingestion rate of species i (kg soil ingested/kg dry diet)

NIR_{totali} = total normalized ingestion rate for species i (kg prey wet weight/kg predator body weight/day)

EC_{soil} = concentration in soil (µg/kg or pCi/kg)

F_{dwi} = conversion factor, dry diet to wet diet for species i (kg dry/kg wet)

θ_i = area use factor for species i (ratio of contaminant area to home range – unitless)

ψ_i = seasonality factor for species i (fraction of year spent at the contaminated site – unitless).

The total normalized ingestion rate for species i is calculated from the equation (EPA 1993):

$$NIR_{totali} = \frac{FMR_i}{W_i \times \sum_{j \neq i} \left(P_{ij} \times ME_j \right)}$$

where:

NIR_{totali} = total normalized ingestion rate for species i (kg prey wet weight/kg predator body weight/day)

FMR_i = free-living metabolic rate of predator (kcal/day)

P_{ij} = wet weight or volume fraction of i's diet consisting of prey j (unitless)

ME_j = metabolizable energy from prey j (kcal/kg prey wet wt)

W_i = body weight of species i (kg wet weight).

The free-living metabolic rate of predator birds is calculated from (EPA 1993):

$$FMR_i = 3.12 \times \left(1000 \times W_i \right)^{0.605}$$

The free-living metabolic rate of predator rodents is calculated from (EPA 1993):

$$FMR_i = 2.514 \times \left(1000 \times W_i \right)^{0.507}$$

The metabolizable energy from prey j is calculated from (EPA 1993):

$$ME_j = GE_j \times AE_j$$

where:

ME_j = metabolizable energy from prey j (kcal/kg prey wet wt)

GE_j = gross energy from prey j (kcal/kg wet weight)

AE_j = assimilation efficiency of prey j (unitless).

4.1.1.2.9 Ingestion of Food

The equilibrium body burden for species i from ingestion of food is calculated (from Hope [1995]) as:

$$C_{ingfi} = D_{ingfi} \times \left(\frac{\alpha_{ingi}}{K_{ei}} \right)$$

where:

C_{ingfi} = equilibrium body burden for species i from ingestion of food (µg/kg or pCi/kg body weight)

D_{ingfi} = applied daily dose to species i from food ingestion (µg/kg/day or pCi/kg/day)

K_{ei} = contaminant-specific depuration rate for species i (1/day).

The applied daily dose to species i from food ingestion is calculated from the equation (modified from Hope [1995] using EPA [1993]):

$$D_{ingfi} = \theta_i \times \psi_i \times \sum_j \left(C_j \times NIR_j \right)$$

where:

D_{ingfi} = applied daily dose to species i from food ingestion (µg/kg/day or pCi/kg/day)

C_j = average contaminant concentration in jth food item (µg/kg or pCi/kg wet weight)

NIR_j = normalized ingestion rate of jth food type on a wet-weight basis (kg prey/kg body weight predator/day)

θ_i = area use factor for species i (ratio of contaminant area to home range – unitless)

ψ_i = seasonality factor for species i (fraction of year spent at the contaminated site – unitless).

The normalized ingestion rate of jth food type on a wet-weight basis is calculated from (EPA 1993) as:

$$NIR_j = P_{ij} \times NIR_{totali}$$

where:

NIR_j = normalized ingestion rate of jth food type on a wet-weight basis (kg prey/kg body weight predator/day)

P_{ij} = wet weight or volume fraction of i's diet consisting of prey j (unitless)

NIR_{totali} = total normalized ingestion rate for species i (kg prey wet weight/kg predator body weight/day).

4.1.1.2.10 Total Ingestion Dose

The applied daily dose for species i from ingestion is calculated from the equation:

$$D_{ingi} = D_{ingfi} + D_{ingsi} + D_{ingwi}$$

where:

    D_{ingi} = applied daily dose for species i from ingestion (µg/kg/day or pCi/kg/day)

    D_{ingfi} = applied daily dose to species i from food ingestion (µg/kg/day or pCi/kg/day)

    D_{ingsi} = applied daily dose to species i from soil ingestion (µg/kg/day or pCi/kg/day)

    D_{ingwi} = applied daily dose to species i from water ingestion (µg/kg/day or pCi/kg/day).

The equilibrium body burden for species i from ingestion is calculated from the equation:

$$C_i = C_{ingfi} + C_{ingsi} + C_{ingwi} + C_{inhi} + C_{deri}$$

where:

    C_i = body burden for species i from ingestion (µg/kg or pCi/kg)

    C_{ingfi} = body burden for species i from ingestion of food (µg/kg or pCi/kg body weight)

    C_{ingsi} = body burden to species i from ingestion of soil (µg/kg or pCi/kg body weight)

    C_{ingwi} = body burden for species i from ingestion of water (µg/kg or pCi/kg)

    C_{inhi} = body burden from inhalation for species i (µg/kg or pCi/kg body weight)

    C_{deri} = body burden from dermal exposure for species i (µg/kg or pCi/kg body weight).

4.1.2   Water-Respiring/Transpiring Species

The basic models used in the risk assessment model to estimate exposures of aquatic organisms to metal or organic contaminants in sediments, pore water, surface water, and the subsequent transfer through the food chain consist of mass-balance equilibrium models originally derived by Thomann (1989) and Thomann et al. (1992, 1995). The basic equilibrium models presented in those papers were further modified by the authors to provide a system of equations generally applicable when only sediment data are available. The essential assumption used in that modification is that the aquatic system is not depurating contaminants, such that the three abiotic compartments (sediment, pore water, and surface water) are in static equilibrium (Thomann et al. 1992). This assumption may only be valid for large lacustrine systems; clearly, it is invalid for streams. However, the basic models may be used directly with only minor modification to address these more dynamic systems.

4.1.2.1   Body Burden for Aquatic Animals

The body burden in a predator species i, V_i, is calculated from direct exposure to contaminated water, ingestion of contaminated prey, and ingestion of contaminated sediment, using the following equation:

$$V_i = \left[BCF_{i,c} \times (b_{pore} \times EC_{pore} + [1 - b_{pore}] \times EC_{surf}) \right] + \left[\frac{\sum_{j \neq i} \left(P_{ij} \times \alpha_{ij} \times I_{ij} \times V_j \right)}{K_i + G_i} \right] +$$

$$\left[EC_{sed} \times SD_i \times \alpha_{i,sed} \times \left(\frac{\sum_{j \neq i} \left(P_{ij} \times I_{ij} \right)}{K_i + G_i} \right) \right]$$

where:

V_i = body burden in predator species i (metals: μg/kg or pCi/kg dry weight [Thomann et al. 1995]; organics: μg/g lipid [Thomann et al. 1992])

$BCF_{i,c}$ = bioconcentration factor for species i and contaminant c (L/kg lipid for organics, L/kg dry weight for inorganics)

b_{pore} = relative exposure to pore water (unitless)

EC_{pore} = contaminant concentration in pore water (μg/L or pCi/L)

EC_{surf} = contaminant concentration in surface water (μg/L or pCi/L)

EC_{sed} = contaminant concentration in sediment (μg/kg or pCi/kg)

P_{ij} = preference for consumption of food item j (unitless)

α_{ij} = chemical assimilation efficiency for contaminant consumed along with prey j (g contaminant assimilated/g contaminant ingested)

$\alpha_{i,sed}$ = chemical assimilation efficiency for contaminant consumed along with sediment (g contaminant assimilated/g contaminant ingested)

I_{ij} = feeding rate of species i on prey item j (organic model: g prey lipid/g predator lipid/day, metal model: g prey dry weight/g predator dry weight/day)

SD_i = feeding rate of species i on sediment as a fraction of total diet intake (kg sediment dry weight/kg prey dry weight/day)

V_j = body burden in prey species j (metals: μg/kg or pCi/kg dry weight [Thomann et al. 1995]; organics: μg/g lipid [Thomann et al. 1992]) or in sediment (metals: μg dry sediment [Thomann et al. 1995]; organics: μg/g organic carbon [Thomann et al. 1992])

K_i = loss rate of contaminant for species i, including depuration and metabolism (1/day)

G_i = growth rate of species i (1/day).

The loss rate of contaminant for species i, including depuration and metabolism, for organic contaminants is calculated from the equation (Thomann 1989):

$$K_i = \left[k_{ui,c} \middle/ \left(\frac{K_{ow}}{1000} \right) \right] + K_{mi}$$

where:

K_i is the loss rate of contaminant for species i, including depuration and metabolism (1/day)

$k_{ui,}$ is the contaminant uptake from dissolved sources for species i for contaminant c (metals: L/g dry weight/day [Thomann et al. 1995]; organics: L/g lipid/day [Thomann et al. 1992])

K_{ow} is the octanol-water partition coefficient (unitless)

K_{mi} is the chemical loss rate in species i due to metabolism and fecal loss (1/day) 1000 represents the conversion factor of 1000 grams per liter of water.

The contaminant uptake from dissolved sources for species i for organic contaminants is calculated from the equation (Thomann 1989):

$$k_{ui,c} = \frac{2.67 \times f_{oci} \times \rho_i \times E_c}{awd_i \times C_0 \times f_{Li}}$$

where:

$k_{ui,c}$ = contaminant uptake from dissolved sources for species i for contaminant c (L/kg lipid/day)

f_{oci} = fraction organic carbon in species i (g organic carbon/g dry weight)

ρ_i = oxygen respiration rate for species i (g O_2/g lipid/day)

E_c = chemical transfer efficiency (unitless)

awd_i = wet-to-dry weight ratio for species i (g wet/g dry)

C_0 = oxygen concentration in the river (mg/L)

f_{Li} = fraction lipid in species i (g lipid/g wet) 2.67 grams of oxygen per gram of carbon.

This equation is not used in the model for metal uptake; instead, the BCF relationship is used and BCFs are obtained from the literature.

The growth rate of species i is given by the regression equation (Thomann et al. 1992):

$$G_i = \delta \times w_i^{-\beta}$$

where δ and β are regression parameters and w_i is the body weight of species i (kg wet weight) (modifier WBMASS on the SPECIE keyword, Section 2.2.11).

The feeding rate of species i on biotic prey item j for organic contaminants is calculated from the following equation (Thomann et al. 1992):

$$I_{ij} = \left(\frac{G_i + \rho_i}{a_i} \right) \times \left(\frac{awd_j}{awd_i} \right) \times \left(\frac{f_{Lj}}{f_{Li}} \right) \times \left(\frac{f_{oci}}{f_{ocj}} \right)$$

where:

I_{ij} = feeding rate of species i on prey item j (organic model: g prey lipid/g predator lipid/day)

G_i = growth rate of species i (1/day)

ρ_i = oxygen respiration rate for species i (1/day)

a_i = organic carbon assimilation rate for species i (g organic carbon assimilated/g organic carbon ingested)

awd_i = wet-to-dry weight ratio for species i (g wet/g dry)

f_{Li} = fraction lipid in species i (g lipid/g wet)

f_{oci} = fraction organic carbon in species i (g organic carbon/g dry weight).

The oxygen respiration rate for species i is calculated from the equation:

$$\rho_i = \phi \times w_i^{-\gamma}$$

where ϕ and γ are regression parameters (Thomann 1989) and w_i is the body weight of species i (kg wet weight) (modifier WBMASS on the SPECIE keyword, Section 2.2.11).

The bioconcentration factor for species i and organic contaminant c is calculated from the equation:

$$BCF_{i,c} = \frac{k_{ui,c}}{K_i + G_i}$$

where:

$BCF_{i,c}$ = bioconcentration factor for species i for contaminant c (L/kg lipid)

$k_{ui,c}$ = contaminant uptake from dissolved sources for species i (L/g lipid/day)

K_i = loss rate of contaminant for species i, including depuration and metabolism (1/day)

G_i = growth rate of species i (1/day).

The equation for I_{ij} for organic contaminants returns values with units of (g prey lipid/g predator lipid/day). The equivalent units for the metal uptake model of Thomann et al. (1995) are (g prey dry weight/ g predator dry weight/day). For the purposes of evaluating metal uptake in aquatic systems, the following conversion was applied to produce consumption rates in the correct units for the feeding rate of species i on biotic prey item j for metallic contaminants:

$$I_{metalij} = I_{ij} \times \left(\frac{awd_i}{awd_j}\right) \times \left(\frac{f_{Li}}{f_{Lj}}\right) = \left(\frac{G_i + \rho_i}{a_i}\right) \times \left(\frac{f_{oci}}{f_{ocj}}\right)$$

where:

$I_{metalij}$ = feeding rate of species i on prey item j (metals model: g prey dry weight/ g predator dry weight/day)

I_{ij} = feeding rate of species i on prey item j (organic model: g prey lipid/g predator lipid/day)

awd_i = wet-to-dry weight ratio for species i (g wet/g dry)

f_{Li} = fraction lipid in species i (g lipid/g wet)

G_i = growth rate of species i (1/day)

ρ_i = oxygen respiration rate for species i (1/day)

a_i = organic carbon assimilation rate for species i (g organic carbon assimilated/g organic carbon ingested)

f_{oci} = fraction organic carbon in species i (g organic carbon/g dry weight).

4.1.2.2 Body Burden for Aquatic Plants

The body burden for aquatic plant species i, V_i, is calculated from the following equation:

$$V_i = k_{ui,c}(b_{pore} \times EC_{pore} + [1 - b_{pore}] \times EC_{surface})$$

where:

V_i = body burden in aquatic plant species i (metals: µg/kg or pCi/kg dry weight [Thomann et al. 1995]; organics: µg/kg lipid [Thomann et al. 1992])

$k_{ui,c}$ = contaminant uptake from dissolved contaminant c for species i (metals: L/kg dry weight [Thomann et al. 1995]; organics: L/kg lipid [Thomann et al. 1992])

b_{pore} = relative exposure to pore water (unitless)

EC_{pore} = contaminant concentration in pore water (µg/L or pCi/L)

$EC_{surface}$ = contaminant concentration in surface water (µg/L or pCi/L).

4.1.2.3 Body Burden as Consumed

The equilibrium body burden for species i from ingestion of metals is calculated from the equation:

$$C_i = V_i / awd_i$$

where:

C_i	=	body burden for species i from ingestion (µg/kg or pCi/kg)
V_i	=	body burden in predator species i (metals: µg/kg or pCi/kg dry weight; organics: µg/kg lipid)
awd_i	=	wet-to-dry weight ratio for species i (g wet/g dry).

The equilibrium body burden for species i from ingestion of organics is calculated from the equation:

$$C_i = 1000 \times V_i \times f_{Li}$$

where:

C_i	=	equilibrium body burden for species i from ingestion (µg/kg or pCi/kg)
V_i	=	body burden in predator species i (metals: µg/kg or pCi/kg dry weight; organics: µg/kg lipid)
f_{Li}	=	fraction lipid in species i (g lipid/g wet) 1000 converts from kilograms to grams

1000 converts from kilograms to grams.

4.1.2.4 Intake of Contaminants from Sediment Ingestion

Thomann et al. (1992, 1995) estimate sediment ingestion as a purposeful portion of the organism's diet (i.e., the organism searches for and consumes the sediment as a carbon source for food). This is a valid assumption for species that consume sediment as the primary portion of their diet. However, sediment intake can be more reasonably viewed as an incidental result of feeding on benthic organisms or plankton. Using this assumption, sediment intake can be expressed as (Thomann et al. 1992):

$$BAF_{ised} = \frac{P_{ised} \times \alpha_{ised} + \sum_{j \neq i} \left(P_{ij} \times \alpha_{ij} \times I_{ij} \right)}{K_i + G_i}$$

where:

BAF_{ised}	=	sediment-to-predator bioaccumulation factor (day - g contaminant assimilated/g contaminant ingested)
P_{ised}	=	preference for consumption of sediment (unitless)
α_{ised}	=	chemical assimilation efficiency for contaminant consumed along with sediment (g contaminant assimilated/g contaminant ingested)
P_{ij}	=	preference for consumption of food item j, including sediment as a separate prey item (unitless)
α_{ij}	=	chemical assimilation efficiency for contaminant consumed along with prey j (g contaminant assimilated/g contaminant ingested)

I_{ij} =   feeding rate of species i on prey item j (organic model: g prey lipid/g predator lipid/day, metal model: g prey dry weight/g predator dry weight/day) or on sediment (organic model: g organic carbon ingested/g predator lipid/day, metal model: g sediment dry weight/g predator dry weight/day)

K_i =   loss rate of contaminant for species i, including depuration and metabolism (1/day)

G_i =   growth rate of species i (1/day).

4.1.2.5   Tissue Benchmark Concentration

The tissue benchmark calculation allows comparison of a body burden to a benchmark threshold. This value is calculated differently for organic and nonorganic analytes.

The tissue benchmark value for both plant and animal aquatic species for organic contaminants is calculated from the following equation:

$$TB_i = 1000 \times V_i \times f_{Li} / BM_i$$

where:

TB_i is the calculated tissue benchmark value for species i (unitless)

V_i is the body burden in predator species i (μg/g lipid or pCi/kg lipid)

f_{Li} is the fraction lipid in species i (g lipid/g wet)

BM_i is the benchmark level for species i (μg/kg lipid or pCi/kg lipid) 1000 is the conversion from kilograms to grams

1000 is the conversion from kilograms to grams.

The tissue benchmark value for both plant and animal aquatic species for nonorganic contaminants is calculated from the following equation:

$$TB_i = \frac{V_i}{BM_i \times awd_i}$$

where:

TB_i is the calculated tissue benchmark value for species i (unitless)

V_i is the body burden in predator species i (μg/kg wet or pCi/kg wet)

awd_i is the wet-to-dry weight ratio for species i (g wet/g dry)

BM_i is the benchmark level for species i (μg /kg or pCi/kg lipid).

4.1.3   Radiological Dose Estimation

The exposure equations return estimates of ingestion exposure to radiological contaminants in units of pCi/kg body mass/day (i.e., in units of radioactive decay rate density). However, radiological effects result from radioactive energy density absorbed by a body in a unit of time, which is usually expressed in units of rads/day. Consequently, decay rates must be converted to energy equivalents. Similarly, an organism can receive external energy from radioactive decay occurring in the abiotic media (air, water, or soil).

4.1.3.1 Internal Dose

The internal total-body dose rate to an organism is the sum of the individual dose rates from each radionuclide in the body. The equation is written as follows:

$$R_{i,int} = \sum_c \left(C_{i,c} \times E_{i,c} \right)$$

where:

$R_{i,int}$	=	radiological dose to organism i from internal radioactive decay (rad/day)
$C_{i,c}$	=	specific body burden of nuclide c in organism i (pCi/kg)
$E_{i,c}$	=	effective absorbed energy rate for nuclide c per unit activity in organism i (kg rad/ pCi/day).

Doses are summed across all radionuclides. As shown in Baker and Soldat (1992), the effective absorbed energy rate for nuclide c per unit activity in organism I can be calculated from the following equation:

$$E_{i,c} = 1 \; Ci/10^{12} \; pCi \times 3.7^{10} \; disintegrations/sec/Ci \times 86,400 \; sec/day \times 1.602^{-11} \; kg \; rad/MeV \times \varepsilon_{i,c}$$

$$E_{i,c} = 5.12^{-8} \times \varepsilon_{i,c}$$

where:

$E_{i,c}$	=	effective absorbed energy rate for nuclide c per unit activity in organism i (kg rad/ pCi/day)
$\varepsilon_{i,c}$	=	is the effective absorbed energy (MeV/disintegration).

4.1.3.2 External Dose

4.1.3.2.1 External Dose from Water Immersion for Aquatic Organisms

The external radiological dose to aquatic organism i from exposure to radioactive decay in water is calculated using the equation:

$$R_{i,imm} = \sum_c \left[(b_{pore} \times EC_{pore,c} + (1 - b_{pore}) \times EC_{surface,c}) \times DF_{imm,c} \times CF_{imm,q} \right]$$

where the sum extends over all radiological contaminants (with index c):

$R_{i,imm}$	=	external radiological dose to organism i from exposure to radioactive decay in water (rad/day)
b_{pore}	=	relative exposure to pore water (unitless)
$EC_{pore,c}$	=	contaminant concentration in pore water for nuclide c (pCi/L)
$b_{surface}$	=	relative exposure to surface water ($b_{surface} = 1 - b_{pore}$) (unitless)
$EC_{surface,c}$	=	contaminant concentration in surface water for nuclide c (pCi/L)
$DF_{imm,c}$	=	water immersion dose factor for nuclide c (mrad/year per pCi/m^3)

$CF_{imm,q}$ = 2.737851×10^{-9} (conversion factor: from (mrad m^3)/(L year) to rad/day).

4.1.3.2.2 External Dose from Water Immersion for Terrestrial Organisms

The external radiological dose to terrestrial organism i from exposure to radioactive decay in water is calculated using the equation:

$$R_{i,imm} = \sum_c \left[EC_{surface,c} \times DF_{imm,c} \times ET_{water,i} \times CF_{imm,t} \right]$$

where the sum extends over all radiological contaminants (with index c):

$R_{i,imm}$ = external radiological dose to organism i from exposure to radioactive decay in water (rad/day)

$EC_{surface,c}$ = contaminant concentration in surface water for nuclide c (pCi/L)

$DF_{imm,c}$ = water immersion dose factor for nuclide c (mrad/year per pCi/m^3)

$ET_{water,i}$ = exposure time of organism i to the water (hour/day)

$CF_{imm,t}$ = 1.140771×10^{-10} (conversion factor: from (mrad m^3)/(L year) to rad/day).

4.1.3.2.3 External Dose from Contact with Sediment for Aquatic Organisms

External dose received from contact with sediment is calculated for aquatic species as the combination of external dose received above the sediment and below the sediment. The equations (Eckerman and Ryman 1993) are:

$$RAbove_{i,sed} = \sum_c \left[EC_{sed,c} \times (1 - b_{pore}) \times DF_{sed,c} \times CF_{elev} \times CF_{above} \right]$$

$$RBelow_{i,sed} = \sum_c \left[EC_{sed,c} \times (1 - b_{pore}) \times DF_{sed,c} \times \gamma_c \times CF_{below} \right]$$

$$R_{i,sed} = RAbove_{i,sed} + RBelow_{i,sed}$$

where the sum extends over all radiological contaminants (with index c):

$R_{i,sed}$ = external radiological dose to organism i from exposure to radioactive decay in sediment (rad/day)

$EC_{sed,c}$ = contaminant concentration in sediment for nuclide c (pCi/kg)

b_{pore} = relative exposure to pore water (unitless)

$DF_{sed,c}$ = sediment dose factor for nuclide c (mrad m^2/pCi/year)

$F_{sed,i}$ = fractional exposure of organism i to the sediment (unitless)

CF_{elev} = 2 if $b_{pore} < 0.5$ or 1 if $b_{pore} >= 0.5$

CF_{above} = conversion factor applicable above the sediment = $0.7^X 5.12^{14 \, X} 1.0^{-6}$ to yield rad kg doses

CF_{below} = conversion factor applicable below the sediment = $1.05^X 5.12^{-2 \, X} 1.0^{-6}$ to yield rad kg doses

γ_c = gamma energy for nuclide c (MeV/disintegration).

4.1.3.2.4 External Dose from Contact with Sediment for Terrestrial Organisms

The external dose received from contact with sediment is calculated for terrestrial species as the combination of external dose received above the sediment and below the sediment. The equations (Eckerman and Ryman 1993) are:

$$RAbove_{i,sed} = \sum_c \left[EC_{sed,c} \times F_{above} \times DF_{sed,c} \times CF_{elev,i} \times CF_{above} \right]$$

$$RBelow_{i,sed} = \sum_c \left[EC_{sed,c} \times (1 - F_{above,i}) \times DF_{sed,c} \times \gamma_c \times CF_{below} \right]$$

$$R_{i,sed} = RAbove_{i,sed} + RBelow_{i,sed}$$

where the sum extends over all radiological contaminants (with index c):

- $R_{i,sed}$ = external radiological dose to organism i from exposure to radioactive decay in sediment (rad/day)
- $EC_{sed,c}$ = contaminant concentration in sediment for nuclide c (pCi/kg)
- $F_{above,i}$ = fractional time for exposure of organism i above the sediment (unitless)
- $DF_{sed,c}$ = sediment dose factor for nuclide c (mrad m2/pCi/year)
- $CF_{elev,i}$ = 2 if Diffhti < 1 or 1 if Diffhti >= 1
- CF_{above} = conversion factor applicable above the sediment = $0.7^X 5.1214^X 1.0^{-6}$ to yield rad kg doses
- CF_{below} = conversion factor applicable below the sediment = $1.05^X 5.12^X 10^{-2 x} 1.0^{-6}$ to yield rad kg doses
- γ_c = gamma energy for nuclide c (MeV/disintegration).

4.1.3.3 Total Dose

Finally, total radiological dose is obtained by summing the above quantities:

$$R_{i,total} = \sum_c \left(R_{i,imm} + R_{i,sed} + R_{i,int} \right)$$

where the doses are summed across all radionuclides:

- $R_{i,imm}$ = external radiological dose to organism i from exposure to radioactive decay in water (rad/day)
- $R_{i,sed}$ = external radiological dose to organism i from exposure to radioactive decay in sediment (rad/day)
- $R_{i,int}$ = radiological dose to organism i from internal radioactive decay (rad/day).

4.2 Code Execution Environment

4.2.1 Location in the Processing Sequence

The Ecological Contaminant Exposure Model (ECEM) code requires access to a number of data files developed by the SAC inventory, release, and transport codes (Eslinger et al. 2002). In particular, every

code on the left side of Figure 1-2 must have been executed to build a suite of concentration data files before the ECEM code can be used to calculate impacts. These concentration data files must have been developed under the control of the same ESD keyword file that the ECEM code reads to determine processing options.

4.2.2   How the Code Is Invoked

ECEM can run under either the Windows or the Linux operating system. Under the Windows operating system (Releases 98, NT, or 2000), ECEM executes in a DOS box. A run of ECEM is initiated by entering the following command line:

```
ECEM "Keyfilename"
```

Under the Linux operating system, ECEM is executed through any of the following Bourne Shell or C Shell commands:

```
ecem.exe "Keyfilename"
```

For these commands, ECEM or ecem.exe is the name of the executable program and "Keyfilename" is the name of an ecological scenario keyword file. Both the name of the executable program and the keyword file may contain path information. If ECEM is invoked without entering the name of the keyword file, the code will prompt the user for the file name. The keyword file, which should be prepared using an editor that can handle ASCII files without leaving embedded control codes, contains text control information describing the run. If ECEM cannot open the keyword file, then the code will terminate execution after writing an error message to the standard output device.

4.2.3   Memory Requirements

The ECEM code uses dynamic memory allocation, so the memory requirements depend on the problem being analyzed. A reasonably large example run where the ECEM code required 2.54 MB of memory (on a Windows 2000 machine) used 10 analytes, 60 time steps, 11 realizations, and 168 locations. It is expected that most, if not all, of the runs of the ECEM code will require less than 4 MB of memory. This run took about 10 minutes to execute on a 933-megahertz system.

4.3   Data Files

The ECEM code reads four or more input files and writes up to five output files. The number of input files depends on the number of contaminants being analyzed. The number of output files depends on the options selected in the ECEM code. These files are described in the following sections.

4.3.1   Input Files

The input files for the ECEM code are keyword files and a suite of concentration data related files. One keyword file controls the case the ECEM code will execute, and it points to the ESD keyword file. The suite of concentration data files are all identified in the ESD keyword file – the user of the ECEM only needs to identify the ESD keyword file. The following are the input files:

- **ESD Keyword File:** The ESD keyword file contains the control information that the inventory and environmental transport codes use to generate concentration data files. Examples of keywords in the ESD file that control the impacts codes, including the ECEM code, are provided in Table 2.1. Definitions for these keywords are given in Section 2.2. Typically, the user of the ECEM code will not modify the ESD keyword file.
- **ECDA Concentration Files:** The ECDA files contain all the concentration data available for the impacts codes. The concentrations for all analytes are based on the same time and location data. There is a "map" file for the ECEM code containing indexing information for each of the concentration data files. In addition, there is a separate concentration data file for every analyte used in the impacts scenario. For example, when running a scenario with seven analytes, there will be one map file and seven concentration data files. The structure of a concentration data file is described in Section 2.3.1.
- **ECEM Keyword File:** The ECEM Keyword file controls the scenario to be analyzed by the ECEM code. The options and data available are constrained by the case defined in the ESD Keyword file. Section 4.4 describes the contents of the ECEM keyword file.

4.3.1.1 Keywords Required from the Environmental Settings File

The ECEM code also reads keywords from the environmental settings file. These keywords are read from a different file and can have a different definition from a keyword defined for internal use in the ECEM code. The environmental settings keywords are defined in Section 2.2. The following keywords are required:

- ANALYTE – definition of analytes in the environmental simulations
- SPECIE – definition of species for the ecological impacts calculations
- RADIUS – effective energy by organism radius
- END – end of the environmental settings keywords
- FILE – file names for the concentration file for each analyte
- LOCATION – locations at which concentrations were generated for the ecological impacts
- REALIZAT – number of realizations for which concentration data were generated for ecological impact calculations
- TIMES – times at which concentrations were generated for the ecological impacts
- TITLE – environmental simulation title.

4.3.1.2 ECEM Keyword File

The ECEM keyword definition file contains control information for the desired impact simulation. Individual keywords are defined in Section 4.4. Table 4.1 contains excerpted keywords for a run of ECEM using 7 realizations, 15 locations, 10 analytes and 57 ecological species. The complete file is 4400 lines long.

Table 4.1 Excerpted Records from an ECEM Keyword File

```
REPORT "Ecem.Rpt"
TITLE   "SAC Example Case - 7 Realizations"
USER    "Paul W. Eslinger"
```

```
SEED 445544
REALIZATIONS 7
EXECUTE
STATISTICS DOSRAD BURDEN CONCEN DOSING DOSINH DOSDER BMTISS SUMRAD
DETAILS    DOSRAD BURDEN CONCEN DOSING DOSINH DOSDER BMTISS SUMRAD
!
FILE ESD      "ESD_Initial.key"
FILE BURDEN   "ECEM.bur"
FILE STATISTI "ECEM_sta.Csv"
FILE HEADER   "ECEM.hdr"
FILE VALUES   "ECEM_Val.Csv"
FILE DETAILS  "ECEM_Det.Csv"
FILE THRESHOL "ECEM_Thres.Csv"
!
TIMES ECOLOGICAL
 1990 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000
GROWTH DELTA=0.002 BETA=0.25
RESPIRE PHI=0.032 GAMMA=0.2
!
VARIABLE COWHDFX=0.0497 EXPOSI=7.9E+8 GASCON=8.314
VARIABLE RFRAC=0.036 AREA=500.0 LENGTH=1000.0 TUPTAKE=0.9
! Node Definitions (Hanford Shore locations)
LOCATION PRIMARY="EL0050" SECOND="EL0049" OUTPUT
LOCATION PRIMARY="EL0102" SECOND="EL0101" OUTPUT
...
LOCATION PRIMARY="EL0618" SECOND="EL0617" OUTPUT
LOCATION PRIMARY="EL0666" SECOND="EL0665" OUTPUT
! Analyte definitions
ANALYTE ID="CCl4"   OUTPUT
ANALYTE ID="CrVI  " OUTPUT
ANALYTE ID="Pu239"  OUTPUT
ANALYTE ID="Cs137"  OUTPUT
ANALYTE ID="I129"   OUTPUT
ANALYTE ID="Sr90"   OUTPUT
ANALYTE ID="Tc99"   OUTPUT
ANALYTE ID="H3"     OUTPUT
ANALYTE ID="U238"   OUTPUT
ANALYTE ID="U"      OUTPUT
! Species Definition
SPECIE ID="AMCOOT"  !OUTPUT
SPECIE ID="AMKSTL"  !OUTPUT
SPECIE ID="AMWPEL"  !OUTPUT
...
SPECIE ID="WOTDTP"  !OUTPUT
SPECIE ID="WAQGS "  !OUTPUT
SPECIE ID="WSTRGN"  !OUTPUT
! Threshold limits for probability calculations
THRESHOLD TYPE="BURDEN" ANALYTE="H3"    SPECIE="MAYFLY" LIMIT1=10.0
LIMIT2=50.0
THRESHOLD TYPE="BURDEN" ANALYTE="Cs137"  SPECIE="HRVMSE" LIMIT1=0.1
LIMIT2=1.0
```

```
! Predation matrix (enter only after all of the species cards)
! This will have 57 rows
PREDATION
 0 0 0 0 0 0 0 0 0 0 0 0.02
  ...
 0 0.0725 0 0 0 0 0 0 0 0
!
STOCHASTIC "CCl4  KOW"   7     436.0  21.8
...
STOCHASTIC "U      KOW"   1      1
STOCHASTIC "CrVI  BCFVEG"  6 9.45E-01 1.03E+00 1.08E+00
...
STOCHASTIC "U     BCFVEG"  6 3.96E-02 4.40E-02 4.84E-02
STOCHASTIC "CCl4  AMCOOTALPHAVAP" 6  3.600E-01  4.000E-01 4.400E-01
  "Inhalation absorption factor for CCl4   and AMCOOT"
STOCHASTIC "CCl4  AMCOOTALPHAPAR" 6  3.600E-01  4.000E-01 4.400E-01
  "Inhalation particulate absorption factor for CCl4   and AMCOOT"
STOCHASTIC "CCl4  AMCOOTALPHAING" 6  5.850E-01  6.500E-01 7.150E-01
  "Ingestion absorption factor for CCl4   and AMCOOT"
STOCHASTIC "CCl4  AMCOOTALPHADS " 6  9.000E-03  1.000E-02 1.100E-02
  "Dermal permeability (soil) for CCl4   and AMCOOT"
STOCHASTIC "CCl4  AMCOOTALPHADW " 6  1.980E-02  2.200E-02 2.420E-02
  "Dermal absorption (water) for CCl4   and AMCOOT"
...
STOCHASTIC "U     WSTRGNALPHAVAP" 6  2.520E-01  2.800E-01 3.080E-01
  "Inhalation absorption factor for U     and WSTRGN"
STOCHASTIC "U     WSTRGNALPHAPAR" 6  2.520E-01  2.800E-01 3.080E-01
  "Inhalation particulate absorption factor for U     and WSTRGN"
STOCHASTIC "U     WSTRGNALPHAING" 6  1.170E-02  1.300E-02 1.430E-02
  "Ingestion absorption factor for U     and WSTRGN"
STOCHASTIC "U     WSTRGNALPHADS " 6  9.000E-04  1.000E-03 1.100E-03
  "Dermal permeability (soil) for U     and WSTRGN"
STOCHASTIC "U     WSTRGNALPHADW " 1 0
  "Dermal absorption (water) for U      and WSTRGN"
STOCHASTIC "AMCOOTFABOVE" 1 1.0
...
STOCHASTIC "WOTDADFABOVE" 1 1.0
STOCHASTIC "CCl4  AMCOOTDEPRATE" 6  7.650E-01  8.500E-01 9.350E-01
  "Depuration rate of AMCOOT for CCl4  "
...
STOCHASTIC "U     WSTRGNDEPRATE" 6  6.300E-01  7.000E-01 7.700E-01
  "Depuration rate of WSTRGN for U238  "
STOCHASTIC "CCl4  CARP  ALPHAIJ" 1 1
  "Chemical assimilation efficiency of CARP   for CCl4  "
...
STOCHASTIC "U     WSTRGNALPHAIJ" 6  1.170E-01  1.300E-01 1.430E-01
  "Chemical assimilation efficiency of WSTRGN for U238   "
STOCHASTIC "CrVI  CARP  BCF" 6  1.800E-02  2.000E-02 2.200E-02
  "Bioconcentration factor of CARP   for CrVI  "
...
STOCHASTIC "U238  WSTRGNBCF" 6  6.300E-06  7.000E-06 7.700E-06
```

```
  "Bioconcentration factor of WSTRGN for U238  "
STOCHASTIC "U     WSTRGNBCF" 6  6.300E-06  7.000E-06 7.700E-06
  "Bioconcentration factor of WSTRGN for U238  "
STOCHASTIC "CCl4  CARP  METBLOSS" 1 0
...
STOCHASTIC "U     WSTRGNMETBLOSS" 1 0
STOCHASTIC "BLCTWDKPS1  " 6  3.060E-03  3.400E-03 3.740E-03
STOCHASTIC "BLCTWDKPA2  " 6  2.970E+03  3.300E+03 3.630E+03
STOCHASTIC "CARP  BPORE " 6  4.500E-02  5.000E-02 5.500E-02
...
STOCHASTIC "WSTRGNBPORE " 6  9.000E-02  1.000E-01 1.100E-01
END
```

4.3.2   Output Files

Up to five output files can be written by the ECEM code. The number of files depends on the options selected in the scenario being analyzed. The following are the output files:

- **Report File:** This required file contains a summary of the scenario being analyzed and contains any error messages. An example report file for the ECEM code is provided in Table 4.2.
- **Stochastic Values File:** This optional file contains the values for every stochastic variable generated in the ECEM code. The description of the VALUES modifier on the FILE keyword (see Table 4.11) explains how to activate writing this file. A subset of the data written to this file for a run using five realizations is provided in Table 4.3.
- **SACView Header File:** This required file contains information used by the interactive SACView program to allow easy extraction of subsets of the results computed by the ECEM code. An example of this file is given in Table 4.4.
- **Detailed Data:** This optional file contains the detailed values for the dose and risk values generated in the ECEM code. The description of the DETAILS modifier on the FILE keyword (see Table 4.11) explains how to activate writing this file. A subset of the data written to this file for a run using five realizations is provided in Table 4.5.
- **Summary Statistics Data:** This optional file contains the summary statistics for the dose and risk values generated in the ECEM code. The description of the STATISTI modifier on the FILE keyword (see Table 4.11) explains how to activate writing this file. A subset of the data written to this file for a run using five realizations is provided in Table 4.6.

4.3.2.1   ECEM Report File

Excerpted records for an example report file for the ECEM code are provided in Table 4.2. This file contains information for a run of the ECEM code using 10 analytes, 10 realizations, 14 locations, and 12 solution times. The omitted records all contained consumption information for different species. This example file is about half the typical size for the report file, provided that no debug options are selected. The size of this file grows rapidly when debug options are selected. For example, this file is about 32 KB in size. If the debug options are turned on, the file grows to 1.6 GB after just seven time steps. A run using all debug options having a large number of locations, analytes, solution times, and realizations could easily generate a report file larger than the 2.1-GB file size limit under the Windows operating system.

Table 4.2 Excerpted Records from an ECEM Report File

```
                    EEEEEEE   CCCCC   EEEEEEE  MM    MM
                    E        C     C  E        M M  M M
                    E        C        E        M  M  M
                    EEEEE    C        EEEEE    M  M  M
                    E        C        E        M     M
                    E        C     C  E        M     M
                    EEEEEEE   CCCCC   EEEEEEE  M     M


                       ECEM       Version 2.00.A.9
                      Last Modified on  4 Feb 2002
                  ----------------------------------------
                     Ecological Contaminant Exposure Model
                   Stochastic Ecological Pathways Risk Analysis
                  ----------------------------------------
                     Developed By Battelle Memorial Institute
                      Pacific Northwest National Laboratories
                              Richland, Washington
                  ----------------------------------------
                              Copyright Notice
                   Copyright © Battelle Memorial Institute, 2000.
                              All Rights Reserved.
                  ----------------------------------------


            Current Run ID = 20020220133056   User Name = Paul W. Eslinger
                   System Date = 02-20-2002   System Time = 13:30:56



            The software used to generate this output is experimental
              and has not been formally tested or peer reviewed.


                            Review Signatures

Input Prepared By: _____     Date: _____

Input Reviewed By: _____     Date: _____


====================== Echo of the Problem Definition ======================

Title: SAC Rev. 0 Initial Case - 11 Realizations
User:  Paul W. Eslinger
   10 Realizations requested

File Name for Input Keyword Data
File: ECEM.Key

File Name for the Report File
File: Ecem.Rpt

File Name for Output Detailed Data
File: ECEM_Det.Csv

...

File Name for Media Concentrations for analyte with ID="CCl4"
File: I:\Initial\Ecda\ECOL_CCl4_Initial.Dat

File Name for Media Concentrations for analyte with ID="CrVI"
File: I:\Initial\Ecda\ECOL_CrVI_Initial.Dat

Debug Flag Information
   No  : Concentration Data
   No  : Stochastic Calculations
```

```
...
   No  : Equations in subroutine NS_QA
   No  : Equations in subroutine NS_TA

Correlated Variables Information
    ALPHADW : Not correlated
    ALPHADS : Not correlated
   ALPHAING : Not correlated
   ALPHAPAR : Not correlated
   ALPHAVAP : Not correlated
        BCF : Not correlated
    DEPRATE : Not correlated

Output Summary Statistics Flag Information
   Yes : BURDEN : Body burden
   Yes : BMTISS : Aquatic species tissue benchmark
   Yes : DOSRAD : Radionuclide dose by nuclide
   Yes : SUMRAD : Summed radionuclide dose
   Yes : DOSDER : Dermal dose by analyte
   Yes : DOSING : Ingestion dose by analyte
   Yes : DOSINH : Inhalation dose by analyte

Starting Problem Execution

    Date: 02/20/2002
    Time: 13:30:59.598

Time Slices Requested: (Index, Calendar Year)
      1 : 1990
     11 : 2000
 ...
    191 : 2900
    211 : 3000
A total of   12 times have been requested.

Locations Requested: (Index, ID, Name)
     50 : EL0050 : Ecological location
    102 : EL0102 : Ecological location
...
    618 : EL0618 : Ecological location
    666 : EL0666 : Ecological location
A total of   14 locations have been requested.

Analytes Requested:
Index    ID    Type Description
----- ------ ---- ------------------------------------------------
    1 H3       NR  Tritium
    2 Sr90     NR  Strontium 90
    3 Tc99     NR  Technetium 99
    4 I129     NR  Iodine 129
    5 Cs137    NR  Cesium 137
    6 U238     NR  Uranium 238
    7 Pu239    NR  Plutonium 239/240
    8 U        NS  Total Uranium
    9 CCl4     NS  Carbon Tetrachloride
   10 CrVI     NS  Hexavalent Chromium
A total of   10 analytes have been requested.

Species Requested
Species information listed in order of computation
Order Out Type   ID    Long Name
----- --- ---- ------ ------------------------------------------------
    5  No   TP  BLCTWD  Black cottonwood
```

```
  18  No   TP  CYLCRS  Columbia yellowcress
  20  No   TP  DENSDG  Dense sedge
...
  40  No   TA  RACOON  Racoon
  52  No   TA  WEASEL  Weasel
  14  No   TA  COYOTE  Coyote
A total of   57 species have been requested.

Consumption information for species 1 : "AMCOOT" : "American coot"
   0.0200 of species  11 : "CLAMS " : "Clams"
   0.0200 of species  17 : "CRYFSH" : "Crayfish"
   0.0350 of species  18 : "CYLCRS" : "Columbia yellowcress"
   0.0400 of species  30 : "MAYFLY" : "Mayfly"
   0.0200 of species  35 : "MUSSEL" : "Mussels"
   0.6000 of species  38 : "PERPHY" : "Periphyton"
   0.0200 of species  50 : "TARTPD" : "Terrestrial arthropods"
   0.0350 of species  51 : "TULE  " : "Tule"
   0.2000 of species  53 : "WMLFOL" : "Water milfoil"
   0.0100 of species  55 : "WOTDTP" : "Woodhouse's toad (tadpole)"


...


No Thresholds Requested that Match with Requested Species and Analytes

Concentration data units conversion factors

    1 : H3     : NR : Seep water    : 1.00000E+09 : From Ci/m^3      to pCi/L
    1 : H3     : NR : Soil          : 1.00000E+12 : From Ci/kg       to pCi/kg
    1 : H3     : NR : Surface water : 1.00000E+09 : From Ci/m^3      to pCi/L
    1 : H3     : NR : Sediment      : 1.00000E+12 : From Ci/kg       to pCi/kg
    1 : H3     : NR : Pore water    : 1.00000E+09 : From Ci/m^3      to pCi/L

    2 : Sr90   : NR : Seep water    : 1.00000E+09 : From Ci/m^3      to pCi/L
    2 : Sr90   : NR : Soil          : 1.00000E+12 : From Ci/kg       to pCi/kg
    2 : Sr90   : NR : Surface water : 1.00000E+09 : From Ci/m^3      to pCi/L
    2 : Sr90   : NR : Sediment      : 1.00000E+12 : From Ci/kg       to pCi/kg
    2 : Sr90   : NR : Pore water    : 1.00000E+09 : From Ci/m^3      to pCi/L
   ...


Ending Problem Execution

    Date: 02/20/2002
    Time: 13:31:10.020

Message originating in routine ECEM
Message: Normal Termination
```

4.3.2.2   ECEM Stochastic Values File

The stochastic values file is an optional output file that contains the values for every stochastic variable generated in the ECEM code. The description of the VALUES modifier on the FILE keyword (see Table 4.11) explains how to activate writing this file. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of the ID of the stochastic variable followed by a value for every generated realization. Table 4.3 provides a subset of the data written to this file for a run using four realizations. Because this file has at most a few thousand entries, the file size is always smaller than 1 MB. For this example case, there were 57 species and 10 analytes. The resulting output file contained 2195 stochastic variables.

Table 4.3 Excerpted Records from the ECEM Stochastic Values File

```
"H3     KOW", 1.00000E+00, 1.00000E+00, 1.00000E+00, 1.00000E+00
"H3     BCFVEG", 4.76008E+00, 5.14824E+00, 4.68511E+00, 4.90057E+00
"H3     AMCOOTALPHAING", 2.99159E-01, 3.20625E-01, 3.12601E-01, 3.32825E-01
"H3     AMCOOTALPHAPAR", 2.95370E-01, 3.02699E-01, 3.07821E-01, 3.18973E-01
"H3     AMCOOTALPHAVAP", 3.03127E-01, 2.97189E-01, 3.12049E-01, 3.33042E-01
"H3     AMCOOTALPHADW", 1.42924E-03, 1.53292E-03, 1.56314E-03, 1.49832E-03
"H3     AMCOOTALPHADS", 7.90622E-04, 8.16154E-04, 7.95349E-04, 7.57446E-04
"H3     AMCOOTDEPRATE", 1.37955E-01, 1.47876E-01, 1.49062E-01, 1.52669E-01
"H3     CARP  BCF", 9.91170E-01, 9.75634E-01, 1.03975E+00, 9.55665E-01
"AMCOOTFABOVE", 1.00000E+00, 1.00000E+00, 1.00000E+00, 1.00000E+00
"AMKSTLFABOVE", 1.00000E+00, 1.00000E+00, 1.00000E+00, 1.00000E+00
"AMWPELFABOVE", 1.00000E+00, 1.00000E+00, 1.00000E+00, 1.00000E+00
"BEAVERFABOVE", 5.00000E-01, 5.00000E-01, 5.00000E-01, 5.00000E-01
"BLCTWDKPS1", 3.28382E-03, 3.15453E-03, 3.69783E-03, 3.46070E-03
"BLCTWDKPA2", 3.30129E+03, 3.26486E+03, 3.53984E+03, 3.13465E+03
"TARTPDFABOVE", 5.00000E-01, 5.00000E-01, 5.00000E-01, 5.00000E-01
"TULE  KPS1", 3.35116E-03, 3.41507E-03, 3.26583E-03, 3.50039E-03
"TULE  KPA2", 3.45243E+03, 3.23831E+03, 3.13824E+03, 3.35585E+03
"TULE  FABOVE", 1.00000E+00, 1.00000E+00, 1.00000E+00, 1.00000E+00
"WEASELFABOVE", 1.00000E+00, 1.00000E+00, 1.00000E+00, 1.00000E+00
"WMLFOLBPORE", 4.92350E-01, 4.97657E-01, 5.28679E-01, 5.16139E-01
"WOTDADFABOVE", 1.00000E+00, 1.00000E+00, 1.00000E+00, 1.00000E+00
"WOTDTPBPORE", 4.93585E-01, 5.35813E-01, 4.94853E-01, 4.74527E-01
"WAQGS FABOVE", 8.00000E-01, 8.00000E-01, 8.00000E-01, 8.00000E-01
"WSTRGNBPORE", 9.33988E-02, 9.83106E-02, 1.03638E-01, 1.07242E-01
```

4.3.2.3   ECEM SACView Header File

The SACView header file is an output file containing information used by the interactive SACView program to allow easy extraction of subsets of the results computed by the ECEM code. This file is required for every run of the ECEM code. An example of this file is given in Table 4.4. The file contains the following sections of information:

- A header section of basic run information
- Solution times selected
- Locations used
- Analytes processed
- Species with output selected
- Solutions selected
- Output file names.

The user only specifies the name of this file; users should not modify the file after it is generated by the ECEM code. See the instructions in Section 7.0 regarding the use of the SACView program. Because this file has at most a few hundred entries, the file size is always much smaller than 1 MB. File names for options not selected are set to null.

Table 4.4 Example Header File from ECEM for the SACView Program

```
type: "Ecological"
title: "SAC Rev. 0 Initial Case - 11 Realizations"
```

```
user: "Paul W. Eslinger"
name: "ECEM"
version: "2.00.A.9"
date: " 4 Feb 2002"
id: "20020220133056"
envfile: "ESD_Initial.key"
realizations:   10
times:   12
 1990
 2000
 2100
 2200
 2300
 2400
 2500
 2600
 2700
 2800
 2900
 3000
locations:   14
"EL0050","Ecological location"
"EL0102","Ecological location"
"EL0150","Ecological location"
"EL0222","Ecological location"
"EL0270","Ecological location"
"EL0314","Ecological location"
"EL0362","Ecological location"
"EL0400","Ecological location"
"EL0444","Ecological location"
"EL0486","Ecological location"
"EL0526","Ecological location"
"EL0574","Ecological location"
"EL0618","Ecological location"
"EL0666","Ecological location"
analytes:   11
"H3    ","NR","Tritium"
"Sr90  ","NR","Strontium 90"
"Tc99  ","NR","Technetium 99"
"I129  ","NR","Iodine 129"
"Cs137 ","NR","Cesium 137"
"U238  ","NR","Uranium 238"
"Pu239 ","NR","Plutonium 239/240"
"U     ","NS","Total Uranium"
"CCl4  ","NS","Carbon Tetrachloride"
"CrVI  ","NS","Hexavalent Chromium"
"-Rads-","XX","Sum of radionuclides"
species:    4
"HRVMSE","TA","Harvest mouse"
"MAYFLY","QA","Mayfly"
"RCANGS","TP","Reed canarygrass"
```

```
"SALMJV","QA","Salmon (juvenile)"
solutions:    7
"BURDEN","Body burden"
"DOSRAD","Radioactive dose"
"DOSDER","Dermal dose"
"DOSING","Ingestion dose"
"DOSINH","Inhalation dose"
"BMTISS","Tissue benchmark"
"SUMRAD","Sum of radioactive dose"
summary: "ECEM_sta.Csv"
detail: "ECEM_Det.Csv"
```

4.3.2.4   ECEM Detailed Data

The detailed data file is an optional output file that contains the detailed values for body burdens and dose generated in the ECEM code. The description of the DETAILS modifier on the FILE keyword (see Table 4.11) explains how to activate writing this file. The solution types that can be written to the file are described in Table 4.10. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of six identifiers followed by a value for every generated realization. A subset of the data written to this file for a run using two realizations is provided in Table 4.5. The header line occupies one line in the file even though it occupies two lines in the table. The following are the six identifiers on each line:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Analyte ID: The identification of the analyte for which the data were computed
- Specie ID: The identification for the species for which data were computed
- Solution type: A flag for solution type
- Units: The units associated with the computed data.

Table 4.5 Excerpted Records from an ECEM Detailed Data File

```
"Time","Location ID","Analyte ID","Specie","Solution Type","Units",
"Values by realization"
1990,"EL0050","H3    ","RCANGS","BURDEN","pCi/kg", 8.01585E+04, 2.06622E+04
1990,"EL0050","H3    ","RCANGS","DOSRAD","rad/day", 2.38039E-05, 6.13585E-06
1990,"EL0050","H3    ","MAYFLY","BURDEN","pCi/kg", 1.76211E+04, 4.70257E+03
1990,"EL0050","H3    ","MAYFLY","BMTISS","unitless", 1.80153E+04, 4.96552E+03
1990,"EL0050","H3    ","MAYFLY","DOSRAD","rad/day", 5.23275E-06, 1.39648E-06
3000,"EL0666","CCl4  ","SALMJV","BURDEN","ug/kg", 2.65356E-02, 2.34807E-02
3000,"EL0666","CCl4  ","SALMJV","BMTISS","unitless", 2.65356E-02, 2.34807E-02
3000,"EL0666","CCl4  ","HRVMSE","BURDEN","ug/kg", 1.66776E-02, 1.18353E-02
3000,"EL0666","CCl4  ","HRVMSE","DOSDER","ug/kg/day", 0.00000E+00, 0.00000E+00
3000,"EL0666","CCl4  ","HRVMSE","DOSINH","ug/kg/day", 0.00000E+00, 0.00000E+00
3000,"EL0666","CCl4  ","HRVMSE","DOSING","ug/kg/day", 2.03146E-02, 1.79998E-02
3000,"EL0666","CrVI  ","HRVMSE","BURDEN","ug/kg", 1.48222E+00, 8.03919E-01
3000,"EL0666","CrVI  ","HRVMSE","DOSDER","ug/kg/day", 0.00000E+00, 0.00000E+00
3000,"EL0666","CrVI  ","HRVMSE","DOSINH","ug/kg/day", 0.00000E+00, 0.00000E+00
3000,"EL0666","CrVI  ","HRVMSE","DOSING","ug/kg/day", 3.80876E+00, 2.32534E+00
```

This file can have several rows of information for every combination of time, location, species, and analyte. Therefore, this file can become very large. As an example, a 2,800 KB file was generated for a case involving 14 locations, 10 analytes, 7 realizations, 12 times, and 4 output species. The file size directly scales with the number of analytes, locations, species, and times. The file size grows more slowly than a direct scaling by the number of realizations. The file size can be reduced by selecting fewer times, locations, output species, or solution types.

