SALMOD

A Population Model
For Salmonids

USERS' MANUAL

Version W3
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By

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INTRODUCTION

SALMOD is a computer model that simulates the dynamics of freshwater salmonid populations, both anadromous and resident. The conceptual model was developed in a workshop setting (Williamson et al. 1993) using fish experts concerned with Trinity River chinook restoration. The model builds on the foundation laid by similar models (see Cheslak and Jacobson 1990). The model's premise is that egg and fish mortality are directly related to spatially and temporally variable micro- and macrohabitat limitations, which themselves are related to the timing and amount of streamflow and other meteorological variables. Habitat quality and capacity are characterized by the hydraulic and thermal properties of individual mesohabitats, which we use as spatial "computation units" in the model. The model tracks a population of spatially distinct cohorts that originate as eggs and grow from one life stage to another as a function of local water temperature. Individual cohorts either remain in the computational unit in which they emerged or move, in whole or in part, to nearby units (see McCormick et al. 1998). Model processes include spawning (with redd superimposition and incubation losses), growth (including egg maturation), mortality, and movement (freshet-induced, habitat-induced, and seasonal). Model processes are implemented such that the user (modeler) has the ability to more-or-less program the model on the fly to create the dynamics thought to animate the population. SALMOD then tabulates the various causes of mortality and the whereabouts of fish.

SALMOD's premise is that physical habitat components (flow dependent micro-habitat and water temperature) are the principal factors limiting the freshwater production. The question of food resources looms as a large question. This model essentially assumes (1) that a stream's underlying food production and delivery processes are inherent to the stream, (2) that production and delivery have been accounted for in the quantification of mesohabitat versus flow relationships through depth, velocity, substrate, and cover requirements, and (3) that these relationships will not be altered by the flow and temperature scenarios explored by the model. In particular, acceptable or preferred habitats are assumed to be those that maximize fitness, including the benefits of maximizing growth potential and minimizing predation risk. Therefore, mesohabitat types with more quantifiably suitable habitat have a higher capacity than those that do not. When these assumptions are not appropriate, SALMOD should either not be the model of choice, or be modified to incorporate new relationships.

In this document, we outline the essential features of the model using examples derived from a Trinity River, California, chinook salmon (*Oncorhynchus tshawytscha*) population. Selected examples from resident trout models are also included. For a more complete understanding of the conceptual basis for SALMOD, and examples from applications, please see the References section at the end of this document.

MODEL DESCRIPTION

Model Resolution

SALMOD is best explained by describing its fundamental structure in terms of temporal, spatial, and biological resolution. These three components are not independent; the size of any computational unit (spatial resolution) has a direct bearing on the distance a fish of a given size (biological resolution) needs to move within one time step (temporal resolution) to encounter alternate habitat conditions. The scale of resolution also affects the way model processes are envisioned and implemented, their assumptions, and their limitations.

Temporal Resolution. We employ a weekly time step for one or more biological years. Biological years typically (but not mandatorily) start with the first week of spawning. All rate parameters (e.g., growth and mortality) are weekly values unless otherwise stated. Physical state variables (e.g., streamflow and water temperature) are represented by weekly averages.

Spatial Resolution. Spatial resolution is consistent with the mesohabitat inventory approach, in which the study area is classified and mapped as discrete mesohabitat types, intermediate between micro- and macrohabitat, that tend to behave similarly in response to discharge fluctuations. Classification is based primarily on channel structure and slope, modified by the general distribution of microhabitat, including cover. These mesohabitat units become the model's computational units.

Streamflow, water temperature, and mesohabitat type are the physical state variables included in this model. The stream can be divided into flow and temperature segments, (i.e., where flows and temperatures are roughly homogeneous) either by distance or by computational unit. Flow and temperature data are organized by river segments and by time step for each segment. Habitat quality is defined by a flow versus habitat relationship for each mesohabitat type.

Currently, SALMOD only sees a linear stream, with no tributaries or branches possible. However, various options control what happens to fish moving out of the collection of computational units defining the study area, either upstream or down.

Biological Resolution. The biological resolution is fairly standard in the sense that we employ a typical categorization of fish life history related to physical morphology, behavior, and reproductive potential (see Figure 1). Fish in the simulated population are tracked by cohorts within computational units. Each cohort is classified by life stages, and class within life stages (Table 1). Life stages 1-4 are adult life stages, defined and ordered as: Male Adult, Male Spawner, Female Adult, and Female Spawner. Adult life stages cannot be further divided. Juvenile life stages can be divided into classes. Life stage 5 is reserved for egg life stages, and is classified by percent development (deposition [0] to emergence [100]). Life stages six through twelve are non-adult life stages classified by size (Table 1). The number of juvenile size classes and their definition can vary, but at least 1 size class must be used to describe each non-adult life stage. As a cohort grows, its life stage and size class attributes are modified when it graduates (or matures) to the next size class or life stage.

The various rate parameters (e.g., growth, mortality) can depend on life stage and class. Non-adult cohorts are tracked individually within a computational unit, but any given cohort's identity may be lost when part or the entire cohort moves into a different computational unit.

Several variables are tracked for each cohort throughout the model, including:
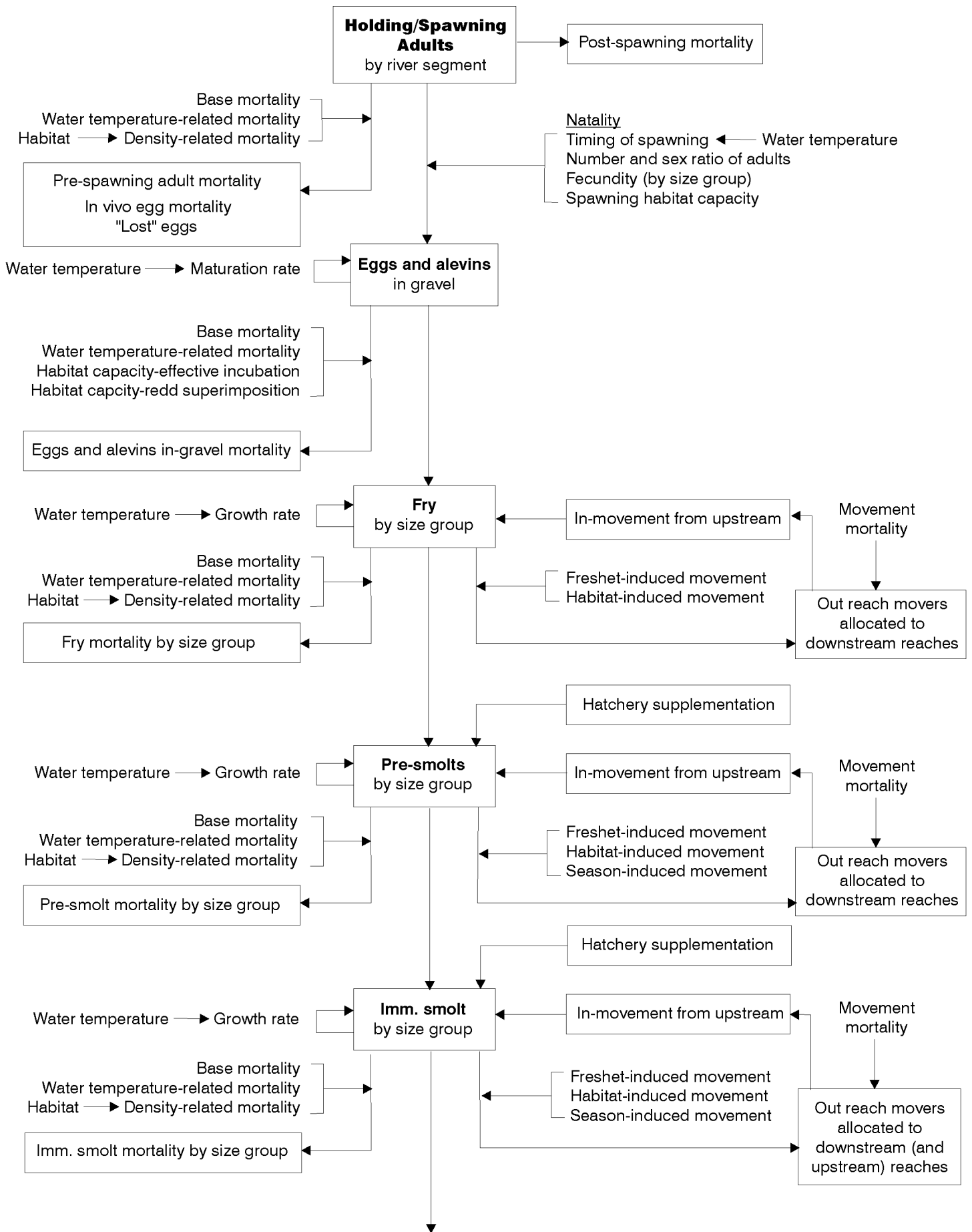
- Number of eggs or fish
- Average weight and length of fish
- Percent egg development (deposition to emergence)
- Number of redds composing an egg cohort
- Number of *in vivo* eggs per gravid spawning female
- Life stage and class of the cohort
- Effective incubation area

Variables are defined only for appropriate cohorts (e.g., the *in vivo* eggs variable only applies to spawning females). Individual measurements such as weight, length, and number of *in vivo* eggs represent the average value for the cohort. Fish growth is computed in weight; length is determined from a weight:length relationship, with the exception that a loss in weight does not result in a loss of length. Fish must regain lost weight prior to new growth in length. Biomass of each cohort is defined for non-egg cohorts as the number in the cohort times the average weight of individuals in the cohort. Biomass of each life stage is the sum over all cohorts in that life stage.

SALMOD is integer based, i.e., only whole animals are ever born or die. This integer formulation was chosen for three reasons. First, so small numbers of fish could be modeled realistically, second, so computations would be as fast as possible, and third, so people quit asking why the model is dealing with fractional animals! Note, however, that just because SALMOD can simulate small numbers of fish does not mean that it is wise to do so. Because the model is deterministic, it relies on parameters that represent population means derived, or supported, by the "law of large numbers". When population numbers are low, mean responses are quickly swamped by environmental stochasticity and individual variability, things that SALMOD was not designed to handle.

Table 1. Example life stage and class structure definition of an anadromous salmonid population along with the model's order of calculation. Classes are defined by percent development (deposition to emergence) for egg stage and by length (mm) for all other life stages.

Life stage name	Calculation order	Class	Class definition		
Spawner	2	sf	Spawning Female		
	4	sm	Non-Spawners		
Adult	1	af	Female		
	3	am	Male		
Egg/Alevin	5	1	0.0%	to	33.3%
		2	33.3%	to	66.7%
		3	66.6%	to	100.0%
Fry	6	f1	34 mm	to	38 mm
		f2	38 mm	to	50 mm
Pre-smolt	7	p1	50 mm	to	60 mm
		p2	60 mm	to	70 mm
		p3	70 mm	to	80 mm
Immature-smolt	8	i1	80 mm	to	90 mm
		i2	90 mm	to	110 mm

Holding/Spawning Adults
by river segment

Post-spawning mortality

Base mortality
Water temperature-related mortality
Habitat → Density-related mortality

Natality
Timing of spawning ◄— Water temperature
Number and sex ratio of adults
Fecundity (by size group)
Spawning habitat capacity

Pre-spawning adult mortality

In vivo egg mortality
"Lost" eggs

Water temperature → Maturation rate

Eggs and alevins
in gravel

Base mortality
Water temperature-related mortality
Habitat capacity-effective incubation
Habitat capcity-redd superimposition

Eggs and alevins in-gravel mortality

Water temperature → Growth rate

Fry
by size group

In-movement from upstream

Movement mortality

Base mortality
Water temperature-related mortality
Habitat → Density-related mortality

Freshet-induced movement
Habitat-induced movement

Out reach movers allocated to downstream reaches

Fry mortality by size group

Hatchery supplementation

Water temperature → Growth rate

Pre-smolts
by size group

In-movement from upstream

Movement mortality

Base mortality
Water temperature-related mortality
Habitat → Density-related mortality

Freshet-induced movement
Habitat-induced movement
Season-induced movement

Out reach movers allocated to downstream reaches

Pre-smolt mortality by size group

Hatchery supplementation

Water temperature → Growth rate

Imm. smolt
by size group

In-movement from upstream

Movement mortality

Base mortality
Water temperature-related mortality
Habitat → Density-related mortality

Freshet-induced movement
Habitat-induced movement
Season-induced movement

Out reach movers allocated to downstream (and upstream) reaches

Imm. smolt mortality by size group

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Model Processes

SALMOD represents the freshwater population dynamics of three life history variants: (1) an anadromous fish species that returns to the stream as an adult to spawn, (2) a resident population of salmonids that complete their entire life cycle in freshwater, or (3) a multiyear variant where juvenile fish remain in the stream for more than one year. The focus is on biological processes that affect the early lifestages of the species. The model simulates (1) spawning, (2) egg development and growth, (3) movement, induced by freshets, time of year, or living space constraints, and (4) various types of mortality. In the *anadromous* variant, adults die after spawning and smolts do not graduate to the adult stage; instead they exit the study area. Thus the population is re-initialized for each biological year. Life history patterns where the juveniles spend more than one year in freshwater are simulated with the *multiyear* variant; this option is much like the *anadromous* variant except that juvenile fish remain in the stream beyond a single biological year. In the *resident* variant, adults do not die after spawning and a juvenile lifestage (e.g., yearlings) may mature to adults capable of spawning.

Each computational process is applied sequentially to each individual cohort for all spatial computational units for a single time step. The model defines the simulation processes and how they function, but the user has a great deal of flexibility over those processes including their execution order and other options useful in hypothesis testing. However, the order of calculations is not always benign. For example, having adult females move before and independently of adult males can influence their effective mortality rates slightly. Some other processes result in stochastic mortality in certain situations. Differences in results, however, should be small.

MODEL IMPLEMENTATION

The SALMOD program is implemented in FORTRAN 90 with a user interface that has been written in C++. The model is almost 100% data-driven, giving the client thorough control over the definition of the life history descriptors and the linking of the life history to the model processes. Data input has been designed to be flexible using a "free format" approach to input data arrays, thus facilitating data import from a wide variety of data base management and spreadsheet software. Data output consists of a variety of graphs and tables. Like the input data formats, output data are arranged to expedite and encourage transfer to other postprocessing software for subsequent analysis or display.

Memory and Hardware Requirements

The executable files associated with SALMOD and its output may require up to 5 megabytes of disk space. We recommend that the user allot 10 megabytes of disk space just for safety's sake. The fastest machine available is recommended to decrease run times and make your use of SALMOD more enjoyable and efficient. A screen resolution of at least 1024 x 768 is recommended.

Installing SALMOD

Install SALMOD like any other Windows-based program.

Running SALMOD

SALMOD is structured to run as most Windows programs, with one exception. The WordPad editor is used to view and edit the array of SALMOD input files, and to view the output files. Therefore WordPad must be available on your computer. You may find it advantageous to change WordPad's default margins to ½ inch to reduce word-wrap in SALMOD's output files. This is done by choosing **File|Page Setup** from Wordpad's menu.

The general sequence of events in running SALMOD is to open one of the special Files.Dat files that contains a list of input files for a SALMOD project, edit one or more of the input files, run the model, look at the graphic and tabular results, and repeat the process, often as part of a calibration or scenario analysis procedure. This documentation will not describe each step. Note that it is usually wise to start with a working set of files to be modified, as the complete set-up can be a daunting task. You cannot create a new set of input files from within SALMOD. If any of the input files are missing, SALMOD will not open the project.

