

GENETICAL ASPECTS OF HUMAN BEHAVIOUR

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by

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PART B
A STUDY OF SOCIAL ATTITUDES

INTRODUCTION

The study of the inheritance of intelligence has a long if somewhat controversial history, as we have seen in Part A. In Part B, we turn to two traits which have interested psychologists and sociologists for some time, but have rarely been subjected to the detailed analysis necessary to determine the causes of variation. In the past, most theorists accepted the untested assumption that all attitudes are developed through experience (Chein, 1948; Doob, 1947), more through conviction than overwhelming empirical evidence. However, the study of evolutionary genetics suggests a biological basis for the determination of attitudes and recognition of this may serve to illuminate certain sociological or psychological perspectives in a more realistic light, by suggesting possible selective advantages for the two traits, how they may have evolved within a social structure and possible changes that may occur in the future.

Indirect evidence for a heritable component of variation in attitudes comes from studies of behavioural traits which may lead an individual to prefer one attitude over another. For example, racial or other prejudices often have an element of active hostility and there is abundant evidence for a heredity component of aggression (e.g. Carthy and Ebling, 1964; Scott and Fuller, 1965; Lorenz, 1966). In a recent book, Dawkins (1976) makes the link between behaviour and evolution which is central to the biological understanding of behaviour, by expressing the distinction between motives and consequences in these terms:

"It is important to remember that the above definitions of altruism and selfishness are behavioural, not subjective. I am not going to argue about whether people who behave altruistically are 'really' doing it for secret or subconscious selfish motives. Maybe they are and maybe they aren't, and maybe we can never know..... My definition is concerned only with whether the effect of an act is to lower or raise the survival prospects of the presumed altruist and the survival prospects of the presumed beneficiary".

It is not how we feel or think we are behaving that are of ultimate importance, but the consequences of the actions (i.e. behaviour), prompted by our emotions or attitudes, which are important for our own survival and, through our offspring, of similar feelings and attitudes in the future.

Attitudes are only of evolutionary consequence in so far as they influence survival. Attitudes may be shaped by underlying personality traits, such as level of aggressiveness, which are known to have a genetic basis. This suggests that there may be a genetic predisposition towards certain attitudes. Conversely, particular forms of behaviour are known to be under genetical control, and insofar as attitudes are shaping this behaviour, it seems likely that the attitudes themselves have some genetic mechanism. All this suggests that attitudes and personality may have a common biological basis, which is related to survival.

The involvement of a genetic mechanism in determining attitudes does not imply that environmental and cultural factors are unimportant. Behavioural differences may have genetical or social consequences either of which may modify the range of behavioural differences in future generations. A change in social system originated by the behaviour of individuals conditioned by that social system may have consequences for the

genetic system. Conversely, selective pressures changing the gene frequencies may alter the social structure. Thus, any change in a population is the result of both genetical and environmental changes upon the behaviour of its members, and to suggest a genetic basis for the attitudes determining behaviour does not preclude the importance of cultural change. Indeed, a new and important area of study is the cultural transmission of social attitudes through genetical differences, acting environmentally, producing cultural change.

Previous work on the genetics of social attitudes comprises two twin studies, which give a consistent picture for the components of variation which can be separated using twins reared together. The work outlined in this thesis contains an analysis of twin data and confirms the results of earlier studies, but also provides a unique opportunity for the resolution of the cultural components of variation and cultural transmission against a background of simple additive genetical differences and the effects of the mating system.

Eysenck became interested in social attitudes and re-examined three early studies (Thurstone, 1934; Carlson, 1934; Ferguson, 1939). In a series of investigations (Eysenck, 1944, 1947) he showed that social and political actions of all kinds are mediated through attitudes and opinions, which are organised into two principal orthogonal factors. These he labelled Radicalism and Toughmindedness. The development and validation of these two dimensions of attitudes was carried out by Coulter (1953), George (1954) and Melvin (1955) and is summarised by Eysenck (1954), together with his own work. Subsequently, the validity of this theory was demonstrated, since the two dimensions showed a relationship with social class and were sufficient to account for the relationship between the different political parties in this country.

(Eysenck, 1951, 1954, 1956). He also showed that the theory could be generalised to populations from the United States, Sweden, Germany and other western countries (Eysenck, 1953; Dator, 1969; Bruni and Eysenck, 1976).

Later, Eysenck showed that the Radicalism-Conservatism dimension could be usefully sub-divided into two components, social conservatism and economic conservatism (the latter being a capitalism-socialism dimension) (Eysenck, 1975, 1976a, b).

A lot of evidence has accumulated in support of the general theory of social attitudes using a variety of questionnaires and types of question (e.g. Rokeach, 1973; Wilson, 1973; Schubert, 1975). Indeed, the data analysed here also confirm the relevance of Radicalism and Toughmindedness and were obtained as responses to one of the most recent types of questionnaire. The most recent study (Hewitt et al, 1977) replicates the findings of the earliest studies after 25 years with remarkable consistency.

Study of the inter-relationship of social attitudes and the whole personality showed that Toughmindedness is related to extraversion and Psychoticism (e.g. Eaves and Eysenck, 1974). In particular there is a distinct tendency for Toughmindedness to be associated with aggressiveness and dominance. Wilson (1975) has suggested personality correlates of Radicalism.

Eaves and Eysenck (1974) also studied the causes of trait variation and covariation in three personality variables and the two dimensions of social attitudes, in order to determine the extent to which variation in personality and opinion share a common genetic basis. They were able to discriminate between simple genetical and simple environmental models and show a heritable component of the observed variation and covariation.

The possibility of common environmental influences was suggested. Genetical differences might account for as much as 65 per cent of variation in Radicalism scores and 54 per cent in Toughmindedness scores. Despite this, parental attitudes will be relatively poor predictors of offspring attitudes, since on the basis of the simple genetical model, given random mating, the parent offspring correlations are expected to be roughly between 0.2 and 0.3. This is substantially lower than correlations reported earlier (e.g. Fuller and Thomson, 1960). Eaves and Eysenck (1974) suggest that if the change is real, it might reflect cultural change over the last 30-40 years and could result from increased social mobility minimising the importance of the family environment, and increasing the importance of genetical differences and environmental experiences unique to the individual. This suggests that attitudes are sensitive to cultural change and may be subject to cultural transmission which is the particular interest of the present work.

Hewitt (1974) analysed the individual dimensions of social attitudes and showed that specific environmental influences, the family environment or the effects of the mating system and additive genetical differences may each account for approximately one third of the total variation in Radicalism. Almost identical results were obtained for the relative contributions of the different sources of variation in a later twin study (Martin, 1976; Martin and Eysenck, 1976). Similarly, both twin studies were consistent with a model for Toughmindedness in which the expression of genes and the effects of the environment are dependent on sex, suggesting that underlying variation in toughmindedness, there is some mechanism of sex limitation mediated genetically or culturally. The

possibility of a cultural component for both traits (demonstrated by Eaves (1977) for Toughmindedness in the earlier twin study), means that some variation in each trait could be produced by the cultural transmission of phenotypic differences. Twin data are unsuitable for the study of cultural transmission since cultural differences and the effects of the mating system are confounded. Thus the earlier studies could only suggest a tempting line of future research. Adoption data is probably the most relevant for the solution of the problem of cultural change and in Part B of this thesis a large body of twin and adoption data are analysed. We hope that this will enable some advance to be made in understanding the inter-relationships of the genetical predisposition of individuals, the different types of environmental factors influencing them and the structure of society and cultural change.

SECTION 1: DESCRIPTION OF THE STUDY

1 THE QUESTIONNAIRE

The structure of the questionnaire used in this study differs radically from that of questionnaires previously used in attempts to elucidate the genetical and environmental components of variation in social attitudes. Eysenck (1957) publishes, in full, an example of the earlier type of questionnaire - the 60 item Public Opinion Inventory - together with its scoring key and a discussion.

Questionnaires used in the work described in the Introduction differ from this only in detail. Subjects respond to explicit statements regarding specific attitudes. Wilson and Patterson (1968) describe semantic problems associated with the conventional manner of framing the questions. They suggest that presenting single nouns with which subjects can agree or disagree might overcome these problems. This led to the development of the Wilson-Patterson Attitudes Questionnaire, presented in Table B1. Wilson (1973) found that responses to this questionnaire could be summarised adequately by reference to two major factors, identified as "Radicalism" and "Toughmindedness".

Eysenck performed detailed analysis, using responses to a 68 item Wilson-Patterson Attitudes Questionnaire, of a quota sample of 1442 adult subjects whose age and sex distributions closely followed those of the whole population. He identified a number of meaningful primary factors, resembling those found in previous studies, whose inter-correlations gave rise to two major higher order factors. These were closely similar in content to the Radicalism and Toughmindedness

TABLE B 1 : ITEMS OF THE WILSON-PATTERSON ATTITUDES QUESTIONNAIRE

Subjects were asked to circle "Yes", "?", or "No", depending on whether they agree with, are uncertain about, or disagree with the following topics.

- | | |
|------------------------|---------------------------|
| 1. Death Penalty | 35. Empire Building |
| 2. Evolution Theory | 36. Licensing Laws |
| 3. School Uniforms | 37. Space Research |
| 4. Strip-tease Shows | 38. Strikes |
| 5. Council Housing | 39. Common Market |
| 6. Sunday observance | 40. Computer Music |
| 7. Hippies | 41. Chastity |
| 8. Women's Lib | 42. Royalty |
| 9. Student Protest | 43. Women Judges |
| 10. Police | 44. Capitalism |
| 11. Surtax | 45. Conventional Clothing |
| 12. Wife-swapping | 46. Teenage Drivers |
| 13. Foreign Aid | 47. Apartheid |
| 14. Pop Music | 48. Nudist Camps |
| 15. Welfare State | 49. Church Authority |
| 16. Tradition | 50. Inheritance Tax |
| 17. Conscription | 51. Astrology |
| 18. The Pill | 52. Disarmament |
| 19. Patriotism | 53. Censorship |
| 20. Modern Art | 54. Birch-ing |
| 21. United Nations | 55. Mixed Marriage |
| 22. Self Denial | 56. Strict Rules |
| 23. Working Mothers | 57. Arab Politics |
| 24. Military Drill | 58. Pacifism |
| 25. Co-Education | 59. Law and Order |
| 26. Law Reform | 60. Casual Living |
| 27. Divine Law | 61. Divorce |
| 28. Socialism | 62. Profit sharing |
| 29. White superiority | 63. Inborn Conscience |
| 30. Cousin Marriage | 64. Coloured Immigration |
| 31. Moral Training | 65. Bible Truth |
| 32. Suicide | 66. Trade Unions |
| 33. Political Systems | 67. Supersonic Airliners |
| 34. Legalised Abortion | 68. Liberals |

factors previously described using conventional types of questionnaire items. Evidence suggests that these factors are partly determined by heredity and are related, genetically and environmentally, to personality variables (Eaves and Eysenck, 1974; Martin, 1976). Despite the novelty of the Questionnaire used, we hope to identify the same factors as previous workers and to compare our genotype-environment analysis of variation in attitudes in society with similar earlier analyses.

THE SUBJECTS

The Wilson-Patterson Attitudes Questionnaire was sent, together with questionnaires on neuroticism, impulsiveness and smoking and drinking behaviour, to twins from the Maudsley Twin Register. This register of twins from the London area has been built up over the years from volunteers who responded to advertisements in the press and journals and have agreed to assist the work of the Institute of Psychiatry (University of London) by occasionally filling in postal questionnaires. The responses to the Wilson-Patterson Attitudes Questionnaire of those twins who returned the forms are the basis of this study.

The present study included 587 pairs of twins from the register whose breakdown by zygosity and sex is given in Table B2. Zygosity was determined on the basis of responses to a questionnaire on physical similarity and mistaken identity in childhood, similar to that described by Kasirel and Eaves (1976). They found an accuracy of 96.1% for their questionnaire method compared with blood-typing, using a sample of 178 pairs of twins and fifteen different blood group systems.

The Attitudes Questionnaire was also sent to individuals who were part of an adoption study. The families, containing adopted individuals, volunteered to take part in research, in response to advertisements in newspapers and women's journals. There are data on 445 individuals who returned the questionnaire. This brings the total number of subjects in the study, including the twin and adoption studies, up to 1619 individuals. Table B3 shows the numbers of each type of individual in the adoption study. They are mainly adopted individuals and adopting

TABLE B 2 : BREAKDOWN OF TWIN SAMPLE BY ZYGOSITY AND SEX

	MZ	DZ	Total Number of Pairs
MALES	83	52	135
FEMALES	233	147	380
OPPOSITE-SEX	-	72	72
TOTAL NUMBER OF PAIRS	316	271	587

KEY: MZ - monozygotic twin pair

DZ - dizygotic twin pair

TABLE B3 : INDIVIDUALS IN THE ADOPTION STUDY

<u>TYPE OF INDIVIDUAL</u>	<u>NUMBER</u>
Adopted son	31
Adopted daughter	239
Adopting father	62
Adopting mother	77
Natural son of adopting parents	12
Natural daughter of adopting parents	13
Second adopted son of adopting parents	9
Second adopted daughter of adopting parents	2
<hr/>	
Total number of individuals	445
<hr/>	

Various Group Totals

Total number of adopted individuals	281
Total number of parents	139
Total number of natural children	25
Total number of males	114
Total number of females	331

parents, but 25 natural children of these parents also took part. Relationships among these 445 individuals are presented in Table B4. The groups shown are not independent, since an individual may be included in more than one group. This precludes any simple analysis of all the summary statistics based on these groups simultaneously. However, the table does provide a useful summary of the sample structure.

TABLE B 4 : RELATIONSHIPS AMONG INDIVIDUALS OF THE ADOPTION STUDY

TYPE OF RELATIONSHIP	NUMBER OF PAIRS
Spouses	61
Adopting father - adopted son	8
Adopting father - adopted daughter	34
Adopting mother - adopted son	21
Adopting mother - adopted daughter	40
Families including one adopted individual and one or both parents	61
Families including one adopted individual and both parents	32
Families including one adopted individual and one parent only	29
Father - son	3
Father - daughter	5
Mother - son	4
Mother - daughter	3
Families including natural child and one or both parents	13
Families including natural child and both parents	9
Families including natural child and one parent only	4
Adopted child - natural child	10
Families with more than two children reared by same parents	15

3 ADEQUACY OF SAMPLING

This is not a random sample, since the subjects were volunteers. Females are clearly over-represented in both parts of the sample (see Tables B2 and B3). It is thought that the lower socio-economic status groups are under-represented. These biases probably reflect the nature of the journals in which advertisements were placed: many were placed in women's magazines.

There is an excess of monozygotic twins; same-sex dizygotic twins are over-represented compared with opposite-sex twins, since we expect equal numbers of the two types of non-identical pair.

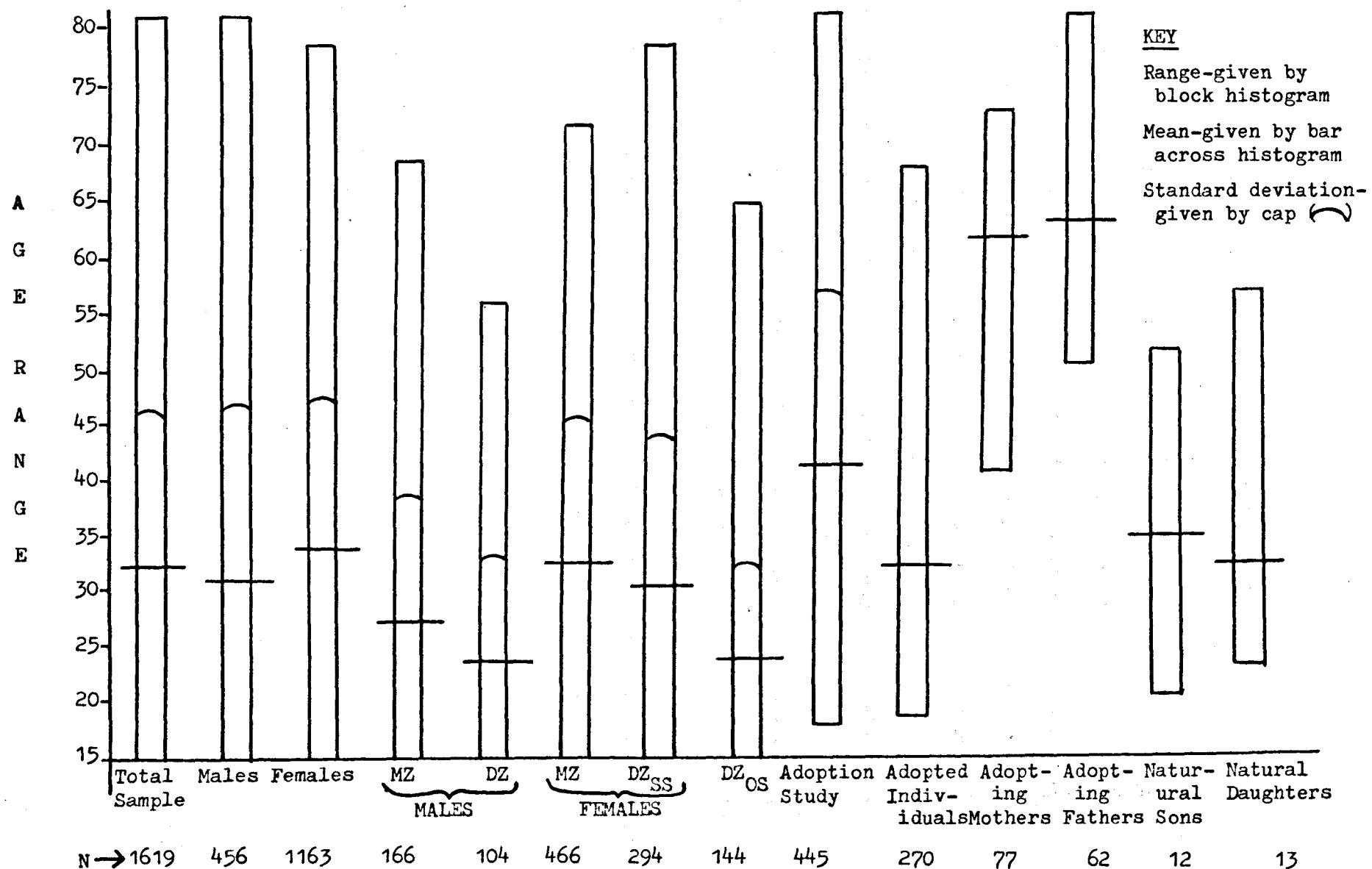
The practical consequences of these biases, for the sampling of Radicalism and Toughmindedness from the population, are not known. However, the sample may not be representative of the population as a whole. There may be a restricted range of genotypes and environments, which could lead to the underestimation of between families effects. This problem will be further discussed when interpreting analyses of the genetical and environmental factors producing variation in attitudes.

AGE DISTRIBUTION IN THE SAMPLE

The age range in the sample, from 15 to 82 years, is wide. The mean age is 32.91 ± 14.88 years. The age distributions in different sub-groups of the data are illustrated in Figure B1. The overall female mean is significantly greater than the male mean ($\chi^2_1 = 6.13$). We notice, also, a tendency for dizygotic twins to be younger than monozygotic twins. The mean ages of the adopted individuals and the twins are similar, but as expected, the adopting parents are much older. Thus, the age structure of the data is such that any relationship between test score and age will make interpretation of the analyses meaningless.

Eysenck (1954) reports evidence that scores on an earlier version of the questionnaire are not age-related. However, we cannot assume that this is true for the present study, since the questionnaire and sample structure are very different. Dependence of attitude score on age will be tested and the appropriate age-corrections made.

FIGURE B1: MEAN AND RANGE OF AGES IN DIFFERENT SUB-GROUPS OF THE DATA



5 ADVANTAGES OF THE DESIGN OF THIS STUDY

The structure of this study has considerable advantages. The large number of twins will enable us to test certain basic models of variation and to compare this study with previous studies. (Eaves and Eysenck, 1974; Martin, 1977). The weakness of the classical twin study of identical and non-identical twins reared together is that it does not allow discrimination between certain hypotheses about the nature of between pairs variation, crucial to our understanding of individual differences in attitudes. The adoption data will enable us to assess the relative importance of cultural effects and assortative mating in producing between families variation and to test the hypothesis of cultural transmission for these traits. Thus, the analysis of individual differences in attitudes will be taken further in this study than has been possible before.

SECTION 2: THE STRUCTURE OF ATTITUDES IN THESE DATA

1

REASONS FOR PERFORMING THE FACTOR ANALYSIS

Previous work with the Wilson-Patterson Attitudes Questionnaire involved large quota samples. Since there may be a restricted range of phenotypes in this study, items may not discriminate adequately between subjects and separation of individuals on the basis of the two major dimensions of Radicalism and Toughmindedness, similar to that achieved in previous studies, may not be possible. Therefore, we will seek evidence that the Radicalism and Toughmindedness scales are appropriate for these data.

THE FACTOR ANALYSIS

A general description of the concepts and theory of factor analysis is given in Appendix C. The particular methods used here will be briefly described, but more detail of Principal Factoring can be found in Section 2 of Part A.

Responses of the 1619 individuals to the 68 items of the Wilson-Patterson Attitudes Questionnaire (coded as 0 = Disagree, 1 = Don't know, 2 = Agree) were entered into the analysis. There were no missing observations. All the computations were carried out on the University of Birmingham's ICL 1906A computer using a program from the library of Biomedical Computer Programs (BMD) (Dixon, 1973).

Principal facturing with interaction was used. The advantages and disadvantages of this method are discussed elsewhere. A 68 x 68 matrix of correlations among the items was calculated. Its' leading diagonal elements were replaced by estimates of the communality for each item. A solution for a specific, predetermined number of factors was then sought, and new communalities were calculated from the multiple correlation with the factors. This procedure was iterated until a specified criterion of convergence was achieved. The problem was to decide the appropriate number of factors and the convergence criterion. In this case, convergence was assumed when the maximum change in the communality estimates was less than 0.001, assuming a two factor model. The final communality estimates, which are estimates of the variance of each item shared in common with the other items are given in Table B5 for the two factor model.

TABLE B 5 : FINAL ITEM COMMUNALITIES FOR A TWO FACTOR MODEL

ITEM	COMMUNALITY	ITEM	COMMUNALITIES
1	224	35	099
2	072	36	150
3	210	37	033
4	153	38	287
5	092	39	079
6	202	40	061
7	341	41	212
8	159	42	249
9	345	43	118
10	138	44	074
11	148	45	120
12	213	46	053
13	188	47	114
14	060	48	222
15	111	49	223
16	198	50	114
17	257	51	007
18	076	52	159
19	232	53	148
20	172	54	184
21	098	55	228
22	133	56	232
23	056	57	040
24	204	58	168
25	093	59	128
26	036	60	255
27	256	61	087
28	225	62	107
29	181	63	055
30	069	64	279
31	202	65	257
32	112	66	201
33	051	67	000
34	071	68	101

NOTE: Decimal points are omitted from the communalities.

Two factors were extracted because we wished to test the hypothesis, suggested by previous work, that the two factor model is appropriate for our data. Inspection of the proportion of the total variation accounted for by the first few principal components showed that this was a reasonable procedure. The first principal component accounted for 10.6% of the total variation and the second for 4.4%. The third component accounted for 3.6% of the total variation, and all subsequent components accounted for substantially less than 2%. The dominance of the first component probably reflects the weight given, when constructing the questionnaire, to discriminating between Radicalism and Conservatism.

Factor loadings for the two orthogonal unrotated factors are given in Table B6. Oblique rotation of these factors for simple loadings was performed by attempting to minimise the squared loadings on each factor using an iterative process. This solution of the factor rotation problem has been called direct quartimin. The oblique rotated factor loadings for each item are given in Table B7.

A correlation of 0.199 was found between the two factors. This is fairly high since earlier work suggested that Radicalism and Toughmindedness are orthogonal. However, it is in line with the correlation of 0.18 found by Eysenck in his quota sample. The two factors obtained were easily identified as Radicalism and Toughmindedness from their item content. Thus, despite earlier misgivings about the unrepresentative nature of the sample, these two major dimensions of attitudes, identified by earlier workers, may be appropriate for our data.

TABLE B 6 : UNROTATED ORTHOGONAL FACTOR LOADINGS FOR A TWO FACTOR MODEL

FACTOR			FACTOR		
ITEM	1	2	ITEM	1	2
1	-388	-271	35	-286	-131
2	256	078	36	-290	256
3	-422	180	37	133	125
4	351	-173	38	529	086
5	194	233	39	018	280
6	-381	238	40	239	064
7	582	051	41	-367	279
8	378	126	42	-445	226
9	565	161	43	053	340
10	-258	268	44	-272	016
11	228	310	45	-318	137
12	352	-299	46	215	084
13	218	375	47	-216	-260
14	244	024	48	463	-085
15	200	267	49	-388	269
16	-329	299	50	294	167
17	-502	-069	51	-058	-057
18	274	039	52	330	225
19	-439	198	53	-329	198
20	396	121	54	-407	-137
21	033	312	55	418	230
22	-194	309	56	-464	129
23	236	028	57	129	153
24	-452	015	58	336	234
25	223	207	59	-260	246
26	053	182	60	483	-148
27	-432	264	61	295	-009
28	440	179	62	162	284
29	-244	-349	63	-161	171
30	262	-020	64	391	355
31	-306	329	65	-437	257
32	319	-101	66	360	268
33	050	220	67	020	-006
34	266	-015	68	064	311

NOTE: Decimal points are omitted from the factor loadings.

TABLE B 7 : OBLIQUE ROTATED FACTOR LOADINGS FOR THE TWO FACTOR MODEL
AND COMPARISON WITH LOADINGS OBTAINED BY E SENCK

ITEM	This Study	Eysenck's Study	T		
			R	This Study	Eysenck's Study
1 Death Penalty	-44	-29		-11	-16
2 Evolution Theory	20	42		14	-03
3 School Uniforms	-05	-02		-44	-29
4 Striptease Shows	02	45		39	15
5 Council Housing	30	13		-01	-06
6 Sunday Observance	02	-28		-45	-31
7 Hippies	34	49		41	20
8 Women's Lib	30	35		20	-18
9 Student Protest	43	46		32	08
10 Police	11	.03		-38	-30
11 Surtax	39	35		-03	-19
12 Wife-swapping	-09	22		47	40
13 Foreign Aid	44	32		-09	-14
14 Pop Music	14	35		17	15
15 Welfare State	34	18		-03	-12
16 Tradition	10	17		-45	-39
17 Conscription	-32	-18		-34	-25
18 The Pill	17	50		18	-00
19 Patriotism	-05	19		-47	-48
20 Modern Art	31	32		22	07
21 United Nations	29	36		-18	-37
22 Self Denial	18	12		-36	-43
23 Working Mothers	14	21		16	-05
24 Military Drill	-22	-08		-36	-32
25 Co-Education	30	37		03	-13
26 Law Reform	19	33		-08	-14
27 Divine Law	02	-08		-51	-39
28 Socialism	38	21		22	05
29 White superiority	-43	-35		05	13
30 Cousin Marriage	16	24		21	28
31 Moral Training	14	20		-46	-44
32 Suicide	07	26		31	20
33 Political Systems	22	33		-11	-32
34 Legalised Abortion	12	43		21	-04

contd...

TABLE B 7 continued.

ITEM	This Study	R	Eysenck's Study	T	This Study	Eysenck's Study
35 Empire Building	-26		-31		-13	-08
36 Licensing Laws	08		-16		-39	-23
37 Space Research	18		47		02	05
38 Strikes	34		41		35	11
39 Common Market	26		35		-17	-20
40 Computer Music	18		28		14	08
41 Chastity	06		04		-47	-45
42 Royalty	-03		-02		-49	-43
43 Women Judges	33		26		-19	-28
44 Capitalism	-12		12		-22	-25
45 Conventional Clothing	-04		05		-34	-21
46 Teenage Drivers	18		35		11	06
47 Apartheid	-34		-28		01	15
48 Nudist Camps	16		54		41	-09
49 Church Authority	04		-15		-48	-31
50 Inheritance Tax	30		19		11	-05
51 Astrology	-08		10		-01	-11
52 Disarmament	37		18		10	03
53 Censorship	01		-19		-39	-38
54 Birchng	-33		-28		-22	-18
55 Mixed Marriage	42		53		17	-00
56 Strict Rules	-12		-21		-44	-24
57 Arab Politics	20		19		-00	-26
58 Pacifism	38		23		10	-06
59 Law and Order	09		04		-36	-30
60 Casual Living	11		17		47	47
61 Divorce	14		39		23	04
62 Profit Sharing	33		21		-07	-11
63 Inborn Conscience	07		30		-24	-38
64 Coloured Immigration	51		34		06	01
65 Bible Truth	01		-29		-51	-38
66 Trade Unions	42		24		10	-05
67 Supersonic Airliners	SOO		26		02	-00
68 Liberals	31		28		-16	-34

Note: Decimal points are omitted from the factor loadings.

3 COMPARISON OF THIS AND AN EARLIER ANALYSIS

For the purpose of comparison, the rotated factor loadings obtained in this study are followed, in Table B7, by those obtained by Eysenck, using the quota sample described in Section 1. Simple inspection shows a striking correspondence between the two sets of factor loadings. Where differences exist, they reflect the ability of the items to discriminate between individuals in the two studies. However, the loadings are so similar on the majority of items, that the organisation of the attitudes tested by the Wilson-Patterson Attitudes Questionnaire along two dimensions broadly similar to those identified by Eysenck (see Section 1) seems to be appropriate in these data.

FACTOR SCORES

The scores of each individual on the Radicalism and Toughmindedness dimensions were estimated and printed by the EMD Library program, used to perform the factor analysis. These "factor scores" are used in all the following analyses of individual differences in social attitudes.

SECTION 3: THE SCALE OF MEASUREMENT

1 CHOICE OF A SCALE

The Radicalism (R) and Toughmindedness (T) scores are a function of the individuals' response to each item and the items' factor loading, summed over items. Thus, the R and T scales are in some sense arbitrary, produced as an artefact of the statistical complexities of factor analysis. Psychological or genetical criteria might lead us to transform the scores if this would facilitate analysis and interpretation of the data, without introducing undesirable statistical properties.

The problem of choosing the most appropriate scale of measurement is discussed in general by Mather and Jinks (1971) and in the context of human behaviour by Eaves et al (1977). Several criteria may be employed in seeking the best scale, which simplifies the analysis and interpretation of data and maximises the predictive value of the results.

1.1 Statistical Criteria

Test scores for continuously varying traits, such as Radicalism and Toughmindedness, are expected to follow the normal distribution, approximately at least. Statistical techniques employed in analysing continuous data are based on the normal distribution and may be inappropriate when significant deviations from normality occur.

Biases in estimates of the components of variation may be produced and

the power of significance tests is usually reduced. Therefore, on statistical grounds, we should seek scales which are normally distributed. However, normality is of secondary importance, compared with psychological and genetical properties of the scale.

1.2 Psychological and Genetical Criteria

Psychological and genetical criteria for choosing a scale of measurement overlap to a large extent. A useful descriptive model for variation in the trait, which allows prediction about behaviour in other situations, is needed on psychological grounds. We are also looking for a scale which facilitates genetical analysis and interpretation of the data and allows predictions to be made about the degree of similarity of other relatives. In both cases, we need a measure where non-additivity is minimised. Psychologically this means that we are looking for a scale with equal intervals so that the discriminating power of the test is equal in all parts of the scale. Reliability should not vary in different parts of the scale. Genetically, we require that the sensitivity of the organism to its environment should be independent of its genotype (i.e. there should be no genotypes x environment interaction.) Finding a scale which satisfies these criteria and minimises non-additivity will increase the predictive value of our results within an economical model.

DISTRIBUTION OF RADICALISM AND TOUGHMINDEDNESS

Two tests for deviations from normality, using third and fourth moments about the mean, were described in detail in Section 2 of Part A. Coefficients of skewness and kurtosis were calculated for the total sample and for various sub-groups of the data, using the Statistical Package for the Social Sciences (SPSS) (Nie et al, 1970). The probabilities of obtaining these coefficients or larger by chance, based on the null hypothesis of normality of the data, were found from Tables in Snedecor and Cochran (1967). The results of these calculations are summarised in Table B8.

There is evidence of negative skewness for Radicalism in the total sample, but no evidence of kurtosis. The negative skewness indicates an excess of individuals below the mean for Radicalism. Two factors are probably contributing to this excess. Eysenck has shown a correlation between conservatism and social class (see Eysenck, 1957). Thus, skewness could be produced by the under-representation of the lower socio-economic status groups. Age effects are probably also contributing to skewness, since the mean age of this sample is high, and it is known that Conservatism increases with age (Eysenck, 1954).

If we consider the sub-groups, skewness is only highly significant where we have pooled over two or more basic groups, although there is some evidence for skewness, significant at the five per cent level, in MZ males and DZ females. This suggests that the overall skewness may have been largely produced by pooling over heterogeneous groups. Since statistics will be calculated separately for each sub-group, most of

TABLE B 8 : COEFFICIENTS OF SKEWNESS AND KURTOSIS FOR THE RAW FACTOR SCORES

		RADICALISM		TOUGHMINDEDNESS	
		Skewness	Kurtosis	Skewness	Kurtosis
Total Sample	1619	-0.331 **	0.0202 NS	0.355 **	0.605 **
All Females	1162	-0.292 **	0.183 NS	0.750 **	0.837 **
All Males	457	-0.428 **	0.222 NS	0.252 *	-0.097 NS
MZ Males	166	-0.341 *	-0.334 NS	0.416 *	0.097 NS
MZ Females	466	-0.178 NS	0.033 NS	0.740 **	0.627 *
DZ Males	104	-0.050 NS	-0.582 NS	0.109 NS	-0.336 NS
DZ Females	294	-0.258 *	-0.275 NS	0.589 **	0.272 NS
DZ Opposite-sex	144	-0.213 NS	-0.588 *	0.343 *	-0.119 NS
Adopted individuals	270	-0.800 **	1.834 **	0.979 **	1.612 **
Adopting mothers	77	-0.303 NS	0.181 NS	2.248 **	7.616 **
Adopting fathers	62	0.014 NS	-0.429 NS	1.077 **	1.387 *
Natural sons	12	-0.355 NS	-1.171 **	0.542 NS	-1.155 **
Natural daughters	13	0.075 NS	-1.581 **	0.437 NS	-1.178 **

KEY : * Significant at the 5% level

** Significant at the 1% level

NS Not significant

which show no significant skewness, the observed deviation from normality in the total sample may not present problems in the analysis of Radicalism. The observed kurtosis in one or two groups is not reflected by kurtosis in the total sample and should not seriously bias our analyses.

For Toughmindedness, there is highly significant skewness and kurtosis in the total sample and evidence for non-normality in nearly every sub-group. Problems produced by non-normality are likely to be far more serious than for Radicalism.

These deviations from normality could reflect the underlying non-normality of the distributions of genetical or environmental effects. However, variation between "item difficulties" or else sampling bias are more likely explanations.

3 INTERNAL STRUCTURE OF THE SCALES

Jinks and Fulker (1970) propose scaling tests for the detection of systematic genotype-environment interaction, employing third degree statistics. Interactions between the genotype and within families variation can be detected using identical twins reared together. Data on MZ twins reared apart are required to detect similar interactions with the between families environmental component (E_2). These GE_2 interactions, if present, will be confounded with estimates of genetical and environmental components of variation, since they cannot be detected in these data.

Interaction of the between families genetical component (G_2) and E_2 will be confounded with the between families effect. Interaction of within families genetical differences (G_1) and E_2 will be confounded with the G_1 component (Eaves, 1976).

The scaling test of Jinks and Fulker (1970) not only detects systematic $G \times E$, but also demonstrates psychometric inadequacies of the scale, since it uses the regression of pair sums onto absolute pair differences. Differences within pairs of MZ twins are produced by both unreliability of measurement and specific environmental differences (E_1). Therefore, any systematic relationship of pair differences with the pair sums (which provide a measure of the genotype and the common family environment) shows that either the reliability varies in some systematic way in different parts of the scale, or that the magnitude of E_1 depends on the genotype of the individual it is affecting (i.e. there is $G \times E$ interaction). Thus, this scaling test provides a test of both genetical and psychological criteria for the adequacy of the scale simultaneously.

Further discussion of the test may be found in Section 6 of Part A, together with details of the methods. Pair sums and absolute pair differences were calculated for all the same-sex twins. Pair sums were regressed onto pair differences using a program from the EMD library. The significance of any linear or quadratic components was tested. Higher order interactions were not calculated since these would be difficult to interpret biologically and psychologically. The analysis was carried out separately for all MZ twins and then separately for males and females. These analyses were repeated for the DZ twins for reasons which will become clear later. The outcome of these analyses is summarised in Table B9.

No significant quadratic regressions were found. A linear component, significant at the 5% level only, was found for Radicalism in the MZ twins as a whole. But strong evidence for a linear component was found in all groups, including the DZ twin groups, for Toughmindedness.

Since there was a relationship between within pairs differences and pair sums in MZ twins, we also expect a regression in DZ twins. The test was made for DZ twins, because a regression in the DZ twins, with no corresponding regression in the MZ twins, would be of great interest. The absence of a regression in the MZ twins would show that the DZ regression was not produced by "G x E" interaction. Therefore, a DZ regression would be produced by the regression of pair sum on genetical differences within pairs. If genetical differences within DZ pairs depend on the scale, then non-additive genetical effects such as dominance and epistasis or unequal gene frequencies must be responsible.

TABLE B 9 : SUMMARY OF SUM-DIFFERENCE REGRESSIONS FOR RAW FACTOR SCORES

	RADICALISM		TOUGHMINDEDNESS	
	Linear	Quadratic	Linear	Quadratic
All monozygotic twins	*	-	***	-
Monozygotic males	-	-	*	-
Monozygotic females	-	-	**	-
All dizygotic twins	-	-	**	-
Dizygotic males	-	-	*	-
Dizygotic females	-	-	*	-

KEY :

- * Significant at the 5% level
- ** Significant at the 1% level
- *** Significant at the 0.1% level
- No significant regression

Since we found no sum-difference regression in DZ twins, there is no evidence for genetical non-additivity in these data. Non-additivity is not precluded, however, since the power of this test is probably low and only a substantial amount of non-additivity could be detected using this test or any other test based on first degree collateral relatives.

In summary, there is little evidence of scalar problems for Radicalism. The slight linear regression in MZ twins taken as a whole might be produced by pooling over sexes. However, absolute differences within pairs increase significantly with Toughmindedness score. Either unreliability increases with Toughmindedness score, or there is genuine G \times E interaction, such that the development of Toughmindedness is more susceptible to specific environmental influences. Both alternatives are plausible and we are unable to discriminate between them. Whichever is true, analysis of Toughmindedness on this scale might produce results which are difficult to interpret and require many parameters to procure satisfactory predictions.

These conclusions are similar to those based on the distributions of Radicalism and Toughmindedness scores. Therefore, we shall analyse the raw Radicalism scale. But since the Toughmindedness scale is clearly inadequate, we shall seek a new scale of measurement for this trait, which minimises the problems of the present scale. We shall do this by making a suitable transformation of the raw scores.

TRANSFORMATION OF THE DATA

Logarithms and square roots of the factor scores were calculated. These transformations are commonly employed with this type of data (Snedecor and Cochran, 1967). Tests for deviations from normality were performed on the transformed data and the results are summarised in Table B10. Transformation has produced non-normal distributions for Radicalism, suggesting that the original scale is more appropriate. For Toughmindedness, the logarithmic transformation produces no improvement over the original scale. However, on the square root scale deviations from normality have largely disappeared. Skewness for males as a whole may be due to pooling data over heterogeneous groups of males. Generally, however, the distribution of test scores on the square root scale is more satisfactory than on the original scale.

Pair sums were regressed onto absolute pair differences in order to determine whether transformation had changed non-additivity in the scales. The results are briefly summarised in Table B11. Both transformations produced sum-difference regressions for Radicalism. A regression remains for Toughmindedness on the logarithmic scale, but the square root transformation has removed the relationship between pair sums and absolute pair differences.

All further analysis will therefore be based on the untransformed Radicalism scores and square roots of the Toughmindedness scores, since non-normality and non-additivity were minimised on these scales.

TABLE B 10: SUMMARY OF TESTS OF NORMALITY FOR THE TRANSFORMED SCALES

	TOUGHMINDEDNESS				RADICALISM			
	Square root		Logarithm		Square root		Logarithm	
	S	K	S	K	S	K	S	K
Total sample	NS	NS	***	***	***	***	***	***
All males	***	NS	***	***	***	***	***	***
All females	NS	NS	***	NS	***	***	***	***
MZ Males	NS	NS	***	***	***	NS	***	NS
MZ Females	NS	NS	***	NS	***	***	***	***
DZ Males	NS	NS	***	NS	NS	NS	*	NS
DZ Females	NS	NS	***	NS	***	NS	***	***
DZ Opposite-sex	NS	NS	***	*	*	NS	***	NS
Adoption study	NS	NS	***	NS	***	***	***	***

KEY : S - skewness (negative in all cases where significant)

K - kurtosis (positive in all cases where significant)

NS - not significant

* - significant at the 5% level

*** - significant at the 1% level

TABLE B 11 : SUMMARY OF SUM-DIFFERENCE REGRESSIONS FOR TRANSFORMED SCALES

	TOUGHMINDEDNESS				RADICALISM			
	Square		Root		Logarithm		Square	
	L	Q	L	Q	L	Q	L	Q
All MZ Twins	-	-	***	-	***	-	***	-
MZ Males	-	-	-	-	**	-	***	-
MZ Females	-	-	***	-	***	-	***	-
All DZ Twins	-	-	**	*	*	-	***	-
DZ Males	-	-	-	*	-	-	-	-
DZ Females	-	-	**	-	**	-	***	-

KEY :

- L - linear component of regression
- Q - quadratic component of regression
- no significant regression
- * regression significant at the 5% level
- ** regression significant at the 1% level
- *** regression significant at the 0.1% level

SECTION 4: AGE EFFECTS IN THESE DATA

1

INTRODUCTION

Since we have a wide age range in these data and the mean ages of the sub-groups differ, any covariation between attitudes score and age may bias our analyses. A regression of test score on age within groups coupled with a mean difference in age between groups, will produce a mean difference in test score between groups. Significance tests for differences in raw score between groups will, therefore, be meaningless. Thus, we must correct the test scores for any significant relationship with age. This will eliminate one source of bias in our analyses and facilitate interpretation of the data.

ANALYSIS OF COVARIANCE

We will consider differences in mean age between groups and their effect on mean differences in Radicalism and Toughmindedness scores, using the analysis of covariance. This statistical technique tests the significance of mean differences in age and test score between groups and also the significance of any regression of test score on age. The means may then be adjusted to remove the age effect and re-tested to see whether any mean differences in test score remain after the age adjustment. The analysis of covariance, thus, combines features of both regression analysis and the analysis of variance. It is discussed by Snedecor and Cochran (1967). Details of the calculations actually performed were described in Section 2 of Part A. We shall confine ourselves to presenting the results of the analysis and discussing their interpretation. The analysis was based on six groups: MZ males, MZ females, DZ males, DZ females, DZ opposite-sex pairs and the individuals of the Adoption Study. The results of this analysis are outlined in the top part of Table Bl2, (labelled: "1. BASED ON ALL GROUPS"). Since the Adoption Study included both adopted individuals and their adopting parents, the age range was wider than in other more restricted groups and the analysis was repeated using the twin groups only. The results are summarised in the bottom part of Table Bl2.

Mean differences in age between groups were significant. The Adoption Study included both adopted individuals and their adopting parents. The mean age ($\bar{x}_{\text{adopted}} = 41.569$) was much higher than that

TABLE B 12 : SUMMARY OF RESULTS OF AN ANALYSIS OF COVARIANCE

	R	T
1. BASED ON ALL GROUPS		
Significance of differences in mean age	***	***
Significance of differences in mean test score	***	***
Significance of differences in mean test score after age-correction	†	***
2. BASED ON TWIN GROUPS		
Significance of differences in mean age	***	***
Significance of differences in mean test score	*	***
Significance of differences in mean test score after age-correction	†	***

NOTES

R - Radicalism

T - Toughmindedness

*** Significant at the 0.1% level

* Significant at the 5% level

† Significant at the 10% level

ALL GROUPS INCLUDED : MZ males, MZ females, DZ males, DZ females,
 DZ opposite-sex pairs and the adoption study
 (i.e. 6 groups)

TWIN GROUPS INCLUDED : MZ males, MZ females, DZ males, DZ females and
 DZ opposite-sex pairs.

of the twins ($\bar{x}_{twins} = 29.625$). The significant mean differences in age might be attributable to this group alone. However, significant mean differences in age persisted when the group comprising the Adoption Study was eliminated from the analysis.

In order to determine the source of the observed mean differences in age between the sub-groups of our sample, some simple comparisons were made amongst group means. The female mean was higher than the male mean ($t_{1617} = 2.682$ $p < 0.01$) and the MZ twin mean was higher than that of the DZ twins ($t_{1028} = 2.719$, $p < 0.01$).

The female mean ($\bar{x}_{females} = 33.538$) could be greater than the male mean ($\bar{x}_{males} = 31.216$) because the mean lifespan of females is greater than that of males. However, samples such as this are not likely to be reflecting population trends, especially since the difference in mean between males and females (2.322 years) is rather big. It is more likely that non-random sampling is introducing a bias. Many individuals volunteered to take part in the study through advertisements in newspapers and women's magazines. The mean age of the readership of the type of magazine in which the advertisements appeared is likely to be higher than that of all women between the age of 18 and 82. This would produce a bias towards older women in the sample. In the case of men replying to newspaper advertisements, the age range was not so likely to be restricted.

It is more difficult to see why monozygotic twins were significantly older than dizygotic twins, but it is almost certainly due to biased sampling. We would suggest that this mean difference may be due to the sex difference in mean age. There are a lot more female monozygotic twins than female dizygotic twins in the sample. This would produce a higher

mean age in monozygotic twins as a function of the sex difference.

Significant mean differences in Radicalism and Toughmindedness scores, which might be attributed to the significant mean differences in age between the groups, were found. So the group means were adjusted for the age effect. Highly significant mean differences in Toughmindedness score persisted after age-adjustment. Inspection of the data suggested that these were mainly sex differences, males being more Toughminded than females.

The age-adjustment reduced the significance of mean differences in Radicalism between groups to the ten per cent level. Although these mean differences are not statistically significant, inspection of the means reveals a tendency for females to score less than males on the Radicalism scale.

REGRESSION OF ABSOLUTE PAIR DIFFERENCES ON AGE

Any regression of absolute pair differences on age would show a tendency for pair similarity to change with age. For example, in the case of monozygotic twins, a significant, positive linear regression might imply that environmental differences within pairs were making twins less alike as they got older. It could also imply that specific environmental influences were more important in the past producing larger differences between members of the older pairs in the sample. Only a longitudinal study could discriminate between these alternatives. A change in the magnitude of differences within pairs of dizygotic twins with age could be produced by specific environmental effects, but also by genetical differences within pairs. (Eaves and Eysenck, 1976). A regression in DZ twins, unaccompanied by a similar regression in MZ twins, would imply that within families genetical effects differ with age. Genes with different properties might be producing variation at different ages.

In order to see whether there is any evidence for environmental effects altering the degree of similarity between twins, or for different genetical systems operating at different ages, absolute differences between pairs of twins were calculated and regressed onto age using a program from the HMD library of computer programs (Dixon, 1973). The analysis was carried out separately for all monozygotic twins and all dizygotic twins and then repeated for each zygosity-sex group separately.

Only one significant regression was found for Toughmindedness: a quadratic component, significant at the 5% level in MZ males. Specific

environmental influences might make males more dissimilar up to a certain age, after which they become more similar again. It is difficult to visualise a mechanism for this and since the effect was only significant at the 5% level and was not reflected in the DZ males, we shall not consider it further.

Radicalism was more interesting. There was no evidence for a significant regression in the MZ twins, but a quadratic component significant at the 5% level was found in the dizygotic twins taken as a whole and was repeated in both males and females. Although, the regressions were only significant at the 5% level, the consistency over sexes suggests that we may be looking at a real effect.

Since there was no regression in the monozygotic twins, changes in pair similarity with age were probably not produced by specific environmental effects. Therefore, genetical differences within families may be implicated. The pairs are most similar at the age of 15. Differences between members of a pair increase until about 40 years of age, when the twins become more similar again. Two possible mechanisms may be visualised.

- i. Developmental rate is the same in both members of the pair i.e. the same operating at a given age. However, they have different alleles of these genes. This produces a difference, at any age, between the individuals. But, at different times in an individual's life, different genes are expressed. If the genes expressed at different times have different non-additive properties (e.g. dominance), then the DZ difference may vary with age as a function of the non-additivity. This seems unlikely for two reasons. Genes controlling developmental rate are

unlikely to be the same in both members of the pair and the non-additive properties of the genes operating would have to change consistently. For example, the dominance of genes being expressed at different times would have to increase up to the age of forty when the maximum DZ difference occurs. After the age of forty, the gradual return to the expression of genes with less non-additivity would have to occur. This situation is illustrated in Figure B2. It implies that the genetic architecture of the trait varies in a consistent manner with age. This is possible but more complex than the second alternative.

ii. This hypothesis suggests that genes producing changes in Radicalism with age are different in the two individuals. Therefore, different genes will be operating in the pair at any time. How this produces the observed relationship between pair difference and age is illustrated in Figure B3.

Both these hypotheses about the origin of the quadratic relationship between absolute pair differences assume that there is a change in Radicalism score with age, and also that this change is probably not linear.