4.3.2.5   ECEM Summary Statistics

This optional file contains summary statistics for dose generated in the ECEM code. The description of the STATISTI modifier on the FILE keyword (see Table 4.11) explains how to activate writing this file. The solution types that can be written to the file are described in Table 4.10. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of six identifiers followed by summary statistics (nine percentiles, mean value, and standard deviation). A subset of the data written to this file for a run using five realizations is provided in Table 4.6. The following are the six identifiers on each line:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Analyte ID: The identification of the analyte for which the data were computed
- Specie ID: The identification for the species for which data were computed
- Solution type: A flag for solution type
- Units: The units associated with the computed data.

The data for each record in this file are too long to present without line-wrapping in this document. Each record in the file occupies two lines in Table 4.6.

Table 4.6 Excerpted Records from the ECEM Summary Statistics File

```
"Time","Location ID","Specie ID","Analyte ID","Result Type","Units","Minimum","5th Percentile","10th Percentile",
"25th Percentile","Median","75th Percentile","90th Percentile","95th Percentile","Maximum","Mean","Standard Deviation"
1990,"EL0050","RCANGS","H3   ","BURDEN","pCi/kg", 2.54241E+01, 2.54241E+01, 2.54241E+01, 2.54241E+01,
2.73537E+04, 3.38985E+04, 4.51161E+04, 4.51161E+04, 8.01585E+04, 3.32611E+04, 2.48229E+04
1990,"EL0050","RCANGS","H3   ","DOSRAD","rad/day", 7.54994E-09, 7.54994E-09, 7.54994E-09, 7.54994E-09,
8.12296E-06, 1.00665E-05, 1.33977E-05, 1.33977E-05, 2.38039E-05, 9.87721E-06, 7.37140E-06
1990,"EL0050","MAYFLY","H3   ","BURDEN","pCi/kg", 1.22778E+01, 1.22778E+01, 1.22778E+01, 1.22778E+01,
6.70630E+03, 8.25514E+03, 1.05390E+04, 1.05390E+04, 1.76211E+04, 7.74609E+03, 5.44027E+03
1990,"EL0050","MAYFLY","H3   ","BMTISS","unitless", 1.23215E+01, 1.23215E+01, 1.23215E+01, 1.23215E+01,
 6.88845E+03, 8.12850E+03, 1.02607E+04, 1.02607E+04, 1.80153E+04, 7.76516E+03, 5.52208E+03
1990,"EL0050","MAYFLY","H3   ","DOSRAD","rad/day", 3.64601E-09, 3.64601E-09, 3.64601E-09, 3.64601E-09,
1.99150E-06, 2.45145E-06, 3.12967E-06, 3.12967E-06, 5.23275E-06, 2.30028E-06, 1.61554E-06
1990,"EL0050","SALMJV","H3   ","BURDEN","pCi/kg", 6.28882E+00, 6.28882E+00, 6.28882E+00, 6.28882E+00,
1.38113E+03, 1.89246E+03, 2.46386E+03, 2.46386E+03, 4.66751E+03, 1.82576E+03, 1.46418E+03
1990,"EL0050","SALMJV","H3   "," BMTISS ","unitless", 6.32028E+00, 6.32028E+00, 6.32028E+00, 6.32028E+00,
1.48005E+03, 1.87565E+03, 2.34242E+03, 2.34242E+03, 4.54303E+03, 1.81281E+03, 1.40662E+03
1990,"EL0050","SALMJV","H3   ","DOSRAD","rad/day", 1.86753E-09, 1.86753E-09, 1.86753E-09, 1.86753E-09,
4.10141E-07, 5.61986E-07, 7.31668E-07, 7.31668E-07, 1.38607E-06, 5.42179E-07, 4.34802E-07
1990,"EL0050","HRVMSE","H3   ","BURDEN","pCi/kg", 1.90977E+01, 1.90977E+01, 1.90977E+01, 1.90977E+01,
1.79798E+04, 2.42002E+04, 3.12386E+04, 3.12386E+04, 5.20661E+04, 2.18047E+04, 1.65240E+04
1990,"EL0050","HRVMSE","H3   ","DOSRAD","rad/day", 5.67125E-09, 5.67125E-09, 5.67125E-09, 5.67125E-09,
```

```
 5.33928E-06, 7.18650E-06, 9.27663E-06, 9.27663E-06, 1.54616E-05, 6.47513E-06, 4.90697E-06
 1990,"EL0050","HRVMSE","H3   ","DOSDER","rad/day", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
 1990,"EL0050","HRVMSE","H3   ","DOSING","rad/day", 3.09753E+01, 3.09753E+01, 3.09753E+01, 3.09753E+01,
  2.85303E+04, 3.52527E+04, 4.67677E+04, 4.67677E+04, 8.33295E+04, 3.45718E+04, 2.57908E+04
 1990,"EL0050","HRVMSE","H3   ","DOSINH","rad/day", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
 1990,"EL0050","RCANGS","CCl4 ","BURDEN","ug/kg", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
 1990,"EL0050","MAYFLY","CCl4 ","BURDEN","ug/kg", 5.06943E-02, 5.06943E-02, 5.06943E-02, 5.06943E-02,
 5.83496E-02, 6.45637E-02, 7.07093E-02, 7.07093E-02, 1.01457E-01, 6.48589E-02, 1.75829E-02
 1990,"EL0050","MAYFLY","CCl4 "," BMTISS ","unitless", 5.06943E-02, 5.06943E-02, 5.06943E-02, 5.06943E-02,
 5.83496E-02, 6.45637E-02, 7.07093E-02, 7.07093E-02, 1.01457E-01, 6.48589E-02, 1.75829E-02
 1990,"EL0050","HRVMSE","CCl4 ","DOSINH","ug/kg/day", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
 1990,"EL0050","HRVMSE","-Rads-","SUMRAD","rad/day", 6.53884E-08, 6.53884E-08, 6.53884E-08, 6.53884E-08,
 5.34093E-06, 7.32354E-06, 9.27913E-06, 9.27913E-06, 1.54730E-05, 6.51136E-06, 4.89722E-06
 1990,"EL0050","MAYFLY","-Rads-","SUMRAD","rad/day", 4.00539E-05, 4.00539E-05, 4.00539E-05, 4.00539E-05,
 9.29692E-05, 1.36747E-04, 2.07406E-04, 2.07406E-04, 3.78735E-04, 1.40443E-04, 1.19386E-04
 1990,"EL0050","RCANGS","-Rads-","SUMRAD","rad/day", 7.54994E-09, 7.54994E-09, 7.54994E-09, 7.54994E-09,
 8.12296E-06, 1.00665E-05, 1.33977E-05, 1.33977E-05, 2.38039E-05, 9.87721E-06, 7.37140E-06
 1990,"EL0050","SALMJV","-Rads-","SUMRAD","rad/day", 2.13907E-06, 2.13907E-06, 2.13907E-06, 2.13907E-06,
 3.69897E-06, 5.16700E-06, 7.70061E-06, 7.70061E-06, 1.60394E-05, 5.71137E-06, 4.94818E-06
```

This file can have several rows of information for every combination of time, location, specie, and analyte. Therefore, this file can become very large. As an example, a 3,890 KB file was generated for a case involving 14 locations, 10 analytes, 7 realizations, 12 times, and 4 output species. The file size directly scales with the number of analytes, locations, species, and times. The file size grows more slowly than a direct scaling by the number of realizations. The file size can be reduced by selecting fewer times, locations, output species, or solution types.

4.4   Keyword Descriptions for the ECEM Code

In the following keyword descriptions, some data are optional and some are required. Data required are enclosed in square brackets. For AB to be required, it would be denoted by [AB]. If only one of the three items AB, BC, CD were required, it would be written as [AB|BC|CD]. The vertical bars indicate to chose one of the items in the list. Optional items are enclosed in normal brackets. For DE to be an optional entry, it would be denoted by {DE}. The {} or [] symbols are indicators of whether the data are required. These symbols are not entered when the keyword is constructed.

In some instances, numerical values or quote strings are associated with a modifier. In this description, the association is indicated by using the equal (=) symbol. The = symbol is not required but may be used when the keyword is constructed. When a numerical value or quote string is associated with a modifier, it must be physically entered on the input line directly after the modifier.

This section defines keywords needed to control the ECEM code directly. The order in which keywords are entered does not matter for many keywords. Several keywords have a required order of appearance, including the following requirements:

- The REPORT keyword must be the first keyword in the file.
- The END keyword must be the last keyword in the file.
- The SPECIES keywords (Section 4.4.15) must all be entered before the PREDATION keyword (Section 4.4.10) is entered.

4.4.1 ANALYTE Keyword for the ECEM Code

The ANALYTE keyword is used to define the analytes to be used in calculating ecological risk metrics. The following is this keyword's syntax:

```
ANALYTE [ID="quote 1"] {ANIMAL} {FUNGUS} {PLANT} {OUTPUT}
```

Analytes chosen must be a subset of the analytes used in the fate and transport activities controlled through the ESD keyword file. Multiple analyte keywords can be entered. A separate ANALYTE keyword is required for each desired analyte. The modifiers can be entered in any order. The modifiers associated with the ANALYTE keyword are described in Table 4.7.

Table 4.7 Modifiers Associated with the ANALYTE Keyword in the ECEM Code

Modifier	Description
ID	The entry associated with the ID modifier is an analyte identification string (up to six characters long). The analyte ID entered must be one of the set of analytes identified in the environmental scenario file.
ANIMAL	If the ANIMAL modifier is present, then the analyte is treated as an animal nutrient.
FUNGUS	If the FUNGUS modifier is present, then the analyte is treated as a fungus nutrient.
PLANT	If the PLANT modifier is present, then the analyte is treated as a plant nutrient.
OUTPUT	The OUTPUT modifier is necessary for data to be output for this species.

The following is an example ANALYTE keyword defining zinc as an analyte that is an animal nutrient:

```
ANALYTE ID="Zn" ANIMAL OUTPUT
```

4.4.2 CORRELATE Keyword for the ECEM Code

The CORRELATE keyword allows a statistical correlation to be defined between sets of two variables. Multiple CORRELATE keywords can be entered. Each entry of the CORRELATE keyword will cause the specific correlation to be defined for all time steps requested (see the TIMES keyword). The following is this keyword's syntax:

```
CORRELATE [BCF | DEPRATE | ALPHAING | ALPHAPAR | ALPHAVAP | ALPHADS |
    ALPHADW]  Pvalue
```

Each occurrence of the CORRELATE keyword must contain only one modifier. The modifier identifies which variable is to be correlated with the input media concentrations. The modifiers associated with the CORRELATE keyword are described in Table 4.8.

Table 4.8 Modifiers Associated with the CORRELATE Keyword in the ECEM Code

Modifier	Description
BCF	This modifier induces a rank correlation of size Pvalue between the bioconcentration factor for a species (depending on the analyte) and the pore water concentration of the analyte. This correlation applies to • aquatic plants combined with analytes that are plant or fungus nutrients • aquatic animals combined with analytes that are plant nutrients
DEPRATE	This modifier induces a rank correlation of size Pvalue between the species depuration rate and pore water concentrations of the analyte. This correlation applies to • Aquatic plants combined with analytes that are plant or fungus nutrients • Aquatic animals combined with analytes that are plant nutrients
ALPHAING	This modifier induces a rank correlation of size Pvalue between the species ingestion absorption factor and analyte surface water concentrations. This correlation applies to terrestrial animals combined with analytes that are animal nutrients.
ALPHAPAR	This modifier induces a rank correlation of size Pvalue between the species inhalation particle absorption factor and analyte concentrations in surface water. This correlation applies to terrestrial animals combined with analytes that are animal nutrients.
ALPHAVAP	This modifier induces a rank correlation of size Pvalue between the species inhalation absorption factor for vapor and analyte concentrations in surface water. This correlation applies to terrestrial animals combined with analytes that are animal nutrients.
ALPHADS	This modifier induces a rank correlation of size Pvalue between the species dermal permeability factor for soil and analyte concentrations in surface water. This correlation applies to terrestrial animals combined with analytes that are animal nutrients.
ALPHADW	This modifier induces a rank correlation of size Pvalue between the species dermal absorption factor for water and analyte concentrations in surface water. This correlation applies to terrestrial animals combined with analytes that are animal nutrients.

The following CORRELATE keyword induces a rank correlation of 0.2 between the variable BCF and the input media concentrations:

```
CORRELATE "BCF" 0.2
```

User Instructions for the Systems Assessment Capability, Rev. 0, Computer Codes
Volume 2: Impact Modules

Use of the CORRELATE keyword is not recommended when using fewer than 10 realizations. When only a few realizations are requested, the computed score matrix can be singular, and the correlation strategy can fail.

4.4.3   DEBUG Keyword for the ECEM Code

The DEBUG keyword is used to activate dumping of intermediate calculations to the report file. It should be used sparingly and with only one or two realizations; otherwise, the volume of output could fill the user's hard drive. The following is the syntax for this keyword record:

```
DEBUG [modifier 1] {modifier 2}…{modifier k}
```

Multiple DEBUG cards can be entered with combinations of modifiers, or a single card can be entered containing all of the modifiers. The modifiers can be entered in any order. Table 4.9 describes the modifiers associated with the DEBUG keyword.

Table 4.9 Modifiers Associated with the DEBUG Keyword in the ECEM Code

Modifier	Description
AIR	Intermediate outputs on calculations for air calculations.
ANALYTE	Intermediate results for analyte information.
CONCENTR	Intermediate outputs for concentration data.
CONSTANT	Intermediate outputs for constant data.
CORRELAT	Intermediate results for correlation information.
RADSUM	Intermediate results for radioactive doses.
GENERATE	Intermediate results for the stochastic variable generation.
LOOP	Messages on the control looping.
SPECIE	Intermediate results for species information.
VERBOSE	Additional messages to the screen showing simulation progress.
OR_QP	Intermediate results for organic radioactive analytes and aquatic plants.
OR_TP	Intermediate results for organic radioactive analytes and terrestrial plants.
OR_QA	Intermediate results for organic radioactive analytes and aquatic animals.
OR_TA	Intermediate results for organic radioactive analytes and terrestrial animals.
NR_QP	Intermediate results for inorganic radioactive analytes and aquatic plants.
NR_TP	Intermediate results for inorganic radioactive analytes and terrestrial plants.
NR_QA	Intermediate results for inorganic radioactive analytes and aquatic animals.
NR_TA	Intermediate results for inorganic radioactive analytes and terrestrial animals.
OS_QP	Intermediate results for organic stable analytes and aquatic plants.
OS_TP	Intermediate results for organic stable analytes and terrestrial plants.

Modifier	Description
OS_QA	Intermediate results for organic stable analytes and aquatic animals.
OS_TA	Intermediate results for organic stable analytes and terrestrial animals.
NS_QP	Intermediate results for inorganic stable analytes and aquatic plants.
NS_TP	Intermediate results for inorganic stable analytes and terrestrial plants.
NS_QA	Intermediate results for inorganic stable analytes and aquatic animals.
NS_TA	Intermediate results for inorganic stable analytes and terrestrial animals.

The following entries provide examples of the use of the DEBUG keyword:

```
DEBUG RADSUM
DEBUG CORRELAT
DEBUG OR_TA NR_TA OS_TA NS_TA
```

There are no quote strings associated with the DEBUG keyword.

4.4.4   DETAILS Keyword for the ECEM Code

The DETAILS keyword is used to control writing detailed data to the output details file for a variety of solution types. The following is this keyword record's syntax:

```
DETAILS [modifier 1] {modifier 2}…{modifier 6}
```

Multiple DETAILS cards can be entered with combinations of modifiers, or a single card can be entered containing all of the modifiers. The modifiers can be entered in any order. Table 4.10 describes the modifiers associated with the DETAILS keyword.

Table 4.10 Modifiers Associated with the DETAILS Keyword in the ECEM Code

Modifier	Description
BURDEN	Presence of the BURDEN modifier initiates output of the body burden (tissue concentrations) for every species and analyte where the species output flag is used (see the SPECIE keyword).
CONCEN	Presence of the CONCEN modifier initiates output of the water, sediment, and soil concentration data used in the calculations. The media identifiers are: • SW denotes surface water (river) • PW denotes pore water (river bottom) • GW denotes groundwater • SE denotes seep water (river bank) • SO denotes soil • SD denotes sediment (river bottom)

Modifier	Description
DOSDER	Presence of the DOSDER modifier initiates output of the dermal dose for terrestrial animal species and all analytes where the species output flag is used (see the SPECIE keyword).
DOSING	Presence of the DOSDER modifier initiates output of the ingestion dose for terrestrial animal species and all analytes where the species output flag is used (see the SPECIE keyword).
DOSINH	Presence of the DOSDER modifier initiates output of the inhalation dose for terrestrial animal species and all analytes where the species output flag is used (see the SPECIE keyword).
DOSRAD	Presence of the DOSRAD modifier initiates output of the radioactive dose for animal and plant species and all radioactive analytes where the species output flag is used (see the SPECIE keyword).
BMTISS	Presence of the BMTISS modifier initiates output of the benchmark comparison for animal and plant species exposed to radioactive analytes where the species output flag is used (see the SPECIE keyword).
SUMRAD	Presence of the DOSRAD modifier initiates output of the radioactive dose summed over all radioactive analytes for animal and plant species when the species output flag is used (see the SPECIE keyword).

The following entries provide examples of the use of the DETAILS keyword:

```
DETAILS DOSRAD SUMRAD
DETAILS SUMRAD
DETAILS DOSING DOSDER BURDEN
```

There are no quote strings associated with the DETAILS keyword.

4.4.5   END Keyword for the ECEM Code

The END keyword signifies the end of all keyword data. It should be the last keyword in the keyword file. All data in the keyword file after the END keyword will be ignored. The following is this keyword record's syntax:

```
END
```

There are no modifiers or quote strings associated with the END keyword.

4.4.6   EXECUTE Keyword for the ECEM Code

The EXECUTE keyword signifies that the user wishes to perform problem execution. If this keyword is not entered, then the inputs are checked for consistency, but the problem will not be executed. This is useful if the run being set up is expected to take a significant amount of computation time. The following is this keyword record's syntax:
```
EXECUTE
```

There are no modifiers or quote strings associated with the EXECUTE keyword.

4.4.7   FILE Keyword for the ECEM Code

The FILE keyword is used to enter the names of input and output files except for the report file. The names of the files providing concentration data are contained in the environmental scenario file rather than in the keyword file. The following is the FILE keyword record's syntax:

```
FILE [modifier1 "quote1"] {modifier2 "quote2"} ... {modifier5 "quote5"}
```

The file names are entered in quote strings, which must be enclosed in double quotation marks. Path names up to 72 characters long are supported. The file name associated with a modifier must be entered before the next modifier is entered. At least one FILE keyword is required for every run of the code. Table 4.11 describes the modifiers associated with the FILE keyword.

Table 4.11 Modifiers Associated with the FILE Keyword in the ECEM Code

Modifier	Description
DETAILS	Optional output file containing detailed solutions by realization.
ESD	Required input keyword file (environmental settings definitions) that contains problem definition information for the release and transport codes and information specific to the ECEM code.
HEADER	Required output file containing header type information associated with all of the other output files identified in this table.
THRESHOL	Optional output file containing exceedance probabilities for user-specified thresholds. See the THRESHOLD keyword (Section 4.4.18) for more detailed information.
STATISTI	Optional output file containing summary statistics for all calculations.
VALUES	Optional output file containing generated values for all stochastic variables. This file is recommended because it contains data required to support uncertainty analyses.

The following two entries define the file for detailed calculations and the header file for use by SACView:

```
FILE DETAILS "TestCase.det"
FILE HEADER "/home/ANALYSIS/Median2/ecem/TestCase.hdr"
```

4.4.8   GROWTH Keyword for the ECEM Code

The GROWTH keyword is used to define the parameters of the growth rate equation described in Section 4.1.2.1:

```
GROWTH   DELTA=value1   BETA=value2
```

These modifiers can be entered in any order, together with their associated data. The following example illustrates the use of the GROWTH keyword:

```
GROWTH  DELTA=0.002 BETA=0.25
```

4.4.9   LOCATION Keyword for the ECEM Code

The LOCATION keyword identifies the locations for ecological impact calculations that will be generated. Multiple LOCATION keywords are allowed. The locations must be a subset of the locations at which environmental data were computed and stored by the inventory, release, and transport modules. The list of desired locations builds sequentially with each LOCATION record. Upon program entry, no locations are active. The following is the LOCATION keyword record's syntax:

```
LOCATION [PRIMARY="quote 1"] {SECOND="quote 2"} (OUTPUT)
```

The ecological impacts module is activated at a location by entering the location ID string in association with the PRIMARY modifier. A separate LOCATION keyword is required for every desired location. The function of the SECOND modifier is to supply concentrations from other locations that may not be computed at the primary location. If the SECOND location is not entered, impacts are calculated using only concentrations available at the primary location. Table 4.12 describes the modifiers associated with the LOCATION keyword.

Table 4.12 Modifiers Associated with the LOCATION Keyword in the ECEM Code

Modifier	Description
PRIMARY	The entry associated with the PRIMARY modifier is an ecological location identification string (up to six characters in length). The location ID entered must be one of the suite of locations identified in the environmental scenario file.
SECOND	The entry associated with the SECOND modifier is an ecological location identification string (up to six characters in length). The location ID entered must be one of the suite of locations identified in the environmental scenario file.
OUTPUT	The OUTPUT modifier is necessary for data to be output for the location.

For example, the primary location may be in the riparian zone, but a food chain including river species is being modeled. The primary location would be on land, and the secondary location should be chosen as the nearest river location. The following are example LOCATION keywords:

```
LOCATION PRIMARY="EL #001"
LOCATION PRIMARY= "EL #002" SECOND="EL #001"
```

4.4.10 PREDATION Keyword for the ECEM Code

The PREDATION keyword is used to describe consumption between species in the food chain. Consumption amounts are entered as fractions of total diet rather than units of mass. The predation data are entered in the form of a square matrix and must be entered only after all of the SPECIES keywords have been entered. The following is the PREDATION keyword record's syntax:

```
PREDATION Value₁, Value₂, … , Valueₙ
```

The number of numerical entries is equal to the square of the number of species being modeled. There are no modifiers or quote strings associated with the PREDATION keyword.

Each row in the matrix consists of the consumption fractions for a species of all the other species. The order of species in the columns (left to right) and rows (top to bottom) are the order in which SPECIES keywords are entered. Each row in the matrix represents a species, and each column represents a species, with each species having both a row and a column.

In the example given below, the first row of the matrix defines the items consumed by the first species with ID of CHCATF (channel catfish). The CHCATF does not eat itself, DAPMAG, or HYALLE, so the first three entries are 0. It gets 0.14 of its diet from MAYFLY, 0.57 from PERPHY, none from PHYPLK, and 0.1 from WMLFOL. The sum of these fractions is only 0.75, which is less than a full diet intake for the catfish. The remaining 0.25 comes from sediment ingestion. Sediment ingestion is defined using the SEDING modifier on the SPECIE keyword in the ESD keyword file (see Section 2.2.11). The value from the ESD keyword file can be overridden using the SEDING modifier on the SPECIE keyword in the ECEM keyword file (see Section 4.4.15). The second row of the matrix specifies that the species DAPMAG (Daphnia magna) obtains its entire diet from PHYPLK (phytoplankton).

The model does not allow cannibal species; thus the diagonal elements of the matrix will always be zero. All entries in the matrix must be between 0 and 1, inclusive. A plant species will have a row consisting of all zeros. The row sum for an animal species must be 1.0 after the sediment ingestion has been added.

An example set of keywords defining seven species and their associated predation matrix is provided here. The SPECIE keywords must all precede the PREDATION keyword. The order of entry of the SPECIE keywords defines the relationship of the rows and columns for the data entered with the PREDATION keyword.

```
SPECIE ID="CHCATF" SEDING=0.25
SPECIE ID="DAPMAG"
SPECIE ID="HYALLE"
SPECIE ID="MAYFLY"
SPECIE ID="PERPHY"
SPECIE ID="PHYPLK"
SPECIE ID="WMLFOL"
PREDATION
  0.00 0.00 0.00 0.14 0.51 0.00 0.10
  0.00 0.00 0.00 0.00 0.00 1.00 0.00
  0.00 0.00 0.00 0.00 0.00 0.50 0.00
  0.00 0.04 0.04 0.00 0.40 0.30 0.12
  0.00 0.00 0.00 0.00 0.00 0.00 0.00
  0.00 0.00 0.00 0.00 0.00 0.00 0.00
  0.00 0.00 0.00 0.00 0.00 0.00 0.00
```

4.4.11 REALIZATION Keyword for the ECEM Code

The REALIZATION keyword defines the number of realizations to generate. The following is this keyword record's syntax:

```
REALIZATION value1
```

The integer value1 has a minimum value of 1 and a maximum of the number of realizations defined in the environmental scenario definition file. If the number of realizations is less than the number of realizations in the concentration data files, then only the first realizations will be used.

The following keyword record sets the number of realizations to 10:

```
REALIZAT 10
```

4.4.12 REPORT Keyword for the ECEM Code

The REPORT keyword is used to define the name of the output report (log) file. It must be the first keyword entered in the keyword file. The following is this keyword record's syntax:

```
REPORT ["quote"]
```

The name of the report file is entered in a quote string. File names up to 72 characters long are supported, and path names can be optionally included. The following is an example REPORT keyword record:

```
REPORT "G:\SAC\SystemCodes\ECEM\Test1.rpt"
```

4.4.13 RESPIRE Keyword for the ECEM Code

The RESPIRE keyword is used to define the parameters of the respiration rate equation described in Section 4.1.2.1. This respiration equation only applies to water-respiring species:

```
RESPIRE  GAMMA=value1  PHI=value2
```

The two modifiers can be entered in any order, together with their associated data. The following example illustrates the use of the RESPIRE keyword:

```
RESPIRE  PHI=0.032 GAMMA=0.2
```

4.4.14 SEED Keyword for the ECEM Code

The SEED keyword sets the value for the seed for the random number generator. The following is this keyword record's syntax:
```
SEED Value1
```

The value for Value1 must be an integer or real number in the range 1 to 999999. The following is an example keyword record:

```
SEED 344443
```

There are no quote strings or modifiers associated with the SEED keyword.

4.4.15 SPECIE Keyword for the ECEM Code

The SPECIE keyword is used to select the species to be simulated in the ECEM code. The following is this keyword's syntax:

```
SPECIE [ID="quote1"] [SEDING=value] {OUTPUT}
```

A separate SPECIE keyword must be entered for every specie being modeled. The ID modifier must be matched with a quote string containing a unique ID that matches one of the species defined in the ESD file (see the SPECIE keyword in Section 2.2.11). The optional OUTPUT modifier initiates output of all information invoked by the DETAILS and STATISTICS keywords for this specie. If no OUTPUT modifiers are entered for any species, then no summary statistics or detailed data will be output.

The modifier SEDING allows the user to override the value in the ESD keyword file for the fraction of diet for this species that comes from ingestion of sediment. This value applies only to animal species. The entered value must be in the range 0 to 1. The sum of all consumption for an animal species (see the PREDATION keyword in Section 4.4.10) must be 1 after sediment ingestion is added.

4.4.16 STATISTIC Keyword for the ECEM Code

The STATISTIC keyword is used to control writing summary statistics to the summary statistics file for a variety of solution types. The following is this keyword record's syntax:

```
STATISTIC [modifier 1] {modifier 2}…{modifier 6}
```

Multiple STATISTIC cards can be entered with combinations of modifiers, or a single card can be entered containing all of the modifiers. The modifiers can be entered in any order. Table 4.13 describes the modifiers associated with the STATISTIC keyword.

Table 4.13 Modifiers Associated with the STATISTIC Keyword in the ECEM Code

Modifier	Description
BURDEN	Presence of the BURDEN modifier initiates output of summary statistics of the body burden (tissue concentrations) for every species and analyte where the species output flag is used (see the SPECIE keyword).
CONCEN	Presence of the CONCEN modifier initiates output of summary statistics for the water, sediment, and soil concentration data used in the calculations. The media identifiers are: • SW denotes surface water (river) • PW denotes pore water (river bottom) • GW denotes ground water • SE denotes seep water (river bank) • SO denotes soil • SD denotes sediment (river bottom)

Modifier	Description
DOSDER	Presence of the DOSDER modifier initiates output of summary statistics of the dermal dose for terrestrial animal species and all analytes where the species output flag is used (see the SPECIE keyword).
DOSING	Presence of the DOSDER modifier initiates output of summary statistics of the ingestion dose for terrestrial animal species and all analytes where the species output flag is used (see the SPECIE keyword).
DOSINH	Presence of the DOSDER modifier initiates output of summary statistics of the inhalation dose for terrestrial animal species and all analytes where the species output flag is used (see the SPECIE keyword).
DOSRAD	Presence of the DOSRAD modifier initiates output of summary statistics of the radioactive dose for animal and plant species and all radioactive analytes where the species output flag is used (see the SPECIE keyword).
BMTISS	Presence of the BMTISS modifier initiates output of summary statistics of the benchmark tissue values for animal and plant species exposed to radioactive analytes where the species output flag is used (see the SPECIE keyword).
SUMRAD	Presence of the DOSRAD modifier initiates output of summary statistics of the radioactive dose summed over all radioactive analytes for animal and plant species when the species output flag is used (see the SPECIE keyword).

The following entries provide examples of the use of the STATISTIC keyword:

```
STATISTIC DOSRAD
STATISTIC DOSING BMTISS
```

There are no quote strings associated with the STATISTIC keyword.

4.4.17 STOCHASTIC Keyword for the ECEM Code

The STOCHASTIC keyword is used to enter the definition of a statistical distribution for stochastic variables. The general syntax for the STOCHASTIC keyword is the following:

```
STOCHASTIC ["Quote1"] [Dist_Index Parameters] {TRUNCATE U1 U2} {"Quote2"}
```
The entry for Quote1 must be a unique character string of up to 20 characters that will be used to identify this stochastic variable in subsequent uses. It is case sensitive and embedded spaces are significant. It is sometimes useful to make the character string some combination of a variable name and other data such that it can be recreated easily when stochastic data are needed. The entry for Quote2 is a description for the stochastic variable that can be up to 64 characters long. An entry for Quote2 is not required.

The entry for Dist_Index must be an integer in the range 1 to 11 that identifies the index of a statistical distribution. The available statistical distributions are defined in Table 10.1. The word Parameters in the general syntax statement indicates the numerical values of parameters required for defining the statistical distribution. The additional modifier TRUNCATE can be used for all distribution types except 1, 3, and 10 (constant, discrete uniform, and user defined). If TRUNCATE is entered, it must be followed by two

values in the interval 0 to 1, inclusive. The lower value must be less than the upper value. These two values specify the tail probabilities at which to impose range truncation for the distribution. Truncation data must be entered after all of the other parameters that define the distribution.

The following is an example stochastic card for a bioconcentration factor that is normally distributed with a mean of 125 and a standard deviation of 5 for a frog exposed to ^{14}C:

```
STOCHASTIC "BCFC14Frog" 7  125.0  5.0  "Example number 1"
```

Although this section gives the general form of a STOCHASTIC keyword entry, it does not describe the entire set of STOCHASTIC keywords required to run the ECEM code. Section 4.5 provides a more complete set of example STOCHASTIC keywords. Table 4.14 provides the example keywords grouped by variable type.

Table 4.14 Cross Reference to Example STOCHASTIC Keywords for the ECEM Code

Dependencies	Cross Reference
Analyte, specie	Table 4.17 Example ECEM Keywords for the Growth Model for Terrestrial Animals.
Analyte	Table 4.18 Example ECEM Keywords for the Root Uptake Model for Terrestrial Plants.
Specie	Table 4.19 Example ECEM Keywords for the Time Fraction Aquatic Animals Spend Above Water.
Analyte, specie	Table 4.20 Example ECEM Keywords for the Depuration Rate for Animal Species.
Analyte, specie	Table 4.21 Example ECEM Keywords for the Chemical Assimilation for Aquatic Animal Species.
Analyte, specie	Table 4.22 Example ECEM Keywords for the Bioconcentration Factor for Aquatic Animal Species.
Analyte, specie	Table 4.23 Example ECEM Keywords for the Metabolism Loss Rate for Aquatic Species.
Specie	Table 4.24 Example ECEM Keywords for Plant-Air Partition Coefficients.
Specie	Table 4.25 Example ECEM Keywords for the Fraction of Time Aquatic Species Spend in Pore Water.

4.4.18 THRESHOLD Keyword for the ECEM Code

As an optional calculation, up to two threshold values can be provided by the user and used to compare calculated doses and body burdens. The values of the thresholds are entered using the THRESHOLD keyword. Two types of threshold can be supplied. The SUMRAD modifier is used for a total radioactive dose only by species. For all other modifiers, the thresholds apply by analyte and species. The following is the THRESHOLD keyword's syntax:

```
THRESHOLD [TYPE=[ BURDEN | DOSDER | DOSING | DOSINH | DOSRAD |
```

```
    BMTISS | SUMRAD ]] [SPECIE="quote1"] {ANALYTE="quote2"}
    {LIMIT1=value1} {LIMIT2=value2}
```

Table 4.15 describes the modifiers for the THRESHOLD keyword.

Table 4.15 Modifiers Associated with the THRESHOLD Keyword in the ECEM Code

Modifier	Description
ANALYTE	The quote string associated with the ANALYTE modifier is an analyte ID. If the SUMRAD modifier is used, the ANALYTE modifier should be omitted (it is ignored). The analyte ID must match with one of the analytes in the ESD file.
TYPE	The quote string associated with the TYPE modifier identifies the type of solution for this threshold calculation. The following are valid entries for the quote string: • BURDEN: Body burden (tissue concentration) • DOSDER: Dermal dose • DOSRAD: Radioactive dose • DOSING: Ingestion dose • DOSINH: Inhalation dose • DOSDER: Dermal dose • BMTISS: Benchmark tissue value for aquatic species • SUMRAD: Sum of the radionuclide dose over analytes
LIMIT1	This modifier identifies a user-specified threshold for calculation of an exceedance probability. The limit is applicable to a specific combination of solution type, species, and analyte.
LIMIT2	This modifier identifies a second user-specified threshold for calculation of an exceedance probability. The limit is applicable to a specific combination of solution type, species, and analyte.

An example of a set of THRESHOLD keywords is given in the following:

```
THRESHOLD TYPE="BURDEN" ANALYTE="C14"  SPECIE="CHCATF"
   LIMIT1=0.005  LIMIT2=0.01
THRESHOLD TYPE="DOSRAD" ANALYTE= "C14"  SPECIE= "CHCATF"
   LIMIT1=0.04  LIMIT2=0.065
THRESHOLD TYPE="SUMRAD" SPECIE="CHCATF" LIMIT2=23.4
```

4.4.19 TIMES Keyword for the ECEM Code

The TIMES keyword identifies the times at which the calculations are to be performed. The following is the keyword's syntax:

```
TIMES [ [T1] {T2} … {Tn} | {ALL} ]
```

The numerical entries T1, T2, …, Tn are the times (whole number years) when outputs are desired. These times must be a subset of the times at which environmental data were computed and stored by the inventory, release, and transport modules. Multiple TIMES keywords can be entered. If the modifier ALL is used, results will be calculated for every time in the ESD keyword file. If the modifier ALL is used, no numerical values should be entered. The following is an example TIMES keyword that requests output for the three years 2020, 2075, and 3014:

```
TIMES 2020 2075 3014
```

There are no quote strings associated with the TIMES keyword.

4.4.20 TITLE Keyword for the ECEM Code

The TITLE keyword is used to define a single-line problem title. The problem title will be written to output files. If the title is not supplied, then the program will error terminate. The following is this keyword record's syntax:

```
TITLE ["quote"]
```

The title is entered in a quote string, which must be enclosed in double quotation marks. Titles up to 72 characters long are supported. The following example defines a title for a run of the code:

```
TITLE "Example title line for the Ecological impacts code."
```

There are no modifiers associated with the TITLE keyword.

4.4.21 USER Keyword for the ECEM Code

The USER keyword is used to identify the user of the program. The user name will be written to output files. If the user name is not supplied, then the program will error terminate. The following is this keyword record's syntax:

```
USER ["quote"]
```

The user name is entered in a quote string, which must be enclosed in double quotation marks. User names up to 16 characters long are supported. The following example defines John Q. Public as the user running the code:

```
USER "John Q. Public"
```

There are no modifiers associated with the USER keyword.

4.4.22 VARIABLE Keyword for the ECEM Code

The VARIABLE keyword is used to enter values for several variables that are constant rather than stochastic. The following is the VARIABLE keyword record's syntax:

```
VARIABLE {TUPTAKE=V1} {COWHDFX=V2} {EXPOSI=V3} {GASCON=V4}
```

```
{RFRAC=V6} {AREA=V7} {LENGTH=V8}
```

Table 4.16 describes the modifiers associated with the VARIABLE keyword. Multiple VARIABLE keywords can be entered, each with a portion of the modifiers. If a modifier is entered more than once, the last definition is the one used in the calculations.

Table 4.16 Modifiers Associated with the VARIABLE Keyword in the ECEM Code

Modifier	Description
TUPTAKE	Fraction root uptake for tritium in terrestrial plants (unitless).
COWHDFX	Cowherd function for terrestrial plants and animals (unitless).
EXPOSI	Exposure interval for terrestrial plants and animals (seconds).
GASCON	Universal gas constant (pascal-m^3/mole-K) used in terrestrial plant calculations.
RFRAC	Respirable fraction for terrestrial plants and animals (gram/m^2-hr).
AREA	Area of contamination for terrestrial plants and animals (cm^2).
LENGTH	Length of side of contaminated area for terrestrial plants and animals (m).

The following are example keywords defining this suite of variables for terrestrial plants:

```
VARIABLE COWHDFX    0.0497 EXPOSI     7.9E+8
VARIABLE GASCON    8.314
VARIABLE RFRAC     0.036
VARIABLE AREA      500.0  LENGTH  1000.0
VARIABLE TUPTAKE    0.9
```

There are no quote strings associated with the VARIABLE keyword.

4.5 Example Stochastic Keywords for the ECEM Code

Typically, a large number of STOCHASTIC keywords are needed for a run of the ECEM code. For example, one run of the code with 10 analytes and 57 species required 4085 STOCHASTIC keywords. The exact number of keywords for a run depends on the number and type of analytes and the number and type of species. The general description of a STOCHASTIC keyword for the ECEM code is provided in Section 4.4.17. Additional information about statistical distributions is provided in Section 10.0.

The general description of the STOCHASTIC keyword uses two quote strings. The first quote string is used to associate a specific statistical distribution to a variable in the code. The second quote string is a descriptive phrase used only for labeling purposes in output files. The first quote string, which must be unique, is a combination of analyte ID, species ID, and variable name. Character case and embedded spaces change the definition of the quote string. Table 4.17 gives example keywords for terrestrial species for a number of variables. In each case, the first quote string is the concatenation of the analyte ID (blank padded to six characters in length if necessary), the species ID (blank padded to six characters in length if necessary), and a variable name.

The first two example keywords in the table define the inhalation absorption factor (ALPHAVAP or α_{vapi}) for terrestrial animals (see Section 4.1.1.2.4). The second set of two example keywords defines the inhalation particulate absorption factor (ALPHAPAR or α_{pari}) for terrestrial animals (see Section 4.1.1.2.5). The third set of two example keywords defines the ingestion absorption factor (ALPHAING or α_{ingi}) for terrestrial animals (see Section 4.1.1.2.7). The fourth set of two example keywords defines the dermal permeability for soil (ALPHADS or α_{dci}) for terrestrial animals (see Section 4.1.1.2.5). The fifth set of two example keywords defines the dermal absorption for water (ALPHADW or K_{pi}) for terrestrial animals (see Section 4.1.1.2.2). If there were 10 analytes and 17 terrestrial animals, then five groups of 170 STOCHASTIC keywords would be required instead of the five groups of two example keywords.

Table 4.17 Example ECEM Keywords for the Growth Model for Terrestrial Animals

Analyte	Species	Variable	Description	Units	Statistical Distribution
CCl4	AMCOOT	ALPHAVAP (α_{vapi})	Inhalation absorption factor for CCl4 and AMCOOT	unitless	Triangular on Lower Limit .36, Mode .4, Upper Limit .44
STOCHASTIC "CCl4 AMCOOTALPHAVAP" 6 3.600E-01 4.000E-01 4.400E-01 "Inhalation absorption factor for CCl4 and AMCOOT"					
Cs137	COYOTE	ALPHAVAP (α_{vapi})	Inhalation absorption factor for Cs137 and COYOTE	unitless	Triangular on Lower Limit .421, Mode .468, Upper Limit .515
STOCHASTIC "Cs137 COYOTEALPHAVAP" 6 4.21E-01 4.68E-01 5.15E-01 "Inhalation absorption factor for Cs137 and COYOTE"					
CCl4	AMCOOT	ALPHAPAR (α_{pari})	Inhalation particulate absorption factor for CCl4 and AMCOOT	unitless	Triangular on Lower Limit .36, Mode .4, Upper Limit .44
STOCHASTIC "CCl4 AMCOOTALPHAPAR" 6 3.600E-01 4.000E-01 4.400E-01 "Inhalation particulate absorption factor for CCl4 and AMCOOT"					
CrVI	CARP	ALPHAPAR (α_{pari})	Inhalation particulate absorption factor for CrVI and CARP	unitless	Triangular on Lower Limit .288, Mode .32, Upper Limit .352

Analyte	Species	Variable	Description	Units	Statistical Distribution
colspan note					

STOCHASTIC "CrVI   CARP   ALPHAPAR" 6 2.88E-01 3.20E-01 3.52E-01
    "Inhalation particulate absorption factor for CrVI and CARP"

| AMCOOT | | ALPHAING (α_{ingi}) | Ingestion absorption factor for CCl4 and AMCOOT | unitless | Triangular on Lower Limit .585, Mode .65, Upper Limit .715 |

STOCHASTIC "CCl4 AMCOOTALPHAING" 6 5.850E-01 6.500E-01 7.150E-01
    "Ingestion absorption factor for CCl4 and AMCOOT"

| CrVI | CARP | ALPHAING (α_{ingi}) | Ingestion absorption factor for CrVI and CARP | Unitless | Triangular on Lower Limit .027, Mode .03, Upper Limit .033 |

STOCHASTIC "CrVI CARP ALPHAING" 6 2.70E-02 3.00E-02 3.30E-02
    "Ingestion absorption factor for CrVI and CARP"

| CCl4 | AMCOOT | ALPHADS (α_{dci}) | Dermal permeability (soil) for CCl4 and AMCOOT | unitless | Triangular on Lower Limit .009, Mode .01, Upper Limit .011 |

STOCHASTIC "CCl4 AMCOOTALPHADS " 6 9.000E-03 1.000E-02 1.100E-02
    "Dermal permeability (soil) for CCl4 and AMCOOT"

| CrVI | CARP | ALPHADS (α_{dci}) | Dermal permeability (soil) for CrVI and CARP | unitless | Triangular on Lower Limit .0031, Mode .00344, Upper Limit .00378 |

STOCHASTIC "CrVI CARP ALPHADS " 6 3.10E-03 3.44E-03 3.78E-03
    "Dermal permeability (soil) for CrVI and CARP"

| CCl4 | AMCOOT | ALPHADW (K_{pi}) | Dermal absorption (water) for CCl4 and AMCOOT | cm/hr | Triangular on Lower Limit .0198, Mode .022, Upper Limit .0242 |

STOCHASTIC "CCl4 AMCOOTALPHADW " 6 1.980E-02 2.200E-02 2.420E-02
    "Dermal absorption (water) for CCl4 and AMCOOT"

Analyte	Species	Variable	Description	Units	Statistical Distribution
Cs137	COYOTE	ALPHADW (K_{pi})	Dermal absorption (water) for Cs137 and COYOTE	cm/hr	Constant 0
STOCHASTIC "Cs137 COYOTEALPHADW " 1 0 "Dermal absorption (water) for Cs137 and COYOTE"					

The model for converting root uptake of analytes to above-ground plant-tissue concentrations requires a value for the octanol-water partitioning coefficient (KOW or K_{ow}) (see Section 4.1.1.1.2). A STOCHASTIC keyword for the KOW variable is needed for every combination of terrestrial plant species and analyte. Table 4.18 provides example keywords for this variable. The first quote string for the STOCHASTIC keywords would hold the concatenation of the analyte ID (blank padded to six characters long, if necessary) and the variable name KOW. A STOCHASTIC keyword is also needed for every combination of terrestrial plant and analytes for the bioconcentration factor for vegetation (BCFVEG or Bv) (see Section 4.1.1.1.2). The first quote string for the STOCHASTIC keywords for bioconcentration values would hold the concatenation of the analyte ID (blank padded to six characters long, if necessary) and the variable name BCFVEG.

Table 4.18 Example ECEM Keywords for the Root Uptake Model for Terrestrial Plants

Analyte	Variable	Description	Units	Statistical distribution
CCl4	K_{ow}	Octanol-water partition coefficient for CCl4	Unitless	Lognormal on Mean – 436.0, Standard deviation of Logarithms 21.8
STOCHASTIC "CCl4 KOW" 7 436.0 21.8 "Octanol-water partition coefficient for CCl4"				
CrVI	K_{ow}	Octanol-water partition coefficient for CrVI	Unitless	Constant 1.0
STOCHASTIC "CrVI KOW" 1 1.0 "Octanol-water partition coefficient for CrVI"				
Sr90	BCFVEG (Bv)	Bioconcentration factor for Sr90 in vegetation	Unitless	Triangular on Lower Limit 14.2, Mode 15.8, Upper Limit 17.4
STOCHASTIC "Sr90 BCFVEG" 6 1.42E+01 1.58E+01 1.74E+01 "Bioconcentration factor for Sr90 in vegetation"				
Tc99	BCFVEG (Bv)	Bioconcentration factor for Tc99 in vegetation	unitless	Triangular on Lower Limit 19.1, Mode 21.2, Upper Limit 23.3

Analyte	Variable	Description	Units	Statistical distribution
STOCHASTIC "Tc99 BCFVEG" 6 1.91E+01 2.12E+01 2.33E+01 "Bioconcentration factor for Tc99 in vegetation"				

Calculation of the external dose from contact with sediment for aquatic species requires information about the fraction of time the species spends above water. The equation for this calculation is given in Section 4.1.3.2. A distinct STOCHASTIC keyword is needed for every aquatic species for this variable, and three examples are given in Table 4.19. The first quote string for the STOCHASTIC keywords would hold the concatenation of the specie ID (blank padded to six characters long, if necessary) and the variable name FABOVE.

Table 4.19 Example ECEM Keywords for the Time Fraction Aquatic Animals Spend Above Water

Species	Variable	Description	Units	Statistical Distribution
AMCOOT	FABOVE	Fraction of time spent above water for AMCOOT	Unitless	Constant 1.0
STOCHASTIC "AMCOOTFABOVE" 1 1.0 "Fraction of time spent above water for AMCOOT"				
AMKSTL	FABOVE	Fraction of time spent above water for AMKSTL	Unitless	Constant 1.0
STOCHASTIC "AMKSTLFABOVE" 1 1.0 "Fraction of time spent above water for AMKSTL"				

Calculation of doses for animal species from dermal contact with contaminants is dependent on the depuration rate of the species (see Section 4.1.1.2.1). A distinct STOCHASTIC keyword is needed for every animal species for this variable, and three examples are given in Table 4.20. The first quote string for the STOCHASTIC keywords would hold the concatenation of the analyte ID (blank padded to six characters in length, if necessary), the specie ID (blank padded to 6 characters in length, if necessary) and the variable name DEPRATE.

Table 4.20 Example ECEM Keywords for the Depuration Rate for Animal Species

Analyte	Species	Variable	Description	Units	Statistical Distribution
CCl4	AMCOOT	DEPRATE (K_{ei})	Depuration rate of AMCOOT for CCl4	1/day	Triangular on Lower Limit .765, Mode .85, Upper Limit .935
STOCHASTIC "CCl4 AMCOOTDEPRATE" 6 7.650E-01 8.500E-01 9.350E-01 "Depuration rate of AMCOOT for CCl4"					
CrVI	CARP	DEPRATE (K_{ei})	Depuration rate of CARP for CrVI	1/day	Triangular on Lower Limit .0468, Mode .052, Upper Limit .0572

Analyte	Species	Variable	Description	Units	Statistical Distribution
STOCHASTIC "CrVI CARP DEPRATE" 6 4.680E-02 5.200E-02 5.720E-02 "Depuration rate of CARP for CrVI"					
Cs137	COYOTE	DEPRATE (K_{ei})	Depuration rate of COYOTE for Cs137	1/day	Triangular on Lower Limit .072, Mode .08, Upper Limit .088
STOCHASTIC "Cs137 COYOTEDEPRATE" 6 7.200E-02 8.000E-02 8.800E-02 "Depuration rate of COYOTE for Cs137"					

Calculation of the body burden for aquatic animal species is dependent on the chemical assimilation of contaminants for the species (see Section 4.1.2.1). A distinct STOCHASTIC keyword is needed for every animal species for this variable, and three examples are given in Table 4.21. The first quote string for the STOCHASTIC keywords would hold the concatenation of the analyte ID (blank padded to six characters long, if necessary), the species ID (blank padded to six characters in length, if necessary) and the variable name ALPHAIJ.

Table 4.21 Example ECEM Keywords for the Chemical Assimilation for Aquatic Animal Species

Analyte	Species	Variable	Description	Units	Statistical Distribution
CCl4	CARP	ALPHAIJ (α_{ij})	Chemical assimilation efficiency of CARP for CCl4	g contaminant assimilated per g contaminant ingested	Constant 1
STOCHASTIC "CCl4 CARP ALPHAIJ" 1 1 "Chemical assimilation efficiency of CARP for CCl4"					
CrVI	CHCATF	ALPHAIJ (α_{ij})	Chemical assimilation efficiency of CHCATF for CrVI	g contaminant assimilated per g contaminant ingested	Triangular on Lower Limit .027, Mode .03, Upper Limit .033
STOCHASTIC "CrVI CHCATFALPHAIJ" 6 2.700E-02 3.000E-02 3.300E-02 "Chemical assimilation efficiency of CHCATF for CrVI"					
CrVI	CLAMS	ALPHAIJ (α_{ij})	Chemical assimilation efficiency of CLAMS for CrVI	g contaminant assimilated per g contaminant ingested	Triangular on Lower Limit .0243, Mode .027, Upper Limit .0297
STOCHASTIC "CrVI CLAMS ALPHAIJ" 6 2.430E-02 2.700E-02 2.970E-02 "Chemical assimilation efficiency of CLAMS for CrVI"					

Calculation of the body burden for aquatic animal species is dependent on the bioconcentration factor of contaminants for the species (see Section 4.1.2.1). A distinct STOCHASTIC keyword is needed for every combination of animal species and nonorganic analyte for this variable, and three examples are given in Table 4.22. The first quote string for the STOCHASTIC keywords would hold the concatenation of the

User Instructions for the Systems Assessment Capability, Rev. 0, Computer Codes
Volume 2: Impact Modules

analyte ID (blank padded to six characters long, if necessary), the species ID (blank padded to six characters long, if necessary), and the variable name BCF.

Table 4.22 Example ECEM Keywords for the Bioconcentration Factor for Aquatic Animal Species

Analyte	Species	Variable	Description	Units	Statistical Distribution
CrVI	CARP	BCF	Bioconcentration factor of CARP for CrVI	L/kg	Triangular on Lower Limit .018, Mode .02, Upper Limit .022
STOCHASTIC "CrVI CARP BCF" 6 1.800E-02 2.000E-02 2.200E-02 "Bioconcentration factor of CARP for CrVI"					
CrVI	CPBLSN	BCF	Bioconcentration factor of CPBLSN for CrVI	L/kg	Triangular on Lower Limit .09, Mode .1, Upper Limit .11
STOCHASTIC "CrVI CPBLSNBCF" 6 9.000E-02 1.000E-01 1.100E-01 "Bioconcentration factor of CPBLSN for CrVI"					
U238	MAYFLY	BCF	Bioconcentration factor of MAYFLY for U238	L/kg	Triangular on Lower Limit .000279, Mode .00031, Upper Limit .000341
STOCHASTIC "U238 MAYFLYBCF" 6 2.790E-04 3.100E-04 3.410E-04 "Bioconcentration factor of MAYFLY for U238"					

Calculation of the body burden for aquatic animal species is dependent on the metabolism loss rate of the analyte for the species (see Section 4.1.2.1). A distinct STOCHASTIC keyword is needed for every combination of animal species analyte for this variable, and three examples are given in Table 4.23. The first quote string for the STOCHASTIC keywords would hold the concatenation of the analyte ID (blank padded to six characters long, if necessary), the specie ID (blank padded to six characters long, if necessary), and the variable name METBLOSS.

Table 4.23 Example ECEM Keywords for the Metabolism Loss Rate for Aquatic Species

Analyte	Species	Variable	Description	Units	Statistical Distribution
CCl4	CARP	METBLOSS (K_{mi})	Metabolism loss rate for CCl4 in CARP	1/day	Constant 0
STOCHASTIC "CCl4 CARP METBLOSS" 1 0 "Metabolism loss rate for CCl4 in CARP"					
Cs137	MAYFLY	METBLOSS (K_{mi})	Metabolism loss rate for Cs137 in MAYFLY	1/day	Constant 0
STOCHASTIC "Cs137 MAYFLYMETBLOSS" 1 0 "Metabolism loss rate for Cs137 in MAYFLY"					

Analyte	Species	Variable	Description	Units	Statistical Distribution
I129	MAYFLY	METBLOSS (K_{mi})	Metabolism loss rate for I129 in MAYFLY	1/day	Constant 0
STOCHASTIC "I129 MAYFLYMETBLOSS" 1 0 "Metabolism loss rate for I129 in MAYFLY"					

The calculation of body burden for terrestrial plants includes the plant-air partition coefficient for air to above-ground plant parts for particulate-bound contaminants (K_{pa2}) and the plant-soil partition coefficient for rain splash (K_{ps1}). See Section 4.1.1.1.4 for a description of K_{pa2} and Section 4.1.1.1.1 for a description of K_{ps1}. A distinct STOCHASTIC keyword is needed for every terrestrial plant species analyte for this variable, and two examples are given in Table 4.24. The first quote string for the STOCHASTIC keywords would hold the concatenation of the species ID (blank padded to six characters long, if necessary), and the variable name KPS1 or KPA2.