The main window for SALMOD looks as shown below. One may open a Files.Dat type file using either **File|Open**, the toolbar button, or one of the files in the *Most Recent Files* list, also found under the **File** menu. **File|Preferences** provides access to a color menu for choosing graph curve colors of your liking.
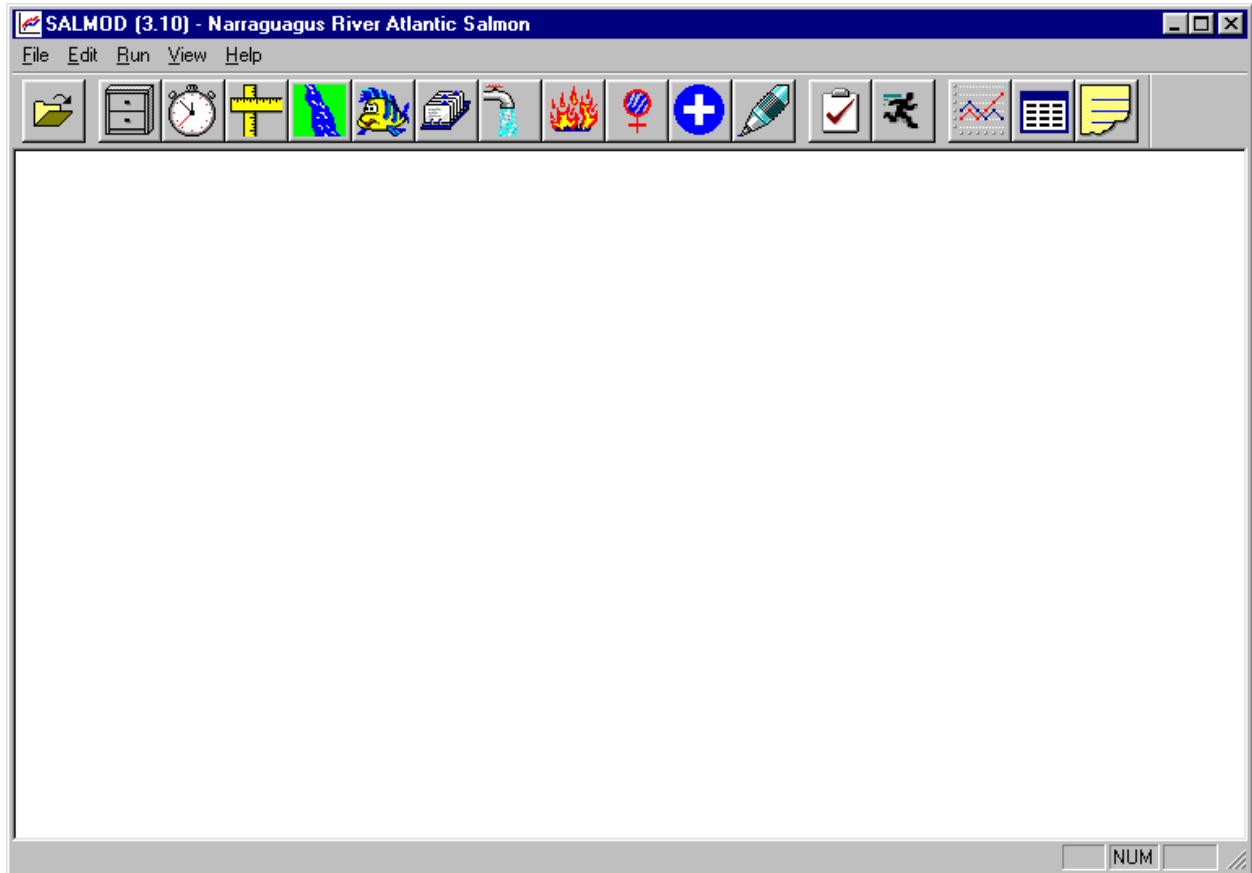
Once a proper Files.Dat is open, successfully read, and all of the files in the list exist, you will find access to each of the editable input files for the SALMOD project under the **Edit** menu:

or via the appropriate button on the toolbar. Holding the mouse cursor over the toolbar buttons will reveal each buttons' specific purpose, also shown in the status bar at the bottom of the main screen. Clicking on the appropriate file or button will transfer control to WordPad so you can look at or edit that file. You may leave any or all input files open on your desktop while you run the SALMOD model, but SALMOD will only use values from those files that have been permanently saved to your hard drive. Since this can become confusing, we recommend keeping

a minimum number of files open at once and saving the contents frequently. If WordPad asks you what format to use to save the file, always choose *Text.*

Also note that if you edit and change file names in FILES.DAT, those names are not available to the SALMOD user interface unless you save the FILES.DAT file to disk before editing them or running the model.

Choosing **Run|Options** brings up an additional menu with the default choices shown below:
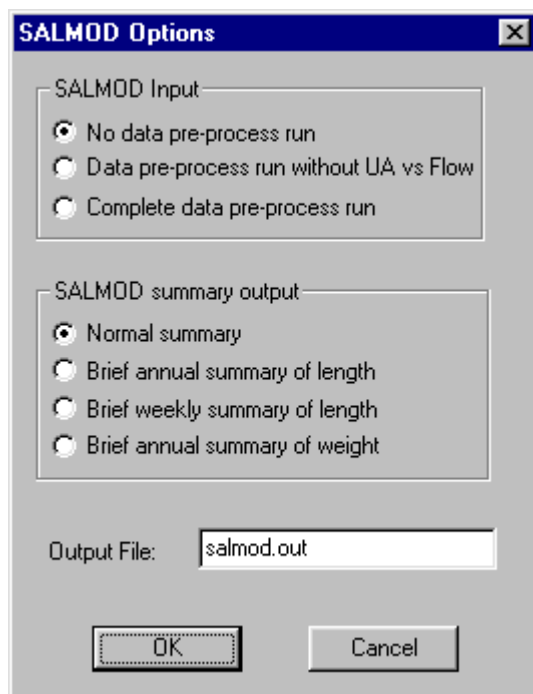
You may select options based on the type and detail of information needed for the *next* simulation run you make. Choosing *Data pre-process run without UA vs Flow* echoes your input data in formatted form to the output file for inspection; it does not calculate and display all weighted usable area values for each flow encountered. That is the purpose of the third radio button, *Complete data pre-process run*. Note that if you have a data set covering many years, the output may exceed WordPad's ability to display the results. However, a DOS program like LIST may work. Once viewed, you must deselect pre-process runs to get normal SALMOD output.

As can be seen, output can be *Normal* or *Brief*, with different kinds of Brief summaries depending on your needs. In general, Brief summaries are easily imported into spreadsheet programs. In addition, you may optionally choose a different name for your standard output file.

When you are ready, choose the **Run** menu item or toolbar button and, if all is well, you will see a small progress bar appear on the screen.
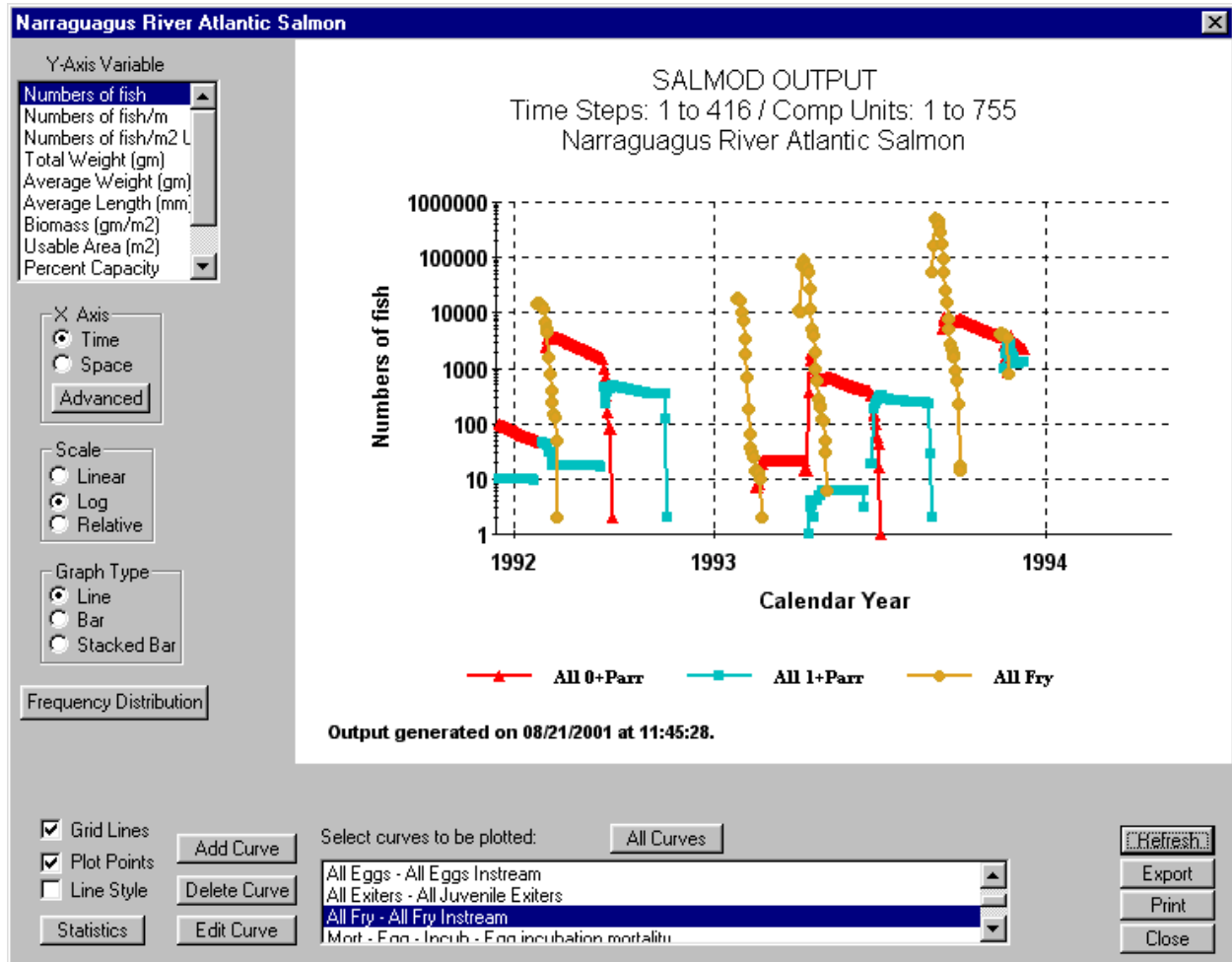
Viewing Tables

When SALMOD runs, it automatically opens up the output file, normally SALMOD.OUT so you can scan for errors and look at results. If this file is already open from a previous run, the contents of SALMOD.OUT will not be refreshed. Therefore, we recommend always closing SALMOD.OUT before you run the model. If you have chosen one of the brief summaries, these results are found in the SUMMARY.OUT file available in the **View** menu or on the toolbar.

Viewing Graphs

To display information about fish production, select the **View|Graph** menu or choose the toolbar button. Depending on how long and complicated your simulation was, it may take a while to bring up the first graph.

NOTE: If a simulation run was aborted, graphic output will be meaningless.

You have almost complete control over what variables are plotted, how they are grouped, what is plotted on the Y-axis, and what is plotted on the X-axis. You must define each curve to be displayed using the facilities provided. Once a curve is defined it is added to a list (stored in the file Curves.Dat) and may simply be selected in the future to display it. Upon first entering the fish production module the curve defaults to the first one in the alphabetical list. The Y-axis variable is numbers of fish and the X-axis is time steps. The figure below illustrates the fish production graphics dialog. Select the curves to be plotted from the list or add a new curve. Always click on *Refresh* to update your display after a change.

Narraguagus River Atlantic Salmon

Y-Axis Variable

Numbers of fish
Numbers of fish/m
Numbers of fish/m2 L
Total Weight (gm)
Average Weight (gm)
Average Length (mm)
Biomass (gm/m2)
Usable Area (m2)
Percent Capacity

X Axis
● Time
○ Space
[Advanced]

Scale
○ Linear
● Log
○ Relative

Graph Type
● Line
○ Bar
○ Stacked Bar

[Frequency Distribution]

SALMOD OUTPUT
Time Steps: 1 to 416 / Comp Units: 1 to 755
Narraguagus River Atlantic Salmon

Numbers of fish

1000000
100000
10000
1000
100
10
1

1992   1993   1994

Calendar Year

——▲—— **All 0+Parr**   ——■—— **All 1+Parr**   ——◆—— **All Fry**

Output generated on 08/21/2001 at 11:45:28.

☑ Grid Lines
☑ Plot Points
☐ Line Style
[Statistics]

[Add Curve]
[Delete Curve]
[Edit Curve]

Select curves to be plotted: [All Curves]

All Eggs - All Eggs Instream
All Exiters - All Juvenile Exiters
All Fry - All Fry Instream
Mort - Egg - Incub - Egg incubation mortality

[Refresh]
[Export]
[Print]
[Close]

To add a curve, click on the *Add Curve* button. The *Add a curve* dialog will be displayed as shown below. Enter a legend key (up to 20 characters) to be used on the graph. Enter a longer more detailed description to help you remember what the curve represents. Select the data type as instream fish, exiters (migrating fish), or mortality. Select a species if more than one species is available, the life stages desired, and any specific classes within life stages if all are not wanted. All classes within a life stage are automatically selected whenever a life stage is selected. Unselect those not wanted. If mortality was selected, select the causes of interest. The *All Stages*, *All Classes*, and *All Causes* buttons select or unselect all items in the respective category. For example, if you wanted a curve of adult mortality due to temperature and density, select Adult Females, Spawning Females, Adult Males, and Spawning Males from the life stage list and Temperature Related and Density Related from the mortality causes list. The new curve will be added to the list of available curves. The procedure for editing curves is the same as for adding a new curve. Select *Delete Curve* if you want to remove a curve from the list. Choose the curve to be deleted from the displayed list.

You may configure the X-axis as time (time steps or dates) or space (computation units or distance). The *Advanced* button allows you to select the X-axis units and set the temporal and spatial extent of the data to be plotted. Use the spin controls to set the beginning and ending time step or computation unit. The corresponding date and distance are displayed in the edit box to the right of the spin control. The dialog for setting advanced features for the X-axis as time is shown below.

Set temporal limits and resolution

X axis units
- ⦿ Time Steps
- ○ Dates

Temporal Resolution
- ⦿ Weekly
- ○ Monthly
- ○ Yearly

[OK]

[Cancel]

Temporal Limits

Beginning   [1]   ▲▼   [10/ 1/1992]

Ending   [156]   ▲▼   [9/30/1995]

[Reset]

Spatial Limits

Upstream   [1]   ▲▼   [0.0 meters]

Downstream   [640]   ▲▼   [100065.3 meters]

[Reset]
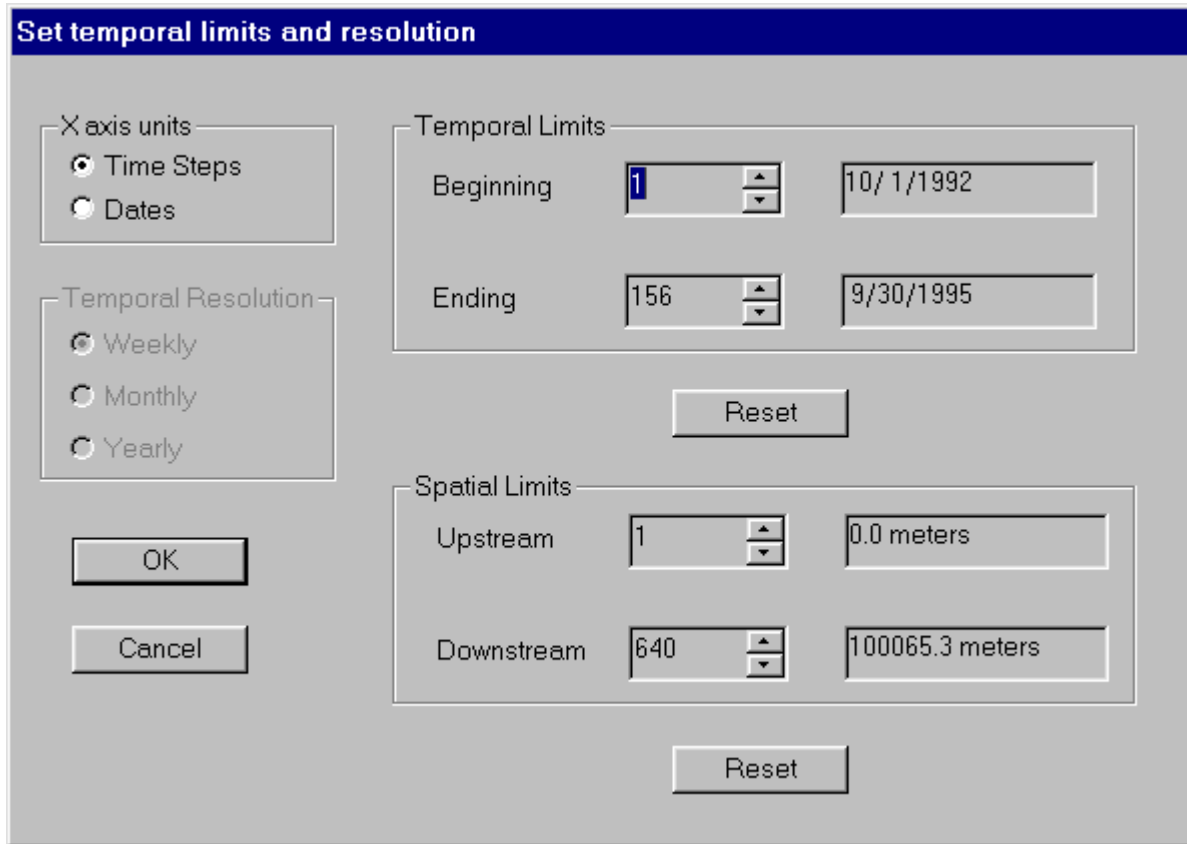
The Y-axis may also be changed on the main graph screen. Note that changing the data type may require the software to read additional data and perform lengthy calculations (especially for items requiring weighted usable area). In addition, you have the facility to plot frequency distributions of length and weight for instream fish and exiters (out-migrants). You may also plot temperatures or flows for stream segments. These are plotted in a separate dialog window that can be moved or minimized to give access to the underlying graph.