FIGURE B2: CHANGES IN GENETIC ARCHITECTURE WITH AGE

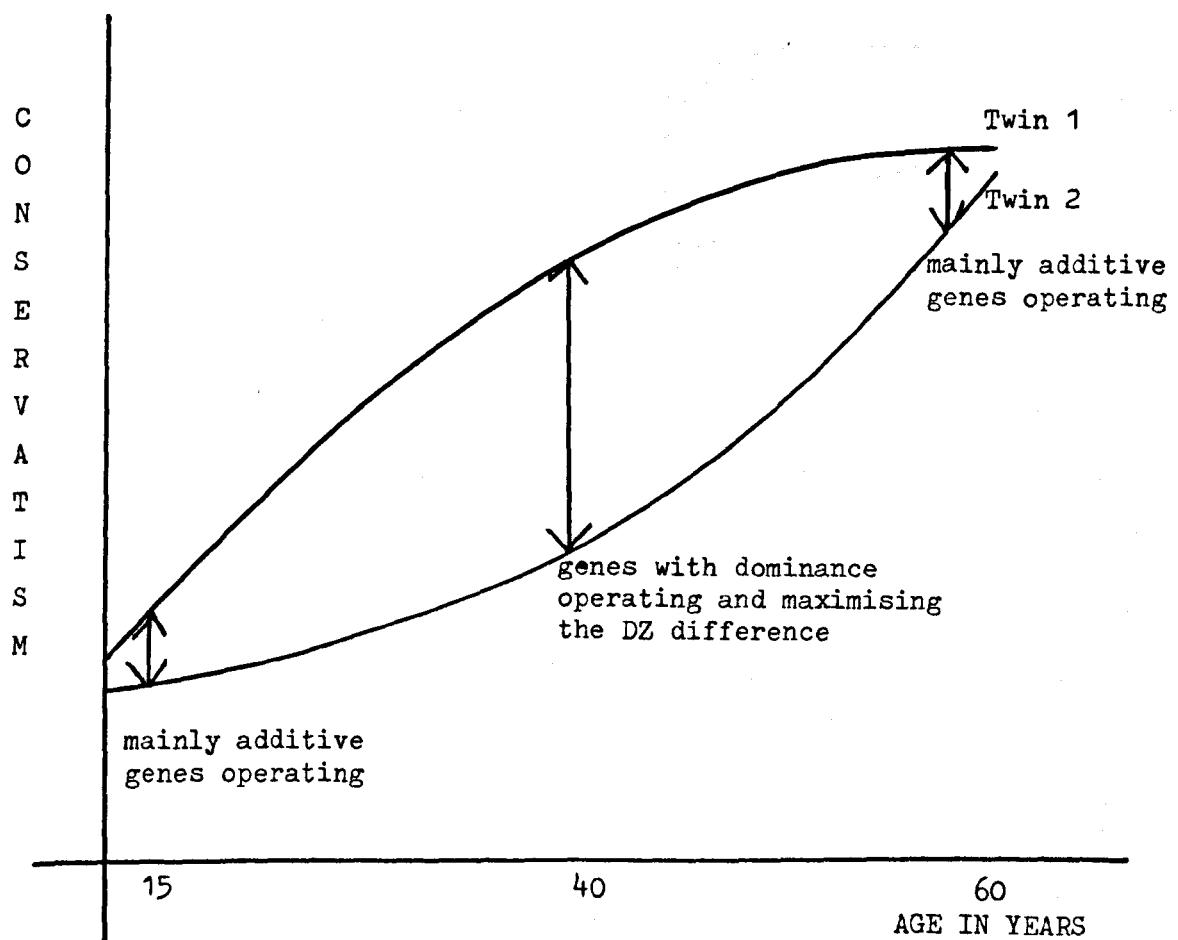
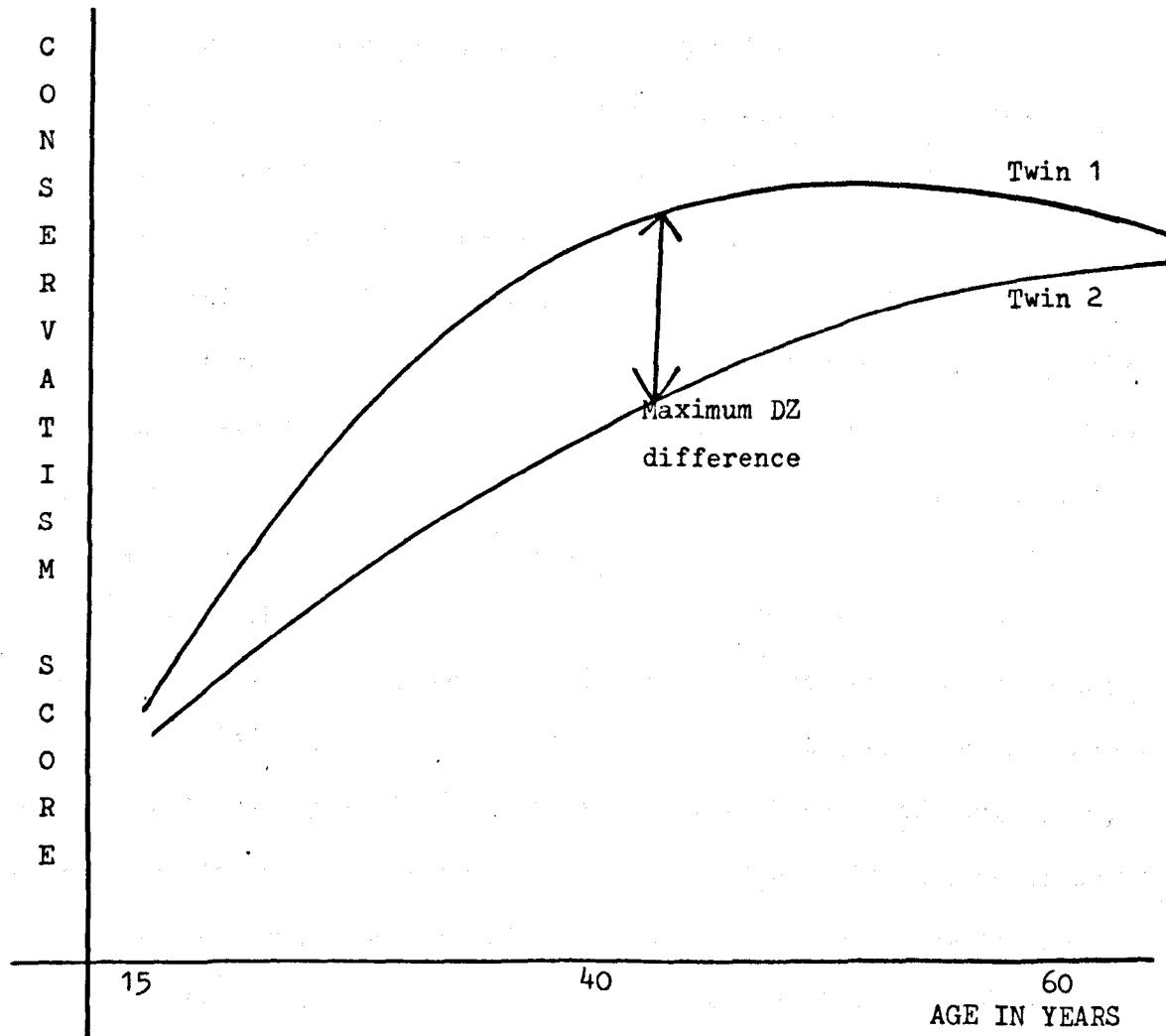


FIGURE B3: CHANGE IN PAIR DIFFERENCE AS A FUNCTION OF DEVELOPMENTAL RATE



NOTE: This graph implies that the increase in Conservatism with age is higher in individuals whose Conservatism score is higher i.e. there is genotypes x ages interaction.

4 REGRESSION OF REAL DIFFERENCES IN OPPOSITE-SEX PAIRS ON AGE

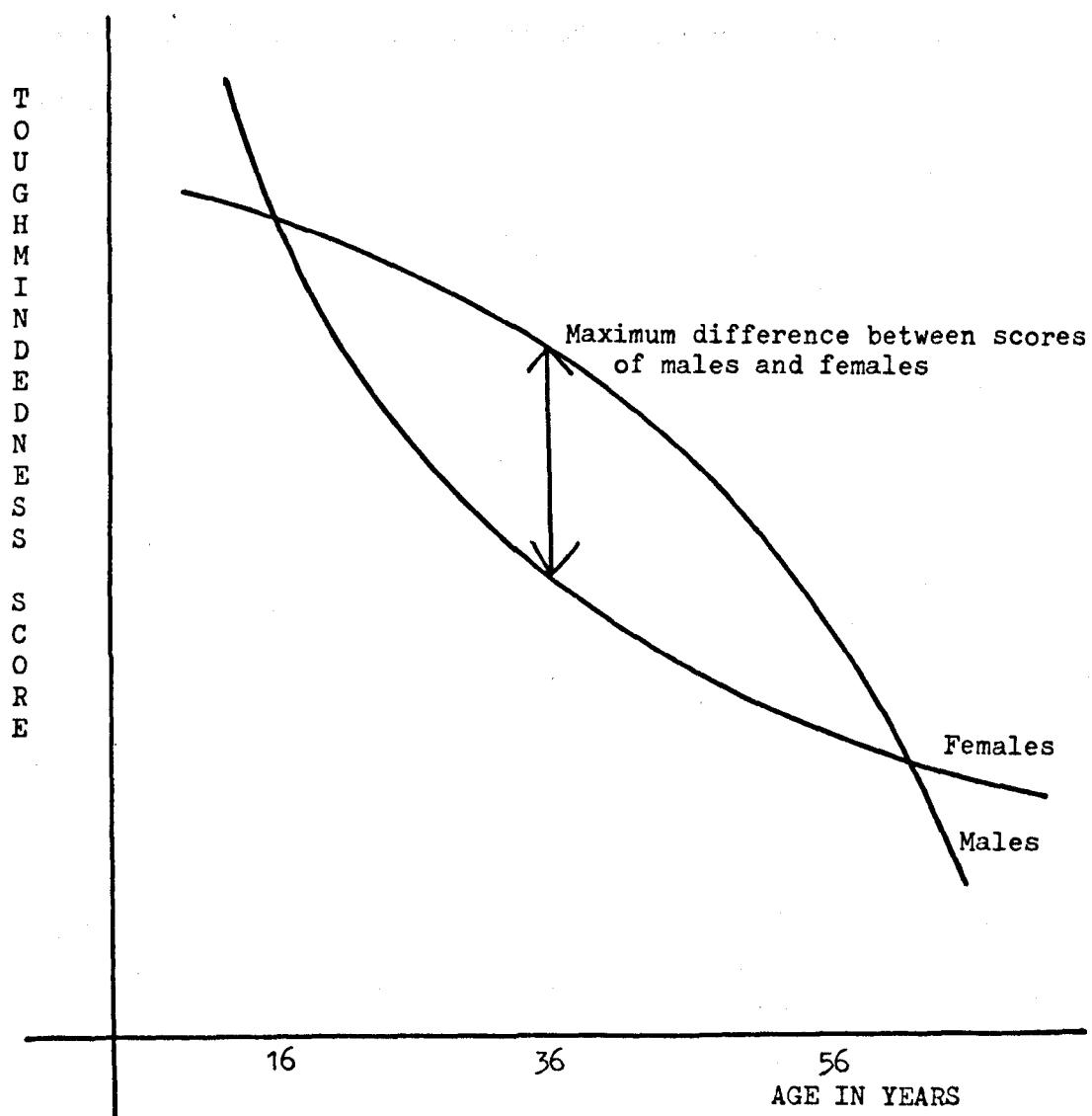
We have already seen that age-adjustment, using the analysis of covariance, does not remove differences in mean Toughmindedness score between sexes. Therefore, the effects of age and sex on test score were examined in more detail, using the opposite-sex pairs. The differences in Radicalism and Toughmindedness scores between males and females were calculated as (Male score - Female score). These differences were then regressed onto pair age.

No significant linear or quadratic component was found for the regression of real differences in Radicalism between members of opposite-sex pairs on age. i.e. the male-female difference does not change with age. This implies that the regression of test score on age will have the same slope in males and females.

Although there was no significant linear component to the regression of differences between members of opposite-sex pairs on age for Toughmindedness, there was a highly significant quadratic component. Males were less toughminded than females below 17 years of age. Then, they gradually become more toughminded compared with females until about 36-40 years of age, when the difference between the sexes begins to decline until, at about 53 years, males are again less Toughminded than females. Thus, males are more Toughminded than females through adulthood, but are less Toughminded in youth and old age.

This regression in opposite-sex pairs leads us to postulate different regressions of Toughmindedness score on age in the two sexes, which are likely to be non-linear (see Figure B4). This is in fact

FIGURE B4: REGRESSION OF TEST SCORE ON AGE IN MALES AND FEMALES,
PREDICTED ON THE BASIS OF THE OPPOSITE-SEX PAIRS



what we find in a later section. Again, we have found an interesting relationship between age, test score and sex for Toughmindedness. We shall now attempt to clarify the relationships between these three effects, by performing an analysis of variance of the opposite-sex pairs.

5 ANALYSIS OF VARIANCE OF THE OPPOSITE-SEX PAIRS

The total variation (143 d.f.) in the opposite-sex pairs may be partitioned into the between pairs (71 d.f.) and the within-pairs (72 d.f.) mean squares. The between pairs mean square may be further partitioned into the variation between pairs produced by the linear regression of score on age (1 d.f.) and the remaining variation between pairs (70 d.f.). The within pairs mean square was partitioned into variation within pairs produced by the sex difference (1 d.f.), by the interaction between age and sex (1 d.f.) and the interaction between pairs and sex (70 d.f.). This analysis of variance is given in Table B13.

Significant variation between pairs was found for Radicalism and Toughmindedness, but the age effect does not reach significance in the opposite-sex pairs (although later we will find a significant regression of test score on age in the data taken as a whole).

Mean differences between the sexes were removed by age-adjustment in the analysis of covariance for Radicalism, but not Toughmindedness. But in this analysis of variance the sex effect is not significant for either trait, although we might expect it to be significant for Toughmindedness. The sex-age interaction mean square which is obtained as the linear regression of real pair differences on age also fails to reach significance. We know, however, from the previous section that there is a significant quadratic component to the regression of real pair differences on age, implying a complex interaction of age and sex for Toughmindedness and suggesting that we may have to perform age-correction of the factor scores separately by sex for this trait.

TABLE B 13 : ANALYSIS OF VARIANCE OF THE OPPOSITE-SEX PAIRS

<u>ITEM</u>	<u>DF</u>	<u>RADICALISM</u>			<u>TOUGHMINDEDNESS</u>			<u>F</u>
		<u>SUM OF SQUARES</u>	<u>MEAN SQUARE</u>	<u>F</u>	<u>SUM OF SQUARES</u>	<u>MEAN SQUARE</u>		
BETWEEN PAIRS	71	172.25	2.43	2.48**	15.91	0.22		2.44**
Age	1	4.71	4.71	1.97NS	0.54	0.54		2.45NS
"Pairs" (error)	70	167.55	2.39		15.37	0.22		
WITHIN PAIRS	72	70.84	0.98		6.49	0.09		
Sex Difference	1	0.99	0.99	1.02NS	0.03	0.03		0.33NS
Sex x Age	1	1.17	1.17	1.21NS	0.00	0.00		0.01NS
pairs x Sex	70	67.70	0.97		6.43	0.09		
TOTAL		143						

KEY : DF degrees of freedom

NS not significant at the 5% level

* significant at the 5% level

** significant at the 1% level

6 REGRESSION OF TEST SCORE ON AGE6.1 Regression of Radicalism and Toughmindedness Scores on Age

Radicalism and Toughmindedness scores were regressed onto age separately for the six sub-groups of the data using a program from the EMD library of computer programs and taking out the linear and quadratic components. The results are summarised in Table Bl4. The major trend in both Radicalism and Toughmindedness is a negative linear component to the regression. This means that older individuals are less Radical and less Toughminded in these data. Therefore, either conservatism and tendermindedness increase with age or else radicalism and toughmindedness have become more dominant in society over the last 60-70 years. Discrimination between these alternative hypotheses about the origin of the regression of test scores on age is not possible without a longitudinal study.

In the two smallest groups (DZ males and DZ opposite-sex pairs), the regression of Radicalism score does not differ significantly from zero. However, we have evidence to suggest that there is a strong linear regression of Radicalism score on age in the data as a whole. A negative quadratic component was significant at the 5% level in two groups (MZ males and DZ females). Visual inspection of the six regression curves suggested that the rate of decline in Radicalism was somewhat faster after the age of 40. For the purposes of age correction we shall ignore this small quadratic component of the regression.

TABLE B 14 : REGRESSION OF TEST SCORES ON AGE

		<u>RADICALISM</u>		<u>TOUGHMINDEDNESS</u>	
		REGRESSION COEFFICIENT OF LINEAR REGRESSION	SIGNIFICANCE LEVEL OF QUADRATIC COMPONENT	REGRESSION COEFFICIENT OF LINEAR REGRESSION	SIGNIFICANCE LEVEL OF QUADRATIC COMPONENT
MZ MALES	166	-0.0139 *	*	-0.0038 *	NS
MZ FEMALES	466	-0.0105 ***	NS	-0.0089 ***	NS
DZ MALES	104	0.0025 NS	NS	-0.0074 *	NS
DZ FEMALES	294	-0.0153 ***	*	-0.0077 ***	NS
DZ OPPOSITE- SEX	144	0.0145 †	NS	-0.0046 †	***
ADOPTION DATA	445	-0.0113 ***	NS	-0.0098 ***	NS

KEY :

- † significant at the 10% level
- * significant at the 5% level
- ** significant at the 1% level
- *** significant at the 0.1% level

The regression of Toughmindedness on age was significant in all groups, apart from the opposite-sex pairs, where the probability was still less than 10%. However, in the opposite-sex pairs there was a highly significant quadratic component. Visual inspection of the six curves showed that the regressions were different in the two sexes as predicted in Section 4.4. There was a tendency towards a negative quadratic component in males and a positive quadratic component in females, neither of which was significant. Together, these produce the highly significant quadratic component observed in the opposite-sex pairs. We expected to find results like this when regressing Toughmindedness score on age from the regression of differences between members of opposite-sex pairs on age.

6.2 Homogeneity of the Regression Lines

The results of the regression analysis lead us to suspect that the regressions found in the six sub-groups of the data may not be homogeneous. Assuming linearity, the homogeneity of the residual variances, the slopes and the elevations of the six regression lines was tested, as described in Snedecor and Cochran (1967). The residual variances and slopes were homogeneous for both Radicalism and Toughmindedness. However, differences between the elevations were significant for Toughmindedness ($p < 1\%$) and approached significance for Radicalism ($5\% < p < 10\%$). This means that the regression of scores on age are similar in all groups, but that the means differ. Significant mean differences in Toughmindedness score may be largely attributed to a sex difference. Similarly males tend to be more

Radical than females although mean differences do not reach significance. Because of these mean differences we will correct the data for the regression of test score on age separately by sex, for both traits.

AGE-CORRECTION OF THE FACTOR SCORES

In order to perform the age-correction, we must obtain regression coefficients for all males and for all females and find the deviation scores (i.e. the difference between the observed score and the score predicted from the regression of test score on age). These scores are the age-corrected factor scores, with males and females varying around their own mean.

The calculations performed are summarised in Table B15, in which the regression analyses and the regression equations obtained from them are given. Predicted scores for each individual were found using these equations, and hence the deviation scores were obtained. These scores are used in all further analyses.

TABLE B15 : REGRESSION OF RADICALISM AND TOUGHMINDEDNESS SCORES ON AGE FOR MALES AND FEMALES

RADICALISM

MALES		$Y = 0.302 - 0.008X$				FEMALES		$Y = 0.444 - 0.013 X$			
ITEM	DF	SUM OF SQUARES	MEAN SQUARE	F	P	ITEM	DF	SUM OF SQUARES	MEAN SQUARE	F	P
Regression	1	8.2569	8.2569	8.98	0.003		1	42.7832	42.7823	56.59	0.000
Residual	451	414.8016	0.9197				1160	877.0118	0.7560		

TOUGHMINDEDNESS

MALES		$Y = 1.865 - 0.009X$				FEMALES		$Y = 1.722 - 0.008X$			
ITEM	DF	SUM OF SQUARES	MEAN SQUARE	F	P	ITEM	DF	SUM OF SQUARES	MEAN SQUARE	F	P
	1	9.2078	9.2078	117.39	0.000		1	16.8979	16.8979	223.24	0.000
	451	35.3738	0.0784				1160	87.8064	0.0757		

SECTION 5: PRELIMINARY ANALYSIS

1 THE MEANS

Means of the age-corrected Radicalism and Toughmindedness scores were calculated for the total sample and for various sub-groups of the data and are presented in Tables B16 and B17. Factor scores were calculated around a mean of zero and subsequently sexes were age-corrected separately around their own mean. Thus all the means are close to zero. However, the overall means of males and females are not exactly zero because they were based on all 1619 individuals, whereas the age-correction was performed on only the 1615 individuals for whom the ages were known.

A simple linear model, specifying the effects of zygosity, sex and their interaction (see Table B18) was fitted to the means by weighted least squares, using the reciprocals of the variances of the means as weights. The procedure is described in Section 3 and Appendix E. The estimates of the effects of zygosity, sex and their interaction on the means were not significant for either Radicalism or Toughmindedness. Since these scores for each sex were adjusted around a mean of zero, lack of significant sex differences between means is no surprise and is not very informative. The absence of zygosity difference suggests no differential sampling bias of the twins. Therefore, we went back to the unagecorrected scores and fitted the linear model to the raw Radicalism factor scores and the square roots of the factor scores for Toughmindedness. The results are presented in Table B18.

TABLE B 16 : MEANS OF AGE-CORRECTED RADICALISM SCORES

	MALES (M)	FEMALES (F)	M + F
MZ TWINS	0.119	-0.013	0.021
SAME-SEX DZ TWINS	-0.121	0.016	-0.019
OPPOSITE-SEX DZ TWINS	0.095	0.137	0.116
ALL TWINS	0.027	-0.002	0.019
All individuals except adopted individuals	-0.003	-0.004	0.012
ADOPTED INDIVIDUALS	-0.292	-0.027	-0.057
ADOPTING PARENTS	-0.115	-0.060	-0.084
NATURAL CHILDREN OF ADOPTING PARENTS	0.497	0.168	0.326
ALL ADOPTION STUDY	-0.104	-0.031	-0.050
ALL DATA	0.005	-0.002	0.000

TABLE B 17 : MEANS OF AGE-CORRECTED, TRANSFORMED TOUGHMINDEDNESS SCORES

	MALES (M)	FEMALES (F)	M + F
MZ TWINS	0.015	-0.026	-0.015
SAME-SEX DZ TWINS	-0.027	0.016	-0.017
OPPOSITE-SEX DZ TWINS	0.013	0.044	0.028
ALL TWINS	-0.001	-0.021	-0.011
ALL INDIVIDUALS EXCEPT ADOPTED INDIVIDUALS	0.022	0.002	-0.008
ADOPTED INDIVIDUALS	0.072	0.059	0.061
ADOPTING PARENTS	-0.048	0.004	-0.019
NATURAL CHILDREN OF ADOPTING PARENTS	0.107	0.019	0.061
ALL ADOPTION STUDY	0.036	0.043	0.041
ALL DATA	0.010	0.001	0.004

TABLE B 18 : SOURCES OF DIFFERENCES IN THE MEANS OF THE TWINS

		MEAN	ZYGOSITY (Z)	SEX (S)	Z X S
	Males	1	2	1	2
Monozygotic Pairs	Females	1	2	-1	-2
	Males	1	-1	1	-1
Dizygotic same-sex pairs	Females	1	-1	-1	1
	Males	1	-1	1	-1
Dizygotic opposite-sex pairs	Females	1	-1	-1	1
	Males	1	-1	1	-1

RADICALISM

Estimate	0.0578	0.0139	0.0079	0.0478
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Significance level	*	NS	NS	**
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TOUGHMINDEDNESS

Estimate	1.5421	-0.0071	0.0895	0.0087
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Significance level	***	NS	***	NS
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There was no significant effect of zygosity on the means for either trait. This shows that being an identical twin rather than a non-identical twin has no effect on attitudes. Although in the total sample males were more Radical than females, the effect of sex on the twin means was not significant. However, there was a sex x zygosities interaction significant at the 5% level. Monozygotic males and dizygotic females were more Radical. There is no obvious explanation for this.

There was a highly significant mean difference between the sexes for Toughmindedness, females being more tenderminded. This confirms the importance of the role of sex for Toughmindedness, which we have already seen during the age-correction, and suggests that this study may support the results of previous workers (Eaves, 1977; Martin, 1977), who found different mechanisms of variation in the two sexes.

2.1 Homogeneity of the Total Variances

Total variances were calculated for age-corrected Radicalism and Toughmindedness scores in the total sample and in various sub-groups of the data. These variances are given in Tables B19 and B20.

Bartlett's test was used to test the homogeneity of the total variances of the main sub-groups i.e. 5 twin groups (MZ males and females, DZ males and females and DZ opposite-sex pairs) and 6 groups from the Adoption Study (adopted males and females, adopting mothers and fathers and natural sons and daughters of the adopting parents). Since these variances were homogeneous for both Radicalism and Toughmindedness, we may regard all types of individual as belonging to one population and attempt to explain variation in all groups simultaneously.

However, more powerful tests may be made by comparison of groups of direct interest. For example, comparison of the total variance of all females with that of all males is significant at the 5% level for Radicalism ($\chi^2_1 = 6.24$) and at the 1% level for Toughmindedness ($\chi^2_1 = 6.70$). This indicates some heterogeneity between the sexes, which could lead to problems in attempting to explain variation in males and females simultaneously.

Eaves (1976a) has shown how competition or co-operation between sibs can lead to a distinct pattern of inequality in the total variances of MZ twins, DZ twins and singletons. For competition we expect:

TABLE B 19 : TOTAL VARIANCES OF AGE-CORRECTED RADICALISM SCORES

	MALES (M)	FEMALES (F)	M + F
MZ TWINS	0.716	0.688	0.698
SAME-SEX DZ TWINS	0.845	0.804	0.816
OPPOSITE-SEX DZ TWINS	1.023	0.755	0.884
ALL TWINS	0.777	0.732	0.761
ALL INDIVIDUALS EXCEPT ADOPTED INDIVIDUALS	1.008	1.038	0.794
ADOPTED INDIVIDUALS	1.672	0.736	0.845
ADOPTING PARENTS	0.971	1.055	1.011
NATURAL CHILDREN OF ADOPTING PARENTS	0.599	1.043	0.824
ALL ADOPTION STUDY	1.189	0.817	0.911
ALL DATA	0.919	0.758	0.803

TABLE B 20 : TOTAL VARIANCES OF TRANSFORMED, AGE-CORRECTED TOUGHMINDEDNESS SCORES

	MALES (M)	FEMALES (F)	M + F
MZ TWINS	0.073	0.078	0.077
SAME-SEX DZ TWINS	0.080	0.067	0.070
OPPOSITE-SEX DZ TWINS	0.081	0.069	0.075
ALL TWINS	0.075	0.074	0.075
ALL INDIVIDUALS EXCEPT ADOPTED INDIVIDUALS	0.173	0.087	0.081
ADOPTED INDIVIDUALS	0.075	0.082	0.081
ADOPTING PARENTS	0.125	0.088	0.104
NATURAL CHILDREN OF ADOPTING PARENTS	0.041	0.098	0.069
ALL ADOPTION STUDY	0.146	0.084	0.100
ALL DATA	0.094	0.077	0.082

MZ < DZ < Singletons and for co-operation: MZ > DZ > Singletons. However, we do not observe either pattern, and the Bartlett test gives no reason to suppose that the total variances are heterogeneous. Thus, there is no evidence that the phenotype of one sib acts environmentally on that of the other, making it either more or less similar to itself.

A priori, it seems likely that cultural effects may be important in determining attitudes and cultural transmission could play a role in producing variation. Eaves (1976b) has shown that when a trait is subject to cultural transmission, the variance of adopted individuals is expected to be greater than that of individuals reared by their natural parents. In these data, the total variance of adopted individuals equals that of individuals reared by their natural parents for Toughmindedness, providing no suggestion of cultural transmission. Variation in Radicalism of the adopted individuals is non-significantly greater than that of individuals reared by their natural parents ($\chi^2_1 = 0.44$, $0.70 > p > 0.50$). Thus, although cultural effects could be important in determining individual differences in attitudes, the total variances provide no evidence for the genotype-environmental covariation which might be expected if cultural transmission were superimposed upon genetically determined differences (Eaves, 1976b).

2.2 Analysis of Variance

Simple one way analyses of variance between and within pairs of twins were carried out for each of the five twin types and the

TABLE B 21 : SIMPLE ONE-WAY ANALYSIS OF VARIANCE OF TWINS RADICALISM SCORES

<u>GROUP</u>	<u>ITEM</u>	<u>DF</u>	<u>SUM OF SQUARES</u>	<u>MEAN SQUARE</u>	<u>F</u>	<u>P</u>	<u>r (intra-class correlation)</u>
MZ MALES	between pairs	81	93.2946	1.1377	3.79	***	0.5824
	within pairs	83	24.9174	0.3002			
MZ FEMALES	between pairs	231	261.9857	1.1292	4.53	***	0.6381
	within pairs	233	58.1424	0.2495			
DZ MALES	between pairs	50	63.7308	1.2496	2.78	**	0.4714
	within pairs	52	23.3449	0.4489			
DZ FEMALES	between pairs	145	177.8865	1.2184	3.11	***	0.5134
	within pairs	147	57.5830	0.3917			
DZ OPPOSITE- SEX	between pairs	70	190.9946	1.2816	2.61	***	0.4411
	within pairs	72	35.3557	0.4911			

TABLE B 22 : SIMPLE ONE WAY ANALYSIS OF VARIANCE OF TOUGHMINDEDNESS SCORES

<u>GROUP</u>	<u>ITEM</u>	<u>DF</u>	<u>SUM OF SQUARES</u>	<u>MEAN SQUARE</u>	<u>F</u>	<u>P</u>	<u>r (intraclass correlation)</u>
MZ MALES	between pairs	81	10.1931	0.1243	5.69	***	0.7004
	within pairs	83	1.8148	0.0219			
MZ FEMALES	between pairs	231	28.3688	0.1224	3.57	***	0.5622
	within pairs	233	7.9998	0.0343			
DZ MALES	between pairs	50	6.3842	0.1252	3.46	***	0.5514
	within pairs	52	1.8826	0.0362			
DZ FEMALES	between pairs	145	13.8700	0.0950	2.43	***	0.4169
	within pairs	147	5.7522	0.0391			
DZ OPPOSITE- SEX	between pairs	70	7.8495	0.1106	2.78	***	0.4698
	within pairs	72	2.8682	0.0398			

results are presented in Tables B21 and B22. One degree of freedom has been lost between pairs in each case by the age-correction, which removed variation between pairs due to the regression of test score on age.

Variation was significantly greater between than within pairs in all groups for both traits, showing that variation is not the result of random differences between individuals. There must be environmental or genetical differences between families. Genetical variation may be indicated since the within pairs mean squares of identical twins are markedly less than those of non-identical twins.

The male within pairs variance is non-significantly larger than the female within pairs variance for both MZ and DZ twins. Conversely, variation in Toughmindedness is greater within female pairs. Evidence for a sex difference in the mechanisms determining individual differences in Radicalism and Toughmindedness is provided by the opposite-sex non-identical twins, whose within pairs variance is greater than that in either male or female DZ pairs for both traits.

Since the total variances of the sub-groups of the data are homogeneous, no information is lost in calculating correlation coefficients from the data. Before proceeding to a more formal investigation of the causes of individual differences in Radicalism and Toughmindedness, the correlation coefficients from the twin and adoption study will be considered, in order to determine what information they yield about individual differences in these data.

3.1 Correlations of the Twins

The intraclass correlation coefficients, calculated from the variance components, are given in Tables B21 and B22. Small, but consistent differences are observed among the correlations. For both Radicalism and Toughmindedness, the MZ twins correlations are higher than those of the DZ twins suggesting either that there is greater genetical similarity between members of an MZ pair or that MZ pairs are treated more alike. A sex effect is observed for both traits. Correlations are higher in females than males for Radicalism. The reverse sex effect is observed for Toughmindedness.

We wish to quantify these observed differences in the correlations and determine whether they are statistically significant. Because the distribution of the correlation coefficient is skewed, the correlations were transformed into z values, which are normally distributed, and the z values were tested for homogeneity as described in Section 4 of Part A.

The five intraclass correlations differed significantly at the 5% level for Toughmindedness ($\chi^2_4 = 10.13$), but not for Radicalism ($\chi^2_4 = 6.57$). The differences between male and female correlations within zygosity noted earlier were not significant for either trait. Therefore, since there was no evidence for the effect of sex, the correlations for each zygosity were pooled over sexes. Pooled MZ and DZ correlations differed significantly at the 5% level for both traits.

Comparison of the pooled same-sex DZ twin correlation with the opposite-sex DZ twin correlation, showed no significant difference for either Radicalism or Toughmindedness. Thus, the correlations provide no evidence for a sex difference in the determination of attitudes, which had been suggested earlier.

A model specifying comparisons between zygosity, sexes and between same and opposite sex twins was written and is given in Table B23. The model was fitted to the z values for Radicalism and Toughmindedness using weighted least squares, as described in Section 4 of Part A. The results are presented in Table B23. The only significant effect for both traits is the mean effect. The overall effects of zygosity, sex and the same-sex vs. opposite-sex comparison were not significant. However, the relative magnitudes of these parameters is informative. Apart from the mean, the zygosity effect is the most substantial effect for both traits. For Toughmindedness, the sex effect is of a similar magnitude. However, the sex effect for Radicalism and the same-sex vs. opposite-sex comparison for both traits are negligible.

We have evidence for significant differences between the MZ and DZ twin correlations from the test of homogeneity of the MZ and DZ twin correlations pooled over sexes. This indicates that there may be a genetical component of variation for these traits, despite the lack of an overall zygosity effect in this analysis.

TABLE B 23 : MODEL AND ESTIMATES FOR CORRELATIONS OF TWINS

GROUP	MEAN	ZYGOSITY	SEX	SAME-SEX VS. OPPOSITE-SEX
MZ Males	1	1	1	0
MZ Females	1	1	-1	0
DZ Males	1	-2/3	1	1
DZ Females	1	-2/3	-1	1
DZ opposite-sex	1	-2/3	0	-2

RADICALISM

Estimate	0.5945	0.1178	-0.0377	0.0212
Standard Error	0.1441	0.1674	0.1576	0.1386
Significance level	***	NS	NS	NS

TOUGHMINDEDNESS

Estimate	0.6160	0.1329	0.1038	0.0088
Standard Error	0.1441	0.1674	0.1576	0.1386
Significance level	***	NS	NS	NS

3.2 Correlation among the individuals of the Adoption Study

Pearson correlation coefficients were calculated among the individuals of the Adoption Study. The 6×6 correlation matrices for Radicalism and Toughmindedness are given in Tables B25 and B24.

There are significant correlations between spouses of 0.4045 and 0.3824 for Radicalism and Toughmindedness respectively, as would have been predicted from previous work. However, these correlations are somewhat lower than the values of about 0.6 reported by Insel (1974) and others, but do not differ significantly from them.

The only other significant correlation for Radicalism is that between adopted daughter and adopting mother, which is based on the largest number of pairs of observations. This correlation suggests that it will be interesting to consider the pattern of the other correlations because although formally they do not differ from zero, they are not significantly different from the foster mother-adopted daughter correlation either.

Firstly, considering Radicalism, the correlations of adopted sons and daughters with their adopting mothers are very similar, whereas those with their fathers differ somewhat (and are not significantly greater than zero). Pooling over sexes, the correlation of an adopted child with its mother is higher than that with its father, suggesting that the role of a mother in providing a child's environment may be more significant in the determination of Radicalism, than the role of a father. Correlations between adopted and natural children reared by the same parents are slightly higher than those between fosterparent

TABLE B 24 : CORRELATION AMONG RADICALISM SCORES

Adopted Male	Adopted Female	Adopting Mother	Adopting Father	Natural Son of Adopting Parents	Natural Daughter of Adopting Parents	Adopted Male
1.0000 (0)	- (9)	0.3160 (5)	0.5153 (5)	(0)	- (1)	Adopted Male
1.0000 (40)	0.3363* (34)	0.0729 (34)	(8)	0.3579 (8)	0.4480 (8)	Adopted Female
1.0000 (47)	0.4045** (3)	0.7554 (3)			0.3679 (5)	Adopting Mother
1.0000 (2)		- (2)			0.5057 (5)	Adopting Father
	1.0000 (1)			- (1)		Natural Son of Adopting Parent
		1.0000 (1)			- (1)	Natural Daughter of Adopting Parent

NOTES :

1. Numbers in brackets give number of pairs on which the correlation was based.

2. Key

* Significant at the 5% level

** Significant at the 1% level

- No correlation could be calculated

TABLE B 25 : CORRELATION AMONG TOUGHMindedNESS SCORES

Adopted Male	Adopted Female	Adopting Mother	Adopting Father	Natural Son of Adopting Parents	Natural daughter of adopting parents	
1.0000	-	0.3369 (9)	0.6468 (5)	-	-	Adopted Male
1.0000	0.0095 (40)	0.2294 (34)	0.5723 (8)	0.1787 (8)	0.5243 (5)	Adopted Female
1.0000	0.3824** (47)	0.8582 (3)	-	0.6081 (5)	0.5243 (5)	Adopting Mother
1.0000	-	(2)	1.0000	-	0.6081 (5)	Adopting Father
1.0000	-	(1)	1.0000	-	0.6081 (5)	Natural son of adopting parents
1.0000	-	(1)	1.0000	-	0.6081 (5)	Natural daughter of adopting parents

and adopted child. Correlations between parents and their natural children are higher than those between adopting parents and their adopted children, which although based on small numbers is consistent with the hypothesis that some of the similarity between natural parents and offspring may be genetic in origin.

Turning now to Toughmindedness, only the marital correlation is significant. The correlations of natural children with their parents tend to be higher than the others, again suggesting a genetical component, but this is all that we can usefully say about them.

The inter-correlations among Radicalism, Toughmindedness and Age, presented in Table B26, are mostly non-significant. However, a few comments will be made. Not surprisingly there is a significant correlation in the age of spouses and also between the ages of parents and adopted children. Two significant correlations between subjects' Radicalism and Toughminded scores are observed, which reflect the non-orthogonality of the traits ($r = 0.19$). Since the data have been age-corrected, we do not expect to find correlations between Radicalism or Toughmindedness and age. However, the correlation between age of mother and Toughmindedness in their adopted daughters is negative and significant at the 5% level. Older mothers who are more Tenderminded themselves, may provide an environment in which their offspring tend to be more tenderminded. However, since we expect one correlation in twenty to be significant at the 5% level, we cannot attach too much importance to this finding.

Overall, looking at the correlations has not been very helpful, apart from demonstrating a marital correlation, because the numbers on which they are based are too few. The causes of variation in the Adoption Study may be elucidated by using all the information available simultaneously, which we shall do in a later section.

TABLE B 26 : CORRELATIONS BETWEEN RADICALISM, TOUGHMINDEDNESS AND AGE

	TOUGHMINDEDNESS						AGE					
	1	2	3	4	5	6	1	2	3	4	5	6
Age	1	-06	-	03	69	-	-	100	-	70*	52	-
	2	-	01	-04	-24	-47	-37	-	100	33*	61**	81*
	3	-41	-34	-06	-04	-83	-15	70*	33*	100	77**	-25
	4	-32	-20	-17	-21	-	-30	52	61**	77**	100	-
	5	-	-05	31	-	-10	-	-	81*	-25	-	100
	6	-	-17	-39	-07	-	-30	-	27	71	14	-
Radicalism	1	-01	-	02	69	-	-	03	-	27	-28	-
	2	-	21**	03	-03	04	11	-	02	-09	17	12
	3	20	14	06	16	85	76	04	-17	-13	-03	30
	4	47	07	14	19	-	-02	46	-00	13	13	-
	5	-	70†	76	-	82**	-	-	-00	-73	-	36
	6	-	26	01	01	-	20	-	58-02	15	-	-36

NOTES :

1. All decimal points are omitted
2. Code numbers are :
 - 1 Adopted Male
 - 2 Adopted Female
 - 3 Adopting Mother
 - 4 Adopting Father
 - 5 Natural son of adopting parents
 - 6 Natural daughter of adopting parents

SECTION 6: SIMPLE MODELS OF VARIATION IN RADICALISM AND TOUGHMINDEDNESS
IN THE TWINS

1

MODEL FITTING PROCEDURES

Throughout this Section, the concepts and methods discussed at length in Section 3 of Part A will be employed to investigate the genetical and environmental mechanisms, producing the pattern of mean squares observed in the twins. This will enable us to compare this study with previous studies, before moving on to examine all the data simultaneously, using methods appropriate to the analysis of unbalanced pedigrees.

Expectations for the ten mean squares will be generated in terms of the genetical and environmental components of variation described in Part A. The most likely explanation of the observed pattern of variation is that employing the least number of parameters representing sources of variation, in a model which satisfies the chisquare criterion of adequacy. Therefore, we first test the adequacy of the simplest models of variation and only incorporate additional parameters into our models when the simpler models are inadequate to explain variation in the data, or when the fitting of an additional parameter produces a significant improvement in fit over simpler models. Thus, certain effects influencing a trait may not be detected and estimated if they do not account for a significant proportion of the variation. The contribution of such effects to the total variation will be small and our explanation of the variation within a parsimonious model will account for the major part of the variation. Biases introduced by accepting as adequate models which are too simple will be calculated in Part C,

where the sample sizes needed to detect different components of variation will also be given.

2 MODELS OF RADICALISM IN THE TWINS

The simplest model of variation, the E_1 model, specifies that all variation is due to random effects such as errors of measurement or environmental influences specific to the individual. This model clearly fails to explain the observed variation ($\chi^2_9 = 178.03$) and its failure indicates that $\sigma^2_b \neq \sigma^2_w$ and $\sigma^2_{w\text{MZ}} = \sigma^2_{w\text{DZ}}$. Environmental differences, such as cultural differences, between families (E_2) might produce the former inequality and differences in E_1 between MZ and DZ twins the latter. Genetical variation would produce both inequalities.

In order to determine whether either genetical or environmental differences between families alone is sufficient to account for the observed residual variation after fitting E_1 , two simple two-parameter models were tested. The simple environmental model (E_1B) specifies that all variation may be accounted for by environmental differences either within or between families. We see from Table B27, that this model is not adequate since significant residual variation remains after fitting it. The simple genetical model (E_1D_R) specifies specific environmental effects, and errors of measurement and also additive genetical variation. Other sources of environmental variation (e.g. cultural differences) and genetical variation (i.e. all non-additive effects: dominance, epistasis genotype-environment interaction, genotype-environment covariation) will lead to failure of this simple model. From Table B27, we see that this model yields a non-significant chisquare. However, the fit is poor indicating that

TABLE B 27 : TWO SIMPLE MODELS FOR RADICALISM IN THE TWINS1. SIMPLE ENVIRONMENTAL MODEL

Parameter	Estimate	Standard Error	Significant Level
E_1	0.3396	0.0198	$p < 0.001$
B	0.4211	0.0361	$p < 0.001$

$$\chi^2_8 = 21.029, \quad p = 0.007$$

2. SIMPLE GENETICAL MODEL

Parameter	Estimate	Standard Error	Significant Level
E_1	0.2536	0.0193	$p < 0.001$
D_R	1.0068	0.0764	$p < 0.001$

$$\chi^2_8 = 14.276, \quad p = 0.075$$

$$\text{Narrow Heritability } (h_N^2) = 0.6650 \pm 0.0284$$

there might be an additional source of variation.

The most obvious three parameter model to try is that incorporating all three sources of variation described so far i.e. the $E_1 D_R B$ model. However, when there is genetical variation, interpretation of the B parameter changes. This parameter specifies between families variation, which may be produced by cultural differences between families as specified in the $E_1 B$ model. *A priori*, we might expect cultural differences to produce variation in Radicalism. However, since the $E_1 D_R B$ model includes additive genetical variation, genetical variation produced by such factors as dominance may contribute to the between families component. Eaves (1972) has shown that the power of the test for detecting dominance, using twins reared together, is extremely low and we would be unlikely to pick up its effect. However, in this study another effect must be considered.

We know from the adoption study that there is a correlation of 0.4045 between spouses in their Radicalism scores. Cultural effects and assortative mating both contribute to variation between families of individuals reared together. If cultural differences are perpetuated by cultural transmission (Eaves, 1976b), then the evolutionary consequences of cultural transmission and assortative mating are likely to be similar in the presence of genetical variation, since both increase apparent genetical variation. Cultural transmission does this by perpetuating environmentally the consequences of genetical segregation in previous generations. Assortative mating does so by associating alleles of like effect. So, when we are looking at twins reared together, we can only determine whether the effects of the mating system and culture are playing a jointly significant role in the determination of differences between families.

The joint contribution of assortative mating and cultural differences is thus summarised by the parameter B in the $E_1 D_R B$ model, which is given in Table B28.

The results of fitting this model to the data are given in Table B29. This model provides an adequate explanation of the data ($\chi^2_7 = 6.198$) and is a significant improvement over the $E_1 D_R$ model ($\chi^2_1 = 8.078$). Despite the fact that we have included all three parameters in this model, each differs significantly from zero and, therefore, represents a significant source of variation. The data are consistent with the interpretation that specific environmental influences and additive genetical effects produce variation in Radicalism. These findings are of limited interest since both D_R and E_1 are random, non-directional effects which could produce variation in a trait that is not biologically or sociologically important (although it is possible that such a trait could be under stabilising selection). However, if there is assortative mating, it seems likely that the trait may be of some evolutionary consequence.

Both assortative mating and cultural differences show that the trait may be sociologically relevant.

We know that either assortative mating or cultural effects or both are producing variation between families, but we cannot determine their relative contribution using the twin data alone. We can only set upper and lower limits for their effects. The total variance is given by ($\frac{1}{2} D_R + E_1 + B$). Therefore, the parameters account for the following percentage of the total variation:

TABLE B 28 : MODEL FITTED TO MEAN SQUARES FOR RADICALISM

TWIN TYPE	MEAN SQUARE	EXPECTED MEAN SQUARE		
		D _R	E ₁	B
MZ _m	b	1	1	2
	w	-	1	-
MZ _f	b	1	1	2
	w	-	1	-
DZ _m	b	$\frac{3}{4}$	1	2
	w	$\frac{1}{4}$	1	-
DZ _f	b	$\frac{3}{4}$	1	2
	w	$\frac{1}{4}$	1	-
DZ _{mf}	b	$\frac{3}{4}$	1	2
	w	$\frac{1}{4}$	1	-

where b = between pairs mean square

w = within pairs mean square

TABLE B 29 : FINAL MODEL FOR RADICALISM IN THE TWINS

Parameter	Estimate	Standard Error	Significance Level
E ₁	0.2687	0.0212	p < 0.001
D _R	0.5765	0.1589	p < 0.001
B	0.2091	0.0734	p < 0.01

$$\chi^2_7 = 6.198 , p = 0.517$$

$$\frac{1}{2}D_R = 37.63\%$$

$$E_1 = 35.08\%$$

$$B = 27.30\%$$

If the contribution to B of assortative mating is zero, then cultural differences may account for as much as 27.30% of the total variation and 37.63% of the variation in Radicalism could be due to genetical differences. However, we know from the adoption study that there is assortative mating. If we now assume assortative mating such that B is entirely genetic in origin, then as much as 64.92% of the variation could be due to genetical differences. In other words anything between 38 and 65% of the variation could be due to genetical differences.

Since we have data on spouses, we can go further than this and resolve the relative contributions of assortative mating and cultural effects. We will take the value of the marital correlation, μ , as 0.4045 and assume that the only influence of parents on their children is genetic. Assortative mating increases the additive genetical variance by associating alleles of like effect. Fisher showed that under certain conditions the contribution of assortative mating to the additive genetical variance is given by $\frac{1}{2}(A/(1-A))D_R$, where A is the correlation between the additive genetical deviations of spouses. "A" can now be calculated from μ and the narrow heritability (h^2_N), where h^2_N is the proportion of the total variation due to additive effects and is given by:

$$h^2_N = \frac{\frac{1}{2}D_R + \frac{1}{2}(A/(1 - A)) D_R}{V_T}$$

$$\text{where } V_T = \frac{1}{2} D_R + E_1 + B$$

This simplifies to:

$$h_N^2 = \frac{\frac{1}{2} D_R ((1/(1 - A)))}{V_T}$$

Making the usual assumption that assortative mating is based on the phenotype, then:

$$A = \mu h_N^2$$

We have estimates of μ and $\frac{1}{2} D_R / V_T$ and can use these to obtain a quadratic in A:

$$A = 0.4045 \times 0.3763 \times 1/(1 - A)$$

which simplifies to:

$$A^2 - A + 0.1522 = 0$$

Solutions for A are 0.8127 and 0.1873. Since the first value is greater than μ , we take $A = 0.1873$. Therefore, assortative mating accounts for $\frac{1}{2} D_R (A/(1 - A))/V_T = 8.67\%$ of the total variance. The difference between this value and the percentage of V_T accounted for by B is 18.63%, which is variation due to environmental differences between families. We can determine the proportion of the total variation due to genetical differences by adding the contribution of assortative mating to that which would still persist if mating were random. Thus, genetical differences account for 46.29% of the total variation.