Table 4.24 Example ECEM Keywords for Plant-Air Partition Coefficients

Species	Variable	Description	Units	Statistical Distribution
BLCTWD	KPS1	Plant-soil partition coefficient for BLCTWD	Kg soil/kg plant wet wt	Triangular on Lower Limit .00306, Mode .0034, Upper Limit .00374
STOCHASTIC "BLCTWDKPS1 " 6 3.060E-03 3.400E-03 3.740E-03 "Plant-Soil partition coefficient for BLCTWD"				
BLCTWD	KPA2	Plant-air partition coefficient for BLCTWD	m^3/kg wet weight	Triangular on Lower Limit 2,970; Mode 3,300; Upper Limit 3,630
STOCHASTIC "BLCTWDKPA2 " 6 2.970E+03 3.300E+03 3.630E+03 "Plant-Air partition coefficient for BLCTWD"				

The calculation of body burden for aquatic species depends in the fraction of the time the species spends in pore water (see Section 4.1.2.1). A distinct STOCHASTIC keyword is needed for every aquatic species for this variable, and two examples are given in Table 4.25. The first quote string for the STOCHASTIC keywords would hold the concatenation of the species ID (blank padded to six characters long, if necessary), and the variable name BPORE.

Table 4.25 Example ECEM Keywords for the Fraction of Time Aquatic Species Spend in Pore Water

Species	Variable	Description	Units	Statistical Distribution
CARP	BPORE	Relative exposure time to pore water for CARP	unitless	Triangular on Lower Limit .045, Mode .05, Upper Limit .055
STOCHASTIC "CARP BPORE " 6 4.500E-02 5.000E-02 5.500E-02 "Relative exposure time to pore water for CARP"				

Species	Variable	Description	Units	Statistical Distribution
CHCATF	BPORE	Relative exposure time to pore water for CHCATF	unitless	Triangular on Lower Limit .09, Mode .1, Upper Limit .11
STOCHASTIC "CHCATFBPORE " 6 9.000E-02 1.000E-01 1.100E-01 "Relative exposure time to pore water for CHCATF"				

5.0   Human Impacts Model (HUMAN)

This section contains instructions for the use of the human exposure and risk models and provides the mathematical formulation for the model is provided.

5.1   Mathematical Formulation for the Human Risk Model

The human risk model is a screening-level chronic exposure model. It is intended for use in situations where the environmental contamination conditions are static or only slowly varying. These conditions are met with the System Assessment Capability contaminant sources, which are slowly released to the accessible environment, primarily via groundwater transport. The models are not appropriate for estimating risks from short-term accidental releases.

The HUMAN code addresses pathways related to long-term contamination of surface water and groundwater, with the associated contaminated media of seeps, springs, and sediments. With these as starting points, the code estimates the contaminant concentrations in surface soil from irrigation, air from resuspension and volatilization, aquatic foods, terrestrial crops, and animal products. Both domestic animals and wild animals may be included. Exposure pathways explicitly modeled include external irradiation, dermal contact, inhalation, and ingestion. Special models are included for unique Native American exposure situations. The code deals with first-order decay of radionuclides but not with degradation processes for chemicals.

The HUMAN code provides flexibility in combining the various pathways into exposure scenarios. Scenarios are defined through the use of representative sets of input parameters to simulate annual average or lifetime average exposure conditions. The scenarios are focused on individual exposures. Individuals are assumed to spend the amounts of time specified in the scenario at the location of analysis; individual mobility throughout the analysis domain is not supported. Population risks are only addressed for the pathway of consumption of drinking water from the Columbia River.

The HUMAN code provides results for radioactive contaminants; non-radioactive but carcinogenic contaminants; and non-radioactive, non-carcinogenic, but still hazardous contaminants. Radiation impacts to people may be calculated as either radiation dose or risk; carcinogenic chemical risks are provided in terms of risk of fatal cancer; risks from hazardous chemicals are provided as Hazard Quotients – the dimensionless ratio of the estimated intake to a standard Reference Dose.

The HUMAN code is designed to accept multiple realizations of concentration of contaminants in the environment. It allows the definition of stochastic exposure parameters, which combine with the uncertainty in the input media concentrations to provide a full range of uncertainty on the final dose or risk to the hypothetical exposed individual.

The following sections provide the mathematical formulations for the human risk model. A more extensive discussion of this model is provided in Chapter 5 of DOE (1998). The equations have been reorganized from that in DOE (1998) and the concentration equations for terrestrial foods (Section 5.1.3.2) have been modified and expanded.

5.1.1   Human Exposure Equations Derived by Pathway

The following equations represent the total exposure of a person to radionuclides or chemicals. These equations describe the exposure or intake and the risk resulting from those exposures. Note that the user may substitute groundwater for seep/spring water in some scenario definitions.

5.1.1.1   External Radiation Exposure

The radiation dose from external radiation sources is computed for a number of activities using the following equation:

$$
\begin{aligned}
\text{Dose}_{ext} = \ & C_{river} \times ET_{swim} \times EF_{swim} \times ED \times DF_{swim} + \\
& C_{river} \times ET_{boat} \times EF_{boat} \times ED \times DF_{boat} + \\
& C_{soil} \times SH_{soil} \times ET_{soil} \times EF_{soil} \times ED \times DF_{soil} + \\
& C_{sed} \times SH_{sed} \times ET_{sed} \times EF_{sed} \times ED \times DF_{soil}
\end{aligned}
$$

where:

C_{river}	=	radionuclide concentration in river water (pCi/L)
C_{sed}	=	radionuclide concentration in sediment (pCi/g)
C_{soil}	=	radionuclide concentration in soil (pCi/g)
DF_{soil}	=	dose conversion factor for soil and sediment (rem/hr per pCi/g)
DF_{swim}	=	dose conversion factor for swimming (rem/hr per pCi/L)
DF_{boat}	=	dose conversion factor for boating (rem/hr per pCi/L)
Dose_{ext}	=	dose from external radionuclides (rem)
ED	=	exposure duration (year)
EF_{boat}	=	exposure frequency for boating (days/year)
EF_{sed}	=	exposure frequency for sediment (days/year)
EF_{soil}	=	exposure frequency for soil (days/year)
EF_{swim}	=	exposure frequency for swimming (days/year)
ET_{boat}	=	exposure time for boating (hours/day)
ET_{sed}	=	exposure time for sediment (hours/day)
ET_{soil}	=	exposure time for soil (hours/day)
ET_{swim}	=	exposure time for swimming (hours/day)
SH_{sed}	=	shielding factor for sediment (unitless)
SH_{soil}	=	shielding factor for soil (unitless).

5.1.1.2   Dermal Exposure (Non-Carcinogenic, Non-Radioactive)

The hazard quotient from dermal contact with non-carcinogenic, non-radioactive materials is computed for a number of activities using the following equation:

$$
\begin{aligned}
DAHQ = \ & C_{soil} \times AF_{soil} \times ABS \times SA_{soil} \times EF_{soil} \times CF1 \times ED \times CF7 \, / \, (\, BW_{adult} \times AT \times HQ) + \\
& C_{sed} \times AF_{sed} \times ABS \times SA_{sed} \times EF_{sed} \times CF1 \times ED \times CF7 \, / \, (\, BW_{adult} \times AT \times HQ) + \\
& C_{seep} \times K_{p} \times SA_{seep} \times ET_{seep} \times EF_{seep} \times CF3 \times ED \times CF7 \, / \, (\, BW_{adult} \times AT \times HQ) + \\
& C_{swim} \times K_{p} \times SA_{river} \times ET_{river} \times EF_{river} \times CF3 \times ED \times CF7 \, / \, (\, BW_{adult} \times AT \times HQ)
\end{aligned}
$$

where:

ABS	=	material-specific absorption factor (unitless)
AF_{sed}	=	adherence factor for sediment (mg/cm^2 per day)
AF_{soil}	=	adherence factor for soil (mg/cm^2 per day)
AT	=	averaging time (year x 365 days/year)
BW_{adult}	=	body weight factor of an adult (kg)
C_{sed}	=	contaminant concentration in sediment (µg/kg)
C_{seep}	=	contaminant concentration in seep/spring water (µg/L)
C_{soil}	=	contaminant concentration in soil (µg/kg)
C_{swim}	=	contaminant concentration for swimming (µg/L)
CF1	=	unit conversion factor (lE-6 kg/mg)
CF3	=	unit conversion factor (1E-3 L/cm^3)
CF7	=	conversion factor (1E-3 mg/µg)
DAHQ	=	hazard quotient from dermal absorption (unitless)
ED	=	exposure duration (year)
EF_{soil}	=	exposure frequency to soil (days/year)
EF_{river}	=	exposure frequency to river water (days/year)
EF_{sed}	=	exposure frequency to sediment (days/year)
EF_{seep}	=	exposure frequency to seep/spring water (days/year)
ET_{river}	=	exposure time to river water (hours/day)
ET_{seep}	=	exposure time to seep/spring water (hours/day)
HQ	=	reference dose (mg/kg per day)
K_p	=	permeability coefficient for a chemical in water through skin (cm/hour)
SA_{soil}	=	body surface area exposed to soil (cm^2)
SA_{river}	=	body surface area exposed to river water (cm^2)
SA_{sed}	=	body surface area exposed to sediment (cm^2)
SA_{seep}	=	body surface area exposed to seep/spring water (cm^2).

5.1.1.3   Dermal Exposure (Carcinogenic, Non-Radioactive)

The risk from dermal contact with carcinogenic, non-radioactive materials is computed for a number of activities using the following equation:

$$
\begin{aligned}
DAR = \; & C_{soil} \,^X AF_{soil} \,^X ABS \,^X SA_{soil} \,^X EF_{soil} \,^X CF1 \,^X ED \,^X SF_{ing} \,^X CF7 / (BW_{adult} \,^X AT) + \\
& C_{sed} \,^X AF_{sed} \,^X ABS \,^X SA_{sed} \,^X EF_{sed} \,^X CF1 \,^X ED \,^X SF_{ing} \,^X CF7 / (BW_{adult} \,^X AT) + \\
& C_{seep} \,^X K_p \,^X SA_{seep} \,^X ET_{seep} \,^X EF_{seep} \,^X CF3 \,^X ED \,^X SF_{ing} \,^X CF7 / (BW_{adult} \,^X AT) + \\
& C_{swim} \,^X K_p \,^X SA_{river} \,^X ET_{river} \,^X EF_{river} \,^X CF3 \,^X ED \,^X SF_{ing} \,^X CF7 / (BW_{adult} \,^X AT)
\end{aligned}
$$

where:

ABS	=	material-specific absorption factor (unitless)
AF_{sed}	=	adherence factor for sediment (mg/cm^2 per day)
AF_{soil}	=	adherence factor for soil (mg/cm^2 per day)
AT	=	averaging time (year x 365 days/year)
BW_{adult}	=	body weight factor of an adult (kg)
C_{sed}	=	contaminant concentration in sediment (µg/kg)

C_{seep}	=	contaminant concentration in seep/spring water (μg/L)
C_{soil}	=	contaminant concentration in soil (μg/kg)
C_{swim}	=	contaminant concentration swimming (μg/L)
CF1	=	unit conversion factor (lE-6 kg/mg)
CF3	=	unit conversion factor (1E-3 L/cm³)
CF7	=	conversion factor (1E-3 mg/μg)
DAR	=	risk from dermal absorption (risk)
ED	=	exposure duration (year)
EF_{soil}	=	exposure frequency to soil (days/year)
EF_{river}	=	exposure frequency to river water (days/year)
EF_{sed}	=	exposure frequency to sediment (days/year)
EF_{seep}	=	exposure frequency to seep/spring water (days/year)
ET_{river}	=	exposure time to river water (hours/day)
ET_{seep}	=	exposure time to seep/spring water (hours/day)
SF_{ing}	=	slope factor (kg per day/mg)
K_p	=	permeability coefficient for a chemical in water through skin (cm/hour)
SA_{river}	=	body surface area exposed to river water (cm²)
SA_{seep}	=	body surface area exposed to seep/spring water (cm²).

5.1.1.4 Inhalation Exposure (Carcinogenic)

The risk from inhalation of carcinogenic materials is computed for a number of activities using the following equation:

$$
\begin{aligned}
INHC = \; & C_{soil} \,^X ML \,^X ET_{soil} \,^X EF_{soil} \,^X ED \,^X IRATE \,^X SF_{inh} \,^X CF7 / (AT \,^X BW_{adult} \,^X CF4) + \\
& C_{seep} \,^X VF \,^X ET_{seep} \,^X EF_{seep} \,^X ED \,^X IRATE \,^X SF_{inh} \,^X CF7 / (AT \,^X BW_{adult} \,^X CF4) + \\
& C_{river} \,^X VF \,^X ET_{river} \,^X EF_{river} \,^X ED \,^X IRATE \,^X SF_{inh} \,^X CF7 / (AT \,^X BW_{adult} \,^X CF4) + \\
& C_{sweat} \,^X CF_{sweat} \,^X ET_{sweat} \,^X EF_{sweat} \,^X ED \,^X IRATE \,^X SF_{inh} \,^X CF7 / (AT \,^X BW_{adult} \,^X CF4)
\end{aligned}
$$

where:

AT	=	averaging time (year x 365 days/year)
BW_{adult}	=	body weight (kg)
C_{river}	=	contaminant concentration in river water (μg/L)
C_{seep}	=	contaminant concentration in seep/spring water (μg/L)
C_{soil}	=	contaminant concentration in soil (μg/kg)
C_{sweat}	=	contaminant concentration in water used in a sweat lodge (μg/L)
CF4	=	unit conversion factor (24 hours/day)
CF7	=	conversion factor (1E-3 mg/μg)
CF_{sweat}	=	volatilization factor for water used in Native American sweat lodges (L/m³)
ED	=	exposure duration (year)
EF_{river}	=	exposure frequency to volatilized river water (day/year)
EF_{seep}	=	exposure frequency to volatilized seep/spring water (day/year)
EF_{soil}	=	exposure frequency to soil (day/year)
EF_{sweat}	=	exposure frequency to a sweat lodge (day/year)
ET_{river}	=	exposure time for breathing volatilized river water (hours/day)

ET_{seep} = exposure time for breathing volatilized seep/spring water (hours/day)
ET_{soil} = exposure time for breathing soil (hours/day)
ET_{sweat} = exposure time for breathing in a sweat lodge (hours/day)
INHC = chronic inhalation risk from carcinogens (risk)
IRATE = inhalation (breathing) rate (m³/day)
ML = mass loading of soil in the air (kg/m³)
SF_{inh} = slope factor for inhalation (kg per day/mg)
VF = volatilization factor (L/m³).

5.1.1.5 Inhalation Exposure (Hazardous)

The hazard quotient from inhalation of non-carcinogenic, non-radioactive, materials is computed for a number of activities using the following equation:

$$
\begin{aligned}
INHQ = \ & C_{soil}{}^X ML {}^X ET_{soil} {}^X EF_{soil} {}^X ED {}^X IRATE {}^X CF7 / (AT {}^X BW_{adult} {}^X CF4 {}^X HQ) + \\
& C_{seep}{}^X VL {}^X ET_{seep} {}^X EF_{seep} {}^X ED {}^X IRATE {}^X CF7 / (AT {}^X BW_{adult} {}^X CF4 {}^X HQ) + \\
& C_{river}{}^X VL {}^X ET_{river} {}^X EF_{river} {}^X ED {}^X IRATE {}^X CF7 / (AT {}^X BW_{adult} {}^X CF4 {}^X HQ) + \\
& C_{sweat}{}^X CF_{sweat} {}^X ET_{sweat} {}^X EF_{sweat} {}^X ED {}^X IRATE {}^X CF7 / (AT {}^X BW_{adult} {}^X CF4 {}^X HQ)
\end{aligned}
$$

where:
AT = averaging time (year x 365 days/year)
BW_{adult} = body weight (kg)
C_{river} = contaminant concentration in river water (µg/L)
C_{seep} = contaminant concentration in seep/spring water (µg/L)
C_{soil} = contaminant concentration in soil (µg/kg)
C_{sweat} = contaminant concentration in water used in a sweat lodge (µg/L)
CF4 = unit conversion factor (24 hours/day)
CF7 = conversion factor (1E-3 mg/µg)
CF_{sweat} = volatilization factor for water used in Native American sweat lodges (L/m³)
ED = exposure duration (year)
EF_{river} = exposure frequency to volatilized river water (day/year)
EF_{seep} = exposure frequency to volatilized seep/spring water (day/year)
EF_{soil} = exposure frequency to soil (day/year)
EF_{sweat} = exposure frequency to a sweat lodge (day/year)
ET_{river} = exposure time for breathing volatilized river water (hours/day)
ET_{seep} = exposure time for breathing volatilized seep/spring water (hours/day)
ET_{soil} = exposure time for breathing soil (hours/day)
ET_{sweat} = exposure time for breathing in a sweat lodge (hours/day)
HQ = reference dose for inhalation (mg/kg per day)
INHQ = chronic inhalation hazard quotient (unitless)
IRATE = inhalation rate (m³/day)
ML = mass loading of soil in the air (kg/m³)
VF = volatilization factor (L/m³).

5.1.1.6 Inhalation Exposure (Radioactive)

The radiation dose from inhalation of radioactive materials is computed for a number of activities using the following equation:

$$
\begin{aligned}
\text{Dose}_{inh} = \quad & C_{soil}\ ^X\ ML\ ^X\ ET_{soil}\ ^X\ EF_{soil}\ ^X\ ED\ ^X\ IRATE\ ^X\ DF5\ /\ CF4\ + \\
& C_{seep}\ ^X\ VF\ ^X\ ET_{seep}\ ^X\ EF_{seep}\ ^X\ ED\ ^X\ IRATE\ ^X\ DF5\ /\ CF4\ + \\
& C_{river}\ ^X\ VF\ ^X\ ET_{river}\ ^X\ EF_{river}\ ^X\ ED\ ^X\ IRATE\ ^X\ DF5\ /\ CF4\ + \\
& C_{sweat}\ ^X\ CF_{sweat}\ ^X\ ET_{sweat}\ ^X\ EF_{sweat}\ ^X\ ED\ ^X\ IRATE\ ^X\ DF5\ /\ CF4
\end{aligned}
$$

where:

C_{river}	=	radionuclide concentration in river water (pCi/L)
C_{seep}	=	radionuclide concentration in seep/spring water (pCi/L)
C_{soil}	=	radionuclide concentration in soil (pCi/kg)
C_{sweat}	=	radionuclide concentration in water used in a sweat lodge (pCi/L)
CF4	=	unit conversion factor (24 hours/day)
CF_{sweat}	=	volatilization factor for water used in Native American sweat lodges (L/m^3)
DF5	=	dose conversion factor for inhalation (rem/pCi)
Dos_{einh}	=	dose from inhalation of radionuclides (rem)
ED	=	exposure duration (year)
EF_{sweat}	=	exposure frequency to materials resuspended during cultural activities (days/year)
EF_{river}	=	exposure frequency to volatilized river water (days/year)
EF_{seep}	=	exposure frequency to volatilized seep/spring water (days/year)
EF_{soil}	=	exposure frequency to volatilized soil (days/year)
ET_{sweat}	=	exposure time for breathing materials suspended during cultural activities (hours/day)
ET_{river}	=	exposure time for breathing volatilized river water (hours/day)
ET_{seep}	=	exposure time for breathing volatilized seep/spring water (hours/day)
EF_{soil}	=	exposure time for breathing volatilized soil (hours/day)
IRATE =		inhalation rate (m^3/day)
ML	=	mass loading of soil in the air (kg/m^3)
VF	=	volatilization factor (L/m^3).

5.1.1.7 Ingestion Exposure (Hazardous)

The hazard quotient from ingestion of non-carcinogenic, non-radioactive materials is computed for a number of activities using the following equation:

$$
\begin{aligned}
\text{INGQ} = \quad & C_{river}\ ^X\ IR_{river}\ ^X\ ED\ ^X\ EF_{river}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{adult}\ ^X\ HQ)\ + \\
& C_{ground}\ ^X\ IR_{ground}\ ^X\ ED\ ^X\ EF_{ground}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{adult}\ ^X\ HQ)\ + \\
& C_{seep}\ ^X\ IR_{seep}\ ^X\ ED\ ^X\ EF_{seep}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{adult}\ ^X\ HQ)\ + \\
& C_{soil}\ ^X\ IR_{soilchild}\ ^X\ ED_{child}\ ^X\ EF_{soil}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{child}\ ^X\ HQ\ )\ + \\
& C_{soil}\ ^X\ IR_{soiladult}\ ^X\ ED_{adult}\ ^X\ EF_{soil}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{adult}\ ^X\ HQ\ )\ + \\
& C_{sed}\ ^X\ IR_{sedchild}\ ^X\ ED_{child}\ ^X\ EF_{sed}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{child}\ ^X\ HQ\ )\ + \\
& C_{sed}\ ^X\ IR_{sedadult}\ ^X\ ED_{adult}\ ^X\ EF_{sed}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{adult}\ ^X\ HQ\ )\ + \\
& C_{leafy}\ ^X\ IR_{leafy}\ ^X\ ED\ ^X\ EF_{leafy}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{adult}\ ^X\ HQ\ )\ + \\
& C_{root}\ ^X\ IR_{root}\ ^X\ ED\ ^X\ EF_{root}\ ^X\ CF7\ /\ (\ AT\ ^X\ BW_{adult}\ ^X\ HQ\ )\ +
\end{aligned}
$$

$$C_{meat} \times IR_{meat} \times ED \times EF_{meat} \times CF7 / (AT \times BW_{adult} \times HQ) +$$
$$C_{milk} \times IR_{milk} \times ED \times EF_{milk} \times CF7 / (AT \times BW_{adult} \times HQ) +$$
$$C_{bird} \times IR_{bird} \times ED \times EF_{bird} \times CF7 / (AT \times BW_{adult} \times HQ) +$$
$$C_{fish} \times IR_{fish} \times ED \times EF_{fish} \times CF7 / (AT \times BW_{adult} \times HQ)$$

where:

AT	=	averaging time (year x 365 days/yr)
BW_{adult}	=	body weight for adult (kg)
BW_{child}	=	body weight for adult (kg)
C_{bird}	=	contaminant concentration in domestic and wild birds (µg/kg)
C_{fish}	=	contaminant concentration in fish (µg/kg)
C_{ground}	=	contaminant concentration in groundwater (µg/kg)
C_{leafy}	=	contaminant concentration in above-ground vegetation (µg/kg)
C_{meat}	=	contaminant concentration in meat (µg/kg)
C_{milk}	=	contaminant concentration in milk (µg/kg)
C_{river}	=	contaminant concentration in river water (µg/kg)
C_{root}	=	contaminant concentration in root vegetables (µg/kg)
C_{sed}	=	contaminant concentration in sediment (µg/kg)
C_{seep}	=	contaminant concentration in seep/spring water (µg/kg)
C_{soil}	=	contaminant concentration in soil (µg/kg)
$CF7$	=	conversion factor (1E-3 mg/µg)
ED	=	lifetime exposure duration (year)
ED_{child}	=	exposure duration for a child (year)
ED_{adult}	=	exposure duration for an adult (year)
EF_{bird}	=	exposure frequency for a bird (days/year)
EF_{fish}	=	exposure frequency for a fish (days/year)
EF_{ground}	=	exposure frequency for ground (days/year)
EF_{leafy}	=	exposure frequency for above-ground vegetation (days/year)
EF_{meat}	=	exposure frequency for meat (days/year)
EF_{milk}	=	exposure frequency for milk (days/year)
EF_{river}	=	exposure frequency for river (days/year)
EF_{root}	=	exposure frequency for a root (days/year)
EF_{sed}	=	exposure frequency for sediment (days/year)
EF_{seep}	=	exposure frequency for seep (days/year)
EF_{soil}	=	exposure frequency for a bird (days/year)
HQ	=	reference dose for ingestion (mg/kg per day)
$INGQ$	=	chronic ingestion hazard quotient (unitless)
IR_{bird}	=	ingestion rate of domestic and wild birds (kg/day)
IR_{fish}	=	ingestion rate of fish (kg/day)
IR_{ground}	=	ingestion rate of groundwater (kg/day)
IR_{leafy}	=	ingestion rate of above-ground vegetation (kg/day)
IR_{meat}	=	ingestion rate of meat (kg/day)
IR_{milk}	=	ingestion rate of milk (kg/day)
IR_{river}	=	ingestion rate of river water (kg/day)
IR_{root}	=	ingestion rate of root vegetables (kg/day)

$IR_{sedadult}$ = ingestion rate of sediment by an adult (kg/day)

$IR_{sedchild}$ = ingestion rate of sediment by a child (kg/day)

IR_{seep} = ingestion rate of seep/spring water (kg/day)

$IR_{soiladult}$ = ingestion rate of soil by an adult (kg/day)

$IR_{soilchild}$ = ingestion rate of soil by a child (kg/day).

5.1.1.8 Ingestion Exposure (Carcinogenic)

The risk from ingestion of carcinogenic, non-radioactive, materials is computed for a number of activities using the following equation:

$$
\begin{aligned}
INGR = \ & C_{river}{}^X IR_{river}{}^X ED{}^X EF_{river}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{ground}{}^X IR_{ground}{}^X ED{}^X EF_{ground}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{seep}{}^X IR_{seep}{}^X ED{}^X EF_{seep}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{soil}{}^X IR_{soilchild}{}^X ED_{child}{}^X EF_{soil}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{child}) + \\
& C_{soil}{}^X IR_{soiladult}{}^X ED_{adult}{}^X EF_{soil}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{sed}{}^X IR_{sedchild}{}^X ED_{child}{}^X EF_{sed}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{child}) + \\
& C_{sed}{}^X IR_{sedadult}{}^X ED_{adult}{}^X EF_{sed}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{leafy}{}^X IR_{leafy}{}^X ED{}^X EF_{leafy}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{root}{}^X IR_{root}{}^X ED{}^X EF_{root}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{meat}{}^X IR_{meat}{}^X ED{}^X EF_{meat}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{milk}{}^X IR_{milk}{}^X ED{}^X EF_{milk}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{bird}{}^X IR_{bird}{}^X ED{}^X EF_{bird}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult}) + \\
& C_{fish}{}^X IR_{fish}{}^X ED{}^X EF_{fish}{}^X SF_{ing}{}^X CF7 / (AT{}^X BW_{adult})
\end{aligned}
$$

where:

AT = averaging time (year x 365 days/yr)

BW_{adult} = body weight for adult (kg)

BW_{child} = body weight for adult (kg)

C_{bird} = contaminant concentration in domestic and wild birds (µg/kg)

C_{fish} = contaminant concentration in fish (µg/kg)

C_{ground} = contaminant concentration in groundwater (µg/kg)

C_{leafy} = contaminant concentration in above-ground vegetation (µg/kg)

C_{meat} = contaminant concentration in meat (µg/kg)

C_{milk} = contaminant concentration in milk (µg/kg)

C_{river} = contaminant concentration in river water (µg/kg)

C_{root} = contaminant concentration in root vegetables (µg/kg)

C_{sed} = contaminant concentration in sediment (µg/kg)

C_{seep} = contaminant concentration in seep/spring water (µg/kg)

C_{soil} = contaminant concentration in soil (µg/kg)

$CF7$ = conversion factor (1E-3 mg/µg)

ED = lifetime exposure duration (year)

ED_{child} = exposure duration for a child (year)

ED_{adult} = exposure duration for an adult (year)

EF_{bird} = exposure frequency for a bird (days/year)

EF_{fish}	=	exposure frequency for a fish (days/year)
EF_{ground}	=	exposure frequency for ground (days/year)
EF_{leafy}	=	exposure frequency for above-ground vegetation (days/year)
EF_{meat}	=	exposure frequency for meat (days/year)
EF_{milk}	=	exposure frequency for milk (days/year)
EF_{river}	=	exposure frequency for river (days/year)
EF_{root}	=	exposure frequency for a root (days/year)
EF_{sed}	=	exposure frequency for sediment (days/year)
EF_{seep}	=	exposure frequency for seep (days/year)
EF_{soil}	=	exposure frequency for a bird (days/year)
INGR	=	chronic ingestion cancer risk (risk)
IR_{bird}	=	ingestion rate of domestic and wild birds (kg/day)
IR_{fish}	=	ingestion rate of fish (kg/day)
IR_{ground}	=	ingestion rate of groundwater (kg/day)
IR_{leafy}	=	ingestion rate of above-ground vegetation (kg/day)
IR_{meat}	=	ingestion rate of meat (kg/day)
IR_{milk}	=	ingestion rate of milk (kg/day)
IR_{river}	=	ingestion rate of river water (kg/day)
IR_{root}	=	ingestion rate of root vegetables (kg/day)
$IR_{sedadult}$	=	ingestion rate of sediment by an adult (kg/day)
$IR_{sedchild}$	=	ingestion rate of sediment by a child (kg/day)
IR_{seep}	=	ingestion rate of seep/spring water (kg/day)
$IR_{soiladult}$	=	ingestion rate of soil by an adult (kg/day)
$IR_{soilchild}$	=	ingestion rate of soil by a child (kg/day)
SF_{ing}	=	slope factor for ingestion (kg per day/mg).

5.1.1.9 Ingestion Exposure (Radioactive)

The dose from ingestion of radioactive materials is computed for a number of activities using the following equation:

$$
\begin{aligned}
Dose_{ing} = \quad & C_{seep}{}^X IR_{seep}{}^X EF_{seep}{}^X ED{}^X DF6 + \\
& C_{river}{}^X IR_{river}{}^X EF_{river}{}^X ED{}^X DF6 + \\
& C_{ground}{}^X IR_{ground}{}^X EF_{ground}{}^X ED{}^X DF6 + \\
& C_{soil}{}^X (IR_{soilchild}{}^X ED_{child} + IR_{soiladult}{}^X ED_{adult}){}^X EF_{soil}{}^X DF6 + \\
& C_{sed}{}^X (IR_{sedchild}{}^X ED_{child} + IR_{sedadult}{}^X ED_{adult}){}^X EF_{sed}{}^X DF6 + \\
& Cleafy{}^X IRleafy{}^X EFleafy{}^X ED{}^X DF6 + \\
& C_{root}{}^X IR_{root}{}^X EF_{root}{}^X ED{}^X DF6 + \\
& C_{meat}{}^X IR_{meat}{}^X EF_{meat}{}^X ED{}^X DF6 + \\
& C_{milk}{}^X IR_{milk}{}^X EF_{milk}{}^X ED{}^X DF6 + \\
& C_{bird}{}^X IR_{bird}{}^X EF_{bird}{}^X ED{}^X DF6 + \\
& C_{fish}{}^X IR_{fish}{}^X EF_{fish}{}^X ED{}^X DF6
\end{aligned}
$$

where:

C_{bird}	=	radionuclide concentration in domestic and wild birds (pCi/kg)
C_{fish}	=	radionuclide concentration in fish (pCi/kg)

C_{ground}	=	radionuclide concentration in groundwater (pCi/kg)
C_{leafy}	=	radionuclide concentration in above-ground vegetation (pCi/kg)
C_{meat}	=	radionuclide concentration in meat (pCi/kg)
C_{milk}	=	radionuclide concentration in meat (pCi/kg)
Criver	=	radionuclide concentration in river water (pCi/kg)
Croot	=	radionuclide concentration in root vegetables (pCi/kg)
Csed	=	radionuclide concentration in sediment (pCi/kg)
Cseep	=	radionuclide concentration in seep/spring water (pCi/kg)
Csoil	=	radionuclide concentration in soil (pCi/kg)
DF6	=	dose conversion factor for ingestion (rem/pCi)
$Dose_{ing}$	=	dose from ingestion (rem)
ED	=	exposure duration (year)
ED_{adult}	=	exposure duration for an adult (year)
ED_{child}	=	exposure duration for a child (year)
EF_{seep}	=	exposure frequency of an adult (days/year)
EF_{river}	=	exposure frequency of an adult (days/year)
EF_{soil}	=	exposure frequency of an adult (days/year)
EF_{sed}	=	exposure frequency of an adult (days/year)
EF_{ground}	=	exposure frequency of an adult (days/year)
EF_{leafy}	=	exposure frequency of an adult (days/year)
EF_{meat}	=	exposure frequency of an adult (days/year)
EF_{fish}	=	exposure frequency of an adult (days/year)
EF_{milk}	=	exposure frequency of an adult (days/year)
EF_{bird}	=	exposure frequency of an adult (days/year)
EF_{root}	=	exposure frequency of an adult (days/year)
IR_{bird}	=	ingestion rate of domestic and wild birds (kg/day)
IR_{fish}	=	ingestion rate of fish (kg/day)
IR_{ground}	=	ingestion rate of groundwater (kg/day)
IR_{leafy}	=	ingestion rate of above-ground vegetation (kg/day)
IR_{meat}	=	ingestion rate of meat (kg/day)
IR_{milk}	=	ingestion rate of milk (L/day)
IR_{river}	=	ingestion rate of river water (kg/day)
IR_{root}	=	ingestion rate of root vegetables (kg/day)
$IR_{sedadult}$	=	ingestion rate of sediment by a child (kg/day)
$IR_{sedchild}$	=	ingestion rate of sediment by a child (kg/day)
IR_{seep}	=	ingestion rate of seep/spring water (kg/day)
$IR_{soiladult}$	=	ingestion rate of sediment by a child (kg/day)
$IR_{soilchild}$	=	ingestion rate of soil by a child (kg/day).

5.1.1.10 Conversion of Exposure to Risk for Radioactive Contaminants

The conversion of dose to risk for radioactive contaminants uses the following equation:

$$Risk\_Rad = Dose^X Dose2Risk$$

where:
    Dose   =   any of the external, inhalation, and ingestion doses calculated above (rem)
    Dose2Risk =   factor converting accumulated radiation dose to risk (risk/rem).

5.1.2   Estimates of Concentrations in Irrigated Soils

The contaminant concentrations in irrigated foods are calculated in a manner similar to that for non-irrigated foods, except the contaminating medium is irrigation water and irrigated farm soil rather than sediment. Concentrations of analytes in farm soil are approximated by assuming accumulation resulting from the irrigation, therefore requiring an irrigation rate input. Baes and Sharp (1981) provide a method for estimating the leach rate of contaminants out of irrigated soils, as:

$$\lambda_L = \frac{P + I - E}{d_s\,\theta\,(1 + \frac{\rho}{\theta}\,K_d)}$$

where:
    λ_L =   leach rate constant, year^{-1}
    P+I-E =   precipitation plus irrigation minus evapotranspiration, the total over-watering rate, taken to be about 15 cm/year
    d_s =   depth of surface soil, taken to be about 15 cm
    ρ =   surface soil density, g/cm^3
    θ =   surface soil volumetric water content, mL/cm^3
    K_d =   soil distribution coefficient, mL/g.

For many types of soil, Baes and Sharp (1981) show the ratio ρ/θ to be about 3. Assuming an average surface soil density of about 1.5 g/cm^3, θ is about 0.5. Therefore:

$$\lambda_L \approx 1 / (0.5 + 1.5\,K_d)$$

For constant water concentration and irrigation rate, surface farm soil concentration would increase until equilibrium was reached. For materials with low-distribution coefficients (zero to about 10), equilibrium will be reached within a few years of the initiation of irrigation. For materials with distribution coefficients (K_d) greater than about 10, equilibrium may not be reached for thousands of years. For this analysis representing current conditions, the average soil concentration over a 70-year lifetime of continuous irrigation was used. This is represented as:

$$C_{soil} = C_{water} \; ^X \; IRR \; ^X \; (1/225 \text{ kg/m}^2) \; ^X \; [(1/\lambda_L) - (1/70\,\lambda_L^2) \; ^X \; (1 - EXP(-\lambda_L \; ^X \; 70))]$$

where:
    C_{soil} =   farm soil concentration, pCi/L or µg/kg
    C_{water} =   irrigation water concentration, pCi/L or µg/L
    IRR =   irrigation rate, L/(m^2 - year)
    225 =   mass of soil of density 1.5 in 1 m2 to a depth of 15 cm.

This reduces to the following equation:

$$C_{soil} = C_{water} {}^X (IRR /225)^X [(0.5 + 1.5 {}^X K_d) - (0.5 + 1.5 {}^X K_d)^2 / 70 {}^X (1 - EXP (-70 /(0.5 +1.5 {}^X K_d)))]$$

Figure 5-1 shows an example plot of the average soil concentration using this equation for a range of soil distribution coefficients. The plot is based on the assumption of a constant concentration of 30 pCi/L in the irrigation water for the entire 70-year period.
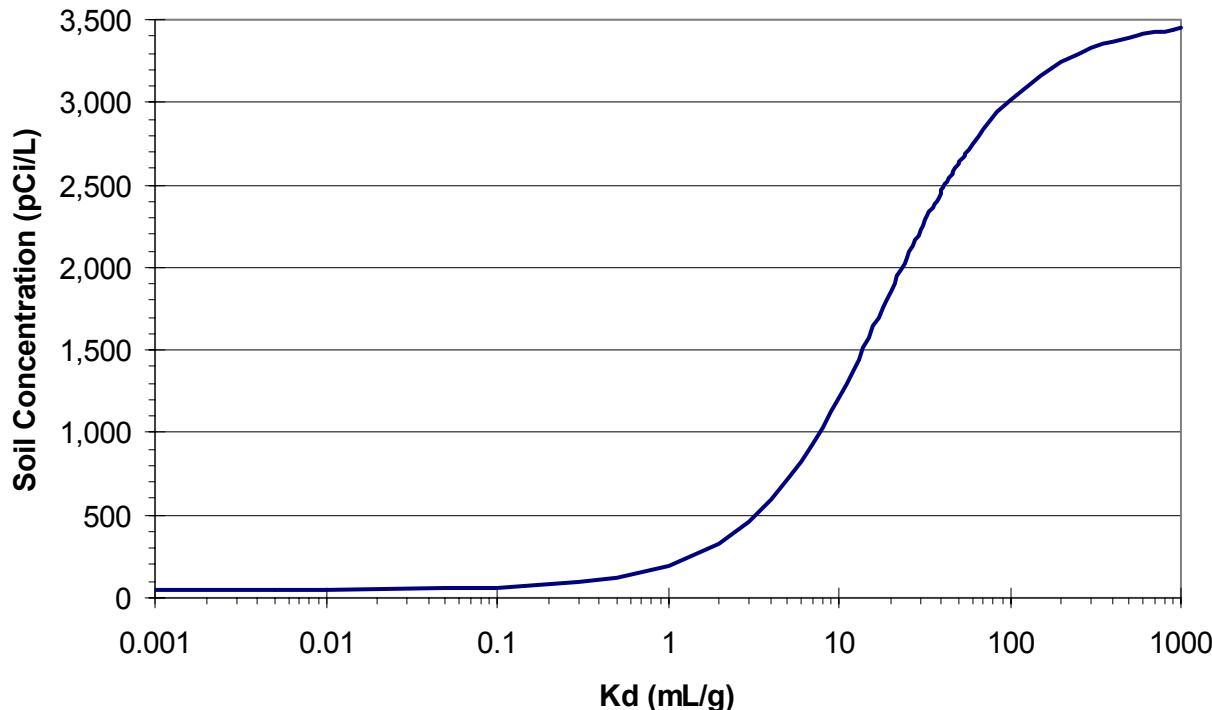
Figure 5-1 Average Soil Concentration over a 70-Year Lifetime for a Range of Soil Distribution Coefficients for Irrigation Water at a Constant Concentration of 30 pCi/L

5.1.3 Estimate of Contaminant Concentrations in Human Foods

The equations for human exposure require the concentrations of contaminants both in water, sediment, and soil and also in food products, such as fish, birds, meat, and vegetables that become contaminated through contact with these media. To determine the concentrations in vegetation, the human exposure model uses transfer coefficients to form a relationship between an environmental concentration and concentration in a food product. The equations for calculating concentrations in food products are described in the following sections.

5.1.3.1 Concentrations in Fish

The contaminant concentration in fish at a river location is computed from the contaminant concentration in Columbia River water (surface water) at that location using the following expression:

$$C_{fish} \quad = \quad C_{river}{}^X BIO_{fish}$$

where:

C_{fish} = analyte concentration in fish (pCi/kg or µg/kg)
C_{river} = analyte concentration in river water (pCi/L or µg/L)
BIO_{fish} = analyte-specific bioaccumulation factor (pCi/kg per pCi/L or µg/kg per µg/kg).

5.1.3.2 Concentrations in Terrestrial Foods

The contaminant concentrations in terrestrial foods are derived from the concentrations of contaminants in soil and water using the following equations:

$$
\begin{aligned}
C_{leafy} \quad &= \quad C_{soil}{}^X CR_{veg} \\
C_{root} \quad &= \quad C_{leafy} \\
C_{milk} \quad &= \quad (C_{leafy}{}^X QP_{milk} + C_{water}{}^X QW_{milk})^X TF_{milk} \\
C_{meat} \quad &= \quad (C_{leafy}{}^X QP_{deer} + C_{water}{}^X QW_{deer})^X TF_{deer} \\
C_{bird} \quad &= \quad (C_{leafy}{}^X QP_{bird} + C_{water}{}^X QW_{bird})^X TF_{bird}
\end{aligned}
$$

where:

C_{bird} = analyte concentration in wild bird flesh (pCi/kg or µg/kg)
C_{leafy} = analyte concentration in leafy vegetables (pCi/kg or µg/kg)
C_{meat} = analyte concentration in animal protein (pCi/kg or µg/kg)
C_{root} = analyte concentration in root vegetables (pCi/kg or µg/kg)
C_{soil} = analyte concentration in soil (pCi/kg or µg/kg)
C_{water} = analyte concentration in irrigation water (pCi/L or µg/L) (the source of irrigation water may be groundwater or surface water from the river)
CR_{veg} = soil-to-vegetation concentration ratio (pCi/kg plant per pCi/kg soil or µg /kg plant per µg /kg soil)
QP_{milk} = quantity of plant matter consumed by cow (kg/day)
QP_{deer} = quantity of plant matter consumed by deer (kg/day)
QP_{bird} = quantity of plant matter consumed by bird (kg/day)
QW_{milk} = quantity of water digested by a cow (L/day)
QW_{deer} = quantity of water digested by a deer (L/day)
QW_{bird} = quantity of water digested by a bird (L/day)
TF_{bird} = feed-to-wild-bird transfer factor derived from ecosystem model (day/kg)
TF_{deer} = feed-to-animal-protein transfer factor derived from ecosystem model (day/kg)
TF_{milk} = feed-to-animal-milk transfer factor derived from ecosystem model (day/L).

5.1.3.3 Concentrations for Special Native American Activities

The only unique Native American pathway defined in the SAC scenarios involves a sweat lodge. The assumption for the sweat lodge was that water would be collected and poured over hot rocks to create steam. The concentration in the sweat lodge water comes from the following expression:

$$C_{sweat} \quad = \quad C_{water}$$

where:

C_{swea} = analyte concentration for water in a sweat lodge (pCi/L or µg/L)

C_{water} = analyte concentration in the water source (pCi/L or µg/L).

The code implementation allows the choice of groundwater, seep water, or surface river water for this calculation.

5.1.4 Population Dose and Risk for Radioactive Contaminants

The population radioactive dose is calculated as the sum of doses to individuals for a set of locations. With the limitation that the code only runs a single exposure scenario at a time, the activities of the people at the different locations can be different. For example, some could be drinking groundwater, and some could be drinking river water; however, they all would be drinking the same amount of water. The equation for this calculation is:

$$\text{Dose}_{pop} = \sum_{loc} \left(\text{Dose}_{ind} * \text{Pop}_{loc} \right)$$

where:

Dose_{pop} = Population dose (person-rem)

Dose_{ind} = Radioactive dose (rem) to an individual at a location

Pop_{loc} = Number of people living at the location (persons).

The sum goes over all locations identified for the specific run of the HUMAN code (see the LOCATION keyword in Section 5.4.9 for further information).

The population risk from radioactive materials is calculated using the following equation:

$$\text{Risk}_{pop} = \text{Dose}_{pop} {}^X \text{Dose2Risk}$$

where:

Risk_{pop} = number of people in the population that are expected to contract a fatal cancer.

5.2 Code Execution Environment

5.2.1 Location in the Processing Sequence

The HUMAN code requires access to a number of data files developed by the SAC inventory, release, and transport codes (Eslinger et al. 2002). In particular, every code on the left side of Figure 1-2 must have been executed to build a suite of concentration data files before the HUMAN code can be used to calculate impacts. These concentration data files must have been developed under the control of the same ESD keyword file that the HUMAN code reads to determine processing options.

5.2.2   How the Code Is Invoked

HUMAN can run under either the Windows or the Linux operating system. Under the Windows operating system (Releases 98, NT, or 2000), HUMAN executes in a DOS box. A run of HUMAN is initiated by entering the following command line:

```
HUMAN "Keyfilename"
```

Under the Linux operating system HUMAN is executed through any of the following Bourne Shell or C Shell commands:

```
human.exe "Keyfilename"
```

For these commands, HUMAN or human.exe is the name of the executable program and "Keyfilename" is the name of a human scenario keyword file. Both the name of the executable program and the keyword file may contain path information. If HUMAN is invoked without entering the name of the keyword file, then the code will prompt the user for the file name. The keyword file, which should be prepared using an editor that can handle ASCII files without leaving embedded control codes, contains text control information describing the run. If HUMAN cannot open the keyword file, then the code will terminate execution after writing an error message to the standard output device.

5.2.3   Memory Requirements

The HUMAN code uses dynamic memory allocation, so the memory requirements depend on the problem being analyzed. A reasonably large example run where the HUMAN code required 3.84 MB of memory (on a Windows 2000 machine) used 7 analytes, 35 times steps, 25 realizations, and 1618 locations. It is expected that most, if not all, of the runs of the HUMAN code will require fewer than 5 MB of memory.

5.3   Data Files

The HUMAN code reads four or more input files and writes up to seven output files. The number of input files depends on the number of contaminants being analyzed. The number of output files depends on the options selected in the HUMAN code. These files are described in the following sections.

5.3.1   Input Files

The input files for the HUMAN code are keyword files and a suite of concentration-data-related files. One keyword file controls the case the HUMAN code will execute, and it points to the ESD keyword file. The suite of concentration data files are all identified in the ESD keyword file – the user of the HUMAN code only needs to identify the ESD keyword file. The following are the input files:

- **ESD Keyword File:** The ESD keyword file contains the control information the inventory and environmental transport codes use to generate concentration data files. Table 2.1 provides examples of keywords in the ESD file that control the impacts codes, including the HUMAN code. Section 2.2 provides definitions for these keywords. Typically, the user of the HUMAN code will not modify the ESD keyword file.

- **HUMAN Keyword File:** The HUMAN Keyword file controls the scenario to be analyzed by the HUMAN code. The options and data available are constrained by the case defined in the ESD Keyword file. Section 5.4 describes the contents of the HUMAN keyword file. Table 5.1 provides excerpted records from a keyword file for the HUMAN code.
- **ECDA Concentration Files:** The ECDA concentration files contain all the concentration data available for the impacts codes. The concentrations for all analytes are based on the same time and location data. There is a "map" file for the HUMAN code containing indexing information for each of the concentration data files. In addition, there is a separate concentration data file for every analyte used in the impacts scenario. For example, when running a scenario with seven analytes, there will be one map file and seven concentration data files.

5.3.1.1 Keyword File for the HUMAN Code

The HUMAN keyword definition file contains control information for the desired impact simulation. Individual keywords are defined in Section 5.4. Table 5.1 contains excerpted keywords from a keyword file for the HUMAN code. The complete file is 530 lines long.

Table 5.1 Excerpted Records from a Keyword File for the HUMAN Code

```
!--------------------------| Top-Level Controls |---------------------------
REPORT "Huser.Rpt"   ! Report File (Must be first non-comment entry)
TITLE  "Upland Scenario - Drinking Local Groundwater"
USER   "Paul W. Eslinger"
REALIZATIONS 5       ! Number of Realizations
SEED  44123466.0     ! Random Seed for Stochastics
SOIL 70.0            ! Soil averaging time for irrigation (years)
AVERAGE 70.0         ! Averaging time for exposure calculations (years)
EXECUTE              ! Execute this problem
SWEAT GROUND         ! Sweat lodge water source
!-----------------------------| File Names |--------------------------------
FILE ESD     "ESD_Initial.Key" ! ESD control keyword file
FILE STATS   "Huser_Sta.csv"  ! Risk summary statistics
FILE DETAIL  "Huser_Dtl.csv"  ! Risk detailed data
FILE FOODS   "Huser_Fod.csv"  ! Food concentration detailed data
FILE FOODSTAT "Huser_Fst.csv" ! Food concentration summary statistics
FILE VALUES  "Huser_Val.csv"  ! Generated stochastic variables
FILE HEADER  "Huser.Hdr"      ! Header file for SACVIEW
!----------------------| Solution Type Identifiers |------------------------
STATISTICS COMB_ANA ! Risk at the combined analyte level
...
STATISTICS PATH_INH ! Risk at the pathway level for inhalation
DETAILS COMB_ANA    ! Risk at the combined analyte level
…
DETAILS PATH_INH    ! Risk at the pathway level for inhalation
!---------------------------| Anaytes to Use |------------------------------
ANALYTE ID="H3"    RADIOACT OUTPUT
ANALYTE ID="Sr90"  RADIOACT OUTPUT
ANALYTE ID="Tc99"  RADIOACT OUTPUT
ANALYTE ID="I129"  RADIOACT OUTPUT
```

```
ANALYTE ID="Cs137"  RADIOACT OUTPUT
ANALYTE ID="U238"   RADIOACT OUTPUT
ANALYTE ID="Pu239" RADIOACT OUTPUT
ANALYTE ID="U"      NONCARCI OUTPUT
ANALYTE ID="CrVI"   CARCINOG OUTPUT
ANALYTE ID="CCl4"   CARCINOG OUTPUT
!----------------------------| Solution Times |-----------------------------
TIMES 2000 2050 2100
!---------------------------| Impact Locations |----------------------------
! Riparian zone locations
LOCATION HUMAN PRIMARY="HL0425" SECOND="HL0426" POP=0 OUTPUT
LOCATION HUMAN PRIMARY="HL0435" SECOND="HL0436" POP=0 OUTPUT
LOCATION HUMAN PRIMARY="HL0443" SECOND="HL0444" POP=0 OUTPUT
! Upland Locations
LOCATION HUMAN PRIMARY="HL3826" IRRIGATE=GRO_WAT POP=0 OUTPUT
LOCATION HUMAN PRIMARY="HL3827" IRRIGATE=GRO_WAT POP=0 OUTPUT
LOCATION HUMAN PRIMARY="HL3828" IRRIGATE=GRO_WAT POP=0 OUTPUT
! Population dose (municipal water intakes)
LOCATION HUMAN PRIMARY="HL0413" POP=34000 OUTPUT ! Richland pumphouse
LOCATION HUMAN PRIMARY="HL0414" POP=32000 OUTPUT ! Pasco water intake
LOCATION HUMAN PRIMARY="HL0415" POP=43000 OUTPUT ! Kennewick water intake
! Other locations
LOCATION HUMAN PRIMARY="HL3050" SECOND="HL0420" IRRIGATE=SUR_WAT POP=0 OUTPUT
LOCATION HUMAN PRIMARY="HL3870" POP=0 OUTPUT
!---------------------| Kd's for Irrigated Locations |----------------------
KDSOIL TERSE ANALYTE="H3"   KDSOIL="KDH"     ! Kd for tritium
KDSOIL TERSE ANALYTE="Sr90"  KDSOIL="KDSr"   ! Kd for Sr-90
…
KDSOIL TERSE ANALYTE="CrVI"  KDSOIL="KDCr"    ! Kd for Hexavalent chrome
KDSOIL TERSE ANALYTE="CCl4"  KDSOIL="KDCCl4" ! Kd for Carbon tetrachloride
!
!----------------------| Scenario Specific Values |--------------------------
! Exposure frequency variables
STOCHASTIC "EFBOAT"  2   5  30 "Exposure frequency for boating (day/yr)"
STOCHASTIC "EFBIRD"   2 270 365 "Exposure frequency for birds (day/yr)"
STOCHASTIC "EFFISH"   2 270 365 "Exposure frequency for fish (day/yr)"
…
! Exposure time variables
STOCHASTIC "ETBOAT"  2  1.0  6.0 "Exposure time for boating (hr/day)"
STOCHASTIC "EDADULT" 2  1.0 64.0 "Exposure duration for an adult (yr)"
…
! Body weight
STOCHASTIC "BWCHILD" 1 16    "Body weight for a child (kg)"
STOCHASTIC "BWADULT" 2 60 90 "Body weight for an adult (kg)"
! Body surface area
STOCHASTIC "SASOIL"  1  5000 "Body surface area - soils (cm^2)"
STOCHASTIC "SASED"   1  5000 "Body surface area - sediments (cm^2)"
…
! Air concentration factor for sweat lodge
STOCHASTIC "CFSWEAT" 2 0.1 0.3 "Air concentration factor - sweat lodge (L/m^3)"
```

```
! Soil and water variables
STOCHASTIC "SHIELDSOIL" 1 0.8     "Soil shielding factor"
STOCHASTIC "SHIELDSED" 1 0.2      "Sediment shielding factor"
…
! Ingestion rate variables
STOCHASTIC "IRATE"      2 20.0 35.0     "Inhalation rate (m^3/day)"
STOCHASTIC "IRRIVER"    2 1.0 3.0       "Ingestion rate, river water (L/day)"
STOCHASTIC "IRROOT"     2 0.1 0.4       "Ingestion rate, root vegetables (kg/day)"
STOCHASTIC "IRMEAT"     2 0.076 3.0     "Ingestion rate, meat (kg/day)"
STOCHASTIC "IRMILK"     2 0.05  0.3     "Ingestion rate, milk (L/day)"
…
!--------------------| Scenario Independent Values |------------------------
STOCHASTIC "DOSE2RISK" 2 2.0E-4 1.0E-3 "Risk/Rem conversion"
!  Radionuclide stochastic dose factors
STOCHASTIC "H3    DFSOIL" 1 0  "H3 dose factor for soil"
STOCHASTIC "H3    DFSWIM" 1 0 "H3 dose factor for swimming"
STOCHASTIC "H3    DFBOAT" 1 0 "H3 dose factor for boating"
STOCHASTIC "H3    DFING" 8 -10.1938,3.01E-01 "H3 dose factor for ingestion"
STOCHASTIC "H3    DFINH" 8 -10.0177,3.01E-01 "H3 dose factor for inhalation"
…
! Stochastic slope factors (cancer potency factor) for carcinogens
STOCHASTIC "CrVI  SFINH" 6 21 42 290 "Cr slope factor for inhalation"
STOCHASTIC "CrVI  SFING" 10 "Cr slope factor for ingestion" 8
 0.0000   0.0   0.7999   0.0   0.8000  21.0   0.8499  21.0
 0.85    42.0  0.8999  42.0   0.90   290.0   1.0    290.0
…
! Stochastic hazard quotients for noncarcinogens
STOCHASTIC "CrVI  HQINH" 6 .001 0.005 0.015  "Cr hazard quotient for inhalation"
STOCHASTIC "CrVI  HQING" 6 .001 0.005 0.015  "Cr hazard quotient for ingestion"
…
! Stochastic transfer and accumulation factors for fish  (IAEA 1994, TRS No. 364)
STOCHASTIC "H3    BIOFISH" 2 0.6 1     "Tritium bioacculation for fish"
STOCHASTIC "Tc99  BIOFISH" 6  2   20   80 "Tc99 bioacculation for fish"
…
! Stochastic transfer factors for birds
STOCHASTIC "H3    TFBIRD" 2 0.5 1.0        "Tritium transfer factor for birds"
STOCHASTIC "I129  TFBIRD" 8 -2.0 0.30103     "I129 transfer factor for birds"
…
STOCHASTIC "QPBIRD" 6 0.35 0.50 0.65 "Ingestion rate of plants for birds (kg/day)"
STOCHASTIC "QWBIRD" 6 0.1  0.25 0.4  "Ingestion rate of water  for birds (L/day)"
!
! Stochastic transfer factors for meat
STOCHASTIC "H3    TFDEER" 2 0.5 1.0          "Tritium transfer factor for deer meat"
STOCHASTIC "Tc99  TFDEER" 4 1.0E-6 1.0E-4       "Tc99 transfer factor for deer meat"
…
STOCHASTIC "QPDEER" 6 58 68  78 "Ingestion rate of plants for deer (kg/day)"
STOCHASTIC "QWDEER" 6 25 68 136 "Ingestion rate of water  for deer (L/day)"
!
! Stochastic transfer factors for milk
STOCHASTIC "H3    TFMILK" 8 -1.82391 0.30103  "Tritium transfer factor for milk"
```

```
STOCHASTIC  "Tc99  TFMILK" 8  0.00002 0.00110  "Tc99 transfer factor for milk"
…
STOCHASTIC "QPMILK" 6 45 55  65 "Ingestion rate of plants for a cow for milk (kg/day)"
STOCHASTIC "QWMILK" 6 25 50 100 "Ingestion rate of water  for a cow for milk (L/day)"
! Stochastic CR (concentration ratio for vegetation) distributions
STOCHASTIC "H3    CRVEG" 6 .05 .1 .2  "Tritium vegetation concentration ratio"
STOCHASTIC "Tc99  CRVEG" 6 1 10 100 "Tc99 vegetation concentration ratio"
…
! Stochastic volatilazion factors
STOCHASTIC "H3    VF" 1 0 "H3 Volatilazation factor"
STOCHASTIC "Tc99  VF" 1 0 "Tc99 Volatilazation factor"
…
! Stochastic skin permeability factors
STOCHASTIC "CrVI  KP" 4 0.03   0.3   "CrVI - Skin permeability coefficient"
…
! Stochastic skin absorption factors
STOCHASTIC "CrVI  ABSORP" 4 0.0001 0.01 "CrVI - Skin absorption coefficient"
…
END
```

5.3.1.2   Keywords Required from the Environmental Settings File

The HUMAN code also reads keywords from the environmental settings file. These keywords are read from a different file and can have a different definition from a keyword defined for internal use in the HUMAN code. The environmental settings keywords are defined in Section 2.2. The following keywords are required:

- ANALYTE – definition of analytes in the environmental simulations
- END – end of the environmental settings keywords
- FILE – file names for the concentration file for each analyte
- KDSOIL – soil to water partition coefficents
- LOCATION – locations at which concentrations were generated for the cultural impacts
- REALIZAT – number of realizations that were simulated
- TIMES – times at which concentrations were generated for the human impacts
- TITLE – environmental simulation title.