Other features are available from the graphing window once you have what you want. Data destination controls are common to all graphic screens and are located in the lower right corner of the graphic screen. These include: *Refresh, Export, Print*, and *Close*. The functions of these buttons are:

Refresh - Redisplays the graphics based on the settings of the controls

Export - Creates a comma separated value file (.csv) containing the data to be graphed. This file can be read easily by MS Excel. **TIP:** You can quickly view the values in Excel by pressing the *Export* button again after the original Export, highlighting the file just saved, right-clicking, and choosing *Open* off of the pop-up menu.

Print - Sends the data to be graphed to your printer after an additional dialog. **Note** that the printed graph will not include the control frame, but will have "footnotes" explaining the composition of the graph. Long, multi-year simulations may present challenges to printers with

little spare memory. In such cases, screen captures (e.g., *Alt-Print Screen*) may be the best alternative. Then paste the graphic into your word processor and print from there.

>   *Close* - Closes the window for this dialog.

An additional button allows you to display a table of statistics for the plotted curves. Click on *Statistics* to display the number of points, minimum curve value, maximum curve value, curve median, curve mean, standard deviation, and totals.

Graph appearance controls determine the appearance of the graph or the form of the data to be graphed. These include: graph type, scale, grid lines, line style, and plot points. The available graph types are line, bar, and stacked bar. Stacked bar are bar graphs where the bars are stacked vertically instead of displayed horizontally. The scale control allows you to change the scale on which the graph is plotted. Options include linear, log, or relative. The relative scale plots values relative to the maximum value (values are 0 to 1). Checking the *Grid Lines* check box will result in grid lines being displayed on the graph. The *Plot Points* check box controls whether individual points are displayed on the graph. If you check the *Line Style* check box, the line style as well as color of each successive curve will be different. Up to 20 curves may be displayed on a single graph. Additional color control is available through the *File|Preferences* dialog that allows changing each line type's red/green/blue attributes. You can set the extents for the Y-axis scale by clicking on the *Set Y-axis* button. Enter the minimum and maximum y values or click on *Use Defaults* to restore the axis to its default values.

Controls that determine what data are displayed include multiple selection list boxes, single selection dropdown lists, and spin control edit boxes. These control the spatial and temporal extent of the data to be displayed.

There are several ways to interact with a graph once it is displayed to examine data more closely, or isolate portions of the graph. Note that for the zoom options, a graphics zoom may not necessarily show axes after the zoom, while an axis zoom shows data with the axes. However, it may not be possible to tell what year of the simulation you are examining.

To scale a graph:
   1. Press *Ctrl*, and hold down both mouse buttons (or the middle button on a 3-button mouse).
   2. Move the mouse down to increase the chart size, or up to decrease chart size.
To move a graph:
   1. Press *Shift*, and hold down both mouse buttons (or the middle button on a 3-button mouse).
   2. Move the mouse to change the positioning of the chart inside the chart area.
Graphics zoom:
   1. Press *Ctrl*, and hold down the left mouse button.
   2. Drag the mouse to select the zoom area, and release the mouse button.
Axis zoom:
   1. Press *Shift*, and hold down the left mouse button.
   2. Drag the mouse to select the zoom area, and release the mouse button.
Reset:

Press the "r" key to remove all scaling, moving, and zooming effects.

Understanding SALMOD's Files

The following table lists executable file names and the common files that make up SALMOD's input data. Each file is described in a section below under its generic name, even though all names may be user defined. Those files listed as data files contain data that the programs use. These files need to be created or modified by the user for the particular application. The internal files are temporary files created by SALMOD and may be directed to a RAM disk in FILES.DAT. SALMOD creates five output files that contain simulation results. These files are designated in the list below by the *.OUT extension. Three internal scratch files are also created and used by the main program.

Program Files	SALMOD_W.EXE	Main user interface program.
	WINSALMOD.EXE	Main simulation program.
	SALOPT.EXE	Flow file optimization program.

Note: The PLOTMORT, PLOTSTAT, PLOT, PLOTINP, and 3DPRINT programs, previously released with SALMOD are no longer supported.

Input Files	FILES.DAT	Lists other input files.
	CONTROL.DAT	Specifies simulation and data parameters.
	FLOW.DAT	Stream flow data for each time step and river segment.
	RELATION.DAT	Movement, mortality, and growth relationships.
	SPAWN.DAT	Spawning parameters and timing.
	SPECIES.DAT	Names species, lifestages, and classes, and gives their length limits.
	STREAM.DAT	Defines the stream computational units, defines flow and temperature segmentation, and controls tally of outmigrants.
	SUPLMENT.DAT	Timing and location of fish to be added to the stream.
	TEMP.DAT	Stream temperature data by time step and river segment.

	WUA.DAT	Flow vs. (weighted) usable area functions for all lifestages and mesohabitat types.
Internal Files	SV.TMP	State Variable Storage.
	HAB.TMP	UA vs. Flow relationships.
	MOVE.TMP	Virtual stream for movers.
	CURVES.DAT	Keeps track of the variety of curves to plot.
	SALMOD.HLP, CNT & GID	Help files.
Output Files	SALMOD.OUT	Standard output is written to this file unless the user overrides the filename in the Options dialog.
	STATS.OUT	Binary population statistics used by graphing program. The actual filename is specified in FILES.DAT.
	TRANS.OUT	Binary population statistics used by graphing program. The actual filename is specified in FILES.DAT.
	SINK.OUT	Binary statistics on numbers exiting the study reach. Used by graphing program, the actual filename is specified in FILES.DAT.
	SUMMARY.OUT	An abbreviated summary of the normal SALMOD.OUT file. The actual filename is specified in FILES.DAT.
	SALMOD.ERR	A small file that contains an error message useful only if SALMOD is run as a child process for another umbrella program, e.g., SIAM.
Optional Files	NOTES.RTF	Optional file in which you may keep notes on origin of input data, assumptions used, simulation options tried, or anything that may be of interest in communicating information to another interested party. NOTES.RTF is not read by SALMOD and may contain any type of information, including graphics, tables, etc. You must add the name for the notes file as the last line of FILES.DAT.

Input Data Files

Data input for a SALMOD project includes a stream definition, mesohabitat classifications, flows, temperatures, and a variety of fish population parameters. The input data have been split into several ASCII files for convenience (well convenience of a sort). Each file contains a single type of information described in the following sections. The filenames can be changed by editing the FILES.DAT.

Input of species, stage, and/or class names is limited to 30 characters, and line length is limited to 80 characters. Note that while the order of information presented in the file is very specific, data lines are almost completely free-format, which means: (1) fields (input values) on a line can be separated by a comma and/or one or more blanks and do not have to be in specific columns, and (2) comments at the end of a line can be included after a semicolon following all fields on a line. **NOTE**, however, that no tabs may be included in the files, and they must be text files, not Word^TM or other word processing files; SALMOD will warn you of these problems.

The input files are explained below by describing each data field and providing an example. If several fields are shown on one line, it is possible to enter them on separate lines in the file; however, if this is done, comments can only be placed after the last field. If the fields are shown on separate lines, they cannot be collapsed into a single line. Indentation with spaces, not tabs, can be used to help structure the input, as shown in the examples. Repetitions of a particular line for an input list are indicated by indexing the fields (i.e., (n) being the subscript). For example, input shown as below indicates that there are two fields per line for 10 lines.

    FIELDA(1), FIELDB(1)
     .
     .
     .
    FIELDA(10), FIELDB(10)

Measurement units for data in the SALMOD set of programs and all of its files are listed in the table below. Please **NOTE** that usable area is in units different from typical PHABSIM output.

Value	Unit
Flow	cfs
Usable Area	ft^2/ft
Length of fish	millimeters
Weight	grams
Growth (juvenile)	% wet weight/day
Growth (egg/alevin)	% of development to emergence
Temperature	$^{\circ}C$
Density	grams/meter^2, or number of fish/m^2
Area	meters^2
Distance (stream lengths)	meters

(Yes, we are aware that units are not consistent.)

FILES.DAT

This file contains the names of the data files, output files, and temporary files. All filenames must be valid filenames up to 30 characters long, including a path (drive, folder, and subfolder if necessary) specification. Temporary files can be assigned to a RAM drive to speed up the operation of SALMOD (e.g., E:SV.Tmp, where E: is a designated RAM drive), though this is rarely necessary on contemporary computers. Generally, it is best to have all files in a single working folder.

Note: Filenames must be entered in the order listed below and the title line must be included.

Format

Title Line
Flow Filename (e.g., Flow.Dat)
Stream Filename (e.g., Stream.Dat)
Spawning Filename (e.g., Spawn.Dat)
Species Filename (e.g., Species.Dat)
Relation Filename (e.g., Relation.Dat)
Temperature Filename (e.g., Temp.Dat)
Weighted Usable Area Filename (e.g., WUA.Dat)
Supplement Filename (e.g., Suplment.Dat)
Control Filename (e.g., Control.Dat)
Sink File Output Filename (e.g., Sink.Out)
Statistics Output Filename (e.g., Stats.Out)
Transactions Output Filename (e.g., Trans.Out)
Summary Output Filename (e.g., Summary.Out)
Habitat Temporary Filename (e.g., Hab.Tmp)
Movement Temporary Filename (e.g., Move.Tmp)
State Variable Temporary Filename (e.g., SV.Tmp)
Optional Notes Filename (e.g., Notes.Rtf)

Example

```
Full Trinity River Model
c:\data95\Flow.dat
c:\data\Stream.dat
c:\data\Spawn.dat
c:\data\Species.dat
c:\data\Relation.dat
c:\data95\Temp.dat
c:\data\Wua.dat
c:\data95\Suplment.dat
c:\data\Control.dat
c:\output\Sink.out
c:\output\Stats.out
c:\output\Trans.out
c:\output\Summary.out
E:Hab.tmp
E:Move.tmp
E:SV.tmp
```

STREAM.DAT

This file describes the river's sequential mesohabitat types. The stream is divided into computational units (also referred to as CU in this document), with a length (in meters) and mesohabitat type supplied for each. A remark, up to 30 characters at the end of each line defining a computational unit, can be used to label that computational unit. Data for computational units must be entered in a downstream order (i.e., the computational unit farthest upstream is entered first.)
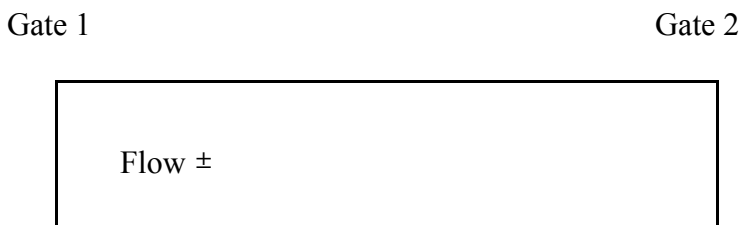
After the lines providing information for each computational unit, flow and temperature segments are defined. Separate sets of data are required for each flow or temperature segment.

For example, if data from only one stream gage are available for the study reach, then one flow segment will be defined for the reach. Temperature and flow segments can be defined in terms of either distance or computational units, both of which are measured from upstream to down. If segment boundaries are defined in distances, a real variable is used (indicated by a decimal in the number). It would be prudent to start and stop flow and temperature segments at computation unit boundaries; errors may occur if this does not hold true. Integer values are used to define segment boundaries by computational units. The whole stream (all computational units) must fall in some flow and temperature segment. The sum of the computational unit lengths must match the total study area length.

The final two lines in the STREAM.DAT file contain the 'gate' definitions for the study area. These gates control the movement of fish into and out of the study area. Each line must contain the gate ID and the gate type. Gate IDs are 'Gate1' for the upstream gate and 'Gate2' for the downstream gate. Gate types define the direction that fish can move through the gates. These can be *downstream* (indicating downstream movement only), *upstream* (indicating upstream movement only), *bidirectional* (allowing movement in both directions), or *barrier* (allowing no movement in or out). Note that barriers may cause fish to "stack up" at the barrier under certain conditions. If fish reach a gate that will not permit movement out of the study area during habitat induced movement and there is no available habitat, the remaining fish are subjected to 100% mortality. Fish caught in a freshet will accumulate in the last computational unit if the downstream gate will not permit movement out of the study area. For seasonal movement, fish moving upstream to a barrier or downstream gate will accumulate in the first computational unit. If fish moving downstream encounter a barrier or upstream gate, they will accumulate in the last computational unit.

During model execution, the gate types will determine the extent of movement of fish into and out of the study area. Gates that allow movement out of the study area (upstream and bidirectional for Gate1, and downstream and bidirectional for Gate2) will have that movement tabulated in the "sink" file as an exiter. Gates that allow movement into the study area permit those fish leaving through the opposite gate to reenter. For example, fish that exit the study area through the downstream gate would reenter through the upstream gate to attempt to simulate an unbounded, representative section of stream. Several examples of how gates can be used follow.

In each example, consider the following diagram:

Gate 1   Gate 2

```
+-----------------------------------------------+
|                                               |
|        Flow ±                                 |
|                                               |
+-----------------------------------------------+
```

Downstream Gate   = --->
Upstream Gate   = <---
Bi-directional Gate = <-->
Barrier   = |

<u>Gate 1</u> <u>Gate 2</u>

--->   --->   In this example, only downstream movement is allowed through both gates. Those fish exiting the study area through Gate2 would be tabulated and would reenter through the upstream gate. This situation would be reversed if both gates were upstream gates. Either situation results in no net migration.

<---   --->   In this example, fish would be allowed to leave the study area and would be tabulated, but no fish could reenter. The gates are set to allow movement out only.

<-->   --->   This situation allows fish to exit the study area through either end; however, fish exiting the downstream gate would reenter the study area upstream. Fish exiting the upstream gate would be tabulated only.

--->   <---   No fish can exit the study area in this situation.

<-->   <-->   In this example, fish are allowed freedom of movement in both directions through both gates. Fish exiting the downstream gate would reenter through the upstream gate and vice-versa; therefore, exiters would be tabulated, but there would be no net migration.

 | --->   This would be a common representation of a stream with a dam (or headwater) allowing no movement out of the system in the upstream direction, but outmigration is allowed and tabulated in the downstream direction.

Note: Title lines and full line comments are not valid in STREAM.DAT.

Format

Number Of Computational Units (n)
Computational Unit Length (1), Mesohabitat type Code (1) ;Label (up to 30 chars. optional)
  . . .
  . . .
  . . .
Computational Unit Length (n), Mesohabitat type Code (n)
Number Of Flow Segments (m)
Beginning Of Flow Segment (1), End Of Flow Segment (1)
  . . .
  . . .
Beginning Of Flow Segment (m), End Of Flow Segment (m)
Number Of Temperature Segments (q)
Beginning Of Temperature Segment (1), End Of Temperature Segment (1)
  . . .
  . . .
Beginning Of Temperature Segment (q), End Of Temperature Segment (q)
Gate ID, Gate Type
Gate ID, Gate Type

NOTE: There may be no blank lines at the end of this file.

Example

```
   6           ; Number of Computational Units
  100    C1    ; First CU  is 100 m  (Two mesohabitat types, C1 and C2 are
defined)
  200    C2    ; Second CU is 200 m long
  400    C1    ; Third CU  is 400 m
  800    C2    ;          ...
 1000    C1
 2000    C2    ; (entire stream is 4500 m long)
   2           ; number of flow segments
    1  3       ; flow seg 1 definition (includes CU's 1-3, note integer values)
    4  6       ; flow segment 2 (includes CU's 4-6)
   2           ; number of temperature segments
   0.0 3000.   ; temp seg 1 (includes 1st 3000m of stream, note decimal points)
  3000.  4500.;  temp segment 2 is the rest of the stream
Gate1  Upstream     ;  Upstream gate
Gate2  Bi-directional;  Downstream gate
```

SPECIES.DAT

The species, stage, and class definitions are provided in the SPECIES.DAT file. The number of species to be modeled (maximum of two) is designated along with species, life stage, and class names. The percent maturation classes for eggs, and length classes for the next sub-adult stages (e.g., fry, fingerlings, and yearlings) are also identified. The number of classes and class definitions can vary among species, but must always be at least one class per stage. Fish length may be either fork length or total length, but just be sure to be completely consistent one way or the other throughout all data files. SALMOD sets the maximum possible length of adults to be the maximum length given in the RELATION.DAT file.