A summary of our final model for the mechanism producing variation in Radicalism is summarised in Table B30. We now wish to compare these results with those of previous studies and then to make

TABLE B 30 : FINAL ANALYSIS OF RADICALISM SCORES FOR 587 PAIRS OF TWINS

Estimates of the components as a percentage of the total variation:

E_1	0.351	
$\frac{1}{2}D_R$	0.376	
B	0.273	
		A.M. 0.087	}
		E2 0.186	0.4629

N.B. A.M. is the percentage of the total variance due to assortative mating.

$$\text{i.e. } A.M. = \frac{1}{2}D_R \left(\frac{A}{1-A} \right) / V_T$$

predictions about the pattern of variances and covariances expected in the adoption study. If the adoption data are consistent with these predictions, we may obtain estimates of genetical and environmental components of variation using all the data simultaneously.

In summary, the most significant feature of this analysis of Radicalism is that the simple models fail. For many traits the simple models fit (see Martin, 1977 for many examples). In some cases, lack of ability to discriminate between simple environmental and simple genetical models indicates that the data are inadequate. However, in others the adequacy of the simple models suggests either that many of the complex mechanisms hypothesised for human variation do not operate in reality or that the traits being studied are not very relevant for our understanding of biology or society.

We have shown that the genetical effects of the mating system and cultural or treatment differences between families are contributing significantly to variation in Radicalism. These effects could reflect the cultural impact of parents on their children. Thus, Radicalism may be a sociologically relevant trait of evolutionary significance, where the joint role of cultural differences and heredity in the transmission of culture can be studied.

3 COMPONENTS OF VARIATION IN RADICALISM IN THREE STUDIES

The results for Radicalism of three studies of social attitudes are presented in Table B31, where the mean squares and proportion of the variation accounted for by the three parameters required to account for the variation are given. These studies (Hewitt, 1974; Martin, 1976; and the present study) are surprisingly consistent, despite the fact that the data were collected at different times, using different questionnaires and with very different aims in mind. Hewitt (1974) states in his thesis that he wished to determine whether the structure of attitudes had altered since the earlier work summarised by Eysenck (1954), as had been suggested by Eaves and Eysenck (1974a), and to examine subjects x items interactions for attitudes using the approach of Eaves and Eysenck (1974b). The collection of this data was initiated by Eaves who wished to study the relationship between personality and social attitudes. Martin's (1976) data were obtained as part of a study designed primarily to examine the determination of individual differences in sexual attitudes and the relationship of these attitudes with other behavioural traits. The data of this twin study were obtained in conjunction with data on smoking and drinking behaviour, neuroticism and impulsiveness. As a result of the consistency of a preliminary analysis of this study by Eaves (personal communication) with that of the other twins studies, the data of the Adoption Study were obtained in order to test hypotheses formulated on the basis of the twin data and to resolve parameters which are inevitably confounded in data on individuals reared together.

TABLE B 31 : COMPARISON OF THREE STUDIES OF RADICALISM

BETWEEN PAIRS MEAN SQUARES

		df	HEWITT MS
MONOZYGOTIC	MALES	141	10.3111
	FEMALES	323	8.36411
DIZYGOTIC	MALES	36	8.8544
	FEMALES	193	9.5146
	OPPOSITE-SEX	126	10.1125

WITHIN PAIRS MEAN SQUARES

MONOZYGOTIC	MALES	142	1.7804
	FEMALES	324	1.9055
DIZYGOTIC	MALES	37	3.2145
	FEMALES	194	2.8950
	OPPOSITE-SEX	126	3.2892

% of Total Variation Accounted For By :

E_1	0.3329
$\frac{1}{2}D_R$	0.3541
B	0.3130
	AM - 0.156
	E_2 - 0.157

μ

0.60

<u>MARTIN</u>		<u>PRESENT STUDY</u>	
df	MS	df	MS
37	356.521	81	1.1377
93	337.97	231	1.1292
15	272.48	50	1.2496
52	365.26	145	1.2184
39	350.61	70	1.2816
39	49.20	83	0.3002
95	61.50	233	0.2495
17	82.38	52	0.4489
54	100.83	147	0.3917
41	129.35	72	0.4911
0.2736		0.3508	
0.4427		0.3763	
0.2736	AM - 0.2736 E ₂ - 0.0000	0.2730	AM - 0.087 E ₂ - 0.186
0.67		0.4045	

63
65
44

Examination of the between pairs mean squares in Table B31 reveals no similarity in their relative magnitudes in the five twin groups in the three studies. However, in all cases, these mean squares were homogeneous and, therefore, the observed patterns in the three studies can be attributed to chance factors. Within pairs mean squares conform to the pattern we expect if there are genetical differences producing variation in Radicalism. MZ twin mean squares are substantially less than DZ twin mean squares. The mean squares within opposite-sex DZ pairs are slightly larger than those within same-sex DZ pairs, indicating slight but non-significant heterogeneity between the sexes.

In all three studies, the most appropriate explanation of the observed pattern of mean squares was found in a model incorporating specific environmental, cultural (or assortative mating) and additive genetical differences. These parameters accounted for a substantial proportion of the total variation in each case.

We first compare the results of the two largest and most reliable studies - Hewitts, based on 824 pairs of twins and the present study based on 587 pairs. These only suffer from the usual problems of sampling associated with twin studies, whereas the response rate in Martin's study was poor (only 30%) because the social attitudes questionnaire was sent out with a questionnaire on sexual attitudes. Problems will be introduced by the low response rate and the likely biases in the type of individual who would return such an anonymous questionnaire.

Hewitt's and the present study yield almost identical estimates of $\frac{1}{2}D_R$ when these are expressed as proportion of the total variance. E_1^A is slightly larger and B slightly smaller in the present study. The

authors' estimates of the relative contributions of assortative mating and cultural effects differ somewhat, but this is explained by the estimates they choose for the value of the marital correlation. Hewitt employs a value suggested by Insel's (1961) study, using the Wilson Conservatism scale, of $\mu = 0.60$. This yields a solution where cultural effects and assortative mating make an equal contribution to the variation. The present analysis uses a lower value of $\mu = 0.40$, obtained from the adoption study, and it is found that cultural effects contribute more than twice as much as assortative mating to the total between families variation. If a value of $\mu = 0.40$ is used with Hewitt's data, rather than the value of $\mu = 0.60$ which he chooses, then cultural effects account for 23.9% of the variation and assortative mating for 7.4% of the total variation, a result very similar to our own. Thus, as is expected, the precise contributions of assortative mating and cultural effects, estimated from the data, depends on the value of μ used. We believe that Insel's correlation may be rather high (as are other correlations he reports; see Eaves and Eysenck (1974)) and that cultural effects may produce more variation in Radicalism than assortative mating. If we assume that \hat{B} is all variation produced by assortative mating, we can easily calculate the value of μ that would be found in the population. For Hewitt's study $\mu = 0.70$ and for the present study $\mu = 0.65$. This value in Hewitt's study is higher than any reported before and the value in our study is considerably higher than the observed correlation. Therefore, although the exact size of their relative contributions is still in question, both cultural effects and assortative mating seem to be playing a role in determining individual differences in Radicalism.

Martin's study might, a priori, be expected to be less reliable because of the sampling procedure and the smaller sample size (246 pairs). Here the value of \hat{B} is about the same as in the other two studies, but $\frac{1}{2}\hat{D}_R$ is larger and \hat{E}_1 is smaller. These estimates are not significantly different to those from the other studies, and overall the studies are in good agreement with one another. However, the size of $\frac{1}{2}\hat{D}_R$ has interesting implications when we look at the distribution of \hat{B} between cultural effects and assortative mating. Martin uses a value of $\mu = 0.67$, reported by Eysenck (1976) for the 88 item Public Opinion Inventory used in his study, in order to calculate the proportion of \hat{B} which can be accounted for by assortative mating. He finds that the quadratic in A has no real solution since $\mu \times \frac{1}{2} D_R / V_T \times 4 > 1$ and concludes that his data are compatible with the explanation that all the between families variation can be accounted for by assortative mating. Assuming again that there is no variation produced by cultural effects and that all \hat{B} is due to assortative mating, we estimate the value of μ as 0.53, which is lower than that used by Martin and explains why no real solution existed for the quadratic. This sets a maximum value of $\mu = 0.53$ for Martin's study (i.e. given that Fishers model is appropriate) and once again suggests that Insel's reported correlations are unusually high or that an entirely different model need be adopted for the findings (e.g. genotype-environment covariance such as that produced by cultural transmission). Using $\mu = 0.4045$ as for the present study, Martin's data yield estimates of assortative mating = 13.5% and cultural effects = 13.9% of the total variation. Thus, depending on which value of μ we use in

the three studies we can get almost any relative contribution of assortative mating and cultural effects to the variation between families. However, from the two largest studies, we believe that both are presented in some degree.

The overall consistency of the three studies, despite the various inadequacies reported by their authors, suggests that our final model of Radicalism in some measure approximates to the true answer and gives some confidence to our efforts to generalise from the study of twins. It now remains to test the generality of this model for other types of individual in order to decide whether or not twins are typical of the population as a whole with respect to the genetical and environmental influences operating on them. We note in passing that so far we have found no evidence for one influence which could differentiate twins from other types of family for this trait, namely competition or co-operation, since the total variances of all twin groups were homogeneous. The adoption data will be used to clarify the position with respect to cultural effects and assortative mating and to test the applicability of the model in the twins to the population as a whole.

4 MODELS OF TOUGHMINDEDNESS IN THE TWINS

Using the same approach as that adopted for Radicalism, the simple E_1 model was first fitted to the data and failed to account for the observed variation. The results of then fitting the two parameter models are given in Table B32. The simple genetical model does not provide an adequate explanation of the data. However the simple environmental model appears to fit quite well, with 46.24% of the variation accounted for by specific environmental factors and 53.40% by between families differences. Therefore, formally at least, we need seek no further than these simple environmental effects for causes of variation in Toughmindedness.

However, as for the previous trait, we fitted the three parameters, E_1 , B and D_R to the data. Although all three parameters were significant, the additional parameter just failed to produce any significant improvement in fit over the simple environmental model ($\chi^2_1 = 3.71$, $5\% < p < 10\%$).

Thus, formally the $E_1 E_2$ model is adequate to account for variation in the twins. However, addition of the D_R parameter produces a substantial although not significant reduction in chisquare and this parameter is significantly greater than zero. Therefore, a small genetical component of variation may be indicated, which might be detected in a larger study of this type or a study with a completely different design (e.g. the Adoption Study).

How do these results compare with those of the two previous twin studies described earlier? The means squares for the three studies are presented together in Table B33 for comparison. Hewitt (1974) found

TABLE B 32 : TWO SIMPLE MODELS FOR TOUGHMINDEDNESS IN THE TWINS1. Simple Environmental Model

Parameter	Estimate	Standard Error	Significance Level
E_1	0.03461	0.00202	$p < 0.001$
E_2	0.03997	0.00352	$p < 0.001$

$$\chi^2_8 = 10.999, \quad p = 0.202$$

2. Simple Genetical Model

Parameter	Estimate	Standard Error	Significance Level
E_1	0.02875	0.00216	$p < 0.001$
D_R	0.08902	0.00744	$p < 0.001$

$$\chi^2_8 = 18.224, \quad p = 0.020$$

$$\text{Narrow Heritability } (h_N^2) = 0.6076 \pm 0.0322$$

TABLE B 33 : COMPARISON OF THREE STUDIES OF TOUGHMINDEDNESS

BETWEEN PAIRS MEAN SQUARES

		<u>HEWITT</u>	
		df	MS
MONOZYGOTIC	MALES	141	7.8197
	FEMALES	323	10.3697
DIZYGOTIC	MALES	36	6.5694
	FEMALES	193	7.5213
	OPPOSITE-SEX	126	8.1251

WITHIN PAIRS MEAN SQUARES

		df	MS
MONOZYGOTIC	MALES	142	3.1980
	FEMALES	324	1.8643
DIZYGOTIC	MALES	37	3.3720
	FEMALES	194	2.9982
	OPPOSITE-SEX	126	4.3155

<u>MARTIN</u>		<u>PRESENT STUDY</u>	
df	MS	df	MS
37	391.03	81	0.12431
93	383.21	231	0.12241
15	548.82	50	0.12518
52	248.89	145	0.09500
39	299.19	70	0.11056
39	93.36	83	0.02187
95	79.48	233	0.03433
17	62.91	52	0.03260
54	125.14	147	0.03913
41	148.63	72	0.03984

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that no model with the same effects in both sexes would fit these data. The simple genetical model was adequate to explain the variation in each sex separately, but the simple environmental model again failed. Eaves (personal communication) later devised a model which could be fitted to both sexes simultaneously by allowing the parameters to take different values in each sex and including a parameter to specify the correlation between an effect in males and females. He found, for Hewitt's study, that a model with separate E_1 's (E_{1M} and E_{1F}), separate D_R 's (D_{RM} and D_{RF}) and an interaction parameter (D_{RMF}) was adequate to explain the variation, but that the fit was poor ($\chi^2_5 = 9.51$: $0.05 < p < 0.10$) (Eaves, 1977). Addition of a parameter summarising cultural differences (or assortative mating) - B - gave a significant improvement in fit over the earlier model and suggested that the mechanism producing variation in the two sexes was very different. Eaves concluded that the principal characteristics of Toughmindedness were those of a trait whose pattern of determination shows a marked interaction with sex. Both sexes seemed to be subject to the effects of the family environment (since B was significant). However, there was only evidence for genetical variation in females. The genes did not appear to be contributing to individual differences in males.

Martin's (1976) study yielded very similar results. Different models of variation were required in males and females. He found that of the two simple two parameter models only the E_1E_2 model would fit in males and only the E_1D_R model would fit in females, which was consistent with the findings of Eaves for Hewitt's data. He found that a similar model to that of Eaves (allowing the parameters to take separate values in the two sexes and allowing for interaction between an effect in males and females) gave the best explanation of his data.

Thus, in both previous studies no simple model would account for variation in both sexes, and the determination of attitudes was markedly different in the two sexes. There was a heritable component of variation in females, but no evidence for genetical variation in males. In this study, there was no heterogeneity between the sexes and no significant genetical component of variation was found in either sex. How can we explain the discrepancy between the two previous studies, which agreed with one another well, and the present study?

The most obvious culprit in such cases is biased sampling. However, this does not seem to be an appropriate reason here, since the findings in all three studies for Radicalism were remarkably consistent. For our explanation, we must turn, I think, to the questionnaire used, since this is the most obvious difference between the previous studies and the present study. Such problems as biased sampling were common to all three studies.

Hewitt's and Martin's studies used different questionnaires, but both were versions of the Public Opinion Inventory where subjects were asked to rate 80 statements from 1 (strongly disagree) to 5 (strongly agree). The present study used the Wilson-Patterson attitudes questionnaire where subjects respond by agreeing or disagreeing with a topic represented by a single noun. This questionnaire was developed from the Wilson Conservatism Scale (1968). A comparison of the Wilson-Conservatism scale and the Wilson-Patterson Attitudes Questionnaire is given for interest in Table B34. Wilson and Patterson (1968) state about the origin of the Conservatism scale that: "Development of the present scale began with a list of characteristics which might be expected in the extreme conservative". Fifty items which were effective

TABLE B 34 : COMPARISON OF WILSON'S (1968) CONSERVATISM SCALE AND THE
WILSON-PATTERSON SOCIAL ATTITUDES QUESTIONNAIRE

ITEMS SPECIFIC TO EARLIER CONSERVATISM SCALE	ITEMS COMMON TO BOTH SCALES	ITEMS SPECIFIC TO SOCIAL ATTITUDES SCALE
Chaperones	1. Death Penalty	5. Council Housing
Student Pranks	2. Evolution Theory	8. Women's Lib
Fluoridisation	3. School Uniforms	9. Student Protest
White Lies	4. Strip-tease Shows	10. Police
Straitjackets	6. Sunday Observance	11. Surtax
Learning Latin	7. Hippies (Beatniks)	13. Foreign Aid
	12. Wife Swapping (Pyjama Parties)	15. Welfare State
	14. Pop Music (Jazz)	16. Tradition
	18. The Pill	17. Conscription
	19. Patriotism	21. United Nations
	20. Modern Art	26. Law Reform
	22. Self Denial	33. Political Systems
	23. Working Mothers	37. Space Research
	24. Military Drill	38. Strikes
	25. Co-Education	39. Common Market
	27. Divine Law	44. Capitalism
	28. Socialism	50. Inheritance Tax
	29. White Superiority	57. Arab Politics
	30. Cousin Marriage	58. Pacificism
	31. Moral Training	59. Law and Order
	32. Suicide	62. Profit Sharing
	34. Legalised Abortion	66. Trade Unions
	35. Empire Building	67. Supersonic Airliners
	36. Licensing Laws	68. Liberals
	40. Computer Music	
	41. Chastity	
	42. Royalty	
	43. Women Judges	
	45. Conventional Clothing	
	46. Teenage Drivers	
	47. Apartheid	
	48. Nudist Camps	

contd.

TABLE B 34 Contd.

ITEMS SPECIFIC TO EARLIER CONSERVATISM SCALE	ITEMS COMMON TO BOTH SCALES	ITEMS SPECIFIC TO SOCIAL ATTITUDES SCALE
-------------------------------------------------	--------------------------------	---------------------------------------------

- 49. Church Authority
- 51. Astrology (Horoscopes)
- 52. Disarmament
- 53. Censorship
- 54. Birchng
- 55. Mixed Marriage
- 56. Strict Rules
- 60. Casual Living
- 61. Divorce
- 63. Inborn Conscience
- 64. Coloured Immigration
- 65. Bible Truth

discriminators on these characteristics, were chosen from a large pool of items, so that half the items scored positively on Conservatism and half negatively. Examination of the items added to this conservatism scale to produce the questionnaire used in the present study does not suggest that they were especially chosen to discriminate between Tough and Tendermindedness. This may be the key to the difference between the present study and earlier studies. Hewitt (1974) reports from his factor analysis of the 60 item Public Opinion Inventory that the first principal component accounted for 14% of the total variation, the second for 10% and all remaining components for 3% or less. Other studies using similar questionnaires to the 60 item Public Opinion Inventory, find that Radicalism and Toughmindedness are two major factors approximately equal magnitude. Eysenck does not report the proportion of variation accounted for by R and T in his analysis of the quota sample described previously. Although the item content and the loadings in the two factors in the present study are closely similar to those found by Eysenck in the quota sample, we do not find that the two factors are of a similar magnitude. The first principal component accounts for 10.6% of the total variation, the second and third for 4.4% and 3.6% and all subsequent components for less than 2%, suggesting that either one or three factors might provide the best description of the items in this study. The picture that emerges for Radicalism, the major factor in this study, agrees remarkably well with that found for previous studies, suggesting that the trait being measured is very similar in all three studies and that a model including specific environmental effects, cultural effects, additive genetical variation and assortative mating may be a close approximation to the true causes of variation in this trait.

In the present study, "Toughmindedness" seems to be only a minor factor and it seems likely that we are not dealing with the same trait as in previous studies. This can be explained by the particular items used in the present scale which emphasize the discrimination between Radicalism and Conservatism. The major factors of Toughmindedness described by Hewitt and Martin show a marked interaction with sex in their determination. Our conclusion is that the trait measured in the present study, which resembles Toughmindedness, is only a minor component of variation. The causes of variation may be much simpler than those for Toughmindedness as measured by conventional types of questionnaires. There is little evidence for a heritable component of variation in this twin study, and the variation can be accounted for by unreliability of measurement, specific environmental influences and environmental differences between families. Although the trait is only a minor component of the attitudes assessed in the Wilson-Patterson Questionnaire, there are differences between families which require explanation. We shall examine in detail the between families component for both "Toughmindedness" and "Radicalism" by now turning to the Adoption Study.

SECTION 7: FITTING MODELS SIMULTANEOUSLY TO THE TWIN DATA AND THE UNBALANCED PEDIGREES OF THE ADOPTION STUDY

1 THE PROBLEM OF UNBALANCED PEDIGREES

The advantages of this study for the resolution of between families effects were discussed in Section 1. Analysis of the twin data has given a broad outline of the major causes of variation in attitudes. Significant between families variation was demonstrated, but we were unable to discriminate between certain hypotheses of considerable interest concerning this variation. For example, the relative contribution of variation produced by assortative mating and cultural effects could not be determined.

Cultural transmission is of great theoretical interest and, a priori, we might expect it to be of some importance in the determination of social attitudes. But since all between families components are inevitably confounded in studies of related individuals reared together, the twin study enabled us to show that cultural differences might contribute to the significant between families component but could provide no positive evidence for the presence of cultural transmission. Many writers have shown that data on adopted individuals provide the most direct test for between families environmental effects. The covariation of genetical and environmental effects which may be generated by the cultural transmission of inherited differences cannot be detected easily without adoption data (Jinks and Fulker, 1970). Cavalli-Sforza and Feldman (1973) comment on the importance of adopted individuals for detection of the components of their model of cultural transmission based

on a single gene. Therefore, in the present study, we hope to use the adoption data to estimate the parameters of a cultural transmission model for attitudes and compare this model with other simpler models in order to determine the likelihood that the non-genetic transfer of information from parents to offspring plays a significant role in the determination of attitudes.

Unfortunately, the design of our study is far from ideal. We have no data on the natural families of adopted children, and information on adoptive families is far from complete. We have a large number of adopted individuals, the adopting parents of a small proportion of these and a few natural and adopted siblings. All these individuals yield some information on effects of interest to us. Our problem is to make use of all this information.

Previously we have considered only balanced pedigrees. The structure of the twin data is consistent from family to family, with no missing observations. Such data are amenable to the analysis of variance. Analysis of such summary statistics as means, correlations and variances was presented in Sections 5 and 6. The procedures used were quick and convenient. We shall show later that using mean squares rather than working on the individual observations involves no serious loss of information when dealing with such regular pedigrees.

In Section 1 we saw that very few pedigrees of the adoption study had a similar structure. Such extremely unbalanced pedigrees present problems when attempting to use conventional summary statistics. Family sizes differ and the same individual may appear in a variety of relationships. Covariances and correlations between relatives are not independent and our usual approach is no longer appropriate.

Data on a large number of individuals with no measured relatives cannot contribute to correlations and covariances but contains a lot of information about total variances of different groups, which would be wasted using the conventional model fitting approach.

We shall present a method which enables the information provided by every individual to be used simultaneously, whatever his position in a particular pedigree. Single individuals are considered to be pedigrees of size one. Because of the awkward experimental "design" of this study, we shall abandon attempts to estimate conventional summary statistics and return to the raw observations. We could attempt to estimate means, variances and covariances between individuals using maximum-likelihood methods and then fit models in the usual way. This would involve using an unrealistically large number of parameters and prove extremely inefficient. The alternative approach is to formulate a model for these statistics and estimate its parameters directly from the raw data using a maximum likelihood method. Such procedures have been previously described (Elston and Stewart, 1971; Lange, Westlake and Spence, 1976). These authors show how to use the full likelihood of a set of pedigrees to obtain estimates of a set of parameters from the data. We will basically follow their approach, but employ more complex models in order to test hypotheses about cultural transmission and another numerical method.

We set up a vector of expected values for the means and an expected variance - covariance matrix for each family. The latter is equivalent to the model specified for the mean squares in Section 6. Then we choose a given set of parameter values which maximises the log

likelihood of observing the observed set of pedigrees. Lange, Westlake and Spence (1976) give a standard expression for the log likelihood of an observed pedigree, given a particular vector of means and an expected covariance matrix. Our main problem is to specify an expected covariance matrix i.e. a model. Lange, Westlake and Spence (1976) illustrate the method using simple models and Spence, Westlake and Lange (1976) have fitted the model to data on dermal ridge counts. They use expectations for simple situations with random mating and environmental differences within families. Additive genetical effects and dominance variation are included in the model. More complex models specifying genotype-environment interaction or genotype-environment covariation are not given. Since we are interested in the latter, we will describe more complex models in the following pages and show how the methods of Lange, Westlake and Spence (1976) may be used to fit them to our data.

2 SOLUTION OF THE NUMERICAL PROBLEM2.1 Specification of the Log Likelihood

We shall follow Lange, Westlake and Spence (1976) in order to specify the likelihood function. They consider a pedigree of n people. In our case, n is the maximum possible pedigree size. Inspection of the data shows that this pedigree has $n = 6$ and is composed of the following members: mother, father, two adopted individuals and two natural siblings.

Let $\mu = (\mu_1 \dots \mu_n)^t$ be a column vector of the expected values of the individuals of the pedigree, where $\mu_i = \mu_m$ or μ_f depending on whether the i^{th} individual is male or female. Males and females thus take separate means, μ_m and μ_f and these are the first two parameters of our model. Other models might be specified for the expected values.

Let $x = (x_1 \dots x_n)^t$ be the observed trait values.

Finally, let Ω be a matrix of expectations for the variances and covariances between members of the pedigree, the expectations being expressed in terms of K parameters. Thus the total number of parameters in our model is $(2 + K)$. The precise expectations for the terms of Ω will be specified later.

Where we do not have a complete pedigree of n individuals (i.e. in most cases), missing members are ignored and μ and Ω reduced in size.

The natural logarithm of the likelihood of the pedigree is then given by:

$$L = -\frac{1}{2} \ln |\Omega| - \frac{1}{2}(x - \mu)^t \Omega^{-1} (x - \mu),$$

(Rao, 1973) (where $|\Omega|$ is the determinant of Ω).

The problem now is to find an appropriate method for choosing a set of values of the $(2 + K)$ parameters which maximises this likelihood summed over families. Some version of Newton's method is most commonly used. This method requires that the first and second derivatives of the likelihood function are specified algebraically, or at least extracted numerically. Lange, Westlake and Spence (1976) produce an algebraic solution, which is complex even for their simple linear model. Since we shall specify far more sophisticated models during our investigation, we would prefer a method for maximising the likelihood which does not rely on the derivatives, or else uses numerical differentiation.

A second problem arises because the likelihood of observing a particular pedigree involves the inverse of the covariance matrix. Therefore, any set of parameter values which would yield a non-positive definite (NPD) covariance matrix will lead to failure of the method.

2.2 Maximising the Log Likelihood

Both these problems may be overcome by using a computer library routine, called E04HAF, supplied by the Nottingham Algorithms Group (NAG) (1977). This routine minimises a function of many independent variables, subject to general inequality and/or equality constraint functions, and bounds on the variables. Therefore, we use the program to minimise minus the log likelihood (i.e. to maximise the log likelihood). E04HAF uses iterative methods and requires initial estimates of the

position of the minimum as trial values. It can overcome the problem of a non-positive definite covariance matrix, if good trial values for a reasonable model are supplied. Otherwise the problem may be overcome by constraining the search for a minimum not to enter an area where Ω is NPD. One method of doing this which is often effective in practise is to use a penalty function technique which devises functions of the parameters which tend to zero when certain constraints are satisfied. The NAG routine uses a penalty function technique due to Lootsma (1972). A routine is supplied by the user to calculate the values of a number of problem functions for any set of values of the variables. To overcome our particular problem and ensure that the $n \times n$ covariance matrix is positive definite, we supply n functions, specifying that all the eigenvalues of the matrix are positive. However, this approach leads to a marked increase in computer time and is, therefore, undesirable. The necessity to specify such constraints may be overcome in most cases by the judicious choice of trial values or rectangular constraints on the parameter values.

The NAG routine provides a choice of three methods for the minimisation. One method, based on the Powell 64 method, relies on the function values only. It has no information on where to search for the solution in the space available and even with good trial values tries widely divergent values for the parameters before coming close to the solution. This means that, without the use of constraints, the covariance matrix often becomes NPD. The use of this method with constraints is extremely time-consuming and it's use is impracticable for our application. However, we did try it several times in this study for simple cases.

The second method uses values and first derivatives in a quasi-Newton method and the third also uses second derivatives in a Newton-type method. It is found, in practise, that the numerical differentiation used by these latter methods gives reasonably satisfactory results, (although it can be time consuming), as long as the iterative process is started with good trial values and a reasonable model is used.

The use of the NAG routine requires that a number of subroutines are supplied by the user. The program incorporating the E04HAF minimisation routine used in the following analyses was written by Dr. L.J. Eaves, Department of Genetics, University of Birmingham and was adapted for the particular problems to be described in the following pages. Further details of the program and methods will be described later when appropriate. All the computations were carried out on a CDC 7600 computer at the University of Manchester Regional Computer Centre via the SWAN link between Manchester and Birmingham's ICL 1904S and 1906A computers.

3 A SIMPLE APPLICATION OF THE METHOD3.1 Comparison of Two Methods

The methods we are about to use are radically different from those employed in conventional model-fitting to twins, as described for the Georgia Twin Study and the Twin Study of Social Attitudes. Therefore, a comparison of the two approaches is highly desirable.

In theory, any discrepancies between the two methods should be due to inadequacies of the conventional approach through model-fitting by weighted least squares. Given normality of the original observations, the new approach should provide the maximum-likelihood solution of our problem, whereas weighted least squares is only equivalent to a maximum-likelihood method given certain assumptions. The most important of these from our point of view is normality of the distribution of the mean squares. Since we have shown that our data are approximately normally distributed and that the mean squares are based on quite large numbers, we do not expect greatly different answers from the two approaches.

The practical problem is somewhat different. The maximum-likelihood method is extremely complex compared with the older method. The NAG routine requires the user to specify the required accuracy of the solution. This is not easy since if the criterion is too stringent, convergence may never be reached. However, relaxing the criterion too far may produce biased parameter estimates. If the estimates from the weighted least squares and maximum-likelihood methods are closely similar, then we can suppose that our convergence criterion is adequate.

In order to compare the two methods, we shall attempt to fit the $E_1 D_R$ and $E_1 BD_R$ models to the twin data using the new method, before attempting to fit models to the twin and adoption data jointly.

3.2 Specification of the Data Structure and of Models

The concepts needed to fit our final complete genetical model will be introduced a few at a time, as they are needed to fit the simpler models that we shall consider first. The first two ideas we need to discuss are the specification of a matrix of relationships and of model matrices.

Before we can specify a model for the means, variances and covariances between relatives, we must uniquely identify each individual type and his relationship with all other members of his family. The following system has been devised for this purpose so that a complete pedigree can be drawn from a matrix of codes (Eaves, personal communication).

The diagonal terms of the matrix represent the individual members of the pedigree in the same order as their scores have been coded and the value of the diagonal term provides information about the individual. The off-diagonal terms contain codes specifying the relationships between all possible pairs of individuals. The system of coding to be used throughout is given in Table B35. An example of a pedigree illustrating the use of these codes is given in Table B36. Family 645 in our study demonstrates the use of all the codes, except that for an adopted son. From this matrix we can draw out the family pedigree without any further information. Eaves (personal communication) has extended this coding system so that pedigrees going back several generations can be specified.

TABLE B 35 : CODES USED IN SPECIFICATION OF PEDIGREES

	CODE	MEANING
Meaning of Diagonal terms	1	Male
	2	Female
	3	Adopted Male
	4	Adopted Female
Relationship specified by off-diagonal terms	20	Spouse of
	21	Natural child of
	22	Natural parent of
	23	Co-sibling of
	80	Adopted child of
	81	Adopting parent of
	82	Adopted sibling of natural child or viceversa
	83	Adopted sibling of an adopted child

TABLE B 36 : EXAMPLE OF A CODED PEDIGREE (FAMILY 645)

	ADOPTED DAUGHTER	MOTHER	FATHER	NATURAL SON	NATURAL DAUGHTER
ADOPTED DAUGHTER	4	80	80	82	82
MOTHER	81	2	20	22	22
FATHER	81	20	1	22	22
NATURAL SON	82	21	21	1	23
NATURAL DAUGHTER	82	21	21	23	2

From Table B36, we can see that the upper and lower triangles of the matrix yield the same information about the family and we could draw the pedigree from either. Thus, when we produce a data file to be used by the computer program, only the upper triangle of the relationship matrix is specified. The data file will contain the following information for each family in turn:

1. The number of individuals in the pedigree
2. The upper triangle of the relationship matrix
3. Scores for each individual (in the same order)

In order to specify a particular model, we now only have to give the expectations appropriate for each code. The program then calculates the expected covariance matrix for each family in turn using the information provided.

In order to generate the expectations for each twin family based on the $E_1^D R$ model, as given in part A of Table B37, we simply attach values to the codes as shown in part B of this Table. In later Sections more complex models will be specified using all the data, but the principle for generating the expected covariance matrix for each family in turn remains the same.

3.3 Obtaining Maximum-Likelihood Solutions of the Parameters

Having specified the data and model, we now attempted to find the set of parameter values which would maximise the log likelihoods, summed over pedigrees, using the program incorporating the NAG library routine, E04HAF, for minimising a function. We have to provide a trial

TABLE 37 : EXPECTATIONS FOR THE $E_1 D_R$ MODEL IN THE TWINS

PART A : Expectations for the Three Types of Twin Family.

	VECTOR OF MEANS	VARIANCE-COVARIANCE MATRIX
Monozygotic Twins	$\begin{pmatrix} \mu_m & \mu_f \\ \mu_m & \text{or} & \mu_f \end{pmatrix}$	$\begin{pmatrix} \frac{1}{2}D_R + E_1 & \frac{1}{2}D_R \\ \frac{1}{2}D_R & \frac{1}{2}D_R + E_1 \end{pmatrix}$
SAME-SEX DIZYGOTIC TWINS	$\begin{pmatrix} \mu_m & \mu_f \\ \mu_m & \text{or} & \mu_f \end{pmatrix}$	$\begin{pmatrix} \frac{1}{2}D_R + E_1 & \frac{1}{2}D_R \\ \frac{1}{2}D_R & \frac{1}{2}D_R + E_1 \end{pmatrix}$
OPPOSITE-SEX DIZYGOTIC TWINS	$\begin{pmatrix} \mu_m & \mu_f \\ \mu_f & \text{or} & \mu_m \end{pmatrix}$	$\begin{pmatrix} \frac{1}{2}D_R + E_1 & \frac{1}{2}D_R \\ \frac{1}{2}D_R & \frac{1}{2}D_R + E_1 \end{pmatrix}$

PART B : Specification for the codes

CODE	VARIANCE	MEAN
1	$\frac{1}{2}D_R + E_1$	μ_m
2	$\frac{1}{2}D_R + E_1$	μ_m
10	$\frac{1}{2}D_R$	-
11	$\frac{1}{2}D_R$	-
Other	-	-

estimate of minus the log likelihood which must be less than the final minimum achieved. Since this was the first run of the program, we had little idea of where the minimum would be. An estimate of -300.0 was given. This turned out to be far less than the actual minimum which was +311.6, corresponding to a log likelihood of -311.6. Convergence takes longer the further the estimate is below the true minimum. However, the program fails if the estimate is greater than the actual minimum. On this first run, a low estimate was used to prevent failure of the program, but on all later runs, more realistic estimates of the minimum were used in order to save computer time.

Trial values of the parameters must also be provided. These were taken from previous analyses of the data and were:

$$\begin{aligned}\mu_m &= 0.005 \\ \mu_f &= -0.002 \\ E_1 &= 0.250 \\ D_R &= 1.000\end{aligned}$$

Since, we expect these trial values to be close to the final parameter estimates, the problem of the search for a minimum entering a region where the expected variance-covariance becomes non-positive definite should be lessened. Therefore, we tried to obtain a solution using the function values only (i.e. the Powell 64 method). The program failed with the expected covariance matrix becoming NPD. In order to overcome this problem, we reran the program, constraining E_1 and D_R to be positive. This time a minimum was quickly reached. The parameter estimates and the corresponding likelihood are given in Part A of Table B38.

TABLE B 38 : COMPARISON OF MODELS FOR RADICALISM OBTAINED BY TWO DIFFERENT METHODS

PART A : THE $E_1 D_R$ MODEL

Estimate	Maximum Likelihood Solution	Weighted least square solution
E_1	0.2536	0.2536
D_R	1.0072	1.0068
μ_m	0.0266	-
μ_f	0.0158	-
L	-315.6243	χ^2 8 14.276

PART B : THE $E_1 B D_R$ MODEL

Estimate	Maximum Likelihood Solution	Weighted least squares solution
E_1	0.2689	0.2687
B	0.2093	0.2091
D_R	0.5753	0.5765
μ_m	0.0265	-
μ_f	0.0160	-
L	-311.6261	χ^2 7 6.198

The $E_1 B D_R$ model, which has been described previously, was similarly specified and a minimum was obtained using the function values only, by constraining E_1 , B and D_R to be positive. The following trial values were used:

$$\begin{aligned} \mu_m &= 0.005 \\ \mu_f &= -0.002 \\ E_1 &= 0.270 \\ B &= 0.210 \\ D_R &= 0.580 \end{aligned}$$

The parameter estimates and the corresponding maximum likelihood are given in Part B of Table B38. This Table also contains the weighted least squares solutions for both models. The estimates obtained by the two methods are closely similar, suggesting that reservations expressed earlier were ill-founded and that the two methods may be regarded as equivalent.

This shows that any problems of accuracy with respect to the maximum likelihood method used are minimal, and indicates its use for analysing the data of the Adoption Study. The comparison between the two methods also serves to provide some evidence concerning several criticisms that have been levelled at the use of weighted least squares for model fitting. One problem is that weighted least squares only provides maximum likelihood solutions when the mean squares are normally distributed. With data such as ours which are approximately normally distributed, no obvious differences are introduced by the use of weighted least squares. Another criticism has been that in using data summaries such as the

analysis of variance, information has been lost. Again, we find no evidence for this from the comparison of the two methods. From a practical point of view, both methods are essentially similar apart from the time taken to reach a solution and it turns out that the maximum likelihood method takes about a hundred times longer than the least squares method to reach convergence for these simple cases, where good trial values are available. With more complex models, or cases where no good trial values are available, time will be an even greater problem.

Model fitting by weighted least squares is clearly the most appropriate method for regular pedigrees where independent summary statistics such as mean squares can be obtained. When we have unbalanced pedigrees such as those of the Adoption study, weighted least squares cannot be used since we cannot easily obtain independent estimates of summary statistics and the equivalent, but more time-consuming method must be used. Before we consider twin and adoption data jointly, it is necessary to introduce another important concept which will be used throughout.

3.4 Hypothesis Testing

Weighted Least Squares has another advantage over the Maximum Likelihood method since it provides a well-defined and explicit test of the model. The residual variation after the model has been fitted follows the chisquare distribution. Since the properties of this distribution are well-known, we can test whether the residual variation differs significantly from that expected by chance. We are unable, at present, to make such a test when the maximum likelihood method is used.

However, it is possible to compare alternative hypotheses about the observed variation, using the likelihood ratio criterion suggested by Elston and Stewart (1971). If H_0 is one hypothesis about the data with a maximum log likelihood of L_0 and H_1 is an alternative, more complex hypothesis with a corresponding likelihood of L_1 , then the statistic, $LR = 2(L_1 - L_0)$, provides a test of the null hypothesis (H_0), since in large samples it follows an approximate chisquare distribution. The number of degrees of freedom is the difference in number of independent parameters between H_0 and H_1 (Rao, 1973; Weiss, 1975). We can illustrate the use of the LR criterion by considering the two models we have already fitted. In Section 6, we saw that the difference between the chisquares for the $E_1 D_R$ and $E_1 BD_R$ models is itself a chisquare for one degree of freedom. This chisquare ($\chi^2_8 - \chi^2_7 - \chi^2_1 = 8.078$) was significant, indicating a significant reduction in the residual variation when the additional parameter is included in the model. The $E_1 BD_R$ model provides a significant improvement in fit over the $E_1 D_R$ model.

Twice the difference between the likelihoods of these two models yields a chisquare for one degree of freedom of 7.9964, which is not substantially different from the chisquare obtained in the weighted least squares analysis, again indicating that the additional parameter is accounting for a significant proportion of the observed variation. The difference between the χ^2_1 's obtained using the two methods is less than 0.1, suggesting that the two methods are equivalent and that no serious loss of information occurs in the conventional weighted least squares analysis.

The likelihood ratio criterion can be used to compare alternative hypotheses about the data. But we would also like a test of the "goodness of fit" of particular models. The value of the log likelihood depends upon a number of factors other than the residual variation and thus cannot be used directly as a criterion for the adequacy of a model (such factors include the number of pedigrees entering into the analysis and the scale of measurement).

A likelihood ratio between a particular model and a model accounting for all the variation, would yield a chisquare, testing the significance of the residual variation after fitting the former model. The latter model might be specified by fitting a separate parameter for each mean, variance, and covariance. This is similar to the approach adopted in weighted least squares analysis. However, in practice, many problems are encountered which have yet to be overcome, and we have been unable to obtain the maximum likelihood solution for all these parameters.

There are two main reasons for this. The first is that the expected covariance matrix easily becomes non-positive definite. Therefore, we have to specify n constraints, where n is the number of unique relationships. Time to convergence is greatly increased using these constraints. Secondly the number of parameters involved is large even when the data structure is simple as in the case of the twin study. As the number of parameters is increased the time taken increases disproportionately. The upper limit on the number of parameters which can reasonably be fitted in this way, using constraints, appears to be about ten.

When we look at the complex structure of the adoption study, the problem is greatly multiplied. However, we made an unsuccessful attempt

to find a solution for the following ten parameter model: μ_m , μ_f one total variance, one correlation for both adopted-adopted and adopted-natural pairs of siblings and one correlation for each other type of relationship. This model would not account for all the variation if there are mean differences other than sex differences or differences in total variance between groups. Its maximum log likelihood might, therefore, be less than that of a model accounting for all the observed variation. Thus, the test of significance, given by $2(L_1 - L_0)$, would in some cases lead us to wrongly accept an inadequate model. However even such an imperfect test would be better than no test, especially since we have no evidence for significant differences means or total variances in our data.

An attempt to find the set of parameter values for this model (maximising the log likelihood summed over pedigrees) was made using all the methods available in EO4HAF. The minimum number of constraints necessary were always used. Estimates of the parameters obtained from previous analyses were used as trial values. Yet despite all this and restarting the program several times with new trial values, we did not manage to achieve convergence.

Two other approaches for testing the model might prove more fruitful. We could attempt to specify our oversimplified model, equivalent to the ' E_1 ' model applied to twin data. For example, we might fit one mean, one total variance and no covariances. This would give some idea of the likely minimum value that the likelihood can take. Then we could at least say which of our models are significantly better than this.

The raw observations to which the model were fitted cannot be predicted from the parameter estimates (as we do in weighted least squares

in order to obtain a chisquare test). Spence, Westlake and Lange (1976) are trying to devise a method similar to the test used in weighted least squares. They take large pedigrees, and use the score of one individual in the pedigree as a baseline, in order to predict the scores of the remaining individuals and obtain a series of observed and expected scores for comparison. Even if a satisfactory test could be made in this way, it would not be very useful for our study, since we have very few pedigrees large enough.

There is an alternative to predicting the observations. We can calculate the covariances between the individuals in our study. We should also be able to predict these covariances from the parameters of our model. Thus it should be possible to devise a suitable test of significance.

However, in the following analyses, we have no test of "goodness of fit". Although in this thesis we are unable to test the adequacy of the models fitted by pedigree analysis, this problem will be returned to at a later date, since the method cannot be regarded as satisfactory until such a test has been found.

Another inadequacy of the pedigree analyses to be described in the following pages is the lack of standard errors for the estimates. This is not a theoretical problem, such as the specification of a test of "goodness of fit" which was described above. In order to obtain standard errors, we need to determine the values of the parameters which will produce a change of 0.5 in the likelihood. We could do this by numerical differentiation and obtain second derivatives. This assumes that the shape of the likelihood surface around the minimum is quadratic. Alternatively, we could plot the likelihood surface around the minimum.

In either case, the minimisation would have to be repeated, which would be expensive in time and money. The standard errors have not been found for the estimates of the parameters obtained in the analyses to be reported here. Standard errors for the parameters of a few of the more important models will be calculated at a later date.

Having shown that the method is satisfactory, we now wish to fit models to the adoption data and all the data jointly and compare these cases with the results from the twin study.

Expectations for all possible code values of the expected variance-covariance matrix are given in Table B39 for the simple $E_1 D_R$ model. Solutions for the parameters of the mean vector and covariance matrix were found for the adoption study (311 families) and then for all the data jointly (898 families), using function values only. The covariance matrix was constrained to be positive definite. The trial values used for the twins were again given. The results of fitting the model to these two data sets are given in Table B40, where the results from the twin study are also tabulated for comparison.

Firstly, we can make some qualitative comparisons of the parameter estimates. These are fairly similar in twin and adoption studies, but E_1 and D_R are both larger in the adoption study, reflecting the greater variance of these data (see Section 5). However, when we look at the genetical variation as a proportion of the total, we see that the additive genetical variation is very similar in the two data sets.

Parameter estimates for all the data jointly lie between those of the two studies, as expected, but are closer to those of the twin study, since there are more twin families (587, compared with 311). Of the 311 families of the adoption study, a large proportion are single individuals who contribute information only about the means and total variances, but not about the covariances.

TABLE B 39 : EXPECTATIONS FOR ALL CODES ON THE $E_1 D_R$ MODEL

CODE	E_1	D_R
1,2,3,4	1	$\frac{1}{2}$
10	-	$\frac{1}{2}$
11,21,22,23	-	$\frac{1}{4}$
20,80,81,82,83	-	-

TABLE B 40 : MODEL FITTING IN ALL DATA JOINTLY, TWIN STUDY AND ADOPTIONSTUDY

	ALL DATA JOINTLY	ADOPTION STUDY	TWIN STUDY
μ_m	-0.02287	-0.12906	0.02656
μ_f	-0.00485	-0.03778	0.01570
E_1	0.25741	0.32999	0.25361
D_R	1.09520	1.14270	1.00720
$\frac{1}{2}D_R$	0.54760	0.57135	0.50360
h_N^2	0.68024	0.63389	0.66507
L	-517.9692	-198.4279	-315.6243

Now we will quantify our comparison of the two data sets by asking whether there is significant heterogeneity between them in respect to the parameters estimated. We cannot compare their log likelihoods directly since these are influenced by such factors as the number of pedigrees involved. We follow Lange, Westlake and Spence (1976) and let the parameter vector of the adoption study be γ_1 and of the twin study be γ_2 . The null hypothesis, H_0 , is that $\gamma_1 = \gamma_2$ and may be tested against the alternative hypothesis, $H_1: \gamma_1 \neq \gamma_2$, using the likelihood ratio statistic: $LR = 2(L_1 - L_0)$, which is approximately distributed as a chisquare with 4 degrees of freedom. L_1 is the sum of the likelihoods for the two studies considered separately and L_0 is the likelihood for the two studies combined. It turns out that $LR = \chi^2_4 = 7.834$ ($5\% < p < 10\%$). Thus, there is little evidence for significant heterogeneity between twin and adoption studies, with respect to the four parameters estimated. If this model adequately explains the observed variation, then we have no evidence to suggest that the two data sets are not drawn from the same population, with common genetical and environmental causes of variation. The best estimates of the parameters are, therefore, those from the analysis of the combined data. However, although formally the $E_1 D_R$ model is adequate to explain the observations in the twins, the fit is poor. The addition of a between families component of variation produces a significant reduction in residual chisquare and the $E_1^{BD} R$ model fits the observations closely. Since \hat{B} is significant in the twins, and the adoption data are more variable than the twin data, in order to be confident that the data are homogeneous, we need to compare the two studies with respect to the parameters of the $E_1^{BD} R$ model.

BETWEEN FAMILIES VARIATION IN THE TWO STUDIES

Adoption data provide a unique opportunity to study components of between families variation. Ultimately, we wish to consider the roles of assortative mating and cultural differences in producing this variation. But in the first instance we will fit a model analogous to the $E_1 D_R B$ model in the twins, in order to determine whether the between families component is homogeneous over twin and adoption data.

Specification of the between families component presents problems because we now have intergenerational as well as collateral relationships. In order to formulate a model, we assume no assortative mating and set the expectation for the covariance between spouses to zero. We are thus assuming that variation estimated as \hat{B} in the twin data is produced only by environmental differences between families (E_2). This assumption will be tested later, when we compare the maximum log likelihoods of models with no assortative mating or E_2 , with either assortative mating or E_2 only and with both effects.

A number of models for the environmental covariance between individuals living together are possible, but we will first consider the model most similar to that fitted to the twins (i.e. $E_1 D_R B$). This model assumes that the environmental factors producing variation in the children are independent of parental phenotype, that the environmental covariance arises anew in each generation and that the environment acts to produce variation in the children. Thus, there is an environmental covariance between collaterals raised in the same home, E_2 , which is added to the expectations for the total variance and all collateral covariances to produce the $E_1 D_R B$ model given in Table B41. This model for the

TABLE B 41 : EXPECTATIONS FOR A MODEL WITH A COMMON ENVIRONMENT FOR
COLLATERALS

CODE	E_1	D_R	E_2
1,2,3,4	1	$\frac{1}{2}$	1
10	-	$\frac{1}{2}$	1
11,23	-	$\frac{1}{4}$	1
20,80,81	-	-	-
21,22	-	$\frac{1}{4}$	-
82,83	-	-	1

environmental variation between families, which is similar to that used in the twins, makes no additional assumptions about the structure of the environment. Therefore, it can be used to determine whether differences between additive genetical or environmental components in the twin and adoption data are significant.

Estimates of \hat{E}_1 , \hat{D}_R and \hat{B} from the twins were used as trial values. The program was run using the function and constraining the covariance matrix to be positive definite. The solution improved very slowly for both the adoption data alone and the combined data. When the time limit was reached the program was rerun with the current solutions as trial values, using the method based on first derivatives. Convergence was quickly reached with the new method. The constraints were removed and the program was rerun using the final solutions as trial values, so that we could compare constrained and unconstrained solutions. The $E_1 D_R B$ model was also rerun in the twins without constraints. Convergence was quickly reached for the combined data and the twin data, but the covariance matrix quickly became non-positive definite for the adoption data. Results for constrained and unconstrained solutions are given, where possible, in Table B42. These are identical to the first six significant figures for the twin study. There is no unconstrained solution for the adoption study. Constrained and unconstrained solutions are somewhat different for the combined data. Unconstrained values of \hat{E}_1 and \hat{E}_2 are somewhat smaller and \hat{D}_R is correspondingly larger. Since the total variance is the same for both solutions, the narrow heritability is larger for the unconstrained case. Its maximum log likelihood is also larger.