5.3.2   Output Files

Up to seven output files can be written by the HUMAN code. The number of files depends on the options selected in the scenario being analyzed. The following are the output files:

- **Report File:** This required file contains a summary of the scenario being analyzed and contains any error messages. An example report file for the HUMAN code is provided in Table 5.2.
- **Stochastic Values File:** This optional file contains the values for every stochastic variable generated in the HUMAN code. The description of the VALUES modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. A subset of the data written to this file for a run using five realizations is provided in Table 5.3.

- **SACView Header File:** This required file contains information used by the interactive SACView program to allow easy extraction of subsets of the results computed by the HUMAN code. An example of this file is given in Table 5.4.
- **Food Concentration Detailed Data:** This optional file contains the detailed values for every food concentration generated in the HUMAN code. The description of the FOODS modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. A subset of the data written to this file for a run using five realizations is provided in Table 5.5.
- **Food Concentration Summary Statistics:** This optional file contains summary statistics for every food concentration generated in the HUMAN code. The description of the FOODSTAT modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. A subset of the data written to this file for a run using five realizations is provided in Table 5.6.
- **Risk Detailed Data:** This optional file contains the detailed values for the dose and risk values generated in the HUMAN code. The description of the DETAIL modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. A subset of the data written to this file for a run using five realizations is provided in Table 5.7.
- **Risk Summary Statistics:** This optional file contains the summary statistics for the dose and risk values generated in the HUMAN code. The description of the STATS modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. A subset of the data written to this file for a run using five realizations is provided in Table 5.8.

5.3.2.1   HUMAN Report File

Table 5.2 provides excerpted records from an example report file for the HUMAN code. This file contains information for a run of the HUMAN code using 10 analytes, 5 realizations, 11 locations, and 3 solution times. This example file is a typical size for the report file, provided that no debug options are selected. The size of this file grows rapidly when debug options are selected. For example, this file is about 12 KB in size. If the debug options are turned on, the file grows to 6.3 MB. A run using all debug options having a large number of locations, analytes, solution times, and realizations could generate a report file larger than 2 GB.

Table 5.2 Excerpted Records from an Example Report File for the HUMAN Code

```
         H        H  U        U  M         M   AAAAA    N        N
         H        H  U        U  MM       MM   A       A  A  NN     N
         H        H  U        U  M M M M   A       A  A  N N    N
         HHHHHHH  U        U  M     M   M   AAAAAAA  N   N  N
         H        H  U        U  M         M   A       A  N     N N
         H        H  U        U  M         M   A       A  N       NN
         H        H   UUUUU   M         M   A       A  N        N


                        Human     2.00.E.2
                   Last Modified on  8 Feb 2002


                   Stochastic Human Risk Analysis
              Systems Assessment Capability (SAC), Revision 0
              ------------------------------------------------
                        Developed By Battelle
                 Pacific Northwest National Laboratory
                        Richland, Washington
              ------------------------------------------------

       Current Run ID = 20020208090905    User Name = Paul W. Eslinger
```

```
                 System Date = 02-08-2002    System Time = 09:09:05



             The software used to generate this output is experimental
                 and has not been formally tested or peer reviewed.



                             Review Signatures

Input Prepared By: _____         Date: _____

Input Reviewed By: _____         Date: _____



====================== Echo of the Problem Definition ======================

Title: Upland Scenario - Drinking Local Groundwater
User:  Paul W. Eslinger
    5 Realizations requested in this run
   25 Realizations available in the concentration files

File Name for Input Keyword Data
File: Huser.key

File Name for Summary Risk Data
File: Huser_Sta.csv

File Name for Detailed Risk Data
File: Huser_Dtl.csv

File Name for Output Food Concentration Details
File: Huser_Fod.csv
... (Deleted records)
File Name for Media Concentrations for analyte with ID="CrVI"
File: I:\Initial\Ecda\HUMA_CrVI_Initial.Dat

Debug Flag Information
   No  : Concentration Data
   No  : Radiological Risk
   No  : Carcinogenic Risk
   No  : Hazard Quotient
   Yes : Stochastic Calculations
   No  : Food concentrations

Soil concentration averaging time for irrigation
   Value =   70.0   Units are years

Averaging time for risk calculations
   Value =  25567.50   Units are days

Sweat lodge option is not used

Location Information based on 1930 possible locations.
  Index : Water Type    : ID     :   Pop. : Location description
  ----- : ------------- : ------ : ------ : ----------------------------
  263 : Dry       :      : HL0413 :  34000 : Richland municipal water intake
  264 : Dry       :      : HL0414 :  32000 : Kennewick municipal water intake
  265 : Dry       :      : HL0415 :  43000 : Pasco municipal water intake
  275 : Dry       :      : HL0425 :      0 : Human location
      : Secondary    : HL0426 :        : Human location
... (Deleted records)
 1182 : Dry       :      : HL3870 :      0 : Human Upland Location-Dense Grid
A total of 11 locations have been requested.
```

```
Analyte Information based on 10 possible analytes.
    1 : H3      : NR : RAD : Tritium
    2 : Sr90    : NR : RAD : Strontium 90
... (Deleted records)
    9 : CCl4    : NS : CAR : Carbon Tetrachloride
   10 : CrVI    : NS : CAR : Hexavalent Chromium
A total of 10 analytes have been requested.


Analyte Concentration Limits
                          Bird       Fish       Meat
                        ---------- ---------- ----------
    1 : H3      : RAD :    None       None       None
... (Deleted records)
   10 : CrVI    : CAR :    None       None       None

Time Slices Requested: (Index, Calendar Year) based on 231 possible times.
   21 : 2000 : Included in this scenario
   31 : 2050 : Included in this scenario
   41 : 2100 : Included in this scenario
A total of    3 times have been requested.


======================= End of the Problem Definition ========================

Starting Problem Execution

   Date: 02/08/2002
   Time: 09:09:06.415

Concentration data units conversion factors

   1 : H3      : NR : Ground water  : 1.00000E+09 : From Ci/m^3  to pCi/L
   1 : H3      : NR : Seep water    : 1.00000E+09 : From Ci/m^3  to pCi/L
   1 : H3      : NR : Soil          : 1.00000E+12 : From Ci/kg   to pCi/kg
... (Deleted records)
  10 : CrVI    : NS : Surface water : 1.00000E+06 : From kg/m^3  to ug/L
  10 : CrVI    : NS : Sediment      : 1.00000E+09 : From kg/kg   to ug/kg

Ending Problem Execution

   Date: 02/08/2002
   Time: 09:09:07.399

Message originating in routine HUMAN
Message: Normal Termination
```

5.3.2.2 HUMAN Stochastic Values File

The stochastic values file is an optional output file that contains the values for every stochastic variable generated in the HUMAN code. The description of the VALUES modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of the ID of the stochastic variable followed by a value for every generated realization. A subset of the data written to this file for a run using five realizations is provided in Table 5.3. Because this file has at most a few hundred entries, the file size is always much smaller than 1 MB.

Table 5.3 Excerpted Records from the Stochastic Values File

```
"DOSE2RISK", 6.63298E-04, 8.95216E-04, 4.28789E-04, 7.61322E-04, 3.24067E-04
"Sr90  DFSOIL", 3.90004E-10, 7.28447E-10, 2.60232E-10, 5.63547E-10, 5.15688E-10
```

```
"Sr90  DFINH", 3.00188E-07, 2.71429E-07, 6.30467E-07, 1.09017E-07, 1.41680E-07
"U    HQINH", 1.00014E+00, 9.98158E-01, 9.94201E-01, 1.00092E+00, 1.00480E+00
"CCl4  SFING", 4.34638E-01, 8.02780E-02, 1.85404E-01, 1.43329E-01, 2.62328E-02
"CCl4  SFINH", 1.75551E-02, 3.65071E-01, 2.56433E-02, 7.24165E-02, 5.14025E-02
"EFBOAT", 2.44306E+01, 1.12904E+01, 1.78827E+01, 5.08665E+00, 2.99136E+01
"ETRIVER", 1.75214E+01, 1.53131E+01, 1.31528E+01, 1.10683E+01, 1.87175E+01
"ED", 1.44600E+01, 1.60701E+01, 6.21335E+01, 4.98780E+01, 2.99073E+01
"EFLEAFY", 3.60858E+02, 3.34866E+02, 2.94225E+02, 3.25261E+02, 2.76094E+02
"QPBIRD", 4.90110E-01, 4.32282E-01, 5.87973E-01, 5.38815E-01, 4.58023E-01
"QWBIRD", 2.22780E-01, 3.69238E-01, 2.49782E-01, 1.42156E-01, 2.92976E-01
"BWADULT", 6.21404E+01, 7.29195E+01, 8.22975E+01, 6.95193E+01, 8.40544E+01
"SASOIL", 5.00000E+03, 5.00000E+03, 5.00000E+03, 5.00000E+03, 5.00000E+03
"SARIVER", 2.00000E+04, 2.00000E+04, 2.00000E+04, 2.00000E+04, 2.00000E+04
"IRSEDCHILD", 2.47929E-04, 4.71712E-04, 3.42739E-05, 2.08821E-04, 3.33628E-04
"IRMEAT", 1.47307E+00, 2.16214E+00, 1.08884E-01, 2.99069E+00, 7.07404E-01
"IRATE", 3.38178E+01, 2.51633E+01, 2.98956E+01, 2.03503E+01, 2.78600E+01
"Sr90  TFDEER", 7.39602E-02, 4.40583E-02, 3.74697E-02, 1.29689E-02, 1.81908E-02
"Sr90  TFBIRD", 5.63319E-01, 2.14527E+00, 1.47448E+00, 2.64039E+00, 6.26559E-02
"IRGRATE", 9.07806E+02, 8.51027E+02, 6.27562E+02, 5.60488E+02, 7.31329E+02
"SHIELDSOIL", 8.00000E-01, 8.00000E-01, 8.00000E-01, 8.00000E-01, 8.00000E-01
"AFSED", 3.96716E-01, 1.41329E-01, 1.28814E-01, 4.29907E-01, 2.54937E-01
```

5.3.2.3 HUMAN SACView Header File

The SACView header file is an output file containing information used by the interactive SACView program to allow easy extraction of subsets of the results computed by the HUMAN code. This file is required for every run of the HUMAN code. An example of this file is given in Table 5.4. The file contains the following sections of information:

- A header section of basic run information
- Solution times selected
- Locations used
- Analytes processed
- Solutions selected
- Food types
- Output file names.

The user only specifies the name of this file; users should not modify the file after it is generated by the HUMAN code. See the instructions in Section 7.0 regarding the use of the SACView program. Because this file has at most a few hundred entries, the file size is always much smaller than 1 MB. File names for options not selected are set to null.

Table 5.4 Example Header File for the SACView Program

```
type: "Human"
title: "Upland Scenario - Drinking Local Groundwater"
user: "Paul W. Eslinger"
name: "Human"
version: "2.00.E.2"
date: " 8 Feb 2002"
id: "20020208090905"
```

```
envfile: "ESD_Initial.Key"
realizations:    5
times:    3
 2000
 2050
 2100
locations:   13
"HL0413","Richland municipal water intake"
"HL0414","Kennewick municipal water intake"
"HL0415","Pasco municipal water intake"
"HL0425","Human location"
"HL0435","Human location"
"HL0443","Human location"
"HL3050","Human Upland Location - Dense Grid"
"HL3826","Human Upland Location - Dense Grid"
"HL3827","Human Upland Location - Dense Grid"
"HL3828","Human Upland Location - Dense Grid"
"HL3870","Human Upland Location - Dense Grid"
"POPDOS","Population dose from radionuclides"
"POPRSK","Population risk from radionuclides"
analytes:   13
"H3    ","RAD","Tritium"
"Sr90  ","RAD","Strontium 90"
"Tc99  ","RAD","Technetium 99"
"I129  ","RAD","Iodine 129"
"Cs137 ","RAD","Cesium 137"
"U238  ","RAD","Uranium 238"
"Pu239 ","RAD","Plutonium 239/240"
"U     ","HAZ","Total Uranium"
"CCl4  ","CAR","Carbon Tetrachloride"
"CrVI  ","CAR","Hexavalent Chromium"
"COMBIN","CAR","Combined carcinogenic analytes"
"COMBIN","HAZ","Combined hazardous analytes"
"COMBIN","RAD","Combined radioactive analytes"
solutions:    8
"EX","External dose"
"IG","Ingestion dose"
"IH","Inhalation dose"
"AL","Analyte dose"
"CB","Combined dose for analyte type"
"DW","Drinking water dose (radioactive)"
"PD","Population dose (radioactive)"
"PR","Population risk (radioactive)"
foods:    8
"CBIRD","Bird tissue concentration "
"CFISH","Fish tissue concentration"
"CLEAFY","Leafy vegetable concentration"
"CMEAT","Meat (deer) concentration"
"CMILK","Cow milk concentration"
"CROOT","Root vegetable concentration"
"CSOIL","Soil (upper layer) concentration"
```

```
"CSWEAT","Sweat lodge item concentration"
statistics_impacts: "Huser_Sta.csv"
detail_impacts: "Huser_Dtl.csv"
statistics_food: "Huser_Fst.csv"
detail_food: "Huser_Fod.csv"
```

5.3.2.4 HUMAN Food Concentration Detailed Data

The food concentration detailed data file is an optional output file that contains the detailed values for every food concentration generated in the HUMAN code. The description of the FOODS modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of six identifiers followed by a value for every generated realization. Table 5.5 provides a subset of the data written to this file for a run using four realizations. The header line occupies only one line in the file even though it shows on two lines in this table. The following are the six identifiers on each line:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Analyte ID: The identification of the analyte for which the data were computed
- Irrigation: A logical (T=true, F=false) flag whether irrigation occurred at this location
- Food: A label identifying the food type
- Units: The units associated with the concentration data.

Table 5.5 Excerpted Records from the Food Concentration Detailed Data File

```
"Time","Location ID","Analyte ID","Irrigation","Food","Units",
"Values by Realization"
2000,"HL0413","H3",F,"LEAFY","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0413","H3",F,"ROOT","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0413","Pu239",F,"BIRD","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0413","Pu239",F,"FISH","pCi/g", 5.15628E+00, 3.78478E+00, 1.55523E+00
2000,"HL0413","Pu239",F,"SWEAT","pCi/L", 0.00000E+00, 0.00000E+00,0.00000E+00
2000,"HL0413","Pu239",F,"SOIL","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0425","CrVI",F,"FISH","mg/g", 2.12795E+05, 4.41670E+05, 8.28373E+05
2000,"HL0425","CrVI",F,"SWEAT","mg/L", 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0443","U",F,"SWEAT","mg/L", 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0443","U",F,"SOIL","mg/g", 1.74405E+00, 2.24946E-01, 2.57270E+00
2000,"HL0443","CCl4",F,"LEAFY","mg/g", 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL3827","Sr90",T,"BIRD","pCi/g", 1.25094E+00, 2.90687E-18, 3.12024E-13
2000,"HL3827","Sr90",T,"FISH","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00
2050,"HL0413","CCl4",F,"FISH","mg/g", 6.67511E+00, 1.91467E+00, 1.61267E+01
2050,"HL0415","Sr90",F,"BIRD","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00
2050,"HL3826","Sr90",T,"MEAT","pCi/g", 4.94571E+01, 1.53114E-15, 2.07545E-10
2050,"HL3826","Sr90",T,"MILK","pCi/L", 2.88256E+00, 1.15078E-16, 1.63727E-12
2100,"HL3828","CrVI",T,"BIRD","mg/g", 1.40425E+01, 5.77752E+00, 1.06295E+01
2100,"HL3828","CrVI",T,"FISH","mg/g", 0.00000E+00, 0.00000E+00, 0.00000E+00
2100,"HL3828","CrVI",T,"SWEAT","mg/L", 0.00000E+00, 0.00000E+00, 0.00000E+00
2100,"HL3828","CrVI",T,"SOIL","mg/g", 3.44492E+02, 2.56305E+02, 2.37438E+02
```

This file will have nine rows of information for every combination of time, location, and analyte. Therefore, this file can become very large. As an example, a 689 KB file was generated for a case involving 1 location, 7 analytes, 25 realizations, and 35 times. The file size directly scales with the number of analytes, locations, and times. The file size grows more slowly than a direct scaling by the number of realizations. As another example, a 484 MB file was generated for a case involving 1618 locations, 6 analytes, 11 realizations, and 35 times.

5.3.2.5   HUMAN Food Concentration Summary Statistics

This file is an optional output file that contains the summary statistics for every food concentration generated in the HUMAN code. The description of the FOODSTAT modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of six identifiers followed by summary statistics (nine percentiles, mean value, and standard deviation). A subset of the data written to this file for a run using five realizations is provided in Table 5.6. The following are the six identifiers on each line:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Analyte ID: The identification of the analyte for which the data were computed
- Irrigation: A logical (T=true, F=false) flag whether irrigation occurred at this location
- Food: A label identifying the food type
- Units: The units associated with the concentration data.

The data for each record in this file are too long to present without with line-wrapping in this document. Each record in the file occupies two lines in Table 5.6.

Table 5.6 Excerpted Records from the Food Concentration Summary Statistics File

```
"Time","Location ID","Analyte ID","Irrigation","Food","Units","Minimum","5th
Percentile","10th Percentile",
"25th Percentile","Median","75th Percentile","90th Percentile","95th
Percentile","Maximum","Mean","Standard Deviation"
1980,"HL3826","H3",T,"CROOT","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
1980,"HL3826","H3",T,"CBIRD","pCi/g", 6.27220E+05, 6.27220E+05, 7.26558E+05,
9.84345E+05, 1.32152E+06,
1.52007E+06, 2.16812E+06, 3.39454E+06, 4.59480E+06, 1.56120E+06, 9.53608E+05
2340,"HL3826","H3",T,"CMEAT","pCi/g", 1.38557E-01, 1.38557E-01, 1.39128E-01, 1.92575E-
01, 3.27591E-01,
4.98474E-01, 6.79826E-01, 9.19843E-01, 1.61333E+00, 4.35308E-01, 3.52671E-01
2360,"HL3826","Cs137",T,"CLEAFY","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2360,"HL3826","Cs137",T,"CMILK","pCi/L", 2.74036E-33, 2.74036E-33, 2.86990E-31,
1.15026E-29, 2.20561E-27,
1.26852E-24, 5.10405E-23, 2.70384E-22, 1.92460E-21, 1.36383E-22, 4.38156E-22
2380,"HL3826","H3",T,"CMEAT","pCi/g", 1.98282E-02, 1.98282E-02, 1.99859E-02, 2.60028E-
02, 4.98622E-02,
7.13764E-02, 1.06772E-01, 1.31404E-01, 3.43755E-01, 6.78115E-02, 6.73055E-02
```

```
2380,"HL3826","Tc99",T,"CMILK","pCi/L", 7.57144E+04, 7.57144E+04, 8.75825E+04,
1.00408E+05, 1.41904E+05,
2.25828E+05, 2.80597E+05, 3.20630E+05, 3.54619E+05, 1.81611E+05, 8.35882E+04
3050,"HL3826","Pu239",T,"CMEAT","pCi/g", 8.04657E-25, 8.04657E-25, 5.73520E-22,
1.24118E-19, 5.71562E-17,
3.02333E-15, 2.24344E-13, 1.86882E-12, 7.87930E-11, 4.19864E-12, 1.62554E-11
3050,"HL3826","Pu239",T,"CFISH","pCi/g", 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
```

This file will have nine rows of information for every combination of time, location, and analyte. Therefore, this file can become very large. As an example, a 676 KB file was generated for a case involving 1 location, 7 analytes, 25 realizations, and 35 times. The file size directly scales with the number of analytes, locations, and times. The file size grows more slowly than a direct scaling by the number of realizations. As another example, a 486 MB file was generated for a case involving 1618 locations, 6 analytes, 11 realizations, and 35 times.

5.3.2.6 HUMAN Risk Detailed Data

The risk detailed data file is an optional output file that contains the detailed values for dose and risk generated in the HUMAN code. The description of the DETAIL modifier on the FILE keyword (see Table 5.12) explains how to activate writing this file. Table 5.11 describes the solution types that can be written to the file. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of six identifiers followed by a value for every generated realization. Table 5.7 provides a subset of the data written to this file for a run using five realizations. The following are the six identifiers on each line:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Analyte ID: The identification of the analyte for which the data were computed
- Analyte Type: A flag for analyte type: 1=radioactive, 2=carcinogen, 3=noncarcinogen
- Solution type: A flag for solution type that has the following definition:
    o EX indicates external dose
    o IG indicates ingestion dose
    o IH indicates inhalation dose
    o AL indicates analyte dose
    o CB indicates combined dose for analyte type
    o DW indicates drinking water dose (radioactive)
    o PD indicates population dose (radioactive)
    o PR indicates population risk (radioactive)
- Units: The units associated with the computed data.

Table 5.7 Excerpted Records from the Risks Detailed Data File

```
"Time","Location ID","Analyte ID","Analyte Type","Solution Type","Units","Values by realization"
2000,"HL0413","H3","RAD","IG","Rem", 1.59834E-05, 5.09257E-05, 1.60365E-04, 6.87785E-05, 5.56380E-05
2000,"HL0413","H3","RAD","IH","Rem", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0413","H3","RAD","EX","Rem", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0413","H3","RAD","DW","Rem", 9.67225E-07, 3.01822E-06, 2.21704E-06, 1.23771E-06, 1.58318E-06
2000,"HL0413","H3","RAD","AL","Rem", 1.59834E-05, 5.09257E-05, 1.60365E-04, 6.87785E-05, 5.56380E-05
2000,"HL0413","H3","RAD","PD","Rem", 3.28856E-02, 1.02619E-01, 7.53793E-02, 4.20823E-02, 5.38282E-02
```

```
2000,"HL0413","H3","RAD","PR","Risk", 2.18130E-05, 9.18666E-05, 3.23219E-05, 3.20382E-05, 1.74439E-05
...
2000,"HL0414","COMBIN","RAD","CB","Rem", 1.51672E-02, 1.43815E-03, 4.61088E-03, 3.55055E-03, 1.01778E-03
2000,"HL0414","COMBIN","RAD","DW","Rem", 1.87235E-02, 1.85456E-03, 1.82662E-03, 6.41806E-03, 7.02531E-04
2000,"HL0414","COMBIN","RAD","PD","Rem", 5.99151E+02, 5.93458E+01, 5.84517E+01, 2.05378E+02, 2.24810E+01
2000,"HL0414","COMBIN","RAD","PR","Risk", 3.97416E-01, 5.31273E-02, 2.50635E-02, 1.56359E-01, 7.28534E-03
...
2000,"HL0414","CCl4","CAR","IG","Risk", 2.44771E-06, 8.10842E-08, 1.44645E-05, 1.51662E-05, 6.47176E-07
2000,"HL0414","CCl4","CAR","IH","Risk", 1.60686E-09, 4.94426E-09, 4.31426E-08, 1.44453E-09, 2.28790E-08
2000,"HL0414","CCl4","CAR","EX","Risk", 1.33223E-07, 4.05942E-09, 3.24008E-08, 7.81486E-08, 4.68123E-09
2000,"HL0414","CCl4","CAR","AL","Risk", 2.58254E-06, 9.00879E-08, 1.45400E-05, 1.52458E-05, 6.74737E-07
…
2000,"HL0414","COMBIN","CAR","CB","Risk", 2.58254E-06, 9.00879E-08, 1.45400E-05, 1.52458E-05, 1.84499E+00
2000,"HL0414","U","HAZ","IG","Unitless", 8.05042E-06, 1.53466E-06, 6.57534E-05, 3.72276E-05, 7.38749E-06
2000,"HL0414","U","HAZ","IH","Unitless", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0414","U","HAZ","EX","Unitless", 3.32978E-07, 1.90871E-07, 2.40724E-07, 8.16859E-06, 2.05838E-07
2000,"HL0414","U","HAZ","AL","Unitless", 8.38340E-06, 1.72553E-06, 6.59941E-05, 4.53962E-05, 7.59333E-06
2000,"HL0414","COMBIN","HAZ","CB","Unitless", 8.38340E-06, 1.72553E-06, 6.59941E-05, 4.53962E-05, 7.59333E-06
...
2100,"POPDOS","POPDOS","RAD","CB","Person-Rem", 6.39394E+02, 6.13426E+01, 7.99459E+01, 8.50341E+02, 1.23211E+02
2100,"POPRSK","POPRSK","RAD","CB","Risk", 4.24109E-01, 5.49149E-02, 3.42799E-02, 6.47383E-01, 3.99285E-02
```

This file can have up to nine rows of information for every combination of time, location, and analyte. Therefore, this file can become very large. As an example, a 227 KB file was generated for a case involving 11 locations, 10 analytes, 5 realizations, and 3 times. The file size directly scales with the number of analytes, locations, and times. The file size grows more slowly than a direct scaling by the number of realizations. As another example, a 463 MB file was generated for a case involving 1618 locations, 6 analytes, 11 realizations, and 35 times, using all details output options. The file size can be reduced by selecting fewer detailed solution types.

5.3.2.7   HUMAN Risk Summary Statistics

This optional file contains summary statistics for dose and risk values generated in the HUMAN code. The description of the STATS modifier on the FILE keyword (see Table 5.12) tells how to activate writing this file. The solution types that can be written to the file are described in Table 5.14. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of six identifiers followed by summary statistics (nine percentiles, mean value, and standard deviation). Table 5.8 provides a subset of the data written to this file for a run using five realizations. The six identifiers on each line are the following:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Analyte ID: The identification of the analyte for which the data were computed
- Analyte Type: A flag for analyte type: 1=radioactive, 2=carcinogen, 3=noncarcinogen
- Solution type: A flag for solution type that has the following definition:
  - EX indicates external dose
  - IG indicates ingestion dose
  - IH indicates inhalation dose
  - AL indicates analyte dose
  - CB indicates combined dose for analyte type
  - DW indicates drinking water dose (radioactive)
  - PD indicates population dose (radioactive)
  - PR indicates population risk (radioactive)

- Units: The units associated with the computed data.

The data for each record in this file are too long to present without with line-wrapping in this document. Each record in the file occupies two lines in Table 5.8.

Table 5.8 Excerpted Records from the Risk Summary Statistics File

```
"Time","Location ID","Analyte ID","Analyte Type","Solution Type","Units","Minimum","5th
Percentile","10th Percentile","25th Percentile","Median","75th Percentile","90th
Percentile","95th Percentile","Maximum","Mean","Standard Deviation"
2000,"HL0413","H3","RAD","IG","Rem", 1.59834E-05, 1.59834E-05, 1.59834E-05, 1.59834E-05,
5.56380E-05, 5.56380E-05, 6.87785E-05, 6.87785E-05, 1.60365E-04, 7.03381E-05, 5.39783E-05
2000,"HL0413","H3","RAD","IH","Rem", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0413","H3","RAD","EX","Rem", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"HL0413","H3","RAD","PD","Person-Rem", 3.28856E-02, 3.28856E-02, 3.28856E-02, 3.28856E-02,
5.38282E-02, 5.38282E-02, 7.53793E-02, 7.53793E-02, 1.02619E-01, 6.13590E-02, 2.80091E-02
2100,"HL0414","Tc99","RAD","IG","Rem", 7.90825E-08, 7.90825E-08, 7.90825E-08, 7.90825E-08,
8.38515E-07, 8.38515E-07, 7.16277E-06, 7.16277E-06, 1.32302E-04, 2.81574E-05, 5.82919E-05
2100,"HL0414","Tc99","RAD","IH","Rem", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2100,"HL0415","U","HAZ","EX","Unitless", 2.13679E-07, 2.13679E-07, 2.13679E-07, 2.13679E-07,
6.95310E-07, 6.95310E-07, 1.37764E-06, 1.37764E-06, 1.67892E-05, 3.87023E-06, 7.23683E-06
2100,"HL0415","U","HAZ","AL","Unitless", 2.48891E-06, 2.48891E-06, 2.48891E-06, 2.48891E-06,
1.75020E-05, 1.75020E-05, 9.33037E-05, 9.33037E-05, 3.77678E-04, 9.97710E-05, 1.59648E-04
2100,"HL0415","COMBIN","HAZ","CB","Unitless", 2.48891E-06, 2.48891E-06, 2.48891E-06, 2.48891E-06,
1.75020E-05, 1.75020E-05, 9.33037E-05, 9.33037E-05, 3.77678E-04, 9.97710E-05, 1.59648E-04
2100,"HL3870","COMBIN","HAZ","CB","Unitless", 3.05987E-20, 3.05987E-20, 3.05987E-20, 3.05987E-20,
9.17589E-07, 9.17589E-07, 3.95330E-06, 3.95330E-06, 4.92935E-04, 9.95633E-05, 2.19907E-04
2100,"POPDOS","COMBIN","RAD","CB","Person-Rem", 6.13426E+01, 6.13426E+01, 6.13426E+01,
6.13426E+01, 1.23211E+02, 1.23211E+02, 6.39394E+02, 6.39394E+02, 8.50341E+02, 3.50847E+02,
3.68026E+02
2100,"POPRSK","COMBIN","RAD","CB","Risk", 3.42799E-02, 3.42799E-02, 3.42799E-02, 3.42799E-02,
5.49149E-02, 5.49149E-02, 4.24109E-01, 4.24109E-01, 6.47383E-01, 2.40123E-01, 2.81275E-01
```

This file can have up to nine rows of information for every combination of time, location, and analyte. Therefore, this file can become very large. As an example, a 398 KB file was generated for a case involving 11 locations, 10 analytes, 5 realizations, and 3 times. The file size directly scales with the number of analytes, locations, and times. The file size grows more slowly than a direct scaling by the number of realizations. As another example, a 466 MB file was generated for a case involving 1618 locations, 6 analytes, 11 realizations, and 35 times, using all details output options. The file size can be reduced by selecting fewer statistics solutions types.

5.4 Keyword Descriptions for the HUMAN Code

In the following keyword descriptions, some data are optional and some are required. Data that are required are enclosed in square brackets. For AB to be required, it would be denoted by [AB]. If only one of the three items AB, BC, CD were required, it would be written as [AB|BC|CD]. The vertical bars indicate that the user must select one of the items in the list. Optional items are enclosed in normal brackets. For DE to be an optional entry, it would be denoted by {DE}. The { } or [ ] symbols indicate whether the data are required; the symbols do not need to be entered when the keyword is constructed. The keyword name can contain any number of characters; however, only the first eight characters are used (for example, REALIZAT = REALIZATION = REALIZATxxx).

In some instances, numerical values or quote strings are associated with a modifier. In this description, the association is indicated by using the equal (=) symbol. The = symbol is not required but may be used when the keyword is constructed. When a numerical value or quote string is associated with a modifier, it must be physically entered on the input line directly after the modifier.

In general, the keywords can be entered in any order. The following are the restrictions on keyword order:

- The REPORT keyword must be the first keyword in the file.
- The END keyword must be the last keyword in the file.

5.4.1   ANALYTE Keyword for the HUMAN Code

The ANALYTE keyword is used to define the analytes to be used in the simulation. The following is this keyword's syntax:

```
ANALYTE [ID="quote1"] {BIRD=N1} {FISH=N2} {MEAT=N3}
    [RADIOACTIVE | CARCINOGEN | HAZARDOUS] {OUTPUT}
```

The analytes requested must be a subset of the analytes for which environmental data were computed and stored by the inventory, release, and transport modules. Table 5.9 describes the modifiers associated with the ANALYTE keyword.

Table 5.9 Modifiers Associated with the ANALYTE Keyword in the HUMAN Code

Modifier	Description
ID	The quote string associated with the ID modifier is an analyte identification string up to six characters long. The analyte identification string is case sensitive, and spaces or hyphens change the definition. All data in the analyte identification strings must satisfy the following conventions: - Only the first entry in the analyte identification string is capitalized - No embedded spaces or hyphens are used, even for radionuclides - Individual elements are defined using the standard element abbreviation
BIRD	The numerical value associated with the BIRD modifier gives the maximum allowable concentration in birds for this analyte (µg/kg or pCi/kg). No limit on the concentration is imposed if this optional modifier is not entered.
FISH	The numerical value associated with the FISH modifier gives the maximum allowable concentration in fish for this analyte (µg/kg or pCi/kg). No limit on the concentration is imposed if this optional modifier is not entered.
MEAT	The numerical value associated with the MEAT modifier gives the maximum allowable concentration in meat for this analyte (µg/kg or pCi/kg). No limit on the concentration is imposed if this optional modifier is not entered.
RADIOACTIVE	The presence of this modifier indicates to treat this analyte as a radioactive analyte.

Modifier	Description
CARCINOGEN	The presence of this modifier indicates to treat this analyte as a chemical carcinogen.
HAZARDOUS	The presence of this modifier indicates to treat this analyte as hazardous but not carcinogenic.
OUTPUT	If the modifier OUTPUT is entered, then outputs requested by the DETAILS and STATISTICS keywords will be written to the output files for this analyte. Otherwise, the calculations will occur, but no data will be output for this analyte.

Even though the HUMAN code can treat each analyte in three different fashions: as a radioactive analyte, as a hazardous chemical, and as a carcinogenic chemical. Each analyte can only be handled in one fashion in a given run of the code. Treating an analyte in all three fashions would require running the code three times.

The following is an example entry for a radioactive analyte that has an upper limit of 1000 pCi/kg in birds:

```
ANALYTE ID="Np237" BIRD=1000 RADIOACTIVE
```

The following is an example entry for a carcinogenic analyte that has no imposed concentration limits:

```
ANALYTE ID="Cr" CARCINOGENIC
```

The following is an example entry for a noncarcinogenic (hazardous) analyte that has no imposed concentration limits:

```
ANALYTE ID="Kerosen" HAZARDOUS
```

The following is an example entry for a noncarcinogenic (hazardous) analyte that has imposed concentration limits on all three foods:

```
ANALYTE ID="Cu" HAZARDOUS BIRD 107500 FISH=25 MEAT=3.475
```

5.4.2   AVERAGE Keyword for the HUMAN Code

The AVERAGE keyword is used to define averaging time for human risk calculations. The following is the keyword's syntax:

```
AVERAGE Value1
```

The entry for Value1 is the number of years in the averaging time. The averaging time has a default value of 70 years, and this record may be omitted if the default averaging time is desired. The following record sets the soil averaging time to 50 years:

```
AVERAGE 50
```

There are no modifiers or quote strings associated with the AVERAGE keyword.

5.4.3   DEBUG Keyword for the HUMAN Code

The DEBUG keyword is used to activate dumping of intermediate calculations to the report file. It should be used sparingly and with only one or two realizations; otherwise, the volume of output could fill the user's hard drive. The following is this keyword record's syntax:

```
DEBUG [modifier 1] {modifier 2}…{modifier 8}
```

Multiple DEBUG records can be entered with combinations of modifiers, or a single record can be entered containing all of the modifiers. The modifiers can be entered in any order. Table 5.10 describes the modifiers associated with the DEBUG keyword.

Table 5.10 Modifiers Associated with the DEBUG Keyword in the HUMAN Code

Modifier	Description
CARCINOG	Intermediate outputs on calculations for carcinogenic analytes.
CONCENTR	Intermediate outputs on reading and processing media concentrations.
FOOD	Intermediate outputs on calculating concentrations in food items.
HAZARDOU	Intermediate outputs on calculations for hazardous analytes.
RADIONUC	Intermediate outputs on calculations for radioactive analytes.
STOCHAST	Write out all generated stochastic values.
DEFINITION	Output the definition of all stochastic variables.
STATISTICS	Output summary statistics for all generated stochastic variables.

The following entries are examples of the use of the DEBUG keyword:

```
DEBUG CARCINOGENIC RADIONUCLIDES STOCHASTIC
DEBUG STOCHASTIC
```

There are no quote strings associated with the DEBUG keyword.

5.4.4   DETAILS Keyword for the HUMAN Code

The DETAILS keyword is used to control writing detailed data for all realizations to the output details file for a variety of solution types. The following is this keyword record's syntax:

```
DETAILS {modifier 1} {modifier 2} … {modifier11}
```

Multiple DETAILS cards can be entered with combinations of modifiers, or a single card can be entered containing all of the modifiers. The modifiers can be entered in any order. The modifiers associated with the DETAILS keyword are given in Table 5.11.

Table 5.11 Modifiers Associated with the DETAILS Keyword in the HUMAN Code

Modifier	Description
COMB_ANA	This modifier activates output of the risk for combined pathways that is also combined over analytes of same type (radioactive, carcinogenic, or hazardous). Detailed information is written out for every time, location, and analyte type combination.
COMB_DWA	This modifier activates output of the risk from drinking water that is combined over all radioactive analytes. Detailed information is written out for every time and location combination.
COMB_PDS	This modifier activates output of the population dose from drinking water that is combined over all radioactive analytes. Detailed information is written out for every time step.
COMB_PRS	This modifier activates output of the population risk from drinking water that is combined over all radioactive analytes. Detailed information is written out for every time step.
EACH_ANA	This modifier activates output of the risk or impact for combined pathways for each analyte. Detailed information is written out for every time, location, and analyte combination.
EACH_PDS	This modifier activates output of the population dose from drinking water for each radioactive analyte. Detailed information is written out for every location, analyte, and time step combination.
EACH_PRS	This modifier activates output of the population risk from drinking water for each radioactive analyte. Detailed information is written out for every location, analyte, and time step combination.
PATH_ING	This modifier activates output of the ingestion pathway impact for each analyte. Detailed information is written out for this pathway for every location, analyte, and time step combination.
PATH_INH	This modifier activates output of the inhalation pathway impact for each analyte. Detailed information is written out for this pathway for every location, analyte, and time step combination.
PATH_EXT	This modifier activates output of the external exposure pathway impact for each analyte. Detailed information is written out for this pathway for every location, analyte, and time step combination.
PATH_DWA	This modifier activates output of the drinking water dose for radioactive analytes. Detailed information is written out for this pathway for every location, analyte, and time step combination.

The following entries provide examples of the use of the DETAILS keyword:

```
DETAILS COMB_ANA
DETAILS COMB_ANA COMB_PDS EACH_PDS
```

There are no quote strings associated with the DETAILS keyword.

5.4.5   END Keyword for the HUMAN Code

The END keyword signifies the end of all keyword data. It should be the last keyword in the keyword file. All data in the keyword file after the END keyword will be ignored. The following is this keyword record's syntax:

```
END
```

There are no modifiers or quote strings associated with the END keyword.

5.4.6   EXECUTE Keyword for the HUMAN Code

The EXECUTE keyword signifies that the user wishes to perform problem execution. If this keyword is not entered, then the inputs are checked for consistency, but the problem will not be executed. This is useful if the run being set up is expected to take a significant amount of computation time. The following is this keyword record's syntax:

```
EXECUTE
```

There are no modifiers or quote strings associated with the EXECUTE keyword.

5.4.7   FILE Keyword for the HUMAN Code

The FILE keyword is used to enter the names of input and output files except for the report file. The names of the files providing concentration data are contained in the environmental scenario file rather than in the keyword file. The following is this keyword record's syntax:

```
FILE [modifier1="quote1"] {modifier2="quote2"} ... {modifier7="quote7"}
```

The file names are entered in quote strings, which must be enclosed in double quotation marks. Path names up to 72 characters long are supported. The file name associated with a modifier must be entered before the next modifier is entered. At least one FILE keyword is required for every run of the code. Table 5.12 describes the modifiers associated with the FILE keyword.

Table 5.12 Modifiers Associated with the FILE Keyword in the HUMAN Code

Modifier	Description
DETAIL	Output file containing the calculated risk for each analyte and segment for every realization of the code. The risks are written in tabular form so they can be imported easily into a spreadsheet or other software. This file is optional. It is required if any modifier is entered on the DETAILS keyword.

Modifier	Description
FOODS	Output file containing the calculated concentration in food for each analyte and location for every realization of the code. The concentrations are written in tabular form so they can be imported easily into a spreadsheet or other software. This file is optional. Entry of this modifier and the file name initiates data output.
FOODSTAT	Output file containing summary statistics on the calculated concentration in food for each analyte and location. This file is optional. Entry of this modifier and the file name initiates data output.
ESD	Input environmental settings definition file that contains the definition of the environmental runs from which impacts are to be calculated.
HEADER	Output file containing information needed by the SACView program to allow easy abstraction of the data output of the data code.
STATS	Output file containing summary statistics on the risks for every analyte at every location. This file is optional. It is required if any modifier is entered on the STATISTICS keyword.
VALUES	Output file containing the generated stochastic values for every stochastic variable used in the run. The values are written in tabular form so they can be imported easily into a spreadsheet or other software. This file is optional. Entry of this modifier and the file name initiates data output.

The following are two example entries:

```
FILE  HEADER "TestCase.hdr"
FILE  FOODS "TestCase.fod"
```

The following set of two entries has the same effect as the single entry above.

```
FILE HEADER="TestCase.hdr"  FOODS="TestCase.fod"
```

5.4.8   KDSOIL Keyword for the HUMAN Code

The KDSOIL keyword identifies the soil to water partition coefficients to be used in irrigation calculations. The syntax for the KDSOIL keyword record is one of the following:

```
KDSOIL LOCATION= "Quote 1" ANALYTE= "Quote 2" KDSOIL= "Quote 3"
```

or

```
KDSOIL TERSE ANALYTE= "Quote 2" KDSOIL= "Quote 3"
```

The modifiers can be entered in any order. Modifiers associated with the KDSOIL keyword are described in Table 5.13. If the LOCATION modifier is used, then a KDSOIL keyword must be entered for combinations of analytes and locations where irrigation is modeled. Thus, if there are 1618 locations

where irrigation will occur and there are 10 analytes, then the user must supply 16180 KDSOIL keywords. If the TERSE modifier is used, then only one KDSOIL keyword is needed for each analyte. Thus, if there are 1618 locations where irrigation will occur and there are 10 analytes, then the user must supply 10 KDSOIL keywords.

Table 5.13 Modifiers Associated with the KDSOIL Keyword in the HUMAN Code

Modifier	Description
ANALYTE	The quote string associated with the ANALYTE modifier must be an analyte ID from the list of ANALYTE keywords in the ESD keyword file.
KDSOIL	The quote string associated with the KDSOIL modifier must be an ID from the list of KDSOIL keywords in the ESD keyword file.
LOCATION	The quote string associated with the LOCATION modifier must be an ID from the list of LOCATION keywords in the ESD keyword file. This modifier and its quote string are not used if the TERSE modifier is used.
TERSE	If the TERSE modifier is entered, it supplants the use of the LOCATION modifier and the quote string associated with the LOCATION modifier. The TERSE modifier indicates that the KDSOIL value for an analyte will be the same for all locations.

The following are example KDSOIL keywords for two analytes and three locations:

```
KDSOIL LOCATION="HL0001" ANALYTE="CrVI"  KDSOIL="KD#001"
KDSOIL LOCATION="HL0001" ANALYTE="Sr90"  KDSOIL="KD#032"
KDSOIL LOCATION="HL0002" ANALYTE="CrVI"  KDSOIL="KD#001"
KDSOIL LOCATION="HL0002" ANALYTE="Sr90"  KDSOIL="KD#032"
KDSOIL LOCATION="HL0003" ANALYTE="CrVI"  KDSOIL="KD#001"
KDSOIL LOCATION="HL0003" ANALYTE="Sr90"  KDSOIL="KD#032"
KDSOIL LOCATION="HL0004" ANALYTE="CrVI"  KDSOIL="KD#001"
KDSOIL LOCATION="HL0004" ANALYTE="Sr90"  KDSOIL="KD#032"
```

The same definitions could be obtained by entering the following two KDSOIL keywords:

```
KDSOIL TERSE ANALYTE="CrVI"  KDSOIL="KD#001"
KDSOIL TERSE ANALYTE="Sr90"  KDSOIL="KD#032"
```

5.4.9   LOCATION Keyword for the HUMAN Code

The LOCATION keyword identifies the locations for human impact calculations that will be generated. Multiple LOCATION keywords are required if more than one location is requested. The locations must be a subset of the locations at which environmental data were computed and stored by the inventory, release, and transport modules. The list of desired locations builds sequentially with each LOCATION record. Upon program entry, no locations are active. The following is the LOCATION keyword record's syntax:

```
LOCATION [PRIMARY="quote 1"] {SECOND="quote 2"} {POP=N1}
    {IRRIGATE} {GRO_WAT | SUR_WAT} {OUTPUT}
```

The human impacts module is activated at a location by entering the location ID string in association with the PRIMARY modifier. A LOCATION keyword is required at each location to activate calculations.

If the SECOND modifier is entered, then it must be paired with a valid location ID string. The function of the SECOND modifier is to supply concentrations from other locations that may not be computed at the primary location. If the SECOND location is not entered, then impacts are calculated from concentrations available at the primary location. For example, the primary location may be inland from the river, but the person will visit the shoreline and spend some time in the river. The primary location would be inland and the secondary location could be in the river. Thus, the primary location would have only a groundwater concentration and the second location would supply surface water, pore water, and sediment concentrations.

If the IRRIGATE modifier is present, then irrigated crops will be grown at that location; otherwise, no irrigation of crops is performed. The default water source is groundwater at the primary location; if surface water is desired, then the modifier SUR_WAT must be entered. The modifier GRO_WAT may be entered for a groundwater source of irrigation water.

The modifier POP may be entered. If it is, it must be associated with the population at the primary location. If the POP modifier is not entered, the population at the location is determined from the entry in the ESD keyword file.

If the modifier OUTPUT is entered, then outputs requested by the DETAILS and STATISTICS keywords will be written to the output files for the location. Otherwise, the calculations will occur, but no data will be output for this location.

The following are example LOCATION keywords:

```
LOCATION PRIMARY="HL #1"
LOCATION PRIMARY= "HL #1" SECOND="HL #23"
```

5.4.10 REALIZATION Keyword for the HUMAN Code

The REALIZATION keyword defines the number of realizations to generate. The following is this keyword record's syntax:

```
REALIZATION value1
```

The integer value1 has a minimum value of 1 and a maximum of the number of realizations defined in the environmental scenario definition file. If the number of realizations is fewer than the number of realizations in the concentration data files, then only the first realizations will be used.

The following keyword record sets the number of realizations to 10:

```
REALIZAT 10
```

5.4.11 REPORT Keyword for the HUMAN Code

The REPORT keyword is used to define the name of the output report (log) file. It must be the first keyword entered in the keyword file. The syntax for this keyword record is the following:

```
REPORT ["quote"]
```

The name of the report file is entered in a quote string. File names up to 72 characters long are supported, and path names can be included. The following is an example REPORT keyword record:

```
REPORT "/SAC/SystemCodes/Cultural/Test1.rpt"
```

5.4.12 SEED Keyword for the HUMAN Code

The SEED keyword sets the value for the seed for the random number generator. The following is this keyword record's syntax:
```
SEED Value1
```

The value for Value1 must be an integer or real number in the range 1 to 999999. The following is an example keyword record:

```
SEED 344443
```

There are no modifiers or quote strings associated with the SEED keyword.

5.4.13 SOIL Keyword for the HUMAN Code

The SOIL keyword is used to define averaging time for soil concentration equations at irrigated locations. The following is the keyword's syntax:

```
SOIL Value1
```

The entry for Value1 is the number of years in the averaging time. The averaging time has a default value of 70 years, and this record may be omitted if the default averaging time is desired. The following record sets the soil averaging time to 120 years:

```
SOIL 120.0
```

There are no modifiers or quote strings associated with the SOILAVG keyword.

5.4.14 STATISTIC Keyword for the HUMAN Code

The STATISTIC keyword is used to control writing summary statistics to the output summary statistics file for a variety of solution types. The following is this keyword record's syntax:

```
STATISTIC [modifier 1] {modifier 2}…{modifier 11}
```

Multiple STATISTIC cards can be entered with combinations of modifiers, or a single card can be entered containing all of the modifiers. The modifiers can be entered in any order. Table 5.14 describes the modifiers associated with the STATISTIC keyword.

Table 5.14 Modifiers Associated with the STATISTIC Keyword in the HUMAN Code

Modifier	Description
COMB_ANA	This modifier activates output of the risk for combined pathways that is also combined over analytes of same type (radioactive, carcinogenic, or hazardous). Summary statistics are written out for every time, location, and analyte type combination.
COMB_DWA	This modifier activates output of the risk from drinking water that is combined over all radioactive analytes. Summary statistics are written out for every time and location combination.
COMB_PDS	This modifier activates output of the population dose from drinking water that is combined over all radioactive analytes. Summary statistics are written out for every time step.
COMB_PRS	This modifier activates output of the population risk from drinking water that is combined over all radioactive analytes. Summary statistics are written out for every time step.
EACH_ANA	This modifier activates output of the risk or impact for combined pathways for each analyte. Summary statistics are written out for every time, location, and analyte combination.
EACH_PDS	This modifier activates output of the population dose from drinking water for each radioactive analyte. Summary statistics are written out for every location, analyte, and time step combination.
EACH_PRS	This modifier activates output of the population risk from drinking water for each radioactive analyte. Summary statistics are written out for every location, analyte, and time step combination.
PATH_ING	This modifier activates output of the ingestion pathway impact for each analyte. Summary statistics are written out for this pathway for every location, analyte, and time step combination.
PATH_INH	This modifier activates output of the inhalation pathway impact for each analyte. Summary statistics are written out for this pathway for every location, analyte, and time step combination.
PATH_EXT	This modifier activates output of the external exposure pathway impact for each analyte. Summary statistics are written out for this pathway for every location, analyte, and time step combination.
PATH_DWA	This modifier activates output of the drinking water dose for radioactive analytes. Summary statistics are written out for this pathway for every location, analyte, and time step combination.