In thinking about lifestage nomenclature and definitions, the best approach to categorization is to think in terms of competition for habitat. For example, you might divide fry from parr based on a length where behavior changes markedly from near-shore habitats to deeper, more open channel habitats. You would then supply mesohabitat versus flow information for each of these two lifestages.

Note: Names of species, life stages, and classes may use the slash (/) character, but if so, the name must be enclosed in single quotes (') when used as a range parameter in the CONTROL.DAT file (see below).

Field definitions
Number of Life Stages   : 12 maximum
Life Stage Name   : 1 - 30 character name
Number Of Species   : 2 species maximum
Species Name   : 1 - 30 character name
Number Of Classes   : 1 - 5 classes
Class Name   : 1 - 30 character class name
Class Lower Limit[*]   : Percent developed or size class lower limit
Class Upper Limit[*]   : Percent developed or size class upper limit

   * class lower limit must be less than upper limit and contiguous size class limits must align within a stage and between stages of a species.

Note: Title lines and full line comments are not valid in SPECIES.DAT.

<u>Format</u>

Number Of Life Stages (m)
Life Stage Name 1 for adult females
Life Stage Name 2 for spawning females
Life Stage Name 3 for adult males
Life Stage Name 4 for spawning males
Life Stage Name 5 for eggs/alevins
Life Stage Name 6 for first juvenile class, e.g., fry
Life Stage Name 7 for second juvenile class, e.g., fingerlings
Life State Name . . . for next juvenile class, e.g., pre-smolts
Life Stage Name 12 for last juvenile class, e.g., smolts
Number Of Species (ns)
Species Name (1)
  Number Of Classes for stage 5 (n)
    Class Name (1)
    Class Lower Limit (1), Class Upper Limit (1)
    Class Name (2)
    Class Lower Limit (2), Class Upper Limit (2)
     . . .
     . . .
     . . .
    Class Name (n)
    Class Lower Limit (n), Class Upper Limit (n)

Repeat for stages 6 – m

Repeat for each species

```
8                       ; -- number of life stages
Adult Females           ; -- names of life stages
Spawning Females
Adult Males
Spawning Males
Eggs/Alevins            ;  (classes are not listed here)
Fry
Pre-Smolts
Immature Smolts
1                       ; -- number of species
Chinook Salmon          ; -- species name
        3               ; -- number of egg classes    (first 4 stages do not
    Prop. Mature        ; -- egg class 1 name            have classes)
      0   .33           ; -- class 1 limits (0-33% maturation)
    Prop. Mature        ; -- class 2 name
     .33  .67           ; -- class 2 limits (33-67% maturation)
    Prop. Mature        ; -- class 3 name
     .67 1.00
        2               ; -- number of fry classes
    F1                  ; -- fry class 1
      34   38           ; -- class 1 limits (32-38 mm length)
    F2                  ; -- fry class 2
      38   50
        3               ; -- number of pre-smolt classes
    P1                  ; -- pre-smolt class 1
      50   55           ; -- class 1 length (50-60 mm length)
    P2                  ; -- pre-smolt class 2
      55   65
    P3                  ; -- pre smolt class 3
      65   80
        3               ; -- number of immature smolt classes
    S1                  ; -- immature smolt class 1
      80   90
    S2                  ; -- immature smolt class 2
      90  110
    S3
     110  200
```

CONTROL.DAT

The CONTROL.DAT file defines the simulation control parameters and is arguably the most complicated file to understand and use effectively. Two types of information are specified in CONTROL.DAT, simulation *options* and simulation *processes*. Simulation options specify certain general rules for the model operation. There are really two kinds of processes: those that may be viewed as principally biological in nature and those that are more computational, though the boundary may be fuzzy for some processes. A brief description of options and processes follows.

Simulation Options

Capacity - The CAPACITY format indicated, either *Numbers* or *Biomass*, must correspond with the habitat capacity data provided in RELATION.DAT. The system default is *Biomass*.

Date - DATE specifies a beginning date (mm/dd/yyyy) for the simulation and associates a specific calendar date with the time steps. The system uses the beginning date to determine weekly dates for the output tables. DATE must be specified or a runtime error will occur.

Population - The POPULATION option determines whether the current fish population remains in the river at the end of the year. When POPULATION = *Anadromous* each year in a multi-year run will begin with a new stock of spawners, and spawners die after spawning. When POPULATION = *Resident*, spawners do not die after spawning and the MATURE process should be included to allow juveniles to mature into adults. POPULATION = *Multiyear* is similar to *Anadromous,* but only adult fish will die at the end of the year , so that immature fish will remain in the system.

Summarize - The SUMMARIZE option creates a report of summary population statistics in the output file. If SUMMARIZE=*Time*, the population status, mortality, and movement statistics during each time step and cumulative statistics at each time step are reported. If SUMMARIZE=*Units*, the same information is provided for each computational unit at each time step. This option can use the */Time=* switch (see discussion of switches below) to limit the time steps in which the summary will be printed. Note that this option will produce a large output file if allowed to run for all time steps. Compared with the DETAILS process switch (described below), the SUMMARIZE option is much easier to read.

Timestep - The TIMESTEP option allows the user to specify the length of the simulation run in weeks. This option must be specified, or the system will default to zero and nothing will happen.

Biological Process Descriptions

Carry - The CARRY process determines when adult females carry eggs. This process calculates the number of eggs for females in a cohort based on their weight and then tracks the number of eggs with them to estimate the *in vivo* egg mortality due to the exposure temperature of the adult female environment. CARRY may span a biological year boundary.

Freshet Movement - The FRESHET process is used to determine if a freshet (an abrupt increase in flow volume) has occurred during the current time step, and if so, displaces the specified stages/classes according to the user-specified parameters governing proportion of fish moved per time period, the distance downstream, and any associated mortality. There are currently three options for defining a freshet (see below) based on either the rate of change in weekly streamflow, or simply user specified. See Godin (1981) for more on freshet movement.

Growth - Cohort growth is a function solely of water temperature in the computational unit and is based on a percent growth per day versus temperature relation. The GROWTH process is typically invoked for each relevant cohort during each time step. **Note** that fish can lose weight through negative growth rates at extreme temperatures. If they do lose weight, they do not lose length; they gain length only after they regain the lost weight. The user may choose to let some cohorts grow and some not if, for example, it is hypothesized that fish moving for a specific reason do not grow. See the Control file later in this document for an example.

Habitat Movement - Habitat-induced movement occurs if the number (or biomass) of fish exceeds the habitat capacity (see Grant and Kramer 1990) of a computational unit for a given lifestage (see Chapman [1962] and Mesick [1988] for more on habitat related movement.) Habitat capacity is governed by a flow versus mesohabitat relationship specified for each lifestage. Movement to alleviate a capacity constraint necessitates mortality in a manner controlled by the user. Habitat-induced movement may be upstream or downstream, or both. Note that one can impose further guidance on HABITAT MOVEMENT through proper use of the size class switches. For example, if you believe that smaller fish are forced to move first if a given computational unit is over capacity, you can order the processes accordingly. See Example 1 below.

As cohorts search for available habitat, they incur mortality that is a function of the distance moved. Mortality occurs prior to putting cohorts into the virtual stream. See Bartholow et al. (1993) and Williamson et al. (1993) for more information on the implementation of habitat-related movement.

As an aside, SALMOD shuffles the order in which it processes computational units for HABITAT MOVEMENT so that there will be no tendency to do anything differently between upstream and downstream.

Mature - When the *resident* variant of the model is used, the MATURE process turns the selected stage/class into adult fish capable of spawning with the sex ratio preset to 50:50. This process is unnecessary if the *anadromous* variant is being used because the SUPPLEMENT process is typically used to introduce adults into the population at a user-specified sex ratio.

Mortality - All mortality not explicitly handled with one of the other processes is computed by the MORTALITY process. This includes temperature (see U.S. Bureau of Reclamation, 1991), density, *in vivo* egg, incubation, and superimposition losses. In addition, a base mortality for all causes not related to any other process is also computed here. Most of the mortality causes are

straightforward functional relations contained in the RELATION file, such as for temperature or density. Superimposition is explained in conjunction with the SPAWN process. Incubation mortality, however, is complicated because it depends so heavily on antecedent conditions.

Imagine that on time step five, there were 100 square meters of spawning habitat available (computed from the flow:habitat area function in the WUA data file) and each redd pocket consumed two square meters (from the SPAWN data file). Imagine also that there were a sufficient number of female spawners to just completely fill the spawning habitat with redds C obviously 50 females C and remember that no superimposition occurs in a computation unit for spawners that spawn <u>within</u> a single time step. (Remember, if there were more than 50 females ready to spawn, all in excess of 50 would shed their eggs with that mortality being tabulated as lost eggs.) Now, at the beginning of time step six, the flow in the computation unit changes and now there are 75 square meters of spawning habitat, but only 90 square meters of incubation habitat (also from the WUA data file). Ten square meters of redds constructed during time step five no longer are viable and die, with all (or a fractional part) of the redds within that area, and the cohort of eggs they represent, dying as well. Suppose further that in time step seven incubation habitat increased to 95 square meters, no problem for redds. However, during time step eight, incubation habitat declined to 80 square meters. In this case, 10 additional square meters of redds (90-80) are lost. And so on through time, all further complicated by other factors such as superimposition of the redds during each spawning time step, but in reality only simple bookkeeping. The important points are that spawning and incubation habitats are independently tracked through time on a computation unit basis. This is the mesohabitat equivalent to PHABSIM¬s cell-by-cell effective spawning calculation routine. As such, it is analogous to effective spawning except that a continuous time series of flows is potentially important and disruptive to a continuous time series of incubating eggs within a computation unit, each cohort of which potentially originated in a different time step and under different spawning conditions. In contrast, PHABSIM deals only with a single pair of flow conditions as representative of the most extreme cases and does not track multiple dates of redd deposition or superimposition. Thus, SALMOD has traded spatial resolution for temporal resolution.

Seasonal Movement - Seasonal movement is similar to the FRESHET process, except it is invoked solely based on time of year. Unlike freshet movement, fish moving in response to the season may move up or downstream. Mortality associated with SEASONAL MOVEMENT will be calculated regardless of the distance moved. For example, fish within 1 km from the downstream-most CU told to move 10 km will still suffer the full complement of mortality and will not be tallied as an exiter. See McDonald (1960) for more on seasonal movement.

Spawn - As its name implies, SPAWN calculates the appropriate fraction of adults that should spawn in the current time step, and then generates from those adult females redd cohorts containing eggs from user supplied parameters detailing acceptable spawning temperatures, area per redd, and number of eggs per female. Several options control the calculation of how pre-existing redds may be superimposed by newly constructed redds. SPAWN also calculates mortality of some eggs that are never successfully deposited. For the condition in which there are too many spawners for the available spawning habitat at the time of spawning, it is assumed that these eggs are shed ("lost") and die with mortality reported as "lost eggs". If spawners fail to

spawn through the duration of the spawn process, their eggs are assumed to die with the adult in the anadromous model and be resorbed in the resident model. In none of these cases do eggs get tallied as being successfully deposited.

Note the differences using the */Time* switch on the SPAWN process for the *Resident* and *Anadromous* variants. It is especially meaningful in the *Resident* variant where the appropriate fraction of adults of both sexes will be treated as spawners for the entire time step during which the SPAWN process is active as specified in the CONTROL.DAT file. This means that adult fish will be subjected to 1) mortality, movement, and growth rates appropriate for spawners as contained in RELATION.DAT, and 2) use the usable area appropriate for spawners as contained in WUA.DAT, all assuming that processes in CONTROL.DAT are specified in that way. In contrast, adults become spawners at the beginning of the SPAWN process in the *Anadromous* variant. As mentioned elsewhere, after spawning, spawners will die in the *Anadromous* variant of the model and revert to adults in the *Resident* variant. There is a special case in the *Anadromous* variant in which a few adult males may be left in the stream post-spawning. This occurs if they were in a computation unit that had, for whatever reason, no spawning females. If you find that this number of adult males is anything other than a trivial number, you probably have something wrong in your process list or timing switches.

Should spawning be delayed due to temperature, spawners remain as spawners awaiting the next possible spawning opportunity, as controlled by the */Time* switch and the temporal limits implied in SPAWN.DAT. It would be only in a case such as this that one would expect to find spawners in the stream at the *end* of a time step, something you will readily note in the postprocessing plot programs. Note, however, that all remaining spawners will be returned to the adult life stages at the beginning of the first time step after spawning has completed. It is advised that one double check the output at the end of a biological year to see if either spawners or adults are still in the system when they should not be. As a general guideline, the times of spawning indicated in SPAWN.DAT should be a subset of the */Time* range of the SPAWN process. In the *Resident* model for example, adults may begin to seek (move to) appropriate spawning habitat a week prior to actual egg deposition. In this case, the */Time* switch should initiate the SPAWN process a week earlier than that given in the SPAWN.DAT file. This would allow movement to spawning habitat a week earlier than egg deposition. See the example CONTROL file for the *Resident* variant later in the manual.

Notes: SPAWN must precede MORTALITY. This version of SALMOD does not make any check to see that the sex ratio within any computation unit is or is not appropriate for spawning to be successful.

Supplement - The SUPPLEMENT process is the way to initialize the stream with adults for spawning in the *anadromous* variant of the model, or to "seed" the stream with pre-existing fish for the *resident* variant; in fact, there is a special */Time=0* option which may be used to force seeding prior to any other process. It may also be used to "supplement" the stream with hatchery fish at specific geographic locations, or to add fish migrating from a tributary. The SUPPLEMENT process introduces fish into the study area in proportion to the habitat available for the given life stage at the time of introduction. Adults are apportioned to spawning habitat in the *anadromous*

variant and proportioned to adult habitat in the *resident* variant of the model. If no habitat for the life stage exists, fish are introduced in proportion to the computation unit lengths.

Computational Process Descriptions

Biomass - The BIOMASS process computes the biomass of each computational unit for each life stage. This process logically precedes both mortality processes dealing with either numbers (or biomass) and habitat capacity, i.e., HABITAT MOVEMENT and density mortality.

Catastrophe - Quite often, a relatively rare event disrupts "normal" population processes. Severe floods or droughts generate abiotic conditions outside the realm of the functional relationships that compose the model. If the user wishes to attempt to mimic unusual mortality events, the CATASTROPHE process allows removal of a given percentage of any class of fish.

Collapse - Large numbers of computational units and a growing number of cohorts due to splits during movement can generate an exponential number of cohorts to track. Earlier versions of SALMOD ran into computer memory limitations that severely degraded simulation times. The COLLAPSE process was a way to reduce the number of cohorts by combining cohorts in the same computational unit and class. A weighted average of the combined cohorts' attributes (length, weight, etc.) was used. Newer compilers and faster computers have reduced, or perhaps eliminated, the need for this process, but the user is free to experiment with it should processing times be a major factor. **Note** that the adult life stages always exist in only one cohort per computation unit, and therefore have no need to be collapsed. Also, SALMOD has a built-in limit of 25 cohorts of a given class that can be in a single computation unit; if this limit is exceeded, an automatic COLLAPSE is performed to alleviate the constraint.

Details - It is not uncommon for a user to be perplexed at the output from a simulation, in effect wondering if he or she is responsible for a given result from a data input error or whether SALMOD has produced a computational error. As the name implies, the DETAILS process triggers SALMOD to print the gory details of the next process in the list to the standard output file (typically SALMOD.OUT) so that details of the computations may be checked. Warning: output may be terse, voluminous, and arcane, but at least it is there. For processes that result in changes to the fish population within a computational unit, DETAILS will produce before and after tables. Switches can be set for the DETAILS process to detail only a subset of the Time, Stage, Class, or CU indicated in the subsequent process.

Graduate - Graduation is the re-classification of cohorts according to growth. The graduation process is typically invoked after all growth (see Growth process) has taken place to advance the non-adult lifestages. Graduation does not, however, create adults from the last juvenile lifestage; the MATURE process is used for that function. **Note** that the juveniles will grow only as large as the largest size listed in SPECIES.DAT.

Immigration - All moving fish (whether habitat-induced, seasonal-induced, or freshet-induced) are placed in a "virtual stream" that conceptually stands beside the real stream. Any movement-

related mortality is removed before fish are put into the virtual stream. While in the virtual stream, fish are not subjected to further processes. The IMMIGRATION process is a computational, rather than biological, process that moves fish from the virtual stream back to the actual stream, typically after all other movement has taken place. Only after fish return to the "real" stream will additional processes affect them.

Process Specifications

The simulation processes outlined above provide the structure for calculation of the population dynamics. The type and order of processes to be performed on the respective species and lifestages are designated by their order in the CONTROL.DAT file and optional switches that accompany them specifying time periods and computational units that indicate when and where each process occurs. The list of processes (up to 30) is performed by SALMOD in order for each time step. Spawning, graduation, and immigration processes can only occur once for each time step, and spawning must precede mortality. A complete list of SALMOD's processes and their optional switches is found in Table 2.