TABLE B 42 : COMPARISON OF CONSTRAINED AND UNCONSTRAINED SOLUTIONS OF THE $E_1 D_R E_2$ (or $E_1 D_R B$) MODEL IN THREE DATA SETS

ESTIMATE	ALL DATA JOINTLY		ADOPTION DATA		TWIN DATA	
	CONSTRAINED	UNCONSTRAINED	CONSTRAINED	UNCONSTRAINED	CONSTRAINED	UNCONSTRAINED
μ_m	-0.0203	-0.0214	-0.1301	-	0.0265	0.0265
μ_f	-0.0060	-0.0060	-0.0395	-	0.0160	0.0160
E_1	0.2931	0.2681	0.2288	-	0.2689	0.2689
D_R	0.5967	0.6779	1.2422	-	0.5753	0.5753
E_2 (or B)	0.2225	0.2061	0.0526	-	0.2093	0.2093
L	-514.2221	-513.6002	-197.9073	-	-311.6261	-311.6261
V_T	0.8140	0.8132	0.9025	-	0.7659	0.7659
$\frac{1}{2} D_R / V_T$	0.3665	0.3669	0.6882	-	0.3756	0.3756
E_2 / V_T	0.2733	0.2532	0.0583	-	0.2733	0.2733
E_1 / V_T	0.3601	0.3297	0.2535	-	0.3511	0.3511

Constrained and unconstrained solutions in the twins were closely similar and we know from the weighted least squares analysis that the $E_1 D_R B$ model is adequate to explain variation in the twins. We have no test of the adequacy of the $E_1 E_2 D_R$ model in the adoption data and combined data. Problems such as slow convergence, differences between constrained and unconstrained solutions or failure to obtain an unconstrained solution might be warning us that the model is inappropriate and maximum likelihood solutions of its parameters are difficult to find. They might equally indicate that we have not chosen the most appropriate method for the particular problem. In either case, caution must be exercised when interpreting the results. In particular, unconstrained solutions will be sought whenever possible since the constrained solution may be less likely and give different parameter estimates.

Comparison of the solutions for the three data sets shows that the total variances of the adoption data, twin data and combined data differ but are similar to those estimated from the data in Section 5 (i.e. $\gamma = 0.911, 0.761$ and 0.803 respectively). Thus, the model cannot be completely inappropriate. A brief look at the estimates from the twin and adoption studies reveals quite substantial differences. Before considering these in detail, we may ask whether there is significant heterogeneity between the two studies with respect to the parameter set as a whole. Using the likelihood ratio criterion described earlier, we find that $LR = \chi^2_5 = 9.3774$ ($5\% < p < 10\%$), based on the likelihoods from the constrained solutions. If we base the likelihood ratio on unconstrained solutions for twin data and combined data and the constrained solution for the adoption data, $\chi^2_5 = 8.1336$ ($10\% < p < 20\%$).

Neither chisquare provides evidence for significant heterogeneity between twin and adoption data. This is interesting in the light of criticism of the twin method which suggests that twins are special and may be subject to different environmental influences than single born children. There is no evidence for such differences between twins and other individuals in this study.

We may now ask what are the likely causes of differences in parameter estimates between twin adoption studies, bearing in mind that we only have the constrained solution for the adoption data, which might indicate that the model is inappropriate. Estimates of \hat{E}_1 are similar, although slightly larger in the twins. However, both \hat{D}_R and $\hat{E}_2(B)$ differ markedly. \hat{D}_R is much greater in the adoption study, accounting for 69% of the total variation, whereas \hat{E}_2 accounts for only 6%. In the twin data, \hat{B} , which provides a biased estimate of E_2 , accounts for 27% of the variation, the contribution of \hat{D}_R being reduced to 38% of the total variation.

Comparing estimates from twin and adoption data with those for the combined data, we see that estimates for the combined data closely resemble those of the twin study, suggesting that the twin study is providing most of the information about these parameters. Using the present model, information about environmental covariance comes only from pairs of collaterals in the adoption study, and there are relatively few of these, whereas parent-offspring and sibling pairs, of which there are many more, provide information about D_R . Thus, we may have a more powerful test for D_R than E_2 in the adoption study. This would be discouraging since we hope to partition the between families component using the adoption data. However, the present model is unrealistic

because we have specified no covariance between spouses (either genetical or environmental) and no environmental covariance between parents and the children they rear. Since we have data on a substantial number of spouses, natural parent-offspring and adopting-parent offspring pairs who would provide information about the family environment on a more realistic model, a detailed study of the between families component of variation may not be precluded.

The discrepancy between the two data sets is most marked when we consider the between families component. In the twin data, we were estimating \hat{B} , which includes both common environmental effects and additive genetical variation produced by assortative mating. In the adoption data, we estimated only \hat{E}_2 . Therefore, the difference between the two estimates, one of \hat{B} and one of \hat{E}_2 , may be due to assortative mating. This seems likely because we know there is a marital correlation, which we have disregarded in performing this analysis.

Another possible reason for differences between the two data sets is that we have used the wrong model for the environmental variation. This model may be adequate to explain the twin data, but not the adoption data where we have intergenerational relationships. We have allowed no environment covariance between parents and children reared by them.

Another model of the environment will now be considered which may be more realistic in light of the known correlations between individuals (see Section 5.3). We assume that environmental covariance arises between individuals, just because they are living together in the same household. Thus we add an E_2' term to the covariance of all individuals of one family. This model is shown in part A of Table B43. There is

TABLE B 43 : EXPECTATIONS AND SOLUTIONS FOR A MODEL WHERE WHOLE FAMILIES
SHARE A COMMON ENVIRONMENT

PART A EXPECTATIONS

CODE	E_1	D_R	E_2^1
1,2,3,4	1	$\frac{1}{2}$	1
10	-	$\frac{1}{2}$	1
11,23	-	$\frac{1}{4}$	1
20,80,81	-	-	1
21,22	-	$\frac{1}{4}$	1
82,83	-	-	1

PART B SOLUTIONS

	ALL DATA JOINTLY	ADOPTION DATA	TWIN DATA
μ_m	-0.0312	-0.1592	0.0265
μ_f	-0.0042	-0.0436	0.0160
E_1	0.2679	0.3668	0.2689
D_R	0.7267	0.6831	0.5753
E_2^1 (or B)	0.1794	0.1911	0.2093 (B)
L	-509.8290	-193.8480	-311.6261
v_T	0.8107	0.8995	0.7659
$\frac{1}{2}D_R/v_T$	0.4482	0.3797	0.3756
E_2^1/v_T	0.2213	0.2125	0.2733
E_1/v_T	0.3305	0.4078	0.3511

now environmental similarity between spouses, parents and children in one family and collaterals living together.

This model was fitted using the method based on first derivatives, with solutions from the previous model as trial values. Convergence was quickly achieved for the combined data and the adoption data, without the necessity to supply constraints. Estimates of the parameters and the maximum log likelihoods are given in part B of Table B43. The solutions for the $E_1 D_R E_2$ model in the twins are again given for comparison.

This model provides a substantially more likely solution than previous models, whether we consider the combined data or only the adoption data. However, we have no degrees of freedom for testing the significance of this improvement. In order to determine the source of the improvement, a similar model was fitted in which we specified environmental covariances between collaterals and between parents and children, but none between spouses (E_2''). A solution was quickly reached for this model, using first derivatives with no constraints and the same trial values as before. The solutions for the combined data and for the adoption data are given in Table B44. The estimates are fairly similar to those for the previous model given in Table B43. However, the likelihoods are substantially lower and are about the same as those based on the model with a single E_2 for collaterals only. Thus, the improvement of the $E_1 D_R E_2'$ model over the $E_1 D_R E_2$ model is undoubtedly due to the addition of a covariance between spouses.

Using the likelihood ratio criterion to provide a measure of the heterogeneity of twin and adoption data with respect to the parameters of the $E_1 D_R E_2'$ model, we find that $\chi^2_5 = 8.7098$ ($10\% < p < 20\%$).

TABLE B 44 : SOLUTIONS FOR A MODEL WITH ENVIRONMENTAL COVARIANCE
BETWEEN COLLATERALS AND PARENT-OFFSPRING PAIRS

	ALL DATA JOINTLY	ADOPTION DATA
μ_m	-0.0291	-0.1458
μ_f	-0.0052	-0.0401
E_1	0.2664	0.4674
D_R	0.8327	0.6285
E_2^{11}	0.1255	0.1185
L	-514.3745	-197.1571
v_T	0.8083	0.9002
$\frac{1}{2}D_R/v_T$	0.5151	0.3492
E_2/v_T	0.1553	0.1316
E_1/v_T	0.3296	0.5192

Again the data are homogeneous with respect to this parameter set. However, the magnitude of the parameters has altered somewhat and the values for the adoption study are much closer to those of the twin study. \hat{D}_R now accounts for only 38% of the variation in the adoption data, rather than 69%. This is very similar to the narrow heritability in the twins. E_1 accounts for a similar proportion of the total variation in the two groups but the percentage is somewhat greater in the adoption data (41%) than the twin data (35%). This is because \hat{E}_2' is still slightly smaller than \hat{B} in absolute size and accounts for only 22% of the variation whereas \hat{B} accounts for 27%. However, the differences between the parameters are now small compared with the previous $E_1 D_R E_2$ model, suggesting we now have a more appropriate model for the environment. However, it is also possible that this model is the most likely so far, simply because we have allowed a covariance between spouses. Thus, the problem of discrimination between cultural or other environmental differences between families and assortative mating has still not been resolved. In order to make this resolution and to test for cultural transmission, we must consider another method of specifying models. Eaves (1976b) model of cultural transmission lets parental phenotype contribute to offspring's environment, leading to cultural differences between families. His paper gives all the expectations we need for our covariance matrix in conventional biometrical-genetical terms. However, his model does not specify the contribution of assortative mating. The extension of Eaves model to include assortative mating is likely to prove a long and difficult task and this has led us to explore another way of specifying the effects of cultural transmission and assortative mating.

simultaneously, which may prove less algebraically demanding than the approach of Eaves and yield simpler expectations. The methods of path analysis which provide a visual representation of the relationships between the genotypes and environments of different individuals, are discussed in the next section.

SECTION 8: AN ALTERNATIVE APPROACH THROUGH THE USE OF PATH MODELS

1

INTRODUCTION

In previous sections, we have used the analysis of variance approach in order to determine the sources of individual differences in several traits, by fitting models to variance components. This methodology was initiated by Fisher (1918) and its use for solving problems in biometrical genetics extended by Mather and Jinks (see Mather and Jinks, 1971). An alternative approach to the problem was taken by Sewall Wright, who treated genetical problems purely as regression problems. The details of his approach are expounded in Wright's books, "The Method of Path Coefficients" and "Systems of Mating" and also in Li's "Population Genetics". Rao, Morton and Yee (1974, 1976) use path models for the analysis of family resemblance and their methods are appropriate for human data. Details of the methods can be found from any of these sources and only the aspects of path analysis necessary for the present study will be discussed as the need arises.

The path model approach suffers from a number of limitations which restrict its use especially in experimental organisms. When we are dealing with man, path models may be useful and the features of the approach which are usually found to be limiting may be put to good use.

The method normally requires two assumptions which we are not willing to accept without some test. Most workers use standardised paths for their models. This introduces all the problems associated with analysing correlation coefficients, which were discussed in Part A.

Use of standardised paths assumes that the total variances of the groups being studied are homogeneous. If this assumption is not justified, biased and misleading estimates of the paths may be obtained. However, the bias can often be found, providing some information from another source is available (e.g. the correlation of parents and natural children not reared by them in the case of genotype-environmental covariance). Since we are interested in cultural differences and cultural transmission, which may lead to genotype-environment covariance, the use of standardised paths is clearly inappropriate, since we do not have such additional information. Eaves (1967a, b) has shown that two mechanisms producing genotype-environment covariance i.e. cultural transmission and sibling effects, both lead to expectations for the total variances which are not the same in all groups. We will derive expectations for the expected covariance matrix using a path model, and, therefore, we will not be using standardised paths.

Another problem of path analysis is that it is essentially a regression method and, therefore, we are unable to say much about the nature of the genes operating. Path models normally assume that all genetical variation is additive, since non-additive effects cannot be specified using path analysis. In contrast, the biometrical-genetical approach provides explicit tests for non-additive effects. Specification of such effects as dominance, epistasis and genotype-environment interaction is possible, and their effects can, therefore, be estimated, given an adequate experimental design.

The chief advantage of path analysis is that, since it is a regression technique, specification of effects at a phenotypic level

is easy. Thus biometrical-genetics is generally superior for analysing genetical variation, whereas the use of path models for analysing environmental variation may be advantageous. This is why we intend to use path models for analysing the between families component of variation in these data. The $E_1 E_R$ model adequately explained variation in the twin data, and there was no evidence to suggest genetical non-additivity. Failure to detect non-additivity in the twin data is not surprising. Eaves (1972) showed that the power of the test for detecting dominance with twin data is very low with the sort of numbers used in this study and also that dominance tends to be counter balanced by E_2 . However, it is possible for dominance to be non-significant in the twins but highly significant in family data where the test is more powerful, leading us to different conclusions in the two sorts of data. Eaves (personal communication) has shown in several instances that inconsistencies between twin and family data may be resolved by introduction of a non-additive component into the model even when there was no evidence for significant non-additivity in the twins alone. He found that estimates of dominance in twin and family data were similar in magnitude, but only significant in family data. However, in the present study no evidence was found for significant heterogeneity between twin and adoption studies and we have no reason to suspect that the genetical system is other than simple and additive. Even if there were some non-additive variation for social attitudes, we have no reason to suppose that we will be able to detect it in these data.

However, we do know that there is significant between families variation due to common environmental effects and/or assortative mating. We shall thus use path analysis to detect and estimate the principal

additive components of the system empirically. We found no evidence for genotype-environment interaction in the twin data. Therefore, the environment seems to be acting additively at the phenotypic level. Assortative mating is assumed to act through the phenotype. The association of like phenotypes leads to a covariance between the genetical similarity of spouses. Since this produces only additive genetical variation, we may specify the effects of assortative mating using path models.

We have some evidence for cultural differences between families and wish to explore the possible role of cultural transmission for social attitudes. Eaves' (1976b) model of cultural transmission gives expectations for variances and covariances expressed in biometrical-genetical terms. However, his model does not include the effects of assortative mating. We have evidence for assortative mating, since we know there are significant marital correlations for both Radicalism and Toughmindedness. Therefore, we wish to fit a model including cultural transmission and assortative mating simultaneously. The extension of Eaves' model to include assortative mating is likely to be a long and difficult task, since the formulation of the basic cultural transmission model was numerically and algebraically complex. In Eaves (1976b) model, the phenotype of the parent contributes to the environment of his offspring, producing variation between families. Since this model is based on phenotypes, the path approach may prove rewarding and allow the formulation of a model for cultural transmission and assortative mating simultaneously. Such a model is likely to prove simpler and algebraically less demanding than attempts reformulate Eaves' model of cultural transmission to include assortative mating.

TWO SIMPLE MODELS

Since the concepts and methods of path analysis have not been discussed before, there are many new ideas to be introduced. We shall, therefore, consider a series of simple and instructive examples, in order to describe the methods to be used in later Sections, when we will fit a full model including cultural transmission and assortative mating. These examples will also be useful in understanding the between families variation.

We shall first consider two extremely simple models to show the use of variances and correlations to specify models for all the elements of the variance-covariance matrices and how we use the maximum likelihood method to obtain solutions for the parameters. We do not need to introduce the concept of path models at this stage. These first two models are unrealistically simple and will, therefore, give some idea of the lowest values the maximum log likelihood can take.

In the first model, we assume the absence of genetical variation, but introduce an environmental covariance between individuals living in the same family. The population variance will be called "V" in this and all subsequent models. The degree of resemblance between individuals produced by the environmental covariance is given by a correlation, r , which is the same for all possible relationships in a family. The diagonal terms of the expected covariance matrix are all V , since the total variances for all individual types are expected to be the same. The covariances may be specified as a product of the variances and the correlation since

$$r = \frac{\text{Cov } x_1 x_2}{\sqrt{Vx_1 Vx_2}}$$

which gives the covariances as rV for all the off-diagonal terms.

Solutions for the four parameters of this basic model were found using the maximum likelihood approach described earlier. Convergence was quickly reached for both Radicalism and Toughmindedness, using the method based on first derivatives, without the necessity to use any constraints. Estimates of the parameters and the maximum log likelihoods are given in Table B45 for both traits. Estimates of V are the same as the total variances for the combined data, calculated in Section 5 (i.e. $V = 0.803$ for Radicalism and $V = 0.082$ for Toughmindedness in Section 5). For both traits the overall correlation between relatives lies between 0.4 and 0.5. We know this model is unrealistic because we saw in Section 5 that the monozygotic twin correlations ($r_{MZ} = 0.62$ for Radicalism and $r_{MZ} = 0.60$ for Toughmindedness) are higher than the DZ correlations ($r_{DZ} = 0.49$ for R and $r_{DZ} = 0.46$ for T), suggesting either greater genetical similarity between MZ twins or else that they are treated more alike. This model is far less likely ($L = -533.7704$) than the $E_1 D_R$ model ($L = -517.9692$), fitted to the data earlier, and we know that the $E_1 D_R$ model is barely adequate to explain the observed variation. This model must be approaching the worst model possible to explain the observations.

A simple extension to the model allows for the observation that MZ twins are more alike than DZ twins. A new parameter, t , is introduced which is the correlation between MZ twins introduced if MZ twins are treated more alike than other siblings. The only expectation which is affected is the covariance for monozygotic twins which is now given by:

$$\text{Covariance}_{MZ} = V(r + t)$$

TABLE B 45 : SIMPLE ENVIRONMENTAL MODEL FOR RADICALISM AND TOUGHMINDEDNESS
FITTED TO ALL DATA JOINTLY

PARAMETER	RADICALISM	TOUGHMINDEDNESS
μ_m	-0.0359	0.0077
μ_f	-0.0012	0.0054
v	0.8038	0.0822
r	0.4837	0.4375
L	-533.7704	1292.5851

We will call "t" the treatment effect, since it affects only the MZ twin correlation. However, since twins provide most of the information, t could also be expressing the greater genetical similarity between MZ twins compared with DZ twins, although we have not given sensible expectations based on genetical theory for the other relationships.

This model was fitted to the Radicalism and Toughmindedness data using the method based on first derivatives. Convergence was quickly reached without the use of constraints. The parameter estimates and maximum log likelihoods for the two traits are given in Table B46. The correlation for individuals reared in the same family is now reduced to 0.3711 for R and 0.3075 for T. The MZ correlations are boosted by the treatment effect to 0.6653 and 0.6162 respectively (i.e. $r + t$). The likelihoods for this model are significantly greater for both traits than those obtained when we estimated a single correlation between relatives.

The two parameter sets just estimated, are purely empirical data summaries, since they do not attempt to explain the variation using a theoretical framework. The second "model", however, which includes an additional correlation between MZ twins which might be predicted as a treatment difference, provides a more adequate summary of the data than the first model, indicating that the resemblance between individuals cannot be adequately represented by a single correlation. It is also somewhat more likely than the E_D model, indicating the inadequacy of the latter, theoretical model to explain the observed variation.

The results found for Radicalism so far will now be summarised since this is likely to be the most interesting trait, when we fit

TABLE B 46 : ENVIRONMENTAL MODEL WITH TREATMENT EFFECTS

PARAMETERS	RADICALISM	TOUGHMINDEDNESS
μ_m	-0.0341	0.0081
μ_t	-0.0019	0.0063
v	0.8112	0.0823
r	0.3711	0.3075
E	0.2942	0.3087
L	-515.8289	1309.0122
r + t	0.6653	0.6162

models specifying genotype-environment covariance. The models, their parameters and corresponding maximum log likelihoods are given in Table B47.

The first model is clearly not an adequate representation of the data, since it is far less likely than any of the other models. If we wanted a four parameter summary of the data, the E_{1R}^D model provides a more likely explanation, suggesting that the degree of similarity between individuals depends on the closeness of their relationship i.e. there is a genetical component of variation. However, the E_{1R}^D model does not account for all the variation since the three 5 parameter models are all significant improvements over the 4 parameter models. The third model is significantly more likely than either of the first two models ($\chi^2_1 = 35.3950$ and $\chi^2_1 = 4.9308$, respectively). This suggests that we need a model including both common environmental effects and a greater similarity in MZ than DZ twins. Both model 4 and model 5 are of this type and are more likely than any other model considered so far, but we cannot test these models against the third model or one another since they all have the same number of parameters, although we see by inspection that Model 5 is the most likely. However, as predicted from the twin study, there is additive genetical and probably common environmental variation.

A comparison of models 5 and 6 suggests that covariance between spouses is also an important factor, and may well account for a substantial proportion of the between families variation.

We wish to investigate the nature of the common environmental variation further, in conjunction with assortative mating, and hopefully

TABLE B 47 : SUMMARY OF MODELS FITTED TO RADICALISM USING PEDIGREE ANALYSIS (BUT NOT PATH MODELS)

<u>DESCRIPTION OF MODEL</u>	<u>NUMBER OF PARAMETERS</u>	<u>PARAMETERS</u>	<u>L</u>
Simple model with one covariance between individuals living together.	4	$\mu_m \mu_f v r$	-533.7704
Simple additive genetical model.	4	$\mu_m \mu_f E_1 D_R$	-517.9692
Simple model with treatment effect.	5	$\mu_m \mu_f v r t$	-515.8289
Simple additive genetical model with environmental covariance between collaterals.	5	$\mu_m \mu_f E_1 D_R E_2$	-513.3635
Simple additive genetical model with environmental covariance between individuals living together.	5	$\mu_m \mu_f E_1 D_R E_2^1$	-509.8290
Simple additive genetical model with environmental covariance between collaterals and parent-child pairs only.	5	$\mu_m \mu_f E_1 D_R E_2^{11}$	-514.3745

b
c
d

find a model which is significantly more likely than any of those in Table B47. Models may be more likely which allow for environmental covariance between spouses and/or covariance between their genetical deviations. We shall attempt to specify such models using the approach of path analysis.

SIMPLE ENVIRONMENTAL PATH MODELS

We introduced, in the last section, the idea of specifying a model for an expected covariance matrix in terms of correlations and a variance, so that an off-diagonal covariance term is simply the product of the total variance and the correlation between the pair of individuals concerned. Such methods were fitted by maximising the log likelihoods, summed over pedigrees. We now want to use the path approach to specify models for the expected covariance matrix in a similar manner and fit these models by maximum likelihood. Thus, we shall not encounter the problems associated with standardised paths, and we will be able to allow the total variances of different groups of individuals to differ.

We shall first look at path models based purely on environmental effects, to determine whether any of these is more likely than the models already considered. This may tell us more about the structure of the environmental covariance and will give us a baseline against which to compare the likelihood of the genetical path models to be introduced later. We wish to consider environmental covariance between relatives and assortative mating simultaneously. We can do this, assuming no genetical variation, if the assortative mating is based on the phenotype. We know that there is a marital correlation. However, we will take this opportunity to determine whether inclusion of a marital correlation provides a significant improvement over simple environmental models, with no marital correlation.

In order to formulate the models, we will make the following assumptions:

1. The total variances of all groups are equal
2. There is no genetical similarity between relatives
3. All children are treated similarly by the parents who rear them regardless of whether they are natural or adopted, twins or single births.

Two basic models, with and without assortative mating, based on the assumptions stated above are given in Figure B5. The first model implies that similarity between parents and children reared by them is produced by the equal environmental impact of the phenotypes of both parents, by the path "p". This model is extremely simple and might be interpreted in other ways.

The second model includes the direct environmental influence of parental phenotype on the offspring through the path "p", but we now specify an environment, E, which is common to all collaterals, but independent of the parents. The path from E to offspring phenotype is called "e".

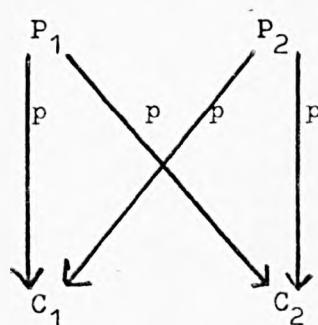
Expectations for parent-offspring, sibling and marital correlations can now be determined using the conventional rules governing paths (Li, 1955). For example, in order to determine the correlation between the two children in model 2B, we can trace back from C_1 to E along path e and then forward along path e from E to C_2 to give us a correlation of e^2 . Tracing paths from C_1 to C_2 via P_1 gives a correlation of ρ^2 . Similarly another term in ρ^2 is obtained from the paths from C_1 to C_2 via P_2 . Correlations of $\rho^2 \mu$ are produced by tracing paths: 1. From C_1 to P_1 to P_2 to C_2 . 2. From C_1 to P_2 to P_1 to C_2 . Adding all the terms, the total correlation becomes:

$$\begin{aligned} r_{\text{siblings}} &= 2\rho^2 + 2\rho^2 \mu + e^2 \\ &= 2\rho^2(1 + \mu) + e^2 \end{aligned}$$

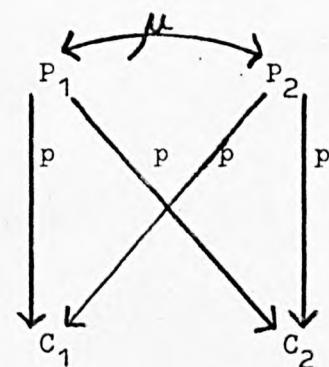
The total variance, as used earlier, is V. Therefore, the covariance

FIGURE B5: ENVIRONMENTAL PATH MODELS

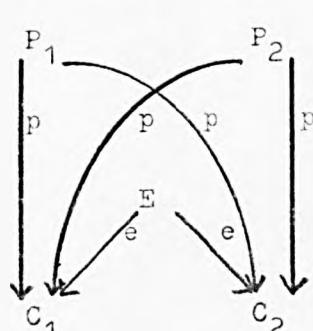
1A.



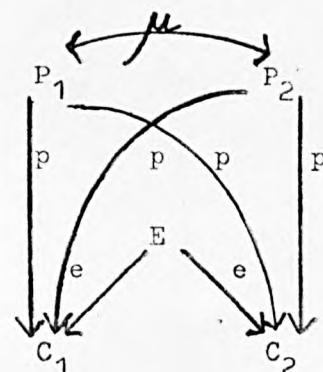
1B.



2A.



2B.

KEY: P_1 First parent P_2 Second parent

C Child

E Environment (see text)

{ }
Paths (see text)

μ Heritability correlation

between siblings is:

$$\text{Cov}_{\text{siblings}} = v(2^2 (1 + \mu) + e^2)$$

The covariances for all four models were calculated and these expectations are given in Table B48. Solutions for the parameters of the four models, which maximised the log likelihood summed over pedigrees were found using the methods described earlier. Estimates of 500.0 and -1500.0, for Radicalism and Toughmindedness respectively, were given for minus the log likelihood. Earlier analyses led us to believe that the final minimum minus the log likelihood would not be below these values and produce failure of the program. The actual values of male and female means, total variances and marital correlations calculated in Section 5 were given as the trial values. Values of 0.5 were used as trial values for the paths, p and e, since we had no idea about their likely magnitude. The covariance matrix was constrained to be positive definite because the trial values for the paths were unlikely to be very realistic. Solutions for models 1A and 1B were obtained using the function values only. The method based on the first derivatives was used to obtain the maximum likelihood solution for models 2A and 2B. Estimates of the parameters and their corresponding maximum log likelihoods are given in Table B49 for Radicalism and Toughmindedness.

Model 1 is clearly inappropriate for these data for both Radicalism and Toughmindedness, whether the marital correlation is included or not, since the likelihoods are substantially lower than those of any of the other models we have considered so far, even the model where only one correlation is specified to account for resemblance between individuals living together in the same family. It is, therefore, not even a useful summary of the data.

TABLE B 48 : EXPECTATIONS FOR SIMPLE ENVIRONMENTAL PATH MODELS

<u>STATISTIC</u>	<u>CODES</u>	
Total variance	1,2,3,4	V
Parent-offspring covariance	21,22,80,81	pV
Sibling covariance	10,11,23,82,83	$2p^2V$
Covariance of spouses	20	0

EXPECTATIONS

MODEL 1B

MODEL 2A

MODEL 2B

v

v

v

$$pV(1+\mu)$$

$$pV$$

$$pV(1+\mu)$$

$$2p^2V(1+\mu)$$

$$V(2p^2+e^2)$$

$$V(2p^2(1+\mu)+e^2)$$

$\bar{v}\mu$

0

$\bar{v}\mu$

463

TABLE B 49 : PARAMETER ESTIMATES FOR SIMPLE ENVIRONMENTAL PATH MODELS

<u>PARAMETER</u>	<u>ESTIMATES</u>							
	RADICALISM				TOUGHMINDEDNESS			
	1A	1B	2A	2B	1A	1B	2A	2B
μ_m	-0.0409	-0.0436	-0.0218	-0.0224	0.0047	0.0073	0.0090	0.0108
μ_f	-0.0048	-0.0002	-0.0066	-0.0056	0.0027	0.0047	0.0056	0.0067
v	0.8100	0.8126	0.8100	0.8167	0.0824	0.0829	0.0827	0.0828
p	0.4752	0.4175	0.1417	0.1335	0.4202	0.3564	0.0052	0.0155
e			0.7200	0.7132			0.7302	0.7299
μ		0.3278		0.3158		0.4662		0.4224
L	-553.7629	-547.4797	-523.4731	-519.4698	1263.5794	1271.9892	1310.6675	1314.7409

V
C
A

Model 2 is more likely than model 1 for Radicalism, but still provides a worse explanation of the data than either the simple environmental model with treatment effects or either of the simple genetical models with common environmental variance. Even Model 2B which includes a marital correlation and is, therefore, a six parameter model, is less likely than any of the five parameter models. This shows that our model is totally inadequate. The problem obviously arises because we have not allowed for closer relatives to be more alike, which we do in all the five parameter models. This reinforces the findings from previous analyses that a genetical component is needed to explain variation in Radicalism.

In the case of Toughmindedness, Model 2A gives a maximum log likelihood of 1310.6675, which is slightly larger than that for the environmental model with treatment effects (ML = 1309.0122, see Table B46). This model is unrealistic because we know there is a correlation between spouses. Model 2B, which includes a marital correlation provides a significant improvement over the environmental model with treatment effects ($\chi^2_1 = 11.4574$, $p < 0.001$). Therefore, for Toughmindedness, it seems that we may not need to allow closer relatives to resemble one another more closely, which agrees with our finding from the twin study that there is little evidence for a genetical component. Model 2B is a significant improvement over model 2A. Therefore, the most likely model from the evidence we have so far is that resemblance between the individuals in our study can be explained in terms of assortative mating between spouses, based on their phenotypes, an environment which is mediated through the phenotype of the parents and also a common environmental component independent of parental phenotype.

We may now ask what the actual values of the parameters tell us. We will consider only the parameters of model 2B, since this is the most likely model for both traits. The values of the total variances are close to those calculated from the data in Section 5, as we expect. However, the marital correlations, $\mu = 0.3148$ and $\mu = 0.4224$ for Radicalism and Toughmindedness respectively are not quite what we expect since we found $\mu = 0.4045$ and $\mu = 0.3824$ for these traits in Section 5. The discrepancy is greater for Radicalism than Toughmindedness and indicates that Model 2B is not accounting for all the variation, particularly in the case of Radicalism.

The relative magnitudes of p and e are quite informative. For both traits, e is substantially larger than p , suggesting that an environmental covariance not dependent upon the parents is of some importance. The value of p is quite large for Radicalism ($p = 0.134$), but is negligible for Toughmindedness ($p = 0.015$). This suggests that the common environment producing similarity in Toughmindedness between individuals living in one family does not depend upon the parents. However, for Radicalism, some substantial part of the environment may depend upon the parents. The size of e shows that a component independent of the parents may also be important. Although e is large for both traits, the greater p for Radicalism means that we are more likely to find cultural transmission as defined by Eaves (1976a) for Radicalism and it is this possibility to which we now turn. The model which we define in the next Section, considers only the environment depend^{ent} on the parent. However, we shall look at the importance of an independent environmental component in later Sections.

4 THE GENETICAL PATH MODEL4.1 The Path Diagram

Eaves' (1976b) model shows how the transmission of cultural differences mediated through the phenotype of the parents leads to genotype-environmental covariance. In order to fit his model to our data, we would have to assume no assortative mating. The observed significant marital correlation in our data, provides direct evidence for assortative mating. Therefore, it is unrealistic to use Eaves' model without reformulating it to include assortative mating. Since this would be difficult, the simplest way to examine genotype-environment covariation and assortative mating simultaneously is to use the technique of specifying effects of interest using the path model approach. The full model including cultural transmission and assortative mating will be described first. Certain simplifying assumptions to be tested will be discussed later as they arise.

The full model yields a very complex path diagram and it has been split into two parts for tracing the paths. These parts are given in figures B6 and B7. These figures can be recombined as shown in Figure B8 to reproduce the original path diagram. Intergenerational relationships may be specified using Figure B6 and collateral relationships using Figure B7. Occasionally we may have to refer to Figure B8 but we shall avoid this as much as possible.

FIGURE B6: PARENT-OFFSPRING RELATIONSHIPS OF A GENETICAL PATH MODEL

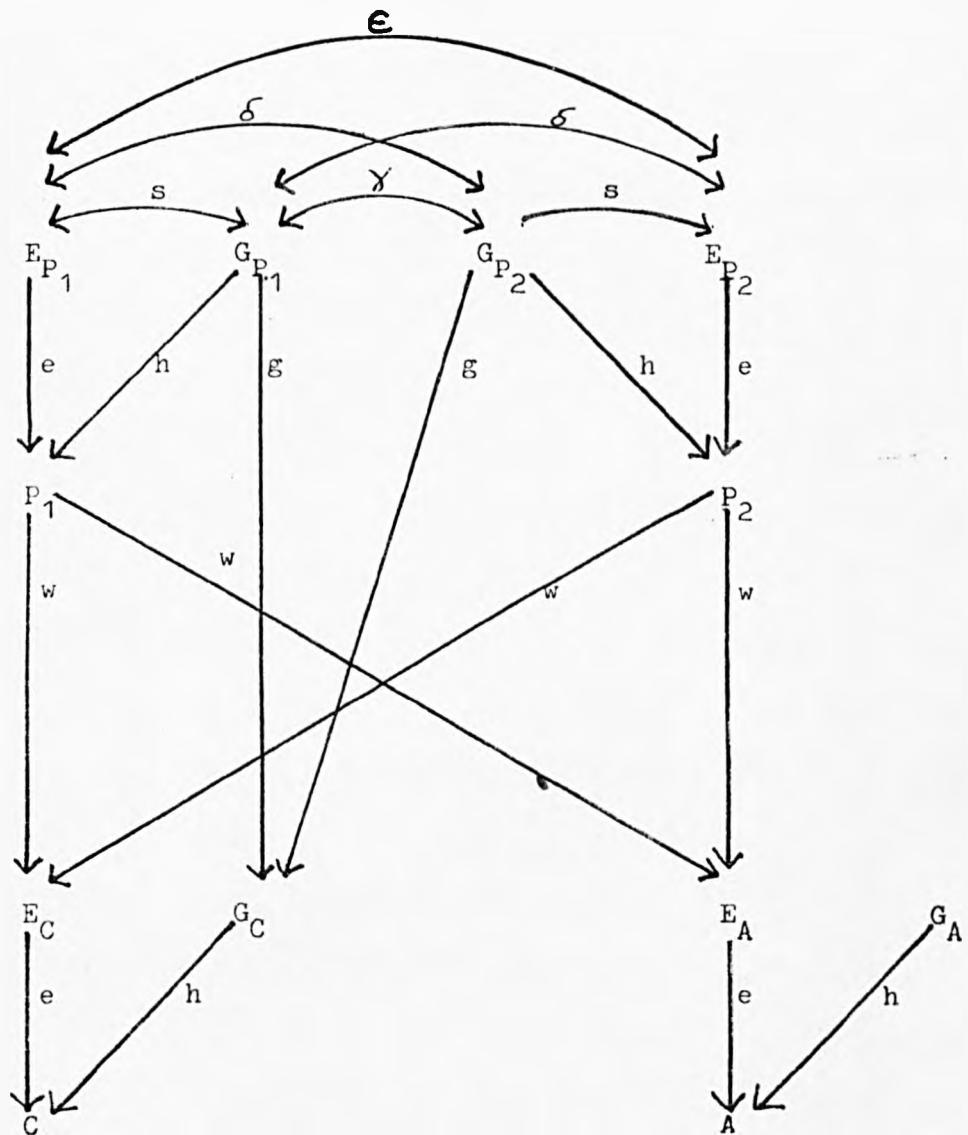


FIGURE B7: COLLATERAL RELATIONSHIPS FOR A GENETICAL PATH MODEL

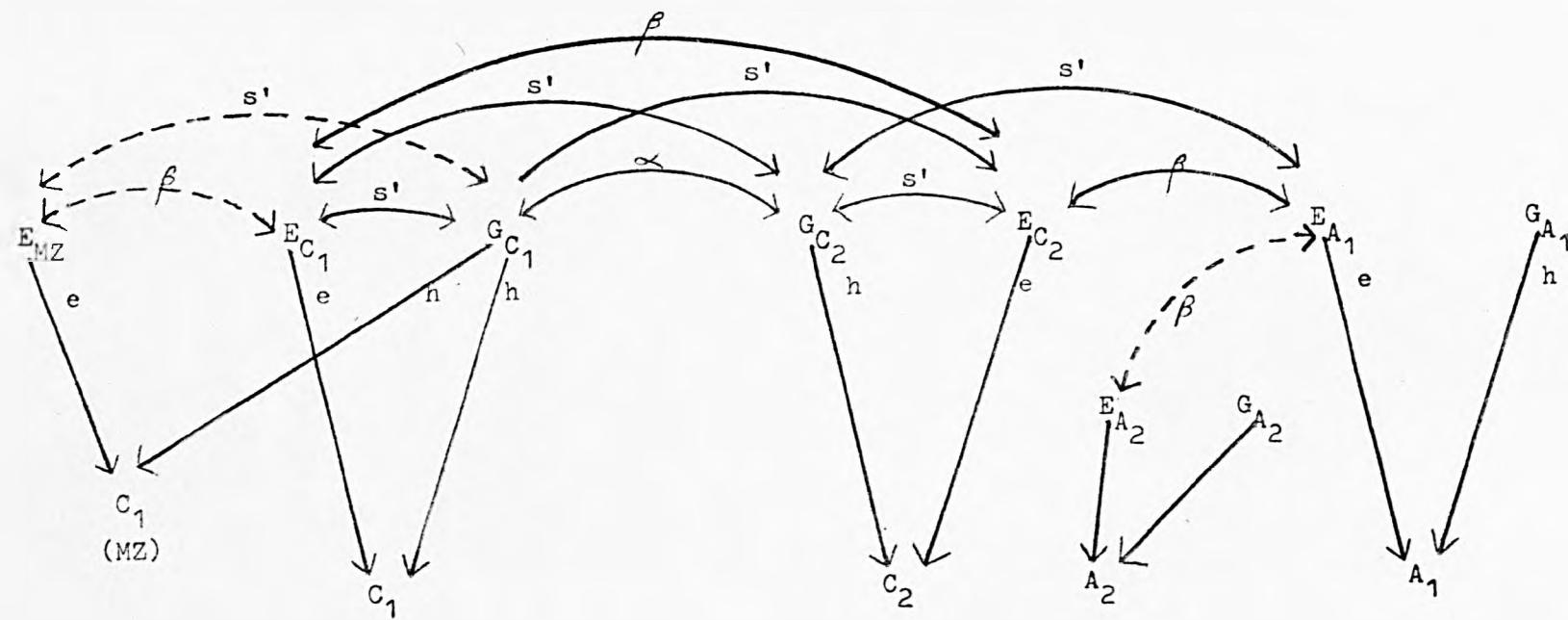
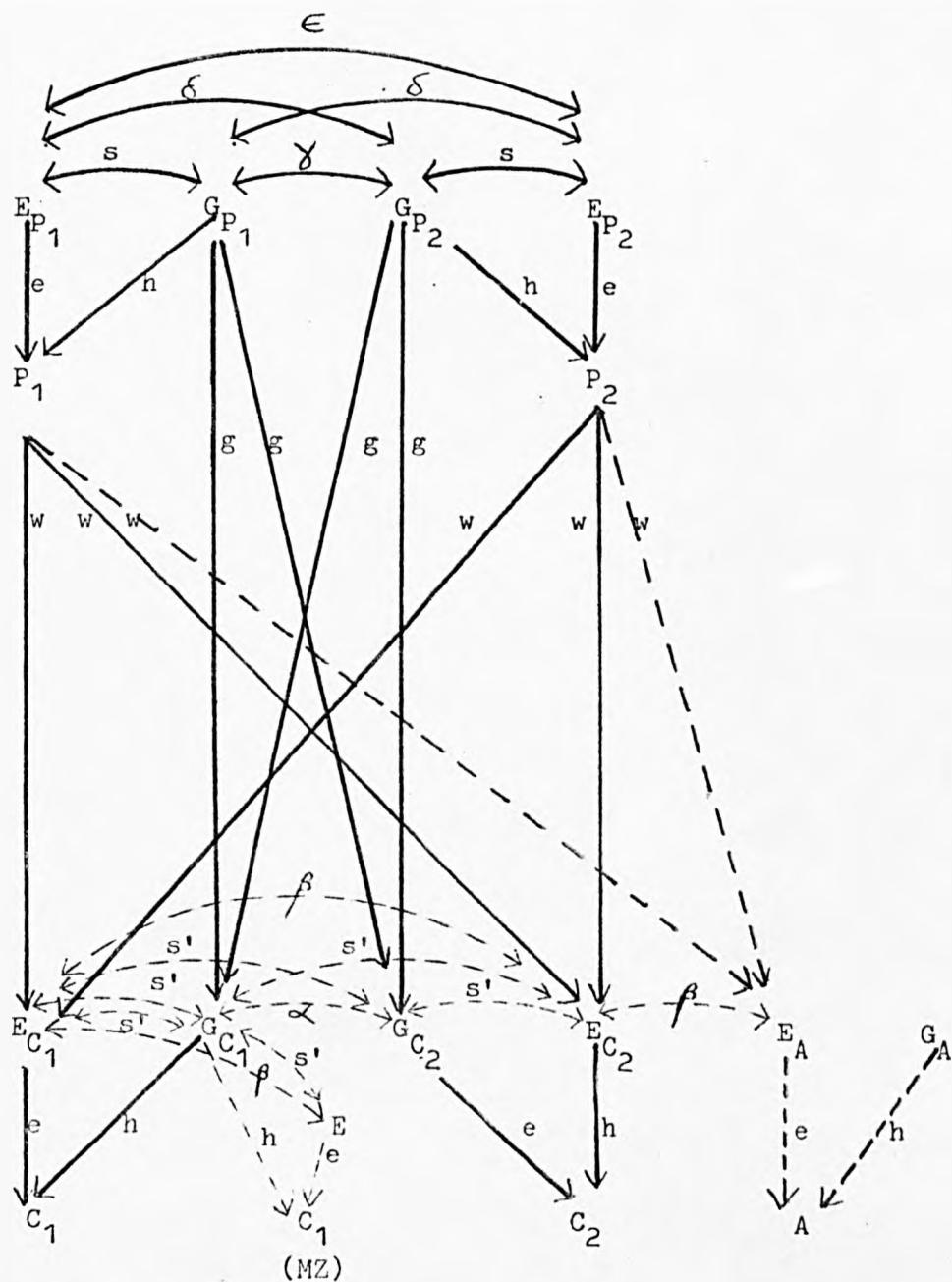


FIGURE B8: A GENETICAL PATH MODEL



4.2 Notation

The main types of individual are specified:

P - Parent

C - Child

A - Adopted Child

Child may sometimes include adopted child, when it is irrelevant whether a child is natural or not i.e. when we are considering environmental effects. C was used to include all types of children in the last section when fitting environmental path models.

Subscripts to P, C and A are used to indicate different individuals, where several individuals of the same type occur in one family e.g. P_1 and P_2 for first and second parent (using mother and father respectively). A special case occurs when we use C_1 twice in order to represent a pair of monozygotic twins.

The other capitals have the following meaning:

G is the genotype (an unknown)

E is the environment (an unknown)

Subscripts to G and E indicate the individual to who the G and E refer.

Paths are always denoted by lower case letters either Roman or Greek.

From Figure B7, α , β and s' are correlations among genotypes and environments implied by the relationships in the preceding generation, and can be expressed in terms of the paths in Figure B6.

Similarly, considering Figure B6, γ , δ , ϵ and s are implied correlations between the genes and environments in the parental generation which could be resolved by reference to the grand-parental generation.

In the collaterals, the correlation between any genotype and environment is given by s' . However in the parental generation genotype-environment correlations are given by s and δ . This is because the collaterals share a common environment provided by their parents and the correlations between G_{C_1} and E_{C_1} and between G_{C_1} and E_{C_2} can be regarded as identical. However in the parental generation, there is no reason why E_{P_1} should be the same as E_{P_2} , since the grandparents providing the environment of the parents are different, and, therefore, separate correlations are needed for the correlation between an individual's own genotype with his environment and the correlation between an individual's own genotype and his spouse's environment. The correlation δ arises because each spouse selects the other on the basis of the phenotype and thus both genetical and environmental correlations exist between them. The correlation s arises as a result of the transmission of genes and environment from the preceding generation, and will be discussed in more depth later.

The implied correlations represent the following:

- s' - correlation between the genes of one sibling and either his own environment or that of his siblings
- s - correlation between a parent's genotype and environment
- δ - correlation between a parent's genotype and his spouse's environment
- α - correlation between the genes of natural siblings, which arises because they have the same parents
- γ - correlation between the genes of spouses, which arises if there is assortative mating

β - correlation between the environments of siblings (natural or adopted). The common environmental covariance is given by $e^2\beta$.

ϵ - correlation between the environments of spouses which arises if there is assortative mating.

The genotype-environment correlation terms can only appear, unless we totally redefine the model, when there is a path from the parents phenotype to the offspring's environment i.e. when there is cultural transmission of the type defined by Eaves (1976b). Eaves (1976a) has shown that genotype-environment covariance can also arise when there is co-operation or competition between siblings i.e. when there is a path from one sibling's phenotype to another's environment. This possibility is not considered in this study and would involve a totally different path diagram. It could also be studied using conventional biometrical-genetical techniques. Another source of genotype-environment-covariance arises when individual's select their own environment. This is not amenable to any sort of analysis since the covariance in this case is always confounded with the individual's genotype in non-experimental populations.

For the purposes of this study, therefore, s , s' and δ cannot appear unless there is a path from parental phenotype to offspring's environment. This path is called w .

The other paths are:

e - path from the environment to the phenotype

g - direct path from parent's genotype to offspring's genotype

h - path from genotype to phenotype

If gene action is purely additive, we expect that $g = \frac{1}{2}$. Therefore,

if we allow g to be a free parameter in the model, and its value differs significantly from $g = \frac{1}{2}$, we are forced to conclude that our model is inappropriate. This may be because of non-additive effects such as dominance or epistasis which cannot be specified using path diagrams, or other inadequacies in the model. The direction of departure from $g = \frac{1}{2}$ depends on such factors as the sample and will not, in general, be systematically related to such effects as dominance.

If there is no genotype-environment covariance, then h^2 is a direct estimate of the proportion of the total variation due to genetical differences. In our full model, h^2 is not an estimate of the heritability since correlations between genes and environment have been specified. However, this will not be the case when we consider several simplifying assumption later.

The model described in this section makes several assumptions. These are:

- i No selective placement of the adopted
- ii No environmental contribution of the true parents to the adopted children
- iii Random distribution of adopting parents throughout the population e.g. they are not concentrated in the higher socio-economic status groups
- iv Maternal and paternal environmental contributions are equal.

4.3 Defining Expectations for the Variances

The model described in the previous sections specifies the effects of cultural transmission based on the phenotype, as described by Eaves (1976b). Such cultural transmission leads to genotype-environment

covariation which is designated s in the parental generation and s' in the offspring generation. If the population is in cultural equilibrium, we expect that $s' = s$. However, we have no reason to suppose that such an equilibrium has been reached for social attitudes, so s and s' will both be treated as free parameters in our model, in the first instance. Later we shall test the hypothesis that the population is in equilibrium by comparing the likelihood when the population is not in equilibrium i.e. $s' \neq s$ with that when we specify that the population is in equilibrium by constraining that $s' = s$.

When s' does not equal s , the total variances of parent's and offspring will differ. This means that, for the first time, we shall allow the diagonal terms of the expected covariance matrix to differ, since $V_p \neq V_c$. Cultural transmission also leads to inequality in the total variances of natural and adopted children. Eaves (1976b) has shown that when his coefficient of cultural transmission, b , is positive the total variance of individuals reared by their own parents, V_c , is greater than that of individuals reared by adopting parents, V_a . When b is negative, then $V_c < V_a$. Thus with the non-equilibrium cultural transmission model depicted in Figures B6, B7 and B8, $V_p \neq V_c \neq V_a$. i.e. we can have three different expected variances on the diagonal of the expected covariance matrix.