The following entries provide examples of the use of the STATISTIC keyword:

```
STATISTIC COMB_ANA
STATISTIC COMB_ANA PATH_ING PATH_DWA EACH_PRS
```

There are no quote strings associated with the STATISTIC keyword.

5.4.15 STOCHASTIC Keyword for the HUMAN Code

The STOCHASTIC keyword is used to enter the definition of a statistical distribution for stochastic variables. The following is the general syntax for the STOCHASTIC record:

```
STOCHASTIC ["Quote1"] [Dist_Index Parameters] {TRUNCATE U1 U2}
    {"Quote2"}
```

The entry for Quote1 must be a unique character string of up to 20 characters that will be used to identify this stochastic variable in subsequent uses. It is case sensitive and embedded spaces are significant. It is sometimes useful to make the character string some combination of a variable name and other data such that it can be recreated easily when stochastic data is needed. The entry for Quote2 is a description for the stochastic variable that can be up to 64 characters long. An entry for Quote2 is not required.

The entry for Dist_Index must be an integer in the range 1 to 13 that identifies the index of a statistical distribution. The statistical distributions are defined in Table 10.1. The word Parameters in the general syntax statement indicates the numerical values of parameters required for defining the statistical distribution. The additional modifier TRUNCATE can be used for all distribution types except 1, 3, and 10. If TRUNCATE is entered, it must be followed by two values in the interval 0 to 1, inclusive. The lower value must be less than the upper value. These two values specify the tail probabilities at which to impose range truncation for the distribution. Truncation data must be entered after all of the other parameters that define the distribution.

The following is an example stochastic record for the ingestion rate of soil for an adult that is uniformly distributed between 0.01 and 0.15:

```
STOCHASTIC "IRSOILADULT" 2 0.01 0.15 "Soil ingestion rate for an adult"
```

Although this section gives the general form of a STOCHASTIC keyword entry, it does not describe the entire set of STOCHASTIC keywords required to run the HUMAN code. A more complete set of example STOCHASTIC keywords is provided in Section 5.5. The example keywords are grouped by variable types as outlined in Table 5.15.

Table 5.15 Cross Reference to Example STOCHASTIC Keywords for the HUMAN Code

Cross-Reference	Multiple Dependencies	Type of Data Defined Using STOCHASTIC Keywords
Table 5.16	None	Exposure frequencies for different human activities.
Table 5.17	None	Exposure times for different human activities.
Table 5.18	None	Ingestion rates for water and food types.
Table 5.19	None	Miscellaneous variables.
Table 5.20	None	Data describing the body variability in humans.

Cross-Reference	Multiple Dependencies	Type of Data Defined Using STOCHASTIC Keywords
Table 5.21	Analyte	Data for transfer of contaminants into food items.
Table 5.22	Analyte	Volatilization and Permeability Data.
Table 5.23	None	Animal food and water variables for computing concentration in animal food products.
Table 5.24	Analyte	Hazard quotients for inhalation and ingestion that are used to compare intake to levels of concern. These data are required only for the analytes modeled as hazardous constituents.
Table 5.25	Analyte	Dose factors for converting external exposure and intake of radionuclides to dose. These data are required only for the radioactive analytes.
Table 5.26	Analyte	Slope factors for inhalation and ingestion that are used to compare intake to risk. These data are required only for the analytes modeled as carcinogenic constituents.

5.4.16 SWEAT Keyword for the HUMAN Code

The SWEAT keyword is used to define the source of water to be used in the sweat lodge calculations. The following is this keyword's general syntax:

```
SWEAT [ GROUND | RIVER | SEEP ]
```

If the SWEAT keyword is not used, then the sweat portion of the impact equations will yield a zero impact. The following is the keyword entry to select river water as the water source for sweat lodge calculations:

```
SWEAT RIVER
```

There are no quote strings or numerical values associated with the SWEAT keyword.

5.4.17 TIMES Keyword for the HUMAN Code

The TIMES keyword identifies the times at which the calculations are to be performed. The following is the keyword's syntax:

```
TIMES [ [T1] {T2} … {Tn} | {ALL} ]
```

The numerical entries T1, T2, …, Tn are the times (whole number years) when human impacts calculations are desired. These times must be a subset of the times at which environmental data were computed and stored by the inventory, release, and transport modules. Multiple TIMES keywords can be entered. If the modifier ALL is used, results will be calculated for every time in the ESD keyword file. If the modifier ALL is used, no numerical values should be entered. The following is an example TIMES keyword that requests output for the three years 2020, 2075, and 3014:

```
TIMES 2020 2075 3014
```

The following is an example TIMES keyword where all times from the ESD keyword file are requested:

```
TIMES ALL
```

There are no quote strings associated with the TIMES keyword.

5.4.18 TITLE Keyword for the HUMAN Code

The TITLE keyword is used to define a single-line problem title. The problem title will be written to output files. If the title is not supplied, then the program will error terminate. The following is this keyword record's syntax:

```
TITLE ["quote"]
```

The title is entered in a quote string, which must be enclosed in double quotation marks. Titles up to 72 characters long are supported. The following example defines a title for a run of the code:

```
TITLE "Example title line for the human impacts code."
```

There are no modifiers associated with the TITLE keyword.

5.4.19 USER Keyword for the HUMAN Code

The USER keyword is used to identify the user of the program. The user name will be written to output files. If the user name is not supplied, then the program will error terminate. The following is this keyword record's syntax:

```
USER ["quote"]
```

The user name is entered in a quote string, which must be enclosed in double quotation marks. User names up to 16 characters long are supported. The following example defines John Q. Public as the user running the code:

```
USER "John Q. Public"
```

There are no modifiers associated with the USER keyword.

5.5   Example Stochastic Keywords for the Human Code

The equations in Section 5.1.1 reference exposure frequencies for a number of activities.

Table 5.16 Example HUMAN Keywords for Entering Exposure Frequencies

Variable	Description	Units	Statistical Distribution
EF_{boat}	Exposure frequency for boating	day/yr	Constant of 5
STOCHASTIC "EFBOAT" 1 5 "Exposure frequency for boating"			
EF_{river}	Exposure frequency to volatile river water	day/yr	Uniform on 270 to 365
STOCHASTIC "EFRIVER" 2 270 365 "Exposure frequency to volatile river water"			
EF_{sed}	Exposure frequency for sediment	day/yr	Uniform on 1 to 20
STOCHASTIC "EFSED" 2 1 20 "Exposure frequency to sediment"			
EF_{seep}	Exposure frequency volatilized seep water	day/yr	Uniform on 270 to 365
STOCHASTIC "EFSEEP" 2 270 365 "Exposure frequency volatile seep water"			
EF_{soil}	Exposure frequency for soil	day/yr	Uniform on 270 to 365
STOCHASTIC "EFSOIL" 2 270 365 "Exposure frequency for soil"			
EF_{swim}	Exposure frequency for swimming	day/yr	Uniform on 1 to 20
STOCHASTIC "EFSWIM" 2 1 20 "Exposure frequency for swimming"			
EF_{sweat}	Exposure frequency for sweat lodge	day/yr	Constant of 0
STOCHASTIC "EFSWEAT" 1 0 "Exposure frequency for sweat lodge"			
EF_{ground}	Exposure frequency for drinking groundwater	day/yr	Uniform on 270 to 365
STOCHASTIC "EFGROUND" 2 270 365 "Exposure frequency for drinking groundwater"			

Variable	Description	Units	Statistical Distribution
EF_{leafy}	Exposure frequency for leafy vegetables	day/yr	Uniform on 270 to 365
STOCHASTIC "EFLEAFY" 2 270 365 "Exposure frequency for leafy vegetables"			
EF_{root}	Exposure frequency for eating root vegetables	day/yr	Uniform on 270 to 365
STOCHASTIC "EFROOT" 2 270 365 "Exposure frequency for eating root vegetables"			
EF_{meat}	Exposure frequency for eating meat	day/yr	Uniform on 270 to 365
STOCHASTIC "EFMEAT" 2 270 365 "Exposure frequency for eating meat"			
EF_{milk}	Exposure frequency for drinking milk	day/yr	Uniform on 270 to 365
STOCHASTIC "EFMILK" 2 270 365 "Exposure frequency for drinking milk"			
EF_{bird}	Exposure frequency for eating birds (poultry)	day/yr	Uniform on 270 to 365
STOCHASTIC "EFBIRD" 2 270 365 "Exposure frequency for eating birds (poultry)"			
EF_{fish}	Exposure frequency for eating fish	day/yr	Uniform on 270 to 365
STOCHASTIC "EFFISH" 2 270 365 "Exposure frequency for eating fish"			

The equations in Section 5.1.1 reference exposure times and durations for a number of activities. Table 5.17 provides example statistical distributions for these activities and the resulting keywords that implement the definitions.

Table 5.17 Example HUMAN Keywords for Entering Exposure Times

Variable	Description	Units	Statistical Distribution
ET_{boat}	Exposure time for boating	hr/day	Constant of 0
STOCHASTIC "ETBOAT" 1 0 "Exposure time for boating"			

Variable	Description	Units	Statistical Distribution
ET_{river}	Exposure time to volatile river water	hr/day	Uniform on 10 to 20
STOCHASTIC "ETRIVER" 2 10 20 "Exposure time to volatile river water"			
ET_{sed}	Exposure time for sediment	hr/day	Constant of 0
STOCHASTIC "ETSED" 1 0 "Exposure time for sediment"			
ET_{seep}	Exposure time volatile seep water	hr/day	Uniform on 10 to 24
STOCHASTIC "ETSEEP" 2 10 24 "Exposure time volatile seep water"			
ET_{soil}	Exposure time for soil	hr/day	Uniform on 8 to 24
STOCHASTIC "ETSOIL" 2 8 24 "Exposure time for soil"			
ET_{swim}	Exposure time for swimming	hr/day	Uniform on 0 to 8
STOCHASTIC "ETSWIM" 2 0 8 "Exposure time for swimming"			
ET_{sweat}	Exposure time for sweat lodge	hr/day	Uniform on 10 to 24
STOCHASTIC "ETSWEAT" 1 0 "Exposure time for sweat lodge"			
ED_{child}	Exposure duration for a child	yr	Uniform on 1 to 6
STOCHASTIC "EDCHILD" 2 1 6 "Exposure duration for a child"			
ED_{adult}	Exposure duration for an adult	yr	Uniform on 1 to 64
STOCHASTIC "EDADULT" 2 1 64 "Exposure duration for an adult"			

The equations in Section 5.1.1 reference inhalation and ingestion rates for a number of foods. Table 5.18 provides example statistical distributions for these activities and the resulting keywords that implement the definitions.

Table 5.18 Example HUMAN Keywords for Entering Ingestion Rates

Variable	Description	Units	Statistical Distribution
IRATE	Inhalation rate	m^3/day	Uniform on 15 to 30
STOCHASTIC "IRATE" 2 15 30 "Inhalation rate"			
IR$_{soilchild}$	Ingestion rate, soil child	kg/day	Uniform on 0.00002 to 0.0005
STOCHASTIC "IRSOILCHILD" 2 0.00002 0.00050 "Soil ingestion rate for a child"			
IR$_{soiladult}$	Ingestion rate, soil adult	kg/day	Uniform on 0.00001 to 0.00015
STOCHASTIC "IRSOILADULT" 2 0.00001 0.00015 "Soil ingestion rate for an adult"			
IR$_{sedchild}$	Ingestion rate, sediment – child	kg/day	Uniform on 0.00002 to 0.0005
STOCHASTIC "IRSEDCHILD" 2 0.00002 0.00050 "Sediment ingestion rate for a child"			
IR$_{sedadult}$	Ingestion rate, sediment – adult	kg/day	Uniform on 0.00001 to 0.00015
STOCHASTIC "IRSEDADULT" 2 0.00001 0.00015 "Sediment ingestion rate for an adult"			
IR$_{river}$	Ingestion rate, river water	L/day	Uniform on 0 to 3
STOCHASTIC "IRRIVER" 2 0 3 "River water ingestion rate"			
IR$_{ground}$	Ingestion rate, ground water	L/day	Uniform on 0 to 3
STOCHASTIC "IRGROUND" 2 0 3 "Ground water ingestion rate"			
IR$_{seep}$	Ingestion rate, seep water	L/day	Constant of 0
STOCHASTIC "IRSEEP" 1 0 "Seep water ingestion rate"			
IR$_{fish}$	Ingestion rate, fish	kg/day	Uniform on 0 to 0.1
STOCHASTIC "IRFISH" 2 0 0.1 "Ingestion rate for fish"			

Variable	Description	Units	Statistical Distribution
IR_{leafy}	Ingestion rate, leafy vegetables	kg/day	Uniform on 0 to 0.5
STOCHASTIC "IRLEAFY" 2 0 0.5 "Ingestion rate for leafy vegetables"			
IR_{root}	Ingestion rate, root vegetables	kg/day	Constant of 0
STOCHASTIC "IRROOT" 1 0 "Ingestion rate for root vegetables"			
IR_{meat}	Ingestion rate, meat	kg/day	Uniform on 0 to 0.25
STOCHASTIC "IRMEAT" 2 0 0.25 "Ingestion rate for meat"			
IR_{milk}	Ingestion rate, milk	L/day	Uniform on 0.1 to 1
STOCHASTIC "IRMILK" 2 0.1 1 "Milk ingestion rate"			
IR_{bird}	Ingestion rate, birds	kg/day	Constant of 0
STOCHASTIC "IRBIRD" 1 0 "Ingestion rate for bird meat"			

The equations in Section 5.1.1 reference several soil and air concentration related variables. Table 5.19 provides example statistical distributions for these activities and the resulting keywords that implement the definitions.

Table 5.19 Example HUMAN Keywords for Entering Concentration Variables

Variable	Description	Units	Statistical Distribution
ML	Mass loading of soil in air	kg/m^3	Constant of 0.00000005
STOCHASTIC "ML" 1 0.00000005 "Mass loading of soil in air"			
AF_{soil}	Adherence factor for soil	$mg/cm^2/day$	Uniform on 0.05 to 0.5
STOCHASTIC "AFSOIL" 2 0.05 0.50 "Adherence factor for soil"			
AF_{sed}	Adherence factor for sediment	$mg/cm^2/day$	Uniform on 0.05 to 0.5
STOCHASTIC "AFSED" 2 0.05 0.50 "Adherence factor for sediment"			

Variable	Description	Units	Statistical Distribution
IRGRATE	Irrigation rate	L/m^2 per yr	Uniform on 500 to 1000
STOCHASTIC "IRGRATE" 2 500 1000 "Irrigation rate"			
SHIELDSOIL	Soil shielding factor	unitless	Constant of 0.8
STOCHASTIC "SHIELDSOIL" 1 0.8 "Soil shielding factor"			
SHIELDSED	Sediment shielding factor	unitless	Constant of 0.2
STOCHASTIC "SHIELDSED" 1 0.2 "Sediment shielding factor"			
CF_{sweat}	Air concentration factor for sweat lodge	L/m^3	Uniform on 0.1 to 0.3
STOCHASTIC "CFSWEAT" 2 0.1 0.3 "Air concentration factor for sweat lodge"			

The equations in Section 5.1.1 reference several body size variables. Table 5.20 provides example statistical distributions for these activities and the resulting keywords that implement the definitions.

Table 5.20 Example Keywords for Entering Body Data in the HUMAN Code

Variable	Description	Units	Statistical Distribution
BW_{child}	Body weight for a child	kg	Constant of 16
STOCHASTIC "BWCHILD" 1 16 "Body weight for a child"			
BW_{adult}	Body weight for an adult	kg	Constant of 70
STOCHASTIC "BWADULT" 1 70 "Body weight for an adult"			
SA_{soil}	Body surface area – soils	cm^2	Constant of 5000
STOCHASTIC "SASOIL" 1 5000 "Body surface area for soil exposure"			
SA_{sed}	Body surface area – sediments	cm^2	Constant of 5000
STOCHASTIC "SASED" 1 5000 "Body surface area for sediment exposure"			

Variable	Description	Units	Statistical Distribution
SA_{seep}	Body surface area - seep water	cm^2	Constant of 20000
STOCHASTIC "SASEEP" 1 20000 "Body surface area for seep water exposure"			
SA_{river}	Body surface area - river water	cm^2	Constant of 20000
STOCHASTIC "SARIVER" 1 20000 "Body surface area for river water exposure"			
SA_{other}	Body surface area - river water	cm^2	Constant of 0
STOCHASTIC "SAOTHER" 1 0 "Body surface area for other (Native American) activities"			
SA_{sweat}	Body surface area - sweat lodge	cm^2	Constant of 20000
STOCHASTIC "SASWEAT" 1 20000 "Body surface area sweat lodge calculations"			

The equations in Section 5.1.1 reference transfer factors for computing concentrations in human food items. These transfer factors must be defined for every analyte. Table 5.21 provides example statistical distributions for these activities and the resulting keywords that implement the definitions.

Table 5.21 Example HUMAN Keywords for Entering Food Transfer Factors

Analyte	Variable	Description	Units	Statistical Distribution
H3	TF_{milk}	Transfer factor for milk for tritium	day/Liter	Lognormal on Mean - 1.82391, Standard deviation of Logarithms 0.30103
STOCHASTIC "H3 TFMILK" 5 -1.82391 0.30103 "Transfer factor for milk for tritium"				
Pu239	TF_{milk}	Transfer factor for milk for Pu-239	day/Liter	Triangular on Lower Limit 3.0E-09, Mode 1.1E-06, Upper Limit 3.0E-06.
STOCHASTIC "Pu239 TFMILK" 6 3.00E-09 1.10E-06 3.00E-06 "Transfer factor for milk for Pu-239"				

Analyte	Variable	Description	Units	Statistical Distribution
CCl4	TF$_{milk}$	Transfer factor for milk for CCl4	day/Liter	Triangular on Lower Limit 0, Mode 3.60E-06, Upper Limit 1.00E-05
STOCHASTIC "CCl4 TFMILK" 6 0.0 3.60E-06 1.00E-05 "Transfer factor for milk for CCl4"				
CrVI	TF$_{milk}$	Transfer factor for milk for chromium	day/Liter	Lognormal on Mean –5, Standard Deviation of Logarithms 0.30103
STOCHASTIC "CrVI TFMILK" 5 -5.0 0.30103 "Transfer factor for milk for chromium"				
Tc99	TF$_{meat}$	Transfer factor for meat for Tc-99	day/kg	Loguniform on Lower Limit 1.00E-06, Upper Limit 1.00E-04
STOCHASTIC "Tc99 TFMEAT" 5 1.00E-06 1.00E-04 "Transfer factor for meat for Tc-99"				
Cs137	TF$_{meat}$	Transfer factor for meat for Cs-137	day/kg	Triangular on Lower Limit 0.01, Mode 0.05, Upper Limit 0.06
STOCHASTIC "Cs137 TFMEAT" 6 1.00E-02 5.00E-02 6.00E-02 "Transfer factor for meat for Cs-137"				
CCl4	TF$_{meat}$	Transfer factor for meat for CCl4	day/kg	Triangular on Lower Limit 0, Mode 1.10E-05, Upper Limit 2.00E-05
STOCHASTIC "CCl4 TFMEAT" 6 0.0 1.10E-05 2.00E-05 "Transfer factor for meat for CCl4"				
CrVI	TF$_{meat}$	Transfer factor for meat for chromium	day/kg	Lognormal on Mean -2.04576, Standard Deviation of logarithms 0.30103
STOCHASTIC "CrVI TFMEAT" 5 -2.04576 0.30103 "Transfer factor for meat for chromium"				
H3	TF$_{bird}$	Transfer factor for birds for tritium	day/kg	Uniform on 0.5 to 1
STOCHASTIC "H3 TFBIRD" 2 0.5 1.0 "Transfer factor for birds for tritium"				

Analyte	Variable	Description	Units	Statistical Distribution
Tc99	TF_{bird}	Transfer factor for birds for Tc-99	day/kg	Triangular on Lower Limit 3.00E-02, Mode 3.50E-02, Upper Limit 2.00E-01
STOCHASTIC "Tc99 TFBIRD" 6 3.00E-02 3.50E-02 2.00E-01 "Transfer factor for birds for Tc-99"				
Pu239	TF_{bird}	Transfer factor for birds for Pu-239	day/kg	Loguniform on Lower Limit 2.00E-05, Upper Limit 3.00E-03
STOCHASTIC "Pu239 TFBIRD" 5 2.00E-05 3.00E-03 "Transfer factor for birds for Pu-239"				
CCl4	TF_{bird}	Transfer factor for birds for CCl4	day/kg	Triangular on Lower Limit 0, Mode 1.10E-05, Upper Limit 2.00E-05
STOCHASTIC "CCl4 TFBIRD" 6 0.00E+00 1.10E-05 2.00E-05 "Transfer factor for birds for CCl4"				
H3	BIO_{fish}	H3 bioaccumulation for fish	pCi/kg per pCi/L	Uniform on 0.6 to 1
STOCHASTIC "H3 BIOFISH" 2 0.6 1.0 "H3 bioaccumulation for fish"				
U238	BIO_{fish}	U-238 bioaccumulation for fish	pCi/kg per pCi/L	Triangular on Lower Limit 2, Mode 10, Upper Limit 50
STOCHASTIC "U238 BIOFISH" 6 2 10 50 "U-238 bioaccumulation for fish"				
CCl4	BIO_{fish}	CCl4 bioaccumulation for fish	pCi/kg per pCi/L	Uniform on 15 to 150
STOCHASTIC "CCl4 BIOFISH" 2 15 150 "CCl4 bioaccumulation for fish"				
CrVI	BIO_{fish}	Chromium bioaccumulation for fish	pCi/kg per pCi/L	Triangular on Lower Limit 40, Mode 200, Upper Limit 2000
STOCHASTIC "CrVI BIOFISH" 6 40 200 2000 "Chromium bioaccumulation for fish"				

Analyte	Variable	Description	Units	Statistical Distribution
H3	CR_{veg}	H3 soil-to-plant ratio	pCi/kg plant per pCi/kg soil	Triangular on Lower Limit 0.05, Mode 0.1, Upper Limit 0.2
STOCHASTIC "H3 CRVEG" 6 0.05 0.1 0.2 "H3 soil-to-plant ratio"				
Tc99	CR_{veg}	Tc99 soil-to-plant ratio	pCi/kg plant per pCi/kg soil	Triangular on Lower Limit 1, mode 10, Upper Limit 100
STOCHASTIC "Tc99 CRVEG" 6 1 10 100 "Tc99 soil-to-plant ratio"				
I129	CR_{veg}	I 129 soil-to-plant ratio	pCi/kg plant per pCi/kg soil	Triangular on Lower Limit 5.00E-05, Mode 5.00E-04, Upper Limit 5.00E-03
STOCHASTIC "I129 CRVEG" 6 5.00E-05 5.00E-04 5.00E-03 "I 129 soil-to-plant ratio"				

The equations in Section 5.1.1 reference volatilization, permeability, and skin absorption variables.
Values for these variables must be entered for every analyte. Table 5.22 provides example statistical
distributions for these activities and the resulting keywords that implement the definitions.

Table 5.22 Example HUMAN Keywords for Volatilization and Permeability Data

Analyte	Variable	Description	Units	Statistical Distribution
CCl4	VF	CCL4 Volatilization Factor	L/m^3	Loguniform on Lower Limit 0.001, Upper Limit 0.1
STOCHASTIC "CCl4 VF" 4 0.001 0.1 "CCL4 Volatilization Factor"				
CrVI	KP	Cr Skin Permeability Coefficient	cm/hr	Loguniform on Lower Limit 0.0003 Upper Limit 0.003
STOCHASTIC "CrVI KP" 4 0.0003 0.0030 "Cr Skin Permeability Coefficient"				
U	ABS	U Skin Absorption Factor	unitless	Loguniform on Lower Limit 0.0001, Upper Limit 0.01
STOCHASTIC "U ABS" 4 0.0001 0.0100 "U Skin Absorption Factor"				

The equations in Section 5.1.1 reference food and water intake by animals. Table 5.23 provides example statistical distributions for these activities and the resulting keywords that implement the definitions.

Table 5.23 Example HUMAN Keywords for Entering Animal Food and Water

Variable	Description	Units	Statistical Distribution
QP_{meat}	Quantity of plants eaten by meat animal	kg(wet)/day	Triangular on Lower Limit 58, Mode 68, Upper Limit 78
STOCHASTIC "QPMEAT" 6 58 68 78 "Quantity of plants eaten by meat animal"			
QP_{milk}	Quantity of plants eaten by milk animal	kg(wet)/day	Triangular on Lower Limit 45, Mode 55, Upper Limit 65
STOCHASTIC "QPMILK" 6 45 55 65 "Quantity of plants eaten by milk animal"			
QP_{bird}	Quantity of plants eaten by bird	kg(wet)/day	Triangular on Lower Limit 0.35, Mode 0.5, Upper Limit 0.65
STOCHASTIC "QPBIRD" 6 0.35 0.50 0.65 "Quantity of plants eaten by bird"			
QW_{meat}	Quantity of water drunk by meat animal	Liter/day	Triangular on Lower Limit 25, Mode 68, Upper Limit 136
STOCHASTIC "QWMEAT" 6 25 68 136 "Quantity of water drunk by meat animal"			
QW_{milk}	Quantity of water drunk by milk animal	Liter/day	Triangular on Lower Limit 25, Mode 50, Upper Limit 100
STOCHASTIC "QWMILK" 6 25 50 100 "Quantity of water drunk by milk animal"			
QW_{bird}	Quantity of water drunk by bird	Liter/day	Triangular on Lower Limit 0.1, Mode 0.25, Upper Limit 0.4
STOCHASTIC "QWBIRD" 6 0.10 0.25 0.40 "Quantity of water drunk by bird"			

The equations in Section 5.1.1 reference hazard quotients (oral reference doses) for hazardous analytes. These values must be entered for every analyte.

Table 5.24 Example HUMAN Keywords for Entering Hazard Quotients

Analyte	Variable	Description	Units	Statistical Distribution
CrVI	HQ$_{inh}$	Cr(VI) hazard quotient for inhalation	mg(intake)/(kg(bodyweight) day)	Triangular on Lower Limit 1.00E-03, Mode 0.005, Upper Limit 0.015
STOCHASTIC "CrVI HQINH" 6 0.001 0.005 0.015 "Cr(VI) hazard quotient for inhalation"				
CrVI	HQ$_{ing}$	Cr(VI) hazard quotient for ingestion	mg(intake)/(kg(bodyweight) day)	Triangular on Lower Limit 0.001, Mode 0.005, Upper Limit 0.015
STOCHASTIC "CrVI HQING" 6 0.001 0.005 0.015 "Cr(VI) hazard quotient for ingestion"				
CCl4	HQ$_{inh}$	CCl4 hazard quotient for inhalation	mg(intake)/(kg(bodyweight) day)	Loguniform on Lower Limit 7.00E-06, Upper limit 7.00E-04
STOCHASTIC "CCL4 HQINH" 5 7.0E-06 7.0E-04 "CCl4 hazard quotient for inhalation"				
CC4	HQ$_{ing}$	CCl4 hazard quotient for ingestion	mg(intake)/(kg(bodyweight) day)	Loguniform on Lower Limit 7.00E-06, Upper Limit 7.00E-04
STOCHASTIC "CCL4 HQING" 5 7.0E-06 7.0E-04 "CCl4 hazard quotient for ingestion"				
U	HQ$_{inh}$	U hazard quotient for inhalation	mg(intake)/(kg(bodyweight) day)	Loguniform on Lower Limit 1.40E-06, Upper Limit 1.40E-03
STOCHASTIC "U HQINH" 5 1.4E-06 1.4E-03 "U hazard quotient for inhalation"				
U	HQ$_{ing}$	hazard quotient for ingestion	mg(intake)/(kg(bodyweight) day)	Loguniform on Lower Limit 3.00E-06, Upper Limit 3.00E-03
STOCHASTIC "U HQING" 5 3.0E-06 3.0E-03 "U hazard quotient for ingestion"				

The equations in Section 5.1.1 reference dose factors for radioactive analytes. The dose factors must be entered for every radioactive analyte. Table 5.25 provides example statistical distributions for these activities and the resulting keywords that implement the definitions.

Table 5.25 Example HUMAN Keywords for Entering Dose Factors

Analyte	Variable	Description	Units	Statistical Distribution
Cs137	DF_{soil}	Cs/Ba137 dose factor for soil	rem/hr per pCi/g	Triangular on Lower Limit 2.50E-08, Mode 5.00E-08, Upper Limit 1.00E-07
STOCHASTIC "U HQING" 5 3.0E-06 3.0E-03 "U hazard quotient for ingestion"				
Cs137	DF_{swim}	Cs/Ba137 dose factor for swimming	rem/hr per pCi/L	Triangular on Lower Limit 4.20E-10, Mode 8.30E-10, Upper Limit 1.70E-09
STOCHASTIC "Cs137 DFSWIM" 6 4.20E-10 8.30E-10 1.70E-09 "Cs/Ba137 dose factor for swimming"				
Cs137	DF_{boat}	Cs/Ba137 dose factor for boating	rem/hr per pCi/L	Triangular on Lower limit 2.10E-10, mode 4.20E-10, Upper Limit 8.30E-10
STOCHASTIC "Cs137 DFBOAT" 6 2.10E-10 4.20E-10 8.30E-10 "Cs/Ba137 dose factor for boating"				
Cs137	DF_{ing}	Cs137 dose factor for ingestion	rem/pCi	Lognormal on Mean -7.30103, Standard Deviation of Logarithms 3.01E-01
STOCHASTIC "Cs137 DFING" 8 -7.30103E+00 3.01E-01 "Cs137 dose factor for ingestion"				
Cs137	DF_{inh}	Cs137 dose factor for inhalation	rem/pCi	Lognormal on Mean -7.49485, Standard Deviation of Logarithms 3.01E-01
STOCHASTIC "Cs137 DFINH" 8 -7.49485E+00 3.01E-01 "Cs137 dose factor for inhalation"				
H3	DF_{soil}	H3 dose factor for soil	rem/hr per pCi/g	Constant of 0
STOCHASTIC "H3 DFSOIL" 1 0 "H3 dose factor for soil"				
H3	DF_{swim}	H3 dose factor for swimming	rem/hr per pCi/L	Constant of 0

Analyte	Variable	Description	Units	Statistical Distribution
STOCHASTIC "H3 DFSWIM" 1 0 "H3 dose factor for swimming"				
H3	DF_{boat}	H3 dose factor for boating	rem/hr per pCi/L	Constant of 0
STOCHASTIC "H3 DFBOAT" 1 0 "H3 dose factor for boating"				
H3	DF_{ing}	H3 dose factor for ingestion	rem/pCi	Lognormal on Mean -10.1938, Standard Deviation of Logarithms 3.01E-01
STOCHASTIC "H3 DFING" 8 -1.01938E+01 3.01E-01 "H3 dose factor for ingestion"				
H3	DF_{inh}	H3 dose factor for inhalation	rem/pCi	Lognormal on Mean -10.0177, Standard Deviation of Logarithms 3.01E-01
STOCHASTIC "H3 DFINH" 8 -1.00177E+01 3.01E-01 "H3 dose factor for inhalation"				

The equations in Section 5.1.1 reference slope factors for carcinogenic analytes. The slope factors must be defined for every carcinogenic analyte. Table 5.26 provides example statistical distributions for these activities and the resulting keywords that implement the definitions.

Table 5.26 Example HUMAN Keywords for Entering Slope Factors

Analyte	Variable	Description	Units	Statistical
CCl4	SF_{inh}	CCl4 slope factor for inhalation	risk per mg(intake)/(kg(bodyweight)/day)	Lognormal on Mean -1.27572, Standard Deviation of Logarithms 0.47712
STOCHASTIC "CCl4 SFINH" 8 -1.27572 0.47712 "CCl4 slope factor for inhalation"				
CCl4	SF_{ing}	CCl4 slope factor for ingestion	risk per mg(intake)/(kg(bodyweight)/day)	Lognormal Mean -0.88606, Standard Deviation of Logarithms 0.47712
STOCHASTIC "CCl4 SFING" 8 -0.88606 0.47712 "CCl4 slope factor for ingestion"				

Analyte	Variable	Description	Units	Statistical
CrVI	SF_{inh}	Cr slope factor for inhalation	risk per mg(intake)/(kg(bodyweight)/day)	Triangular on Lower Limit 21, Mode 42, Upper Limit 290
STOCHASTIC "CrVI SFINH" 6 21 42 290 "Cr slope factor for inhalation"				
CrVI	SF_{ing}	Cr slope factor for ingestion	risk per mg(intake)/(kg(bodyweight)/day)	User-defined cumulative distribution function
STOCHASTIC "CrVI SFING" 10 "Cr slope factor for ingestion" 8 (0,0) (0.7999,0) (0.8,21) (0.8499,21) (0.85,42) (0.8999,42) (0.9,290) (1,290)				

6.0   Tri-Cities Economic Regional Model (TCERM)

6.1   Mathematical Formulation for the Economics Impacts Model

The following sections give the mathematical formulations for TCERM, the Tri-Cities Economic Risk Model. TCERM is divided into three primary sections: TRIGGER calculations, EFFECTS calculations, and economic change (ECONCHG) calculations.

6.1.1   Trigger Mechanisms

The trigger mechanisms are the set of equations that use input environmental concentrations and user-specified threshold levels to determine if an economic effect is present. The cost of filtering or replacing a contaminated water supply is also calculated within the TRIGGER subroutine.

6.1.1.1   Comparison to Environmental Standards

The first function in the TRIGGER routine is to compare the environmental concentrations for a location to the standards selected for each contaminant. This information is then used in various combinations to set economic activity reduction factors used in the EFFECTS module of TCERM. The environmental concentrations provided for a site are surface water used as drinking water, surface water used for recreation (swimming, boating, etc.), surface water used for irrigation, groundwater used for drinking water, groundwater used for irrigation, and fish tissue concentrations for selected species calculated by the ECEM model. Not all of these environmental concentrations need be supplied for a single location. For example, only one type of drinking water would be supplied, either surface water or groundwater, as appropriate.

6.1.1.1.1   Trigger for Fish Tissue Concentrations

For each species, the fish tissue concentrations calculated by ECEM are compared to user-specified threshold concentrations for each analyte. The variable BBT is set to one of three levels depending on the comparison to the body burden threshold for a given species S at a location L.

$$BBT(L,S) = 0, \quad \text{If } BB(L,S,C) < 0.01^{X} \text{ ALBB}(S,C)$$
$$BBT(L,S) = 1, \quad \text{If } 0.01^{X} \text{ ALBB}(S,C) \leq BB(L,S,C) \leq ALBB(S,C)$$
$$BBT(L,S) = 2, \quad \text{If } BB(L,S,C) > ALBB(S,C)$$

where:
  $BB(L,S,C)$ =   Body burden for analyte C in species S at location L (pCi/L or µg/kg)
  $AL_{BB}(S,C)$ =   Threshold concentration for the body burden concentration for analyte C in
        species S (pCi/L or µg/kg).

At each location, the user specifies the fractional contribution to recreational fishing for six fish species. If the body burden concentration for a species exceeds the user-specified threshold for at least one analyte, then the maximum body burden trigger for the species is 2, and the fishing

reduction fraction for the location is incremented by the contribution fraction for that fish at that location.

```
FRF(L) = FRF(L) + FWT(L,S)
```

where:
    FWT(L,S) =   The percentage of the game fish at location L represented by species S (unitless).

6.1.1.1.2   *Trigger for Surface Water Drinking Water Concentrations*

The trigger for surface water drinking water is used in the calculation of the cost or filtering or replacing the drinking water supply. If the surface water concentration for an analyte exceeds the threshold, then the filtering cost for the analyte is added to the total cost of filtering the water supply. The drinking water source is specified as private or public.

```
FT_SW(L) = FT_SW(L) + FF_SW(L,C), If SW_DW(L,C) > AL_DW(C)
```

where:
    $FF_{SW}(L,C)$ = Cost of filtering the drinking water supply for analyte C at location L (\$ per 1,000 gallons)
    $SW_{DW}(L,C)$ = Surface water drinking water concentration for analyte C at location L (pCi/L or µg/L)
    $AL_{DW}(C)$ = Threshold concentration for the drinking water concentration for analyte C (pCi/L or µg/L).

6.1.1.1.3   *Trigger for Surface Water Contact Water Concentrations*

The surface water concentration specified for contact in recreation is used to determine the reduction fractions for recreational activities.

```
SWTCON(L) = 0,  If SWCON(L,C) < 0.01 X ALCON(C)
SWTCON(L) = 1,  If 0.01 X ALCON(C) ≤ SWCON(L,C) ≤ ALCON(C)
SWTCON(L) = 2,  If SWCON(L,C) > ALCON(C)
```

where:
    $SW_{CON}(L,C)$ = Surface water contact concentration for analyte C at location L (pCi/L or µg/L)
    $AL_{CON}(C)$ = Threshold concentration for the surface water contact for analyte C (pCi/L or µg/L).

Factors for reduction in recreational activity caused by regulatory action and voluntary avoidance are set based on the contact surface water trigger. All reduction fractions for contact water are sampled from user-specified statistical distributions. Regulatory reduction in recreational activities occurs when environmental concentrations exceed regulatory limits.

```
SWCF_RR (L) = RRWQ(L,A) , If Max(SWT_CON(L)) = 2
```

where:

RRWQ(L,A) = Stochastically generated fraction based on water quality for activity A at location L (unitless).

Voluntary avoidance of recreational activities may result when environmental concentrations are either above or below regulatory limits. There is no reduction in activity if the water concentrations are below one percent of the threshold concentration for contact water for all analytes. There is a moderate voluntary avoidance of recreation if the water concentration for any analyte is greater than one percent of the threshold but does not exceed the threshold. There is a greater voluntary reduction in recreational activity if any analyte contact water concentration exceeds its threshold concentration.

```
SWCFVA (L) = 0 , If Max(SWTCON(L)) = 0
SWCFVA (L) = RRS1(L,A) , If Max(SWTCON(L)) = 1
SWCFVA (L) = RRS2(L,A) , If Max(SWTCON(L)) = 2
```

where:
RRS1(L,A) = Stochastically generated step 1 fraction for activity A at location L (unitless)
RRS2(L,A) = Stochastically generated step 2 fraction for activity A at location L (unitless).

6.1.1.1.4 Trigger for Surface Water Irrigation Water Concentrations

The surface water irrigation concentration is used to determine the reduction fractions for agricultural activities.

```
SWTAG(L) = 0,  If SWIRR(L,C) < 0.01 X ALAG(C)
SWTAG(L) = 1,  If 0.01 X ALAG(C) ≤ SWIRR(L,C) ≤ ALAG(C)
SWTAG(L) = 2,  If SWIRR(L,C) > ALAG(C)
```

where:
SWIRR(L,C) = Surface water irrigation concentration for analyte C at location L (pCi/L or µg/L)
ALAG(C) = Threshold concentration for the surface water contact for analyte C (pCi/L or µg/L).

6.1.1.1.5 Trigger for Groundwater Drinking Water Concentrations

The trigger for groundwater drinking water is used in the calculation of the cost of filtering or replacing the drinking water supply. If the groundwater concentration for an analyte exceeds the threshold, then the filtering cost for the analyte is added to the total cost of filtering the water supply. The drinking water source is specified as private or public.

$$FT_{GW}(L) = FT_{GW}(L) + FF_{GW}(L,C), \text{ If } GW_{DW}(L,C) > AL_{DW}(C)$$

where:
$FF_{GW}(L,C)$ = Cost of filtering the drinking water supply for analyte C at location L ($/1,000 gal/d)
$GW_{DW}(L,C)$ = Groundwater drinking water concentration for analyte C at location L (pCi/L or µg/L)

$AL_{DW}(C)$ = Threshold concentration for the drinking water concentration for analyte C (pCi/L or μg/L).

6.1.1.1.6 *Trigger for Groundwater Irrigation Water Concentrations*

The groundwater irrigation concentration is used to determine the reduction fractions for agricultural activities.

```
GWTAG(L) = 0,  If GWIRR(L,C) < 0.01 X ALAG(C)
GWTAG(L) = 1,  If 0.01 X ALAG(C) ≤ GWIRR(L,C) ≤ ALAG(C)
GWTAG(L) = 2,  If GWIRR(L,C) > ALAG(C)
```

where:
$GW_{IRR}(L,C)$ = Groundwater irrigation concentration for analyte C at location L (pCi/L or μg/L)
$AL_{AG}(C)$ = Threshold concentration for the surface water contact for analyte C (pCi/L or μg/L).

6.1.1.2 Reduction in Recreational Activity Due to Regulation

The regulatory reduction fractions for recreational activity are equal to the surface water contact reduction fractions as defined in Section 6.1.1.1.3.

```
RRFRR(L,A) = SWCFRR (L)
```

6.1.1.3 Reduction in Recreational Activity Due to Avoidance

The reduction fraction for voluntary avoidance of fishing is set based on both the surface water contact trigger and the fish body burden trigger.

```
RRFVA(L,A) = SWCFVA (L),  If  SWCFVA (L) >0
RRFVA(L,A) = 0,  If  SWCFVA (L) =0 and FRF(L) = 0
RRFVA(L,A) = RRWQ(L,A) X FRF(L),  If  SWCFRR (L) =0 and FRF(L) > 0
```

For all other activities, the reduction fraction for voluntary avoidance is set to the surface water contact trigger.

```
RRFVA(L,A) = SWCFVA (L)
```

6.1.1.4 Reduction in Agricultural Supply Due to Regulation

The regulatory reduction fractions for agriculture are based on both the surface water for irrigation and the groundwater for irrigation. If the surface water for irrigation exceeds a threshold, then the agricultural reduction fraction is incremented by the product of a stochastically generated reduction fraction for surface water times the portion of agricultural product P that is irrigated with surface water at location L. If the groundwater for irrigation exceeds a threshold, then the agricultural reduction fraction is incremented by the product of a stochastically generated reduction fraction for

groundwater times the portion of agricultural product P that is irrigated with groundwater at location L.

```
ARF_RR(L,P)  = 0,   If SWT_AG(L)=0 and GWT_AG(L)=0
ARF_RR(L,P)  = GWARF_RR(L,P) ^X IRRFRAC_GW(L,P), IF SWT_AG(L)=0 and GWT_AG(L)>0
ARF_RR(L,P)  = SWARF_RR(L,P) ^X IRRFRAC_SW(L,P), IF SWT_AG(L)>0 and GWT_AG(L)=0
ARF_RR(L,P)  = SWARF_RR(L,P) ^X IRRFRAC_SW(L,P) ^X GWARF_RR(L,P) ^X IRRFRAC_GW(L,P),
    If SWT_AG(L)>0 and GWT_AG(L)>0
```

where:

$GWARF_{RR}(L,P)$ = Stochastically generated fraction for reduction of groundwater irrigation of product P at location L (unitless)

$IRRFRAC_{GW}(L,P)$ = Fraction of product P that is irrigated with groundwater at location L (unitless)

$SWARF_{RR}(L,P)$ = Stochastically generated fraction for reduction of surface water irrigation of product P at location L (unitless)

$IRRFRAC_{SW}(L,P)$ = Fraction of product P that is irrigated with surface water at location L (unitless).

6.1.1.5 Reduction in Agricultural Value of Production Due to Avoidance

Voluntary avoidance of agricultural products may result when environmental concentrations are either above or below regulatory limits. There is no reduction in activity if the water concentrations are below one percent of the threshold concentration for irrigation water for all analytes for both groundwater and surface water used for irrigation. There is a moderate voluntary avoidance of recreation if the water concentration for any analyte is greater than one percent of the threshold but does not exceed the threshold. There is a greater voluntary reduction in an agricultural product if any analyte irrigation water concentration exceeds its threshold concentration.

```
ARF_VA(L,P)  = 0,   If SWT_AG(L)=0 and GWT_AG(L)=0
ARF_VA(L,P)  = VAS1(L,A),   If SWT_AG(L)=1 or GWT_AG(L)=1
ARF_VA(L,P)  = VAS2(L,A),   If SWT_AG(L)=2 or GWT_AG(L)=2
```

where:

$VAS1(L,P)$ = Stochastically generated step 1 fraction for product P at location L (unitless)

$VAS2(L,P)$ = Stochastically generated step 2 fraction for product P at location L (unitless).

6.1.1.6 Cost of Drinking Water Source Replacement

For the appropriate water type used for drinking water at location L, the annual cost of filtering and using the water for drinking water is:

```
Cost_FILT(L)  = FT(L) ^X FLOW(L) ^X 365.25
```

where:

$FT(L)$ = $FT_{SW}(L)$ or $FT_{GW}(L)$, depending on the source of drinking water at location L ($/1,000 gal/d)

FLOW(L) = Flow rate of water supply at location L (1,000 gal/d)
365.25 = Number of days per year (d).

The annualized cost of replacing the drinking water source at location L is:

```
Cost_REPL(L) = (FLOW(L) X COST(L) X RATE) / (1 - (1+RATE)^-YRS)
```

where:
COST(L) = Replacement cost for the drinking water supply ($/(1,000 gal/d))
RATE = Annual discount rate (unitless)
YRS = Financing period (yr).

6.1.2 Economic Effects

The effects calculations are the set of equations that use the reduction fractions calculated in the TRIGGER subroutine to determine the costs associated with regulatory reduction or voluntary avoidance of recreational activities and agricultural products. These costs are then apportioned to industries and economic sectors for input to the ECONCHG subroutine.

6.1.2.1 Agricultural Impact

Agricultural impact is calculated for a number of agricultural products. The change in production, change in producer's surplus, revenue change, and cost change are calculated for each product, and then the effects are summed and allocated over the sectors of the regional economy. All agricultural impacts are calculated separately for each requested time.

6.1.2.1.1 Change in Value and Production of Agricultural Products

The change in production of agricultural products is a reduction in production due to either regulatory action or voluntary avoidance. The minimum of these two alternatives is chosen because both will be negative numbers. This means that the maximum impact is selected.

```
CHG_PROD(L,P) = Min( Prod(L,P) X (-ARF_RR(L,P)), Prod(L,P) X IFSW(L,P) X (-
    ARF_VA(L,P)) )
```

where:
CHG_PROD(L,P) = The change is production of product P at location L (bu or tons or cwt)
Prod(L,P) = The production of product P at location L (bu or tons or cwt)
IFSW(L,P) = The fraction of product P that is irrigated with surface water at location L (unitless).

The change in producer's surplus for agricultural product P at location L is an increase in the value of unsold product as a result of regulatory action or voluntary avoidance. If the value calculated for the change is producer's surplus is less than zero, then it is set to zero.

```
CHG_PS(L,P) = 0.5 X Min( (Price(P) - LSP(P)) X Prod(L,P) X (- ARF_RR(L,P)),
    (Price(P) - LSP(P)) X Prod(L,P) X IFSW(L,P) X (-ARF_VA(L,P)) )
```

where:

Price(P) = Price of agricultural product P in the region ($/bu or ton or cwt)

LSP(P) = Lowest supply price for agricultural product P at location L ($/bu or ton or cwt).

The change in revenue from the sale of product P at location L is the price times the change in production.

$$CHG_{REV}(L,P) = Price\ (P)\ ^X\ CHG_{PROD}(L,P)$$

The change in cost of product P at location L is the change in revenue minus the change in producer's surplus.

$$CHG_{COST}(L,P) = CHG_{REV}(L,P) - CHG_{PS}(L,P)$$

6.1.2.1.2   *Effect of Agricultural Products on the Regional Economy*

The two quantities needed to determine the impact on the regional economy of agriculture in the ECONCHG module are the change in procurements and the change in labor cost for agriculture.

$$CHGPROC(L,P) = CHGCOST(L,P)\ ^X\ (1- Labor)$$

where:

Labor = The percentage of the agricultural cost that is labor (unitless).

The change in the labor cost of agriculture is the change in cost times the labor percentage.

$$CHG_{LAB}(L,P) = CHG_{COST}(L,P)\ ^X\ (Labor)$$

The changes in labor and non-labor expenditures on agriculture are allocated over economic industries in proportion to their contribution to final demand spending by consumers in the local economy (for labor) or for agricultural spending (non-labor).

$$AgEffPROC(L,P,I) = CHGPROC(L,P)\ ^X\ AgIP(I)$$
$$AgEffINC(L,P,I) = CHGLAB(L,P)\ ^X\ AgIP(I)$$

where:

AgIP(I) = The percentage of total spending on agriculture allocated to industry I (unitless).

The industry percentage for each product is calculated by dividing the baseline agricultural spending on agriculture by the sum of the expenditures for agriculture over all industries.

$$AgIP(I) = Base(I)\ /\ TotInd$$

where:

Base (I) = The baseline spending in industry I by agriculture ($M)

TotInd = Total spending by agriculture over all industries in the regional economy ($M).

The input to the final module of TCERM, ECONCHG, requires that the change in procurements and income for agriculture be allocated over economic sectors in proportion to their contribution to the economy. When each industry is defined, it is assigned to an economic sector. The sector totals are calculated by adding the baseline agricultural spending for each industry assigned to the sector.

$$\text{AgEff}_{\text{PROC}}(L,P,S) = \text{CHG}_{\text{PROC}}(L,P) ^{X} \text{AgSP}(S)$$
$$\text{AgEff}_{\text{INC}}(L,P,S) = \text{CHG}_{\text{inc}}(L,P) ^{X} \text{AgSP}(S)$$

where:

RecSP(A,S) = The percentage of total spending on activity A allocated to sector S (unitless).

6.1.2.2   Recreational Impact

Recreational impact is calculated for four activities: fishing, boating, swimming, and water skiing. The value and effect are calculated for each activity, and then the effects are summed and allocated over the sectors of the regional economy.

6.1.2.2.1   *Value of Recreational Activities*

The value of the recreational activities is calculated separately for each requested time. The total value of an activity at a location is the daily value per person times the number of trips per person times the participating population for that activity.

$$V(L,A) = \text{VD}(A) ^{X} \text{Trips}(A) ^{X} \text{Pop}(L,A)$$

where:

V(L,A)   = Total value of recreational activity A at location L ($)
VD(A)   = Value per activity day of recreational activity A at location L ($)
Trips(A) = Number of recreational days per member of the population for activity A at location L (person^{-1})
Pop(L,A) = Participating population for recreational activity A at location L (persons).

The daily per person value of fishing is a regression equation involving a base value and several measures of the quality of the fishing activity. The daily value of the other recreational activities is constant. The daily value of fishing is not location-specific within the regional economy.

$$\text{VD}(A) = \text{BV}(A) + C_Q ^{X} \text{SQF}(A) + C_{SA} ^{X} \text{SAF}(A) + C_{COV} ^{X} \text{COV}(A) + C_{TT} ^{X} \text{TT}(A) +$$
$$C_{SUBS} ^{X} \text{SUBS}(A) + C_{IOF} ^{X} \text{IOF}(A) + C_{HV} ^{X} \text{HV}(A)$$

where:

BV(A)   = base value of recreational activity A in the region ($/d)
C_Q = Regression coefficient for site quality (unitless)
SQF(A) = Regional site quality factor (unitless)
C_{SA} = Regression coefficient for specialized activity (unitless)
SAF   = Specialized activity factor (unitless, 0 or 1)
C_{COV} = Regression coefficient for sample coverage (unitless)
COV(A) = sample coverage factor (unitless)

C_{TT}	=	Regression coefficient for travel time cost (unitless)
TT(A)	=	Travel time cost factor (unitless)
C_{SUBS}	=	Regression coefficient for substitution (unitless)
SUBS(A)	=	Substitution variable factor (unitless)
C_{IOF}	=	Regression coefficient for individual observation (unitless)
IOF(A)	=	Individual observation factor (unitless)
C_{HV}	=	Regression coefficient for household production (unitless)
HV(A)	=	Household production factor (unitless).

The number of trips at location L to pursue activity A on a per-person basis.

$$\text{Trips(A)} = \text{EXP}(\ C_{base} + C_{Dist}\ ^{X}\ \text{LN(Dist)} + C_{QUAL}\ ^{X}\ \text{LN(QUAL(A)}\ ) + C_{sub}\ ^{X}\ \text{LN}(Q_{sub})\ )$$

where:

C_{base}	=	Base number of trips (person^{-1})
C_{Dist}	=	Regression coefficient for travel distance (unitless)
Dist	=	Travel distance factor (unitless)
C_{QUAL}	=	Regression coefficient for site quality (unitless)
QUAL(A)	=	Fishing quality for the site (unitless, 1 if A is not fishing)
Csub	=	Regression coefficient for substitute site (unitless)
Qsub	=	Ratio of site quality to distance of substitute site (unitless).

6.1.2.2.2 *Effect of Recreational Activities on the Regional Economy*

The effect on the regional economy due to changes in recreational activity is measured by the change in expenditures on recreational activities due to contamination in the environment. The change in spending results in a reduced number of trips per person and is reduced by the maximum of the regulatory reduction and the voluntary avoidance factors calculated in the TRIGGER routine.

$$\text{ExpChg(L,A)} = -1\ ^{X}\ \text{Pop(L,A)}\ ^{X}\ (\ \text{Trips(A)}\ ^{X}\ \text{Max}(RRF_{RR}(L,A), RRF_{VA}(L,A)\ )\ ^{X}\ \text{Spend(L,A)}$$

where:
    Spend(L,A) =   Spending per person per trip at location L on recreational activity A.

The change in expenditures on recreation is allocated over economic industries in proportion to their contribution to the economy.

$$\text{RecEff(L,A,I)} = \text{ExpChg(L,A)}\ ^{X}\ \text{RecIP(A,I)}$$

where:
    RecIP(A,I) =   The percentage of total spending on activity A allocated to industry I (unitless).

The industry percentage for each activity is calculated by dividing the baseline recreational spending for an activity by the sum of the expenditures for the recreational activity over all industries.

```
RecIP(A,I) = Base(A,I) / TotInd(A)
```

where:

Base (A,I) = The baseline spending in industry I on recreational activity A ($).

TotInd(A) = Total spending on recreational activity A over all industries in the regional economy ($).