Table 2. Alphabetical list of SALMOD processes as specified in the CONTROL file, their applicable optional switches, and defaults. Note that the /SPECIES switch may be used for ALL processes if necessary.

Process name	Description	Switches	Defaults
BIOMASS	Computes biomass in each computational unit in order to calculate capacity limits.	None allowed	None
CARRY	Determines when females carry eggs for calculation of *in vivo* egg mortality.	/TIME	All
CATASTROPHE	Allows for mortality due to any catastrophic event.	/DATE (mm/dd/yyyy) /RATE (percent)	Required Input 100%
COLLAPSE	Collapses cohorts of like stage/class to reduce the overall number of cohorts. Only necessary if computation time is a problem.	/TIME	All
DETAILS	Prints details for the process immediately following the details line.	/TIME /CU /STAGE /CLASS	All All All All
FRESHET MOVEMENT	Performs fish movement due to freshet events.	/TIME /STAGE /CLASS /CU /OPTION	All All All All 2xPorA (see below)

GRADUATE	Updates stage/class of fish based on their length.	/TIME /STAGE /CLASS /CU /EMERGE /INITDEV	All All All All -99.0 0
GROWTH	Calculates growth as a function of water temperature.	/TIME /STAGE /CLASS /CU	All All All All
HABITAT MOVEMENT	Performs movement based on habitat constraints.	/TIME /STAGE /CLASS /CU /MOVE /ORDER	All All All All Down100 1
IMMIGRATION	Moves fish from the "virtual stream@back into the stream. This is a mechanical, rather than biological, process.	None allowed	None
MATURE	Allows juvenile fish to mature into adults.	/TIME /STAGE /CLASS /CU	Time step 52 All All All
MORTALITY	Performs mortality based on mortality functions specified in RELATION.DAT.	/INVIVO	none
SEASONAL MOVEMENT	Performs movement based on time of year.	/TIME /STAGE /CLASS /MOVE	All All All Down100
SPAWN	Performs spawning based on the parameters in SPAWN.DAT. (Must precede MORTALITY)	/SI /TIME*	Random All
SUMMARIZE	Creates a report of summary population statistics in the output file.	/TIME /CU	All All
SUPPLEMENT	Adds returning spawners or hatchery fish to the stream based on the parameters in SUPLMENT.DAT.	/Time /Time=0**	All

* TIME may be used for these processes; however as the time steps are defined in the data files specifying the time in the process is largely redundant.
** Special case to seed the stream prior to any process.

<u>Process Switches</u>

Switches can be added to processes listed in the control file to provide limits or option selections for the various processes. Many processes can be repeated several times with the same or different process switches. Some switches are applicable to all processes whereas some switches are process specific. Switches applicable to all processes may have one or two values listed. For example, the *Time*, *Species*, *Stage*, *Class*, and *CU* switch values for a process can be given as a range or single value. If a range or value is not provided, SALMOD defaults to performing the process for the complete range (i.e., all time periods, all species, etc.). Single values represent the specific value for the switch. For example, */Time*=10 will result in the associated process being run only during the tenth time step of a year. If two values are used, they are separated by a comma and represent a range of values. For example, */Time*=10,20 will result in the associated process being run during each time step between 10 and 20 inclusive. A range is always defined by only two values, one the lower value and one the upper, never a list of values.

Notes: When values are entered for the */Time* switch, these time steps are relative to the beginning of the simulation year. Therefore, if *Timesteps*=104 is entered, and */Time*=10,52 is specified for a process, the process will be executed in time steps 10 through 52 and time steps 62 through 104 (relative time steps 10 through 52 in the second year). As mentioned, the */Time=0* option may be used for the Supplement process to seed the stream prior to any other process. Legal values for process times are 1 to 52 only and, with the exception of the Carry process, may not "wrap" the biological year boundary. Even if fish are supplemented at time step 55, this will be dealt with by the Supplement process during time step 3 in the second year. Time parameters entered in "reverse," such as 40,10 will get "turned around" to be 10,40 and not work as expected. Again, because the CARRY process may wrap the biological year, its time step parameters will not be "turned around." If you need to span a biological year boundary for a process other than Carry, simply use two process lines, one for early in the year and one for later.

When entering values for the stage switch, the names entered for the stages in SPECIES.DAT may be used, or the numerical ID may be used. Each stage is assigned a numerical ID based on the order listed in SPECIES.DAT. Values used for the class switch are entered in a similar fashion. **Note** that ranges for lifestages do not "wrap around" the life stage/class continuum in terms of the calculation order shown in Table 1, though SALMOD automatically adjusts the order in the specified range (i.e., *fry, immature smolts* is equivalent to *immature smolts, fry*). That is, if you wish to include all stages except eggs, the process must be invoked at least twice, once for lifestages "below" eggs and once for those "above."

Movement processes have switches specific to movement. The Freshet movement process has a */Option*=<option> switch that defines how a freshet event will be identified. The options currently available are defined as follows:

2xPorA - a freshet event occurs when the current time step's flow is greater than or equal to twice the previous time step's flow *or* when the current flow is greater than or equal to twice the average of the previous three flows.

2xPandA - a freshet event occurs when the current time step's flow is greater than or equal to twice the previous time step's flow *and* is greater than or equal to twice the average of the three previous time step's flows.

Userspec - a freshet event occurs when the flow for a given time step is entered as a negative number. These must be defined by the user in FLOW.DAT.

The SEASONAL and HABITAT MOVEMENT processes have a switch, /*Move*=<option>, to determine the direction of movement. The format for the option is either *Upxxx* or *Downxxx*, where xxx is the percent moving in the given direction and is specified as an integer from 1 to 100. No spaces should be entered between the direction and the percent value. For example, /*Move=Up*15 would result in 15% of the moving fish in the specified move to move upstream and the remaining 85% to move downstream. The default for both processes is 100% downstream. Movement in the FRESHET MOVEMENT process is always downstream.

Note: The three movement processes (habitat, freshet, seasonal) collectively present a special case. In each case, the moving fish are placed into a "virtual stream" for storage until the immigration process is executed. Fish in the virtual stream are not affected by any other in-stream processes; therefore, they will not be subjected to further movement and the associated mortality. For example, in a test run the number of out-migrant pre-smolts was 40% lower when seasonal movement occurred after habitat movement as opposed to before habitat movement. The user must decide the appropriate sequence for movement processes, generally placing the process with the most dominant effect first.

The SPAWN process has an *SI* switch to determine the method for redd superimposition (McNeil 1967). Available methods are *Random*, *Contagious*, and *Avoidance*. In the *random* method spawners first choose from available spawning area randomly. For the *avoidance* method, spawners avoid previously constructed redds to the degree they can, and in the *contagious* method, spawners choose previously constructed redd sites. If this option is not specified, the system will default to the Random model.

A summary of process switches may be found in Table 3.

Table 3. Summary of optional process switches.

Switch name	Description	Number of arguments	Argument options	Argument notes
Time	Limits time steps.	1 or 2	Valid time step.	See special notes for SPAWN and Supplement processes
Species	Limits species	1 or 2	Valid species name.	For multi-species runs
Stage	Limits stage.	1 or 2	Valid stage name.	
Class	Limits class.	1 or 2	Valid class name.	
CU	Limits computational units.	1 or 2	Valid comp unit.	
Option	Determines method of defining freshets.	1	2xPorA 2xPandA Userspec	See text
Move	Determines percent of fish moving up or down stream.	1	UP*xxx* DOWN*xxx*	Only one is used with remaining fish moving in the opposite direction.
Order	Determines order of leaving CU in response to HABITAT MOVEMENT	1	1 2 3	1 = Last in first out (default) 2 = First in first out 3 = Increasing condition factor, i.e., proportional to length^3/weight
SI	Determines redd superimposition type.	1	Random Contagious Avoidance	See text
Invivo	Limits time for *in vivo* egg mortality.	1 or 2	Valid time step	
Emerge	Minimum temperature for emergence.	1	Temperature	Defaults to -99.0
Initdev	Uniform random deviate to add/subtract to the initial fry length (mm) on emergence, e.g., " 5 mm	1		Warnings issued if deviation would cause initial length to fall outside limits defined by SPECIES.DAT; Recommend setting Initdev equal to twice the SD
Date	Catastrophic event date.	1		Event data in format mm/dd/yy
Rate	Catastrophic event mortality rate.	1	Percent	This is the percent of fish that die when the event occurs.

Processing CONTROL.DAT

Errors that may occur reading the various switches in CONTROL.DAT may not cause execution of the model to stop; rather, default values may be used. For example, if a /Time switch is used and an invalid number is read, the system will default to running the model for timesteps 1 through 52. If any errors of this type occur, SALMOD will note the problem in the output file and continue execution with the default values.

Note: Title lines are not valid in this file; however, full line comments are.

Format

TIMESTEP=Number of time steps;
DATE=Begin Date in format mm/dd/yy;
CAPACITY=NUMBERS or BIOMASS;
SUMMARIZE=UNITS/CU=A, B or TIME/Time=x, y;
POPULATION=ANADROMOUS or RESIDENT;

Then, for each process (maximum 30), the following format is used:

PROCESS NAME /*Time*=A<,B> /*Stage*=C<,D> /*Class*=E<,F> /*CU*=G<,H>/*other*;

where the <> delimiters indicate an optional parameter. That is, if the switch has a single parameter, such as a single time step, it only applies to that time step. If two parameters are used to define a range, the switch applies to the range, inclusive. In no case can there be more than two parameters for a given switch.

Example 1 - *Anadromous* Model

```
; Options
Timesteps=52;
Date=9/2/1986;
Capacity=Biomass;
Population=Anadromous;
; Processes
Supplement /Time=0,15;
Spawn /Time=1,15 /SI=Random;
Freshet Movement /Stage=Fry, Immature Smolts /Option=2xPorA;
Seasonal Movement /Time=35,39 /Stage=Fry, Immature Smolts;
Biomass computation;
;Habitat moves in the following order force smallest size classes
; to move first
Habitat Movement /Time=10,52 /Stage=Fry /Class=F1;
Habitat Movement /Time=10,52 /Stage=Fry /Class=F2;
Habitat Movement /Time=10,52 /Stage=Pre-smolts /Class=P1;
Habitat Movement /Time=10,52 /Stage=Pre-smolts /Class=P2;
Habitat Movement /Time=10,52 /Stage=Pre-smolts /Class=P3;
Habitat Movement /Time=10,52 /Stage=Immature smolts /Class=S1;
Habitat Movement /Time=10,52 /Stage=Immature smolts /Class=S2;
Growth /Stage=Eggs, Immature Smolts;
Detail;
Mortality;
Immigration /Stage=Fry, Immature Smolts;
Graduate /Stage='Eggs/Alevins',Immature Smolts;
```

In the preceding example, SALMOD will run for a total of 52 time steps with a starting date of September 2, 1986, with an anadromous population. Habitat capacity for each computational unit will be determined by total biomass rather than number of fish, and HABITAT MOVEMENT has been structured to move the smallest fish first to relieve that constraint. Redd superimposition will be determined randomly, and spawners will be distributed temporally based on the data supplied in SPAWN.DAT.

Sixteen processes have been specified in the process list. During each time step, the processes will be executed in the order given. For the above example, SUPPLEMENT will be executed in time step zero, followed by the processes beginning in time step one, in the following order: SUPPLEMENT, SPAWN, FRESHET MOVEMENT, BIOMASS COMPUTATION, GROWTH, MORTALITY, IMMIGRATION, AND GRADUATION. HABITAT MOVEMENT is not executed in time step one, as the time switch specifies execution from time step 10 to 52 only. Likewise, SEASONAL MOVEMENT will be executed beginning time step 35 and ending time step 39. Movement for HABITAT and SEASONAL MOVEMENT is 100% downstream. Detailed output will be provided for the MORTALITY process in each time step.

As mentioned, processes are executed in the order listed in CONTROL.DAT. Note in the example above that GRADUATE is the last process listed. Even though the habitat moves have been governed by the computational unit capacity, any particular computational unit could find itself several thousand percent over capacity due to graduation of one stage to the next. This is particularly true with eggs graduating to fry. Thus, any over capacity "problems" will show up in the next time step. Process order is also important for the habitat moves and the biomass

computation. The habitat moves will be based on the previously executed BIOMASS computation; therefore, it is advisable to place the biomass computation prior to the habitat moves in CONTROL.DAT.

Our advice is to carefully plan out the order of processes and make sure you carefully understand the implications of that order prior to making your first run. At times, it may not be possible to achieve exactly what you want, but you can probably get close. Then, periodically review the order in light of the output you are getting to see if the order of calculations is influencing any problematic results.

Example 2 - *Resident* Model

```
; Sample brown trout model
Timesteps=286;
Date=09/27/1991;
Capacity=Numbers;
Population=Resident;
Supplement /Time=0; Step 0 establishes standing crop by seeding stream
Biomass computation;
; Habitat movement must be done in two steps so eggs don't try to move
Habitat Movement /Time=1,52 /Stage=Adult Females, Spawning Males /Move=UP050;
Habitat Movement /Time=1,52 /Stage=Fry, Yearlings /Move=UP050;
Growth /Stage='Eggs/Alevins',Fry; moving fry don't grow
Growth /Stage=Adult Females;
Growth /Stage=Adult Males;
Growth /Stage=Parr, Yearlings;
; Immigration from virtual stream must be done in two steps
; because of life stage order
Immigration /Stage=Adult Females, Spawning Males;
Immigration /Stage=Fry, Yearlings;
Carry /Time=50,7;
Spawn /Time=1,7 /SI=Random; Puttnam per. comm.
Mortality;
Graduate;
Mature /stage=yearlings /class=Y3;
```

SPAWN.DAT

Spawning information and distribution are provided in SPAWN.DAT. Allowable spawning temperatures, area per redd, number of *in vivo* eggs per female, and time steps when spawning occurs are indicated for each species. The proportion spawning in each time step is entered as a decimal, and the sum of all proportions must equal 1.0. SALMOD assumes that the temporal pattern of spawning is the same each biological year. Note that if water temperatures are outside of the specified minimum-maximum range, adults simply hold in place and are subject to "normal" movement and mortality.

Note: Title lines and full line comments are not valid.

Format

Species Name (1)
  Average Area Per Redd Pocket
  Minimum spawn temp, maximum spawn temp
  Average weight of fry upon emergence (maturation from alevins)
  Beginning Spawning Time step (b)
  Proportion Spawning in time step b
  Proportion Spawning in time step b+1
  . . .
  . . .
  . . .
  Proportion Spawning in time step b+n   **Note**: proportions must total 1.0!
      (n need not be fixed ahead of time)
  . . .
  . . .
  . . .
Species Name (Number Of Species)
  Average Area Per Redd Pocket
  Minimum spawn temp, maximum spawn temp
  Average weight of fry upon emergence (maturation from alevins)
  Beginning Spawning Time Step (b)
  Proportion Spawning in time step b
  Proportion Spawning in time step b+1
  . . .
  . . .
  . . .
  Proportion Spawning in time step b+n (n need not be fixed ahead of time)

Example

```
Chinook Salmon    ;identifies species for multi-species runs
4.5               ;average area per redd (m**2)
5.6 13.9          ;min-max spawn temperatures(C)
.396              ;average wt of fry upon emergence(g)
1                 ;beginning spawn time step within year
   .01            ;spawn distribution (fraction spawn in each time step)
   .01
   .04
   .03
   .11
   .18
   .34
   .16
   .04
   .05
   .02
   .01
```

RELATION.DAT

RELATION.DAT contains information on movement and mortality rates. The relationships provided are described below in order of appearance in the file. In cases where a value required by SALMOD falls between two values listed in the file, the required value will be interpolated. No extrapolation will be performed; if a value is outside the range of the pairwise values, the relevant maximum or minimum value will be used after an appropriate warning message. To eliminate warning messages, simply increase the outside range if possible.

Freshet Movement parameters include the distance moved, proportion moved, and associated mortality rate. These parameters are required for each juvenile life stage in the *Anadromous* model, and all life stages in the *Resident* model, by size class.

Seasonal Movement parameters include the time-step when seasonal movement occurs, the distance moved, the proportion moved, and the associated mortality rate. Seasonal Movement parameters are required for each juvenile life stage in the *Anadromous* model, and all life stages in the *Resident* model, by size class.

A *Temperature vs. Growth relationship* is required for every non-adult life stage and provides the weekly growth factor for specific temperature values. These values are also required for adult life stages in the *Resident* model. We have found Crisp (1981, 1988) very helpful for egg incubation and (Shelbourne et al. 1973) for juvenile growth.

The *Base Mortality Rate* indicates the proportion of the population dying each week from causes other than movement or temperature. A base mortality rate is required for every life stage.