The variance of adopteds, using standard path notation is given by:

$$R^2 = h^2 r_{AG} + e r_{AE}$$

$$\therefore R^2 = h^2 + e^2$$

Since $R^2 = 1$, we have:

$$1 = h^2 + e^2$$

i.e. the total variance has been standardised to unity. In order to work with variances, we multiply this equation by the total variance of the adopteds, to obtain:

$$V_A = V_A (h^2 + e^2).$$

This result is a tautology for the case of the adopteds, since $h^2 + e^2 = 1$. However, it proves useful in defining V_C and V_P .

We now define the unit variance of children reared by their natural parents as:

$$\begin{aligned} R^2 &= hr_{CG} + er_{CE} \\ \therefore R^2 &= h(h + es') + e(e + s'h) \\ \text{i.e. } R^2 &= h^2 + 2ehs' + e^2 \end{aligned}$$

Therefore, as the non-standardised total variance we obtain:

$$V_C = V_A (h^2 + 2ehs' + e^2)$$

$$\rightarrow V_C = V_A (1 + 2ehs')$$

i.e. we obtain the same result as Eaves (1976b) since when s' is positive, $V_C > V_A$ and vice versa.

We may similarly define V_P :

$$V_P = V_A (1 + 2ehs)$$

We can see, therefore, that when the population is in cultural equilibrium that $V_P = V_C = V_A$.

4.4 Defining Expectations for the Covariances

In Figure B7, the two individuals marked C_1 are identical twins, since they share a common G. Following the usual rules of path analysis,

(Li, 1955), we can show from this diagram that the covariance of MZ twins is given by:

$$\text{COV}_{\text{MZ}} = v_C (h^2 + 2ehs' + e^2 \beta)$$

Similarly if C_1 and C_2 are either siblings or dizygotic twins, the covariance is given by:

$$\text{COV}_{\text{DZ}} = \text{COV}_{\text{SIB}} = v_C (h^2 \alpha + 2ehs' + e^2 \beta)$$

If we look at the difference between MZ and DZ twins,

$$\text{COV}_{\text{MZ}} - \text{COV}_{\text{DZ}} = v_C h^2 (1 - \alpha)$$

which is equivalent to G_1 in conventional biometrical genetical terminology i.e. the variation within families produced by the segregation of the genes.

The covariance of the two adopted individuals, A_1 and A_2 may be expressed:

$$\text{COV}_{AA} = v_A (e^2 \beta)$$

This differs from the covariance of adopted and natural siblings reared together, because the total variance of the two groups differs. This is given by:

$$\text{COV}_{AC} = \sqrt{v_A \times v_C} (e^2 \beta)$$

It would be possible to define the marital correlation:

$$\mu = h^2 \gamma + 2eh\delta + e^2 \epsilon$$

However, this would mean that we could not resolve γ , δ , ϵ and s in terms of the other parameters and we shall, therefore, estimate the marital correlation directly from the data by specifying the covariance between spouses:

$$\text{COV}_{P_1 P_2} = V_P \mu$$

The expectation for the natural parent-offspring covariance is complex. We derive this from figure B6. In order that the reader may follow the derivation of this expectation, we will write out the paths in full in the order in which they are traced. This gives:

$$\text{COV}_{PC} = \sqrt{V_P \times V_C} (hgh + hgse + hg\gamma h + hg\delta e$$

$$+ ew + ewh\delta h + ewh\delta e + ewe\delta h + ewe\epsilon e)$$

which simplifies to:

$$\text{COV}_{PC} = \sqrt{V_P \times V_C} (gh^2(1+\gamma) + egh(s+\delta) + ew(1+h^2\gamma + 2eh\delta + e^2\epsilon))$$

The adopting parent-offspring covariance may be similarly traced from Figure B6 and turns out to be:

$$\text{COV}_{PA} = \sqrt{V_P \times V_A} (ew(1 + h^2\gamma + 2eh\delta + e^2\epsilon))$$

Thus, we now have expectations for all possible elements of the expected covariance matrix. These involve fifteen parameters. We could not hope to estimate this many parameters from the data. However, these parameters are not all free parameters and we can resolve some of them in terms of the others to give us a final model of eight parameters:

$$\mu_m, \mu_f, V_A, g, h, w, s \text{ and } \mu.$$

Thus, from Figure B8, we can show that:

$$\alpha = 2g^2(1 + \gamma)$$

$$\beta = 2w^2(1 + 2eh\delta + e^2\epsilon + h^2\sigma)$$

$$s' = 2gw(es + h\delta + h + h\gamma)$$

which eliminates three of the original fifteen parameters. Similarly from Figure B6, we can show that:

$$\gamma = \mu (h + es)^2$$

$$\sigma = \mu (hs + e)(h + es)$$

$$\epsilon = \mu (e + hs)^2$$

Also, we know that $e = \sqrt{1 - h^2}$. Therefore, making these substitutions into the expectations for the variances and covariances, we arrive at a final non-equilibrium model of 8 parameters. These expectations are summarised in Table B50, in terms of all the paths and implied correlations. The substitutions that can be made in order to simplify the number of parameters to eight are given below the expectations. These substitutions were never made into the expectations by hand, but were specified in the computer program.

4.5 Fitting the Full Eight Parameter Path Model

This model, described above, includes genetical and environmental effects, genotype-environment covariation produced by cultural transmission and assortative mating. In order to fit this model, we set up the data files in the usual way, as described in Section 7. The model is specified in the program as described earlier. In order to specify estimates of minus the maximum log likelihood, we examined previous analyses. Since the estimates must be less than the final solutions for minus the log likelihood, based on the present model, we chose fairly low values of 500.0 and -1350.0 for Radicalism and Toughmindedness respectively.

The only remaining problem is to choose sensible trial values. The values calculated from the data in Section 5 were given for μ_m ,

TABLE B 50 : EXPECTATIONS FOR THE TERMS OF THE COVARIANCE MATRIX

<u>VARIANCE OR COVARIANCE OF :</u>	<u>EXPECTATION</u>
ADOPTED CHILDREN (v_A)	$v_A (h^2 + e^2)$
NATURAL CHILDREN (v_C)	$v_A (h^2 + 2ehs^1 + e^2)$
PARENTS (v_p)	$v_A (h^2 + 2ehs + e^2)$
MZ TWINS	$v_C (h^2 + 2ehs^1 + e^2\beta)$
DZ TWINS OR SIBLINGS	$v_C (h^2 + 2ehs^1 + e^2\beta)$
NATURAL AND ADOPTED CHILDREN	$\sqrt{v_A \times v_C} (e^2\beta)$
TWO ADOPTED CHILDREN	$v_A (e^2\beta)$
NATURAL PARENT CHILD	$\sqrt{v_p \times v_C} (gh^2(1+\gamma) + egh(s+\delta) + ew(1+h^2\gamma + 2eh\delta + e^2\epsilon))$
ADOPTING PARENT CHILD	$\sqrt{v_p \times v_A} (ew(1+h^2\gamma + 2eh\delta + e^2\epsilon))$
SPOUSES	v_p / μ

The following substitutions can be made into the above expectations:

$$\begin{aligned}
 e &= \sqrt{1-h^2} \\
 \gamma &= \mu(h+es)^2 \\
 \delta &= \mu(hs+e)(h+es) \\
 \epsilon &= \mu(e+hs)^2 \\
 \alpha &= 2g^2(1+\gamma) \\
 \beta &= 2w^2(1+2eh\delta + e^2\epsilon + h^2\gamma) \\
 s^1 &= 2gw(es+h(1+\gamma+\delta))
 \end{aligned}$$

μ_f , V_A , and μ , and trial values of 0.5 were given for the paths g , h , w and s . Convergence took some time, but was achieved using the method based on first derivatives and no constraints were necessary. Parameter estimates for Radicalism and Toughmindedness and their corresponding maximum log likelihoods are presented in Table B51. Values for the variances, implied correlations and paths which may be specified in terms of the parameters of the model were calculated and given in the lower part of Table B51. We will not consider the values of the parameters of this model in any detail since we want to move on and compare this model with a similar but simplified model. However, we shall briefly compare the maximum log likelihoods with those found for earlier models. For both traits, the maximum log likelihoods based on this model are greater than those for any of our previous models. In the case of Radicalism, this model does not provide a significant improvement in fit over the $E_1 D_R E_2'$ model ($\chi^2_3 = 1.5972$, $50\% < p < 70\%$), but it does enable us to partition the between families variation into that due to assortative mating and that due to environmental differences dependent upon parental phenotype.

This genetical path model provides a significant improvement in fit over the most likely model we have found for Toughmindedness. This was the environmental path model 2B whose maximum log likelihood was 1314.7409. Thus, using the likelihood ratio criterion, $\chi^2_2 = 28.8022$, $p < 0.1\%$. The main difference between the two models is that in the latter model, there is genetical variation and genotype-environmental covariance leading to inequality of the total variances of parents, natural children and adopted children. In Section 5, we saw differences in total variance between these three groups. However, there was no

TABLE B 51 : FULL EIGHT PARAMETER GENETICAL PATH MODEL

PARAMETER	RADICALISM	TOUGHMINDEDNESS
μ_m	-0.0172	0.0093
μ_f	-0.0042	0.0065
v_A	0.8489	0.1010
g	0.5477	0.5652
h	0.8489	0.8988
w	-0.0539	-0.2106
s	0.0156	-0.1103
μ	0.3173	0.4692
L	-509.0304	1329.1420
e	0.5286	0.4386
γ	0.2331	0.3393
δ	0.1474	0.1355
ϵ	0.0932	0.0541
α	0.7398	0.8557
β	0.0077	0.1234
s^1	-0.0697	-0.3040
v_c	0.7958	0.0768
v_p	0.8608	0.0922

evidence for any genetical variation in the twin data. This model may provide a significant improvement over previous models because it predicts differences in the total variances or it may be the first indication that we have for genetical variation in Toughmindedness. We will consider the implications of this possibility and why there was no evidence for it in the twin data later.

4.6 A Seven Parameter Genetical Path Model

In the previous model, eight parameters were fitted which included g , the path from parental genotype to offspring genotype. The value of this path should be 0.5 if all the variation is additive. But if g differs significantly from 0.5, we may take this as evidence for some form of non-additivity in the data. We see that $g = 0.5477$ for Radicalism and $g = 0.5652$ for Toughmindedness. These values are close to 0.5, but we need a test of significance to determine whether we can regard them as estimates of the genetical path which differ from 0.5 only by sampling error. In order to make this test of significance we shall fit a simplified model to the data.

This model is similar to that specified in Table B50, but 0.5 is substituted for g in all the expectations. This yields a 7 parameter genetical path model: μ_m , μ_f , V_A , h , w , s and μ . In order to obtain the maximum likelihood solutions for these parameters, we reran the computer program using the new expectations (with $g = \frac{1}{2}$), the same estimates of minus the log likelihood and the solutions for the parameters from Table B51 as trial values. The method based on first derivatives was used for both traits. Convergence was reasonably quickly reached

for Radicalism. However, in the case of Toughmindedness the program failed after a number of iterations, with the covariance matrix becoming non-positive definite. The matrix was constrained to be positive definite by specifying that all its eigenvalues must be greater than zero and the program was rerun. This time convergence was quickly achieved. The parameter estimates and the maximum log likelihoods are given in Table B52 for the unconstrained solution for Radicalism and the constrained solution for Toughmindedness.

Now we will compare the likelihoods for $g = \frac{1}{2}$ and $g \neq \frac{1}{2}$. Using the likelihood ratio criterion, the eight parameter model for Radicalism does not provide a significant improvement over the seven parameter model. ($\chi^2_1 = 1.0618$, $30\% < p < 50\%$). Therefore, we have no reason to suppose that g takes any other value than 0.5 i.e. there is no evidence for genetical non-additivity. This is consistent with our analysis of the twin study.

However, in the case of Toughmindedness, we find a different picture. The likelihood ratio criterion gives us a value of chisquare: $\chi^2_1 = 4.0894$, $2\% < p < 5\%$, which is significant at the five per cent level. We can attribute this significant difference between the seven and eight parameter models to the fact that $g \neq \frac{1}{2}$. This indicates the inadequacy of the additive model for these data.

4.7 Discussion of Toughmindedness

In Section 6, we found no evidence for any genetical component of Toughmindedness, as measured by the Wilson-Patterson Attitudes

TABLE B 52 : SEVEN PARAMETER MODEL, CONSTRAINING THAT ALL GENETICAL VARIATION IS ADDITIVE

<u>PARAMETER</u>	<u>RADICALISM</u>	<u>TOUGHMINDEDNESS</u>
μ_m	-0.0221	0.0104
μ_f	-0.0048	0.0069
v_A	0.8462	0.0998
h	0.8573	0.8976
w	-0.0543	-0.1704
s	0.0655	0.0422
μ	0.4306	0.5802
L	-509.5613	1327.0973
g	0.5000	0.5000
e	0.5148	0.4408
γ	0.3419	0.4870
δ	0.2191	0.2545
ϵ	0.1404	0.1329
α	0.6710	0.7435
β	0.0087	0.0941
s^1	-0.0745	-0.2695
v_c	0.7905	0.0785
v_p	0.8951	0.1031

Questionnaire and concluded that variation could be explained by unreliability of measurement, specific environmental effects and a common environmental component. Yet now we find that the genetical path model provides a significant improvement over environmental models. It is difficult to understand this discrepancy, but two explanations are possible.

The first is that the great improvement of this model over previous models is purely a result of relaxing the constraint that the total variances are equal. In Section 5, we saw that $V_p = 0.104 > V_A = 0.100 > V_C = 0.075$. This model allow the variances to differ in this order given appropriate values of s and s' .

If this is not the reason for the genetical path model providing the best explanation of the data, then there may be genetical variation determining individual differences in Toughmindedness. Why then did we not detect genetical variation in the twin data? Perhaps non-additive variation and interactions could produce the sort of results we have found, if they were confounded with estimates of E_1 and E_2 in the twins, but not in the adoption data. Since $g \neq \frac{1}{2}$, we know that the genetical path model for Toughmindedness is not appropriate. Non-additivity of environmental effects or sex interactions, without a genetical background, might provide the most appropriate explanation for our findings. Our tentative conclusion is that there may be some genetical variation for Toughmindedness of which a large proportion is non-additive. (We recall that $\chi^2_1 = 3.71$, $5\% < p < 10\%$, when we compared $E_1 BD_R$ and $E_1 E_2$ models in the twins, which approaches significance and that all three parameters of the $E_1 BD_R$ model were significant. Thus, genetical variation was not strongly precluded in the twins). However, it is also possible that

the variation may be explained by unequal environmental effects in the different groups, which lead to inequality of the total variances; non-additive environmental effects, or sex interactions.

A comparison of the means, total variances and marital correlation calculated from the data and calculated from the estimates of the seven parameter and eight parameter genetical path models is given in Table B53. Estimates of the means and total variances are similar in all cases, giving us no additional information. Estimates of the marital correlation based on the two models are rather high. However, the estimate of μ based on the eight parameter model is closer to the true value than that based on the seven parameter model, providing additional evidence that the eight parameter model is more appropriate for our data.

In both models w is negative. However, s and s' take the same sign in the eight parameter model whereas in the seven parameter model, only s' is negative. A mechanism whereby the covariance would differ in direction between the generations is hard to visualise, and the eight parameter model in which s and s' are both negative again seems more reasonable. Considering now only the eight parameter model, the genotype-environment correlations are quite large and s' is substantially bigger than s . i.e. the negative covariance between genotype and environment has increased between the two generations. This suggests that the population is not in equilibrium. The concept of cultural equilibrium, its algebraic definition and the solution of an equilibrium model will be discussed later in reference to Radicalism. However, the simplest way to achieve an equilibrium solution for the parameters of the path model using the computer program is simply to specify the constraint that $s = s'$. This was done for the seven and eight

TABLE B 53: COMPARISON OF ESTIMATES FROM THREE SOURCES FOR TOUGHMINDEDNESS

	ESTIMATES FROM SECTION	ESTIMATES FROM SEVEN PARAMETER MODEL	ESTIMATES FROM EIGHT PARAMETER MODEL
μ_m	0.010	0.010	0.009
μ_f	0.001	0.007	0.007
v_A	0.100	0.100	0.101
v_c	0.075	0.079	0.077
v_p	0.104	0.103	0.092
μ	0.382	0.580	0.469

parameter models. The values of the unconstrained solution were given as trial values. Solutions were sought using function values only.

The method using first derivatives and the method using second derivatives. In all cases the covariance matrix became non-positive definite and the programs failed. They were rerun with the additional constraints needed to ensure that the covariance matrix remained positive definite. These programs ran for some time and were restarted using the current solutions as new trial values. However, movement towards convergence was very slow and was obviously not going to be reached in a reasonable amount of time. Thus solutions for the parameters of the equilibrium solution were never found. The great difficulty encountered suggests that the equilibrium model may be inappropriate and that the population is not in equilibrium. This is reasonable in view of the large difference between the covariance terms of the two generations.

Thus, the eight parameter, non-equilibrium genetical path model remains our most likely model for Toughmindedness. Values of the implied correlations and the paths all seem reasonable and lie within the expected range. However, we will defer further discussion of Toughmindedness until we have considered the likelihoods of certain simplified models.

4.8 Discussion of Radicalism

Since we have considerable genetical variation for Radicalism, but have found no evidence to suggest non-additivity, the seven parameter genetical path model is more appropriate than the eight parameter model. Although this model is not significantly more likely

than the $E_1 D E_2$ ' model, it provides a more useful parameterisation, which enables us to consider certain effects of interest.

A comparison of estimates of the means, variances and marital correlation calculated from the data in Section 5 and calculated from the two genetical path models is given in Table B54. Estimates of the means and total variances are similar and the total variances take the same order i.e. $V_p > V_A > V_C$. However, we have no evidence that lifting the constraint that the total variances must be equal significantly improves the likelihood, when we compare the likelihoods based on this model and that based on the $E_1 D E_2$ ' model. Again, estimates of the marital correlation differ in the three cases, and the estimate from the most likely model is closest to the true value, providing further evidence that the seven parameter model is the most appropriate.

Estimates of the paths and implied correlations seem reasonable and internally consistent. However, we will defer discussion of the relative magnitudes of the parameters and their interpretation until we have considered the equilibrium solution.

4.9 Equilibrium Solution for Radicalism

The path from parents' phenotype to offspring's genotype is negative suggesting that the environmental effect of more radical parents is to make their children less radical and vice versa. The effect is only small, as judged by the size of w . The genotype-environment correlation is also small but differs between the two generations by a small amount.

TABLE B 54 : COMPARISON OF ESTIMATES FROM THREE SOURCES FOR RADICALISM

	ESTIMATES FROM SECTION 5	ESTIMATES FROM SEVEN PARAMETER MODEL	ESTIMATES FROM EIGHT PARAMETER MODELS
μ_m	0.005	-0.022	-0.017
μ_f	-0.002	-0.005	-0.004
v_A	0.845	0.846	0.849
v_c	0.762	0.791	0.796
v_p	1.011	0.895	0.861
μ	0.405	0.431	0.317

If the population is in equilibrium we expect that s and s' will be equal. We would like to know whether s and s' differ significantly i.e. whether population is in equilibrium. In order to do this we need to fit a model assuming equilibrium and compare the maximum log likelihoods of equilibrium and non-equilibrium solutions.

In order to assume equilibrium we let $s' = s$. In Table B50, we saw that s' may be expressed in terms of s , as follows

$$s' = 2gw (es + h(1 + \gamma + \delta))$$

Now at equilibrium $s' = s$. Therefore, substituting and transferring terms in s to the left hand side we find:

$$s(1 - 2egw) = 2gwh(1 + \gamma + \delta) \quad \dots 1$$

which simplifies to:

$$s = \frac{2gwh(1 + \gamma + \delta)}{1 - 2egw}$$

However, from Table B50, we see that γ and δ contain terms in s . Therefore, substituting in equation 1, we obtain:

$$s(1 - 2egw) = 2gwh(1 + \mu h(e+h) + s\mu(e+h)^2 + s^2\mu e(e+h))$$

which we may express:

$$s^2(2eghw\mu(e+h)) + s(\mu(e+h)^2 - (1 - 2egw)) + 2ghw(1 + \mu h(e+h)) = 0$$

This quadratic in s may be expressed as:

$$As^2 + Bs + C = 0, \text{ where}$$

$$A = 2eghw\mu(e+h)$$

$$B = \mu(e+h)^2 - (1 - 2egw)$$

$$C = 2ghw(1 + \mu h(e+h))$$

Therefore, s is given by:

$$s = - \frac{B \pm \sqrt{B^2 - 4AC}}{2A} \quad ...2$$

This equation has two roots and thus two solutions of s are possible which produce an equilibrium. Clearly, in practise only one of these solutions is likely to be sensible. However, we have no way of knowing which this will be, and it may turn out not to be the same root in all situations.

In order to fit the equilibrium path model using our expression for s , defined by equation 2, we would have to reformulate the expectations in Table B50. Moreover, we would have to set up two sets of expectations based on the two possible roots for s , and attempt to find solutions for each of these sets of expectations, which would be expensive in computer time. It might not even be possible to achieve a solution in this way, because oscillation might occur between two minima. However, we can easily overcome these problems by constructing a penalty function, added to L , which tends to zero when $(s' - s) = 0$. In order to obtain solutions for the equilibrium model of the seven and eight parameter genetical models, we used the estimates from the non-equilibrium model as trial values. The method based on first derivatives was used to obtain the maximum log likelihood solution for the parameters of the model. Convergence was rapidly reached without the need to constrain the covariance matrix to be positive definite. The ease with which a solution was found for Radicalism suggests that perhaps the equilibrium model is appropriate, whereas for Toughmindedness it was clearly not appropriate and an equilibrium solution could not be found.

Estimates of the parameters for eight and seven parameter-models and their likelihoods are given in Tables B55 and B56 respectively. The paths and implied correlations which can be resolved in terms of these parameters were calculated and are given in the bottom part of these tables. Comparison of the maximum log likelihoods of these models with those of the non-equilibrium models will show whether the non-equilibrium solution is more likely than the equilibrium solution. Since there is one less free parameter in the equilibrium model, we can use the likelihood ratio criterion to make a test of significance. For the eight parameter model $\chi^2_1 = 0.8926$, $30\% < p < 50\%$, and for the seven parameter model $\chi^2_1 = 2.6202$, $10\% < p < 20\%$. Whichever model we consider, specifying the constraint that $s' = s$ does not produce a significant reduction in the likelihood. Thus there is no evidence that the genotype-environment correlation differs in the two generations being considered.

Comparing the eight and seven parameter model using the likelihood ratio criterion, we find that $\chi^2_1 = 2.6894$, $10\% < p < 20\%$. Therefore, we have no reason to suppose that g differs significantly from 0.5. The most appropriate path model for our data so far is the model whose solutions are given in Table B56. In this model, there is additive genetical variation, assortative mating and cultural transmission as defined by Eaves (1976b), with the population in cultural equilibrium. The value of h is large suggesting that there is a large heritable component of variation. Following on from this we see that there is a large genetical correlation between siblings, α . The assortative mating leads to a substantial correlation between the genes of spouses i.e. $\gamma = 0.2224$, but a much lower correlation between their

TABLE B 55 : EQUILIBRIUM SOLUTION FOR FULL EIGHT PARAMETER MODEL

PARAMETER	RADICALISM
μ_m	-0.0176
μ_f	-0.0043
v_A	0.8315
g	0.5473
h	0.8311
w	-0.0234
s	-0.0305
μ	0.3152
M_L	-509.4767
e	0.5561
γ	0.2089
δ	0.1362
ϵ	0.0888
α	0.7242
β	0.0014
s^1	0.0282
v_c	0.8532
v_p	0.8080

TABLE B 56 : EQUILIBRIUM SOLUTION FOR SEVEN PARAMETER MODEL

PARAMETER	RADICALISM
μ_m	-0.0190
μ_f	-0.0043
v_A	0.8302
h	0.8405
w	-0.0257
s	-0.0290
μ	0.3270
ML	-510.8214
g	0.5000
e	0.5418
γ	0.2224
δ	0.1396
ϵ	0.0875
ζ	0.6112
β	0.0017
s^1	-0.0290
v_c	0.7828
v_p	0.8083

environments, $E = 0.0875$. The correlation between the environments of siblings provided by their parents is small: $\beta = 0.0017$, suggesting that any common environmental component dependent upon the parents is quite small. This is a consequence of the low value of the path, w , from parental phenotype to offspring's environment, which suggests that cultural transmission may be making only a minimal contribution to the total variation. The small genotype-environment correlation which arises as a result of cultural transmission is estimated to be small suggesting that any effect of cultural transmission is minimal. We, therefore, need to test whether the effect of cultural transmission is significant by comparing the likelihood of this model with that based on a simplified model in which there is no cultural transmission.

5 SIMPLIFIED GENETICAL PATH MODELS

5.1 Introduction

We know from the twin data that there is evidence for a between families component produced by either common environmental influences or by assortative mating. This was confirmed by fitting biometrical-genetical models to all the data jointly using the methods of pedigree analysis. However, we were still unable to discriminate properly between the two alternative sources of the between families component.

In the last section we considered the possibility that both assortative mating and cultural differences mediated through the phenotype of the parents were important. We found that the assortative mating parameters were substantial, but that the path, w , and the genotype-environment covariance were minimal for Radicalism. This suggested that there might be no significant variation produced by cultural transmission. How then can we interpret the between families component? There are two possibilities. All the between families component could be due to assortative mating. Alternatively there could be a common environmental effect independent of the parents. Or, both these effects might be contributing.

If we test the first possibility by specifying a path model with no cultural transmission, but with assortative mating, we can use this model to test the significance of the variation produced by cultural transmission, by comparing it with the model discussed at length in Section 8.4.

We can also specify a model with a common environmental component and determine whether this gives us a more likely explanation of the observed variation in attitudes.

5.2 Simplified Genetical Path Model

A path diagram for a genetical model with assortative mating but no common environmental component is given in Figure B9, by the solid lines. The model is similar to that used in Section 8.4, except that there is now no path from parental phenotype to offspring environment. Since we do not have this path, specifying cultural transmission, we no longer have any genotype-environment covariation i.e. there are no implied correlations: s , and s' . Considering the model given by the solid lines, there is no correlation between the environment of siblings i.e. there is no common environmental component. E now represents only specific variation. A correlation between the genes of siblings is produced by the genetic system. Assortative mating gives rise to correlations between the genes of spouses and between their environments, since it is based on the phenotype. However, there is no longer any genotype-environment covariance in the parental generation. In effect, we now have an additive genetical model, with assortative mating and specific environmental variation.

This model is much simpler than the full model described in Section 8.4 and derivation of expectations for the expected covariance matrix presents no problems. These expectations, worked out from the solid lines in Figure B6 are given in Table B57.

FIGURE B9: SIMPLIFIED GENETICAL PATH MODEL

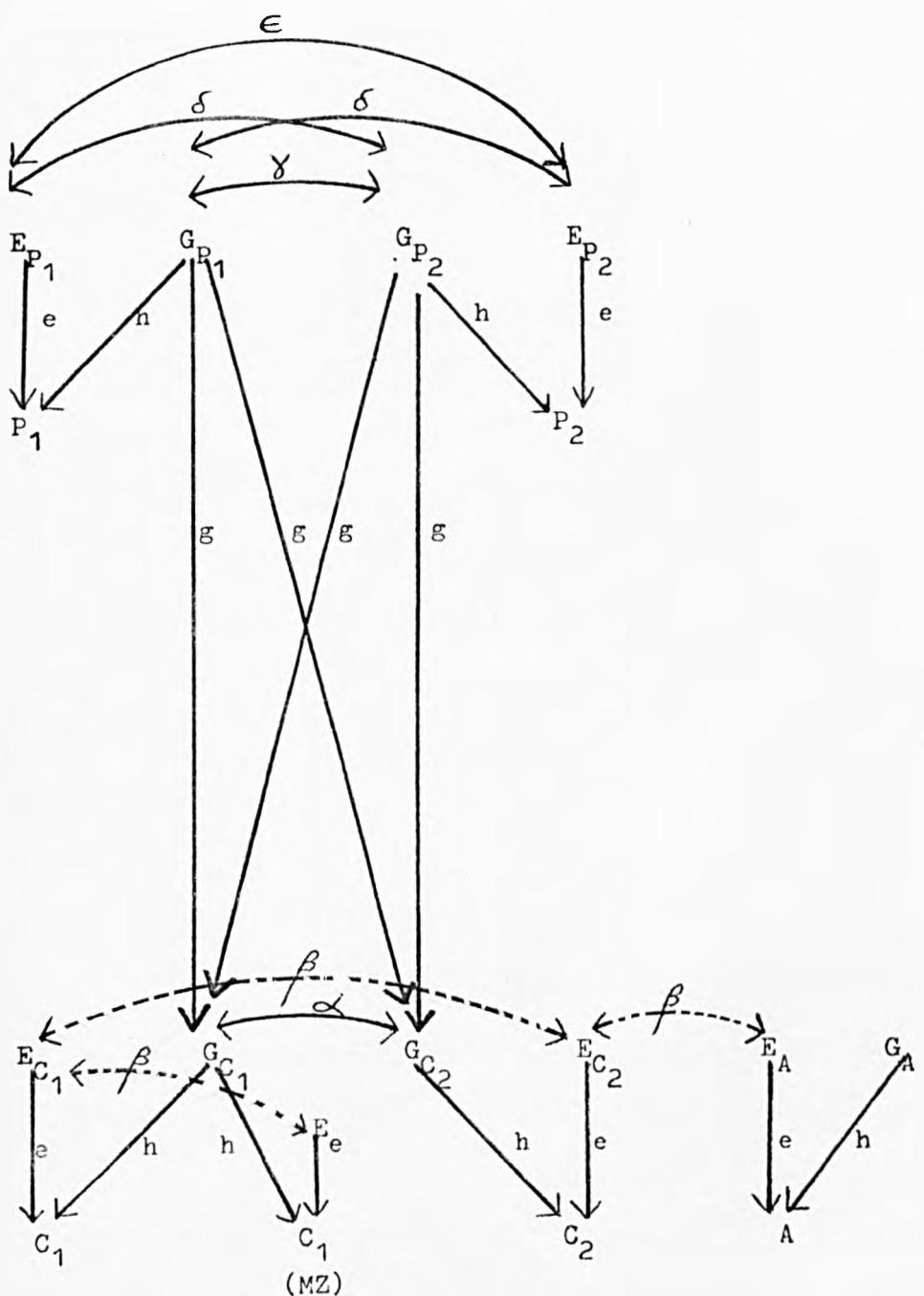


TABLE B 57 : EXPECTATIONS FOR A SIMPLIFIED GENETICAL MODEL

<u>VARIANCE OR COVARIANCE</u>	<u>EXPECTATION</u>
TOTAL VARIANCE	v
MZ TWINS	$v h^2$
DZ TWINS OR SIBLINGS	$v h^2 \alpha$
NATURAL AND ADOPTED CHILDREN	0.0
TWO ADOPTED CHILDREN	0.0
NATURAL PARENT-CHILD	$vgh^2(1 + \gamma)$
ADOPTING PARENT-CHILD	0.0
SPOUSES	$v \mu$

The following substitutes can be made into the above expectations

$$\epsilon = \sqrt{1 - h^2}$$

$$\gamma = \mu h^2$$

$$\epsilon = \mu \epsilon^2$$

$$\alpha = 2g^2 (1 + \gamma)$$

We fitted this model to both Radicalism and Toughmindedness in order to determine whether it provides a more economical explanation of the data than the full genetical path model described in Section 8.4. The data file for the program was set up in the usual way. Two models were specified; one in which g was allowed to take its own value (6 parameters); the other where g was fixed at 0.5, by substituting 0.5 into the expectations given in Table B57 (i.e. 5 parameters). Values of 500.0 and -1350.0 were again given for the trial minus log likelihoods for Radicalism and Toughmindedness respectively. The solutions from the appropriate full genetical path model were given as trial values. The program was run using the method based on first derivatives. In each case the covariance matrix became non-positive definite and the program failed. However, when the program was rerun using the method based on second derivatives, convergence was rapidly reached for both models for Radicalism and Toughmindedness. The maximum likelihood solutions of the parameters and the log likelihoods are given in Tables B58 and B59 for the six and five parameter models respectively. Values of e and the implied correlations were calculated from the estimated parameters and are given below the likelihoods in these tables. We will defer discussion of these models until we have looked at a final model with a common environment independent of the parents, when we will compare the results for all the models fitted and determine which is the "best" model for each trait.

TABLE B 58 : SIMPLIFIED GENETICAL PATH MODEL WITH $g = \frac{1}{2}$

PARAMETER	RADICALISM	TOUGHMINDEDNESS
μ_m	-0.0247	0.0111
μ_f	-0.0053	0.0099
v	0.8114	0.0833
g	0.5412	0.5672
h	0.8148	0.7860
μ	0.3400	0.4398
L	-509.1514	1324.7638
e	0.5845	0.6182
γ	0.2257	0.2717
ϵ	0.1162	0.1681
κ	0.7180	0.8183

TABLE B 59 : SIMPLIFIED GENETICAL PATH MODEL WITH $g = \frac{1}{2}$

PARAMETER	RADICALISM	TOUGHMINDEDNESS
μ_m	-0.0243	0.0116
μ_f	-0.0049	0.0097
v	0.8106	0.0831
h	0.8228	0.8001
μ	0.3893	0.5022
L	-510.0310	1322.7811
g	0.5000	0.5000
e	0.5683	0.5999
γ	0.2636	0.3215
ϵ	0.1257	0.1807
α	0.6318	0.6608
h^2	0.6770	0.6402
e^2	0.3230	0.3599

5.3 Simplified Genetical Path Model with an Independent Common Environment

We found some evidence from the environmental path models in Section 8.3 that the effect of an environment dependent on the parents was relatively small, whereas an environment independent of the parents was important in determining individual differences in attitudes. In order to test the importance of an independent common environment, we shall specify a model including its effect and compare its likelihood with that based on the model specified in the previous section. This model is given in Figure B9, if we consider both solid and broken lines. The model is similar to that described in the previous section, except that we now introduce a covariance between the environments of siblings reared together, which we call β . This changes our expectations for the covariances between collaterals. These expectations may be easily traced from the path diagram and are presented in Table B60.

In order to obtain the maximum likelihood solution for this model, we respecified the expected covariance matrix as shown in Table B60. The same trial values were used as for the previous model and a trial value of 0.2 was arbitrarily specified for β . Convergence was quickly reached in all cases using the method based on second derivatives. Solutions for the situations where $g \neq \frac{1}{2}$ and where $g = \frac{1}{2}$ are given in Tables B61 and B62 for Radicalism and Toughmindedness.

Having the results for all our models we are now in a position to determine the most appropriate model for the observed variation in all the data for each trait and to discuss the implications of this model.

TABLE B 60: EXPECTATIONS FOR SIMPLIFIED GENETICAL MODEL WITH COMMON ENVIRONMENT INDEPENDENT OF THE PARENTS.

<u>VARIANCE OR COVARIANCE</u>	<u>EXPECTATION</u>
TOTAL VARIANCE	v
MZ TWINS	$v(h^2 + e^2\beta)$
DZ TWINS OR SIBLINGS	$v(h^2\alpha + e^2\beta)$
NATURAL AND ADOPTED CHILDREN	$v e^2\beta$
TWO ADOPTED CHILDREN	$v e^2\beta$
NATURAL PARENT-CHILD	$v gh^2(1+\gamma)$
ADOPTED PARENT CHILD	0.0
SPOUSES	$v\mu$

The following substitutions can be made into the above expectations

$$e = \sqrt{1 - h^2}$$

$$\gamma = \mu h^2$$

$$\epsilon = \mu e^2$$

$$\alpha = 2g^2(1+\gamma)$$

TABLE B 61 : SEVEN PARAMETER MODEL WITH COMMON ENVIRONMENT INDEPENDENT
OF THE PARENTS. $\alpha \neq \frac{1}{2}$

PARAMETER	RADICALISM	TOUGHMINDEDNESS
μ_m	-0.0237	0.0104
μ_f	-0.0055	0.0092
v	0.8117	0.0833
s	0.5327	0.5642
h	0.7603	0.6911
μ	0.3376	0.4295
β	0.2058	0.2715
L	-509.0011	1325.7574
e	0.6496	0.7228
γ	0.1952	0.2051
ϵ	0.1425	0.2244
α	0.6783	0.7672

TABLE B 62 : SIX PARAMETER MODEL WITH COMMON ENVIRONMENT INDEPENDENT
OF THE PARENTS, $\sigma = \frac{1}{2}$

PARAMETER	RADICALISM	TOUGHMINDEDNESS
μ_m	-0.0226	0.0106
μ_f	-0.0055	0.0087
v	0.8114	0.0830
h	0.7021	0.6428
μ	0.3462	0.4466
β	0.3482	0.3717
L	-509.2089	1324.8996
g	0.5000	0.5000
e	0.7121	0.7660
γ	0.1707	0.1845
ϵ	0.1756	0.2620
α	0.5854	0.5923

5.4 The Final Model for Radicalism

In order to decide which model of those we have fitted is the most appropriate for Radicalism we have prepared a summary of all the models fitted, which is given in Table B63. This Table gives the parameters of the models and their corresponding maximum log likelihoods.

The model with the highest maximum log likelihood is number 17, with $L = -509.0011$. This model, specifying the effects of genes, assortative mating and a common environment independent of the parents, will be used as a baseline against which to compare all the other models. We see immediately that models based purely on environmental variation between individuals (i.e. models 1, 2, 7, 8, 9, 10) are all significantly less likely than model 17. Therefore, our first conclusion, which confirms the results of the twin study, is that genetical differences determine differences between individuals in their Radicalism scores.

These environmental models, although not the most likely explanations of the data do contribute useful information. A comparison of the simple correlation models (1 and 2) shows that monozygotic twins are significantly more alike than dizygotic twins, suggesting either a genetical component of variation or that MZ twins are treated more alike. The importance of assortative mating is indicated by the comparison of model 7 with 8 and of 9 with 10. In both cases, the addition of the assortative mating parameter produces a significant difference in the likelihood, as measured by the likelihood ratio criterion. Using this criterion, we found that models including an environment independent of

TABLE B 63: SUMMARY OF MODELS FOR RADICALISM

<u>MODEL</u>	<u>PARAMETERS</u>	<u>LIKELIHOOD</u>	
1	$\mu_m \mu_f V r$	-533.7704	
2	$\mu_m \mu_f V r t$	-515.8289	
3	$\mu_m \mu_f E_1 D_R$	-517.9692	
4	$\mu_m \mu_f E_1 D_R E_2$	-513.3635	
5	$\mu_m \mu_f E_1 D_R E_2^1$	-509.8290	
6	$\mu_m \mu_f E_1 D_R E_2^{11}$	-514.3745	
7	$\mu_m \mu_f V p$	-553.7629	
8	$\mu_m \mu_f V p \mu$	-547.4797	
9	$\mu_m \mu_f V p \alpha$	-523.4731	
10	$\mu_m \mu_f V p \alpha \mu$	-519.4698	
11	$\mu_m \mu_f V_A g h w s \mu$	-509.0304	
12	$\mu_m \mu_f V_A h w s \mu$	-509.5613	
13*	$\mu_m \mu_f V_A g h w s \mu$	-509.4767	
14*	$\mu_m \mu_f V_A h w s \mu$	-510.8214	
15	$\mu_m \mu_f V g h \mu$	-509.1514	
16	$\mu_m \mu_f V h \mu$	-510.0310	
17	$\mu_m \mu_f V g h \beta \mu$	-509.0011	
18	$\mu_m \mu_f V h \beta \mu$	-509.2089	

NOTE

Models marked with a "*" are the equilibrium models.

the parents produced significantly more likely solutions than models without it. The importance of an independent environmental component compared with a common environment depending on the parents was confirmed by inspection of the relative magnitudes of the paths p and e .

The most likely biometrical-genetical model was number five, which specifies specific environmental variation, additive genetical variation and a covariance between all individuals living together. The likelihood for this model does not differ significantly from that of our baseline model, number 17. Since this model summarises the pattern of variation using five parameters and model 17 uses seven parameters, we might consider model 5 to be a more satisfactory and parsimonious explanation of individual differences in Radicalism. However, the way in which the common family covariance has been specified does not allow us to achieve a separation between the effects of the common environment and assortative mating, since both these would contribute to the E_2' term. Therefore, we might prefer one of the path models as a more useful way of looking at the data.

The full genetical path models (models 11-14) showed us that the data are consistent with additive genetical variation. There was no reason to suppose, from comparing the likelihoods of model 11 with 12 and 13 with 14, that g was significantly different from 0.5 i.e. this path represents only additive effects. We also saw that any effect of cultural transmission was small and that there was no evidence (from comparing models 11 with 13 and 12 with 14) that the population was not in equilibrium.

Given that the path, w , and the genotype-environment correlations are so small, have we any reason to suppose that they are significantly

greater than zero i.e. is the effect of cultural transmission producing significant variation? We fitted models 15 and 16 with genetical variation and no assortative mating to test this possibility. Models 15 and 16 do not differ significantly, again confirming that $g = \frac{1}{2}$ and that genetical variation is additive. Thus in order to determine whether there is any significant effect of cultural transmission we compared models 14 and 16. It turns out the difference in likelihood between these models is small and that the maximum log likelihoods of the five parameter and more complex eight parameter model do not differ significantly. Thus, there is no evidence that variation produced by cultural transmission is needed in order to explain individual differences in Radicalism.

However, this does not mean that there is no common environmental component and so we fitted models in which we specified genetical variation, assortative mating a shared environment not dependent upon the parents. The likelihoods for these models are given in Table B63 next to models 17 and 18. Again there is no evidence that g differs from 0.5 and we consider that model 18 is the most appropriate of this pair. Using the likelihood ratio criterion we tested whether model 18 is more likely than model 16. It turns out that $\chi^2_1 = 1.6442$, which is not significant. Again, we have no evidence for significant between families environmental variation.

Thus, in the final analysis we can explain variation between individuals in their Radicalism scores in terms of unreliability of the scale of measurement, specific individual experiences and additive genetical variation. The between families component found using the twins can be attributed to the effects of assortative mating in the

population. The importance of assortative mating is emphasized by the magnitude of the marital correlation ($\mu = 0.3893$), which is close to that calculated from the data in Section 5, and by the correlation of 0.2636 between the genes of the parents.

Estimates of the means and total variance are also similar to those found previously. Since there is no genotype-environment covariance, the proportion of the total variation produced by additive genetical effects is given by h^2 . Thus additive variation accounts for 67.7% of the total variation and specific environmental variation for only 32.3%. These figures agree closely with those estimated in Section 6 from the twin data by assuming that the between families component could be explained purely in terms of assortative mating. We therefore have no evidence for cultural differences between families which cannot be explained in terms of their genotypes, and no evidence for significant cultural transmission. How the determination of man's cultural background affects variation cannot be studied in these data. We could turn to another trait to study this problem. Alternatively, more data collected on a larger sample of adopted individuals, might prove informative, since the value of $\beta = 0.2$ is large although not significant in this study.

5.5 The Final Model for Toughmindedness

The story for Toughmindedness is not so straightforward as that for Radicalism as we can see from Table B64, which summarises the models we have fitted and their corresponding likelihoods. The most likely model, which will act as our baseline model against which to compare

TABLE B 64: SUMMARY OF MODELS FOR TOUGHMINDEDNESS

<u>MODEL</u>	<u>PARAMETERS</u>	<u>LIKELIHOOD</u>
1	$\mu_m \mu_f v r$	1292.5851
2	$\mu_m \mu_f v r \mu$	1309.0122
3	$\mu_m \mu_f v p$	1263.5794
4	$\mu_m \mu_f v p \mu$	1271.9892
5	$\mu_m \mu_f v p e$	1310.6675
6	$\mu_m \mu_f v p e \mu$	1314.7409
7	$\mu_m \mu_f v_A g h w s \mu$	1329.1420
8	$\mu_m \mu_f v_A h w s \mu$	1327.0973
9	$\mu_m \mu_f v g h \mu$	1324.7638
10	$\mu_m \mu_f v h \mu$	1322.7811
11	$\mu_m \mu_f v g h \beta \mu$	1325.7574
12	$\mu_m \mu_f v h \beta \mu$	1324.8996

the adequacy of other models is model 7. In the case of Toughmindedness, the full non-equilibrium genetical path model, with g not equal to 0.5, is the most likely model with $L = 132.9.1420$. Model 8, where $g = \frac{1}{2}$, is the next most likely model, but using the likelihood ratio criterion we see that $\chi^2_1 = 4.0894$, $2\% < p < 5\%$, indicating that model 8 provides a significantly worse explanation of the data than model 7. Since the likelihoods of all the other models are lower than that of model 8, these too fail to explain the observed variation as well as model 7. A purely environmental path model cannot account for individual differences in Toughmindedness when we consider all the data jointly. Yet in the twin data, a simple environmental model adequately explained the observed variation. How can we account for this? In Section 8.4.7 we discussed how model 7 might be more likely than other models because it does not constrain equality of the total variances in parents, natural children and adopted children. This seems possible since the total variances are heterogeneous ($\chi^2_2 = 19.97$).

Another possibility is that variation is really all environmental, but we have specified the wrong model for the environment. Further work is needed to devise more sophisticated environmental models and test these. However, for the present we must conclude that this genetical model is the most appropriate for our data despite the fact that we detected no genetical variation in the twins. This model breaks the constraint that $g = \frac{1}{2}$, if genetical variation is additive. This may indicate non-additive effects and complex interactions in the data which were not detected in the twins. This seems feasible since detection of non-additivity using twin data is notoriously difficult (Eaves, 1972). It has also been shown in several cases (Eaves, 1977) that significant

non-additivity may be detected using family data which was not apparent for twin data. Thus on our present evidence the most likely model for Toughmindedness seems to be one in which there is genetical variation, additive and non-additive variation, assortative mating, and a substantial environmental component dependent on the parents, which suggests the possibility of cultural transmission. However, these are only tentative conclusions and cannot be taken seriously until further evidence has been collected. Environmental non-additivity, sex interactions or differences in environmental components between groups might provide as likely an explanation if we fitted a model including their effects.

SECTION 9: DISCUSSION

Our overall conclusion from this study of social attitudes confirms earlier results in that a simple picture emerges for Radicalism which is consistent with previous work, whereas Toughmindedness presents something of an enigma. There was no evidence for genetical variation or complex sex effects on the variances in the twin data for Toughmindedness and this led us to suggest that the trait assessed as Toughmindedness by the Wilson-Patterson Attitudes Questionnaire was not the same as that analysed by previous workers (Eaves and Eysenck, 1974; Hewitt 1974; Martin 1976; Eaves, 1977), whose results were fairly similar. Some evidence was found for this by examining the structure of the questionnaire used in the present study. Our trait of "Toughmindedness" clearly has a different mechanism producing differences between individuals than that of the earlier workers. A picture consistent over twin and adoption studies for the genetical and environmental determinants of this trait has not emerged. The twin data shows the importance of a between families environmental component but provides no evidence for significant genetical variation. The importance of the common environmental component is confirmed for all the data jointly and can be resolved in terms of a model of cultural transmission, since there is evidence for genetical variation when we consider the combined data. Clearly a lot more work needs to be done on Toughmindedness before we can be at all sure of the causes of variation. The trait needs to be defined more precisely, so that we can ascertain the differences between our trait and "Toughmindedness" as measured by previous workers. More family and adoption data is clearly needed in order to provide information on relationships about which we

know little at the moment. Then we can attempt to specify more realistic environmental models for comparison with those we have already tried. We can also explore further the suggestion we had from this study of non-additivity or complex interactions. We know, for example, that there were sex interactions with age which do not appear to be influencing our model fitting but which we would like to study in more detail. We could fit the model of Eaves (1977) which allows for the correlation between relatives to decline with age, following a simple decay curve. This might provide some leverage on the problem of sex interactions in Toughmindedness. It would also be interesting to fit dominance to family data, although dominance could not be detected in the twins. Its effects, or sex interactions might explain the non-additivity we have found. The analysis of Toughmindedness has thus left us with many questions and our main conclusion is that we have an interesting trait on which more work needs to be done.

Radicalism has provided far more clear cut results, which agree closely with those of previous workers. Estimates of specific environmental variation, additive genetical variation and a between families component, \hat{B} , are very similar to those obtained in older studies (see Eaves and Eysenck, 1974; Hewitt, 1974; Martin, 1976 and Eaves, 1977). Analogous models to the $E_1 D_R B$ model in twins were fitted to the adoption data and the combined data and it was found that twin and adoption studies were homogeneous as far as the E_1 , D_R and different E_2 parameters were concerned. Results for Radicalism are thus consistent over different questionnaires at different times and using different family groupings.

Fitting genetical path models to the data showed that the between families component, B , could be interpreted purely as a result of

assortative mating. There was no convincing evidence for environmental differences between families dependent upon the phenotype of the parents, and therefore, no cultural transmission, as defined by Eaves (1976b) or Cavalli-Sforza and Feldman (1973), was found. There was a suggestion that a common environment independent of the parents might be relevant, but its effect was not significant.

Once again, further work needs the collection of more data. In order to provide a more powerful test for a common environment independent of parental phenotype, more adopting parent-child, adopted-adopted child, adopted-natural child and natural sibling pairs are needed. However, other work on this data set would still be desirable despite its deficiencies. Having shown that there is no cultural transmission and that the between families component, \hat{B} , can be interpreted in terms of assortative mating, it would be interesting to fit Fisher's model of assortative mating to the data. It would also be useful to fit a genetical path model with no assortative mating to the data. It would also be useful to fit a genetical path model with no assortative mating but with an environmental covariance, although the results from Section 7, suggest that this would be less likely than the genetical model with assortative mating only. Again it would be relevant to look for non-additive effects such as dominance or age effects in view of the recent work of Eaves (personal communication). Another desirable addition to the present work would be to extend Eaves (1976b) model of cultural transmission to include the effects of assortative mating, which was unfortunately not within the scope of this study.