The input to the final module of TCERM, ECONCHG, requires that the change in expenditures on recreation be allocated over economic sectors in proportion to their contribution to the economy. When each industry is defined, it is assigned to an economic sector. The sector totals are calculated by adding the baseline recreational spending for each industry assigned to the sector.

```
RecEff(L,A,S) = ExpChg(L,A) X RecSP(A,S)
```

where:

RecSP(A,S) = The percentage of total spending on activity A allocated to sector S (unitless).

6.1.3   Economic Change Analysis

The economic change analysis is the set of equations that use the agricultural and recreational effects calculated in the EFFECTS subroutine to determine the impact on the regional economy in terms of changes in output, wages, and employment.

6.1.3.1   Change in Output

A sector-by-sector matrix M is provided in which the entries in each column represent purchases from each industry per dollar of output in the industry that defines the sector. The data for this matrix are can be obtained from routine U.S. Department of Commerce, Bureau of Economic Analysis publications. The matrix M is subtracted from the identity matrix, and the resulting matrix is inverted using the LU decomposition method. The matrix M_{INV} is a square matrix of dimension number of sectors by number of sectors.

```
M_INV = (I-M)^-1
```

The change in output due to change in agricultural procurements is a matrix multiplication of the matrix M_{INV} and the vector of changes in the agricultural sector's non-labor procurements calculated in the EFFECTS routine.

```
AgOut_PROC(L,S) = M_INV X AgEff_PROC(L,S)
```

The change in output due to change in agricultural income is a matrix multiplication of the matrix M_{INV} and the vector of changes in spending of agricultural income calculated in the EFFECTS routine.

```
AgOut_INC(L,S) = M_INV X AgEff_INC(L,S)
```

The change in output due to change in recreational spending is a matrix multiplication of the matrix M_{INV} and the vector of changes in recreational spending calculated in the EFFECTS routine. The change in recreational output is summed over all recreational activities.

```
RecOut(L,S) = Σ (M_INV ^X RecEff(L,A,S)), A=1 to 4
```

The total change in output for a sector is the sum of the changes in output due to changes in agricultural and recreational spending.

```
Output(L,S) = AgOut_PROC(L,S)+ AgOut_INC(L,S) + RecOut(L,S)
```

6.1.3.2 Change in Wages

The change in wages is the product of the change in output and the base wages per dollar of output for a given sector.

```
Wages(L,S) = Output(L,S) ^X BaseWage(S)
```

where:
    BaseWage(S) =   Dollars of earnings per dollars of output for sector S.

6.1.3.3 Change in Employment

The change in employment is the product of the change in output and the base employment per million $ of output for a given sector.

```
Employ(L,S) = Output(L,S)/1.0E+6 ^X BaseEmp(S)
```

where:
    BaseEmp(S) =   jobs per million dollars of output for sector S.

6.2 Code Environment

6.2.1 Location in the Processing Sequence

The TCERM code requires access to a number of data files developed by the SAC inventory, release, and transport codes (Eslinger et al. 2002). In particular, every code on the left side of Figure 1-2 must have been executed to build a suite of concentration data files before the TCERM code can be used to calculate economic impacts. These concentration data files must have been developed under the control of the same ESD keyword file that the TCERM code reads to determine processing options.

6.2.2 How the Code Is Invoked

TCERM can run under either the Windows or the Linux operating system. Under the Windows operating system (Releases 98, NT, or 2000), TCERM executes in a DOS box. A run of TCERM is initiated by entering the following command line:

```
TCERM "Keyfilename"
```

Under the Linux operating system, TCERM is executed through the following Bourne Shell or C Shell command:

```
tcerm.exe "Keyfilename"
```

For these commands, TCERM or tcerm.exe is the name of the executable program and "Keyfilename" is the name of an economic scenario keyword file. Both the name of the executable program and the keyword file may contain path information. If TCERM is invoked without entering the name of the keyword file, the code will prompt the user for the file name. The keyword file, which should be prepared using an editor that can handle ASCII files without leaving embedded control codes, contains text control information describing the run. If TCERM cannot open the keyword file, then the code will terminate execution after writing an error message to the standard output device.

6.2.3   Memory Requirements

The TCERM code uses dynamic memory allocation, so the memory requirements depend on the problem being analyzed. An example run where the TCERM code required 1.9 MB of memory (on a Windows 2000 machine) used 10 analytes, 202 times steps, 1 realization, and 4 locations. It is expected that most if not all of the runs of the TCERM code will require fewer than 4 MB of memory.

6.3   Data Files

The TCERM code reads four or more input files and writes up to five output files. The number of input files depends on the number of contaminants being analyzed. The number of output files depends on the options selected in the TCERM code. These files are described in the following sections.

6.3.1   Input Files

The input files for the TCERM code are two keyword files and a suite of concentration data related files, plus a fish body burden file for scenarios that include recreational fishing. One keyword file controls the case the TCERM code will execute, and it points to the ESD keyword file. The suite of concentration data files are all identified in the ESD keyword file – the user of the TCERM only needs to identify the location and name of the ESD keyword file. The following are the input files:

- **TCERM Keyword File:** The TCERM Keyword file controls the scenario to be analyzed by the TCERM code. The options and data available are constrained by the case defined in the ESD Keyword file. Section 6.3.1.1 describes the contents of the TCERM keyword file.
- **ESD Keyword File:** The ESD keyword file contains the control information that the inventory and environmental transport codes use to generate concentration data files. Table 2.1 provides examples of keywords in the ESD file that control the impacts codes, including the TCERM code. Section 2.2 provides definitions for these keywords. Typically, the user of the TCERM code will not modify the ESD keyword file.

- **ECDA Concentration Files:** The ECDA files contain all the concentration data available for the impacts codes. The concentrations for all analytes are based on the same time and location data. There is a "map" file specific to the TCERM code containing indexing information for each of the concentration data files. In addition, there is a separate concentration data file for every analyte used in the impacts scenario. For example, when running a scenario with seven analytes there will be one map file and seven concentration data files. The structure of a concentration data file is described in Section 2.3.1.

- **Fish Body Burden File:** Scenarios in TCERM that include recreational fishing require an additional input file. This file is generated by the ECEM code and contains the body burden for selected fish species for all analytes to be modeled. Section 6.3.1.2 provides an example fish body burden file.

6.3.1.1 TCERM Keyword File

Table 6.1 provides excerpted records from a keyword file for TCERM. Data from each major section of the inputs are provided, but many lines were omitted to reduce the size of the file. This file was originally over 1350 lines long.

Table 6.1 Excerpted Records from a TCERM Keyword File

```
! Report File (Must be first Entry)
REPORT "tcerm.rpt"
TITLE  "Production run of the TCERM Code for SAC Rev. 0"
USER   "Terri B. Miley"
EXECUTE
! Input file names
FILE ESD       "/home/ANALYSIS/Median2/ESD_Median2.key"
FILE BURDEN    "/home/ANALYSIS/Median2/Bg/ecem/Ecem_Fish_Det_Bg.csv"
! Output file names
FILE TRIGGERD  "TRIG_Det.csv"
FILE TRIGGERS  "TRIG_Sta.csv"
FILE EFFECTSD  "EFF_Det.csv"
FILE EFFECTSS  "EFF_Sta.csv"
FILE ECONCHGD  "ECHG_Det.csv"
FILE ECONCHGS  "ECHG_Sta.csv"
FILE HEADER    "tcerm.hdr"
FILE STOCHAST  "tcerm_val.csv"
!
! Output summary statistics
STATISTICS TRIGGER
STATISTICS EFFECTS
!
! Output detailed data
DETAILS TRIGGER
DETAILS EFFECTS
!
! Random Seed for Stochastics
SEED 445544
!
! Number of Realizations
```

```
REALIZATION 1
!
! Times to be used
TIMES ECONOMIC   2000 2050
!
! Locations to be used
LOCATION ECONOMIC ID="EN001" NAME="Richland region"
  SWDW="EN0011" SWCON="EN0012" SWIRR="EN0013" GWIRR="EN0014" FISH="EL0118"
  DWSOURCE="PUBSW" SWFLWPUB=18000.0  SWCSTPUB=1000.0 GWFLWPUB=2000.0
GWCSTPUB=0.0
LOCATION ECONOMIC ID="EN002" NAME="Kennewick region"
  SWDW="EN0021" SWCON="EN0022" SWIRR="EN0023" FISH="EL0240"
  DWSOURCE="PUBSW" SWFLWPUB=3000.0 SWCSTPUB=1000.0
  GWFLWPUB=4500.0  GWCSTPUB=1000.0
LOCATION ECONOMIC ID="EN003" NAME="Pasco region"
  SWDW="EN0031" SWCON="EN0032" SWIRR="EN0033" FISH="EL0384"
  DWSOURCE="PUBSW" SWFLWPUB=8800.0  SWCSTPUB=1000.0
LOCATION ECONOMIC ID="EN004" NAME="Snake to McNary region"
  SWDW="EN0041" SWCON="EN0042" SWIRR="EN0043" FISH="EL0548"
  DWSOURCE="PVTSW" SWFLWPVT=2300.0  SWCSTPVT=67.0
  GWFLWPVT=2300.0  GWCSTPVT=45.0
!
! Analytes to be used
ANALYTE "H3" "Tc99"
!
! Species to be used
SPECIE "SALMAD" "RTRTAD" "SMBASS" "CARP  " "WSTRGN" "CRYFSH"
!
! Fish weighting factors by species and location
! These factors must sum to 1 for each location
FISHWT
 0.4   0.3   0.2   0.3   ! SALMAD
 0.1   0.1   0.2   0.1   ! RTRTAD
 0.2   0.2   0.2   0.2   ! SMBASS
 0.1   0.2   0.1   0.1   ! CARP
 0.1   0.1   0.2   0.2   ! WSTRGN
 0.1   0.1   0.1   0.1   ! CRYFSH
!
! Recreational Activity Definitions
RECACT ID="FISHNG" NAME="Fishing"        OUTPUT
RECACT ID="BOATNG" NAME="Boating"        OUTPUT
...
! Spending on recreational activities by activity and location
SPEND LOCATION="EN001" RECACT="FISHNG" 38.6
SPEND LOCATION="EN002" RECACT="FISHNG" 38.6
...
! Population in recreational activities by activity and location
PARTIC LOCATION="EN001" RECACT="FISHNG"  37600.0
PARTIC LOCATION="EN002" RECACT="FISHNG"   1100.0
...
!
```

```
! Discount rate for drinking water source replacement capital costs
DISCOUNT 0.07
!
! Drinking water filter cost ($/1000 gal/day)
FILTER LOCATION="EN001" ANALYTE="CCl4" PUBSW=5.0
FILTER LOCATION="EN002" ANALYTE="CCl4" PUBGW=5.0
...
! Agricultural Product Definitions
! Field crops
AGPROD ID="SPRWHT" NAME="Spring wheat"      OUTPUT
AGPROD ID="WINWHT" NAME="Winter wheat"      OUTPUT
...
! Vegetables
AGPROD ID="ASPARA" NAME="Asparagus"         OUTPUT
AGPROD ID="CARFRS" NAME="Fresh carrots"     OUTPUT
...
! Percent of agricultural cost that is labor (unitless)
AGLABOR 0.55
!
! Lowest supply price and total production by location of ag products
AGPARAM AGPROD="SPRWHT"  LOCATION="EN001"  LOWPRICE=2.83
AGPARAM AGPROD="WINWHT"  LOCATION="EN001"  LOWPRICE=2.50
...
AGPARAM AGPROD="HOGPIG"  LOCATION="EN004"  LOWPRICE=39.00
AGPARAM AGPROD="SHPPRO"  LOCATION="EN004"  LOWPRICE=46.20
!
! Fraction of agricultural product by location that is irrigated with GW
IRRFRACG
  0.0   0.0   0.0   0.0   ! SPRWHT
  0.0   0.0   0.0   0.0   ! WINWHT
...
  0.0   0.0   0.0   0.0   ! HOGPIG
  0.0   0.0   0.0   0.0   ! SHPPRO
!
! Fraction of agricultural product by location that is irrigated with SW
IRRFRACS
  0.0   0.0   0.0   0.0   ! SPRWHT
  0.65  0.65  4.57  3.47  ! WINWHT
...
  0.0   0.0   0.0   0.0   ! SHPPRO
!
! Sector Definitions
SECTOR ID="AGRICU" NAME="Ag, Forestry, Fishery"
  BASE_EMP=13.22937384  BASE_WAG=0.200201976 OUTPUT
SECTOR ID="AGSVCS" NAME="Ag Services"
  BASE_EMP=45.79844691  BASE_WAG=0.43577533  OUTPUT
...
SECTOR ID="CONSVC" NAME="Contract Research & Consulting"
  BASE_EMP=21.80  BASE_WAG=0.4527 OUTPUT
SECTOR ID="GOVERN" NAME="Government"
  BASE_EMP=21.98070593  BASE_WAG=0.833478636 OUTPUT
```

```
!
! Industry Definitions
! Recreational baseline order is Fishing, Boating/Skiing, Swimming
INDUSTRY ID="AGCRPS" NAME="AGG 1 AG CROPS"
  SECTOR="AGRICU" AGBASELINE=11.806 RECBASELINE=0 0 0 0 OUTPUT
INDUSTRY ID="AGLVST" NAME="AGG 2 AG LIVESTOCK"
  SECTOR="AGRICU" AGBASELINE=1.155  RECBASELINE=0 0 0 0 OUTPUT
...
INDUSTRY ID="CONRES" NAME="AGG 87 CONTRACT RESEARCH"
  SECTOR="CONSVC" AGBASELINE=0.370  RECBASELINE=0 0 0 0 OUTPUT
INDUSTRY ID="GOVERN" NAME="AGG 90 GOVERNMENT"
  SECTOR="GOVERN" AGBASELINE=15.901 RECBASELINE=0 0 0 0 OUTPUT
!
! Sector by Sector Make-Use Matrix
MAKEUSE
 0.024024073 0.0 0.0 0.0 0.085639176 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
  ...
 0.011306241 0.014708226 0.005611014 0.014811406 0.002796793
!
! Threshold Concentrations
THRESHOLD ANALYTE="CCl4" DRINK    0.25   ! ug/L
THRESHOLD ANALYTE="CCl4" SUR_CON  0.25   ! ug/L
...
THRESHOLD ANALYTE="U238" SPECIE="WSTRGN"  FISH_BUR 1.5E+3    ! pCi/kg
THRESHOLD ANALYTE="U238" SPECIE="CRYFSH"  FISH_BUR 1.5E+3    ! pCi/kg
!
! Lowest supply price
STOCHASTIC "SPRWHTPRICE"  6 2.83 3.82 4.95
  "Price for spring wheat      ($/bu )"
STOCHASTIC "WINWHTPRICE"  6 2.5 3.67 4.81
  "Price for winter wheat      ($/bu)"
...
!  Total production by location and agricultural product
STOCHASTIC"EN001 SPRWHTTOTPROD" 1 0.0
  "Total production of Spring Wheat at location EN001 in bu"
STOCHASTIC"EN001 WINWHTTOTPROD" 6 76011 101348 126685
  "Total prod of Winter Wheat at location EN001 in bu"
...
STOCHASTIC "EN004 SWIMNGVAREC_S2" 6  0.2 0.5  0.8
  "Reg red in rec due to water quality at EN004 for SWIMNG"
STOCHASTIC "EN004 SKIINGVAREC_S2" 6  0.2 0.5  0.8
  "Reg red in rec due to water quality at EN004 for WSKING"
!
END
```

6.3.1.2 Fish Body Burden File

The TCERM code requires the analyte concentrations in fish (body burdens) for the recreational activities calculations. These body burdens are input using a file structure the same as that written by ECEM (see Section 4.3.2.4). If desired, this file can be generated using a run of the ECEM code

selecting the BURDEN solution type on the DETAILS keyword (see Section 4.4.4). Table 6.2 provides the first 13 records from a body burden file that uses only one realization of data. The first record occupies only one line in the file even though it shows as two lines in the table.

Table 6.2 Excerpted Records from a Fish Body Burden File for TCERM

```
"Time","Location ID","Analyte ID","Specie","Solution Type","Units",
"Values by realization"
1990,"EL0118","H3    ","SALMAD","BURDEN","pCi/kg",  4.15060E+00
1990,"EL0118","H3    ","SMBASS","BURDEN","pCi/kg",  4.26955E+00
1990,"EL0118","H3    ","CARP  ","BURDEN","pCi/kg",  4.28114E+00
1990,"EL0118","H3    ","CRYFSH","BURDEN","pCi/kg",  4.99664E+00
1990,"EL0118","H3    ","RTRTAD","BURDEN","pCi/kg",  4.24874E+00
1990,"EL0118","H3    ","WSTRGN","BURDEN","pCi/kg",  4.20176E+00
1990,"EL0118","Tc99  ","SALMAD","BURDEN","pCi/kg",  2.00817E-04
1990,"EL0118","Tc99  ","SMBASS","BURDEN","pCi/kg",  4.73804E-04
1990,"EL0118","Tc99  ","CARP  ","BURDEN","pCi/kg",  4.94875E-04
1990,"EL0118","Tc99  ","CRYFSH","BURDEN","pCi/kg",  8.58488E-04
1990,"EL0118","Tc99  ","RTRTAD","BURDEN","pCi/kg",  4.31910E-04
1990,"EL0118","Tc99  ","WSTRGN","BURDEN","pCi/kg",  2.73174E-04
```

6.3.2   Output Files

Up to nine output files can be written by the TCERM code. The number of files depends on the options selected in the scenario being analyzed. The following are the output files:

- **Report File:** This required file contains a summary of the scenario being analyzed and contains any error messages. This file is described in Section 6.3.2.1.
- **SACView Header File:** This required file contains information used by the interactive SACView program to allow easy extraction of subsets of the results computed by the TCERM code. This file is described in Section 6.3.2.2.
- **Stochastic Values File:** This optional file contains the values for every stochastic variable generated in the TCERM code. This file is described in Section 6.3.2.3.
- **Trigger Detailed Data:** This optional file contains the detailed values for the economic change trigger data generated in the TCERM code. This file is described in Section 6.3.2.4.
- **Trigger Summary Statistics Data:** This optional file contains the summary statistics for the economic change trigger data generated in the TCERM code. This file is described in Section 6.3.2.5.
- **Effects Detailed Data:** This optional file contains the detailed values for the economic effects generated in the TCERM code. This file is described in Section 6.3.2.6.
- **Effects Summary Statistics Data:** This optional file contains the summary statistics for the economic effects generated in the TCERM code. This file is described in Section 6.3.2.7.
- **Economic Change Detailed Data:** This required file contains the detailed values for the economic change data generated in the TCERM code. This file is described in Section 6.3.2.8.
- **Economic Change Summary Statistics Data:** This required file contains the summary statistics for the economic change data generated in the TCERM code. This file is described in Section 6.3.2.9.

6.3.2.1 TCERM Report File

Table 6.3 provides excerpted records for an example report file for the TCERM code. This file contains information for a run of the TCERM code using 2 analytes, 4 locations, 31 agricultural products, and 62 industries in 36 sectors. This file is about 12 KB in size. The size of this file grows rapidly when debug options are selected. A run using all debug options having a large number of locations, analytes, solution times, and realizations could easily generate a report file of 2 GB or larger.

Table 6.3 Excerpted Records from a TCERM Report File

```
              TTTTTTT  CCCCC  EEEEEEE RRRRRR  MM      MM
                 T    C     C E       R     R M M   M M
                 T    C       E       R     R M  M M  M
                 T    C       EEEE    RRRRRR  M   M   M
                 T    C       E       R  R    M       M
                 T    C     C E       R   R   M       M
                 T     CCCCC  EEEEEEE R    R  M       M


                  TCERM          Version 1.00.A.6
                  Last Modified on 28 Mar 2002
              ----------------------------------------------
                  SAC Rev. 0 Economic Impacts Model
              ----------------------------------------------
              Developed By Battelle Memorial Institute
               Pacific Northwest National Laboratories
                        Richland, Washington

        Current Run ID = 20020410073226   User Name = Terri B. Miley

          System Date = 04-10-2002   System Time = 07:32:26.817

        The software used to generate this output is experimental
           and has not been formally tested or peer reviewed.

                         Review Signatures

Input Prepared By: _____     Date: _____

Input Reviewed By: _____     Date: _____

======================= Echo of the Problem Definition =======================

Title: Production run of the TCERM Code for SAC Rev. 0
User:  Terri B. Miley
   1 Realizations requested in this run
   1 Realizations available in the concentration files

File name for input keyword data
File: tcerm.key

File name for input ESD keyword data
File: /home/ANALYSIS/Median2/ESD_Median2.key

File name for input ECEM body burden data
File: /home/ANALYSIS/Median2/Bg/ecem/Ecem_Fish_Det_Bg.csv


...

File Name for Media Concentrations for analyte with ID="Tc99"
```

```
File: /home/ANALYSIS/Median2/ecda/ECON_Tc99_Median2.Dat

Seed for random number generator =  445544.0
...

Analyte Information based on 10 possible analytes.
     1 : H3      : Tritium
     2 : Sr90    : ===> Not used
     3 : Tc99    : Technetium 99
     4 : I129    : ===> Not used
     5 : Cs137   : ===> Not used
     6 : U238    : ===> Not used
     7 : Pu239   : ===> Not used
     8 : U       : ===> Not used
     9 : CCl4    : ===> Not used
    10 : CrVI    : ===> Not used
A total of  2 analytes have been requested.

Location Information
  Index : ID     : Location description
  ----- : ------ : ----------------------------------------
      1 : EN001  : Richland region
      2 : EN002  : Kennewick region
      3 : EN003  : Pasco region
      4 : EN004  : Snake to McNary region
A total of 4 locations have been requested.

Agricultural Products
  Index : ID     : Product name
  ----- : ------ : ----------------------------------------
      1 : SPRWHT : Spring wheat
      2 : WINWHT : Winter wheat
      3 : BARLEY : Barley
...
     29 : BEEF   : Beef
     30 : HOGPIG : Hogs and pigs
     31 : SHPPRO : Sheep, lambs and wool

Recreational Activities
  Index : ID     : Activity name
  ----- : ------ : ----------------------------------------
      1 : FISHNG : Fishing
      2 : BOATNG : Boating
      3 : SWIMNG : Swimming
      4 : SKIING : Water skiing

Industry Definitions
  Index : ID     : Industry definition
  ----- : ------ : ----------------------------------------
      1 : AGCRPS : AGG 1 AG CROPS
      2 : AGLVST : AGG 2 AG LIVESTOCK
      3 : AGSVCS : AGG 7 AG SERVICES
...
     60 : MEMORG : AGG 86 MEMBERSHIP ORGS
     61 : CONRES : AGG 87 CONTRACT RESEARCH
     62 : GOVERN : AGG 90 GOVERNMENT

Sector Definitions
  Index : ID     : Sector definition
  ----- : ------ : ----------------------------------------
      1 : AGRICU : Ag, Forestry, Fishery
      2 : AGSVCS : Ag Services
      3 : MINING : Mining
...
```

```
     34 : MEMORG : Membership orgs
     35 : CONSVC : Contract Research & Consulting
     36 : GOVERN : Government

Fish Species
  Index : ID     : Species name
  ----- : ------ : -------------------------------------
      1 : SALMAD : Salmon (adults)
      2 : RTRTAD : Rainbow trout (adults)
      3 : SMBASS : Smallmouth bass
      4 : CARP   : Carp
      5 : WSTRGN : White sturgeon
      6 : CRYFSH : Crayfish

Time Slices Requested: (Index, Calendar Year) based on 211 possible times.
 Index : Year : Use description
 ----- : ---- : -----------------------------------
     1 : 2000 :  : Included in this scenario
    11 : 2050 :  : Included in this scenario
A total of    2 times have been requested.

====================== End of the Problem Definition ========================

Concentration data units conversion factors

    1 : H3     : NR : Ground water  :  1.00000E+09 : From Ci/m^3       to pCi/L
    1 : H3     : NR : Surface water :  1.00000E+09 : From Ci/m^3       to pCi/L

    3 : Tc99   : NR : Ground water  :  1.00000E+09 : From Ci/m^3       to pCi/L
    3 : Tc99   : NR : Surface water :  1.00000E+09 : From Ci/m^3       to pCi/L

Ending Problem Execution

    Date: 04/10/2002
    Time: 07:32:36.534

Message originating in routine TCERM
Message: Normal Termination
```

6.3.2.2   TCERM SACView Header File

The SACView header file is an output file containing information used by the interactive SACView program to allow easy extraction of subsets of the results computed by the TCERM code. This file is generated by every run of the TCERM code. Table 6.4 provides an example of this file. The file contains the following sections of information:

- A header section of basic run information
- Solution times selected
- Locations used
- Agricultural products used
- Recreational activities modeled
- Economic sectors modeled
- Economic change variables
- Change trigger variables
- Effects variables
- Output file names.

The user only specifies the name of this file; users should not modify the file after it is generated. See the instructions in Section 7.0 regarding the use of the SACView program. Because this file has at most a few hundred entries, the file size is always much smaller than 100 KB. File names for options not selected are set to null.

Table 6.4 Example Header File from TCERM for the SACView Program

```
type: "Economic"
title: "Production run of the TCERM Code for SAC Rev. 0"
user: "Terri B. Miley"
name: "TCERM"
version: "1.00.A.6"
date: "28 Mar 2002"
id: "20020410073226"
envfile: "/home/ANALYSIS/Median2/ESD_Median2.key"
realizations:    1
times:    2
 2000
 2050
locations:    4
"EN001","Richland region"
"EN002","Kennewick region"
"EN003","Pasco region"
"EN004","Snake to McNary region"
agprods:   31
"SPRWHT","Spring wheat"
"WINWHT","Winter wheat"
"BARLEY","Barley"
"OATS","Oats"
"CORNGR","Corn for grain"
"CORNSI","Corn for silage"
"DRYBNS","Dry beans"
"POTATO","Potatoes"
"HAY","Hay"
"ALFSED","Alfalfa seed"
"OTHGRS","Other grass"
"ASPARA","Asparagus"
"CARFRS","Fresh carrots"
"CARPRO","Processed carrots"
"GRNPEA","Green peas"
"ONIONS","Onions"
"SWTCRN","Sweet corn"
"APPLES","Apples"
"APRICO","Apricots"
"SWTCHR","Sweet cherries"
"TRTCHR","Tart cherries"
"BARTPR","Bartlett pears"
"OTHRPR","Other pears"
"PEACHS","Peaches"
"PRUNES","Prunes"
```

```
"GRPCON","Concord and Niagra grapes"
"GRPWIN","Wine grapes"
"MILK","Milk"
"BEEF","Beef"
"HOGPIG","Hogs and pigs"
"SHPPRO","Sheep, lambs and wool"
recacts:    4
"FISHNG","Fishing"
"BOATNG","Boating"
"SWIMNG","Swimming"
"SKIING","Water skiing"
sectors:   36
"AGRICU","Ag, Forestry, Fishery"
"AGSVCS","Ag Services"
"MINING","Mining"
"CONSTR","Construction"
"FODPRO","Food Processing"
"PRIPUB","Printing & Publishing"
"CHEMIC","Chemical Mfg"
"STONGL","Stone, Clay, & Glass Mfg"
"METALS","Primary & Fabricated Metals Mfg"
"MISMFG","Other Manufacturing"
"RAILRD","Railroads"
"TRNSPT","Transportation Services"
"COMMUN","Communications"
"UTILIT","Utilities"
"WHOLSL","Wholesale Trade"
"GENMER","General Merchandise & Apparel"
"FODSTO","Food Stores"
"AUTODL","Automotive Dealers"
"EATDRK","Eating & Drinking Establishments"
"OTHRET","Other Retail Trade"
"BANKNG","Banking"
"INSURE","Insurance"
"OTHFIN","Other Financial Services"
"REALES","Real Estate"
"LODGNG","Hotels And Lodging Places"
"PERSVC","Personal Services"
"BUSSVC","Business Services"
"AUTSVC","Automotive Services"
"REPSVC","Repair Services"
"AMUSEM","Amusement & Recreation Services"
"HEASVC","Health services"
"PRIEDU","Private education"
"OTHSVC","Other services"
"MEMORG","Membership orgs"
"CONSVC","Contract Research & Consulting"
"GOVERN","Government"
echgvars:    3
"OUTPUT","Output in $M"
"WAGES","Wages per $M of output"
```

```
"EMPLOY","Employment per $M of output"
trgvars:     6
"RRREC_FRAC","Regulatory reduction in recreational activity"
"VAREC_FRAC","Voluntary avoidance of recreational activity"
"RRAG_FRAC","Regulatory reduction in agricultural activity"
"VAAG_FRAC","Voluntary avoidance of agricultural products"
"FILTCOST","Cost to filter and use the present drinking water supply"
"REPLCOST","Cost to replace the present drinking water source"
effvars:     7
"DAYVAL","Value of a day of participation in a recreational activity"
"PERSONTRIP","Number of day trips per person participating in recreational
activity"
"TOTVAL","Total value of a recreational activity"
"PRODCHG","Change in production of an agricultural product"
"PRODSURPCHG","Producer surplus of an agricultural product"
"COSTCHG","Change in cost of an agricultural product"
"REVCHG","Change in revenue from an agricultural product"
echgsum: "ECHG_Sta.csv"
echgdet: "ECHG_Det.csv"
trigsum: "TRIG_Sta.csv"
trigdet: "TRIG_Det.csv"
effsum: "EFF_Sta.csv"
effdet: "EFF_Det.csv"
```

6.3.2.3   TCERM Stochastic Values File

The stochastic values file is an optional output file that contains the values for every stochastic variable generated in the TCERM code. The description of the STOCHAST modifier on the FILE keyword (see Section 6.4.10) explains how to activate writing this file. The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of the ID of the stochastic variable followed by a value for every generated realization. Table 6.5 provides a subset of the data written to this file for a run using one realization. Because this file has at most a few hundred entries, the file size is always smaller than 100 KB. For this example case, there were 2 analytes, 4 locations, 31 agricultural products, and 62 industries in 36 sectors. The resulting output file contained 513 stochastic variables.

Table 6.5 Excerpted Records from the TCERM Stochastic Values File

```
"SPRWHTPRICE", 4.39686E+00
"WINWHTPRICE", 4.11085E+00
"BARLEYPRICE", 2.63601E+00
"OATS  PRICE", 1.38742E+00
"CORNGRPRICE", 3.15596E+00
"CORNSIPRICE", 2.78145E+01
...
"SPRWHTVAAG_S1", 5.15985E-02
"WINWHTVAAG_S1", 6.94639E-02
"BARLEYVAAG_S1", 9.13993E-02
"OATS  VAAG_S1", 8.53741E-02
"CORNGRVAAG_S1", 5.36837E-02
...
"GRPWINVAAG_S2", 3.00518E-01
```

```
"MILK  VAAG_S2", 3.85969E-01
"BEEF  VAAG_S2", 4.65310E-01
"HOGPIGVAAG_S2", 6.64737E-01
"SHPPROVAAG_S2", 4.65067E-01
"EN001 SPRWHTTOTPROD", 0.00000E+00
"EN001 WINWHTTOTPROD", 1.06814E+05
```

6.3.2.4   TCERM Trigger Detailed Data File

The trigger detailed data file is an optional output file that contains the detailed values for economic trigger calculations in the TCERM code. Output to this file is activated by entering the TRIGGER modifier on the DETALS keyword (see Section 6.4.6). The file name for this file is entered using the TRIGGERD modifier on the FILE keyword (see Section 6.4.10). The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. After the one-line header, each line of the file consists of four identifiers followed by a value for every generated realization. Table 6.6 provides a subset of the data written to this file for a run using one realization. The following are the four identifiers:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Solution Category: The identification of the solution category for which data were computed
- Solution Type: The identification of the solution type for which data were computed.

Table 6.6 Excerpted Records from the TCERM Trigger Detailed Data File

```
"Time","Location ID","Solution Category","Solution Type",
"Values by realization"
2000,"EN001 ","FISHNG","RRREC_FRAC", 0.00000E+00
2000,"EN001 ","FISHNG","VAREC_FRAC", 0.00000E+00
2000,"EN001 ","BOATNG","RRREC_FRAC", 0.00000E+00
2000,"EN001 ","BOATNG","VAREC_FRAC", 0.00000E+00
2000,"EN001 ","SWIMNG","RRREC_FRAC", 0.00000E+00
2000,"EN001 ","SWIMNG","VAREC_FRAC", 0.00000E+00
2000,"EN001 ","SKIING","RRREC_FRAC", 0.00000E+00
2000,"EN001 ","SKIING","VAREC_FRAC", 0.00000E+00
2000,"EN001 ","SPRWHT","RRAG_FRAC", 0.00000E+00
2000,"EN001 ","SPRWHT","VAAG_FRAC", 5.95562E-01
2000,"EN001 ","WINWHT","RRAG_FRAC", 0.00000E+00
2050,"EN004 ","HOGPIG","VAAG_FRAC", 0.00000E+00
2050,"EN004 ","SHPPRO","RRAG_FRAC", 0.00000E+00
2050,"EN004 ","SHPPRO","VAAG_FRAC", 0.00000E+00
2050,"EN004 ","PVTSW","FILTER", 0.00000E+00
2050,"EN004 ","PVTSW","REPLACE", 1.24184E+04
```

This file can have several rows of information for every combination of time, location, and crop. For a typical run, this file is several thousand lines long.

6.3.2.5   TCERM Trigger Summary Statistics File

This optional file contains summary statistics for the detailed economic trigger data generated in the TCERM code. Output to this file is activated by entering the TRIGGER modifier on the STATISTICS keyword (see Section 6.4.23). The file name for this file is entered using the

TRIGGERS modifier on the FILE keyword (see Section 6.4.10). The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of four identifiers followed by summary statistics (nine percentiles, mean value, and standard deviation). Table 6.7 provides a subset of the data written to this file for a run using five realizations. The following are the four identifiers on each line:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Solution Category: The identification of the solution category for which data were computed
- Solution Type: The identification of the solution type for which data were computed.

The data for each record in this file are too long to present without line-wrapping in this document. Each record in the file occupies two lines in Table 6.7.

Table 6.7 Excerpted Records from the TCERM Trigger Summary Statistics File

```
"Time","Location ID","Solution Category","Solution Type","Minimum","5th Percentile","10th
Percentile","25th Percentile","Median","75th Percentile","90th Percentile","95th
Percentile","Maximum","Mean","Standard Deviation"
2000,"EN001 ","FISHNG","RRREC_FRAC", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"EN001 ","FISHNG","VAREC_FRAC", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"EN001 ","BOATNG","RRREC_FRAC", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"EN001 ","SPRWHT","VAAG_FRAC", 5.95562E-01, 5.95562E-01, 5.95562E-01, 5.95562E-01, 5.95562E-
01, 5.95562E-01, 5.95562E-01, 5.95562E-01, 5.95562E-01, 5.95562E-01, 0.00000E+00
2000,"EN001 ","WINWHT","RRAG_FRAC", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"EN001 ","WINWHT","VAAG_FRAC", 5.67366E-01, 5.67366E-01, 5.67366E-01, 5.67366E-01, 5.67366E-
01, 5.67366E-01, 5.67366E-01, 5.67366E-01, 5.67366E-01, 5.67366E-01, 0.00000E+00
2000,"EN001 ","BARLEY","RRAG_FRAC", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
2000,"EN001 ","BARLEY","VAAG_FRAC", 5.77696E-01, 5.77696E-01, 5.77696E-01, 5.77696E-01, 5.77696E-
01, 5.77696E-01, 5.77696E-01, 5.77696E-01, 5.77696E-01, 5.77696E-01, 0.00000E+00
2000,"EN001 ","OATS  ","RRAG_FRAC", 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00,
0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00, 0.00000E+00
```

This file can have several rows of information for every combination of time, location, and crop. For a typical run, this file is several thousand lines long.

6.3.2.6 ECEM Effects Detailed Data File

The economic effects detailed data file is an optional output file that contains the detailed values for economic effect calculations in the TCERM code. Output to this file is activated by entering the EFFECTS modifier on the DETAILS keyword (see Section 6.4.6). The file name for this file is entered using the EFFECTS modifier on the FILE keyword (see Section 6.4.10). The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. After the one-line header, each line of the file consists of four identifiers followed by a value for every generated realization. Table 6.8 provides a subset of the data written to this file for a run using one realization. The four identifiers are the following:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Solution Category: The identification of the solution category for which data were computed
- Solution Type: The identification of the solution type for which data were computed.

Table 6.8 Excerpted Records from the TCERM Economic Effects Detailed Data File

```
"Time","Location ID","Solution Category","Solution Type",
"Values by realization"
2000,"EN001 ","FISHNG","DAYVAL", 6.49410E+01
2000,"EN001 ","FISHNG","PERSONTRIP", 1.16078E+01
2000,"EN001 ","FISHNG","TOTVAL", 2.83437E+07
2000,"EN001 ","BOATNG","DAYVAL", 2.61350E+01
2000,"EN001 ","BOATNG","PERSONTRIP", 9.19832E+00
2000,"EN001 ","BOATNG","TOTVAL", 2.64438E+05
2000,"EN001 ","SWIMNG","DAYVAL", 2.61350E+01
2000,"EN001 ","SWIMNG","PERSONTRIP", 9.19832E+00
2000,"EN001 ","SWIMNG","TOTVAL", 0.00000E+00
2000,"EN001 ","SKIING","DAYVAL", 2.61350E+01
2000,"EN001 ","SKIING","PERSONTRIP", 9.19832E+00
2000,"EN001 ","SKIING","TOTVAL", 0.00000E+00
2000,"EN001 ","SPRWHT","PRODCHG", 0.00000E+00
2000,"EN001 ","SPRWHT","PRODSURPCHG", 0.00000E+00
2000,"EN001 ","SPRWHT","COSTCHG", 0.00000E+00
2000,"EN001 ","SPRWHT","REVCHG", 0.00000E+00
2000,"EN001 ","WINWHT","PRODCHG",-3.93915E+04
2000,"EN001 ","WINWHT","PRODSURPCHG", 0.00000E+00
2000,"EN001 ","WINWHT","COSTCHG",-1.61932E+05
2000,"EN001 ","WINWHT","REVCHG",-1.61932E+05
2000,"EN001 ","BARLEY","PRODCHG", 0.00000E+00
2000,"EN001 ","BARLEY","PRODSURPCHG", 0.00000E+00
2000,"EN001 ","BARLEY","COSTCHG", 0.00000E+00
2000,"EN001 ","BARLEY","REVCHG", 0.00000E+00
2000,"EN001 ","OATS  ","PRODCHG", 0.00000E+00
2000,"EN001 ","OATS  ","PRODSURPCHG", 0.00000E+00
```

This file can have several rows of information for every combination of time, location, and crop. For a typical run, this file is several thousand lines long.

6.3.2.7 ECEM Effects Summary Statistics File

This optional file contains summary statistics for the detailed economic effects data generated in the TCERM code. Output to this file is activated by entering the EFFECTS modifier on the STATISTICS keyword (see Section 6.4.23). The file name for this file is entered using the EFFECTS modifier on the FILE keyword (see Section 6.4.10). The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of four identifiers followed by summary statistics (nine percentiles, mean value, and standard deviation). Table 6.9 provides a subset of the data written to this file for a run using five realizations. The following are the four identifiers on each line:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Solution Category: The identification of the solution category for which data were computed
- Solution Type: The identification of the solution type for which data were computed.

The data for each record in this file are too long to present without line-wrapping in this document. Each record in the file occupies two lines in Table 6.9.

Table 6.9 Excerpted Records from the TCERM Economic Effects Summary Statistics File

```
"Time","Location ID","Solution Category","Solution Type","Minimum","5th Percentile","10th
Percentile","25th Percentile","Median","75th Percentile","90th Percentile","95th
Percentile","Maximum","Mean","Standard Deviation"
2000,"EN001 ","FISHNG","DAYVAL", 6.49410E+01, 6.49410E+01, 6.49410E+01, 6.49410E+01, 6.49410E+01,
6.49410E+01, 6.49410E+01, 6.49410E+01, 6.49410E+01, 6.49410E+01, 0.00000E+00
2000,"EN001 ","FISHNG","PERSONTRIP", 1.16078E+01, 1.16078E+01, 1.16078E+01, 1.16078E+01,
1.16078E+01, 1.16078E+01, 1.16078E+01, 1.16078E+01, 1.16078E+01, 1.16078E+01, 0.00000E+00
2000,"EN001 ","FISHNG","TOTVAL", 2.83437E+07, 2.83437E+07, 2.83437E+07, 2.83437E+07, 2.83437E+07,
2.83437E+07, 2.83437E+07, 2.83437E+07, 2.83437E+07, 2.83437E+07, 0.00000E+00
2000,"EN001 ","BOATNG","DAYVAL", 2.61350E+01, 2.61350E+01, 2.61350E+01, 2.61350E+01, 2.61350E+01,
2.61350E+01, 2.61350E+01, 2.61350E+01, 2.61350E+01, 2.61350E+01, 0.00000E+00
2000,"EN001 ","BOATNG","PERSONTRIP", 9.19832E+00, 9.19832E+00, 9.19832E+00, 9.19832E+00,
9.19832E+00, 9.19832E+00, 9.19832E+00, 9.19832E+00, 9.19832E+00, 9.19832E+00, 0.00000E+00
2000,"EN001 ","BOATNG","TOTVAL", 2.64438E+05, 2.64438E+05, 2.64438E+05, 2.64438E+05, 2.64438E+05,
2.64438E+05, 2.64438E+05, 2.64438E+05, 2.64438E+05, 2.64438E+05, 0.00000E+00
2000,"EN001 ","SWIMNG","DAYVAL", 2.61350E+01, 2.61350E+01, 2.61350E+01, 2.61350E+01, 2.61350E+01,
2.61350E+01, 2.61350E+01, 2.61350E+01, 2.61350E+01, 2.61350E+01, 0.00000E+00
```

This file can have several rows of information for every combination of time, location, and crop. For a typical run, this file is several thousand lines long.

6.3.2.8 TCERM Economic Change Detailed Data File

The economic change detailed data file is a required output file that contains the detailed values for economic change calculations in the TCERM code. The file name for this file is entered using the ECONCHGD modifier on the FILE keyword (see Section 6.4.10). The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. After the one-line header, each line of the file consists of four identifiers followed by a value for every generated realization. Table 6.10 provides a subset of the data written to this file for a run using one realization. The following are the four identifiers:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Solution Category: The identification of the solution category for which data were computed
- Solution Type: The identification of the solution type for which data were computed.

Table 6.10 Excerpted Records from the TCERM Economic Change Detailed Data File

```
"Time","Location ID","Solution Category","Solution Type",
"Values by realization"
2000,"EN001 ","AGRICU","OUTPUT",-3.44122E+03
```

```
2000,"EN001 ","AGRICU","WAGES",-6.88939E+02
2000,"EN001 ","AGRICU","EMPLOY",-4.55252E-02
2000,"EN001 ","AGSVCS","OUTPUT",-8.75477E+02
2000,"EN001 ","AGSVCS","WAGES",-3.81511E+02
2000,"EN001 ","AGSVCS","EMPLOY",-4.00955E-02
2000,"EN001 ","MINING","OUTPUT",-8.76162E+00
2000,"EN001 ","MINING","WAGES",-3.32251E+00
2000,"EN001 ","MINING","EMPLOY",-9.04338E-05
2000,"EN001 ","CONSTR","OUTPUT",-2.85485E+03
2000,"EN001 ","CONSTR","WAGES",-1.21060E+03
2000,"EN001 ","CONSTR","EMPLOY",-3.65421E-02
2000,"EN001 ","FODPRO","OUTPUT",-1.79937E+04
2000,"EN001 ","FODPRO","WAGES",-3.01344E+03
2000,"EN001 ","FODPRO","EMPLOY",-8.27248E-02
2000,"EN001 ","PRIPUB","OUTPUT",-1.96714E+03
2000,"EN001 ","PRIPUB","WAGES",-6.47606E+02
2000,"EN001 ","PRIPUB","EMPLOY",-2.67759E-02
2000,"EN001 ","CHEMIC","OUTPUT",-5.18538E+03
2000,"EN001 ","CHEMIC","WAGES",-9.20565E+02
2000,"EN001 ","CHEMIC","EMPLOY",-1.54273E-02
```

This file can have several rows of information for every combination of time, location, and crop. For a typical run, this file will be several thousand lines long.

6.3.2.9 TCERM Economic Change Summary Statistics File

The economic change summary statistics file is a required output file that contains the detailed values for economic change calculations in the TCERM code. The file name for this file is entered using the ECONCHGS modifier on the FILE keyword (see Section 6.4.10). The values are written as text in comma-separated format so they can be imported easily into a spreadsheet or other software. Each line of the file consists of four identifiers followed by summary statistics (nine percentiles, mean value, and standard deviation). Table 6.11 provides a subset of the data written to this file for a run using five realizations. The four identifiers on each line are the following:

- Time: Year for which the data are valid
- Location ID: The location identifier where the data are valid
- Solution Category: The identification of the solution category for which data were computed
- Solution Type: The identification of the solution type for which data were computed.

The data for each record in this file are too long to present without line wrapping in this document. Each record in the file occupies two lines in Table 6.11.

Table 6.11 Excerpted Records from the TCERM Economic Change Summary Statistics File

```
"Time","Location ID","Solution Category","Solution Type","Minimum","5th Percentile","10th
Percentile",
"25th Percentile","Median","75th Percentile","90th Percentile","95th
Percentile","Maximum","Mean","Standard Deviation"
2000,"EN001 ","AGRICU","OUTPUT",-3.44122E+03,-3.44122E+03,-3.44122E+03,-3.44122E+03,-3.44122E+03,
-3.44122E+03,-3.44122E+03,-3.44122E+03,-3.44122E+03,-3.44122E+03, 0.00000E+00
2000,"EN001 ","AGRICU","WAGES",-6.88939E+02,-6.88939E+02,-6.88939E+02,-6.88939E+02,-6.88939E+02,
-6.88939E+02,-6.88939E+02,-6.88939E+02,-6.88939E+02,-6.88939E+02, 0.00000E+00
```

```
2000,"EN001 ","AGRICU","EMPLOY",-4.55252E-02,-4.55252E-02,-4.55252E-02,-4.55252E-02,-4.55252E-02,
-4.55252E-02,-4.55252E-02,-4.55252E-02,-4.55252E-02,-4.55252E-02, 0.00000E+00
2000,"EN001 ","AGSVCS","OUTPUT",-8.75477E+02,-8.75477E+02,-8.75477E+02,-8.75477E+02,-8.75477E+02,
-8.75477E+02,-8.75477E+02,-8.75477E+02,-8.75477E+02,-8.75477E+02, 0.00000E+00
2000,"EN001 ","AGSVCS","WAGES",-3.81511E+02,-3.81511E+02,-3.81511E+02,-3.81511E+02,-3.81511E+02,
-3.81511E+02,-3.81511E+02,-3.81511E+02,-3.81511E+02,-3.81511E+02, 0.00000E+00
2000,"EN001 ","AGSVCS","EMPLOY",-4.00955E-02,-4.00955E-02,-4.00955E-02,-4.00955E-02,-4.00955E-02,
-4.00955E-02,-4.00955E-02,-4.00955E-02,-4.00955E-02,-4.00955E-02, 0.00000E+00
2000,"EN001 ","MINING","OUTPUT",-8.76162E+00,-8.76162E+00,-8.76162E+00,-8.76162E+00,-8.76162E+00,
-8.76162E+00,-8.76162E+00,-8.76162E+00,-8.76162E+00,-8.76162E+00, 0.00000E+00
2000,"EN001 ","MINING","WAGES",-3.32251E+00,-3.32251E+00,-3.32251E+00,-3.32251E+00,-3.32251E+00,
-3.32251E+00,-3.32251E+00,-3.32251E+00,-3.32251E+00,-3.32251E+00, 0.00000E+00
2000,"EN001 ","MINING","EMPLOY",-9.04338E-05,-9.04338E-05,-9.04338E-05,-9.04338E-05,-9.04338E-05,
-9.04338E-05,-9.04338E-05,-9.04338E-05,-9.04338E-05,-9.04338E-05, 0.00000E+00
2000,"EN001 ","CONSTR","OUTPUT",-2.85485E+03,-2.85485E+03,-2.85485E+03,-2.85485E+03,-2.85485E+03,
-2.85485E+03,-2.85485E+03,-2.85485E+03,-2.85485E+03,-2.85485E+03, 0.00000E+00
2000,"EN001 ","CONSTR","WAGES",-1.21060E+03,-1.21060E+03,-1.21060E+03,-1.21060E+03,-1.21060E+03,
-1.21060E+03,-1.21060E+03,-1.21060E+03,-1.21060E+03,-1.21060E+03, 0.00000E+00
```

This file can have several rows of information for every combination of time, location, and crop. For a typical run, this file will be several thousand lines long.

6.4 Keyword Descriptions for the TCERM Code

In the following descriptions, some data are optional and some are required. Data required are enclosed in square brackets. For AB to be required, it would be denoted by [AB]. If only one of the three items AB, BC, CD were required, it would be written as [AB|BC|CD]. The vertical bars indicate to choose one of the items in the list. Optional items are enclosed in normal brackets. For DE to be an optional entry, it would be denoted by {DE}. The {} or [] symbols are indicators of whether the data are required; they are not actually entered when the keyword record is constructed.

In general, the order in which keywords are entered does not matter. However, the REPORT keyword must be the first keyword in the file and the END keyword must be the last keyword in the file.

6.4.1 AGLABOR Keyword for the TCERM Code

The AGLABOR keyword is used to determine the percentage of agricultural value generated that is labor cost. The following is this keyword record's syntax:

```
AGLABOR value
```

The first value is the percentage of agricultural value that is labor. The following is an example of the AGLABOR keyword record:

```
AGLABOR 0.55
```

6.4.2 AGPARAM Keyword for the TCERM Code

The AGPARAM keyword is used to provide the lowest price for an agricultural product at a location. It is assumed that if the price drops below this price, then no product will be produced. The following is this keyword record's syntax:

```
AGPARAM AGPROD="quote1" LOCATION="quote2" LOWPRICE=value
```

The first quote string contains an agricultural product ID. The second quote string contains a location ID. The lowest supply price for the product and location provided follows the LOWPRICE modifier on the AGPARAM keyword card. The following is an example of the AGPARAM keyword record:

```
AGPARAM AGPROD="SPRWHT"  LOCATION="EN001"  LOWPRICE=2.83
```

6.4.3 AGPROD Keyword for the TCERM Code

The AGPROD keyword is used to provide the lowest price for an agricultural product at a location. It is assumed that if the price drops below this price, no product will be produced. The following is this keyword record's syntax:

```
AGPROD ID="quote1" NAME="quote2" {OUTPUT}
```

The first quote string contains an agricultural product ID. The second quote string contains a location ID. The modifier OUTPUT is included if information for this agricultural product should be written to the output files. The following is an example of the AGPROD keyword record:

```
AGPROD ID="SPRWHT" NAME="Spring wheat" OUTPUT
```

6.4.4 ANALYTE Keyword for the TCERM Code

The ANALYTE keyword is used to define the analytes to be used in calculating economic risk metrics. The following is this keyword's syntax:

```
ANALYTE ["quote 1"] {"quote "}…{"quote n"}
```

The entry for each quote string must be an analyte identification string (up to six characters in length). The analyte identification string is case sensitive, and spaces or hyphens change the definition. Care must be taken that all data follow the convention that only the first entry in the analyte name is capitalized and that no embedded spaces or hyphens are used. The analytes selected must be a subset of the set of analytes identified in the environmental scenario file. Multiple analyte keywords can be entered. The following ANALYTE keyword selects the two analytes strontium-90 and zinc for analysis:

```
ANALYTE "Zinc" "Sr90"
```

6.4.5 DEBUG Keyword for the TCERM Code

The DEBUG keyword is used to activate dumping of intermediate calculations to the report file. It should be used sparingly and with only one or two realizations; otherwise, the volume of output could fill the user's hard drive. The following is this keyword record's syntax:

```
DEBUG [modifier1] {modifier2}{modifier3}
```

Multiple DEBUG records can be entered with combinations of modifiers, or a single record can be entered containing all of the modifiers. The modifiers can be entered in any order. Table 6.12 describes the modifiers associated with the DEBUG keyword:

Table 6.12 Modifiers Associated with the DEBUG Keyword in the TCERM Code

Modifier	Description
TRIGGER	Intermediate outputs on calculations for area calculations.
EFFECTS	Intermediate outputs on calculations for distance calculations on specific sites.
ECONCHG	Intermediate outputs on calculations for generating map data.
ANALYTE	Media concentration data are output to the report file.
DEFINITION	Output the definition of all stochastic variables.
STATISTICS	Output summary statistics for all generated stochastic variables.

The following entries provide examples of the use of the DEBUG keyword:
```
DEBUG TRIGGER
DEBUG EFFECTS
DEBUG TRIGGER EFFECTS ECONCHG
DEBUG ANALYTE
DEBUG DEFINITION STATISTICS
```

6.4.6   DETAILS Keyword for the TCERM Code

The DETAILS keyword is used to activate reporting of calculations of TRIGGER or EFFECTS calculations by realization to output files. The following is this keyword record's syntax:

```
DETAILS {TRIGGER} {EFFECTS}
```

Multiple DETAILS keywords can be entered with combinations of modifiers, or a single record can be entered. The following is an example that activates reporting for detailed data for both trigger and effects calculations:

```
DETAILS  TRIGGER  EFFECTS
```

6.4.7   DISCOUNT Keyword for the TCERM Code

The DISCOUNT keyword is used to supply the discount rate for calculation of the capital cost of drinking water source replacement in the EFFECTS subroutine. The following is this keyword's syntax:

```
DISCOUNT value1
```

The entry for the value must be a fraction between 0 and 1. The fraction represents the interest rate in a payment calculation. The following is an example of the DISCOUNT keyword record:

```
DISCOUNT 0.07
```

6.4.8   END Keyword for the TCERM Code

The END keyword signifies the end of all keyword data. It should be the last keyword in the keyword file. All data in the keyword file after the END keyword will be ignored. The following is this keyword record's syntax:

```
END
```

There are no modifiers or quote strings associated with the END keyword.