A *Temperature-induced Mortality Rate* is also required for every life stage. This relationship indicates the proportion of the population dying each week at various temperatures.

The *Temperature-induced in vivo Egg Mortality Rate* indicates the proportion of eggs dying each week at various temperatures. This relationship is required for each species.

A *Weight vs. Length relationship* is also required for each species.

The *Habitat-induced Movement Mortality Rate* indicates the proportion of the population that dies from moving a certain distance. The last distance provided in this distance versus mortality rate relationship is the maximum distance that a fish can move in one time step. Any fish required to move beyond this maximum distance dies. This relationship is required for each juvenile stage in the *Anadromous* model, and all life stages in the *Resident* model, by size class.

The *Density-induced Mortality Rate* is required for each life stage. This relationship is expressed in density as number of fish in number/m^2 (or biomass in gm/m^2, depending on **Capacity** designation in CONTROL.DAT) per unit area versus the weekly mortality rate. The density levels provided are significant even if the mortality rate does not vary. The upper density limit

provided is the habitat carrying capacity that triggers habitat-induced movement. This parameter is obviously a key to SALMOD dynamics. Note that we are assuming that the upper density limit per unit habitat is fixed for each lifestage and does not vary across mesohabitat types or throughout the period of food availability. Both of these assumptions must be considered in applying SALMOD and considering how the habitat qualities are measured and how finely to divide the lifestage descriptors.

A *Female Weight vs. Number of Eggs* relationship for each species is the final relationship contained in this file.

Note: Converting rates from time periods other than a week to a weekly rate is best illustrated as a two-step process. First convert the reference rate you may have to a daily instantaneous rate by:

$$M_1 = 1 - (1 - M_n)^{1/n}$$

where M is the mortality rate and n is the number of days in the reference period. Then convert the daily instantaneous rate to a 7-day rate as:

$$M_7 = 1 - (1 - M_1)^7$$

For example, suppose you know that temperature mortality is 80% at 15 days of mean water temperature of 16.1°C. Then

$$M_1 = 1 - (1 - .8)^{1/15} = 1 - 0.898 = 0.102$$

and

$$M_7 = 1 - (1 - 0.102)^7 = 1 - 0.472 = 0.528$$

Notes: Title lines and full line comments are not valid.
Relation.Dat must end with a blank line.

<u>Format</u>

[Freshet Movement Parameters - repeats for each class, stage, and species]
Species
  Stage
    Class
      Distance Moved, Proportion Moved, Proportion Dying
[Seasonal Movement Parameters - repeats for each class, stage and species]
Species
  Stage
    Class
      Timestep, Distance Moved, Proportion Moved, Proportion Dying

[Temperature vs. Growth Parameters - repeats for each stage and species]
Species
  Stage
    Temperature1, Daily Growth Rate1
    Temperature2, Daily Growth Rate2
     . . .   . . .
     . . .   . . .
[Base Mortality Rate - repeats for each stage and species]
Species
  Stage
    Proportion Dying per week

[Temperature Mortality Rate - repeats for each stage and species]
Species
  Stage
    Temperature1, Proportion Dying per week1
    Temperature2, Proportion Dying per week2
     . . .   . . .
     . . .   . . .
[Temperature vs. In vivo Egg Mortality Rate - repeats for each species]
Species
  Temperature1, Proportion Dying1
  Temperature2, Proportion Dying2
   . . .   . . .
   . . .   . . .
[Weight vs. Length Parameters - repeats for each species]
Species
  Weight1, Length1
  Weight2, Length2
  . . . . . .
  . . . . . .
[Distance vs. Mortality Parameters - repeats for each class, stage and species]
Species
  Stage
    Class
      Distance Moved1, Proportion Dying1
      Distance Moved2, Proportion Dying2
       . . .   . . .
       . . .   . . .

. . .   . . .
[Density vs. Mortality Parameters - repeats for each stage and species]
Species
  Stage
    Density1, Proportion Dying1
    Density2, Proportion Dying2
     . . . . . .
     . . . . . .
[Weight vs. Number of Eggs Parameters - repeats for each species]
Species
  Weight1, Number of Eggs1
  Weight2, Number of Eggs2

  . . .   . . .

  . . .   . . .

<u>Example</u>

```
Chinook Salmon              ; freshet movement parameters
Fry
 F1
   3780 .90   .1            ; Distance Moved, Prop. Moved, Prop. Dying
 F2
   4860 .10   .1
Pre-Smolts
 P1
   5940 .8    .05
 P2
   7020 1.0   .04
 P3
   8100 .8    .03
Immature Smolts
 S1
   9180 .8    .02
 S2
 10260 .8     .01
Chinook Salmon              ; seasonal movement parameters
Pre-Smolts
 P1
35  20000 .80   .05         ;  time, distance, proportion, mortality
36  20000 .80   .05
 P2
35  20000 .85   .04
36  20000 .85   .04
 P3
35  20000 .90   .03
36  20000 .90   .03
Immature Smolts
 S1
35  20000 .95   .02
36  20000 .95   .02
 S2
35  20000 1.0   .01
36  20000 1.0   .01
Chinook Salmon              ; temperature vs. growth relation
Eggs/Alevins               ;           -per/day (additive)
            0 0.0022
            1 0.0028
            2 0.0034
```

```
               3 0.0042
               4 0.0051
               5 0.0061
               6 0.0072
               7 0.0085
               8 0.0098
               9 0.0112
              10 0.0126
              11 0.0141
              12 0.0156
              13 0.0170
              14 0.0184
              15 0.0196
              16 0.0207
              17 0.0216
              18 0.0222
              19 0.0227
              20 0.0229
Fry                                 ; - per day (multiplicative)
           1                0.008
           5                 .021
          10                 .05
          15                 .065
          20                 .06
          24                -.002
Pre-Smolts                          ;    -per day (multiplicative)
           1                0.003
           5                0.009
          10                 .018
          15                 .025
          20                 .017
          24                -.002
Immature Smolts                     ;    -per day (multiplicative)
           1                0.002
           5                0.0075
          10                 .0125
          15                 .014
          20                 .011
          24                -.002
Chinook Salmon                      ; base mortality rate
Eggs/Alevins
0.02
Fry
0.06
Pre-Smolts
0.016
Immature Smolts
0.004
Adult Females
0.001
Spawning Females=Adult Females
Adult Males=Adult Females
Spawning Males=Adult Females
Chinook Salmon           ; temperature vs. mortality relation - per week (mult)
Eggs/Alevins
         0.00    .00
        13.33    .00
        15.00    .081
        15.56    .272
        16.11    .460
        16.67    .867
        17.22    .934
```

```
        17.78    1.000
        19.00    1.000          ; maximum allowable value before warning message
Fry
         0.00     0.00
        12.22     0.00
        13.39    .2500
        17.44    .5000
        19.78    .7500
        21.11    1.0
        37.78    1.0
Pre-Smolts
         0.00     0.00
        12.22     0.00
        13.39    .2500
        17.44    .5000
        19.78    .7500
        21.11    1.00
        37.78    1.00
Immature Smolts
         0.00     0.00
        12.22     0.00
        13.39    .2500
        17.44    .5000
        19.78    .7500
        21.11   1.0000
        37.78   1.0000
Adult Females
            0        0
         12.8        0
           24      0.7
           35      0.7
Spawning Females=Adult Females
Adult Males=Adult Females
Spawning Males=Adult Females
Chinook Salmon               ;   temperature vs. in vivo egg mortality relation
         0.00     .00
        13.33     .00
        13.89    .028
        14.44    .048
        15.00    .084
        15.56    .257
        16.11    .317
        16.67    .455
        17.22    .483
        17.78    .652
        19.00    .652
Chinook Salmon               ; weight vs. length relation
        0.31       30
        0.74       40
        1.44       50
        2.48       60
        3.94       70
        5.89       80
        8.38       90
       11.50      100
        . . .
     5888.00      800
     7062.44      850
     8383.50      900
```

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```
Chinook Salmon          ; distance moved vs. mortality rate relation - per step
Fry                     ; --- last distance specified is the maximum distance
  F1
    0    .0
    500  1.0
  F2
    0    .0
    750  1.0
Pre-Smolts
  P1
    0    .00
    2000 1.0
  P2
    0    .00
    3000 1.0
  P3
    0    .00
    7000 1.0
Immature Smolts
  S1
    0    .00
    10000 1.0
  S2
    0    .00
    10000 1.0
Chinook Salmon       ;   density vs. mortality relation - weekly
Fry                  ;   --- density is biomass (gm)/m**2
    0  0.00          ;   Even if there is no direct density-dependent mortality
    25 0.01          ;     the upper limit of density triggers the habitat-
Adult Females        ;     induced movement
    0  0.00
    1800 0.00
Immature Smolts
    0  0.00
    25 0.20
Eggs/Alevins
    0  0.0           ;  --- density-independent relationship
    1000 0.0         ;      upper bound not relevant for eggs
Pre-Smolts
    0  0.0
    15 0.04
Spawning Females=Adult Females
Adult Males=Adult Females
Spawning Males=Adult Females
Chinook Salmon                     ;  weight vs. # eggs relation
2000  2666
4000  3732
7000  4666
```

WUA.DAT

This data file contains the detailed (weighted) usable area versus flow data for each mesohabitat type, species, and life stage. Flow is in cubic feet per second and usable area in square feet per foot of stream. There is a limit of 30 flow versus usable area pairs per lifestage. The indentation shown is simply for readability and is not required. Information on more mesohabitat types than required can be included in this file. This flexibility allows the user to create one WUA.DAT file that can be used for a number of model runs with different CONTROL.DAT and STREAM.DAT file configurations.

Note: Title lines and full line comments are not valid. There should be no extra blank line at the end.
Note: Usable area values are in ft^2/ft, not $ft^2/1000$ ft as would be typical PHABSIM output.

<u>Format</u>

```
Mesohabitat Type Name (1)
  Species Name (1)
   Life Stage Name        ; Life stages can be in any order
     Flow Value, UA       ; however, each life stage must be
     . . .                ; accounted for.
     . . .
     . . .
     Flow Value, UA
   . . .
   . . .
   . . .
   Life Stage Name
     Flow Value, UA
     . . .
     . . .
     . . .
     Flow Value, UA
  . . .
  . . .
  . . .
  WUA for life stages can also be listed by their relationship to previously defined life stages in the format:
   Life Stage Name = Previously defined Life Stage Name * Multiplier
  Species Name (Number Of Species)
   Life Stage Name
     Flow Value, UA
     . . .
     . . .
     . . .
     Flow Value, UA
  . . .
  . . .
  . . .
   Life Stage Name
```

Flow Value, UA
. . .
. . .
Flow Value, UA
. . .
. . .
Mesohabitat Type Name (Number Of Mesohabitat Types)
. . .
. . .

Example

```
    C1                   ; Mesohabitat Type
    Chinook Salmon      ; Species
    Fry           ; Life Stage
 150    7.7          ; Flow - WUA pairs
 350    4.8
 450    3.8
 800    2.5
2000   33.3
    Pre-Smolts          ; Life Stage 2
 150   48.0          ; Flow - WUA pairs
 350   28.7
 450   27.2
 800   17.7
2000   32.1
    Spawning Females    ; Life Stage 3
150    5.1841             ; Flow - WUA pairs
350   15.2016
800    8.8439
Adult Females=Pre-Smolts*5.0  ; Life Stage 4
Adult Males=Adult Females     ; Life Stage 5
Spawning Males = Adult Males  ; Life Stage 6
Eggs/Alevins=Spawning Females*3.0        ; Life Stage 7
Immature Smolts=Pre-Smolts    ; Life Stage 8
    C2                   ; Second Mesohabitat Type
    Chinook Salmon      ; Same Species
    Fry
 150    5.5
 350    4.5
 450    6.9
 800    6.6
2000    4.6
    Pre-Smolts
 150   28.3
 350   23.2
 450   20.7
 800   16.1
2000   21.4
   Spawning Females
150    2.0219
350    2.7536
800    0.172
Adult Females=Pre-Smolts*5.0
Adult Males=Adult Females
Spawning Males = Adult Males
Eggs/Alevins=Spawning Females*3.0
Immature Smolts=Pre-Smolts
```

FLOW.DAT

This is the stream flow data file. One set of flows can be provided for the entire study reach, or the stream can be divided into 'flow segments' with a corresponding set of flow data provided for each segment. Data on each line represent flows at a single time step. The flow segments are defined in the STREAM.DAT file. Note that if /Option=UserSpec is used with the freshet movement process, then flow values for those time steps where freshet events are to occur must be entered as negative values.

Note: Full line comments are valid in FLOW.DAT.

<u>Format</u>

Flow(1,1) Flow(1,2) ... Flow(1, Number Of Flow Segments)
. . .
. . .
. . .
Flow(Number Of Time Steps, 1) ... Flow(Number Of Time Steps, Number Of Flow Segments)

<u>Example</u>

```
  351.57    354.00     ;water year 1986 beginning Sept. 2
  349.88    352.00
  326.71    334.00
  333.29    335.00
  326.86    330.00
…
  317.86    320.00
  319.00    320.00
  314.43    320.00
  310.43    311.00
  308.14    309.00
  312.29    322.00
  305.57    308.00
  311.00    314.00
  307.14    309.00
  463.57   1260.00     ;(see note below)
 1211.43   1750.00     ;(          |          )
 2581.43   2680.00     ;(          |          )
 3840.00   6150.00     ;(          |          )
 6200.00   6250.00     ;(          V          )
 2847.57   5730.00
  423.57    518.00
  427.86    480.00
        .  .  .
        .  .  .
        .  .  .
  624.43    631.00
  609.57    623.00
  485.86    503.00
  299.14    302.00
  301.43    305.00
  304.43    308.00
```

Note: Looking at the section of the FLOW.DAT file noted, for flow segment 1, the values 1211.43 and 2581.43 above would produce freshet events under options 1 (2xPorA) and 2 (2xPandA). The values 3840 and 6200 would produce freshet events under option 2 only. For flow segment 2, the value 1260 would produce a freshet event under option 1 or 2, while the values 1750 and 2680 would produce freshet events under option 1 only. The value 6150 would again produce a freshet event under option 1 or 2.

SUPLMENT.DAT

This file provides information for the model to add fish into the population at the appropriate time and location. Most of SALMOD's references to time are weeks within a biological year. SUPPLEMENT is different in that the time steps specified are a sequential count from the beginning of the simulation run, and may optionally include zero for seeding the stream prior to any other process. For example, if spawning occurred regularly, SUPPLEMENT may be used for time step one, fifty three, etc. Location can be given as a range of either computational units (indicated as integer values) or distances from the top of the study reach (indicated as real values). Fish are apportioned to the range of CU's designated in proportion to the habitat available for their lifestage at the time that they are introduced, with adults going to adult habitat in the *resident* variant and to spawning habitat in the *anadromous* variant. If no habitat is available for the computation units specified for the flow at the time of introduction, the fish will be apportioned based on length of the computation units alone, with a warning message issued.

If adding adult fish, the locations, number of adults, sex ratio (actually ratio of spawners to non-spawning adults), and the weight for males and females are indicated. For juveniles, enter the location where they appear, the number of fish, and weight only; the sex ratio will be assumed to be 50:50. In other words, adults get six parameters and non-adults get four.

Note: Title lines and full line comments are not valid.

<u>Format</u>

Time Step
  Species Name
    Upstream Comp Unit # or Distance, Downstream Comp Unit # or Distance, # adults, Sex ratio (F:M),
      weight for males, weight for females
  . . .
  . . .
  . . .
    Upstream Comp Unit # or Distance, Downstream Comp Unit # or Distance, # adults, Sex ratio (F:M),
      weight for males, weight for females
  . . .
  . . .
  . . .
  Species Name

Upstream Comp Unit # or Distance, Downstream Comp Unit # or Distance, # adults, Sex ratio (F:M), weight for males, weight for females

. . .

. . .

. . .

Upstream Comp Unit # or Distance, Downstream Comp Unit # or Distance, # juveniles, weight

. . .

. . .

. . .

Time Step

Species Name

Upstream Comp Unit # or Distance, Downstream Comp Unit # or Distance, # adults, Sex ratio (F:M), weight for males, weight for females

. . .

. . .

. . .

Upstream Comp Unit # or Distance, Downstream Comp Unit # or Distance, # adults, Sex ratio (F:M), weight for males, weight for females

. . .

. . .

. . .

Species Name

Upstream Comp Unit # or Distance, Downstream Comp Unit # or Distance, # adults, Sex ratio (F:M), weight for males, weight for females

. . .

. . .

. . .

Upstream Comp Unit # or Distance, Downstream Comp Unit # or Distance, # juveniles, weight

Example