This study has also proved fruitful in extending the methodology for analysing human variation. The usual combination of maximum likelihood

estimation and pedigree analysis with path model techniques has proved a useful tool in analysing these data. The problems of unbalanced pedigrees discussed in Section 7 have been successfully overcome and maximum likelihood estimates of the parameters of complex models have been obtained, without losing any information by having to omit some types of pairs of individuals from the analysis because there were so few of them. However, the pedigree analysis approach still needs further work. Its chief disadvantage is in its lack of any test of the "goodness-of-fit" of the model. It is useful to be able to pick out the most likely of a series of models. But ultimately we want to be able to determine whether any given model gives an adequate account of the observed variation. Otherwise we may never know about certain important components of variation in our data. Suggestions for ways in which a test of significance might be devised were given in Section 7.

When satisfactory tests of significance have been formulated for the pedigree analysis approach, it should prove the ideal tool for analysing human variation. The need for balanced family structures will disappear and advances in the genetics of human behaviour will no longer have to rely on "nature's experiments", such as twins, which may turn out to be special cases and mislead us about the causes of variation in the population as a whole. The use of pedigree analysis will allow data to be usefully collected on families as they naturally occur, no matter what their structure. Thus random sampling of the variation in any population will be easier and collection of large bodies of data will be practicable and cheaper since we will no longer be looking for rare individuals. Thus, we will be able to make powerful tests of many hypotheses for a variety of different traits and arrive at unequivocal answers about the causes of human variation.

PART C
A STUDY OF POWER AND BIASES
IN HUMAN BEHAVIOUR GENETICS

INTRODUCTION

There are several reasons why the work to be discussed in the final part of this thesis was undertaken. Problems which arose during the analysis of the twins studies, particularly the Georgia Twin Study, suggested that it would be useful to know, before embarking on a long and expensive programme of data collection, the optimal experimental design and the number of individuals needed to detect effects of interest and to discriminate between alternative hypotheses/ causes of variation ^{about} in the population. Where the optimal experimental design cannot be used, because of time, expense or the rarity of the individuals required or when analysing data collected by others, then effects of interest may be confounded, may not be statistically significant or may, if we wrongly accept an inappropriate model, be biased by other components of variation than those included in the wrong model. In such cases, it would be desirable to know precisely the biases which may occur.

These problems have not, until recently received widespread attention, but have been considered by members of my own department in experimental organisms (Kearsey, 1970; Mather, 1974) and in man (Eaves, 1969, 1970, 1972, 1977; Martin, 1976).

This work continues that above by considering the power of the test for detecting certain effects and discriminating between alternative hypotheses and the precise estimation of biases introduced where an inappropriate model is accepted.

In the Georgia Twin Study, effective discrimination between the simple genetical and simple environmental models could not be made for several measures of ability and it was suggested that the sample size

was too small to make rejection of the simple environmental model possible given the heritabilities of these particular tests. The genetical model was preferred for other tests, also purporting to measure ability, because an environmental model was unable to explain variation. This raises the problem of how big a sample must be in order to reject a false model at a particular level of probability with a given a given degree of confidence. The power of the test for rejecting false models is discussed by Martin (1976), Eaves (1977) and Eaves, Last, Martin and Jinks (1977), in relation to the classical twin study of monozygotic and dizygotic twins reared together. Martin (1976) assumed various proportions of each type of twin, and generated four statistics (the between and within pairs mean square for MZ and DZ twins), for a series of "populations" with different causes of variation. He considered populations with different combinations and amounts of the following parameters: E_1 , E_2 , D_R , M (additive variance produced by assortative mating) and H_R . Then, by fitting false models to these populations he obtained the non-centrality parameter of the non-central chisquare distribution of the observed deviations, and from this was able to calculate the number of pairs of twins needed to reject these false models, at the 5% level in 95% of cases, using the chisquare criterion.

Two of his calculations were relevant in the context of the Georgia Twin Study. When he generated mean squares assuming that $E_1 = E_2 = 0.5$ (using a total variance of 1.0) and fitted the $E_1 D_R$ model to these "data", he found that 430 pairs of twins (i.e. 215 pairs each of MZ and DZ twins) were needed before the $E_1 D_R$ model would be rejected at the 5% level in 95% of cases. Conversely, when the $E_1 E_2$

model was fitted to data assuming that $\frac{1}{2}D_R = E_1 = 0.5$, he found that 640 pairs were needed for rejection of the false model. The Georgia Twin Study contained 364 pairs of twins. Therefore, it could have been predicted that discrimination between the two simple models would be difficult if the heritability of any of the tests was approximately 0.5. Indeed, for those tests where both the E_1E_2 and E_1D_R models fitted the data, the narrow heritability obtained by fitting the E_1D_R model was about 0.5. Thus, since one of the main aims of the Georgia Twin Study was to detect and compare genetical variation in Blacks and Whites, more data should have been collected.

Obviously then, before embarking on any major study, it would be useful to know the results of power calculations, such as those performed by Martin, so that data on an adequate number of individuals could be collected to be reasonably certain of discriminating between the hypotheses that the study is designed to test. Collection of data on fewer individuals than those indicated by the power calculations would clearly be a waste of time and resources.

An allied problem to that of discriminating between alternative hypotheses, concerns the power of the test for detecting particular effects. Given that a particular effect produces variation in a population, the question arises as to how many individuals would be needed for that effect to be significant at the 5% level in 95% of cases in any given experimental design. Kearsey (1970) calculated the sample size needed for the detection of dominance with four different crossing schemes that may be used in experimental organisms, in order to determine the most efficient design. Similar work by Eaves (1972) compared the power of the test for detecting dominance in man in three

different data sets which in theory allow the separation of additive and non-additive components of variation. He showed that sample sizes needed for the detection of dominance variation in human data, using second degree statistics are considerably larger than those normally employed.

Problems of power in a study of MZ and DZ twins reared together, in which the zygosity was not known, were considered by Eaves and Jinks (1972). In this study, the intraclass correlations were determined using the opposite-sex pairs (to provide an estimate of DZ twin correlation) and the known proportion of the two types of twin. They showed that about three times as many pairs of twins would be needed to obtain the same power as in a sample where the zygosity was determined directly using genetic markers or a questionnaire. The methods used by them to determine the power of the test for a genetical component, based on the difference between transformed correlations of MZ and DZ twins, were used in the Georgia Twin Study to determine the number of pairs needed to reject the null hypothesis that there is no genetical component of variation at the 5% level in 95% of cases, given different levels of broad heritability and in the presence and absence of assortative mating. This number was greater than the sample size of the Georgia Twin Study (364 pairs) unless the broad heritability was 0.8 or higher, no matter what the mating system. This showed that the failure to detect significant genetical variation for several measures of ability could not be taken as proof of its absence since the power of the test was too low for those tests whose MZ intraclass twin correlations were below 0.8.

In more recent work, Klein (1974) presented Tables of the power for estimates of heritability and "genetic correlation" obtained from four relationships: offspring-mid-parent, offspring-single parent, full sibs and half sibs. He also showed that large samples are required for the comparison of heritabilities between populations, estimated from each of these relationships.

The problems of the power for rejecting false hypotheses and for detecting genetical and environmental components of variation will be discussed in the following pages. However, the main purpose of the analyses, was to consider the biases that will be introduced into parameter estimates when a false model is wrongly accepted as an adequate explanation of variation. This is likely to happen when the power of the test for detecting certain effects present in a population is too low.

Eaves (1970) considered this problem for the case of dominance, since his power calculations showed that the detection of dominance is likely to be difficult, unless sample sizes are large. Given that dominance is present in a population, he asked how dominance will bias the estimates obtained from fitting false models, which may be adequate to account for the observed variation. He showed, for example, that in studies of twins reared together, when the $E_1 E_2 D_R$ model is fitted to a population in which E_2 and H_R are both present, then

$$\hat{D}_R = D_R + \frac{3}{4} H_R$$

and $\hat{E}_2 = E_2 - \frac{1}{8} H_R$

In studies of twins reared together, it is not possible to separate the contributions of E_2 and dominance. Thus, fitting an $E_1 D_R H_R$ model, when E_2 and H_R are present, then:

$$\hat{D}_R = D_R + E_2$$

and

$$\hat{H}_R = H_R - 8E2.$$

Thus, E_2 and H_R tend to balance one another and if both are present in a population negative estimates of E_2 or H_R may be obtained depending on their relative magnitude. Such studies of biases can obviously prove useful in interpreting the possible causes of biologically meaningless results.

Mather (1974) derived expectations for the components of variation in terms of three types of epistasis and showed how epistatic interactions will affect estimates of D_R and H_R when allele frequencies are not equal.

The work of Eaves and Mather emphasises how two different sources of non-additive variation can bias estimates of genetical and environmental effects. Here, the biases introduced by genotype-environment interaction (GXE) and genotype-environment covariation (CovGE) will be specified. There is a substantial literature claiming the intractability of GXE and CovGE (e.g. Block and Dworkin, 1974a, b; Layzer, 1974; Linn, 1974; Moran, 1973). However, the specification of these effects, their analysis and their biological significance is still the subject of much confusion. The theory and analysis of GXE in species other than man has been the subject of much research (e.g. Haldane, 1946; Mather and Jones, 1958; Bucio-Alanis et al, 1969; Jinks and Perkins, 1970; Jinks and Connolly, 1975; Mather and Caligari, 1975) and attempts have been made to specify empirically CovGE in man (e.g. Cattell, 1960; Loehlin, 1965). Jinks and Fulker (1970) systematically treat the principles underlying the detection and analysis of GXE and CovGE in man. More recent work by Eaves (1976a,b) has provided a satisfactory theoretical formulation of different sources of CovGE.

However, a number of authors suggest that GXE and CovGE preclude any worthwhile analysis of individual differences in human populations (e.g. Moran, 1973; Layzer, 1974; Lewontin, 1974; Feldman and Lewontin, 1975). They express the view that GXE and CovGE are important in determining individual differences in behaviour, but cannot be detected and separated from other components of variation. Thus, attempts to estimate and interpret other population parameters may be seriously in error. It is suggested that the biases introduced generally lead to inflation of heritability estimates. The problems of detecting and estimating genotype-environment interaction and genotype environment covariation have been adequately answered in the work mentioned above. Whether GXE and CovGE are widespread and produce a substantial amount of variation in behaviour in human populations can only be determined by practical investigation of a number of traits using the methods already available. In many cases, the presence of GXE and CovGE will lead to failure of simple models. However, the amount of systematic GXE and CovGE which might remain undetected and the biases this would introduce into parameter estimates can be investigated theoretically.

Plomin et al (1977) make some attempt to assess how GXE and CovGE may bias estimates of genetical and environmental components of variation in twin data, but not in adoption data. However, CovGE produces biases in both types of data. The weakness of their study is that they only suggest what biases may occur. They make little attempt to quantify the biases or deal with the problem in a systematic way.

In order to satisfy criticisms that GXE and CovGE seriously bias parameter estimates and lead to overestimation of the heritability, we will attempt a systematic treatment of the problems discussed by Plomin et al. We will determine under what conditions GXE and CovGE will remain

undetected by performing a series of power calculations and also calculate precisely how different parameters will be biased in a variety of situations. Similar analyses will be performed for variation produced by additive effects and dominance in order to confirm and extend earlier work (Eaves, 1969, 1970, 1972; Martin, 1976).

The results of this study, which are presented in a series of reference Tables in Appendix G, are too extensive to be presented in detail. The reader may extract from the Tables the information most pertinent to his particular problem or interest. However, those findings that are relevant to the arguments about whether GXE and CovGE preclude worthwhile analysis of individual differences in human populations will be discussed.

Part of this work is included in a paper which discusses in detail problems of non-additivity and genotype-environment covariance and attempts to provide a comprehensive framework of theory and method in which these and other contributions to individual differences can be critically assessed. This paper (Eaves, Last, Martin and Jinks, 1977) is included as Appendix F.

SECTION 1: THE "DATA" SETS

1

THE EXPERIMENTAL DESIGN

In order to determine the power for detecting genetical and environmental effects, the power for rejecting false hypotheses and the biases produced by fitting the "wrong" model to particular hypothetical populations, we will consider only one experimental design. In practice a variety of designs are used and ideally we would like to repeat the work to be described here for a variety of the most commonly used designs.

The experimental design adopted here is rather more demanding than those usually employed in studies of human behaviour. It has the disadvantage that it requires certain rare types of individual e.g. monozygotic twins reared apart, and is, therefore, unlikely to be used in practice. However, it is extremely useful in our context because it allows us to separate all effects of interest and, to make powerful tests for them.

The mean squares from the ideal study to which we shall fit models are derived from the following individuals:

Monozygotic twins reared together;

Dizygotic twins (full-sibs) reared together;

Monozygotic twins reared apart;

Dizygotic twins (full-sibs) reared apart;

Unrelated individuals reared together; and

Singletons, reared by their natural parents.

Eleven mean squares can be derived from this study i.e. a between and within pairs mean square for each of the twin types and the total variance of singletons. We could, therefore, fit models including up to ten

parameters and still have one degree of freedom left for testing the adequacy of the model. Thus the complexity of the model we can fit will not be limiting and, in fact, the most complicated models fitted were those involving five parameters. In the classical twin study considered by Martin (1976), only three parameters can be fitted and components of variation such as dominance and the common environmental effect cannot be separated.

In order to specify certain models, it is necessary to have information about the rearing conditions of those related individuals who have been reared apart. For the purposes of this investigation, we will assume that such individuals have been reared as singletons in randomly chosen foster homes. Eaves et al (1977) discuss the effect of placement on family resemblance.

2.1 The Populations

The analyses will be performed for a series of populations with different sources of environmental and genetical variation. There are five main areas of interest: additive effects, dominance, genotype-environment interaction, genotype-environment covariation produced by cultural transmission (Eaves, 1976b) and sibling effects (Eaves, 1976a). Each of these effects will be considered in combination with other sources of variation. The total of fourteen populations is given in Key B in Appendix G. Within each of the five main areas, the causes of variation are of increasing complexity.

2.2 General Considerations for Generating the Populations

Each population type may vary considerably in the proportion of the total variation accounted for by each of its parameters. We will consider a series of possibilities for each population, in order to demonstrate how power changes depending upon the relative magnitudes of different components of variation.

The expected values of the second degree statistics obtained from the study described above will be produced for a variety of systems of causation, which may be represented by various combinations of nine parameters. The contributions of these parameters to the mean squares are given in Table C1.

TABLE C1: CONTRIBUTION OF POPULATION PARAMETERS TO ELEVEN MEAN SQUARES

	MEAN SQUARES		EXPECTATIONS						
	E_1	E_2	D_R	M	H_R	I	C	D_R''	D_R'
Between MZT	1	2	1	1	$\frac{1}{2}$	1	2	1	2
Within MZT	1
Between DZT	1	2	$\frac{3}{4}$	1	$\frac{5}{16}$	$\frac{3}{4}$	2	$\frac{3}{4}$	$1\frac{1}{2}$
Within DZT	1	.	$\frac{1}{4}$.	$\frac{3}{16}$	$\frac{1}{4}$.	$\frac{1}{4}$	$-\frac{1}{2}$
Between MZA	1	1	1	1	$\frac{1}{2}$	$\frac{1}{2}$.	.	.
Within MZA	1	1	.	.	.	$\frac{1}{2}$.	.	.
Between DZA	1	1	$\frac{3}{4}$	1	$\frac{5}{16}$	$\frac{1}{2}$.	.	.
Within DZA	1	1	$\frac{1}{4}$.	$\frac{3}{16}$	$\frac{1}{2}$.	.	.
Between UT	1	2	$\frac{1}{2}$	1	$\frac{1}{4}$	$\frac{1}{2}$.	$\frac{1}{2}$	1
Within UT	1	.	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{1}{4}$	$\frac{1}{2}$.	$\frac{1}{2}$	-1
Singletions	1	1	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{1}{4}$	$\frac{1}{2}$	1	.	.

In order to produce numerical expectations for the eleven mean squares in any population, we must specify values for its parameters. These are arbitrary, but some sets of values are more consistent with the existing body of information about the causes of variation in human populations. In all cases, we will start with a value of 225 for the total variance (σ^2_T). Certain effects will lead to a change in σ^2_T when we fix the population values (e.g. CovGE produced by sibling effects). We will consider two general levels of broad heritability of 0.5 and 0.9, which roughly correspond to values found for personality traits and social attitudes on the one hand and measures of ability on the other. Thus the total environmental variation (E) will be either

$$E = \frac{1}{2} \times 225 = 112.5$$

or

$$E = \frac{1}{10} \times 225 = 22.5$$

Even in cases where genotype-environment covariance leads to a change in σ^2_T , these values for E will be used. The contributions of E_1 and E_2 to E are determined empirically for any real set of data. However, we will assume that $E_1 = E_2$ throughout so that the only possible values for E_1 and E_2 are:

$$E_1 = 112.5 \text{ or } E_1 = E_2 = 56.25$$

and

$$E_1 = 22.5 \text{ or } E_1 = E_2 = 11.25$$

The particular values taken by the other population parameters, vary depending on the particular combination of causes of variation, and will be described for each population in turn. The values of the parameters are summarised in the Tables in Appendix G.

2.3 Population 1: $E_1 D_R$

In the simplest, random mating population, there is specific environmental variation and additive genetical variation. Two cases only will be considered, according to the general criteria given above.

These are:

$$a \quad \frac{1}{2}D_R = E_1 = 112.5$$

$$b \quad \frac{1}{2}D_R = 9E_1 = 202.5 \quad \text{i.e. } E_1 = 22.5$$

2.4 Population 2: $E_1 E_2 D_R$

In this population, there is additive gene action and environmental variation within and between families. When $h_B^2 = 0.5$, we have $\frac{1}{2}D_R = 112.5$ and $E_1 = E_2 = 56.25$. In the second case, $h_B^2 = 0.9$ and we have $\frac{1}{2}D_R = 202.5$ and $E_1 = E_2 = 11.25$.

2.5 Population 3: $E_1 D_R^M$

There is specific environmental variation and additive genetical variation as in Population 1, but now there is also additive variation produced by assortative mating. As in population 1, we will consider two cases where

$$a. \quad \frac{1}{2}D_R = E_1 = 112.5$$

$$\text{and } b. \quad \frac{1}{2}D_R = 9E_1 = 202.5$$

Assortative mating leads to an increase in additive genetical variance until at equilibrium, the contribution of the additional variation is

given by $\frac{1}{2}(A/(1-A))D_R$, where A is the correlation between the additive genetical deviations of spouses. By analogy with D_R , we will define M as $(A/(1-A))D_R$, so that the contribution of assortative mating to σ_T^2 is $\frac{1}{2}M$.

Assuming Fisher's model of assortative mating (Fisher, 1918), $A = \mu h^2_N$, where μ is the correlation between the phenotypes of spouses. In order, to generate the populations, we will assume values for A which are likely to represent values found for measures of ability (Vandenberg, 1972) and lie within the range of values found for other behavioural traits.

The values of A chosen were 0.25 and 0.45 for the two cases. From these values of A, M was found as $(A/(1-A))D_R$ which was 75.0 when $\frac{1}{2}D_R / \sigma_T^2 = E_1$; and 331.4 when $\frac{1}{2}D_R / \sigma_T^2 = 9E_1$. This procedure enables reasonable values of M to be calculated for given D_R , E_1 and A, remembering that $A = h^2_N \mu$ at equilibrium. We may calculate equilibrium values of h^2_N , μ and σ_T^2 . We can find $\sigma_T^2 = E_1 + E_2 + \frac{1}{2}D_R + \frac{1}{2}M = 262.5$ for case 1 and $\sigma_T^2 = 390.7$ for case 2.

Thus assortative mating can lead to a substantial increase in variation.

We calculate $h^2_N = \frac{1}{2}D_R + \frac{1}{2}M / \sigma_T^2$, which gives us:

- a. $h^2_N = 0.57$
- b. $h^2_N = 0.94$

The marital correlation can now be estimated as $\mu = A/h^2_N$ to give:

- a. $\mu = 0.44$
- b. $\mu = 0.48$

The final parameters for these populations are summarised in Table C2.

TABLE C2: PARAMETERS OF SIMPLE POPULATIONS WITH ASSORTATIVE MATING

PARAMETER	POPULATION			
	3a	3b	4a	4b
E_1	112.5	22.5	56.25	11.25
E_2	-	-	56.25	11.25
D_R	225.0	405.0	225.00	405.00
M	75.0	331.4	75.00	331.36
σ_T^2	262.5	390.7	262.50	390.68
h_N^2	0.57	0.94	0.57	0.94
A	0.25	0.45	0.25	0.45
μ	0.44	0.48	0.44	0.48

2.6 Population 4: $E_1 E_2 D_R M$

This is similar to the previous population, but we now have two sources of environmental variation. Since M is defined purely in terms of D_R and A, the only parameters which differ between this population and the previous population are E_1 and E_2 . The two cases where $h^2_N = 0.57$ and $h^2_N = 0.94$ are summarised in Table C2.

2.7 Population 5: $E_1 D_R H_R$

This population contains specific environmental variation and additive genetical variance, as in all previous populations, but now contains dominance. We will consider two levels of heritability and two levels of dominance to provide four combinations. As before when $h^2_B = 0.5$, $E_1 = 112.5$ and when $h^2_B = 0.9$, $E_1 = 22.5$.

We will consider the cases where dominance is complete i.e. where the ratio, $\sqrt{D_R/H_R}$ (i.e. dominance ratio when allele frequencies are equal) is 1 and where dominance is intermediate. For intermediate dominance, a dominance ratio of 0.5 is used.

In order to perform the calculations, we let $\sqrt{R} = \sqrt{D_R/H_R}$.

Therefore, H_R is given by:

$$H_R = D_R \cdot R^2$$

The total genetical variance, $\sigma_G^2 = \frac{1}{2} D_R + \frac{1}{4} H_R$. This may be partitioned into components due to additive genetical and dominance variation:

$$D_R = \frac{\sigma_G^2}{\frac{1}{2} + \frac{1}{4} R^2}$$

$$H_R = D_R \cdot R^2$$

For $h_B^2 = 0.5$, given equal allele frequencies, a dominance ratio of 1 will give $D_R = H_R = 150$ and a dominance ratio 0.5 gives $D_R = 200$ and $H_R = 50$. In each case the contribution of D_R and H_R to the total variation, given by $\frac{1}{2}D_R + \frac{1}{4}H_R$, is 112.5. Similarly, when $h_B^2 = 0.9$, we find $D_R = H_R = 270$ for a dominance ratio of 1 and $D_R = 360$ with $H_R = 90$ for a dominance ratio of 0.5.

2.8 Population 6: E_1 E_2 D_R H_R

This is similar to the previous population, but there is now between families environmental variation. The calculations involved in obtaining D_R and H_R for the two levels of heritability and dominance ratio are identical to those in 2.7, yielding the same values as before. The only difference is that now when $h_B^2 = 0.5$, $E_1 = E_2 = 56.25$ and when $h_B^2 = 0.9$, $E_1 = E_2 = 11.25$.

2.9 Population 7: E_1 D_R H_R M

In this population both dominance and assortative mating are present. The values for D_R and H_R are calculated as in 2.7, and are, identical to those given for the $E_1 D_R H_R$ population for the four cases. Variation produced by assortative mating is added to the total variation as in 2.5. Calculating M as before, we find four different values for M:

- a. $M = 30.00$ when $E_1 = 112.5$ and $R = 1$
- b. $M = 115.71$ when $E_1 = 22.5$ and $R = 1$
- c. $M = 57.14$ when $E_1 = 112.5$ and $R = \frac{1}{2}$
- d. $M = 240.00$ when $E_1 = 22.5$ and $R = \frac{1}{2}$

(using $A = 0.156, 0.239, 0.197, 0.261$, respectively).

This gives new values of σ_T^2 of 240.00, 282.86, 253.57 and 345.

The true narrow and broad heritabilities are, therefore:

	h_N^2	h_B^2
a.	0.375	0.531
b.	0.682	0.920
c.	0.507	0.556
d.	0.870	0.935

The values of the marital correlation in the four populations respectively are: 0.416, 0.350, 0.389, and 0.300).

2.10 Population 8: E_1 E_2 D_R H_R M

This population has identical values for D_R , H_R and M as the previous population. However, at the lower and higher levels of heritability, $E_1 = E_2 = 11.25$ and $E_1 = E_2 = 56.25$ respectively.

2.11 Population 9: E_1 E_2 D_R I

This population and the two that follow contain genotype-environment interaction, which is specified using the parameter "I".

This population is randomly mating and there is additive gene action and environmental variation within and between families. Environmental differences between families are independent of genetical differences, but the two sources of variation interact, producing variation due to the interactions of D_R and E_2 . The contribution of GXE to the total variance is $\frac{1}{2}I$. Interactions involving E_1 are not included since these are inevitably confounded with estimates of E_1 .

We will consider the two cases where $E_1 = E_2 = 56.25$ and $E_1 = E_2 = 11.25$. The remaining 50 per cent of the variation in the former case and 90 per cent in the latter case will be assigned to the additive effects of genes and their interaction with environmental differences between families i.e. $\frac{1}{2}D_R + \frac{1}{2}I = 112.5$ and 202.5 respectively. Two levels of interaction will be used. In experimental organisms, it is seldom found that more than 20 per cent of the variation can be attributed to GXE. Therefore, values of 20 per cent and 10 per cent of the total variation will be used for GXE in order to examine its effect in extreme and less extreme cases. Ten per cent of the total variation is 22.5 and twenty per cent is 45. Therefore, values of 45 and 90 were given to I. D_R , which is given by $2 \times (225 - (E_1 + E_2) - \frac{1}{2}I)$, takes the values 180 and 360 when $\frac{1}{2}I$ accounts for 10 per cent of the variation and $h_B^2 = 0.5$ or 0.9 where $h_B^2 = \frac{\frac{1}{2}D_R + \frac{1}{2}I}{\sigma_T^2}$.

When $\frac{1}{2}I$ accounts for 20 per cent of the variation, D_R takes the values 135 and 315 respectively.

2.12 Population 10: $E_1 E_2 D_R I M$

Both GXE and assortative mating are found in this population. The

four sets of parameter values involving E_1 , E_2 , D_R and I which were calculated in the last section are again used. Then variation produced by assortative mating is calculated and added to the total variance as described in 2.5.

Values of A of 0.2, 1.15, 0.4 and 0.35 are used. We can, therefore, calculate M as $(A/(1 - A)) D_R$, which gives values of 45.00, 23.82, 40.00 and 169.62. Therefore, the total variances become: 247.5, 236.91, 345 and 309.81. The values for h^2_N in this population are calculated as:

$$h^2_N = \frac{1}{2}D_R + \frac{1}{2}M/\sigma_T^2$$

This gives values of: 0.45, 0.34, 0.87 and 0.78. If we define the broad heritability as:

$$h^2_B = \frac{\frac{1}{2}D_R + \frac{1}{2}I + \frac{1}{2}M}{\sigma_T^2}$$

we obtain values: 0.55, 0.53, 0.93 and 0.93. The marital correlations given as $\mu = A/h^2_N$ become: 0.89, 0.88, 0.92 and 0.90.

2.13 Population 11: E_1 E_2 D_R H_R I

In this population we may vary the broad heritability, the dominance ratio and the amount of GXE interaction. Using $h^2_B = 0.5$ or $h^2_B = 0.9$, dominance ratios of 1 and $\frac{1}{2}$ and GXE accounting for 10 or 20 per cent of the total variation yields eight possible situations. These are given in Table 9B of Appendix G.

In order to generate the population values the following steps were taken:

1. Values of E_1 and E_2 were fixed at either $E_1 = E_2 = 56.25$ or $E_1 = E_2 = 11.25$. This leaves 112.5 or 202.5 to be assigned to the remaining sources of variation.
2. Either 10 per cent or 20 per cent of the remaining variation was assigned to $\frac{1}{2}I$, to produce values of I of 45 and 90 respectively. Subtracting these from the remaining variation leaves 90 for $E_1 = E_2 = 56.25$ when $\frac{1}{2}I = 22.5$ and 67.5 when $\frac{1}{2}I = 45$; and 180 for $E_1 = E_2 = 11.25$ when $\frac{1}{2}I = 22.5$ and 157.5 when $\frac{1}{2}I = 45$.
3. The remaining variation is partitioned between D_R and H_R for the two dominance ratios as described in 2.7. This produces eight pairs of values for D_R and H_R : 120, 120; 160, 40; 90, 90; 120, 30; 240, 240; 320, 80; 210, 210; 280, 70; where the dominance ratio changes fastest, then the amount of GXE and then finally the broad heritability. This is made clear in Table 9B of Appendix G.

2.14 Population 12: E_1 E_2 D_R C

This population contains environmental variation within and between families, additive genetical variation and CovGE arising as a result of the cultural impact of parents on their offspring. Earlier work (Cattell, 1960; Loehlin, 1965) made no attempt to specify a theoretical basis for the causes of CovGE, merely demonstrating the contributions of the empirical parameters, E_2 and CovGE, to the total variation. Eaves (1976a, b) has described several mechanisms by which CovGE may arise. One mechanism is cultural transmission (Eaves, 1976b) whereby phenotypic variation in the parents is perpetuated culturally as well as genetically in the offspring generation. The parameters E_2 and CovGE can thus be reformulated:

$$E_2 = \left(\frac{2b^2}{1-2b^2} \right) \left[\left(\frac{1+b}{1-b} \right) \frac{1}{2} D_R + E_1 \right]$$

and

$$2\text{CovGE} = \frac{2b}{1-b} \left(\frac{1}{2} D_R \right) \text{ for } |b| < \frac{1}{2}$$

where b is the regression of offspring family environment on parental phenotype. The symbol "C" is used to denote 2CovGE throughout. We consider only the simplest population where E_1 , E_2 , D_R and C are present. Thus, common environmental effects not dependent upon the parents are excluded in these analyses, but could occur in principle.

Two possibilities are considered for the values of D_R and E_1 . We let $\frac{1}{2}D_R = 2E_1 = 112.5$ or else $\frac{1}{2}D_R = 2E_1 = 202.5$, corresponding to narrow heritabilities of 0.67 and 0.95, in the absence of cultural transmission. If we now assume that cultural transmission is entirely responsible for common environmental effects, values for E_2 and CovGE can be calculated if the magnitude of b is fixed. We chose to consider values of b which were low ($b = 0.1$) and intermediate ($b = 0.25$). For $b = 0.1$, we get $E_2 = 61.61$ and $C = 150.00$ when $\frac{1}{2}D_R = 2E_1 = 112.50$ and $E_2 = 98.04$ and $C = 270.00$ when $\frac{1}{2}D_R = 2E_1 = 202.50$. Similarly we find $E_2 = 6.76$ and $C = 50.00$ when $\frac{1}{2}D_R = 2E_1 = 112.50$ and $E_2 = 10.33$ and $C = 90.00$ when $\frac{1}{2}D_R = 2E_1 = 202.50$.

2.15 Population 13: E_1 D_R D_R'' D_R'

Populations 13 and 14 both consider another source of genotype-environment covariance, namely sibling effects. (Eaves, 1976a). The genotype-environment covariance in this instance arises because the phenotypes of siblings form a part of the environment of their co-siblings

In population 13, we consider a simple system in which all gene effects are additive and all the between families environmental component is due to the genetical covariance between members of a sibling pair. The total variance of singletons is thus: $\sigma^2_S = \frac{1}{2}D_R + E_1$, since there is no variation due to sibling effects in individuals reared alone. The total variance of singletons is 225 and we will consider two levels of heritability. When $h^2_N = 0.5$, $E_1 = 112.5$ and $D_R = 225.0$. For $h^2_N = 0.9$, $E_1 = 22.5$ and $D_R = 405.0$. Variation produced by sibling effects must now be specified. Eaves (1976a) uses two parameters to summarise this variation. These are:

- D_R'' - the variation produced by the contribution of the additive genetical deviations of siblings to the environment of their co-siblings (the "genetic environmental" variance due to sibling effects) and
- D_R' - the covariance between genotype and environment produced by the contribution of siblings phenotypes to the environments of their co-siblings.

Table C1 shows the contribution of D_R'' and D_R' to the mean squares for the hypothetical experiment described earlier, which depend upon the degree of relationship between members of the pair contributing to a particular statistic. We may contrast this with the situation when E_2 and CovGE are specified empirically.

For each level of heritability, we will consider both $D_R'' = D_R$ and $D_R'' = \frac{1}{2}D_R$. The specification of D_R' is more difficult. For the purpose of these simulations, we will define

$$\rho_{ge} = D_R' / \sqrt{(D_R D_R'')}$$

Since D_R' is in effect a measure of association between the direct effects of genes on an individual's phenotype and their indirect effect, mediated through the environment, on the phenotype of a sibling.

ρ_{ge} is the proportion of loci having both direct effects on the phenotype and indirect effects on the phenotype of siblings, under certain conditions stated by Eaves et al (1977). Values of $\rho_{ge} = 1.0$ and $\rho_{ge} = 0.5$ were used in this study. We now have two variables for each heritability level. When $h_N^2 = 0.5$. $D_R = 225.0$ and D_R'' takes either the value 225.0 or 112.5. For each of these possibilities D_R' may take two values depending on ρ_{ge} . Thus we have:

$$\begin{array}{ll}
 \text{a. } D_R = D_R'' = D_R' = 225 & \left. \begin{array}{l} \\ \end{array} \right] \rho = 1 \\
 \text{b. } D_R = 2D_R'' = 225; \quad D_R' = 159.1 & \left. \begin{array}{l} \\ \end{array} \right] \rho = 1 \\
 \text{c. } D_R = D_R'' = 2D_R' = 225 & \left. \begin{array}{l} \\ \end{array} \right] \rho = \frac{1}{2} \\
 \text{d. } D_R = 2D_R'' = 225; \quad D_R' = 79.55 & \left. \begin{array}{l} \\ \end{array} \right] \rho = \frac{1}{2} \\
 \text{e. } D_R = D_R'' = D_R' = 405 & \left. \begin{array}{l} \\ \end{array} \right] \rho = 1 \\
 \text{f. } D_R = 2D_R'' = 202.5; \quad D_R' = 286.38 & \left. \begin{array}{l} \\ \end{array} \right] \rho = 1 \\
 \text{g. } D_R = D_R'' = 2D_R' = 405 & \left. \begin{array}{l} \\ \end{array} \right] \rho = \frac{1}{2} \\
 \text{h. } D_R = 2D_R'' = 405; \quad D_R' = 143.19 & \left. \begin{array}{l} \\ \end{array} \right] \rho = \frac{1}{2}
 \end{array}$$

$h_N^2 = 0.5$

$h_N^2 = 0.9$

These values assume that the CovGE is positive i.e. that there is co-operation and the high performance of one sib produces an environmental effect enhancing performance of a co-sib. The converse situation of competition is also possible in which the CovGE is negative and the high performance of one sib is achieved at the cost of another. In this case, the same absolute values for $E_1 D_R$, D_R'' are D_R' are used, but D_R' is now negative. This gives a total of sixteen possible situations for a population in which $E_1 D_R$, D_R'' and D_R' are present (see Table 11B).

2.16 Population 14: $E_1 E_2 D_R D_R'' D_R'$

This population is similar to the previous one, except that we have now introduced environmental variation between families. The values of D_R , D_R'' and D_R' are identical to those used previously, but now $E = E_1$ is replaced by $\frac{1}{2}E = E_1 = E_2$. Thus $E_1 = E_2 = 56.25$ when $h^2_N = 0.5$ and $E_1 = E_2 = 11.25$ when $h^2_N = 0.9$. The parameters of these populations are given in Table B12 in Appendix G.

2.17 Generating the Mean Squares from the Populations

In order to proceed, we must now generate the eleven mean squares which could be derived in our hypothetical experiment for each situation for each population type. This involves a considerable number of sets of mean squares, but the procedure followed is the same in each case. We will illustrate this by reference to the simplest population ($E_1 D_R$), when $h^2_N = 0.5$.

The vector of parameters used to generate the statistics is in this case:

$$\begin{pmatrix} E_1 \\ D_R \end{pmatrix} = \begin{pmatrix} 112.5 \\ 112.5 \end{pmatrix}$$

The expected values of the statistics which can be derived from this population in our experiment are obtained by post multiplying the model matrix which can be derived from the appropriate columns of Table C1 by this vector of population parameters:

$$\begin{pmatrix} 1 & 1 \\ 1 & 0 \\ 1 & \frac{3}{4} \\ 1 & \frac{1}{4} \\ 1 & 1 \\ 1 & 0 \\ 1 & \frac{3}{4} \\ 1 & \frac{1}{4} \\ 1 & \frac{1}{2} \\ 1 & \frac{1}{2} \\ 1 & \frac{1}{2} \end{pmatrix} \times \begin{pmatrix} 112.5 \\ 112.5 \end{pmatrix}$$

For example, this produces the first expected mean square for MZT as:

$$\begin{aligned} MS_{bMZT} &= E_1 + D_R \\ &= 112.5 + 112.5 \\ &= 225 \end{aligned}$$

and the within pairs mean square for MZT as:

$$\begin{aligned} MS_{wMZT} &= E_1 + (0 \times D_R) \\ &= 112.5 \end{aligned}$$

The mean squares for the wide variety of situations considered in this study are not given, but can easily be derived for any situation of interest by the procedure used above, using the appropriate vector of population parameters which can be found from Tables 1B to 12B in Appendix G and the model matrix derived from the appropriate columns of Table C1.

SECTION 2: THE ANALYSES

1. FITTING MODELS

The procedures to be described in this Section are general and will be applied to each of the "data sets" generated in turn.

Population 1 ($E_1 D_R$) will be used to illustrate the analyses. The case where $E_1 = \frac{1}{2} D_R = 112.5$ will be considered.

The three types of calculation to be performed have a common starting point. A model is fitted to the mean squares from a simulated population by an iterative weighted least squares procedure, in which the expected values generated by fitting the model are used to produce new weights for each iteration. The principles and methods of weighted least squares are described in some detail in Section 3 of Part A and Appendix E.

Estimates of the parameters of the model are given by $(\underset{\sim}{A}' \underset{\sim}{W} \underset{\sim}{A})^{-1} \underset{\sim}{A}' \underset{\sim}{W} \underset{\sim}{x}$,

where $\underset{\sim}{x}$ is the vector of mean squares

$\underset{\sim}{A}$ is a model matrix

$\underset{\sim}{W}$ is a diagonal matrix of weights

The weights are given by:

$$w_i = \frac{n_i}{2v_i^2} \quad (i = 1, 11)$$

where v_i is the value of the i th mean square for the first iteration, but is evaluated from the parameter estimates in subsequent iterations.

n_i is the degrees of freedom for the i th mean square.

We have described the structure of a hypothetical experiment which produces eleven mean squares but have not yet fixed its size. For the

purposes of these calculations, there are 200 pairs of each twin type and one hundred singletons. The n_i used in calculating the weights were each taken to be 100. This is an approximation since the degrees of freedom between pairs should be one less than those within pairs. This simplification facilitates repetition of the calculations, and has only a trivial effect on the results, since the degrees of freedom are large.

Standard errors of the estimates (σ_{θ}) be obtained from the covariance matrix of the estimates, which is given by:

$$\hat{Z} = \left(\begin{smallmatrix} A' \\ \sim \sim \sim \end{smallmatrix} \right) W A^{-1}$$

Dividing the estimates ($\hat{\theta}$) by their standard errors ($\hat{\sigma}_{\theta}$) yields a vector of normal deviates (C), which are the expected values of $\hat{\theta}_i / \hat{\sigma}_{\theta_i}$ for samples of this size and are used to test the significance of the estimates in real data. In our case, the expected values of the normal deviate will be used to assess the power of the test for detecting particular effects.

The significance of the residuals after a model has been fitted to real data is given by

$$\chi^2_{N-k} = (o_i - E_i)^2 w_i$$

where N is the number of statistics

k is the number of parameters

o_i are the observed mean squares

E_i are the mean squares predicted from the parameter estimates

w_i is the weights matrix evaluated from the estimates which

minimise the value of χ^2_{N-k}

Normally when fitting models to real data $\sum \chi^2_{N-k} = N-k$ when the model fits because the mean squares are estimated with error from the population. However, when fitting a "false" model, the mean squares from the hypothetical populations are known exactly and $\sum \chi^2_{N-k} = N-k + \lambda$, where λ is the non-centrality parameter of a non-central chisquare with $N-k$ degrees of freedom. It turns out that the weighted residual sum of squares which we calculate by fitting "wrong" models to expected mean squares is approximately equal to the non-centrality parameter and can be used to calculate the power of the test of goodness of fit of false hypotheses.

The final calculations we make will estimate the biases introduced into parameter estimates, when the model fitted is not the true model of variation.

2 THE POWER OF THE TEST FOR DETECTING EFFECTS

Two models were fitted to the meansquares derived from the population to be used as an example throughout. These are the $E_1 E_2$ and $E_1 D_R$ models. A number of other models were also fitted to the mean squares from the remaining populations. The full set of models is given in Key C of Appendix G. The most complex model fitted to any set of mean squares was one with the same number of parameters as the causes of variation in the population from which the mean squares were derived. In most cases, more complex models would contain the true causes of variation as a subset of their parameters and it would not make sense to fit them since no residual variation will remain after all the true causes of variation have been fitted because the mean squares from our populations are known without error. In real data fitting a model which is too complex should produce non-significant residuals.

The $E_1 D_R$ model is the "true" model for the causes of variation in our example population and a "true model" will be fitted to each population in turn. A series of false models will also be fitted as exemplified by the $E_1 E_2$ model for our example. For more complex populations a whole series of false models are possible and were fitted to the mean squares. These models can be found for each population type in the tables in Appendix G.

When the $E_1 D_R$ model was fitted to the mean squares, the variance-covariance matrix was obtained:

$$\mathbf{Z} = (\mathbf{A}' \mathbf{W} \mathbf{A})^{-1}$$

where \mathbf{W} was an 11×11 diagonal matrix of weights. The off-diagonal terms are zero because the mean squares are independent.

The covariance matrix is:

$$\begin{matrix} & E_1 & D_R \\ E_1 & \left(\begin{array}{cc} 103.6688 & -170.2078 \\ -170.2078 & 671.7273 \end{array} \right) \\ D_R & \end{matrix}$$

Thus, the estimates and their standard errors are:

$$\begin{matrix} & E_1 & D_R \\ E_1 & \left(\begin{array}{cc} 112.50 & 10.18 \\ 225.00 & 25.92 \end{array} \right) \\ D_R & \end{matrix}$$

Dividing each estimate by its standard error we obtain a vector of expected normal deviates:

$$c = \begin{pmatrix} 11.05 \\ 8.68 \end{pmatrix}$$

These are the values of c expected for samples of 1100 in an experiment of this design, where individual differences are determined equally by specific environmental variation and additive genetical variation. Normally a two-tailed test of significance is performed, although the components of variation are expected to be positive if the model is appropriate, because, in practise, we may fit inappropriate models and significant negative estimates would indicate that the model was wrong. Thus, we may determine whether a model provides an adequate explanation of the data by looking at the significance of the residuals, or by deciding whether parameter estimates are consistent with biological theory. As can be seen from the Tables in Appendix G, negative estimates are often

obtained when inappropriate models are fitted and in these circumstances it is impossible to mislead ourselves about the true causes of variation.

The expected values of c show that we would have no difficulty in detecting both E_1 and D_R as effects significantly different from zero in a sample of this size and structure. However, this sample is larger than those frequently used in practise and we may ask how many individuals would be required for these parameters to be significant at the 5 per cent level in, for example, 95 per cent of cases. The method used is outlined in Eaves' (1972) paper.

The expected value of c for any parameter is a function of the square root of the total sample size. Thus, the value of c , c_x , for a sample of size x can be calculated, given the expected value of c_e and the sample size in this experiment:

$$c_x = c_e \sqrt{1100/x}$$

or x may be calculated

$$x = \left(\frac{c_e}{c_x} \right)^2 \times 1100 \quad ...1$$

We want a value of x , such that the null hypothesis that θ is not greater than zero will be rejected at the 5 level in 95% of cases. Thus, the power of the test is the probability that $\hat{\theta} > 1.96$ given that $\theta > 0$. For this probability to be 0.95, we require sample sizes which would produce an expected value of $1.96 + 1.65 = 3.61$ for θ/σ_θ . We may substitute for c in equation 1:

$$x = \frac{13.03}{2} \times 1100$$

For E_1 we have $c_x = 11.05$ and for D_R $c_x = 8.68$. Therefore, we can calculate x as 117 for E_1 and 190 for D_R .

Thus the sample sizes needed to detect E_1 and D_R , in a population where these are the true causes of variation are by no means prohibitive. Corresponding sample sizes when $h^2_N = 0.9$, are 141 for E_1 and 41 for D_R , so that D_R can be detected with very few individuals. This will not be the case for some of the effects present in particular populations, as we shall see in the discussion, where we confirm, for example the work of Eaves (1972) and show that extremely large numbers of individuals are needed for the detection of dominance in four different population types, where dominance is present in association with a variety of other sources of variation (Tables B5 to B8).

Following the procedure outlined above, we also fitted the false E_1E_2 model to the population in which E_1 and D_R were the true causes of variation (and $h^2_N = 0.5$), producing the following estimates (θ_F), standard errors (σ_{θ_F}) and values for the normal deviate (c_F);

$$\begin{pmatrix} E_1 \\ E_1 \end{pmatrix} \quad \begin{pmatrix} 168.75 \\ 56.25 \end{pmatrix} \quad \begin{pmatrix} 12.89 \\ 12.67 \end{pmatrix} \quad \begin{pmatrix} 13.09 \\ 4.44 \end{pmatrix}$$

$$\begin{matrix} \theta_F \\ \sim \end{matrix} \quad \begin{matrix} \sigma_{\theta_F} \\ \sim \end{matrix} \quad \begin{matrix} c_F \\ \sim \end{matrix}$$

The number of individuals needed for these "false" estimates to be significant in a two tailed test at the 5 per cent level in 95% of cases was calculated in the same way as for the "true" estimates. We found that 84 and 728 individuals for E_1 and E_2 respectively would be needed when $h^2_N = 0.5$ and 90 and 205, when $h^2_N = 0.9$. Thus, we can obtain "sensible" and significant estimates for a source of variation

which does not exist in a population, with a reasonably small number of individuals. The number of individuals needed to detect biased estimates in other more complex situations will be discussed later.

3 THE POWER OF THE TEST FOR REJECTING FALSE HYPOTHESES

We have discussed two criteria for determining whether a model is a satisfactory explanation of variation in a population. If any estimate of a variance component is significantly negative, the model is deemed inappropriate immediately, although as we shall see later, when certain estimates are negative, alternative more suitable hypotheses are suggested by this fact. A well known example is that of dominance and common environmental variance. A negative value for estimates of one of these effects in twin studies is strongly indicative that the other is present (Eaves, 1970).

A second criterion often used in determining whether a model is adequate is the significance of its parameters. We are suspicious of models in which certain estimates are not significant even if we have no reason to suppose that the residuals are other than zero. In such cases, we may have a misleading parameterisation of the causes of variation. We shall see that the sample sizes needed to detect sources of variation which are not present in a population are usually so high as to make it unlikely that they will be significant at the 5 per cent level in any experiment of the scale normally adopted. However, as we have seen, in certain cases significant estimates of "non-existent" sources of variation may be obtained. In such cases, our usual criterion of the significance of the residuals in a chisquare test is the only one we have. This brings us to the question of the power of this test for rejecting false models. We have already seen that this is particularly relevant for studies of fairly typical sample sizes where discrimination between simple models of variation (i.e. $E_1 E_2$ and $E_1 D_R$) is not possible (see Part A, the Georgia Twin Study and Martin, 1976). Martin (1976) has already

considered the "Power of the Classical Twin Study", for populations in which the causes of variation are fairly simple. We shall repeat his calculations, for our experimental design and also consider the more complex populations which were specified earlier.

The approach of Martin (1976) is based on the non-central chisquare distribution and was suggested by Lewontin's power calculations for the rejection of the null hypothesis of Hardy-Weinberg equilibrium (Lewontin and Cockerham, 1959). He gives the following proof supplied by Dr. Paul Davies which is based on a paper by Mitra (1958).

Given a set of observed statistics, O_i , their expected values calculated on the basis of a "true" model of variation, E_i , and the expected values calculated on the basis of a false model, F_i , we wish for each i , to test the null hypothesis:

$$H_0 : O_i = E_i$$

against the alternative hypothesis

$$H_1 : O_i = F_i = E_i + \mu_i / \sqrt{\delta_i}$$

where μ_i is a deviation from the expected value E_i , δ_i is the degrees of freedom and $\mu_i = \sqrt{\delta_i} (F_i - E_i)$. If δ_i is large and H_0 is true, then: $O_i \sim N(E_i, 2E_i^2/\delta_i)$ while if H_1 is true, then:

$O_i \sim N(F_i, 2F_i^2/\delta_i) \sim \text{approx. } N(F_i, 2E_i^2/\delta_i(1 + o(\delta_i^{-\frac{1}{2}})))$
where $o(\delta_i^{-\frac{1}{2}})$ denotes a term of the order $\delta_i^{-\frac{1}{2}}$.

$$\text{Thus, } \frac{\delta_i(O_i - E_i)}{\sqrt{2E_i^2}} \sim N\left\{ \frac{\sqrt{\delta_i}(F_i - E_i)}{\sqrt{2E_i^2}}, 1 + o(\delta_i^{-\frac{1}{2}}) \right\}$$

and the asymptotic power function of $\frac{\delta_i(O_i - E_i)^2}{2E_i^2}$

is non-central chi-square with non-centrality parameter: $\lambda = \frac{\delta_i(F_i - E_i)^2}{2E_i^2}$

In general, to test $H_0: \frac{O_i}{\sqrt{n}} = \frac{E_i}{\sqrt{n}}$ against $H_1:$

$$\frac{O_i}{\sqrt{n}} - \frac{E_i}{\sqrt{n}} = \frac{\mu_i}{\delta_i}$$

we use

$$\chi^2_{n-k} = \sum_i \frac{(O_i - E_i)^2}{2E_i^2}$$

with limiting power function being non central χ^2_{n-k} with non centrality parameter $\sum_i \frac{(F_i - E_i)^2}{2E_i^2}$.