6.4.9   EXECUTE Keyword for the TCERM Code

The EXECUTE keyword signifies that the user wishes to perform problem execution. If this keyword is not entered, then the inputs are checked for consistency, but the problem will not be executed. This is useful if the run being set up is expected to take a significant amount of computation time. The following is this keyword record's syntax:

```
EXECUTE
```

There are no modifiers or quote strings associated with the EXECUTE keyword.

6.4.10   FILE Keyword for the TCERM Code

The FILE keyword is used to enter the names of input and output files except for the report file. The names of the files providing concentration data are contained in the environmental scenario file rather than in the keyword file. The following is the FILE keyword record's syntax:

```
FILE [modifier1 "quote1"] {modifier2 "quote2"} ... {modifier5 "quote5"}
```

The file names are entered in quote strings, which must be enclosed in double quotation marks. Path names up to 72 characters long are supported. The file name associated with a modifier must be entered before the next modifier is entered. At least one FILE keyword is required for every run of the code. Table 6.13 describes the modifiers associated with the FILE keyword.

Table 6.13 Modifiers Associated with the FILE Keyword in the TCERM Code

Modifier	Description
BURDEN	Input data file containing fish body burden concentrations produced by the ECEM code.
ESD	Input environmental scenario file that contains the definition of the environmental runs from which impacts are to be calculated.
HEADER	Output file containing header type information associated with all of the other output files identified in this table.
STOCHASTIC	Output file containing the generated values for all stochastic variables used in the run. This is an optional file that is recommended to support uncertainty analyses. Entry of this modifier and the file name activates output of the data.

Modifier	Description
BURDEN	Input data file containing fish body burden concentrations produced by the ECEM code.
TRIGGERD	Output file containing the calculated data, by realization, for each of the trigger calculations. This file is required only if the TRIGGER modifier is used on the DETAILS keyword.
TRIGGERS	Output file containing summary statistics for each of the trigger calculations. This file is required only if the TRIGGER modifier is used on the STATISTICS keyword.
EFFECTSD	Output file containing the calculated data, by realization, for each of the effects calculations. This file is required only if the EFFECTS modifier is used on the DETAILS keyword.
EFFECTSS	Output file containing summary statistics for each of the effects calculations. This file is required only if the EFFECTS modifier is used on the STATISTICS keyword.
ECONCHGD	Output file containing the calculated annual change in the economy by economic sector for each realization, location, and time. This file is always required.
ECONCHGS	Output file containing summary statistics for the annual economic change by economic sector for each location and time. This file is always required.

The following is an example entry:

```
FILE  HEADER "TestCase.hdr"  EFFECTSD "TestCase.efd"
```

The following set of two entries has the same effect as the single entry above.

```
FILE  EFFECTSD "TestCase.efd"
FILE  HEADER "TestCase.hdr"
```

6.4.11 FILTER Keyword for the TCERM Code

The FILTER keyword is used to provide the cost of filtering the water supply at a location for a given analyte. The following is the keyword's syntax:

```
FILTER LOCATION="quote1" ANALYTE="quote2"
    [PUBSW | PUBGW | PVTSW | PVTGW] value1
```

The entry for the value is the filtration cost in $/1000 gal/day. The following is an example of the FILTER keyword record:

```
FILTER LOCATION="EN003" ANALYTE="Sr90" PUBSW=5.0
```

6.4.12 FISHWT Keyword for the TCERM Code

The FISHWT keyword is used to input the matrix that identifies the relative importance of each species to recreational fishing at each location. There are no modifiers to the FISHWT keyword. The FISHWT keyword must be followed by NUMSPC lines, each containing NUMNOD values. The order of the species must match the number and order of species input through the SPECIE keyword. The values must match the order and number of the nodes supplied in the NODE keyword. For each location (column of values), the weights must sum to 1 (100%). The following is an example of the FISHWT keyword:

```
FISHWT
    0.4     0.3     0.2     0.3     ! SALMAD weights
    0.1     0.1     0.2     0.1     ! TROUT weights
    0.2     0.2     0.2     0.2     ! BASS weights
    0.1     0.2     0.1     0.1     ! CARP weights
    0.1     0.1     0.2     0.2     ! STURGEON weights
    0.1     0.1     0.1     0.1     ! CRAYFISH weights
```

6.4.13 INDUSTRY Keyword for the TCERM Code

The INDUSTRY keyword is used to define the local industries. The syntax for this keyword record takes one of the following forms:

```
INDUSTRY  ID="quote1" NAME="quote2" SECTOR="quote3"
    AGBASELINE=value1 RECBASELINE=value2 value3 value4 value5 {OUTPUT}
```

The first quote string contains an industry ID. The second quote string contains a short description of the industry. The first value is the baseline agricultural value for the industry. The second through fifth values are the baseline recreational values for the industry. One value is provided for each of the four recreational activities, in the order in which they are supplied on the RECACT keyword card. The third quote string contains the sector ID identifying the sector to which this industry aggregates. The following is an example of the INDUSTRY keyword record:

```
INDUSTRY ID="FODSTR" NAME="Food Stores"  SECTOR="FODSTO"
    AGBASELINE=52.349  RECBASELINE=15.573 14.381 0.0 14.381 OUTPUT
```

6.4.14 IRRFRACG Keyword for the TCERM Code

The IRRFRACG keyword is used to input the matrix that identifies the percentage of water supplied through irrigation for each agricultural product at each location. There are no modifiers to the IRRFRACG keyword. The IRRFRACG keyword must be followed by NUMAGP lines, each containing NUMLOC values. The order of the agricultural products must match the number and order of agricultural products input through the AGPROD keyword. The values must match the order and number of the locations supplied in the LOCATION keyword. The following is an example of the IRRFRACG keyword:

```
IRRFRACG
    0.4     0.3     0.2     0.3   ! SPRWHT
```

```
       0.1     0.1     0.2     0.1     ! WINWHT
       0.2     0.2     0.2     0.2     ! ALFSED
       0.1     0.2     0.1     0.1     ! ASPARA
       0.1     0.1     0.2     0.2     ! SWTCHR
       0.1     0.1     0.1     0.1     ! APPLES
```

6.4.15 IRRFRACS Keyword for the TCERM Code

The IRRFRACS keyword is used to input the matrix that identifies the percentage of water supplied through irrigation for each agricultural product at each location. There are no modifiers to the IRRFRACS keyword. The IRRFRACS keyword must be followed by NUMAGP lines, each containing NUMLOC values. The order of the agricultural products must match the number and order of agricultural products input through the AGPROD keyword. The values must match the order and number of the locations supplied in the LOCATION keyword. The following is an example of the IRRFRACS keyword:

```
   IRRFRACS
       0.4     0.3     0.2     0.3     ! SPRWHT
       0.1     0.1     0.2     0.1     ! WINWHT
       0.2     0.2     0.2     0.2     ! ALFSED
       0.1     0.2     0.1     0.1     ! ASPARA
       0.1     0.1     0.2     0.2     ! SWTCHR
       0.1     0.1     0.1     0.1     ! APPLES
```

6.4.16 MAKEUSE Keyword for the TCERM Code

The MAKEUSE keyword is used to input the make-use matrix required by the ECONCHG routine. There are no modifiers to the MAKEUSE keyword. The MAKEUSE keyword must be followed by NUMSCT lines, each containing NUMSCT values. These values are the make-use fractions for the economic sectors defined by the SECTOR keyword. The values must match the order and number of the sectors supplied in the SECTOR keyword. The following is an example of the MAKEUSE keyword:

```
   MAKEUSE
       0       0.6     0.05     0.05   0
       0       0       0        0      0
       0       0.5     0        0      0
       0       1.0     0        0      0
       0       0       0.05     0.05   0
```

6.4.17 LOCATION Keyword for the TCERM Code

The LOCATION keyword is used to define the nodes to be used in calculating economic risk metrics. One LOCATION record must be entered for each node to be assessed. The following is the keyword's syntax:

```
   LOCATION [PRIMARY="quote1"] {SECOND="quote2"} DWSOURCE="quote3"
       SWFLOW_PUB=value1 GWFLOW_PUB=value2
       SWFLOW_PVT=value3 GWFLOW_PVT=value4
       SWCOST_PUB=value5 GWCOST_PUB=value6
       SWCOST_PVT=value7 GWCOST_PVT=value8
```

The entry for each quote string must be a location identification string (up to six characters long). The location identification string is case sensitive, and spaces or hyphens change the definition. Care must be taken that all data follow the convention that only the first entry in the location name is capitalized and that no embedded spaces or hyphens are used. The locations selected must be a subset of the set of locations identified in the environmental scenario file. The available environmental concentrations will be taken from the PRIMARY location, and any additional environmental concentrations will be taken from the SECONDARY location if any are available. The following LOCATION keyword selects the location EN-01 and defines the associated variables:

```
LOCATION ECONOMIC ID="EN001" NAME="Richland region"
    SWDW="EN0011" SWCON="EN0012" SWIRR="EN0013" GWIRR="EN0014"
    FISH="EL0118" DWSOURCE="PUBSW" SWFLWPUB=18000.0  SWCSTPUB=1000.0
    GWFLWPUB=2000.0 GWCSTPUB=0.0

LOCATION PRIMARY="EN-01" SECOND="EN-04" SWFLOW_PUB=150 GWFLOW_PUB=150
    SWFLOW_PVT=1 GWFLOW_PVT=1 SWCOST_PUB=100 GWCOST_PUB=100 SWCOST_PVT=50
    GWCOST_PVT=50
```

6.4.18 RECACT Keyword for the TCERM Code

The RECACT keyword is used to determine the recreational activities to be analyzed and to provide the necessary input data by activity. The syntax for this keyword record takes one of the following forms:

```
RECACT  ID="quote1" NAME="quote2" SPEND=value1 PARTIC=value2
```

The first quote string contains an activity ID. The second quote string contains a short description of the activity. The first value is the average expenditure on the activity per outing. The second value is the number of inhabitants who participate in the activity. The following is an example of the RECACT keyword record:

```
RECACT  ID="FISH" NAME="Recreational fishing" SPEND=20.00 PARTIC=10000
```

6.4.19 REPORT Keyword for the TCERM Code

The REPORT keyword is used to define the name of the output report (log) file. It must be the first keyword entered in the keyword file. The following is the keyword record's syntax:

```
REPORT ["quote"]
```

The name of the report file is entered in a quote string. File names up to 72 characters long are supported, and path names can be included. The following is an example REPORT keyword record:

```
REPORT "/SAC/SystemCodes/Economic/Test1.rpt"
```

6.4.20 SECTOR Keyword for the TCERM Code

The SECTOR keyword is used to provide the sector definitions for aggregating from industries in the effects calculations. The following is the SECTOR keyword's syntax:

```
SECTOR ID="quote1" NAME="quote2" BASE_OUTPUT=value1 BASE_EMPLOY=value2
   BASE_WAGES=value3
```

Each economic sector is defined by entering a SECTOR keyword. The first quote string contains an identifying label for the sector and is limited to six characters. The second quote string provides a brief sector description and is limited to 72 characters. The list of sectors listed on SECTOR keyword records must exactly match the list, in order, of sectors listed in the sector make-use file. Sector data are provided through the use of modifiers on the sector keyword record. The following is an example for this keyword:

```
SECTOR ID="Sect01" NAME="Ag, Forestry, Fishery" OUTPUT=??
```

6.4.21 SEED Keyword for the TCERM Code

The SEED keyword is used to supply the random seed for stochastic variable generation. The following is the SEED keyword's syntax:

```
SEED value1
```

6.4.22 SPECIE Keyword for the TCERM Code

The SPECIE keyword identifies those species whose body burdens will be read from an ECEM output file and used for the recreational fishing trigger.
```
SPECIE "id 1" … "id n"
```

The following is an example of the SPECIE keyword:

```
SPECIE  "HYALLE" "LMSUCK" "SALMAD"
```

6.4.23 STATISTICS Keyword for the TCERM Code

The STATISTICS keyword is used to activate reporting of summary statistics from calculations of TRIGGER or EFFECTS calculations to output files. The following is this keyword record's syntax:

```
STATISTICS {TRIGGER} {EFFECTS}
```

Multiple STATISTICS keywords can be entered with combinations of modifiers, or a single record can be can be entered. The following is an example that activates reporting of summary statistics for both trigger and effects calculations:

```
STATISTICS TRIGGER  EFFECTS
```

6.4.24 STOCHASTIC Keyword for the TCERM Code

The STOCHASTIC keyword is used to enter the definition of a statistical distribution for stochastic variables. The following is the general syntax for the STOCHASTIC record:

```
STOCHASTIC ["Quote₁"] [Dist_Index Parameters] {TRUNCATE U1 U2}  {"Quote₂"}
```

The entry for Quote₁ must be a unique character string of up to 20 characters that will be used to identify this stochastic variable in subsequent uses. It is case sensitive and embedded spaces are significant. It is useful to make the character string some combination of a variable name and other character data such that it can be recreated easily when stochastic data are needed. The entry for Quote₂ is a description for the stochastic variable that can be up to 64 characters long. An entry for Quote₂ is not required.

The entry for Dist_Index must be an integer in the range 1 to 11 that identifies the index of a statistical distribution. The statistical distributions are defined in Section 10.0. The word Parameters in the general syntax statement indicates the numerical values of parameters required for defining the statistical distribution. The additional modifier TRUNCATE can be used for all distribution types except 1, 3, and 10. If TRUNCATE is entered, it must be followed by two values in the interval 0 to 1, inclusive. The lower value must be less than the upper value. These two values specify the tail probabilities at which to impose range truncation for the distribution. Truncation data must be entered after all of the other parameters that define the distribution.

The TCERM code uses a suite of STOCHASTIC keywords. The following paragraphs describe the required STOCHASTIC keywords by functional group. A run of TCERM using 4 recreational activities, 4 locations, and 31 agricultural products requires 513 STOCHASTIC keyword entries.

The lowest supply price for agricultural products is entered using the STOCHASTIC keyword. In this case, the value for Quote₁ is the agricultural product ID (blank filled to six spaces, if necessary) followed by the word PRICE. A separate STOCHASTIC keyword must be entered for every agricultural product. The following are example keywords:

```
STOCHASTIC "SPRWHTPRICE" 6 2.83 3.82 4.95 "Price for spring wheat ($/bu)"
STOCHASTIC "WINWHTPRICE" 6 2.5 3.67 4.81 "Price for winter wheat ($/bu)"
```

The total production is also entered using the STOCHASTIC keyword for each combination of location and agricultural products. In this case, the value for Quote₁ is the location ID (blank filled to six spaces, if necessary) followed by agricultural product ID (blank filled to six spaces, if necessary) followed by the word TOTPROD. A separate STOCHASTIC keyword must be entered for every combination of location and agricultural product. The following are example keywords:

```
STOCHASTIC "EN001 SPRWHTTOTPROD" 1 0.0
    "Total production of Spring Wheat at location EN001 in bu"
STOCHASTIC"EN002 WINWHTTOTPROD" 6 76011 101348 126685
    "Total production of Winter Wheat at location EN002 in bu"
```

The reduction fraction in total production due to regulatory limits being exceeded in surface water irrigation supplies is also entered using the STOCHASTIC keyword for each combination of location and agricultural products. In this case, the value for Quote₁ is the location ID (blank filled to six spaces, if necessary) followed by agricultural product ID (blank filled to six spaces, if necessary) followed by the word RRAG_SW. A separate STOCHASTIC keyword must be entered for every combination of location and agricultural product. The following are example keywords:

```
STOCHASTIC "EN001 SPRWHTRRAG_SW" 1 1.0
    "Reg reduction in ag due to SW at EN001 for SPRWHT"
STOCHASTIC "EN004 SPRWHTRRAG_SW" 1 1.0
    "Reg reduction in ag due to SW at EN004 for SPRWHT"
```

The reduction fraction in total production due to regulatory limits being exceeded in groundwater irrigation supplies is also entered using the STOCHASTIC keyword for each combination of location and agricultural products. In this case, the value for Quote$_1$ is the location ID (blank filled to six spaces, if necessary) followed by agricultural product ID (blank filled to six spaces, if necessary) followed by the word RRAG_SW. A separate STOCHASTIC keyword must be entered for every combination of location and agricultural product. The following are example keywords:

```
STOCHASTIC "EN001 SPRWHTRRAG_GW" 1 1.0
    "Reg reduction in ag due to GW at EN001 for SPRWHT"
STOCHASTIC "EN002 SPRWHTRRAG_GW" 1 1.0
    "Reg reduction in ag due to GW at EN002 for SPRWHT"
```

The voluntary avoidance of agricultural products due to step 1 concentration limits being exceeded is also entered using the STOCHASTIC keyword for each agricultural product. In this case, the value for Quote$_1$ is the agricultural product ID (blank filled to six spaces, if necessary) followed by the word VAAG_S1. A separate STOCHASTIC keyword must be entered for every agricultural product. The following are example keywords:

```
STOCHASTIC "SPRWHTVAAG_S1" 6 0.0 0.05 0.25
    "Voluntary avoid of ag step 1 for SPRWHT"
STOCHASTIC "WINWHTVAAG_S1" 6 0.0 0.05 0.25
    "Voluntary avoid of ag step 1 for WINWHT"
```

The voluntary avoidance of agricultural products due to step 2 concentration limits being exceeded is also entered using the STOCHASTIC keyword for each agricultural product. In this case, the value for Quote$_1$ is the agricultural product ID (blank filled to six spaces, if necessary) followed by the word VAAG_S2. A separate STOCHASTIC keyword must be entered for every agricultural product. The following are example keywords:

```
STOCHASTIC "SPRWHTVAAG_S2" 6 0.2 0.3 0.8
    "Voluntary avoid of ag step 2 for SPRWHT"
STOCHASTIC "WINWHTVAAG_S2" 6 0.2 0.3 0.8
    "Voluntary avoid of ag step 2 for WINWHT"
```

The reduction fraction in recreation due to regulatory limits being exceeded in surface water is also entered using the STOCHASTIC keyword for each combination of location and recreational activity. In this case, the value for Quote$_1$ is the location ID (blank filled to six spaces, if necessary) followed by recreational activity ID (blank filled to six spaces, if necessary) followed by the word RRREC_WQ. A separate STOCHASTIC keyword must be entered for every combination of location and recreational activity. The following are example keywords:

```
STOCHASTIC "EN001 FISHNGRRREC_WQ" 6 0.6 0.8 0.9
    "Regulatory red in rec due to water quality at EN001 for FISHNG"
STOCHASTIC "EN001 BOATNGRRREC_WQ" 6 0.6 0.8 0.9
```

```
    "Regulatory red in rec due to water quality at EN001 for BOATNG"
STOCHASTIC "EN001 SWIMNGRRREC_WQ" 6 0.6 0.8 0.9
    "Regulatory red in rec due to water quality at EN001 for SWIMNG"
STOCHASTIC "EN001 SKIINGRRREC_WQ" 6 0.6 0.8 0.9
    "Regulatory red in rec due to water quality at EN001 for WSKING"
```

The voluntary avoidance of recreational activities due to step 1 concentration limits being exceeded is also entered using the STOCHASTIC keyword for each combination of location and recreational activity. In this case, the value for Quote$_1$ is the location ID (blank filled to six spaces, if necessary) followed by recreational activity ID (blank filled to six spaces, if necessary) followed by the word VAREC_S1. A separate STOCHASTIC keyword must be entered for every combination of location and recreational activity. The following are example keywords:

```
STOCHASTIC "EN001 BOATNGVAREC_S1" 6 0.0 0.05 0.2
    "Voluntary avoid of rec step 1 at EN001 for BOATNG"
STOCHASTIC "EN001 SWIMNGVAREC_S1" 6 0.1 0.25 0.5
    "Voluntary avoid of rec step 1 at EN001 for SWIMNG"
```

The voluntary avoidance of recreational activities due to step 2 concentration limits being exceeded is also entered using the STOCHASTIC keyword for each combination of location and recreational activity. In this case, the value for Quote$_1$ is the location ID (blank filled to six spaces, if necessary) followed by recreational activity ID (blank filled to six spaces, if necessary) followed by the word VAREC_S2. A separate STOCHASTIC keyword must be entered for every combination of location and recreational activity. The following are example keywords:

```
STOCHASTIC "EN001 FISHNGVAREC_S2" 6 0.2 0.35 0.6
    "Voluntary avoid of rec step 1 at EN001 for FISHNG"
STOCHASTIC "EN001 BOATNGVAREC_S2" 6 0.0 0.1 0.5
    "Voluntary avoid of rec step 1 at EN001 for BOATNG"
```

6.4.25 THRESHOLD Keyword for the TCERM Code

The TRIGGER keywords reference thresholds for their calculations. The values of the thresholds are entered using the THRESHOLD keyword. The action levels apply by analyte, media, and usage. The following is the THRESHOLD keyword's syntax:

```
THRESHOLD ["quote"] [DRINK | SUR_CON | SUR_AG | FISH_BUR] [N1]
```

The entry for the quote string is the analyte identification string. The different threshold types possible are the following:

- DRINK = drinking water limit
- SUR_CON = surface water limit
- SUR_AG = surface water limit for agricultural use
- FISH_BUR = tissue concentration limit.

6.4.26 TIMES Keyword for the TCERM Code

The TIMES keyword identifies the times at which the calculations are to be performed. The following is the keyword's syntax:

```
TIMES [T1] {T2} … {Tn}
```

The numerical entries T1, T2, …, Tn are the times (whole number years) when outputs are desired. These times must be a subset of the times at which environmental data were computed and stored by the inventory, release, and transport modules. Only one TIMES record should be entered. The times entered will apply to all AREA, SITE, and MAP calculations. The following is an example TIMES keyword that requests output for the three years 2020, 2075, and 3014:

```
TIMES 2020 2075 3014
```

There are no modifiers or quote strings associated with the TIMES keyword.

6.4.27 TITLE Keyword for the TCERM Code

The TITLE keyword is used to define a single-line problem title. The problem title will be written to output files. If the title is not supplied, then the program will error terminate. The following is the keyword's syntax:

```
TITLE ["quote"]
```

The title is entered in a quote string, which must be enclosed in double quotation marks. Titles up to 72 characters long are supported. The following example defines a title for a run of the code:

```
TITLE "Example title line for the economic impacts code – Test #1."
```

There are no modifiers associated with the TITLE keyword.

6.4.28 USER Keyword for the TCERM Code

The USER keyword is used to identify the user of the program. The user name will be written to output files. If the user name is not supplied, then the program will error terminate. The following is the keyword's syntax:

```
USER ["quote"]
```

The user name is entered in a quote string, which must be enclosed in double quotation marks. User names up to 16 characters long are supported. The following example defines John Q. Public as the user running the code:

```
USER "John Q. Public"
```

There are no modifiers associated with the USER keyword.

6.5 Keywords Required from the Environmental Settings File

The TCERM code also reads keywords from the environmental settings file. These keywords are read from a different file and can have a different definition from a keyword defined for internal use in the TCERM code. The environmental settings keywords are defined in Section 2.2. The following keywords are required:

- ANALYTE – Definition of analytes in the environmental simulations
- END – End of the environmental settings keywords
- FILE – File names for the concentration file for each analyte
- LOCATION – Locations at which concentrations were generated for the economic impacts
- REALIZAT – Number of realizations that were simulated
- SPECIE – The species for which tissue concentrations were generated for the ecological impacts
- TIMES – Times at which concentrations were generated for the economic impacts
- TITLE – Environmental simulation title.

7.0   SAC Data Viewer (SACView)

This section contains instructions for using the SACView data extraction tool. SACView has a Windows user interface and simplifies viewing the contents of environmental concentration data files and the results files generated by all of the impacts programs. SACView allows creation of smaller customized data sets from the large data files that can be further analyzed using a spreadsheet or graphical analysis tool. SACView assists the user in defining the customized data set by presenting screens that allow the user to select from the various elements within the larger data set.

The following are references to other parts of this document that will help clarify the data types that can be retrieved by SACView:

- Concentration analysis will consist of selecting information from files that were created by the inventory, release, and transport codes. Data that can be viewed through concentration analysis reside in the ECDA (see Sections 2.3 and 2.3.1).
- Cultural analysis will consist of selecting information from files that were created by cultural impacts model (see Section 3.3.2).
- Ecological analysis will consist of selecting information from files that were created by the ecological impacts model (see Section 4.3.2).
- Human analysis will consist of selecting information from files that were created by the human impacts model (see Section 5.3.2).
- Economic analysis will consist of selecting information from files that were created by the Tri-Cities economic regional model (see Section 6.3.2).

The following conventions are used in the descriptions for using the SACView tool:

- Screen names are capitalized (DATA SOURCE)
- Button and check box names appear in bold (**Human**, **Summary Data**)
- Framed categories (sections of a screen) and tab labels appear in italics (*Level of Analysis*).

7.1   Getting Started

SACView is written in Visual Basic and runs only under the Windows operating system; however, the data files to be viewed can reside either on a Windows system or a Linux system. SACView is launched from the Windows Start menu. The first screen displays a series of buttons, along with the version, date, and time the SACView application was built. This screen is called IMPACT SELECTION. Use the buttons that appear in the upper right corner of this screen (see Figure 7-1) to select the impact type. You must always select an impact type whether impact data or concentration data will be viewed. The default is **Human**, as indicated by its different color and appearance when clicked.

Figure 7-1 Selecting an Impact Type in SACView

As indicated in Figure 7-2, SACView can receive input from the impact codes (human, ecological, economic, and cultural) and can read concentration data that resides in the Environmental Concentration Data Accumulator (see Section 2.3). You must choose either the **Impacts** or **Concentrations** button to continue. The **Impacts** button is the default selection.
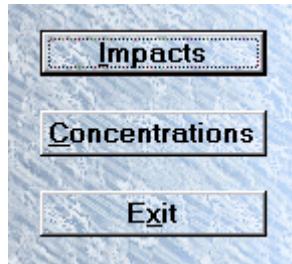
Figure 7-2 Selecting the Data Type to View in SACView

To terminate the SACView run from this screen, click the **Exit** button. To exit the program after you have continued to other screens, click the **Cancel** button found on that screen. SACView will state that selections will be lost and then return to the IMPACT SELECTION screen where you can click **Exit**.

7.2   Data Source Screen

After selecting one of the impact types and either **Impacts** or **Concentrations**, you must open a header file that contains information based on these selections. The purpose of the DATA SOURCE screen shown in Figure 7-3 is to navigate to the header file that contains details about this data set. A *drive selection* window, a *directory selection* window, and a *file selection* window assist in this process.

Instructions associated with Figure 7-3 include the following:

- To select a drive, open the drop-down list and highlight the desired drive.
- To open a directory, double-click the desired directory.
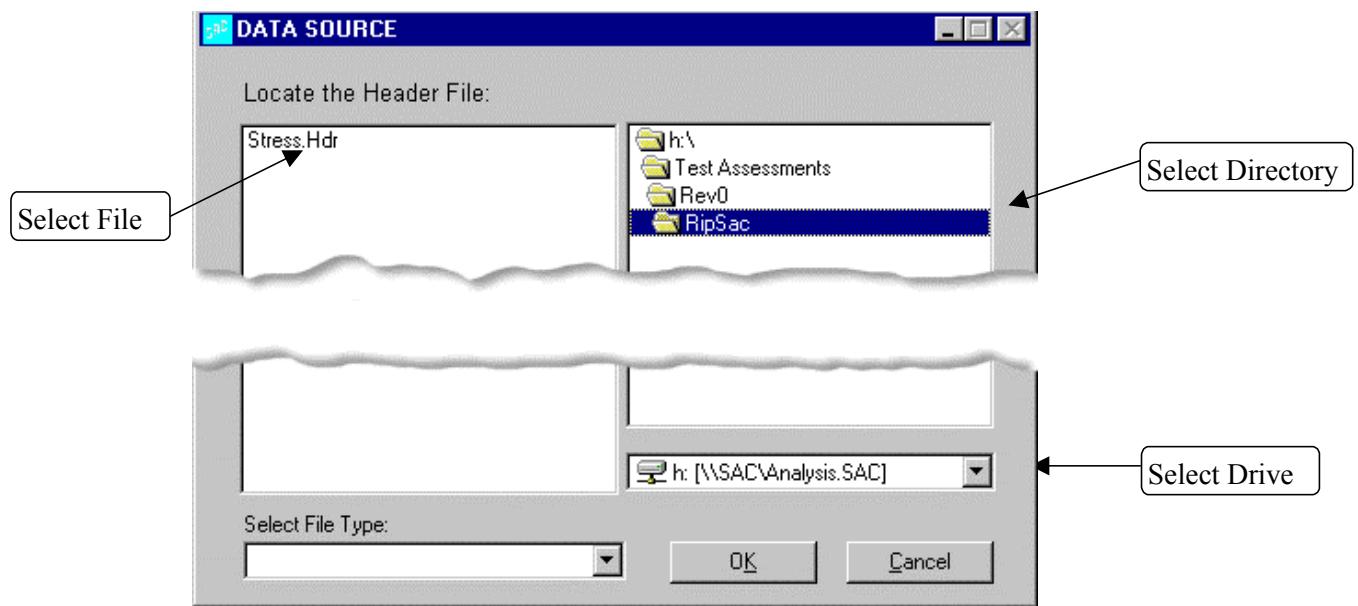
Figure 7-3 Navigating to the Header File in SACView

- You can open the selected header file one of two ways:
  - ○ Single-click the file name and click **OK**.
  - ○ Double-click the file name.

The purpose of the *Select File Type* option is to be able to filter the types of files that appear in the *file selection* frame. The list starts with the default file type that has an .hdr extension (such as Stress.Hdr in Figure 7-3). The result is that only files with the .hdr extension will appear in the list. Others may be added by entering a file name or type in the *Select File Type* box (for example, *.* and *.txt). The selected file should be the header file that defines the desired data set. Examples of header files are found in the following tables:

- Table 3.3 for the cultural impacts model
- Table 4.4 for the ecological impacts model
- Table 5.4 for the human impacts model
- Table 6.4 for the economic impacts model.

If the selected header file does not match the selections you made on the IMPACT SELECTION screen, an error message will appear. After you click the **OK** button in the message box, SACView will remain at the DATA SOURCE screen to allow you to select a header file that matches your previous selections. If the impact type or the type of data you selected is incorrect, click **Cancel** to return to the IMPACT SELECTION screen and select the correct impact and/or data type.

7.3 Displaying the Contents of the Header File

Once you have selected the correct header file type, click **OK**. The HEADER CONTENTS screen will open. A label at the top of the screen confirms the impact type or concentration type that was selected on the IMPACT SELECTION screen.

7.3.1 Summary Run Information

A block of information is displayed at the top of the screen that defines the data set described in the header file. Table 7.1 provides the data from an example run.

Table 7.1 Summary Information from Header File displayed by SACView

Title:	SACView Rev 0 Initial case – 11 realizations
User:	Paul W. Eslinger
Name	ECEM
Version:	2.00.A.9
Date of Run:	4 Feb 2002
Run ID:	20020220133056

7.3.2 Level of Analysis and Other Options for Selection

At the bottom of the HEADER CONTENTS screen, you must make two selections that further define the data to be extracted. The *Level of Analysis* determines whether summary or detailed data are to be extracted. You must select the *Level of Analysis* first: **Summary Data** or **Detailed Data**. The *Other Options* vary depending on the impact type you selected. When changing the *Level of Analysis*, any *Other Options* that were selected will not be preserved.

Figure 7-4 shows the Human model options. Both **SummaryData** and **Detailed Data** data have *Other Options* of **Human Impacts** or **Foods**.
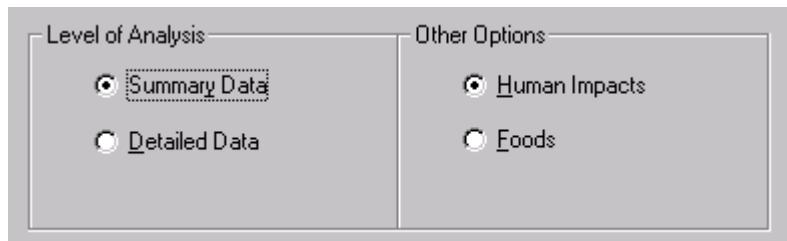

Figure 7-4 Human Model Options in SACView

Figure 7-5 shows the Ecological model options. There are no *Other Options* currently available for this impact type.
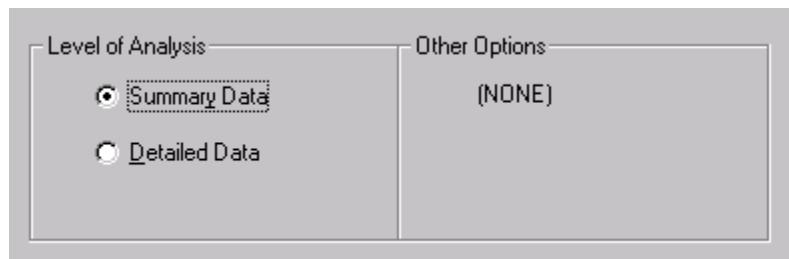
Figure 7-5 Ecological Model Options in SACView

Figure 7-6 shows the Economic model options. Both **Summary Data** and **Detailed Data** can have all three *Other Options* available — **Triggers**, **Effects**, and **Economic Change**.
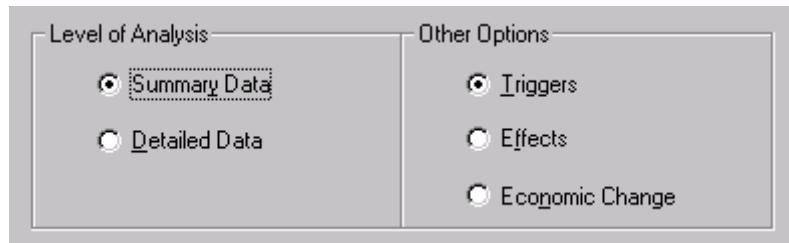
Figure 7-6 Economic Model Options in SACView

Figure 7-7 and Figure 7-8 show the Cultural model options. **Summary Data** and **Detailed Data** can have **Sites** or **Areas** as other options. **Map Data** has no *Other Options*.
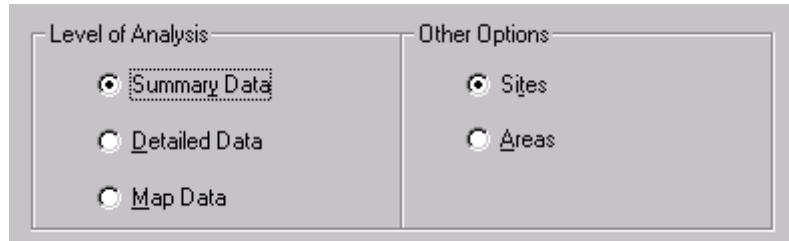
Figure 7-7 Cultural Model Options for **Summary Data** and **Detailed Data** in SACView
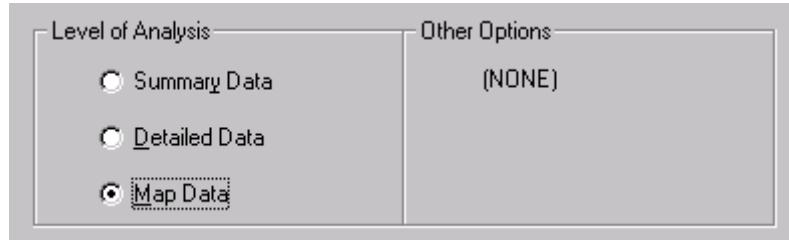
Figure 7-8 Cultural Model Options for **Map Data** in SACView

Figure 7-9 shows Concentration data options. These options apply to data for all impacts types. The data found in the ECDA can only be viewed at the **Detailed Data** *Level of Analysis*, and there are no *Other Options* available.
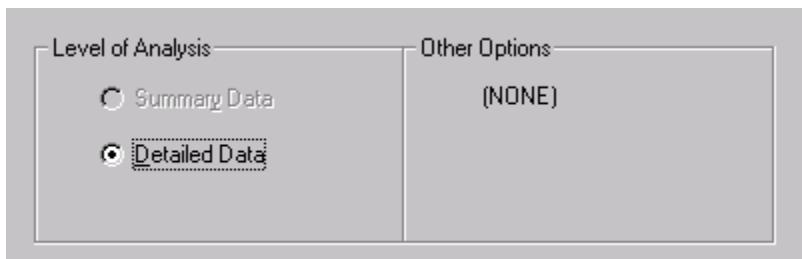
Figure 7-9 Concentration Data Options in SACView

Often, a set of data may not have all the options available. This is determined by the choices made when the particular impacts data set was created. As indicated in Figure 7-10, if the file does not contains a particular data type, then the option will be grayed out (not enabled).
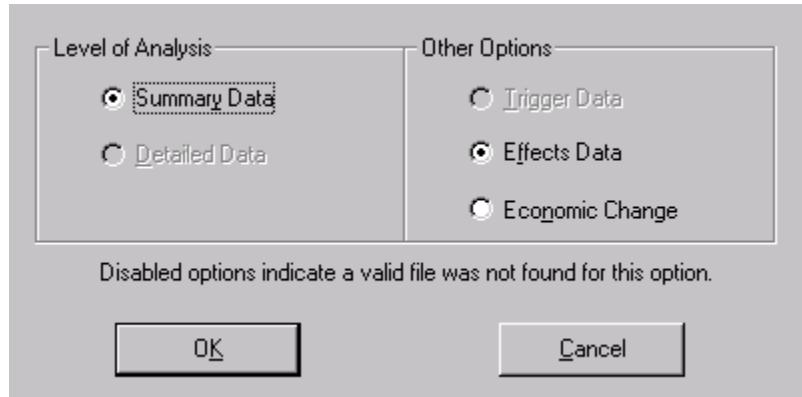
Figure 7-10 Unavailable Options for *Level of Analysis* and *Other Options*

Click the **OK** button to bring up the next screen, which presents the next set of items to select from. To return to the main screen, IMPACT SELECTION, click the **Cancel** button; all selections made to this point will be lost.

7.4   Impact Screens

Although the next screen will be referred to by the name IMPACT SCREEN, one of the following names will appear at the top of the screen. The one that appears depends on your previous selections.

- Human Impacts
- Ecological Impacts
- Economic Impacts
- Cultural Impacts
- Human Concentrations
- Ecological Concentrations
- Economic Concentrations.

SACView is now prepared to display header information specific to the impact type, the type of data (impacts or concentrations), the level of analysis (detailed, summary or map), and other options that are selected.

The name of the header file appears in the lower left corner along with the number of realizations that make up this data set. All impact screens are designed around a series of tabs. On each tab are lists of elements that describe the data set. Specific directions are given here about how to make selections from these lists. The purpose of this process is to refine the data set that will be extracted. Figure 7-11 gives an example of the tabular design used to display the information:


Figure 7-11 Tabular Design to Categorize the Information

The lists that appear on the tabs sometimes have columns to display multiple sets of information concerning the topic. In Figure 7-11, there are four columns. Often the data displayed in a column is longer than the default column width. You may drag the bars left or right to widen the viewing area to display a greater portion of the information in the column. Often, scroll bars are available to make viewing a long list possible.

You must make selections from each tab type. Some tabs, particularly *Analytes* and *Species*, may have more than one list. If a required selection is not made, then SACView will not continue; instead, a warning message will be displayed to notify you of a required selection. Click the **OK** button in the warning box and SACView will return to the tab that needs completing. Make a selection, and click the **OK** button again.

Each tab on the final data selection screen will have **Select ALL** and **Clear ALL** options (see Figure 7-12). When the checkbox for **Select ALL** is checked, all options that appear in the tab will become selected. A strategy that can be used to select most of the items is to choose **Select ALL** and then uncheck individual items that are not to be included. The **Clear ALL** checkbox will remove all selected items.

Figure 7-12 **Select ALL** or **Clear ALL** Options for Lists

7.4.1   Human Impact

While selecting the *Level Of Analysis* and *Other Options* on the HEADER CONTENTS screen as described in Section 7.3.2, if you select **Summary Data** or **Detailed Data** and **Human Impacts**. The IMPACT SCREEN displays has three tabs: *Times, Locations*, and *Analytes and Solutions*. You must make at least one selection on each tab except for the *Analytes and Solutions* tab. The analytes have been categorized into three separate lists (see Figure 7-13) to help you in the selection process. The lists are *Radioactive Analytes*, *Hazardous Analytes*, and *Carcinogenic Analytes*. At least one selection must be made in one of the three lists. At least one selection must be made in *Solution Types*. Therefore, a minimum of two selections must be made on this tab.

Figure 7-13 Selection Analytes and Solution Types for the Human Impact

If you selected **Summary Data** or **Detailed Data** and **Foods** while on the HEADER CONTENTS screen, four tabs will appear on the IMPACT SCREEN. The labels of these tabs are *Times*, *Locations*, *Analytes*,

and *Foods*. There are no *Solution Types* available for Foods. At least one selection must be made on each tab. The *Foods* tab will have *Irrigation* and *Foods*. As shown in Figure 7-14, *Irrigation* is defaulted to "Both."

Figure 7-14 Irrigation Selections for the Human Impacts Model

A selection must be made from the *Foods* list that appears below *Irrigation* as shown in Figure 7-15.

Figure 7-15 Foods Selections for the Human Impacts Model

7.4.2   Ecological Impact

The Ecological IMPACT SCREEN has only one set of tabs because there were no *Other Options* to select on the HEADER CONTENTS screen. The tabs that are displayed on the IMPACT SCREEN for both **Summary Data** and **Detailed Data** will be *Times*, *Locations*, *Analytes*, *Species*, and *Media and Solutions*.

The *Analytes* are grouped into the following categories:

- Organic radioactive analytes
- Non-organic (inorganic) radioactive analytes

- Organic stable analytes
- Non-organic (inorganic) stable analytes.

The *Species* are grouped into the following categories:

- Terrestrial plants
- Aquatic plants
- Terrestrial animals
- Aquatic animals.

The following are the available *Media Types*:

- SW denotes surface water (river)
- PW denotes pore water (river bottom)
- GW denotes ground water
- SE denotes seep water (river bank)
- SO denotes soil
- SD denotes sediment (river bottom).

The following are the available *Solution Types*:

- DOSDER – Dermal Dose
- DOSING – Ingestion Dose
- DOSINH – Inhalation Dose
- BMTISS – Benchmark Tissue Value
- CONCEN – Media Concentration
- SUMRAD – Sum of Radioactive Dose.

The rules for selecting data ecological are more complex than for other impact types.

- A *Time* and *Location* must always be selected.
- If the goal is to view concentrations only, then one or more *Analytes*, one or more *Media Type*, and the **CONCEN** *Solution Type* must be selected. This will allow viewing of the concentration data used in the calculations.
- If the goal is to view species data, then one or more *Analytes*, one or more *Species*, and one or more *Solution Types* must be selected. Occasionally, the user may only be interested in viewing the summed radionuclide dose. In this case, select only *Species* and the **SUMRAD** *Solution Type*. The output will consist of the radioactive dose summed over all radioactive analytes for the animal and/or plant species that are selected.
- Other combinations can be made. An *Analyte*, *Species*, **SUMRAD**, **CONCEN**, and other *Solution Types* may be selected simultaneously. Please note, however, if a *Species* is selected, then there must always be a *Solution Type* selected. The media types and CONCEN are tied together (see Figure 7-16). When selecting **CONCEN**, all items in the *Media Type* list will be selected. When selecting a media type, then the **CONCEN** solution will become selected.
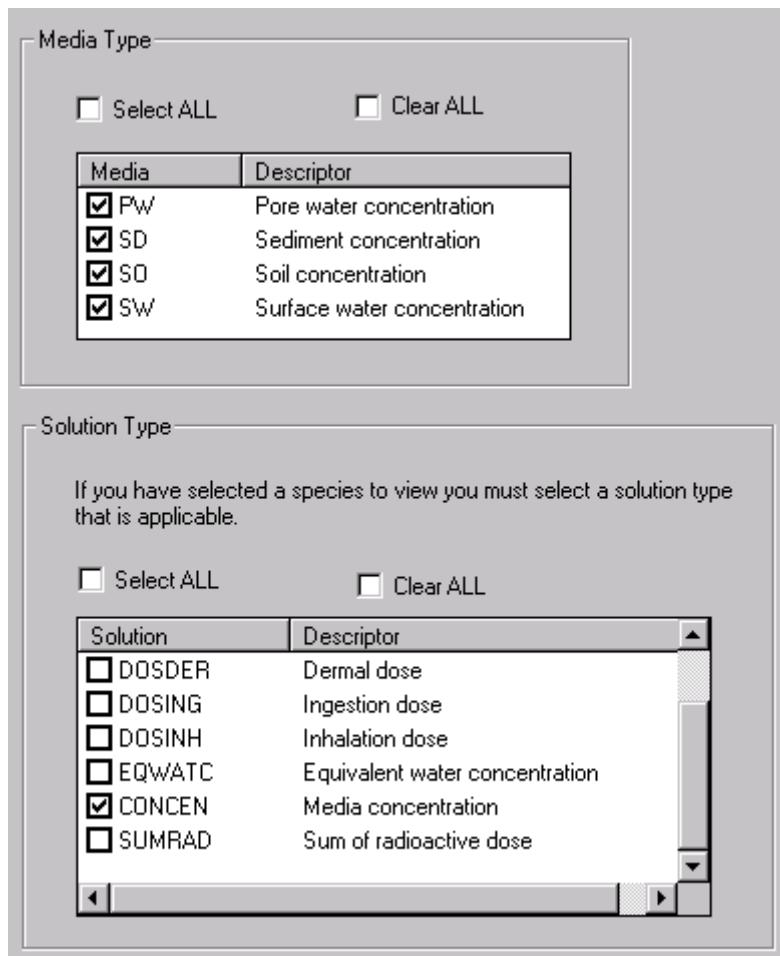
Figure 7-16 Selections of Media Type and Solution Type

Table 7.2 summarizes the grouping of ecological selections.

Table 7.2 Summary of Ecological Selection Options

Analyte Selected	*Species Selected*	*Media Type Selected*	*Solution Type*	**Data Viewed**
Yes	No	Yes	CONCEN	Concentration data only.
No	Yes	No	SUMRAD	Radioactive dose summed over all radioactive analytes for the selected species.
Yes	Yes	No	See other solutions in Table 4.10	Results listed per analyte, species, and solution combinations selected.
Yes	Yes	Yes	CONCEN plus another solution or SUMRAD	Data will be included as defined in the previous three table rows.

7.4.3 Economic Impact

Four tabs will appear on the IMPACT SCREEN if **Summary Data** or **Detailed Data** and **Triggers** are selected on the HEADER CONTENTS screen when choosing the *Level Of Analysis* and *Other Options* as described in Section 7.3.2. The tabs will be labeled *Times, Locations, Products and Activities*, and *Triggers*. At least one selection is required on each tab except for the *Products and Activities* tab, which requires at least one selection for *Agricultural Product* and *Recreational Activity*. On the final tab, a *Trigger* must be selected.

If **Effects** is selected instead of **Triggers** on the HEADER CONTENTS screen, then the tabs will look the same as described above except for the fourth tab, which will now have *Effects* instead of *Triggers*. At least one selection must be made from each list just as described for *Triggers*.

If **Economic Changes** is selected instead of **Triggers** on the HEADER CONTENTS screen, the tabs will be labeled *Times*, *Locations, Sectors*, and *Impacts*. There will be only one list per tab and a selection will be required on each list.

7.4.4 Cultural Impact

The Cultural Impact screen has only two tabs no matter what selections are made on the previous screen.

7.4.4.1 Cultural Summary and Detailed Selections

If **Summary Data** or **Detailed Data** and **Sites** are selected on the HEADER CONTENTS screen, there will be tabs containing lists of *Times* and *Sites*. One selection must be made on each tab. If, however, **Areas** is selected, there will be lists of *Times* and *Areas*. One selection must be made on each tab.

7.4.4.2 Cultural Map Selections

If the *Level of Analysis* selected is **Maps**, two tabs will display *Times* and *Maps*. One selection must be made on each tab.

7.4.5 Concentrations

To view concentration data, select from data sets that were created during the execution of the inventory, release, and transport codes represented by the left side of the diagram described in Figure 1-2. The results created by these codes are in binary format and can be read by SACView. As mentioned in Section 2.3.2, a separate data file is created for each impact and analyte combination. You must select the impact type from the main screen. The IMPACT SCREEN will display *Times, Locations*, and *Analytes and Media* and a selection is required in each list.

7.4.6 Saving the Data to File (SACView output files)

At the bottom of each IMPACT SCREEN (see Figure 7-17), there is a button that provides the capability for saving the extracted data to a file that can be opened by a spreadsheet or other analysis program. All output data are in ASCII comma-delimited format. Data will not be saved until a file name is provided. A warning is displayed on the screen to remind you that this information has not yet been provided.
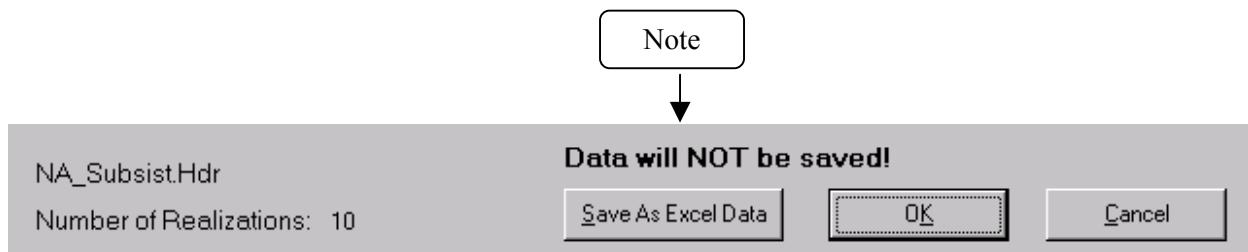
Figure 7-17 Saving the Data to File

To save the selected data in SACView, use the FILE NAME REQUEST screen to locate the drive and directory and enter a file name. This screen is shown in Figure 7-18.
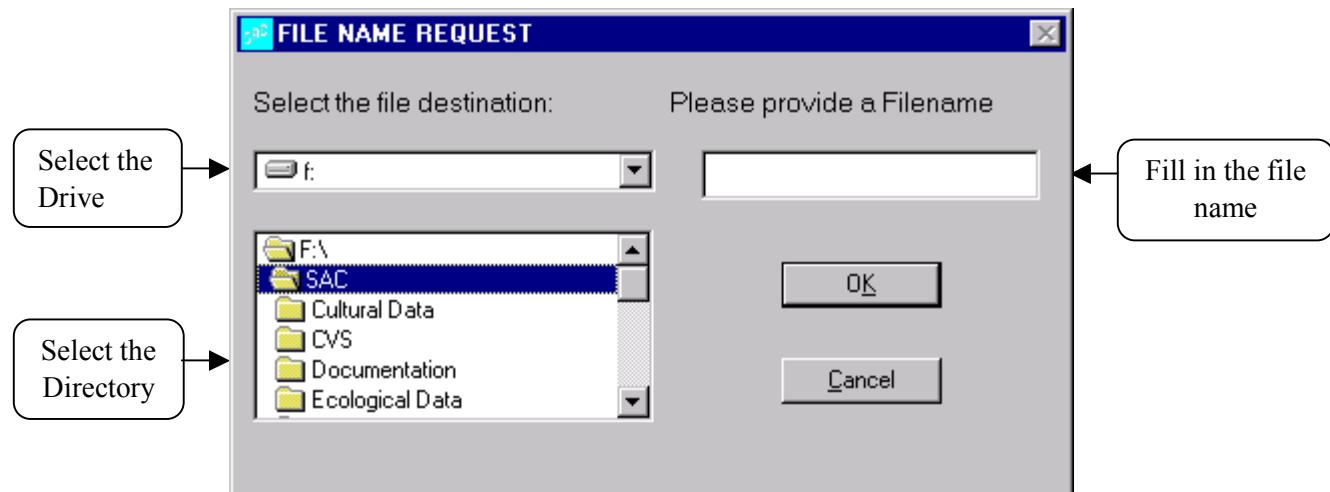
Figure 7-18 FILE NAME REQUEST Screen

The lists on the left of the screen are designed to assist in locating where the file is to be saved. In the input box located in the upper right corner, enter the file name to be used. The output is a comma-delimited file in ASCII format. If the ".csv" extension is used, the file can be imported without further conversions into Microsoft Excel.

After you provide a file name and click "OK," SACView will return to the IMPACT SCREEN. The warning that appears above the **Save** button is changed to read "Data WILL be saved" as shown in Figure 7-19.
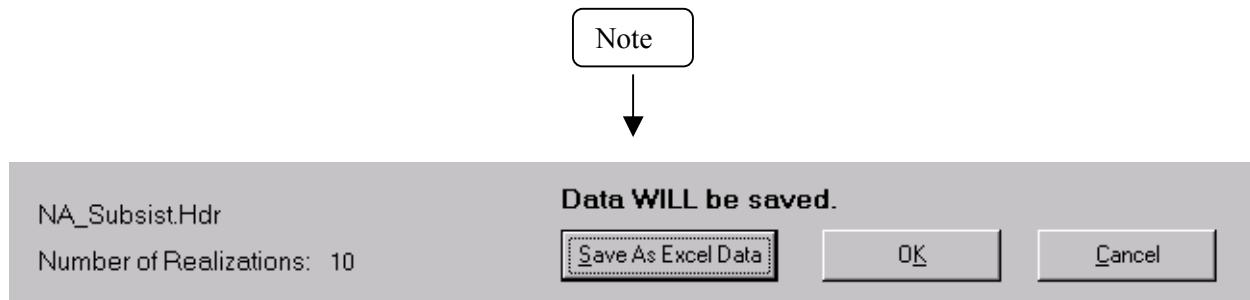
Figure 7-19 Verification Screen for the Data Save Option

If the impact type is Cultural and the **Map Data** option is selected, the **Save** button will display the caption "Save As Map Data." In this case, data are output using comma-separated triple pairs: the first two entries of the triple are the easting and northing coordinates, and the last entry is the data value. The coordinates are expressed as meters in the Lambert Projection on the Washington State Plane (NAD 83).

7.5 Data Display Screen

The results are output to a grid on a screen labeled either IMPACT DATA DISPLAY or CONCENTRATIONS DATA DISPLAY. Scroll bars are available to make viewing the entire list possible. The columns in this display are not adjustable. Data that do not fit in the columns can be viewed by saving to a file and reviewing the data in a spreadsheet tool. A maximum of 3,000 lines of data is displayed on the grid, and a maximum of 65,000 lines of data may be saved to a file. Figure 7-20 shows an example impact data display.