```
0                                    ; Zero time step to seed stream
Chinook Salmon                       ; Species Name
     0.0   1794.4 3788 .33 4000 4000 ; Upstream Distance, Downstream distance, # Adults
 1794.4 27814.8 4508 .33 4000 4000   ; Proportion of spawners (F:M), male and female
27814.8 39934.8  402 .33 4000 4000         ; weights
25                                   ; Time step 25
Chinook Salmon                       ; Species name
 95 95 2500 1.25                     ; Juveniles entering at a specific computation unit
53                                   ; Only time step 53
Chinook Salmon
     0.0   1794.4 3788 .33 4000 4000
 1794.4 27814.8 4508 .33 4000 4000
27814.8 39934.8  402 .33 4000 4000
```

TEMP.DAT

The stream temperature data are provided in a file similar to the stream flow file. Temperatures are entered one time step per line. If data are available for more than one location, the stream is divided into the ☐temperature segments' defined in STREAM.DAT. Temperatures contained in the file should be representative of those encountered by the lifestage(s) present at the appropriate time of year. For instance, eggs buried in the gravel may be warmer during the winter months than measured free-flowing water temperatures (Shepherd et al. 1986). Adjusting the temperatures accordingly, to the degree necessary, should be considered.

Note: Full line comments are valid.

Format

Temp(1,1) Temp(1,2) ... Temp(1, Number Of Temp Segments)
.
.
.
Temp(Number Of Time Steps, 1)...Temp(Number Of Time Steps, Number Of Temp Segments)

Example

```
     9.44     11.11        ;Seg 1 is Lewiston to Grass Valley
     9.44     10.56        ;Seg 2 is Grass Valley to Douglas City
     9.17     10.00
     8.89      9.44
     8.61      8.89
       . . .
       . . .
       . . .
     7.78      7.78
    10.00     11.11
    10.00     11.39
    10.00     11.67
    10.00     12.22
    10.00     12.22
    10.00     12.22
```

SALMOD s PROGRAM LIMITS

SPECIES LIMITS
       Maximum number of fish species modeled (2)
       Maximum number of life stages for each species (12)
       Maximum number of size classes for fry - juveniles (5)

STREAM LIMITS
       Maximum number of computational units (1000)
       Maximum number of stream segments defining flow regime (15)
       Maximum number of stream segments for temperature regimes (15)
       Maximum number of mesohabitat classification types (60)
       Maximum number of stream segments for supplementing fish (20)

RELATION LIMITS
       Maximum number of density: mortality pairs (20)
       Maximum number of distance: mortality rate pairs (10)
       Maximum number of flow values to for flow : WUA relation (30)
       Maximum number of temperature :mortality, temperature: growth pairs (30)
       Maximum number of weight:length pairs (30)
       Max number of seasonal time step movements (15)

SPAWN LIMITS
       Maximum number of time steps for spawning (30)

OTHER LIMITS
       Maximum number of characters in filenames (30)
       Maximum number of cohorts per species per computational unit (25)
       Maximum number of population processes to perform per time step (30)
       Maximum number of usable area versus discharge pairs in WUA.DAT (50)

STEPS IN ORGANIZING AND RUNNING SALMOD

1. Decide if SALMOD is appropriate for your problem or situation. The program should have a measure of "face validity" for the type of problem you are facing, i.e., is habitat a principal limiting factor in your situation? Are the management objectives, potential control options, and constraints (data, legal, regulatory, and economic) such that using a model like SALMOD, with its spatial and temporal resolution, would be helpful. Is there a simpler model, consistent with data and the problem at hand, that will work?

2. Assemble data, using sample data sets as a guideline. To the degree possible, make sure the physical data (flows, temperatures, mesohabitat types) are well specified so that level of uncertainty is "removed" from the model, leaving the biological realm as the most uncertain. Data assembly can be a daunting task; however, procrastination will get you nowhere. This can cause you to ask excellent questions!

3. All simulation models contain unobservable or poorly quantified values. Annotate data files (and keep a cumulative set of additional notes in NOTES.RTF) with:
   a. the source of all data
   b. any assumptions you have made about the input data
   c. the implications for the domain of the model's applicability, i.e., what are the ranges of flows and water temperatures within which the model should be appropriate?

4. Verify data by running SALMOD with the *preprocess* options.
   a. look for any messages in SALMOD.OUT. In particular, 1) look for error, warning, or informative messages, 2) correct the errors, and 3) be satisfied about the meaning of the others.
   b. compare data in formatted listing with original data files,
   c. review the formatted process list to insure the processes and their switches are what you expected.

5. Run SALMOD for a single biological year. Examine SALMOD.OUT and SUMMARY.OUT for meaningful results. Do they corroborate the knowledge of local experts? Try seeding the system with only a few adults and let them all spawn at once, rather than try to sort out all the dynamics of a multi-year simulation.

   Steps 4 and 5 collectively imply scrutinizing several things. Do fish graduate appropriately from one life stage to another? Is the timing right? If spawning occurs on date X does emergence occur on date Y? Once emerged, do fish grow at about the right rate? Do the causes of mortality seem in about the right ballpark? Remember that much if not most of the literature available is poor in being explicit. One person's definition of a parr may be quite different from another's. One study area may have water temperatures quite different from another's. All of these differences may confound thorough tests for reasonableness. Do NOT pay any attention to number of fish at this point (unless there are none!).

Remember that SALMOD employs a strictly descriptive and deterministic relationship between temperature and lifestage-specific growth rate. One could "calibrate" growth by shifting the curvilinear relationship left or right based on race-specific attributes, or shift the curve up or down based on relative food supply perhaps using Shelbourne et al. (1973) as guidance. One may fairly ask the question "How might the temperature-growth relationship change if there was (1) substantial channel change resulting in more shallow edge-water habitat and/or (2) a reduction in fine gravel now clogging the cobble? Both could alter the food producing value of the habitat.

6. Examine the graphs to explore the population's dynamics. Look to see if the model is behaving as you might expect. If not, try the DETAILS and/or SUMMARIZE switches.

7. If appropriate, run SALMOD for multiple years, under different environmental conditions, looking for reasonable behavior. Set the model at risk by trying extreme conditions. Extreme conditions can also include non-varying conditions. Turn various control options off and on to confirm their effect. Does the model behave plausibly? I recommend keeping a set of notes chronicling your observations for this step as well as steps 8 and 9.

8. Data permitting, calibrate SALMOD to growth, numbers, outmigrants, etc., by adjustment of parameters within a reasonable range to improve the agreement between model output and real-world observations. Calibrating the "parts" is better than trying to do everything at once. For example, get your emergence timing right by carefully scrutinizing the spawn time, water temperatures, and egg development rate. Simple goodness-of-fit measures are all that are necessary with SALMOD as the data are likely too noisy to do much else. Beware using single measures; one that captures trend (like R^2) and one that captures closeness of fit (like RMSE) would be preferable. Again, data permitting, run the calibrated model for other data sets (typically years) to see if it holds up to additional scrutiny. This helps to confirm the calibration.

9. If you haven't already effectively done so, determine the sensitivity of the model by noting those parameters causing significant change in the model's behavior. Though there are various forms of sensitivity analysis, SALMOD lends itself to simple first-order analysis by varying relevant parameters by a set percentage up and down.

10. Decide if the model mimics the real world well enough to satisfy your purposes. This implies that you have objective measures of what "good enough" means.

11. Combining elements of steps 6, 7, 8, 9, and 10, decide how much confidence to place in inferences about the real system based on model results. Clearly state whether your confidence is qualitative or quantitative. *All models are wrong, but some are useful*.

12. Exercise SALMOD in the evaluation of alternatives.

13. Organize the results for communication to others. Include all important assumptions, noting which were modified through learning ⊂ a model is an assumption analyzer.

14. Document adjustments necessary to the model and/or to the observed data to improve the whole modeling process. Both are moving targets.

15. Resources permitting, attempt to invalidate the model by comparing *a priori* predictions against real-world measures, the so-called post-audit validation.

Note: For a reasonable, if long winded, discussion of testing (verifying and validating) ecological models, see Rykiel (1996).

SALMOD's VERSION HISTORY

Version 1 - This version is the original version.

Version 1.01 - Modifications made from 6/14/93 to 8/6/93
1 - Upstream and downstream movement has been incorporated.
2 - Gates have been installed at each end of the study area to regulate movement into and out of the study area.
3 - The appropriate tables have been added to the output for the upstream sink.
4 - Last in first out changes made.
5 - Comp Units processed in a random order.

Version 1.02 - Modifications made from 8/6/93 to 8/23/93
1 - Call InitMovement Statistics to clear out old data when a new year begins.
2 - Main routine modified to call SALMODINIT, SALMODCLOSE, and SALMODPROC in preparation for link with the water model.
3 - Added switch to turn on the resident model. ex. POPULATION=Resident
4 - Added a process to mature immature smolts to adults at a specified time step. Used in the resident model. ex. MATURATION /Time=1 /Stage=Yearlings
5 - Modified movement to allow adults to move without searching for an empty group in new comp units. Adults are kept in a single cohort, saving memory for juvenile cohorts.
6 - Went to old version of mort.for as mortality calculations were determined to be more accurate.

Version 1.03 - Modifications made from 8/24/93 to 2/2/94
1 - Modified the binary search code in ReadHabLabel. Old version would return a value in certain conditions where a match was not found.
2 - SI option now a switch on SPAWN process. ex. SPAWN /SI=Random
3 - CARRY process specifies when females carry eggs. This process is required. If CARRY is not included in the Control file, females will never carry eggs. ex. CARRY /Time=1,52 (Currently defaults to 1,52)
4 - Invivo switch added to MORTALITY process. Specifies when *in vivo* egg mortality is calculated. ex. MORTALITY /Invivo=1,52 (Currently defaults to 0,0)

Version 1.04 - Modifications made from 2/3/94 to 3/10/94
1 - New process call CATASTROPHY. Specify species, stage, class to be affected by CATASTROPHY as with other processes.   Specify date of catastrophe as /DATE=mm/dd/yyyy. This will only occur on the specified date. Specify percent losses with /RATE=xx where xx is a whole number expressing percent losses.
2 - New switch added to the GRADUATE process. Temperature above or equal to emergence can occur.   /EMERGENCE TEMPERATURE = xx.x where xx.x is temperature in C.

Version 1.5 - Modifications made from 3/11/94 to 9/9/94
1 - Modified output subroutine so all textual output is within double quotes.
2 - Modified the -I option to include all user comments.
3 - Added -b and -b1 switches to create brief summaries.

Version 1.51 - Modification made 9/16/94
1 - Fixed a bug in the SUPPLEMENT process. The previous version allowed some adult fish to not be added to the river under conditions where the last computation unit in the list for a spawn segment had no weighted usable area.
2 - Fixed a bug in the subroutine that reads input files. Previous version was not reading computation units for spawning segment definitions.

Version 2.00 - Modifications made 5/97
1 - SUPPLEMENT process modified to allow juvenile fish to be added to the system.
2 - Model=Spawner option was removed.
3 - General bug fixes to SALMOD in general and the Population=Resident option in particular.
4 - Fixes to PLOTSTAT to accommodate SALMOD's new limits.

Version 2.01 - Modifications made from June to August, 1997
1 - Limit on the number of flow and/or temperature segments was increased to 10.
2 - CreateSpawners was moved from the beginning of the spawn process to the beginning of the time step in which spawning occurs.
3 - Created the "Salmod.err" file. This file is created at the beginning of a SALMOD run and is deleted at the end. If the file exists, SALMOD bombed. This was created primarily for SIAM to allow the system to detect if SALMOD run successfully or not.
4 - Fixed a bug in the initialization routine to remove resident population stage requirements from anadromous populations.

Version 2.05 - Modifications September, 1997
1 - Modified the SUPPLEMENT process to apportion fish based on comp unit length if there is no habitat. Also added the */Time=0* option.
2 - Fixed a bug where adult cohorts did not have a stage setting. This caused some adult cohorts to be ignored in some processes. Fixing this bug fixed several apparent problems in the output.
3 - The "Numbers Reaching Stage" table was modified to a "Mass Balance" table. This involved adding adult stages to the table and tallying supplements, graduates, mortality, exiters, and those remaining instream.
4 - Added the RemoveSpawners subroutine. This subroutine is called at the beginning of the first time step after spawning has completed, and returns any remaining spawners back to the adult stages.
5 - A bug in the mortality rate calculation was fixed.

Version 2.06 - Modifications November, 1997

1 - Modified the SUPPLEMENT process to create spawners at the beginning of any time step during which spawning occurs for the *anadromous* variant. Note that it has been problematic getting spawning to "work" properly for both model variants, and for both a single and a multi-year run

Version 2.07b - Modifications July, 1998.

1 - Added -w switch to print weight instead of length in summary output for SALOPT.

Version 2.08 - Modifications January through March, 1999

1 - Fixed bug where adults did not grow.
2 - Fixed bug where eggs per female were reset by immigration process.
3 - Allowed Carry process to span biological year boundaries, but Carry is now a required process.
4 - Changed output file to:
    - increase decimal places for weight and length
    - added total kilograms to output
    - calculate coefficient of variation (CV%) on brief output
    - write filenames to summary/brief output similar to .out file.
5 – Changed "Habitat loss" to "Lost eggs"

Version 2.1 – Modifications October through April, 2000

1 – Added the GRADUATE process switch for *INITDEV*
2 – Added the HABITAT MOVEMENT process switch for *ORDER*
3 – Increased maximum number of flow and thermal segments from 10 to 15
4 – Replaced PLOTMORT and PLOTSTAT with SALPLOT
5 – Cosmetic changes to documentation

Version 3.1 – Modifications to implement WindowsTM GUI through August 2001

1 – All of the enhancements associated with the Windows implementation
2 – Added *Multiyear* simulation option
3 – Added *Barrier* gate type
4 – Put cap on maximum growth
5 – Corrected the computational shuffle prior to habitat movement
6 – Made the Summary file not so hard wired for the Trinity data set
7 – Corrected some problems with summary mortality statistics
8 – Increased the number of flow:WUA pairs to 50
9 – Several cosmetic changes to output tables and "pre-process" input listing
10 – Corrected problem with adult mortality after spawning
11 – Corrected problem with "disappearing" movers
12 – Added Flow and temperature to output graphics
13 – Added a frequency distribution module for weight and length to output graphics
14 – Add a notes file capability
15 – Added check for non-text files as input files and for tabs in the input files

SAMPLE SALMOD MODEL OUTPUT

It has been our desire to make SALMOD's output useful, relatively easy to read and deal with, and understandable without being too lengthy. Simultaneously achieving these goals is always difficult, if not impossible, with a computer program such as SALMOD.

Some items in the *mortality table* require explanation:
- the *Spawned* category, for both male and female spawners, tallies fish that die after spawning.
- the *InVivo* category tallies eggs that died within their mother due to water temperatures. These eggs are not counted in the mass balance table as they were never successfully deposited.
- the *Resorbed eggs* category tallies eggs that "belonged" to female *resident* spawners who had not spawned by the completion of the spawning season for whatever reason and return to the adult female lifestage. These eggs are not counted in the mass balance table, as they were never successfully deposited. In the *anadromous* variant, non-spawned adults should die and these eggs are not tallied anywhere.
- the *Lost eggs* category tallies eggs that die when there is not enough spawning habitat for all the spawning females in a computation unit when they spawn. It is assumed that these eggs are shed, but as they are alive when leaving the female spawners, they are tallied in the mass balance table.
- the *Incubation Loss* category tallies eggs lost if redds (or portions of redds) are lost due to changing egg incubation habitat through the duration of the incubation season. This is based on whether egg habitat declines relative to that available when the eggs were deposited and reflects (1) drying of eggs in redds near the margins of the channel if streamflow drops, or (2) scour if flows get too high.

The Mass Balance table also requires explanation. Columns in the Mass Balance table represent the following information:

Entrants	Fish entering the system through the supplement process, upstream or downstream gates, or as deposited eggs.
Graduates	Fish reaching the specific stage through graduation or maturation from the prior stage.
Exiters	Fish exiting the system through either the upstream or downstream gates.
Deaths	Total mortality for the stage.
Instream	Those fish for the given stage remaining in the stream at the end of the year.

	Total	Total number of fish reaching the stage. This number is cumulative, so will increase each year.

Mass Balance Example

Consider the following supplements when viewing the Mass Balance Tables that follow.