The larger the degrees of freedom, δ_i , the larger the deviations, μ_i , may be from E_i before the distribution departs from non central chisquare.

The non centrality parameter, λ' , can be obtained when we fit a "false" model to a set of statistics derived from one of our hypothetical populations. The procedure is the same as that used to obtain chi-square, when we fit models to real data. We defined $\chi^2_{n-k} = (O_i - E_i)^2 w_i$ and since $w_i = \delta_i / 2E_i^2$, and our mean squares for the hypothetical populations are known without error, then $\chi^2_{n-k} = \lambda'$.

We can use the value of λ' in conjunction with tables of non-central chisquare to determine the sample sizes necessary to reject a "false" hypothesis at a certain level of probability with a given degree of confidence. The procedure is best illustrated by reference to the simple example population containing E_1 and D_R .

When the false $E_1 E_2$ model was fitted to this population, we obtained $\chi^2_9 = \lambda'$ (with 9df) = 46.3611. In order to be 95 per cent certain of rejecting the "false" model at the 5 per cent level, we must ensure that $\lambda = 23.589$, which is the value of $\lambda(0.05, 0.95, 9)$ tabulated by Pearson and Hartley (1972). The number of individuals required is given by $N = \lambda / \lambda'$ for unit sample size. Since our "experiment" was based on 1100 individuals, N becomes:

$$N = \frac{\lambda}{\lambda'} \times 1100 = \frac{23.589}{46.3611} \times 1100 \\ = 562$$

When the calculations were repeated for the population in which $h^2_N = 0.9$, we found $N = 147$. Thus, although as we saw earlier very few individuals are required for the estimate of E_2 to be significant at the 5 per cent level, the false hypothesis may be rejected with only a modest experiment when $h^2_N = 0.9$. However, even with the optimal experimental design used here, as many as 562 individuals are required to discriminate between simple environmental and simple genetical hypotheses when $h^2_N = 0.5$. This may be a more realistic level of heritability to consider particularly for personality and social attitudes. Thus it seems that if we are to learn anything useful about the causes of individual differences for many behavioural traits we must be prepared to embark on extensive data collection programmes.

4 CALCULATION OF BIASES WHEN FALSE MODELS ARE FITTED

We have considered three ways in which "false" models may be rejected:

1. Negative estimates of variance components
2. Parameters not significant
3. Residuals significant in a chi-square test

We have also described a method for determining the number of individuals needed to detect particular effects when they are present in a population and we fit the correct model. From the Tables in Appendix G, we see that this number is unrealistically high in several cases (e.g. dominance, genotype-environment interaction). This provides some evidence for the claims of several authors, mentioned earlier, that such effects as genotype-environment interaction and genotype-environment covariation may remain undetected even in the most extensive studies of human variation. We may now ask what basis there is for the accompanying claim that such undetected effects seriously bias our estimates.

The calculations needed in order to estimate the biases which occur when a "false" model is fitted are easily performed. When we fitted the $E_1 E_2$ model to the mean squares derived from a population in which $\frac{1}{2}D_R = E_1 = 112.5$, the parameter estimates were obtained as $(A'WA)^{-1} A'Wx$. If B is the "true" model for the mean squares from the populations, then we may obtain the contribution of the "true" parameters to these estimates by substituting B in the above expression i.e. from the rows of $(A'WA)^{-1} A'WB$. For our example, we obtain

$\sim \sim \sim \sim \sim \sim$

$$\begin{pmatrix} E_1 \\ E_2 \end{pmatrix} = \begin{pmatrix} 1 & 0.25 \\ 0 & 0.25 \end{pmatrix} \begin{pmatrix} E_1 \\ D_R \end{pmatrix}$$

i.e. $\hat{E}_1 = E_1 + \frac{1}{4}D_R$

$$\hat{E}_2 = \frac{1}{4} D_R$$

The algebraic specification of these biases does not depend directly upon the magnitude of the "true" population parameters, but only on the sources of variation present, the experimental design and the weights. Obviously the numerical value of the biases does depend on the parameter values. However, there is only one set of biases for each model for each of the fourteen population types described earlier. These are present for all the possibilities we considered in the "A" tables of Appendix G.

SECTION 3: THE RESULTS

1

GENERAL COMMENTS

The analyses described in the previous section performed on the different "data sets" derived from the fourteen hypothetical populations have produced results which are far too extensive to discuss in all their details. These results are summarised in the tables in Appendix G and largely speak for themselves, so that the reader can draw his own conclusions from the particular tables most relevant to the problem he is likely to encounter when planning experiments designed to detect and estimate certain effects. In this discussion we shall confine ourselves to making points which illustrate the general usefulness of the Tables and to considering particular effects which have been the subject of much controversy in recent years i.e. genotype-environment interaction and genotype-environment covariation (e.g. Moran, 1973; Block and Dworkin, 1974a, 1974b; Layzer, 1974; Lewontin, 1974; Linn, 1974; Feldman and Lewontin, 1975; Plomin et al, 1977). We will attempt to answer critics who claim that the complexity of the causes of variation in human behaviour makes any experiments designed to elucidate these causes not only worthless, but also misleading. We will do this by integrating information from the different analyses described earlier in order to determine the likelihood of seriously misleading ourselves in a variety of different circumstances. We will also consider claims that the biases that occur usually lead to the overestimation of heritabilities.

2 POPULATIONS WITH ADDITIVE VARIATION

We considered four population types in which variation was only produced by additive effects:

1. $E_1 D_R$
2. $E_1 E_2 D_R$
3. $E_1 D_R M$
4. $E_1 E_2 D_R M$

These populations contain various combinations of the contributions of specific environmental variation, between families environmental variation, additive genetical variation and additional variation produced by assortative mating.

For the very simplest population (containing E_1 and D_R), rejection of the null hypothesis of no genetical variation should not prove difficult unless the heritable component accounts for less than 50 per cent of the variation, when over 600 individuals will be required. If we were to mistakenly accept the $E_1 E_2$ model as an adequate explanation of our data, E_1 and E_2 would be equally biased by $\frac{1}{4}D_R$. The contribution of D_R to E_1 and E_2 is always $\frac{1}{4}$, when we omit to fit D_R when it is a source of variation in a population.

Detection of D_R is generally not too difficult, but experimental sizes of about 600 are required to detect E_2 when it accounts for 25% of the variation and over 1000 are needed when its contribution falls to 5%. Thus, we might fail to detect E_2 as significant in a modest experiment and in such an experiment we would be unlikely to reject the $E_1 D_R$ model because over a thousand individuals are needed to reject this model when the true population contains $E_1 E_2 D_R$ and E_2 accounts for 25% of the total variation. Similarly, quite large numbers are needed to reject the $E_1 D_R$ and $E_1 D_R M$ models when the true causes of variation are $E_1 E_2 D_R M$. From Tables 1A and 2A we see that failure to fit E_2 when it is

in fact present leads to biases of all the other parameters we might fit. If we fail to detect significant E_2 , we are most likely to take $E_1 D_R$ as the true explanation for variation. In this case, the contribution of E_2 to $\frac{1}{2}D_R$ is slightly greater than that to E_1 , thus leading to over-estimation of the narrow heritability in this experimental design.

The number of individuals required to detect assortative mating, when $h^2_N = 0.9$ is quite small (i.e. about 300), but when the heritability drops to 0.5, over 5000 individuals are required. Obviously we may fail to detect significant assortative mating when it is present. Both E_2 and M contribute to the same statistics in studies of twins reared together and it is possible in such cases that estimates of their joint effect may be significant when fairly small experimental sizes are used.

For the $E_1 D_R M$ population, we might easily accept $E_1 D_R$ as an adequate explanation of the data since the number of individuals needed to reject this false hypothesis is over a thousand for $h^2_N = 0.9$ and over 12000 for $h^2_N = 0.5$. For the $E_1 E_2 D_R M$ population either $E_1 D_R$ or $E_1 E_2 D_R$ might be accepted depending upon the sample size. The contribution of M to E_1 and E_2 is very small and $\frac{1}{2}D_R$ is estimated approximately as $\frac{1}{2}D_R + \frac{1}{2}M$. However, the direction of the bias although small is such that in the case of the $E_1 D_R$ model, the true narrow heritability ($h^2_N = \frac{1}{2}D_R + \frac{1}{2}M / \frac{2}{T}$) is overestimated by the narrow heritability based on the false $E_1 D_R$ model. When the $E_1 E_2 D_R$ model is accepted for the $E_1 E_2 D_R M$ model, estimates of narrow heritability are not biased.

In these simple situations, narrow heritabilities may thus be overestimated, providing some support for the claims of critics. However, these same critics express the opinion that the causes of individual differences in human behaviour are not simple and so the situation for more complex populations must be examined.

3

POPULATIONS WITH DOMINANCE

The results for four populations are presented in Appendix G: $E_1 D_R H_R$, $E_1 E_2 D_R H_R$, $E_1 D_R H_R M$, $E_1 E_2 D_R H_R M$. We will discuss mainly the simplest of these.

Eaves (1972) showed that the detection of dominance using several experimental designs involved prohibitive sample sizes. We amply confirm his findings in each of the four types of population considered here. The smallest sample in which dominance could be detected in any of the populations was 4643 in the $E_1 D_R H_R M$ population, when the broad heritability was 0.93 and the dominance ratio was 0.5. In most other cases the numbers required were much higher. Thus detection of dominance seems to be virtually impossible even with this "ideal" experimental twin design. In practice, in more restricted data sets, we will be extremely unlikely to detect dominance, so that the collection of twin data is likely to prove of little use for the study of genetic architecture (Mather, 1943) in human populations. Inbreeding studies or data on other types of relationships (e.g. half siblings, grandparents, etc.) are needed if we wish to detect dominance (see Jinks and Fulker, 1970).

When E_1 , D_R and H_R are the true causes of variation in the population, the "false" $E_1 D_R$ model is most easily rejected when $h^2_N = 0.90$ and the dominance ratio is 1.0. Even in this case 16042 individuals are required before rejection at the 5 per cent level will occur in 95% of cases, and the false $E_1 D_R$ model will be accepted as representing the true causes of variation.

From Table 3A, we find that:

$$\hat{E}_1 = E_1 + 0.02 H_R$$

$$\hat{D}_R = D_R + 0.47 H_R$$

In other words, estimates of E_1 are not seriously biased and H_R contributes to the estimate of additive genetical variation. Estimates of the narrow heritability obtained by fitting the $E_1 D_R$ model include both additive and dominance variation and give us the broad heritability for the trait.

If we now consider an additional source of environmental variation, so that the true population contains E_1 , E_2 , D_R and H_R , we find that the number of individuals required to reject the $E_1 D_R$ model drops considerably to about 1100, when $h_N^2 = 0.9$ and 2100, when $h_N^2 = 0.5$. This number is still fairly large and in many typical experiments, we would accept the $E_1 D_R$ model as the true explanation of the observed variation.

If we did this, we would estimate:

$$\begin{aligned}\hat{E}_1 &= E_1 + 0.46 E_2 + 0.01 H_R \\ \hat{D}_R &= 1.05 E_2 + D_R + 0.49 H_R\end{aligned}$$

H_R again only contributes to \hat{D}_R , but our estimates of \hat{E}_1 and \hat{D}_R are biased by the E_2 component which we have also failed to detect.

Estimates of h_N^2 are thus inflated by the E_2 component, as we saw in the last section.

If we had performed an experiment of well over 2500 individuals, we would probably reject the $E_1 D_R$ model. In this case we would then fit a series of three parameter models: $E_1 E_2 D_R$, $E_1 D_R H_R$, $E_1 D_R M$. From Table 4B.1, we can see that the $E_1 D_R H_R$ model would almost certainly be rejected but that either the $E_1 E_2 D_R$ or $E_1 D_R M$ models would probably be retained as possible models for variation.

The contribution of the two parameters to the estimates for the $E_1 E_2 D_R$ model is:

$$\begin{aligned}\hat{E}_1 &= E_1 + 0.01 H_R \\ \hat{E}_2 &= E_2 - 0.01 H_R \\ \hat{D}_R &= D_R + 0.51 H_R \approx 2 V_G,\end{aligned}$$

where V_G is all the genetic variation.

For the $E_1 D_R M$ model it is:

$$\begin{aligned}\hat{E}_1 &= E_1 + 0.51 E_2 \\ \hat{D}_R &= D_R + 0.55 E_2 + 0.67 H_R \\ \hat{M} &= 1.38 E_2 - 0.16 H_R\end{aligned}$$

Thus, the $E_1 E_2 D_R$ model would lead us to estimate the narrow heritability as the proportion of variation produced by all genetical effects i.e. the broad heritability and we would not underestimate the importance of environmental effects.

In the case of the $E_1 D_R M$ model, the narrow heritability will be inflated, but the importance of the environmental components will be overestimated.

Our conclusion then is that in populations in which either E_1 , D_R and H_R or E_1 , E_2 , D_R and H_R are the true causes of variation, we will not overestimate the importance of genetical effects except when we are unable to reject the $E_1 D_R$ model for the $E_1 E_2 D_R H_R$ population because the power of the test for E_2 is not high enough. Samples of over a thousand will be needed to reject this model when $h^2_N \approx 0.5$ and of over two thousand when $h^2_N \approx 0.9$.

Similar conclusions emerge when we consider additional variation produced by assortative mating. When E_1 , D_R , H_R and M are the true causes of variation, it is difficult to reject the $E_1 D_R$ model and we may estimate:

$$\hat{E}_1 = E_1 + 0.01 H_R - 0.05 M$$

$$\hat{D}_R = D_R + 0.48 H_R + 1.18 M \leq 2V_G$$

Again, all genetical effects are estimated largely with \hat{D}_R and estimates of narrow heritability reflect all variation produced by genetical differences between individuals.

In the population where $E_1 E_2 D_R H_R$ and M produce variation over 1000 individuals are needed for rejection of the $E_1 D_R$ model. If we fail to reject this model, parameter estimates will be biased by E_2 and the proportion of variation attributable to environmental effects will be underestimated. If E_2 is fitted, then \hat{E}_1 and \hat{E}_2 are virtually unbiased and \hat{D}_R contains all the genetical variation produced by D_R , H_R and M .

In the last two sections we have seen that failure to detect H_R does not introduce biases of the sort that lead us to underestimate the importance of environmental factors. Failure to detect E_2 is also likely with typical sample sizes, and this may lead to overestimation of the importance of genetical factors.

GENOTYPE-ENVIRONMENT INTERACTION

We have generated four populations in which there is variation produced by genotype-environment interaction, where additive genetical effects interact with the common family environmental component:

1. $E_1 E_2 D_R I$
2. $E_1 E_2 D_R I M$
3. $E_1 E_2 D_R H_I$

From Tables 7B to 10B, we can see that the number of individuals needed to detect I as significant at the 5 per cent level in 95 per cent of similar experiments is prohibitive. The number needed to detect the E_2 component is also large. The population where we are most likely to detect GXE is one in which the true causes of variation are E_1 , E_2 , D_R and I and $h^2_N = 0.9$ and GXE accounts for twenty per cent of the total variation. Even in this case 2958 individuals are needed. Thus, GXE which is not systematically related to genetical or environmental deviations, and is, therefore, not detectable by other methods, is unlikely to be detected by fitting linear models to mean squares unless the contribution of GXE to the total variation is much larger than 20 per cent. Work in other organisms suggests that GXE is not likely to be much larger than this. There is thus some evidence that GXE may remain undetected in man, as claimed by several authors. We may now ask whether this will lead to serious biases of parameter estimates from models found adequate to account for variation using the chi-square criterion.

The number of individuals needed to reject the $E_1 D_R$ model is moderate in this instance:

h^2_B	I	N
0.5	10%	802
0.5	20%	636
0.9	10%	689
0.9	20%	479

When the heritability is high and GXE accounts for 20 per cent of the variation, only a relatively small experiment is required. But when the heritability is lower and GXE accounts less than 10% of the variation, then approaching 1000 individuals may be needed. If our experimental size is such that we mistakenly accept the $E_1 D_R$ model, then we estimate:

$$\hat{E}_1 = E_1 + 0.45 E_2 + 0.25 I$$

$$\hat{D}_R = D_R + 1.07 E_2 + 0.25 I$$

The GXE contributes equally to E_1 and D_R , which means that it biases the contribution of E_1 to the total variation twice as much as that of D_R , since the contribution of D_R to the total variation is only $\frac{1}{2}$. This would lead to the underestimation of h^2_N but for the fact that we have failed to fit E_2 and as before this leads to the over-estimation of h^2_N .

If we have a reasonable experimental size, we are likely to reject the $E_1 D_R$ model. We would then fit three 3 parameter models: $E_1 E_2 D_R$, $E_1 D_R M$ and $E_1 D_R H_R$. Rejection of the $E_1 D_R H_R$ model would be immediate, not only because few individuals are required, but also because estimates of H_R would be non-significant and negative. However, both the $E_1 E_2 D_R$ and the $E_1 D_R M$ model would fit the data, leading to estimates:

1. $E_1 E_2 D_R$ model

$$\begin{aligned}\hat{E}_1 &= E_1 + 0.07 I \\ \hat{E}_2 &= E_2 + 0.25 I \\ \hat{D}_R &= D_R + 0.43 I\end{aligned}$$

2. $E_1 D_R M$ model

$$\hat{E}_1 = E_1 + 0.51 E_2 + 0.25 I$$

$$\hat{D}_R = D_R - 0.53 E_2 + 0.50 I$$

$$\hat{M} = 1.36 E_2$$

In the latter case, all estimates are biased and our failure to fit E_2 leads to overestimate of the narrow heritability.

When we fit $E_1 E_2 D_R$ to the "data", \hat{E}_1 is virtually unbiased. However, both \hat{E}_2 and \hat{D}_R are quite strongly biased by the GXE, when its effect is ignored in fitting the model. Since the contributions of additive genetical variation and cultural effects to the total variation are $\frac{1}{2}D_R$ and E_1 , these effects are almost equally biased by I.

We find that estimates of the narrow heritability calculated on the assumption of no GXE are inflated, and that we are likely to overestimate the true contribution of additive genetical variance, when the estimate is based on the relatives in our experimental design.

This provides some justification for the criticisms of certain authors (e.g. Moran, 1973; Layzer, 1974; Feldman and Lewontin, 1975) that unsystematic GXE, if it is an important source of variation in human populations may remain undetected and inflate heritability estimates. However, this will not be the case for all experimental designs. GXE could lead to the underestimation of D_R in transgenerational data (e.g. parent-offspring covariances).

We may be interested in analysing variation in human behaviour for two main reasons. The first is a desire to discover the biologically important sources of variation in human behaviour and the second a desire for environmental intervention to enhance the phenotypes of those whose genetic predisposition is for a lower phenotype of some particularly desirable attribute. In either case, we should not exaggerate the

significance of our findings about the difficulties that face those who attempt to detect non-systematic GXE. The existence of GXE systematically related to genetical or environmental deviations is likely to be far more meaningful biologically and could suggest suitable medical or educational strategies for the enhancement of particular phenotypes. Several tests have been proposed for the detection of such systematic GXE (Jinks and Fulker, 1970) and these are discussed in earlier parts of this thesis.

5.1 Cultural Transmission

In this population, genotype-environment covariation arises as a result of the cultural impact of parents on their offspring. The specification of this population was described in Section 1.2.13. Since only one new parameter, b , was involved in the specification of E_2 and $\text{Cov } g_2 e_2$, we could have estimated E_1 , D_R and b by the more powerful approach of non-linear weighted least squares (Eaves, 1975). However, the approach described in Section 2 was continued and four parameters were estimated: E_1 , D_R , E_2 , C , where C is the genotype-environment covariance produced by cultural transmission. The constraint upon the values of E_2 and $\text{Cov } g_2 e_2$ implied by the cultural transmission model was, therefore, not enforced, but since real data may not exactly follow our model, this may be a more useful approach.

From Table 10B.2, we can see that the detection of variation produced by cultural transmission is not likely to be so difficult as for some of the effects considered previously. When $b = 0.25$, the number of individuals required to detect C was 631 and 461, for the two levels of heritability. Detection of E_2 was also feasible (635 and 249 individuals). When $b = 0.1$, larger (but not unreasonable) samples are required for C (2000 and 1231) although the detection of E_2 was not so likely (25332 and 1521). Sample sizes, of course, increase as the heritability increases and there is a corresponding decrease in the size of E_2 and C .

Another heartening feature of Tables 10B.1 and 10B.2 is that the number of individuals needed to reject false models is generally lower

than that seen in previous Tables. This suggests that we will be less likely to mislead ourselves about the true causes of variation when cultural transmission is present.

We can obtain the linear combination of the observed statistics which yields the weighted least squares estimate of $2 \text{ Cov } g_2 e_2$. The coefficients of the eleven statistics in the estimator of $2 \text{ Cov } g_2 e_2$ for the case when $b = 0.25$ and $\frac{1}{2}D_R = 2E_1 = 112.5$ are:

<u>Mean square</u>	<u>Coefficient</u>
Between MZT	0.1616
Within MZT	0.4507
Between DZT	0.1974
Within DZT	-0.1048
Between MZA	-0.1209
Within MZA	-0.2304
Between DZA	-0.1395
Within DZA	-0.1964
Between UT	-0.1564
Within UT	-0.1433
Singletions	0.2821

This shows that the test for $\text{Cov } g_2 e_2$ depends largely upon a comparison of the total variances of individuals reared by their natural parents with that of individuals reared by foster parents. It does not matter whether the individuals are twins or not, or even whether they are reared in pairs. Thus, information about genotype-environment covariance produced as a result of cultural transmission would be best sought in adoption studies, as suggested by Jinks and Fulker, (1970) and Cavall-Sforza and Feldman (1973). The use of such adoption studies

for the detection and estimation of the parameters of cultural transmission was discussed extensively in Part B: A Twin Study of social attitudes.

There has been discussion in the literature about the contribution of dominance and genotype-environment covariation to variation in intelligence. We fitted several models incorporating dominance to the four data sets generated from the population where E_1 , E_2 , D_R and C were contributing to variation:

1. $E_1 D_R H_R$
2. $E_1 D_R H_R M$
3. $E_1 E_2 D_R H_R$

In all cases, estimates of dominance were small and negative. The $E_1 E_2 D_R H_R$ population is the most similar to the "true population" containing $E_1 E_2 D_R C$. Even in the situation most favourable for the detection of the false H_R effect, 1417 individuals were needed for H_R to be significant in this experimental design. When $b = 0.25$, fairly small sample sizes only are required for the false $E_1 E_2 D_R H_R$ model to be rejected at the 5 per cent level in 95 per cent of cases, although rather more were needed when $b = 0.1$.

The likely failure of the $E_1 E_2 D_R H_R$ model and the negative values obtained for dominance variation suggests that we would not accept the $E_1 E_2 D_R H_R$ model, but would seek an alternative explanation for the pattern of variation. It may, however, be possible to mistake negative genotype-environmental covariance with dominance in borderline cases, because some of the consequences of negative CovGE may reproduce certain of the effects of dominance. This may be true for Cov GE produced both by cultural transmission and also by sibling effects

(in the case of competition). We have specified populations in which competition is operating (see Section 1.2.15 and 1.2.16) and so we can study the likelihood of being mislead about the true causes of variation in such cases.

5.2 Sibling Effects

A second source of genotype-environment covariation was defined by Eaves (1976a) in which the Cov GE arises because the phenotype of a sibling produces an environmental effect on the phenotype of his co-sibling. An advantageous phenotype in one sibling may enhance the environment necessary for a co-sibling to develop high levels of the advantageous trait (i.e. cooperation), or an advantageous phenotype may develop in one sibling at the expense of a co-sibling (competition). These lead to positive and negative genotype-environment covariance respectively.

Power calculations and estimation of biases were carried out for two populations: $E_1 D_R D_R'' D_R'$ and $E_1 E_2 D_R D_R'' D_R'$ and the results are presented in Tables 11A.1 to 12B.15. The discussion will be confined mainly to a consideration of the first population type, of which we considered sixteen different cases with the relative contributions of the parameters varying according to h_N^2 , the direction of the covariance, the relative magnitude of D_R'' compared with D_R and the value of ρ_{ge} .

The correct $E_1 D_R D_R'' D_R'$ model was fitted to each data set and the number of individuals needed to detect the four sources of variation was determined as described earlier. From Table 11B.6, it can be seen

that no more than 142 individuals are needed to detect E_1 in an experiment of this design and no more than 327 are needed to detect D_R . The numbers needed to detect D_R'' and D_R' vary considerably depending on the values of the population parameters. If we average the numbers required over values of ρ_{ge} and relative magnitudes of D_R'' compared to D_R' , then when $h^2_N = 0.5$, 1969 individuals are required to detect D_R'' and only 513 for D_R' . When $h^2_N = 0.9$, the numbers are 989 and 244.

Thus generally we notice that it is easier to detect D_R' and D_R'' as the heritability increases. It is considerably easier when the environmental effect of the alleles equals their direct effect upon the genotype i.e. when $D_R'' = D_R'$. If the proportion of loci contributing to both D_R and D_R' is one, the likelihood of detecting D_R' is considerably increased at the expense of the power of the test for detecting D_R'' . The power of the test for detecting sibling effects is greater when these covary with the direct effects of genetical differences (i.e. when ρ_{ge} is positive). The fact that far fewer individuals are needed to detect D_R' than D_R'' arises because the test of D_R'' depends merely on a comparison between the total variances of individuals reared as pairs and singletons, whereas the significance of D_R' depends upon a very precise pattern of expectations which involve the individual mean squares as well as the total variances.

It seems that the detection of both competition and cooperation should be relatively easy in the majority of non-extreme situations which we have considered. In order to emphasize this further we may list the other models which might be fitted to mean squares derived from populations in which E_1 , D_R , D_R' and D_R'' are the true causes of variation and show why we might reject those in most cases.

1. $E_1 E_2$ - significant residuals (and estimates of \hat{E}_2 non-significant or negative when D_R' negative)
2. $E_1 D_R$ - residuals significant in most situations
3. $E_1 E_2 D_R$ - significant residuals or negative estimates of \hat{E}_2 or non-significant estimates of \hat{E}_2
4. $E_1 D_R H_R$ - significant residuals, estimates of \hat{D}_R or \hat{H}_R negative and non-significant, depending on whether ρ_{ge} is positive or negative
5. $E_1 D_R M$ - significant residuals or M sometimes non significant (or negative when ρ_{ge} negative)
6. $E_1 E_2 D_R H_R$ - significant residuals and negative or non-significant estimates of \hat{D}_R or \hat{H}_R or \hat{E}_2 depending on the particular situation.
7. $E_1 E_2 D_R I$ - negative estimates of \hat{E}_2 or \hat{I}
8. $E_1 E_2 D_R M$ - estimates of \hat{E}_2 and M non-significant or negative, residuals significant
9. $E_1 D_R H_R M$ - \hat{D}_R or M negative. \hat{D}_R , \hat{H}_R and \hat{M} often non-significant. Residuals often significant

In all these cases, if we fitted a "false" model to the "data", we would find some reason for rejecting the false model in this experimental design. Thus, it is not easy to be mislead about the true causes of variation in a population when these are E , D_R , D_R'' and D_R' .

The cases of the $E_1 D_R H_R$ and $E_1 E_2 D_R H_R$ models are particularly pertinent in view of the discussion of the roles of dominance and Cov GE in the determination of I.Q. We suspected that it might be possible to confuse these two effects when Cov GE is negative. However, from the information provided in Tables 11B.4 and 11B.7, it seems that

this would be unlikely. Overall, we have every reason to be optimistic about our chances of detecting Cov GE produced by sibling effects and rejecting alternative false models.

SECTION 4:

DISCUSSION

In this work, we have attempted to provide precise statements about the power of tests for detecting components of variation and for rejecting false models. Biases in estimated parameters can be calculated mathematically given that we simulate a series of possible populations, from which mean squares can be derived for a particular experimental design. Thus, we have quantified many of the arguments which are discussed, without evidence, in the field of human behaviour genetics. We have done this for two main reasons:

1. In order to provide a rational basis for the discussion of criticisms of the analysis of individual differences in human behaviour.
2. In order to provide a quantitative framework for the planning of future research.

We have shown that in some cases the critics may have a case, although they had no evidence for this themselves. Consider, for example, the case of GXE, where we have shown that its effects may remain undetected even in extensive twin studies and can bias estimates of the components of variation, leading to an overestimate of the importance of genetical differences between individuals. This provides some support for authors such as Moran, (1973), Layzer (1974a) and Feldman and Lewontin (1975). However, it does not support the claim that GXE precludes any worthwhile analysis of individual differences in human populations. Non-systematic genotype-environment interaction may be detected with more appropriate experimental designs, and in any case systematic GXE is likely to be more biologically and socially relevant. This source of variation can be detected using several scaling tests (Jinks and Fulker, 1970).

In contrast to this, we have found that the detection of Cov GE produced by either cultural transmission or sibling effects should prove relatively easy. Much of the misunderstanding and controversy surrounding non-additive effects such as GXE and Cov GE arises because previously the specification of these effects was purely empirical. However, the work of Eaves (1976a, 1976b) has provided a theoretical framework from which a knowledge of the consequences of Cov GE in particular populations can be developed through simulation and practical studies.

These simulations have provided a wealth of information about the sorts of experiments that should be conducted in order to test certain hypotheses about the causes of individual differences, mainly in terms of the sample sizes required and the biases that may be introduced when false models of variation are retained because of an inadequate experimental design.

The disadvantage of such simulations is that while they may tell us a lot about what we may expect given one particular constellation of relatives, they cannot be generalised to other experimental designs. Other types of relatives or studies may detect effects which cannot be detected in this study. The precise nature of the biases and the powers of particular tests need to be determined for each specific situation.

This leads us to suggest a future development of the present work. A simulation package of computer programs should be developed for use by psychogeneticists. This package would produce any desired population type, and calculate the mean squares derived from this population for specified experimental designs, and then perform the

calculations we have described in Section 2. Thus before embarking on a study designed to test a specific hypothesis, a worker could determine the optimal experimental design within his resources and would know beforehand the probability of detecting particular effects and the biases he could expect. In this way many fruitless research programmes would not be started, and hopefully the concentration of resources on a few efficient experiments would do much to increase our understanding of the nature of individual differences in human behaviour.

GENERAL SUMMARY AND DISCUSSION

This discussion will be brief since each part of the thesis is largely self-contained and has already been discussed in some detail. The general significance of the findings and their implications for future research will be considered.

Human behaviour genetics uses the methods of modern genetics to study traits which were once considered solely as the interest of psychology and shows the importance of the biological basis of behaviour for understanding the evolution of culture and a social system in man. The relationship between biology and behaviour can only be understood by studying the evolution of behavioural traits through their contribution to fitness and the dependence of an organism on and its sensitivity to the environment. The determination of genetic architecture and understanding of genotype-environment interaction and the non-genetic, as well as the genetic, transfer of information from generation to generation are essential. The analysis of a few twin correlations and unreliable estimation heritabilities are clearly inadequate for this purpose, although in the past most studies were confined to these simple aims. The limitations of this approach, suggested by Jinks and Fulker (1970), were illustrated using the data from the Georgia Twin Study and the advantages of the analysis of variance components was shown. Whites were more variable than Blacks, a fact which would have remained undiscovered in an analysis of correlations, leading to biased estimates of genetical and environmental effects and probable errors of inference about the causes of individual differences in ability. The greater variability of Whites could be partly attributed to greater between families differences, due to cultural differences

within populations or the greater genetical heterogeneity of Whites. Some of this heterogeneity could be attributed to differences in mean performance between Whites from different regions. The roles of the mating system and culture in maintaining differences between sub-populations and Whites in the United States could provide a constructive area for future investigation.

Although the analysis of variance components represents an advance over the analysis of correlations, the test battery and the size and design of the experiment proved limiting factors in the Georgia Twin Study. High levels of test specific variation were found for certain Spatial tests, and produced many ambiguities during the analyses. This suggests that great care should be taken at the initiation of an enquiry in choosing reliable, standardised tests. More work is obviously needed to determine the tests most suitable for use with White and Black populations.

The unreliability of certain tests, leads to inflated within families variation in MZ twins and reduced MZ twin correlations. This made discrimination between simple genetical and simple environmental models difficult with the sample sizes used here. Power calculations showed that the number of twins required to reject one of these hypotheses at the 5% level in 95% of cases is greater than the number in this study, when the MZ twin correlation is about 0.5 - 0.6. A larger twin study of Blacks and Whites in the US using a more carefully chosen test battery would enable the causes of variation in ability, particularly Spatial ability, to be determined more satisfactorily.

The twin study of social attitudes was large enough to test the genotype-environmental models that can be specified for twins. Estimates

of additive genetical variation, specific environmental variation and a between families component were remarkably consistent with those from two previous studies. However, the resolution of the between families component into variation produced by cultural differences and the mating system is not possible with data only on twins reared together. Twin studies can be useful in the early stages of an investigation for providing powerful tests of certain simple hypotheses, but do not permit the detailed investigation of sources of variation. Thus, there is a general trend towards the collection of other types of data, and particularly data on whole families. In Birmingham and London, a study of ability, personality and attitudes is attempting to combine the features of twin and family data. Mothers and fathers are being tested, as well as the twins themselves in an extensive programme. Thus, many additional hypotheses can be tested concerning, for example, the causes of variation in adults compared with children and sex-linkage. Nance and Corey (1976) and Eaves (personal communication) have suggested an improved design which allows the detection and estimation of most effects of interest. This includes measurements on pairs of adult identical and non-identical twins, their spouses and offspring and thus provides covariances between twins, spouses and parents and offspring. Relationships among the children of a pair of MZ twins provide the equivalent of half sibling and sibling covariances. Similarly the offspring of DZ twins provide sibling and cousin covariances. However, for the resolution of cultural differences, adoption data provide powerful tests (although the equivalent of covariances between parent and offspring (not reared by him) is provided by an MZ twin and the offspring of his co-twin). Adoption data were used to investigate the role of cultural transmission for social attitudes.

Both twin and adoption data are open to the criticism that the individuals may be atypical of the population as a whole. The collection of data on a random sample of families as they naturally occur in the population would provide sufficient numbers of most types of relationships if large enough samples were employed and would overcome the problem of individuals being atypical. However, the unbalanced pedigrees obtained could make analysis difficult and wasteful of information. The method of maximum likelihood estimation by pedigree analysis, used for analysing the adoption data of the social attitudes study shows how this problem may be overcome. In this case there were too few individuals of some types e.g. natural-adopted sibling pairs, which meant that tests of hypotheses of particular interest were not adequate. There was no evidence for the significant effect of cultural transmission and the between families component could apparently be explained by reference to the mating system in these data. However, the power of the test was probably low.

In Part C, methods were introduced for estimating the power of the test for detecting particular effects, the power for rejecting false hypotheses and for calculating biases when false models are fitted. It was shown that large samples are needed for the detection of genotype-environment interaction, but not for genotype-environment covariance. The exclusion of CovGE from models of variation leads to failure of alternative models with relatively small sample sizes, and is unlikely to lead to overestimation of the genetical component. This is not true when GXE is mistakenly omitted from analyses, but the biases are not necessarily large.

The limitation of all such simulations is their specificity to

particular experimental designs, populations and actual models fitted. However, the methods may be generalised and used to estimate biases and determine probable errors of inference in other situations. One aim of future work should, therefore, be to construct a general simulation package which enables the possibilities for any experimental design, population and model to be tested. This would be useful in determining the errors of inference that might have occurred when interpreting results. However, its main value would be in the optimisation of experimental designs for the detection and estimation of effects of interest before a study is undertaken. This should prevent waste of time and resources on inefficient studies which in the end cannot make powerful tests of the hypotheses they were designed to test.

Many of the problems of power and unreliability in the Georgia Twin Study were overcome by extracting and analysing a "general factor" of ability. A factor analysis of the data showed that the tests could be regarded as belonging either to a Verbal Arithmetic factor or to a Spatial factor. In order to consolidate the conclusions from this study, scores of the two factors should be obtained and analysed. An alternative approach would be to analyse the structure of the variance and covariance between tests into its genetical and environment components, using method already available (Joreskog, 1973; Martin and Eaves, 1977).

However, the main development of the work in this thesis should be in the analysis of the environment. An analysis of "genotype-environment interaction" showed that, for ability, many apparent interactions between genotypic and environmental differences may be regarded simply as a property of the scale of measurement rather than the

individuals sensitivity to his environment. Little evidence for "GXE interactions" could be found for social attitudes. Thus, the analysis of cultural differences and cultural transmission is our main problem in relating the environment to the phenotype of an organism. When the environment is provided by the phenotype of the parents, cultural transmission may arise. The work in this thesis suggests further study of the effects of culture in the evolution of man's behaviour using studies appropriately designed with the aid of computer simulations. Simulation studies could also be used to study the consequences of cultural transmission and assortative mating for the pattern of variation. Alternatively, family data could be collected and analysed using the methods of pedigree analysis. In this thesis the problem of the joint role of assortative mating and cultural differences has been resolved in terms of path models. Future work should include the development of Fisher's (1918) model of assortative mating to include cultural transmission as specified by Eave's (1976b) model. This would enable further advances to be made in understanding one of the most interesting current problems in human behavioural genetics - the evolution of the behaviour leading to cultural differences and cultural change and the development of society.

APPENDIX A: FINAL DETERMINATION OF ZYGOSITY FOR ELEVEN PAIRS OF TWINS
OF UNCERTAIN ZYGOSITY

Twin Pair No.233 - These 16 year old white girls were called MZ by the discriminant analysis program and DZ by AID. The girls were exactly the same height but different by 14.5% in weight. Differences in head length and breadth were also significant. One sister was right-handed; the other ambidextrous. The twins reported they were rarely misidentified. They believe they are DZ. Twin A says, "There is no resemblance. Everything is unlike." Final classification, DZ.

Twin Pair No.277 - In terms of biometric measurements, these 14 year old Negro girls appear to be identical. They are the same height. Head length and head breadth are also the same. There are only slight differences in the other physical measurements. However, Twin A is right-handed; Twin B is not. The test for colour blindness probably convinced the investigator. Final classification, DZ.

Twin Pair No.282 - These 14 year old Negro boys were classified MZ by AID and DZ by the discriminant analysis program. Weight difference was 6%; face length difference, 8%. Twin A was colour blind; Twin B, not. A is left-handed; B is right-handed. Final classification, DZ.

Twin Pair No.284 - These 15 year old Negro girls were not classified the same way by the computer programs. Examination of their files convinced the investigator they were DZ. The twins say they are fraternal. A is left-handed; B is right. Both say they don't look alike. Both twins say that Twin A is darker skinned and heavier. But also both say that their nose, mouth and eyes look alike. Teachers, parents, and friends sometimes mistake one for the other. Differences in head length and breadth both are significant at the .01 level from Verschuer tables. Final classification, DZ.

Twin Pair No.309 - This pair of 17 year old white girls was classified DZ by AID and MZ by discriminant analysis. The girls differ by 8% in height

and 27% in weight. Twin A is right-handed; B is left-handed. The attending physician said they were DZ and the girls believe they are fraternal. Final classification DZ.

Twin Pair No. 317 - These are 14 year old white girls. A says she knows she is an MZ twin; B is just as confident she is DZ because the attending physician said they were DZ. In the questionnaire B said their noses were not alike. This, in fact, is the case since their noses differ in length by 9%. Height difference is 5%; weight 13%. A is right-handed; B is left-handed. Final classification, DZ.

Twin Pair No. 347 - This pair of 14 year old white girls says their attending physician said they are identical. However, Twin B says, "We look nothing alike." A's hair is brown; B's auburn. They never, or only rarely, are mistaken by teachers and parents. Differences in nose length, face length, head length, and height all support final diagnosis of DZ.

Twin Pair No. 362 - These 13 year old Negro boys "know they are identical." But Twin A says that B's hair grows faster than his. They are only occasionally mistaken by teachers, friends and parents. Differences in five biometric measurements, height, weight, head breadth, nose length and face length convinced the investigator of the final DZ classification.

Twin Pair No. 373 - These 13 year old Negro girls know they are fraternal. A is right-handed; B is left-handed. They are rarely mistaken by friends, teachers or parents. A's hair is lighter and thinner than B's. Both twins report their face, legs, and head to be different. The AID program called them DZ; the discriminant analysis MZ. Final classification DZ.

Twin Pair No. 375 - These 17 year old white girls say they are identical but rarely misidentified. They indicate their nose, fingers, hands, stomach and bust to be similar. The discriminant analysis program classifies the girls as DZ, the AID program as MZ. Rorhrer's Index of Body Structure and Kaup's Index both support the diagnosis of DZ. Differences in nose length and face length confirm the final DZ classification.

Twin Pair No. 379 - These 16 year old Negro boys say they look alike and know they are identical because their attending Physician said they were. They are seldom misidentified. Face length difference is the only biometric measure that supports a DZ diagnosis. Other measurements are within MZ limits. Final classification MZ.

APPENDIX B:

PSYCHOLOGICAL TESTS

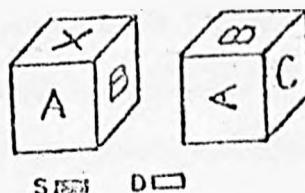
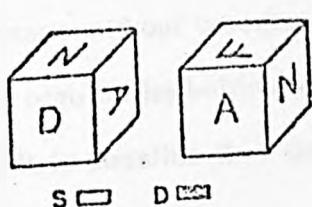
CALENDAR TEST (*calendar*)

On the Calendar Test, developed by Remondino (1962), the examinee is asked to check the exactness of 50 sentences pertaining to the relationship of the days of the week. In a factor analysis, Remondino found that this test loaded on the Number factor. Following are examples of the type of questions asked:

If today is Sunday then tomorrow will be Monday. T F
 If yesterday was Wednesday then today is Saturday. T F

CUBE COMPARISONS TEST (*Cubes*)

The Cube Comparisons Test was developed from Thurstone's Cubes. Each item presents two drawings of a cube, such as shown below. Assuming no cube can have two faces alike, the subject has to decide whether the two drawings can represent the same cube or must represent different cubes. The instructions indicate that the task can be performed (1) by mentally turning one of the cubes so that the face of one cube is oriented in the same way as the like face of the second cube and then comparing the sides one by one or (2) by noting whether two faces which are side by side have the same letters or numbers in the same position relative to one another. The process of obtaining the answers by the second method consists largely of verbal reasoning although it does require a "static" awareness of three-dimensional relations as opposed to a more "dynamic" moving around of the blocks in space.



SIMPLE ARITHMETIC TEST (Arithmetic)

The Simple Arithmetic Test, taken from an unpublished study by Mukherjee (1963), contains seven parts, each consisting of a number of simple arithmetical problems. Part 1 contains 15 problems; part 2, 20 problems; and parts 3 through 7 each contains 25 problems. Speed is an important factor in this test since the examinee is allowed only two minutes per test. This is a multiple-choice test with five alternatives for each problem. The complexity of the problems decreases from part 1 to part 7. Examples contained in each part are given below:

$$\text{Part 1: } \frac{4(77+39-4)}{7} = 60\ 68\ 74\ 64\ 84$$

- Part 2: $5(69+18-3) = 420\ 400\ 410\ 415\ 425$
- Part 3: $69+25-9 = 85\ 95\ 90\ 89\ 80$
- Part 4: $640 \div 5 = 120\ 128\ 88\ 136\ 126$
- Part 5: $8 \times 91 = 738\ 728\ 732\ 739\ 737$
- Part 6: $19 - 7 = 12\ 13\ 14\ 15\ 16$
- Part 7: $83 + 17 = 90\ 110\ 100\ 109\ 101$

WIDE RANGE VOCABULARY TEST (Vocabulary)

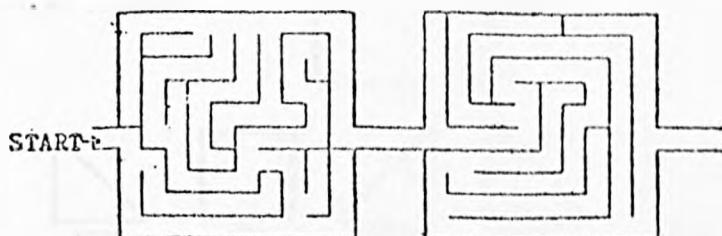
The Wide Range Vocabulary Test, which was adapted from a Cooperative Vocabulary Test (ETS; French, Ekstrom, & Price, 1963) is a five-choice synonym test having items ranging from very easy to very difficult. Samples of the items follow:

- JOVIAL: 1. refreshing 2. scare 3. thickset 4. wise 5. jolly
- DULLARD: 1. peon 2. duck 3. braggart 4. thief 5. dunce

THE MAZES TEST (Mazes)

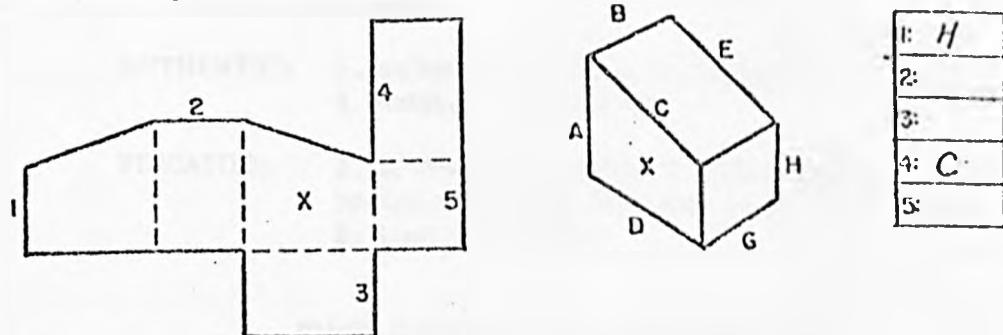
The Mazes Test was taken from a laboratory manual by McKinnon and Henle. The task, typical of earlier Maze problems, is to draw a line from one end to the other of the maze without crossing any line or entering blind alleys. Although this test does not require the holding of a 3-dimensional or even of a 2-dimensional figure in mind, it is possible that solution of the task will be facilitated by the ability

to remember briefly sections of the correct path before one draws a line. A sample maze is shown below.



SURFACE DEVELOPMENT TEST (Surface development)

The Surface Development Test is adapted from Thurstone. In this test the subject has to imagine or visualize how a piece of paper can be folded to form some kind of object. Each item consists of a drawing of a piece of paper which can be folded on the dotted lines to form the object drawn at the right. (See sample below.) The subject is to imagine the folding, to figure out which of the lettered edges on the object are the same as the numbered edges on the piece of paper at the left, and to identify the letters of the answers in the numbered spaces at the far right. He is told that the side of the flat piece marked with the X will always be the same as the side of the object marked with the X. It appears that this task does require mental movement of the parts of the pattern and it is not likely that the subject can perform this task by verbal reasoning only.



FORM BOARD TEST (Form board)

Each item of the Form Board Test presents five shaded drawings of pieces some or all of which can be put together to form a figure presented in outline form.

The task is to indicate which of the pieces when fitted together will form the outline. An example follows:



SELF-JUDGING VOCABULARY TEST (Heim)

The Self-Judging Vocabulary Test, developed by Heim et al (1965), contains two parts. The first part contains 128 words each of which the examinee marks with an A, B, or C (A = I know this word and could explain it to someone unfamiliar with it, B = I am doubtful as to what this word means, C = I have never seen this word before and have no idea what it means.) The second part of the test consists of the first 80 words of the 128 word list presented as a multiple-choice test with six alternatives. The second part of the test combines the advantages of the multiple-choice and creative answer techniques by allowing the examinee who thinks he knows the word but dislikes the six alternatives offered to write his answer in his own words below the six choices. In this study only the second part of the test is used. Examples of test items are given below:

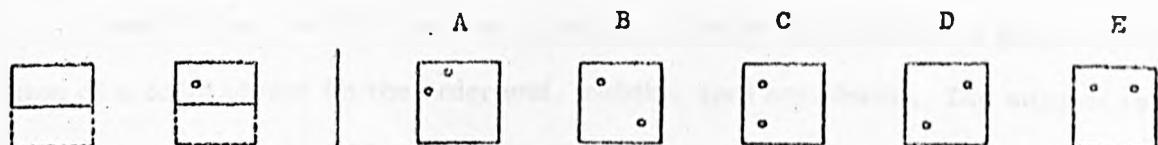
AUTHENTIC: 1. writer 2. to allow 3. respectful 4. a bargain
5. antique 6. genuine

VERSATILE: 1. of varied activities 2. pouring out 3. form of poetry 4. having masculine vigor 5. intense 6. kind of turnstile

PAPER FOLDING TEST (Paper folding)

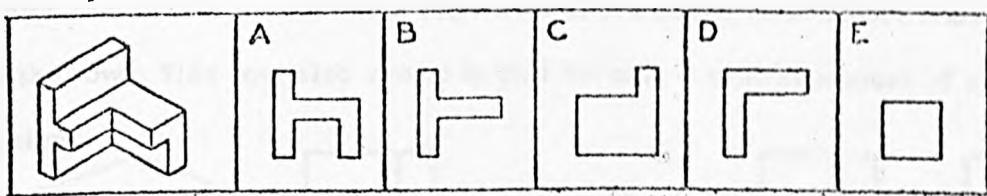
The Paper Folding Test was suggested by Thurstone's Punched Holes. For each item, successive drawings illustrate two or three folds made in a square sheet of paper. A drawing of the folded paper shows where a hole is punched in it. The

subject selects one of five drawings to show how the sheet would appear completely unfolded. While it is probable that the problems can be solved more quickly if one can easily imagine the folding and unfolding, one can also solve these problems by verbal reasoning. Such verbal reasoning, however, is more likely to lead to incorrect answers. A sample appears below.