Figure 7-20 Example of Extraction Results Displayed in SACView

Summary information about the selections that were made is displayed at the bottom of the screen. In the frame to the left, the composite selection path that was taken to get to this point is summarized. The total number of records that are displayed in the grid is reported in the center frame. A frame that informs the

user of the processing status indicates **Loading Complete** in Figure 7-21. While the data are being processed and loaded into the grid, this frame will display "LOADING DATA" in large black letters.

Occasionally, a message will appear informing that no data can be found. In this case, you have selected a set of options that does not match with any computed data. In this case, you should try a different set of selection options. For example, ECEM can compute equivalent water concentrations, which apply only to aquatic animals. The same run could also compute body burdens that apply to both aquatic and terrestrial animals. For example, it is possible to select options that identify a harvest mouse and the equivalent water concentration solution. However, because the harvest mouse is a terrestrial animal, the equivalent water concentration solution does not apply.

Figure 7-21 Summary of Information Extracted with SACView

When concentration data are being extracted, a button is displayed to provide access to the units that were used in the calculations for the various media types. This button is illustrated in Figure 7-22.

Figure 7-22 Accessing the Media Units

Click the **Media Units** button to open a small screen (see Figure 7-23) that lists the data units for each media type.
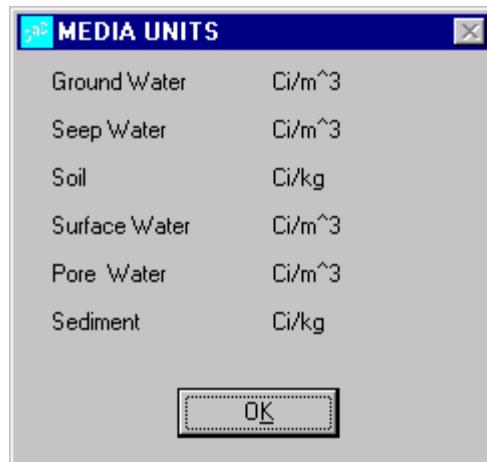
Figure 7-23 Display of Data Units for Media Concentrations

7.6   Reselect/Exit

Figure 7-24 shows the terminal screen that appears following the extraction of a customized data set in SACView. Four options are presented:

- **New Impact** – Click this button to discard all selections except the impact type and return to the IMPACT SELECTION screen described in Section 7.1. A new impact may be selected as well as the type of data to extract.
- **Summary / Detailed** – Click this button to discard all elemental selections made on the IMPACT SCREEN and return to the HEADER CONTENTS screen described in Section 7.3. A new *Level of Analysis* and/or *Other Options* may be selected to continue the extraction process. At this level, the current impact and type of data (impacts or concentrations) remain the same.
- **Elemental Selections** – Click this button to save all selections within SACView and return to the IMPACT DISPLAY screen described in Section 7.4. New selections may be made from these same lists that define the current impact type.
- **Exit** – Click this button to exit the application. In order to prevent inadvertent loss of work, SACView will ask you to confirm the requested action.
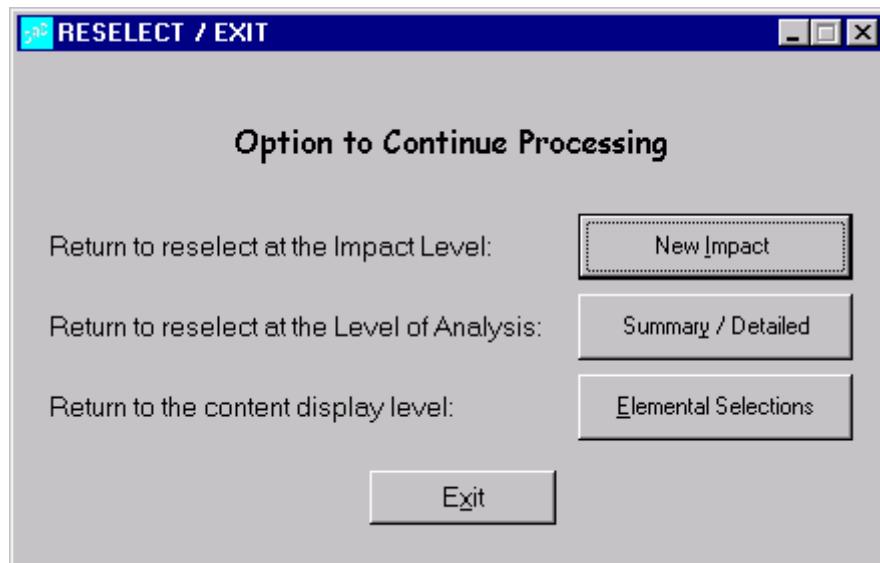
Figure 7-24 Reselect or Exit Screen

8.0   Impacts Differencing Tool (ImDiff)

8.1   Overview

The river transport model in the SAC Rev. 0 computer codes can be run with or without background concentrations from upriver sources. A typical method of analyzing a Hanford-related problem is to run the river code with two data sets. First, a transport run is made using background values, but no source term from the Hanford Site is introduced. Then, another transport run is made that is identical to the first run except a Hanford source term is introduced. If the impacts codes are run using these two data sets, then their results can be differenced to determine the contribution from Hanford sources.

The differencing does not currently apply to impacts based on groundwater concentrations. The groundwater model in SAC, Rev. 0, is not set up to model background concentrations.

A utility code called ImDiff is provided to facilitate differencing the results from the impacts models. This code handles all four impacts models: cultural, ecological, economic, and human. Two computer runs of an impacts model are required to use ImDiff. The impacts runs to be differenced must be identical with the exception of the concentration files they use.

8.1.1   Location in the Processing Sequence

The ImDiff code requires access only to data files developed by the SAC impacts codes. In particular, every code on the left side of Figure 1-2 must have been executed to build a suite of concentration data files, and then one or more impacts codes from the right side of Figure 1-2 must also have been executed.

8.1.2   How the Code Is Invoked

ImDiff can run under either the Windows or the Linux operating system. Under the Windows operating system (Releases 98, NT, or 2000), ImDiff executes in a DOS box. A run of ImDiff is initiated by entering the following command line:

```
ImDiff "Keyfilename"
```

Under the Linux operating system, ImDiff is executed through the following Bourne Shell or C Shell command:

```
imdiff.exe "Keyfilename"
```

For these commands, ImDiff or imdiff.exe is the name of the executable program and "Keyfilename" is the name of a differencing scenario keyword file. Both the name of the executable program and the keyword file may contain path information. If ImDiff is invoked without entering the name of the keyword file, then the code will prompt the user for the file name. The keyword file, which should be prepared using an editor that can handle ASCII files without leaving embedded control codes, contains text control information describing the run. If ImDiff cannot open the keyword file, then the code will terminate execution after writing an error message to the standard output device.

8.1.3 Memory Requirements

The ImDiff code uses dynamic memory allocation, so the memory requirements depend on the problem being analyzed. It is expected that most if not all of the runs of the ImDiff code will require fewer than 1.2 MB of memory.

8.2 File Definitions

The ImDiff keyword file and the report file are unique to the ImDiff code. All other files used by ImDiff were generated by an impacts code (CULTURE, ECEM, HUMAN, or TCERM) or have the same format as files generated by the impacts codes.

8.2.1 Input Files

The input files for the ImDiff code are a keyword file and a suite of impacts files. The following are the input files:

- **ImDiff Keyword File:** The ImDiff keyword file defines which impacts are to be differenced and controls the differencing. An example ImDiff keyword file that differences results for all four impacts models is provided in Table 8.1. Section 8.3 provides definitions for these keywords.
- **CULTURAL Model Files:** The top-level input files for the cultural impacts code are the header files for SACView (see Section 3.3.2.2) for both the background and combined data runs. These files point to the other input files needed for the AREA, MAP, and SITE computation options.
- **ECOLOGICAL Model Files:** The top-level input files for the ecological impacts code are the header files for SACView (see Section 4.3.2.3) for both the background and combined data runs. These files point to the other input files needed for the RESULTS computation option.
- **HUMAN Model Files:** The top-level input files for the human impacts code are the header files for SACView (see Section 5.3.2.3) for both the background and combined data runs. These files point to the other input files needed for the FOOD and IMPACTS computation options.
- **ECONOMIC Model Files:** The top-level input files for the economics impacts code are the header files for SACView (see Section 6.3.2.2) for both the background and combined data runs. These files point to the other input files needed for the CHANGE, EFFECTS, and TRIGGER computation options.

Table 8.1 provides an example ImDiff keyword file that differences results for all four impacts models. The ImDiff code can be used to difference results from any combination of impact models during a single run.

Table 8.1 Example Keyword File for the ImDiff Code

```
REPORT  "Test_01.rpt"
USER    "Paul W. Eslinger"
TITLE   "Test differencing for all impact models in the ImDiff code"
EXECUTE
!
MODEL HUMAN
BACKGROUND  HEADER = "\Test_01\Human\Human_Background.Hdr"
```

```
COMBINED    HEADER = "\Test_01\Human\Human_Combined.Hdr"
DIFFERENCED HEADER = "\Test_01\Human\Human_Differenced.Hdr"
OPTION FOOD
  DETAILS    = "\Test_01\Human\Human_Differenced_Food.Csv"
  STATISTICS = "\Test_01\Human\Human_Differenced_Food_Statistics.Csv"
OPTION IMPACTS
  DETAILS    = "\Test_01\Human\Human_Differenced_Impacts.Csv"
  STATISTICS = "\Test_01\Human\Human_Differenced_Impacts_Statistics.Csv"
ENDMODEL
!
MODEL ECOLOGICAL
BACKGROUND  HEADER="\Test_01\Ecologic\Ecologic_Background.Hdr"
COMBINED    HEADER="\Test_01\Ecologic\Ecologic_Combined.Hdr"
DIFFERENCED HEADER="\Test_01\Ecologic\Ecologic_Differenced.Hdr"
OPTION RESULTS
  DETAILS    = "\Test_01\Ecologic\Ecologic_Dif_Results.Csv"
  STATISTICS = "\Test_01\Ecologic\Ecologic_Dif_Results_Statistics.Csv"
ENDMODEL
!
MODEL ECONOMIC
BACKGROUND  HEADER="\Test_01\Economic\Econ_Bck.hdr"
COMBINED    HEADER="\Test_01\Economic\Econ_Com.Hdr"
DIFFERENCED HEADER="\Test_01\Economic\Econ_Dif.Hdr"
OPTION CHANGE
  DETAILS="\Test_01\Economic\ECHG_01_Dif_Det.Csv"
  STATISTICS="\Test_01\Economic\ECHG_01_Dif_Sta.Csv"
OPTION EFFECTS
  DETAILS="\Test_01\Economic\EFF_01_Dif_Det.Csv"
  STATISTICS="\Test_01\Economic\EFF_01_Dif_Sta.Csv"
OPTION TRIGGER
  DETAILS="\Test_01\Economic\TRIG_01_Dif_Det.Csv"
  STATISTICS="\Test_01\Economic\TRIG_01_Dif_Sta.Csv"
ENDMODEL
!
MODEL CULTURAL
BACKGROUND  HEADER="\Test_01\Cultural\Cult_Bck.hdr"
COMBINED    HEADER="\Test_01\Cultural\Cult_Com.hdr"
DIFFERENCED HEADER="\Test_01\Cultural\Cult_Dif.hdr"
OPTION AREA
  DETAILS="\Test_01\Cultural\Cult_Dif_Det_Area.Csv"
  STATISTICS="\Test_01\Cultural\Cult_Dif_Sta_Area.Csv"
OPTION MAP
  DETAILS="\Test_01\Cultural\Cult_Dif_Det_Map.Csv"
OPTION SITE
  DETAILS="\Test_01\Cultural\Cult_Dif_Det_Sites.Csv"
  STATISTICS="\Test_01\Cultural\Cult_Dif_Sta_Sites.Csv"
ENDMODEL

END
```

8.2.2   Output Files

The output files for the ImDiff code are a report file and a suite of impacts files. The following are the output files:

- **ImDiff Report File:** The ImDiff report file echoes information from the run of the code. Table 8.2 provides an example ImDiff report file for a run that differences results for all four impacts models.
- **CULTURAL Model Files:** The following are the output differenced files for the economic impacts code:
  - o **Header File for SACView** – This file format is described in Section 3.3.2.2
  - o **Area Detailed Data** – This file format is described in Section 3.3.2.3
  - o **Area Summary Statistics** – This file format is described in Section 3.3.2.4
  - o **Map Detailed Data** – This file format is described in Section 3.3.2.5
  - o **Site Detailed Data** – This file format is described in Section 3.3.2.6
  - o **Site Summary Statistics** – This file format is described in Section 3.3.2.7
- **ECOLOGICAL Model Files:** The following are the output differenced files for the ecological impacts code:
  - o **Header File for SACView** – This file format is described in Section 4.3.2.2
  - o **Results Detailed Data** – This file format is described in Section 4.3.2.4
  - o **Results Summary Statistics** – This file format is described in Section 4.3.2.5
- **HUMAN Model Files:** The following are the output differenced files for the human impacts code:
  - o **Header File for SACView** – This file format is described in Section 5.3.2.3
  - o **Food Concentration Detailed Data** – This file format is described in Section 5.3.2.4
  - o **Food Concentration Summary Statistics** – This file format is described in Section 5.3.2.5
  - o **Risk Detailed Data** – This file format is described in Section 5.3.2.6
  - o **Risk Summary Statistics** – This file format is described in Section 5.3.2.7
- **ECONOMIC Model Files:** The following are the output differenced files for the economic impacts code:
  - o **Header File for SACView** – This file format is described in Section 6.3.2.2
  - o **Economic Change Detailed Data** – This file format is described in Section 6.3.2.8
  - o **EconomicChange Summary Statistics** – This file format is described in Section 6.3.2.9
  - o **Effects Detailed Data** – This file format is described in Section 6.3.2.6
  - o **Effects Summary Statistics** – This file format is described in Section 6.3.2.7
  - o **Trigger Detailed Data** – This file format is described in Section 6.3.2.4
  - o **Trigger Summary Statistics** – This file format is described in Section 6.3.2.5

Table 8.2 Example ImDiff Report File That Differences All Four Impacts Models

```
IIIIIII   MM    MM  DDDD      IIIIIII  FFFFFFF  FFFFFFF
   I      M M M M   D    D       I     F        F
   I      M   M   M D      D      I     F        F
   I      M   M   M D        D     I     FFFF     FFFF
   I      M       M D      D       I     F        F
   I      M       M D    D        I     F        F
IIIIIII   M       M DDDD      IIIIIII  F        F
```

```
                         ImDiff     Version 1.00.A.5
                        Last Modified on 19 Feb 2002
                     Hanford and Background Impacts Differencing
                  -------------------------------------------------
                      Systems Assessment Capability, Rev. 0
                    Stochastic Ecological Pathways Risk Analysis
                  -------------------------------------------------
                      Developed By Battelle Memorial Institute
                       Pacific Northwest National Laboratories
                                 Richland, Washington
                  -------------------------------------------------


            Current Run ID = 20020219131143   User Name = Paul W. Eslinger
                  System Date = 02-19-2002   System Time = 13:11:43.441


              The software used to generate this output is experimental
                 and has not been formally tested or peer reviewed.



                                 Review Signatures

Input Prepared By: _____        Date: _____

Input Reviewed By: _____        Date: _____


Problem title for this run
Title: Test a the Economics Model in the ImDiff code


Keyword file for this run
File: "Test_01.key"


User name for this run
User: Paul W. Eslinger


Cultural model information --------------------------------------------

     Cultural background header
     File: "F:\Sac\Codes\ImDiff\Test_01\Cultural\Cult_Bck.hdr"

     Cultural combined header
     File: "F:\Sac\Codes\ImDiff\Test_01\Cultural\Cult_Com.hdr"

     Cultural differenced header
     File: "F:\Sac\Codes\ImDiff\Test_01\Cultural\Cult_Dif.hdr"


Ecological model information ------------------------------------------

     Ecological background header
     File: "F:\Sac\Codes\ImDiff\Test_01\Ecologic\Ecologic_Background.Hdr"
```

```
     Ecological combined header
     File: "F:\Sac\Codes\ImDiff\Test_01\Ecologic\Ecologic_Combined.Hdr"

     Ecological differenced header
     File: "F:\Sac\Codes\ImDiff\Test_01\Ecologic\Ecologic_Differenced.Hdr"

Economic model information -------------------------------------------

     Economic background header
     File: "F:\Sac\Codes\ImDiff\Test_01\Economic\Econ_Bck.hdr"

     Economic combined header
     File: "F:\Sac\Codes\ImDiff\Test_01\Economic\Econ_Com.Hdr"

     Economic differenced header
     File: "F:\Sac\Codes\ImDiff\Test_01\Economic\Econ_Dif.Hdr"

Human model information -------------------------------------------------

     Human background header
     File: "F:\Sac\Codes\ImDiff\Test_01\Human\Human_Background.Hdr"

     Human combined header
     File: "F:\Sac\Codes\ImDiff\Test_01\Human\Human_Combined.Hdr"

     Human differenced header
     File: "F:\Sac\Codes\ImDiff\Test_01\Human\Human_Differenced.Hdr"


-----------------------------------------------------------------------
---------------- Cultural model information processing ---------------
-----------------------------------------------------------------------
. . . (Deleted records)
25 Lines Processed in PROCESS_CULTURAL_AREAS
161 Lines Processed in PROCESS_CULTURAL_MAPS
9 Lines Processed in PROCESS_CULTURAL_SITES


-----------------------------------------------------------------------
---------------- Economic model information processing ---------------
-----------------------------------------------------------------------
. . . (Deleted records)
8 Lines Processed in PROCESS_ECONOMIC_CHANGE
1152 Lines Processed in PROCESS_ECONOMIC_TRIGGER
2176 Lines Processed in PROCESS_ECONOMIC_EFFECTS


-----------------------------------------------------------------------
-------------- Ecological model information processing ---------------
-----------------------------------------------------------------------
. . . (Deleted records)
10051 Lines Processed in PROCESS_ECOLOGIC_RESULTS
```

```
-------------------------------------------------------------------
---------------- Human model information processing ----------------
-------------------------------------------------------------------
. . .
97 Lines Processed in PROCESS_HUMAN_FOOD
51 Lines Processed in PROCESS_HUMAN_IMPACTS
```

8.3   Keyword Definitions for the ImDiff Code

This section defines keywords needed to control the ImDiff code directly. The order in which keywords are entered does not matter for many keywords. Two keywords have a required order of appearance:

- The REPORT keyword must be the first keyword in the file.
- The END keyword must be the last keyword in the file.

The MODEL and ENDMODEL keywords must be paired. The BACKGROUND, COMBINED, DIFFERENCED, and OPTION keywords must be nested within a MODEL … ENDMODEL pair of keywords. Other keywords cannot be used within a MODEL … ENDMODEL pair of keywords.

In the following keyword descriptions, some data are optional and some are required. Required data are enclosed in square brackets. For AB to be required, it would be denoted by [AB]. If only one of the three items AB, BC, CD were required, it would be written as [AB|BC|CD]. The vertical bars indicate a choice of one of the items in the list. Optional items are enclosed in curly brackets; for example, the optional item DE would be denoted by {DE}. The {} or [] symbols are not entered when the keyword is constructed.

In some instances, numerical values or quote strings are associated with a modifier. In this description, the association is indicated by using the equal (=) symbol. The = symbol is not required but may be used when the keyword is constructed. When a numerical value or quote string is associated with a modifier, it must be physically entered on the input line directly after the modifier.

8.3.1   BACKGROUND Keyword for the ImDiff Code

The BACKGROUND keyword is used to point to the header file defining a data set that was generated using only background concentrations in the impact calculations. The following is this keyword's syntax:

```
BACKGROUND [HEADER="quote 1"]
```

The data set is defined by information contained in the header file developed for use by the SACView program. The name of the header file is entered in the quote string.

This keyword is only valid when entered between a MODEL and ENDMODEL pair of keywords and then applies only to the single model type. The following is an example use of this keyword for the human impacts model:

```
MODEL HUMAN
BACKGROUND HEADER= "F:\SAC\Test_01\Human\Human_01.Hdr"
COMBINED keyword
DIFFERENCED keyword
ENDMODEL
```

8.3.2 COMBINED Keyword for the ImDiff Code

The COMBINED keyword is used to point to the header file defining a data set that was generated using both Hanford derived analytes and background analytes in the impact calculations. The following is this keyword's syntax:

```
COMBINED [HEADER="quote 1"]
```

The data set is defined by information contained in the header file developed for use by the SACView program. The name of the header file is entered in the quote string.

This keyword is only valid when entered between a MODEL and ENDMODEL pair of keywords and then applies only to the single model type. The following is an example use of this keyword for the economic impacts model:

```
MODEL ECONOMIC
COMBINED HEADER="F:\SAC\Test_01\Economic\Economic_01.Hdr"
BACKGROUND keyword
DIFFERENCED keyword
ENDMODEL
```

8.3.3 DEBUG Keyword for the ImDiff Code

The DEBUG keyword is used to initiate intermediate data output statements. The following is this keyword's syntax:

```
DEBUG
```

This keyword should not be used when a large data set is being processed because it may result in a very large output file. There are no modifiers or quote strings associated with the DEBUG keyword.

8.3.4 DIFFERENCED Keyword for the ImDiff Code

The DIFFERENCED keyword is used to define the header file that will be created for the difference between a data set that has both Hanford-derived analytes and background analytes in the impact calculations and the data set that has only Hanford-derived analytes. The following is this keyword's syntax:

```
DIFFERENCED [HEADER="quote 1"]
```

The modifier HEADER identifies a file name ("quote 1") for the header file for the differenced data set. SACView can use this header file for data extraction purposes.

This keyword is only valid when entered between a MODEL and ENDMODEL pair of keywords and then applies only to the single model type. The following is an example use of this keyword for the economic impacts model:

```
MODEL ECONOMIC
DIFFERENCED HEADER="F:\SAC\Test_01\Economic\Economic_01.Hdr"
BACKGROUND keyword
COMBINED keyword
ENDMODEL
```

The differenced data is computed by subtracting the data from the background-only run from the correspond data for the combined run. Up to numerical accuracy of the solutions, the differences should be greater than or equal to zero.

8.3.5 END Keyword for the ImDiff Code

The END keyword signifies the end of all keyword data. It should be the last keyword in the keyword file. All data in the keyword file after the END keyword will be ignored. The following is this keyword's syntax:

```
END
```

There are no modifiers or quote strings associated with the END keyword.

8.3.6 ENDMODEL Keyword for the ImDiff Code

The ENDMODEL keyword is used to terminate impact model type associations initiated by a MODEL keyword. The following is the general syntax for the ENDMODEL keyword:

```
ENDMODEL
```

There are no quote strings or modifiers associated with the ENDMODEL keyword.

8.3.7 EXECUTE Keyword for the ImDiff Code

The EXECUTE keyword signifies that the user wishes to perform problem execution. If this keyword is not entered, the inputs are checked for consistency, but the problem will not be executed. This is useful if the run being set up is expected to take a significant amount of computation time. The following is this keyword record's syntax:

```
EXECUTE
```

There are no modifiers or quote strings associated with the EXECUTE keyword.

8.3.8   MODEL Keyword for the ImDiff Code

The MODEL keyword is used to select an impact model type that applies to model associations with the following keywords. The following is the keyword's general syntax:

```
MODEL [HUMAN|ECONOMIC|CULTURAL|ECOLOGICAL]
```

The MODEL keyword must always be paired with an ENDMODEL keyword. Once a MODEL keyword is entered, all BACKGROUND, COMBINED, DIFFERENCED, and OPTION keywords apply only to the chosen model. The following is an example use of this keyword to define inputs for the human impacts model:

```
MODEL HUMAN
```

There are no quote strings associated with the MODEL keyword.

8.3.9   OPTION Keyword for the ImDiff Code

The OPTION keyword is used to define the options for data differencing. The following is the general syntax for the keyword:

```
OPTION [MODIFIER1] [DETAILS= "quote1"] {STATISTICS="quote2"}
```

This keyword is only valid when entered between a MODEL and ENDMODEL pair of keywords and then applies only to the single model type. Table 8.3 describes the modifiers associated with the OPTION keyword.

Table 8.3 Modifiers Associated with the OPTION Keyword in the ImDiff Code

Model	Modifier	Action
Human	IMPACTS	Differencing will be conducted for all of the human impact metrics that were calculated in the previous runs of the HUMAN code. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.
Human	FOOD	Differencing will be conducted for the human food concentration data. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.

Model	Modifier	Action
Cultural	AREA	Differencing will be conducted for all of the area calculations that were evaluated in previous runs of the CULTURE code. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.
Cultural	MAP	Differencing will be conducted for all of the map calculations that were evaluated in previous runs of the CULTURE code. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.
Cultural	SITE	Differencing will be conducted for all of the site proximity calculations that were evaluated in previous runs of the CULTURE code. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.
Ecological	RESULTS	Differencing will be conducted for all of the ecological impact metrics that were calculated in the previous runs of the ECEM code. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.
Economic	CHANGE	Differencing will be conducted for all of the economic change calculations that were evaluated in previous runs of the TCERM code. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.
Economic	EFFECTS	Differencing will be conducted for all of the economic effect calculations that were evaluated in previous runs of the TCERM code. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.
Economic	TRIGGER	Differencing will be conducted for all of the economic trigger calculations that were evaluated in previous runs of the TCERM code. The detailed differenced data will be written to the file name entered in quote1. If the STATISTICS modifier is entered, summary statistics for the differenced data will be computed and written to the file name entered in quote2.

The following is an example set of option keywords for the economic model. In this suite of keywords, summary statistics are not computed for the economic change differenced data.

```
MODEL ECONOMIC
DIFFERENCED keyword
BACKGROUND keyword
COMBINED keyword
OPTION EFECTS DETAILS= "Dif_Eff_Det.csv"
STATISTICS="Dif_Eff_Sta.csv"
OPTION TRIGGER DETAILS= "Dif_Trig_Det.csv"
STATISTICS="Dif_Trig_Sta.csv"
OPTION CHANGE DETAILS= "Dif_Chan_Det.csv"
ENDMODEL
```

8.3.10 REPORT Keyword for the ImDiff Code

The REPORT keyword is used to define the name of the output report (log) file. It must be the first keyword entered in the keyword file. The following is this keyword record's syntax:

```
REPORT ["quote"]
```

The name of the report file is entered in a quote string. The following is an example REPORT keyword record:

```
REPORT "/SAC/SystemCodes/ECEM/Test1.rpt"
```

There are no modifiers associated with the REPORT keyword.

8.3.11 TITLE Keyword for the ImDiff Code

The TITLE keyword is used to define a single-line problem title. The problem title will be written to output files. If the title is not supplied, then the program will error terminate. The following is this keyword record's syntax:

```
TITLE ["quote"]
```

The title is entered in a quote string, which must be enclosed in double quotation marks. Titles up to 72 characters long are supported. The following example defines a title for a run of the code:

```
TITLE "Example title line for the ImDiffcode."
```

There are no modifiers associated with the TITLE keyword.

8.3.12 USER Keyword for the ImDiff Code

The USER keyword is used to identify the user of the program. The user name will be written to output files. If the user name is not supplied, then the program will error terminate. The following is this keyword record's syntax:

```
USER ["quote"]
```

The user name is entered in a quote string, which must be enclosed in double quotation marks. User names up to 16 characters long are supported. The following example defines John Q. Public as the user running the code:

```
USER "John Q. Public"
```

There are no modifiers associated with the USER keyword.

9.0 Keyword Language Syntax

Each line of a keyword data file is parsed into numeric and character data. These are interpreted to set up control information and define input parameters. An input line can contain up to 180 characters of information. Lines longer than 180 characters are truncated to 180 characters.

Every line of the input data file is considered a keyword record, continuation record, or a comment record. Keyword records contain a keyword beginning in column 1. The keyword is used to determine the purpose of the subsequent data. Continuation records are used when a keyword record requires too much data to be placed on one line. Comment lines are ignored by the reading software but are useful for annotating the input file.

The information from each keyword record and subsequent continuation lines is moved into storage arrays. Data that can be deciphered as numeric values are placed into a numeric array. Other data are classified either as "secondary keywords" (called "modifiers") or "quote strings." Secondary keywords are stored as character images in an array. All such keywords or modifiers read from the input file are changed to uppercase before being stored. Quote strings are text strings that are enclosed in double quotation marks. These are stored exactly as they are read from the input file.

9.1 Keyword Records

Keyword records start in column 1 with any letter from A to Z, in either upper- or lowercase. The first eight letters of a keyword are stored in a variable and are used by the modeling software to determine the actions desired by the program user. All subsequent lines of text that do not have an alphabetic character or comment character in column 1 are treated as continuation lines. The following is an example keyword record (where SAMPLEKEY starts in column 1):

```
SAMPLEKEY 2 0 500 1 100
```

The word SAMPLEKEY is the keyword. The numbers 2, 0, 500, 1, and 100 are numeric data.

9.2 Continuation Records

Continuation records start with any valid separator character (except a double quotation mark). These are treated as additional data to the previous keyword record. Section 5.5 identifies valid separator characters. The combined data on a keyword line and on the subsequent continuation line(s) are treated as a single block of information. All numeric values and character strings on those lines are used as input data relevant to the keyword of the keyword line. The two following keyword entries contain the same information:

```
SAMPLEKEY 2 0 500 1 100


SAMPLEKEY 2 0
  500 1 100
```

9.3 Comment Records

Any line with the characters $, !, /, or * in column 1 will be treated as a comment record. These lines are ignored by the input data record reader. Both the $ and the ! can also be used to signify in-line comments (not in column 1). Any information that follows a $ or a ! will be ignored. The * and / characters indicate a comment only if one is the first character on the input line. The * character is also used as a repetition factor in the input. The following are some examples of comment lines:

```
$This is a comment line
/This is a comment line
!This is a comment line
*This is a comment line
```

The following are some examples of in-line comments:

```
SAMPLEKEY 3 4.0 5.0 !Trailing information is ignored after the !
SAMPLEKEY 3 4.0 5.0 $Trailing information is ignored after the $
```

9.4 Input Data Handling

Each line of the input is read and parsed into numeric and character values. All numeric values are converted to real numbers (as opposed to FORTRAN integer). All data that cannot be interpreted as numeric information are stored as character values.

Numeric data can include a leading sign (+ or -), integer characters 0 through 9, a decimal point, and an exponent indication ("E" or "e"). The FORTRAN "double precision" exponent indicator "D" is not valid. A maximum of 10 digits is allowed when entering numeric data.

Secondary keywords, or modifiers, are character strings that could not be interpreted as numeric values. These are converted to uppercase, where necessary, and stored in an array. The number of secondary keywords that are moved into the array is stored for internal use.

Only the first eight characters of any keyword are significant. Keywords fewer than eight characters long are left justified and blank-filled.

9.4.1 Quote Strings

Quote strings are strings of literal text that must be used exactly as given in the input line. They are enclosed by double quotation marks and are typically used for passing file names into a program. Only the first 72 characters of a quote string are saved. Each quote string must begin and end on a single line of the input file. When an unclosed quote is encountered, an implied quote is created at the end of that line. The following is an example of quote string usage:

```
FILE "c:\apps\human\test.dat"
```

9.4.2   Data Separators

Keywords, numeric data, and secondary keywords must be separated by any one of the following data "separators": space character, comma, equal sign, colon, semicolon, left parenthesis, right parenthesis, single quotation mark, double quotation mark, and tab character.

Also, any character with a ASCII character storage code of less than 10 is treated as a separator character. This is used mainly to identify the ASCII tab character as a data separator. Double quotation marks are used differently than the other separators. They indicate text strings that are stored without conversion by the program. Double quotation marks cannot be used as the first character of a continuation line. As an illustration of the use of separator characters, the following keyword records all contain the same information:

```
SAMPLEKEY 3 4.5 5.6 6.7
SAMPLEKEY 3 (4.5,5.6,6.7)
SAMPLEKEY 3 ( 4.5=5.6'6.7 )
SAMPLEKEY 3:4.5  5.6:6.7
```

10.0   Stochastic Variable Generation

Many of the codes in SAC, Rev. 0, generate values for stochastic variables. All of the codes use the same suite of statistical routines to do this generation. The following are some major considerations for this process:

- Each distribution is generated using the Probability Integral Transformation method (Mood et al. 1974, p. 202).
- The uniform number generator uses a linear congruential method (Lewis, Goodman, and Miller 1969).
- Stratified sampling is used when the number of values to be generated is greater than 1.
- Most distributions may be truncated between two limits that are specified as limits in the uniform domain on the interval 0 to 1.
- The user may specify a cumulative distribution function in the form of a table of values.
- Information about a stochastic variable is linked to a unique character ID. Access to all information about the variable is available through use of the variable ID.

The following are the available statistical distributions:

- Constant value
- Uniform distribution between two limits
- Discrete uniform distribution on a set of contiguous integers
- Loguniform (base 10) distribution between two limits
- Loguniform (base e) distribution between two limits
- Triangular distribution defined using a lower limit, mode, and an upper limit
- Normal distribution with a mean and standard deviation
- Lognormal (base 10) distribution specified by the mean and standard deviation of the logarithms of the data
- Lognormal (base e) distribution specified by the mean and standard deviation of the logarithms of the data
- User-specified cumulative distribution function input as a table of probabilities and exceedance values
- Beta distribution that can be shifted and scaled from the standard (0,1) interval
- Log-ratio from a normal distribution
- Hyperbolic arcsine from a normal distribution.

10.1 Stochastic Keyword

The STOCHASTIC keyword is used in each of the impacts codes to enter the definition of a statistical distribution for stochastic variables. The following is the general syntax for the STOCHASTIC record:

```
STOCHASTIC ["Quote1"] [Dist_Index Parameters] {TRUNCATE U1 U2} {"Quote2"}
```

The entry for Quote1 must be a unique character string of up to 20 characters that will be used to identify this stochastic variable in subsequent uses. It is case sensitive and embedded spaces are significant. It is sometimes useful to make the character string some combination of a variable name and other data so that it can be recreated easily when stochastic data is needed. The entry for Quote2 is a description for the stochastic variable that can be up to 64 characters long and is used for output labeling purposes. The entry for Quote2 is optional.

The entry for Index must be an integer in the range 1 to 13 that identifies the index of a statistical distribution. The statistical distributions are defined in Table 10.1. The word Parameters in the general syntax statement indicates the numerical values of parameters required for defining the statistical distribution. The additional modifier TRUNCATE can be used for all distribution types except 1, 3, and 10. If TRUNCATE is entered, it must be followed by two values in the interval 0 to 1, inclusive. The lower value must be less than the upper value. These two values specify the tail probabilities at which to impose range truncation for the distribution. Truncation data must be entered after all of the other parameters that define the distribution.

Table 10.1 Statistical Distributions Available in All Impacts Codes

Index	Distribution	Truncate	Parameters Required
1	Constant	No	Single value.
2	Uniform	Yes	Lower limit, upper limit.
3	Discrete Uniform	No	Smallest integer, largest integer.
4	Loguniform (base 10)	Yes	Lower limit, upper limit.
5	Loguniform (base e)	Yes	Lower limit, upper limit.
6	Triangular	Yes	Lower limit, mode, upper limit.
7	Normal	Yes	Mean, standard deviation.
8	Lognormal (base 10)	Yes	Mean, standard deviation of logarithms.
9	Lognormal (base e)	Yes	Mean, standard deviation of logarithms.
10	User Defined	Yes	Number of pairs, data for pairs of values $(Prob(X_i),X_i)$.
11	Beta	Yes	Alpha, beta, lower limit, upper limit. The mean of the distribution would be alpha/(alpha+beta) if the limits were 0 and 1.
12	Log ratio	Yes	Mean, standard deviation (of normal), lower limit, upper limit.
13	Hyperbolic arcsine	Yes	Mean, standard deviation (of normal).

The following is an example stochastic keyword for a variable assigned a constant of 234.432:

```
STOCHASTIC "Unique1" 1 234.432 "Define a constant distribution"
```

The constant can take any value.

The following is an example stochastic keyword for a variable assigned a uniform distribution on –2 to 7:

```
STOCHASTIC "Unique2" 2 -2.0 7 "Define a uniform distribution on -2 to 7"
```

The two limits can take any values as long as the second value is strictly greater than the first value.

The following is an example stochastic keyword for a variable assigned a discrete uniform distribution on the integers 6 to 70:

```
STOCHASTIC "Unique3" 3 6 70 "Discrete uniform distribution on 6 to 70"
```

The two limits must be integers where the second integer is strictly greater than the first integer.

The following is an example stochastic keyword for a variable assigned a loguniform (base 10) distribution on the interval 10^{-7} to 10^{-3}:

```
STOCHASTIC "Unique4" 4 1.0E-7 1.0E-3
    "Define a loguniform (base 10) distribution on 0.0000001 to 0.001"
```

The two limits must both be greater than zero and the second limit must be greater than the first limit.

The following is an example stochastic keyword for a variable assigned a loguniform (base e) distribution on the interval 10^3 to 10^6:

```
STOCHASTIC "Unique5" 5  1.0E3  1E+6
    "Define a loguniform (base e) distribution on 1000 to 1000000"
```

The two limits must both be greater than zero and the second limit must be greater than the first limit.

The following is an example stochastic keyword for a variable assigned a triangular distribution with a minimum of 2, a mode of 3, and a maximum of 7:

```
STOCHASTIC "Unique6" 6  2 3 7  "Triangular distribution on (2,3,6)"
```

The three values that define the triangular must all be different, and they must be entered in increasing order.

The following is an example stochastic keyword for a bioconcentration factor that is normally distributed with a mean of 125 and a standard deviation of 5 for a frog exposed to ^{14}C:

```
STOCHASTIC "BCFC14Frog" 7  125.0  5.0  "Example normally distributed frog"
```

The mean value can be any number, but the standard deviation must be greater than zero.

The following keyword would define a different stochastic variable from the one just entered because the identification string (Quote1) is case sensitive:

```
STOCHASTIC "BCFC14FROG" 7  125.0  5.0  "Example normally distributed frog"
```

The following keyword entry would define a lognormal (base 10) distribution where the mean and standard deviation (of the logarithms) are –2.0 and 0.5:

```
STOCHASTIC "Unique8"  8  -2  0.5 "Lognormal (base 10) variable"
```

The mean value can be any number, but the standard deviation must be greater than zero.

The following keyword entry would define a lognormal (base e) distribution where the mean and standard deviation (of the logarithms) are –2.0 and 0.5. In addition, the lognormal distribution will be truncated between the lower 0.025 and upper 0.99 probabilities.

```
STOCHASTIC "Unique9" 9 -2 .5 TRUNCATE 0.025 0.99
    "Example for a truncated lognormal variable"
```

The mean value can be any number, but the standard deviation must be greater than zero.

The following keyword entry illustrates the use of the user-defined distribution (distribution type 10). This example entry uses seven pairs of values. The first pair of numbers uses a probability of 0 to define the lower limit of the distribution at 8.4 E-7. The last pair of numbers uses a probability of 1 to define the upper limit of the distribution at 1.73E-6. The other values are associated with the probability levels of .025, .167, .5, .833, and .975. The probability data and distribution percentiles must be entered in strictly increasing order.

```
STOCHASTIC "Sr90Con" 10  7
   0  8.40E-7
   2.50E-02  9.20E-7
   1.67E-01  1.06E-6
   5.00E-01  1.21E-6
   8.33E-01  1.37E-6
   9.75E-01  1.58E-6
   1  1.73E-6
```

The first pair of numbers uses a probability of 0 to define the lower limit of the distribution. The last pair of numbers uses a probability of 1 to define the upper limit of the distribution. The intervening pairs define probability levels and the associated data values. The probabilities and data values must be entered in strictly increasing order.

The following keyword entry would define a beta distribution with parameters 1.1 and 2.1 on the interval (0,1):

```
STOCHASTIC "Unique11-1"  11  1.1  2.1  0.0  1.0
    "Beta (1.1,2.1) on the interval 0,1"
```

Let the first parameter be denoted by α and the second parameter be denoted by β. The mean of the beta distribution would be $\alpha/(\alpha+\beta)$ if the limits were 0 and 1. Both α and β must be greater than zero. The lower limit must be less than the upper limit.

The following keyword entry would define a beta distribution with parameters 1.1 and 2.1 but on the interval –2 to 4:

```
STOCHASTIC "Unique11-2"  11  1.1  2.1  -2.0  4.0
   "Beta (1.1,2.1) on the interval (-2,4)"
```

The following keyword entry would define a log ratio distribution from a normal (-1.459,1.523) distribution on the interval -5.756 to 4.33:

```
STOCHASTIC "Test1203" 12 -1.459  1.523 -5.756 4.330
   "Log ratio from Normal(-1.4,1.5) on (-5.756,4.330)"
```

The entry for the normal standard deviation (a value of 1.523 in this example) must be greater than zero. The last two numerical values define the interval for the generated values, so the lower limit must be smaller than the upper limit.

The following keyword entry would define a hyperbolic arcsine distribution from a normal (0.189,0.146) distribution:

```
STOCHASTIC "Test1302" 13 0.189  0.146
   "Hyperbolic Arcsine from Normal(0.189,0.146)"
```

The entry for the normal standard deviation (a value of 0.189 in this example) must be greater than zero.

10.2 Probability Concepts

The distribution of a continuous random variable X (the term *continuous* indicates that the random variable is defined over a continuum of values) is completely described by its probability density function, f(x). The interpretation of the probability density function is that the area under f(x), for an interval a<x<b, equals the probability that the random variable, X, will fall in the interval (a,b), denoted P[a<X<b]. One cannot make the statement P[X=t], because there is no area under the probability density function at any given point. Two axioms of probability theory (Mood et al. 1974, p. 22) are that the probability of any event is between zero and one, and the integral of the probability density function over the entire support (the interval [L,U]) of X equals 1. The integral of the probability density function from the lower bound L to some value x (suppose it is less than the upper bound U) represents the probability that X will be observed in the interval (L,x). This integral operation defines the cumulative distribution function for the random variable X. The cumulative distribution function is denoted by F(x) (the capital F for the cumulative distribution function corresponds to the lowercase f for the probability density function) and mathematically is represented by:

$$F(x) = \int_{L}^{U} f(s)ds$$

The inverse cumulative distribution function, $[F^{-1}(\bullet)]$, is single-valued if x is in the interval (L,U). Hence if p'= F(x') is known, in theory x'= F^{-1}(p') can be obtained.

10.3 Probability Integral Transform Method

Generation of a random variable from a given distribution typically involves the use of information either about f or F. There are two philosophical approaches to generating random numbers: exact methods and approximate methods. The algorithms embedded in SAC employ exact methods. Exact methods can be further categorized into probability integral transform methods and functional methods. The probability integral transform method is employed in SAC.

In the probability integral transform method, the random variable of interest is expressed as a function of a U(0,1) random variable, where U(0,1) denotes the continuous random variable ranging uniformly over the interval (0,1). The probability density function of the uniform random variable is g(u)=1 if u∈(0,1) and is zero elsewhere. The cumulative distribution function for this random variable takes the exceedingly simple form G(u)=u. It can be shown that any cumulative distribution function evaluated at a random value X (instead of being evaluated at a known value x as in the previous discussion) is distributed uniformly over the interval (0,1) (Mood et al. 1974, p. 202). Therefore, given a realization u of the U(0,1) random variable and a selected statistical distribution (known cumulative distribution function), one can set u=F(x) and solve to obtain x=F^{-1}(u). The value x thus obtained is a random realization from the selected statistical distribution.

In principle, one can obtain an exact solution for x given any specific cumulative distribution function and value u. In reality, there exist some distributions, such as the normal and beta distributions, for which no closed-form analytical expression for F^{-1} exists, and hence approximation methods must be applied.

The probability integral transform method allows efficient sampling from a subregion of the interval (L,U), such as (c,d), where L<c<d<U. In this case one would find the corresponding interval in the uniform domain, say (c',d'), and sample uniformly over that interval, by sampling from the rescaled uniform distribution [for example, u'=(d-c)u+c] and then obtaining x as usual using x=F^{-1}(u'). The rescaled uniform distribution takes the form g(u)=1/(d'-c') for u∈(c',d') and is zero elsewhere. For any distribution with probability density function f(x) and cumulative distribution function F(x), the probability density function, under truncation to the interval (c,d), is f_T(x) = f(x)/[F(d)-F(c)]. The divisor ensures that f_T(x) integrates to unity.

10.4 Stratified Sampling

Stratified sampling can easily be implemented when generating random deviates using the probability integral transform method. This is accomplished by dividing the uniform interval (0,1) into subintervals, or strata, and sampling a specified number of times within each stratum, each time obtaining the corresponding value of x. Within SAC, the strata intervals are assigned equal probability, and exactly one value is sampled within each stratum. The method generates samples from each stratum, and then randomly shuffles the entire set of realizations using a variation of the Quicksort algorithm (Singleton 1969). The primary purpose of stratified sampling is to achieve more evenly spaced (in a probability sense) samples from the distribution of a random variable than would result from randomly sampling over the whole range of the distribution. Iman and Conover (1982) have shown that stratified sampling can result in more efficient estimation of simulation results for a variety of estimators than when using simple random sampling.

10.5 Generation Algorithms

Table 10.1 summarizes the statistical distributions available in the SAC codes. The following paragraphs describe the generation algorithms.

10.5.1 Algorithm for the Uniform Distribution

Algorithms that generate truly random uniform numbers do not exist, although many algorithms generate pseudo-random deviates (hereafter loosely referred to as random numbers). The selection of a random-number generator is based on four considerations: 1) computer implementability, 2) degree of independence within a sequence of deviates, 3) periodicity or cyclic length of a sequence, and 4) uniform coverage of sequences (occurrence) over the interval (0,1), the square (0,1) X (0,1), etc., up to the hypercube (0,1) in k dimensions.

Commonly used random-number generation techniques on digital computers involve feedback shift register and linear congruential methods (Kennedy and Gentle 1980, pp. 136, 150). The SAC codes use a linear congruential random number generator. The linear congruential generator generates random integers from an algorithm of the form $S_i = (A \cdot S_{i-1} + C) \mod M$. where S_i is the ith generated random integer, A and C are constants, M is the modulus of the generated integers, and mod denotes the remainder function. These integers are converted to approximate uniform (0,1) numbers by the division $U_i = S_i / M$.

The period of a sequence $\{U_i\}$ of generated deviates is the minimal value k such that $U_i = U_{i+k}$ (this occurs independent of i for linear congruential generators). It can be shown that the period of any congruential generator does not exceed M. Therefore, if one is generating many uniform deviates, it is desirable that M be large. The performance of each congruential generator (each choice of A, C, and M) can thus be examined with respect to criteria proceeding from the four considerations given above. The SAC implementation uses A=16807, C=0, and M=2147483647. These choices yield a sequence $\{U_i\}$ that 1) is implementable on a 32-bit computer without machine language coding, 2) is sufficiently independent on an element-by-element basis, 3) possesses a long cycle (period), and 4) has a reasonable degree of coverage over all hypercubes of dimension less than k. These conclusions proceed from results from tests described in Fishman and Moore (1986).

Any value, x, generated from the uniform (a,b) distribution in the SAC codes makes use of a value, y, from the U(0,1) distribution. The value y is first generated, and then x is evaluated as x=a+(b-a)y. The uniform (a,b) distribution will be denoted by U(a,b).

10.5.2 Algorithm for the Discrete Uniform Distribution

The probability density function for the discrete uniform distribution is f(x)=1/N for each of the N integers ranging in the interval L to U. The generation algorithm for the discrete uniform distribution is:

$$F^{-1}(u) = L + \text{int}[u(U - L + 1)]$$

where the int($\cdot$) function returns the integer portion of its argument.

10.5.3 Algorithm for the Loguniform Distribution

The probability density function for the loguniform random variable of base b is:

$$f(x) = \frac{I(b^c < x < b^d)}{x(d-c) \bullet \ln(b)}$$

for $-\infty < c < d < \infty$, where I is an indicator function (0 if false, 1 if true), b is the logarithm base (either 10 or the natural constant e), and ln(b) denotes the natural logarithm of b.

The inverse cumulative distribution function algorithm used to generate a value, x, from the loguniform distribution first generates a value, y, from the U(c,d) distribution and then evaluates the expression $x=b^u$.

10.5.4 Algorithms for the Triangular Distribution

The triangular distribution has probability density function:

$$f(x) = \begin{cases} 2(x-a)/[(b-a)(c-a)] & \text{for} \quad a < x \le b \\ 2(c-x)/[(c-b)(c-a)] & \text{for} \quad b \le x < c \end{cases}$$

and takes the value 0 elsewhere.

The following equation provides the generation algorithm for the triangular distribution:

$$F^{-1}(u) = \begin{cases} a + \sqrt{u(c-a)(b-a)} & \text{for} \quad 0 \le u \le (b\text{-}a)/(c\text{-}a) \\ c - \sqrt{(1-u)(c-a)(c-b)} & \text{for} \quad (b\text{-}a)/(c\text{-}a) \le u \le 1 \end{cases}$$

10.5.5 Algorithms for the Normal Distribution

A normal (μ, σ^2) random deviate, y, is obtained by generating a N(0,1) deviate, x, and then transforming that value using the equation $y=\mu+\sigma x$. The normally distributed random variable with mean μ and variance σ^2, denoted as $N(\mu, \sigma)$, has the probability density function:

$$f(x) = \frac{e^{-(x-\mu)^2/(2\sigma^2)}}{\sigma\sqrt{2\pi}}$$

for $-\infty < x < \infty$, $-\infty < \mu < \infty$ and $\sigma > 0$.

The inverse cumulative distribution function for the N(0,1) random variable does not have a closed form expression. It is approximated by:

$$F^{-1}(p) = \begin{cases} q\,A(q^2)/B(q^2) & \text{for } |q| < 0.42 \\ \text{sgn}(q)C(r)/D(r) & \text{otherwise} \end{cases}$$

where q=p-0.5, and r=$\sqrt{\ln(0.5-|q|)}$. The quantity (0.5-|q|) is formed as p or, to avoid cancellation if p is small, as (1-p). The letters A, B, C, and D represent polynomials of order 3, 4, 3, and 2, respectively, whose coefficients are given in Beasley and Springer (1985), and sgn(q)=1 if q>0 and -1 if q<0.

10.5.6 Algorithms for the Lognormal Distribution

The logarithm of a random variable that is lognormally distributed is distributed as a normal $N(\mu, \sigma^2)$ random variable (thus the name lognormal). The probability density function of the lognormal distribution is:

$$f(x) = \frac{A}{x\sigma\sqrt{2\pi}} e^{-[\log(x)-\mu]^2/2\sigma^2}$$

for x>0 and σ>0. Because this distribution is available in both base 10 and natural logarithm base form, the constant A is $1/\log_e 10$ for base 10 and 1 for the natural logarithm base. The logarithm log(x) is also evaluated in terms of the chosen base.

A lognormal random variable, x, is generated using a two-step process. First, a value, y, is generated from the $N(\mu, \sigma^2)$ distribution. This value is then used in the expression x=b^y, where the base b is either 10 or the natural constant e as desired.

10.5.7 Algorithms for the User-Defined Distribution

In addition to selecting from parametric families of distributions, the user may implement any other distribution by supplying a table of data pairs corresponding to the pairs [F(x),x]. Thus, the user provides the SAC code with discrete evaluations of the cumulative distribution function. The algorithm linearly interpolates between these points to solve for F^{-1} when generating a random deviate.

10.5.8 Algorithms for the Beta Distribution

The beta random variable, x, is described by the probability density function:

$$f(x) = \frac{x^{p-1}(1-x)^{q-1}}{B(p,q)}$$

for p>0, q>0, and 0<x<1. This variable can be transformed to the interval (a,b) and the resulting probability density function for the random variable, y, takes the form:

$$f(x) = \frac{(b-a)^{-(p+q+1)}(y-a)^{p-1}(b-y)^{q-1}}{B(p,q)}$$

for p>0, q>0, and a<y<b. The second expression for the probability density function can be obtained from the first by the change of variable y=(b-a)x+a.

A closed form expression for the beta inverse cumulative distribution function does not exist. The algorithm implemented is provided in Algorithm AS 64/AS 109 (Griffiths and Hill, 1985, p. 121). Algorithm AS 64/AS 109 requires the logarithm of B(p,q). Using the relationship between the beta and gamma functions (Mood et al. 1974, p.535), B(p,q)=G(p+q)/{G(p)G(q)}, where G(·) denotes the gamma function, the logarithm of B(p,q) is computed using Algorithm ACM 291 (Pike and Hill, 1966). Algorithm AS 64/AS 109 uses approximate starting values and a Newton-Rhapson iterative method to achieve a final solution.

10.5.9 Algorithms for the Log Ratio Distribution

Let y denote a random variable from the log ratio distribution on the interval (a,b). The probability density function for y is:

$$f(y) = \frac{(b-a)e^{-(\ln\{(y-a)/(b-y)\}-\mu)^2/(2\sigma^2)}}{\sigma(y-a)(b-y)\sqrt{2\pi}}$$

where a<b and a<y<b.

A random variable, y, from the log ratio distribution is generated using a two-step process. First, a value, x, is generated from the $N(\mu,\sigma^2)$ distribution. This value is then used in the expression:

$$F^{-1}(x) = \frac{a+be^x}{1+e^x}$$

10.5.10 Algorithms for the Hyperbolic Arcsine Distribution

Let the random variable x be a normally distributed random variable with mean μ and variance σ^2. Then, let y be a random variable defined as $y = \sinh^{-1}(x)$. The probability density function for y is:

$$f(y) = \frac{0.5(e^u + e^{-u})e^{-(\sinh(y)-\mu)^2/(2\sigma^2)}}{\sigma\sqrt{2\pi}}$$

for $-\infty<y<\infty$, $-\infty<\mu<\infty$ and $\sigma^2>0$.

A random variable, y, from the hyperbolic arcsine distribution is generated using a two-step process. First, a value, x, is generated from the $N(\mu,\sigma^2)$ distribution. This value is used in the expression:

$$F^{-1}(x) = \sinh(x)$$

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