```
Supplements in time step 0, 1992

        30638       adults
         2268       parr
         6369       fingerlings
        28499       yearlings
```

```
1992 Mass Balance for Brown Trout

                       Incoming                    Remaining   Cumulative
    Stage     Entrants Graduates  Exiters   Deaths  Instream    Total
------------------------------------------------------------------------
Adult Females    18383     11941        0     1993     28331      30324
Adult Males      12255     11941        0     1722     22474      24196
Eggs/Alevins  11066145         0        0 11044614         0   11066145
Fry                  0     21531        0    17570         0      21531
Parr              2268      3961        0     2151      2810       6229
Fingerlings       6369      1268        0      556       610       7637
Yearlings        28499      6471        0     4751      6337      34970
```

For the 1992 mass balance (see above), the total number of adult male (12255) and female (18383) entrants is equal to the number of supplemented adults (30638), the total number of entrants for Eggs/Alevins (11066145) will be the number of eggs successfully deposited through the spawn process, and the total number of entrants for the juvenile stages will equal the number of supplemented fish for the stage (2268 parr, 6369 fingerlings, and 28499 yearlings.)

In the first year of a simulation, the "Total" column equals the number of entrants plus the number of graduates during that year. In subsequent years, the "Total" column equals the sum of the number of entrants, the number of graduates, and the previous total.

In any given year, the following equation holds true:

Graduates(B) =   Instream(A, previous year) + Entrants(A) + Graduates(A) - Exiters(A) - Deaths(A) - Instream(A)

where A = any particular lifestage, and B = the next lifestage after A. (See note below for the case where B represents the adult life stages.)

Some examples for the 1992 mass balance:

```
          Adult Males Entrants     18383
          Adult Females Entrants +12255
          ------------------------------
          Supplemented Adults      30638
```

```
          Fry Entrants         0
          Fry Graduates    +21531
          Fry Exiters      -     0
          Fry Deaths       -17570
          Fry Instream     -     0
          ----------------------
          Parr Graduates     3961
```

Some examples for the 1993 mass balance:

```
        Fingerlings Instream (from 1992)   610
        Fingerling Entrants              +    0
        Fingerling Graduates             + 2691
        Fingerling Exiters               -    0
        Fingerling Deaths                -  198
        Fingerlings Instream             -  544
        -------------------------------------
        Yearling Graduates                  2559
```

```
        Yearlings Instream (from 1992)   6337
        Yearling Entrants                +    0
        Yearling Graduates               + 2559
        Yearling Exiters                 -    0
        Yearling Deaths                  -  131
        Yearlings Instream               - 3233
        -----------------------------------
                         -
        Adult Graduates                    5532
        -----------------------------------
                         -
        Adult Male Graduates               2766
        Adult Female Graduates             2766
```

Note that Graduates to the Adult lifestages is always at a 50:50 sex ratio, unlike the Supplement process for which the sex ratio may be specified.

Full Trinity River Model - Biological Year 88-89

Input Files from Files.Dat

```
Flow Data            : Q8889.PRN
Stream Definition    : ..\Stream.DAT
Spawning Parameters  : Spawn.88
Population Definition : ..\Species.DAT
Functional Relations : ..\Relation.DAT
Temperature Data     : T8889.REG
Useable Area Functions: ..\Wua.DAT
Returning Spawners   : Suplment.88
Process Definition   : Control.88
```

Output Files

```
Exiting Smolts       : Sink.dat
Numbers/Biomass Stats : Stats.dat
Transactions         : Trans.dat
Summary              : summary.out
```

Temporary Files

```
Habitat-Flow Functions: Hab.tmp
Mover Temporary File  : move.tmp
State variable Storage: SV.tmp
Comment Line:  Options
Comment Line:  Processes
```

Comment Line: Don't let freshet and seasonal movement overlap in time

Full Trinity River Model - Biological Year 88-89

"**********************************"
"Yearly/Final summary - 1989   "
"**********************************"

"Numbers remaining in stream   "
"--------------------------   "

"---------------   "
"Stream Summary   "
"---------------   "
"Chinook Salmon   "
"---------------------------------"
"# of cohorts = 3307   " "Numbers" "Avg Wt " "Avg Len" " Repr.
"
"   " "   " "(grams)" " (mm)   "
"#eggs/fem"

"--
"

	Numbers	Avg Wt (grams)	Avg Len (mm)	Repr. #eggs/fem
Adult Females	0	.0	.00	0.
Spawning Females	0	.0	.00	0.
Adult Males	17	2000.0	553.75	
Spawning Males	0	.0	.00	
Eggs/Alevins	0			
Prop. Mature 0-.33	0			
Prop. Mature .33-.67	0			
Prop. Mature .67-1.00	0			
Fry	0	.0	.00	
F1	0	.0	.00	
F2	0	.0	.00	
Pre-Smolts	70902	2.4	62.68	
P1	8105	1.8	57.27	
P2	59759	2.4	62.91	
P3	3038	3.6	72.60	
Immature Smolts	300	5.8	85.41	
S1	300	5.8	85.41	
S2	0	.0	.00	
S3	0	.0	.00	
Total Young	71202	2.4	62.78	

Full Trinity River Model - Biological Year 88-89

"Cumulative Mortality Statistics"
"------------------------------"

"Chinook Salmon	"	"Number"	"Percent"	"Rate"
" Adult Females	"			
" All	"	315.	1.000	.0271
" Base	"	60.	.190	.0052
" Temperature	"	255.	.810	.0220
" Density Dependent	"	0.	.000	
" Habitat Movement	"	0.	.000	
" Freshet Movement	"	0.	.000	
" Seasonal Movement	"	0.	.000	
" Spawning Females	"			
" All	"	11290.	1.000	
" Base	"	0.	.000	
" Temperature	"	0.	.000	
" Density Dependent	"	0.	.000	
" Habitat Movement	"	0.	.000	
" Freshet Movement	"	0.	.000	
" Seasonal Movement	"	0.	.000	
" Spawned	"	11290.	1.000	
" Adult Males	"			
" All	"	653.	1.000	.0303
" Base	"	130.	.199	.0060
" Temperature	"	523.	.801	.0243
" Density Dependent	"	0.	.000	
" Habitat Movement	"	0.	.000	
" Freshet Movement	"	0.	.000	
" Seasonal Movement	"	0.	.000	
" Spawning Males	"			
" All	"	20884.	1.000	
" Base	"	0.	.000	
" Temperature	"	2.	.000	
" Density Dependent	"	0.	.000	
" Habitat Movement	"	0.	.000	
" Freshet Movement	"	0.	.000	
" Seasonal Movement	"	0.	.000	
" Spawned	"	20882.	1.000	
" InVivo Eggs	"	127156.		

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"	Eggs/Alevins	"			
"	All	"	20885840.	1.000	.6967
"	Base	"	11675010.	.559	.3894
"	Temperature	"	1466.	.000	.0000
"	Density Dependent	"	0.	.000	
"	Incubation Loss	"	759884.	.036	.0253
"	Superimposition	"	8438848.	.404	.2815
"	Lost eggs	"	10625.	.001	.0004
"	Catastrophic	"	0.	.000	
"	Fry	"			
"	All	"	6469095.	1.000	.7113
"	Base	"	245156.	.038	.0270
"	Temperature	"	0.	.000	
"	Density Dependent	"	0.	.000	
"	Habitat Movement	"	6203480.	.959	.6821
"	Freshet Movement	"	20459.	.003	.0022
"	Seasonal Movement	"	0.	.000	
"	Catastrophic	"	0.	.000	
"	Pre-Smolts	"			
"	All	"	1535699.	1.000	.5907
"	Base	"	99822.	.065	.0384
"	Temperature	"	14009.	.009	.0054
"	Density Dependent	"	0.	.000	
"	Habitat Movement	"	984105.	.641	.3785
"	Freshet Movement	"	0.	.000	
"	Seasonal Movement	"	437763.	.285	.1684
"	Catastrophic	"	0.	.000	
"	Immature Smolts	"			
"	All	"	1823.	1.000	.1231
"	Base	"	1.	.001	.0001
"	Temperature	"	264.	.145	.0178
"	Density Dependent	"	0.	.000	
"	Habitat Movement	"	0.	.000	
"	Freshet Movement	"	0.	.000	
"	Seasonal Movement	"	1558.	.855	.1052
"	Catastrophic	"	0.	.000	

```
"Cumulative Movement Statistics "
"----------------------------- "
"Chinook Salmon               "
"                             ""      ""Dying Movers""        " "  ""Surviving Movers""     "
"                             ""Groups" "Number" "Avg Dist" "Groups" "Number" "Avg Dist"
"                             "                   "(meters)"                   "(meters)"
"Fry                          "
"  F1                         "
"     Habitat                 "    7527   6073272    297.     3234   1962460     188.
"     Freshet                 "     300     12943  20000.      300       260   20000.
"     Seasonal                "       0         0      0.        0         0       0.
"  F2                         "
"     Habitat                 "    2114    130208    367.      899    238155     219.
"     Freshet                 "     448      7516  20000.      455     17499   20000.
"     Seasonal                "       0         0      0.        0         0       0.
"Pre-Smolts                   "
"  P1                         "
"     Habitat                 "   14162    670144    620.     4151    731346     363.
"     Freshet                 "       0         0      0.        0         0       0.
"     Seasonal                "    3907    128542   7000.     3998    774202    7000.
"  P2                         "
"     Habitat                 "   16120    305688    805.     4152    371497     436.
"     Freshet                 "       0         0      0.        0         0       0.
"     Seasonal                "   16859    203288  14000.    18696   1315286   14000.
"  P3                         "
"     Habitat                 "    1915      8273    459.      819     46521     305.
"     Freshet                 "       0         0      0.        0         0       0.
"     Seasonal                "   11574    105933  21000.    13986    681400   21000.
"Immature Smolts              "
"  S1                         "
"     Habitat                 "       0         0      0.        0         0       0.
"     Freshet                 "       0         0      0.        0         0       0.
"     Seasonal                "     566      1558  28000.     1260     13594   28000.
"  S2                         "
"     Habitat                 "       0         0      0.        0         0       0.
"     Freshet                 "       0         0      0.        0         0       0.
"     Seasonal                "       0         0      0.        0         0       0.
"  S3                         "
"     Habitat                 "       0         0      0.        0         0       0.
"     Freshet                 "       0         0      0.        0         0       0.
"     Seasonal                "       0         0      0.        0         0       0.


Note: Surviving Movers represent ALL moves and cohorts
        that move more than once in a given category will
        be tabulated for each move.
```

```
1989 Mass Balance for Chinook Salmon

    Stage         Entrants   Graduates   Exiters    Deaths   InStream     Total
----------------------------------------------------------------------------------
Adult Females       11605          0          0      11605          0      11605
Adult Males         21554          0          0      21537         17      21554
Eggs/Alevins     29980091          0          0   21012991          0   29980091
Fry                     0    9094256      25230    6469095          0    9094256
Pre-Smolts              0    2599931     978517    1535699      70902    2599931
Immature Smolts         0      14813      12690       1823        300      14813
```

```
              "      Summary of Out-Migrant Fish      "
              "--------------------------------------"


              "   ***    Upstream Out-Migrants   ***   "
              "   -------------------------------   "

              "            No Out-Migrants            "


              "   ***  Downstream Out-Migrants  ***   "
              "   -------------------------------   "
```

```
"Out-Migrants at time step =   24  Date =  2/10/1989"
"Chinook Salmon                   "
"--------------------------------"
"# of cohorts =     2             "  "Numbers" "Avg Wt " "Avg Len" "  Repr.
"
"                                 "  "          " "(grams)" " (mm)   "
"#eggs/fem"
"--------------------------------------------------------------------------"
" Adult Females                   "         0        .0       .00         0.
" Spawning Females                "         0        .0       .00         0.
" Adult Males                     "         0        .0       .00
" Spawning Males                  "         0        .0       .00
" Eggs/Alevins                    "         0
"    Prop. Mature 0-.33           "         0
"    Prop. Mature .33-.67         "         0
"    Prop. Mature .67-1.00        "         0
" Fry                             "      3594        .5     35.91
"    F1                           "      3594        .5     35.91
"    F2                           "         0        .0       .00
" Pre-Smolts                      "         0        .0       .00
"    P1                           "         0        .0       .00
"    P2                           "         0        .0       .00
"    P3                           "         0        .0       .00
" Immature Smolts                 "         0        .0       .00
"    S1                           "         0        .0       .00
"    S2                           "         0        .0       .00
"    S3                           "         0        .0       .00
" Total Young                     "      3594        .5     35.91
```

Other outmigrant summaries for time steps omitted here

```
"Out-Migrants summarized across time"
"--------------------------------"
"Chinook Salmon                  "
"--------------------------------"
"# of cohorts = 19767            " "Numbers" "Avg Wt " "Avg Len" "  Repr.
"
"                                " " "          " "(grams)" " (mm)   "
"#eggs/fem"
   "-----------------------------------------------------------------------"
   " Adult Females                "        0       .0        .00         0.
   " Spawning Females             "        0       .0        .00         0.
   " Adult Males                  "        0       .0        .00
   " Spawning Males               "        0       .0        .00
   " Eggs/Alevins                 "        0
   "   Prop. Mature 0-.33         "        0
   "   Prop. Mature .33-.67       "        0
   "   Prop. Mature .67-1.00      "        0
   " Fry                          "    25230       .6      39.07
   "   F1                         "     9432       .5      35.91
   "   F2                         "    15798       .7      40.95
   " Pre-Smolts                   "   978517      2.7      65.05
   "   P1                         "    34446      1.5      53.71
   "   P2                         "   465795      2.2      60.90
   "   P3                         "   478276      3.2      69.92
   " Immature Smolts              "    12690      5.0      81.66
   "   S1                         "    12690      5.0      81.66
   "   S2                         "        0       .0        .00
   "   S3                         "        0       .0        .00
   " Total Young                  "  1016437      2.7      64.61
```

Sample output file when using the -b1 switch.

```
" Date : 8/24/1994"
" Time : 8:52      "
" Title:     Full Trinity River Model - Biological Year 88-89        "
```

"Week"	"Fry" "Numbers"	"Ave." "Length"	"Pre-Smolts" "Numbers"	"Ave." "Length"	"Immature" "Numbers"	"Ave." "Length"	"Smolts" "Total" "Numbers"
1	0.	.00	0.	.00	0.	.00	0.
2	0.	.00	0.	.00	0.	.00	0.
3	0.	.00	0.	.00	0.	.00	0.

.
. *weeks 4 through 14 listed here*
.

"Week"	Fry Numbers	Ave. Length	Pre-Smolts Numbers	Ave. Length	Immature Numbers	Ave. Length	Total Numbers
15	0.	.00	0.	.00	0.	.00	0.
16	8260.	35.91	0.	.00	0.	.00	8260.
17	30.	35.91	0.	.00	0.	.00	30.
18	7847.	35.91	0.	.00	0.	.00	7847.
19	313.	39.14	0.	.00	0.	.00	313.
20	254.	36.45	0.	.00	0.	.00	254.
21	5288.	36.12	0.	.00	0.	.00	5288.
22	0.	.00	0.	.00	0.	.00	0.
23	4793.	35.91	653.	51.05	0.	.00	5446.
24	36.	38.64	682.	50.64	0.	.00	718.
25	4737.	36.03	2237.	51.89	0.	.00	6974.
26	0.	.00	282.	51.17	0.	.00	282.
27	20478.	40.00	66992.	55.47	0.	.00	87470.
28	650.	41.51	5157.	57.15	0.	.00	5807.
29	7491.	35.91	287.	53.40	0.	.00	7778.
30	14675.	35.91	1158.	53.45	0.	.00	15833.
31	4942.	35.91	0.	.00	0.	.00	4942.
32	2183.	36.39	154078.	62.39	0.	.00	156261.
33	2183.	35.91	325892.	59.47	0.	.00	328075.
34	1908.	36.74	364505.	60.06	0.	.00	366413.
35	842.	35.91	318717.	59.31	58.	81.09	319617.
36	315.	35.91	336154.	57.82	6919.	80.77	343388.
37	642.	35.91	343708.	56.35	8350.	82.24	352700.
38	0.	.00	192519.	55.79	4309.	84.57	196828.
39	0.	.00	97624.	55.74	1952.	87.12	99576.
40	0.	.00	25516.	54.90	283.	89.39	25799.
"MIN"	0."	"	0."	"	0."	"	0.
"MAX"	20478."	"	364505."	"	8350."	"	366413.
"AVE"	2197."	"	55904."	"	547."	"	58647.
"MED"	15."	"	0."	"	0."	"	516.
"STD"	4357."	"	115723."	"	1812."	"	116660.

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FEEDBACK

We are interested in your constructive feedback on SALMOD, or otherwise. Obviously, we are interested in extending the features of SALMOD if the needs warrant. Some features that have been suggested are (1) adding other "gates" in the middle of the study area to simulate diversions and associated passage problems, (2) adding river network topology to handle tributary production, (3) beefing up the handling of adults, such as tabulating their movement and allowing size classes, (4) fixing known bugs, and (5) adding age as a cohort attribute so that processes such as mature could operate as a function of age as well as length or lifestage. The *preprocess input option* should check that flow and temperature segments fall at computation unit boundaries. Let us know. Feedback may be sent to John_Bartholow@USGS.Gov or to the address/phone listed on the cover.