OBJECT APERTURE TEST (Object aperture)

This test of spatial visualization, developed by Philip H. DuBois and Goldine C. Gleser, consists of a number of items similar to the sample below. A three-dimensional object is shown at the left, followed by outlines of five apertures or openings. The subject is to imagine how the object looks from all directions; then to select from the five apertures outlined the opening through which the solid object would pass directly if the proper side were inserted first. This usually requires the subject to mentally turn the object into other positions.



IDENTICAL PICTURES TEST (Identical pictures)

The Identical Pictures Test consists of items similar to the one shown below. The subject is to select from the five figures or pictures on the right the one which is identical to the figure at the left of the row. This is a test of perceptual speed.

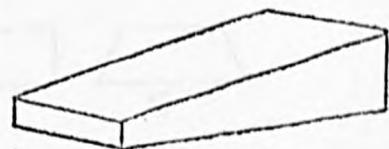
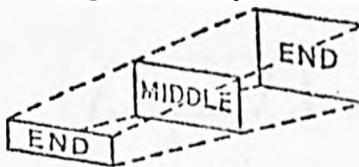
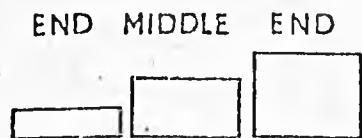


NEWCASTLE SPATIAL TEST (Spatial ability)

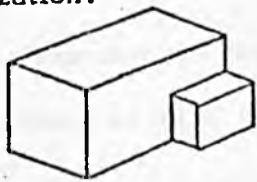
The Newcastle Spatial Test, developed by I. McFarlane Smith and J. S. Lawes for the National Foundation for Educational Research in England and Wales, consists of six different sub-tests ranging in difficulty from simple recognition of selections of regular solids to the more complex problems of surface development.

Test 1 consists of ten sets of drawings in which the end views and middle section of a solid object (in the order end, middle, end) are shown. The subject is to determine which one of 12 solid objects on the opposite page fits each set of drawings. (See sample below.) It appears that this test does not require a very strongly developed spatial ability beyond some idea of perspective drawing.

Imagine them placed like this: and you see they form this:



A sample of test 2 is shown below. This test requires the subject to indicate which one of four choices is a view from above of the solid model shown at the left of the row. This test also seems to call for only a modest amount of spatial visualization.



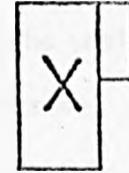
MODEL



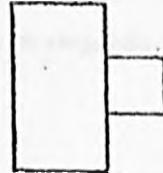
A



B



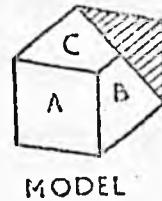
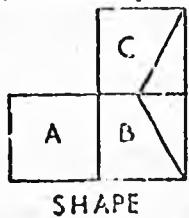
C



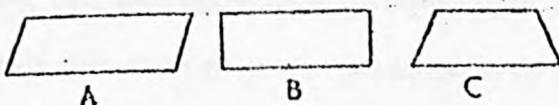
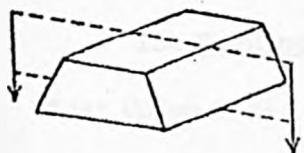
D

Test 3 consists of items similar to the sample below. In each item the subject is given three sides of a cube in a flat pattern and a drawing of a solid cube, part of which is shaded. The subject is to draw lines on the pattern to indicate where he would cut to remove the parts shown shaded on the solid model. One would

probably use spatial visualization to solve this problem although it seems possible to perform the task by verbal reasoning.

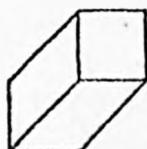


In test 4 each item shows a block of wood. The subject is to imagine a cut made where shown by the dotted lines and to indicate which of the three drawings on the right shows the shape of the cut face. A sample is shown below. It appears that for this task no highly developed ability to visualize 3-dimensional objects is needed.



In each item on test 5 there is a drawing of a solid object, called Shape, and a place to copy it, called Framework. The subject is to put circles around the crosses in the Framework which could be joined to make the Shape. An example is shown below. It appears that it is not necessary to visualize the shape in three dimensions in order to copy it. In fact, the task may be easier if one regards the shape as a flat pattern and merely counts units of distance.

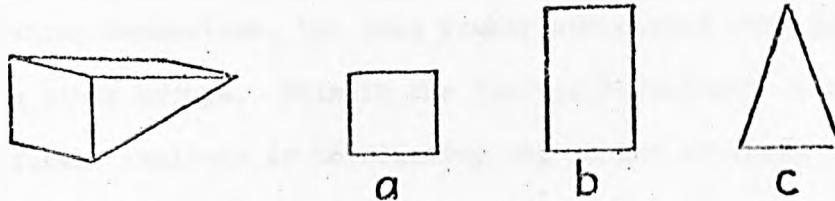
SHAPE E



FRAMEWORK F

1X 2X 3X 4X 5X
1X 2X 3X 4X 5X

Each item in test 6 (see example below) shows a model built from the shapes shown next to it. The subject is required to indicate the number of times each shape was used to make the model. Although one could rely largely on verbal reasoning to solve these problems, visualization would probably allow him to work much faster.



SPELLING ACHIEVEMENT TEST (Spelling)

The Spelling Achievement Test was taken from the Metropolitan Achievement Test (Allen et al, 1946). In this test each word was pronounced by the examiner, used in a sentence, and then pronounced again. The student was then instructed to write the word. The test, consisting of 60 words, was administered to small groups of subjects by trained examiners in accordance with standard procedures. Examples are given below:

garage
instructor
tuberculosis

I keep my car in a garage.
One who teaches is an instructor.
Tuberculosis is a serious lung disease

garage
instructor
tuberculosis

APPENDIX C: THE CONCEPT AND THEORY OF FACTOR ANALYSIS

In psychological and biological studies, many measurements are often made on each individual in the sample. Usually the observed measurements will be correlated. Within the correlation or covariance matrices, the observed variables will tend to fall into groups of variables which are highly correlated among themselves, but only weakly correlated with variables belonging to other groups. This is the "factor structure" of the data. The purpose of factor analysis is to discover the number of common factors underlying the variables and give the covariance between them. The variables with significant specific variation and the proportion of variance accounted for by the specific variation are established. Finally factor analysis shows which factors contribute to variation in which variables allowing inferences about the common causal relationships between the variables.

Factor analysis analyses the original p correlated variables into a small number (m) of uncorrelated variables called common factors, with an uncorrelated residual or specific component remaining for each variable which is also uncorrelated with any of the other variables.

Thus, only a proportion of the variances in the diagonal of the correlation or covariance matrix are assumed to be due to the common factor. This is one advantage of Factor Analysis over Principal Components analysis, which is sometimes used as an approximation to Factor Analysis, in the study of behavioural traits. Principal Components Analysis is superficially similar to Factor analysis, but makes certain assumptions that are untenable in the behavioural context. For example, Principal Components Analysis (PCA) does not allow for some of the variance being specific to certain variables.

The decomposition of the variables into factors does not have a unique solution unless certain restrictions are imposed and the problem of which decomposition to choose is known as the problem of rotation. The clustering of variables into groups or common factors may be considered to occur in

a multidimensional space in which the common factors extracted are the axes. Simple transformations of the factors or, as it is otherwise known, rotation of the axes, will produce an infinite number of solutions from which we have to choose the most appropriate. PCA assumes a unique solution to the problem of rotation such that the orthogonal axes of the principal components solution are the axes of greatest variance. However, the axes of greatest variance are not necessarily the easiest to interpret psychologically. In Factor Analysis, the axes of the common factors are rotated to new orthogonal or oblique axes so that they are clearly interpretable in terms of theoretical ideas about the underlying structure of the traits. This is another advantage of Factor Analysis over Principal Components Analysis as far as determining the underlying structure of psychological variables is concerned.

We must now turn to a more precise formulation of the factor analytic model and a more rigorous discussion of the problems of rotation.

Formulation of the Model

The theory of Factor Analysis has been described by many authors (Joreskog, 1963; Seal, 1964; Harman, 1967; Morrison, 1967; Hope, 1968; Lord and Novick, 1968). We shall follow the notation of Seal in describing the factor analytic model.

Firstly, let p = number of observed variables e.g. the fourteen tests of the Georgia Twin Study

m = the number of underlying factors (i.e. latent variables)

Now, we may define X as a $p \times 1$ row vector of p observed variables, having finite variances, which is $N(\mu, \Sigma)$. The purpose of the factor analysis is to explain the correlational structure of the observed variables in terms of a small number of common factors, the residual variance of each variable being specific. Therefore, let f be a row vector of m common factors with $m < p$. Both X and f are defined in some fixed population of persons.

Now let T be a $p \times m$ matrix of weights relating X to f . These weights are known as factor loadings. If we also specify that each column of T has

at least two non-zero elements then each element of f must be a common factor, since this implies that each such element is common to at least two of the observed variables. The $p \times 1$ vector, μ which is $N(0, \Delta)$ and independent of f , contains specific factors corresponding to the elements of X . These are the residuals after the common factors have been extracted. The $p \times p$ variance - covariance matrix of μ is called Δ . This is a diagonal matrix with non-negative elements. This implies that Δ really contains specific variances since the elements of Δ are uncorrelated. The matrix TT' must be of rank $m < p$.

Now the linear factor analytic model may be written:

$$X = \mu + T f + u \dots \dots \dots (1)$$

We can decompose the variance-covariance matrix of X , Σ , into two parts.

$$\begin{aligned}
 \Sigma &= \varepsilon ((x - \mu)(x - \mu)^T) \\
 &= \varepsilon ((Tf + u)(Tf + u)^T) \\
 &= \varepsilon (Tf(Tf)^T + Tf u^T + u(Tf)^T + uu^T) \\
 &= \varepsilon (Tff^T T^T) + \varepsilon (uu^T)
 \end{aligned}$$

Now since $\mathcal{E}_u = 0$ and $\mathcal{E}_f = 0$ and u and f are independent,

This equation is the basis of factor analysis. Many solutions have been proposed which are mostly approximate and not independent of scale change. Kendall (1957) criticises such approximations because the factors and residuals estimated by these methods have unknown distributions and valid tests of significance cannot be made.

We will discuss two commonly used solutions of this equation. However, first there are two points worth making. It has been assumed throughout that the sample of multivariate observations has been drawn from the multivariate Normal distribution and the methods described here should only be applied to data which conforms to this assumption.

If Δ are the specific variances, then

$$T \varepsilon (ff^1) T^1 = \Sigma - \Delta$$

will have diagonal terms which correspond to the common variances. The communalities of the observed variables, X , are defined as the diagonal elements of the matrix, $D^{-1} T \varepsilon (ff^1) T^1 D^{-1}$ where $D^{-1} = \text{diag } \Sigma$. The communality of a variable corresponds to the squared multiple correlation coefficient between the variable and the set of common factors.

The Principal Factor Solution

The values of T and Δ must be estimated from the sample of observations, which presents problems since we have two unknowns:

$$\Sigma = T (\varepsilon ff^1) T^1 + \Delta$$

The Δ obviously cannot be known until the T has been estimated. Therefore an iterative solution has to be used starting from assumed values of Δ , or else, likely values of Δ can be inserted according to known properties of the data. Therefore, we can write:

$$\hat{\Sigma} - \hat{\Delta} = T (\varepsilon ff^1) T^1$$

We can estimate the T from a Principal Components Analysis working with the matrix of $\hat{\Sigma} - \hat{\Delta}$. Any matrix of the form BB^1 is symmetric and all its eigen-values are non-negative. So, if there are negative values among the largest m eigen values of $\hat{\Sigma} - \hat{\Delta}$ then either $\hat{\Delta}$ is an inappropriate estimate or $\hat{\Sigma} - \hat{\Delta}$ cannot be written as $T \varepsilon (ff^1) T^1$. Therefore, we write

$$|(\hat{\Sigma} - \hat{\Delta}) - k I| = 0$$

and proceed to calculate the m largest roots. Next, we calculate

$$\hat{\Delta} = \text{diag} (\hat{\Sigma} = T (\varepsilon ff^1) T^1)$$

The estimation of T is repeated using new values of $\hat{\Delta}$ until two successive estimates of T change only by a certain specified amount. After completion of the iterations,

$$\text{diag} (T \varepsilon (ff^1) T^1 + \hat{\Delta}) = \text{diag} \hat{\Sigma}$$

but,

$$\text{non-diag}, T (\varepsilon ff^1) T^1 \neq \text{non-diag} \hat{\Sigma}$$

Therefore, we can test the "correctness" of m by asking whether the last

$(p-m)$ roots of the final iteration are sufficiently close to zero for the differences between $\hat{\Sigma}$ and $\hat{T} \hat{T}' + \Delta$ to be explained by sampling variation.

The use of Principal Factoring to obtain estimates of T may be criticised because different results are produced when X is re-scaled.

Canonical Factor Analysis

A solution which does not vary according to the scale of X is given by Canonical Factoring. This solves the equation:

$$|\hat{\Delta}^{-\frac{1}{2}}(\hat{\Sigma} - \hat{\Delta})\hat{\Delta}^{-\frac{1}{2}} - vI| = 0$$

The solution of this equation gives the maximum likelihood solution of Lawley (1940, 1942). An iterative solution was proposed by Maxwell (1961, 1964) using the principal components of the data as the first approximation. The Principal Factoring method has been used in all Factor Analysis carried out in this study.

Rotation of the Factors

The problem of rotation has been briefly described in the introduction to this Appendix. We have pointed out that the decomposition of the p variables into m factors does not have a unique solution. Let T be an orthogonal non-singular matrix of order m , then:

$$\underset{\tilde{\Sigma}}{T'T} = I = \underset{\tilde{\Sigma}}{TT'}$$

$$\text{and } (\underset{\tilde{\Sigma}}{T}) (\underset{\tilde{\Sigma}}{T})^{-1} = T TT' T \\ = T T'$$

Therefore, $\Sigma = T T' + \Delta$, irrespective of T . Therefore if a factor analytic solution exists for some value of m , it follows that there are an infinite number of solutions. Going from one solution to another is known as rotation.

The number of possible solutions may be reduced by introducing certain restraints. One such restraint commonly applied is to require that the T common factors are orthogonal and not oblique. This reduces the number of solutions considerably, but does not solve the problem since this restraint will not produce a unique solution. Also, it is often not a very useful

restraint since oblique factors are often found to make more sense, psychologically, than orthogonal factors. Thurstone (1945) has produced a number of criteria which must be satisfied in order to produce "simple structure" of the $p \times m$ T matrix of rotated factor loadings. These criteria ensure that variables fall into mutually exclusive groups, having high loadings on one factor, possibly intermediate loadings on a few other factors and virtually no loading on the remaining factors. Thus, Thurstone's criteria allow for either orthogonal, or oblique solution of the rotation problem.

Originally, an approximation to simple structure was sought graphically by pair-wise rotation of the factor axes. Morrison (1967) illustrates graphical rotation by means of several examples. When the angle of rotation has been determined, new loadings on the rotated factors may be obtained approximately as the projections of the variables on the rotated axes, or may be determined directly by post-multiplying the factor loadings on the old axes by the transformation matrix:

$$T = \begin{pmatrix} \cos & \sin \\ -\sin & \cos \end{pmatrix}$$

However, graphical rotation is very tedious and time-consuming, especially as the number of factors and variables increases. Therefore, later workers have proposed several analytical solutions for orthogonal or oblique rotation, using various criteria in an attempt to approximate simple structure. Ferguson (1954) and Nehaus and Wrigley (1954) independently produced solutions for orthogonal rotation based on what is now known as the quartimax criterion for rotation. Quartimax rotation attempts to maximise the fourth powers of the factor loadings. Carroll (1953) also used the quartimax criterion for achieving simple structure, but his formulation permitted oblique as well as orthogonal solutions.

Kaiser (1958) proposed a different criterion for producing simple

structure, known as the varimax criterion, which attempts to maximise the squared loadings in each column of the factor matrix. Harman (1967) has made a comparison of the loadings obtained through quartimax and varimax rotation, and shown that the varimax criterion produces solutions which more nearly approximate simple structure than the quartimax criterion. Hendrickson and White (1964) have proposed an alternative method of oblique rotation to simple structure known as the Promax method.

APPENDIX D: MULTIPLE REGRESSION ANALYSIS

The most general form of multiple regression analysis will be discussed here, where q error free measurements are used to explain p interconnected variates. A full discussion of multiple regression analysis may be found in Seal (1968), and we follow Seal in writing the full model as:

$$\begin{aligned} x_{ij} &= \beta_{10} z_{0j} + \beta_{11} z_{1j} + \beta_{12} z_{2j} + \beta_{13} z_{3j} + \dots + \beta_{1q} z_{qj} + e_{1j} \\ x_{2j} &= \beta_{20} z_{0j} + \beta_{21} z_{1j} + \beta_{22} z_{2j} + \beta_{23} z_{3j} + \dots + \beta_{2q} z_{qj} + e_{2j} \\ x_{pj} &= \beta_{p0} z_{0j} + \beta_{p1} z_{1j} + \beta_{p2} z_{2j} + \beta_{p3} z_{3j} + \dots + \beta_{pq} z_{qj} + e_{pj} \end{aligned}$$

where x_p are the p-variates.

β_{pj} are the pj regression coefficients for the p variates and the q measurements.

j is the number of units on which the measurements are made - usually the number of individuals.

e_{pj} are the error terms.

N.B. The first term on the right hand sides (i.e. z_{0j}) is the mean value and the following terms up to z_{qj} represent the explanatory variables.

The p component vectors of x measurements are:

$$x_1 = \begin{bmatrix} x_{11} \\ x_{12} \\ x_{13} \\ \vdots \\ \vdots \\ x_{1j} \end{bmatrix} \quad x_2 = \begin{bmatrix} x_{21} \\ x_{22} \\ x_{23} \\ \vdots \\ \vdots \\ x_{2j} \end{bmatrix} \quad \dots \quad x_p = \begin{bmatrix} x_{p1} \\ x_{p2} \\ x_{p3} \\ \vdots \\ \vdots \\ x_{pj} \end{bmatrix}$$

Let $X = [x_1 \ x_2 \ \dots \ x_p]$

The same notation is used for e_1, e_2 and E

$$\text{Now } Z = \begin{bmatrix} z_{01} & z_{02} & \dots & z_{0j} \\ z_{11} & z_{12} & \dots & z_{1j} \\ z_{21} & z_{22} & \dots & z_{2j} \\ \vdots & \vdots & & \vdots \\ \vdots & \vdots & & \vdots \\ z_{q1} & z_{q2} & \dots & z_{qj} \end{bmatrix}$$

$$\text{and } \beta_1 = \begin{bmatrix} \beta_{10} \\ \beta_{11} \\ \beta_{12} \\ \vdots \\ \vdots \\ \beta_{1q} \end{bmatrix}, \quad \beta_2 = \begin{bmatrix} \beta_{20} \\ \beta_{21} \\ \beta_{22} \\ \vdots \\ \vdots \\ \beta_{2q} \end{bmatrix}, \quad \beta_p = \begin{bmatrix} \beta_{p0} \\ \beta_{p1} \\ \beta_{p2} \\ \vdots \\ \vdots \\ \beta_{pq} \end{bmatrix}$$

Therefore, following the previous notation

$$B = [\beta_1 \ \beta_2 \ \dots \ \beta_p]$$

The full model may now be re-written as follows:

$$\underset{(jxp)}{X} = \underset{(jxq)}{Z'} \underset{(qxp)}{B} + \underset{(jxp)}{E}$$

Now premultiplying by Z and replacing B by \hat{B} its least squares estimate
 (NB $\Sigma(E) = 0$ and $\Sigma(E'E) = \Sigma$, where O is a jxp matrix of zeros and

$$\Sigma = \begin{bmatrix} \sigma_{11} & \sigma_{12} & \dots & \sigma_{1p} \\ \sigma_{21} & \sigma_{22} & \dots & \vdots \\ \vdots & \vdots & & \vdots \\ \sigma_{p1} & \sigma_{p2} & \dots & \sigma_{pp} \end{bmatrix}, \text{ i.e.}$$

the variance - covariance matrix), we now obtain:

$$Z X = Z Z' \hat{B}$$

from whence

$$\hat{B} = (Z Z')^{-1} Z X$$

This full model is designated Ω and assumes that all q measurements are affecting the p -variates. The next stage is to eliminate s rows of the B_{Ω} and write the reduced models designated by W as:

$$\begin{matrix} X \\ (jxp) \end{matrix} = \begin{matrix} Z' \\ (jx(q-s)) \end{matrix} \begin{matrix} B \\ ((q-s)x p) \end{matrix} + \begin{matrix} E \\ (jxp) \end{matrix}$$

The s rows which are eliminated depend on the design of the experiment and the effects we are interested in. When the W model has been written we proceed to test the validity of the reduced model by comparing the two sets of residuals from Ω and W respectively. We calculated $(N-q) \hat{\Sigma}_{\Omega}$ and $(N-S) \hat{\Sigma}_W$ where

$$f \hat{\Sigma} = X'X - \hat{B}' ZZ' \hat{B} \quad (\text{See Seal})$$

and B and Z refer to either Ω or W provided f is adjusted appropriately. The ratio of the determinants is written $U_p, q-s, f$ and the variate - $[f - \frac{1}{2}(p-q s + 1)]$. In $U_p, q-s, f$ is distributed approximately as chisquare with $p(q-s)$ degrees of freedom. If the chisquare is significant, then the significance of the $p(q-s)$ values of B omitted from the model are considered to be significant.

This technique is often useful in psychological studies when different psychological variables can be partly explained in terms of age, socio-economic status and other similar causes. It enables a correction to be made to the data for the predictor variables so that variation in the variable due to other causes can be estimated without being biased by the effects of the criterion variables.

APPENDIX E: MAXIMUM-LIKELIHOOD ESTIMATION AND WEIGHTED LEAST SQUARES.

MAXIMUM-LIKELIHOOD ESTIMATION

A problem exists when we wish to estimate population parameters from a sample and several estimators exist. The criteria used to determine the "best" estimator are based on the distributions of estimates produced by the estimators. Four properties of estimators are important in discriminating between them and in choosing the "best" estimator.

CONSISTENCY

Consistency is a limiting property, affecting the behaviour of estimators (t 's) as sample size (n) approaches infinity. A consistent estimator is one where the probability that estimates (θ 's) are close to the true values of the parameters (θ 's) approaches unity, as the sample size tends to infinity.

Lack of Bias

An unbiased estimator is one where:

$$\mathbb{E}(t) = \theta$$

for all values of n and θ . Thus, a consistent estimate may be biased, but consistent estimators must tend to be unbiased as the sample size approaches infinity. It is possible that there may be no unbiased estimator for a parameter.

Efficiency

If we choose consistent, unbiased estimators, then estimators with a smaller variance will deviate less, on average, from the true parameter value, than estimators with a larger variance. This is known as the criterion of minimum variance and an estimator with minimum variance as the sample size tends to infinity, is known as an efficient estimator.

Sufficiency

Fisher (1921,1925) defined the criterion of the sufficiency of estimators. A sufficient estimator is one which uses all the information in the sample about the parameter being estimated.

In order to find an estimator that satisfied these criteria, the method of Maximum-likelihood is used. Kendall and Stuart (1961) outline the principles and show how the best estimator of an effect may be found by the method of maximum-likelihood. Fisher has shown that the maximum-likelihood estimator satisfies most of the criteria specified above. Maximum-Likelihood estimators are consistent, although they are not necessarily unbiased. They are sufficient, where a sufficient estimator exists, and have minimum variance in large samples (i.e. they are efficient) and sometimes in small samples also. The Maximum-Likelihood estimator is asymptotically normally distributed (i.e. its distribution approaches normality as the sample size approaches infinity) and shows the property of functional invariance (i.e. if $\hat{\theta}$ is the maximum-likelihood estimate of θ , then $f(\hat{\theta})$ is the maximum-likelihood estimate of $f(\theta)$).

WEIGHTED LEAST SQUARES

When we wish to explain a set of statistics in terms of a linear combination of the parameters of a model, then the method of least squares provides maximum-likelihood estimates of the parameters, given certain assumptions.

These assumptions are:

1. That the observations are independent
2. That the observations are normally distributed

When the statistics are each based on the same number of observations, then least squares is used. Where the sample size differs with each statistic, the statistics are not known with equal precision and estimates of the parameters obtained by least squares are not independent. However, this problem may be overcome and maximum-likelihood estimates of the parameters obtained by appropriately weighting the statistics. In the method of weighted least squares, the statistics are weighted by the inverse of their variances. For normally distributed estimates, the inverse of the variance is equivalent to the amount of information about that estimate.

We may now formulate the linear equation for which we wish to find the least squares estimator:

$$\tilde{X} = \tilde{A} \tilde{W} \tilde{\theta} + \tilde{e}$$

where \tilde{X} is an $n \times 1$ vector of statistics

\tilde{A} is an $n \times k$ matrix of the coefficients of the model

\tilde{W} is an $n \times n$ diagonal matrix of weights

$\tilde{\theta}$ is a $k \times 1$ vector of the parameters of the model

and \tilde{e} is an $n \times 1$ vector of error terms

The expected value of \tilde{e} , $E(\tilde{e}) = 0$, and the variance-covariance matrix of \tilde{e} is given by $V(\tilde{e}) = E(e e') = \sigma^2 \tilde{I}$ where \tilde{I} is the $n \times n$ identity matrix. Thus, we are assuming that the e 's are uncorrelated, have zero means and the same variance.

To obtain the least squares estimator of θ , we must minimise the sum of squares of $\tilde{X} - \tilde{A} \tilde{W} \tilde{\theta}$ for variation in θ , which is given by:

$$\text{Sum of Squares} = S = (\tilde{X} - \tilde{A} \tilde{W} \tilde{\theta})' (\tilde{X} - \tilde{A} \tilde{W} \tilde{\theta})$$

In order to minimise S , we must let $\frac{ds}{d\theta} = 0$.

Differentiating, we find:

$$2\tilde{A}'\tilde{W}(\tilde{X} - \tilde{A} \tilde{W} \tilde{\theta}) = 0$$

which gives the least squares estimator as:

$$\hat{\theta} = (\tilde{A}'\tilde{W}\tilde{A})^{-1}(\tilde{A}'\tilde{W}\tilde{X}) \dots \dots \dots (1)$$

The matrix $(\tilde{A}'\tilde{W}\tilde{A})$ is the weighted information matrix. This matrix comprises the weighted sums of squares and products of the elements of the column vectors of A , the model matrix. The inverse of the information matrix yields the variance - covariance matrix of the estimates. The parameter estimates are obtained by evaluating equation (1). The variances of these estimates are given by the diagonal terms of the variance-covariance matrix. The estimates may be tested for significant departures from zero by use of the t test. The one-tailed test is used when we expect an estimate to take a particular sign. In the absence of any expectation for the sign of a parameter estimate,

the two-tailed test is used.

If parameter estimates turn out to be non-significant, the expectations for these parameters may be dropped from the model and a simpler model may be fitted. We now have the problem of deciding which of our models are adequate to explain variation in our observations. The "goodness of fit" of a given model may be found since the sum of squares of the residuals (i.e. the \hat{e} 's), $(n-k)s^2/\sigma^2$, is a chisquare with $n-k$ degrees of freedom. If this chisquare is significant, the model we have fitted is not adequate to explain variation in the trait we are interested in and further models must be tested.

APPENDIX G: TABLES OF BIASES AND POWER

This appendix contains twelve tables, providing information about fourteen types of population, each with different genetical and environmental causes of variation. The population parameters have been specified in the text of part C. The meaning of the symbols used for the parameters is briefly summarised in Key A and their contribution to the total variation is also given. All the keys are placed immediately before the Tables.

The genetical and environmental effects contributing to variation in each of the fourteen population types are summarised in Key B. Key B also indicates the number of the Table in which information about a particular population can be found.

The fourteen populations have been classified into five groups, whose main interests are additive effects, dominance, genotype-environment interaction, cultural transmission and sibling effects. This classification forms the basis of the discussion in the text.

A number of models have been fitted to each population, using the methods described in Section 3 of Part A and Appendix E, in order to determine:

1. The contribution of "true" population parameters to parameters estimated using the "wrong" model i.e. the biases which may occur in model fitting.
2. How heritabilities may be biased when the wrong model is fitted.
3. The number of individuals required for a given estimated parameter to be significant at the 5% level in 95% of cases.

4. The number of individuals required for rejection of the wrong model at the 5% level to occur in 95% of cases.

The models which were used and appear in the Tables are summarised in Key C. The information obtained is presented in two types of table, labelled A and B. Additional numbering is used when more than one page is required for any table e.g. Table 1B.2 refers to the second page of Table 1B.

The "A" Tables

These Tables contain the biases introduced into parameter estimates when a wrong model is fitted to a particular population type. The contribution of the "true" population parameters to the parameters estimated using the wrong model is tabulated. The "true" parameters form the column headings. The models fitted to the population are numbered downwards. The estimated parameters of the wrong model can be read in terms of the "true" parameters e.g. when the $E_1 E_2$ model is wrongly fitted to a population in which the true causes of variation are E_1 and D_R , it can be seen from Table 1A that E_1 would be estimated as $E_1 + \frac{1}{2} D_R$ and E_2 as $\frac{1}{2} D_R$.

The following additional points must be noted.

1. No decimal places are given when the contribution of the "true" parameter to the estimated parameter is an integer.
2. In other cases, two decimal places only are given.
3. A value of 0.00 indicates that the contribution of the "true" parameter to the estimated parameter is less than 0.005.
4. A " - " indicates no contribution of the "true" parameter to the estimated parameter.

The "B" Tables

1. The columns headed "True Parameter Values" give the variance produced by the true population parameters, given particular levels of heritability, assortative mating, dominance, genotype-environment interaction, genotype-environment covariance produced by cultural transmission and genotype-environment covariance produced by sibling effects. For any population type there are a series of different populations in which the variation produced by the true parameters differs. These are labelled a, b, c, etc. in Tables 1-10. In Tables 11 and 12, the different populations are characterised by the two parameters h_N^2 and ρ , where h_N^2 is the narrow heritability and ρ is the proportion of loci which contribute both to D_R and D_R'' i.e. the proportion of loci having both direct effects on the phenotype and indirect effects on the phenotype of siblings (see text for conditions under which this is true). How the different populations were specified is explained in the text of Part C.
2. The models fitted to the populations are numbered downwards, and their parameters can be determined as the parameters under which there are entries in the columns headed 'Sample Sizes Needed to Detect:'
3. The entries in these columns give the number of individuals required for estimated parameters to be significant at the 5% level in 95% of cases.
4. The number of individuals required for rejection of a wrong model at the 5% level in 95% of cases is given in the column headed "R".
5. Estimates of narrow (h_N^2) and broad (h_B^2) heritability are also given, where h_N^2 is defined as:

$$h^2_N = \frac{\frac{1}{2} D_R + \frac{1}{2} M}{V_T}$$

and h^2_B is defined, somewhat unconventionally as:

$$h^2_B = \frac{\frac{1}{2} D_R + \frac{1}{2} M + \frac{1}{4} H_R + \frac{1}{2} I + C + \frac{1}{2} D_R'' + D_R'}{V_T}$$

and V_T is the total variance.

The following additional points must be noted.

- a. Models marked by an asterix are the correct models for the population to which they are being fitted.
- b. Where the sample size needed to detect an effect is followed by a "X", the estimated value of the effect is negative.
- c. A value given as " ∞ ", indicates that the number was greater than 99,999.

KEY A: SYMBOLS USED FOR GENETICAL AND ENVIRONMENTAL PARAMETERS

SYMBOL	COMTRIBUTION TO TOTAL VARIATION	MEANING OF SYMBOL
E_1	1	Specific environmental variation
E_2	1	Common environmental variation
D_R	$\frac{1}{2}$	Additive genetical variation
M	$\frac{1}{2}$	Additive genetical variation produced by assortative mating
H_R	$\frac{1}{4}$	Dominance variation
I	$\frac{1}{2}$	Systematic genotype-environment interaction
C	1	Variation produced by cultural transmission
D_R''	$\frac{1}{2}$	Variation produced by the contribution of the additive genetical deviations of siblings to the environment of their co-siblings
D_R'	1	Covariance between genotype and environment produced by the contribution of the phenotypes of sibs to the environments of their co-sibs.

KEY B: GENETICAL AND ENVIRONMENTAL FACTORS CONTRIBUTING TO VARIATION
IN FOURTEEN POPULATIONS

POPULATION	TABLE	POPULATION PARAMETERS	
1	1	$E_1 D_R$	
2	1	$E_1 E_2 D_R$	
3	1	$E_1 D_R M$	Additive effects
4	2	$E_1 E_2 D_R M$	
5	3	$E_1 D_R H_R$	
6	4	$E_1 E_2 D_R H_R$	
7	5	$E_1 D_R H_R M$	Dominance
8	6	$E_1 E_2 D_R H_R M$	
9	7	$E_1 E_2 D_R I$	
10	8	$E_1 E_2 D_R I M$	Genotype-environment interaction
11	9	$E_1 E_2 D_R H_R I$	
12	10	$E_1 E_2 D_R C$	Cultural transmission
13	11	$E_1 D_R D_R'' D_R'$	
14	12	$E_1 E_2 D_R D_R'' D_R'$	Sibling effects

KEY C: MODELS FITTED TO THE POPULATIONS

 $E_1 E_2$ $E_1 D_R$ $E_1 E_2 D_R$ $E_1 D_R M$ $E_1 D_R H_R$ $E_1 E_2 D_R M$ $E_1 E_2 D_R H_R$ $E_1 D_R H_R M$ $E_1 E_2 D_R I$ $E_1 E_2 D_R C$ $E_1 D_R D_R' D_R'$ $E_1 E_2 D_R H_R M$ $E_1 E_2 D_R H_R I$ $E_1 E_2 D_R D_R' D_R'$ $E_1 D_R D_R' D_R' M$

TABLE 1A

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS	
		<u>E₁</u>	<u>D_R</u>
1	<u>E₁</u>	.1	0.25
	<u>E₂</u>	-	0.25
1	<u>E₁</u>	<u>E₁</u>	<u>D_R</u>
	<u>E₂</u>	-	0.25
2	<u>E₁</u>	1	0.46
	<u>D_R</u>	-	1.05
3	<u>E₁</u>	1	0.5
	<u>D_R</u>	-	3
	<u>H_R</u>	-	-4
4	<u>E₁</u>	1	0.51
	<u>D_R</u>	-	-0.50
	<u>M</u>	-	1.34
1	<u>E₁</u>	<u>E₁</u>	<u>D_R</u>
	<u>E₂</u>	-	0.25
2	<u>E₁</u>	1	-
	<u>D_R</u>	-	1.16
3	<u>E₁</u>	1	-
	<u>E₂</u>	-	0.12
	<u>D_R</u>	-	1.03
4	<u>E₁</u>	1	-
	<u>D_R</u>	-	3.18
	<u>H_R</u>	-	-4.17

TABLE 1B.1

MODEL	TRUE PARAMETER VALUES			SAMPLE SIZES NEEDED TO DETECT:					R	h_N^2	h_B^2
	E_1	E_2	D_R	E_1	E_2	D_R	H_R	M			
1a	112.50	-	225.00	84	728	-	-	-	562	-	-
b	22.50	-	405.00	90	205	-	-	-	147	-	-
2a	112.50	-	225.00	117	-	191	-	-	-	0.50	-
b	22.50	-	405.00	141	-	41	-	-	-	0.90	-
1a*	56.25	56.25	225.00	91	160	-	-	-	440	-	-
b*	11.25	11.25	405.00	91	160	-	-	-	137	-	-
2a	56.25	56.25	225.00	127	-	105	-	-	1085	0.63	-
b	11.25	11.25	405.00	142	-	38	-	-	2215	0.92	-
3a*	56.25	56.25	225.00	221	633	207	-	-	-	0.50	-
b*	11.25	11.25	405.00	282	1361	42	-	-	-	0.90	-
4a	56.25	56.25	225.00	139	-	1114	$13444^X_{\infty X}$	-	1010	0.88	0.63
b	11.25	11.25	405.00	144	-	749	-	-	2151	0.98	0.93
5a	56.25	56.25	225.00	132	-	1040	-	4544	1237	0.45	0.62
b	11.25	11.25	405.00	142	-	157	-	89594	2171	0.89	0.92

TABLE 1B.2

MODEL	TRUE PARAMETER VALUES			SAMPLE SIZES NEEDED TO DETECT:				R	h_N^2	h_B^2
	E_1	D_R	M	E_1	E_2	D_R	H_R			
1a	112.5	225.0	75.0	86	424	-	-	-	401	-
b	22.5	405.0	331.4	92	123	-	-	-	108	-
2a	112.5	225.0	75.0	122	-	126	-	-	12066	0.59
b	22.5	405.0	331.4	142	-	36	-	-	948	0.94
3a	112.5	225.0	75.0	176	39354	174	-	-	14315	0.57
b	22.5	405.0	331.4	284	67914	37	-	-	919	0.94
4a	112.5	225.0	75.0	136	-	1160	10244 ^x	-	28214	0.87
b	22.5	405.0	331.4	144	-	142	400 ^x	-	3549	1.84
5a*	112.5	225.0	75.0	129	-	1222	-	6771	-	0.57
b*	22.5	405.0	331.4	144	-	207	-	377	-	0.94

TABLE 2A

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS			
		E ₁	E ₂	D _R	M
1	E ₁	1	-	0.25	0.16
	E ₂	-	1	0.25	0.38
2	E ₁	1	0.47	-	-0.03
	D _R	-	1.02	1	1.12
3	E ₁	1	-	-	-0.04
	E ₂	-	1	-	0.09
	D _R	-	-	1	0.94
4	E ₁	1	0.50	-	0.00
	D _R	-	3	1	3.24
	H _R	-	-4	-	-4.27
5	E ₁	1	0.51	-	-
	D _R	-	-0.37	1	-
	M	-	1.22	-	1
6	E ₁	1	0.52	-	-0.03
	D _R	-	0.84	1	1.01
	D _R	-	-0.49	-	0.08
	D _R	-	0.86	-	0.17
7	E ₁	1	-	-	-0.01
	E ₂	-	1	-	0.05
	D _R	-	-	1	3.02
	H _R	-	-	-	-4.02
8	E ₁	1	-	-	-0.01
	E ₂	-	1	-	0.26
	D _R	-	-	1	1.16
	I	-	-	-	-0.58
9	E ₁	1	0.49	-	-
	D _R	-	-4.26	1	-
	H _R	-	5.57	-	-
	M	-	2.25	-	1

TABLE 2B.1

MODEL	TRUE PARAMETER VALUES				SAMPLE SIZES NEEDED TO DETECT:						R	h_N^2	h_B^2
	E_1	E_2	D_R	M	E_1	E_2	D_R	H_R	D_R''	D_R'			
1a	56.25	56.25	225.00	75.00	91	140	-	-	-	-	313	-	-
b	11.25	11.25	405.00	331.36	92	110	-	-	-	-	98	-	-
2a	56.25	56.25	225.00	75.00	130	-	83	-	-	-	904	0.70	-
b	11.25	11.25	405.00	331.36	142	-	35	-	-	-	611	0.96	-
3a	56.25	56.25	225.00	75.00	238	604	154	-	-	-	11680	0.56	-
b	11.25	11.25	405.00	331.36	286	1221	37	-	-	-	890	0.94	-
4a	56.25	56.25	225.00	75.00	140	-	513	2582 ^x	-	-	1036	1.19	0.68
b	11.25	11.25	405.00	331.36	144	-	133	358 ^x	-	-	1281	1.88	0.96
5a	56.25	56.25	225.00	75.00	132	-	170	-	70304 ^x	982	1545	0.68	-
b	11.25	11.25	405.00	331.36	144	-	79	-	62248	1166	753	0.95	-

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TABLE 2B.2

MODEL	TRUE PARAMETER VALUES				SAMPLE SIZES NEEDED TO DETECT:						R	h_N^2	h_B^2
	E_1	E_2	D_R	M	E_1	E_2	D_R	H_R	I	M			
6a	56.25	56.25	225.00	75.00	135	-	1099	-	-	1533	1334	0.67	-
b	11.25	11.25	405.00	331.36	144	-	188	-	-	339	2195	0.96	-
7a	56.25	56.25	225.00	75.00	256	665	1020	7722 ^x	-	-	44181	0.85	0.57
b	11.25	11.25	405.00	331.36	285	1289	140	382 ^x	-	-	3579	1.84	0.94
8a	56.25	56.25	225.00	75.00	273	1044	190	-	21113 ^x	-	15962	0.59	0.51
b	11.25	11.25	405.00	331.36	286	1078	39	-	1357 ^x	-	1310	0.94	0.70
9a*	56.25	56.25	225.00	75.00	256	802	822	-	-	6133	-	0.57	-
b*	11.25	11.25	405.00	331.36	285	1393	185	-	-	363	-	0.94	-
10a	56.25	56.25	225.00	75.00	140	-	∞	34466	-	3815 ^x	1300	0.37	0.67
b	11.25	11.25	405.00	331.36	144	-	39430	∞	-	3097	2107	0.91	0.96

TABLE 3A

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS		
		E_1	D_R	H_R
1	E_1	1	0.25	0.15
	E_2	-	0.25	0.10
2	E_1	1	-	0.02
	D_R	-	1	0.47
3	E_1	1	-	0.02
	E_2	-	-	-0.01
	D_R	-	1	0.49
4	E_1	1	-	0.01
	D_R	-	1	0.63
	M	-	-	-0.13

TABLE 3B

MODEL	TRUE PARAMETER VALUES			SAMPLE SIZES NEEDED TO DETECT:					R	h_N^2	h_B^2
	E_1	D_R	H_R	E_1	E_2	D_R	H_R	M			
1a	112.5	150.0	150.0	84	820	-	-	-	587	-	-
b	22.5	270.0	270.0	89	232	-	-	-	156	-	-
c	112.5	200.0	50.0	84	756	-	-	-	567	-	-
d	22.5	360.0	90.0	90	213	-	-	-	152	-	-
2a	112.5	150.0	150.0	116	-	199	-	-	71089	0.49	-
b	22.5	270.0	270.0	141	-	41	-	-	13405	0.90	-
c	112.5	200.0	50.0	117	-	193	-	-	∞	0.50	-
d	22.5	360.0	90.0	141	-	41	-	-	∞	0.90	-
3a	112.5	150.0	150.0	153	∞^x	260	-	-	72038	0.49	-
b	22.5	270.0	270.0	270	∞^x	42	-	-	13048	0.90	-
c	112.5	200.0	50.0	156	∞^x	255	-	-	∞	0.50	-
d	22.5	360.0	90.0	270	∞^x	42	-	-	∞	0.90	-
4a*	112.5	150.0	150.0	134	-	9505	40853	-	-	0.33	0.50
b*	22.5	270.0	270.0	144	-	2311	8464	-	-	0.60	0.90
c*	112.5	200.0	50.0	134	-	5208	∞	-	-	0.44	0.50
d*	22.5	360.0	90.0	144	-	1206	68433	-	-	0.80	0.90
5a	112.5	150.0	150.0	123	-	863	-	78126 ^x	∞	0.50	-
b	22.5	270.0	270.0	142	-	151	-	12976 ^x	38499	0.90	-
c	112.5	200.0	50.0	123	-	951	-	∞^x	∞	0.50	-
d	22.5	360.0	90.0	142	-	159	-	∞^x	∞	0.90	-

TABLE 4A

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS			
		E_1	E_2	D_R	H_R
1	E_1	1	-	0.25	0.15
	E_2	-	1	0.25	0.10
2	E_1	1	0.46	-	0.01
	D_R	-	1.05	1	0.49
3	E_1	1	-	-	0.01
	E_2	-	1	-	-0.01
	D_R	-	-	1	0.51
4	E_1	1	0.50	-	-
	D_R	-	3	1	-
	H_R	-	-4	-	1
5	E_1	1	0.53	-	0.01
	D_R	-	0.80	1	0.49
	D_R	-	0.46	-	0.02
	D_R	-	0.85	-	-0.02
6	E_1	1	0.51	-	0.00
	D_R	-	0.55	1	0.67
	M	-	1.38	-	-0.16
7	E_1	1	-	-	0.01
	E_2	-	1	-	-0.04
	D_R	-	-	1	0.47
	I	-	-	-	0.09
8	E_1	1	-	-	0.00
	E_2	-	1	-	0.01
	D_R	-	-	1	0.68
	M	-	-	-	-0.18
9	E_1	1	0.49	-	-
	D_R	-	-4.05	1	-
	H_R	-	5.21	-	1
	M	-	2.23	-	-

TABLE 4B.1

MODEL	TRUE PARAMETER VALUES				SAMPLE S	
	E ₁	E ₂	D _R	H _R	E ₁	E ₂
1a	56.25	56.25	150.00	150.00	91	171
b	56.25	56.25	200.00	50.00	91	164
c	11.25	11.25	270.00	270.00	90	181
d	11.25	11.25	360.00	90.00	91	168
2a	56.25	56.25	150.00	150.00	127	-
b	56.25	56.25	200.00	50.00	127	-
c	11.25	11.25	270.00	270.00	142	-
d	11.25	11.25	360.00	90.00	142	-
3a	56.25	56.25	150.00	150.00	218	677
b	56.25	56.25	200.00	50.00	221	408
c	11.25	11.25	270.00	270.00	282	1415
d	11.25	11.25	360.00	90.00	282	1379
4a	56.25	56.25	150.00	150.00	139	-
b	56.25	56.25	200.00	50.00	139	-
c	11.25	11.25	270.00	270.00	144	-
d	11.25	11.25	360.00	90.00	144	-
5a	56.25	56.25	150.00	150.00	128	-
b	56.25	56.25	200.00	50.00	128	-
c	11.25	11.25	270.00	270.00	142	-
d	11.25	11.25	360.00	90.00	142	-

SIZES NEEDED TO DETECT:

R h_N^2 h_B^2

D_R	H_R	D_R''	D_R'				
-	-	-	-	464	-	-	-
-	-	-	-	450	-	-	-
-	-	-	-	147	-	-	-
-	-	-	-	137	-	-	-
108	-	-	-	1154	0.63	-	6
107	-	-	-	1110	0.63	-	67
38	-	-	-	2024	0.93	-	63
38	-	-	-	2229	0.93	-	63
208	-	-	-	49593	0.50	-	-
208	-	-	-	∞	0.50	-	-
42	-	-	-	12124	0.90	-	-
42	-	-	-	∞	0.90	-	-
1800	∞^x	-	-	1120	0.71	0.63	-
1296	22779 ^x	-	-	1105	0.82	0.63	-
1760	11524	-	-	2161	0.68	0.93	-
969	∞	-	-	2156	0.88	0.93	-
217	-	41965 ^x	1363	1868	0.61	-	-
213	-	36568 ^x	1217	1892	0.61	-	-
85	-	∞^x	∞	1877	0.93	-	-
85	-	∞^x	62658	2112	0.93	-	-

TABLE 4B.2

MODEL	TRUE PARAMETER VALUES				SAMPLE SIZES NEEDED TO DETECT:						R	h_N^2	h_B^2
	E_1	E_2	D_R	H_R	E_1	E_2	D_R	H_R	I	M			
6a	56.25	56.25	150.00	150.00	132	-	868	-	-	9112	1222	0.61	-
b	56.25	56.25	200.00	50.00	132	-	975	-	-	5629 ^x	1237	0.61	-
c	11.25	11.25	270.00	270.00	142	-	144	-	-	29198 ^x	2034	0.93	-
d	11.25	11.25	360.00	90.00	142	-	170	-	-	∞	2151	0.93	-
7a*	56.25	56.25	150.00	150.00	249	668	8184	30420	-	-	-	0.33	0.50
b*	56.25	56.25	200.00	50.00	249	661	4427	∞	-	-	-	0.44	0.50
c*	11.25	11.25	270.00	270.00	284	1369	2232	7968	-	-	-	0.60	0.90
d*	11.25	11.25	360.00	90.00	284	1364	1162	64018	-	-	-	0.80	0.90
8a	56.25	56.25	150.00	150.00	268	1829	326	-	∞	-	56711	0.49	0.52
b	56.25	56.25	200.00	50.00	269	1572	315	-	∞	-	∞	0.50	0.51
c	11.25	11.25	270.00	270.00	286	∞	43	-	42457	-	14324	0.90	0.95
d	11.25	11.25	360.00	90.00	286	84269	43	-	∞	-	∞	0.90	0.92
9a	56.25	56.25	150.00	150.00	250	713	625	-	-	42184 ^x	∞	0.50	-
b	56.25	56.25	200.00	50.00	250	722	700	-	-	∞ ^x	∞	0.50	-
c	11.25	11.25	270.00	270.00	285	1340	141	-	-	11588 ^x	38622	0.90	-
d	11.25	11.25	360.00	90.00	285	1363	150	-	-	89691 ^x	∞	0.90	-
10a	56.25	56.25	150.00	150.00	139	-	∞ ^x	11798	-	6146	1237	0.11	0.62
b	56.25	56.25	200.00	50.00	139	-	∞	19049	-	6140	1217	0.22	0.62
c	11.25	11.25	270.00	270.00	144	-	19753	16544	-	∞	2097	0.55	0.92
d	11.25	11.25	360.00	90.00	144	-	9170	76414	-	∞	2092	0.75	0.92

TABLE 5A

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS			
		E ₁	D _R	H _R	M
1	E ₁	1	0.25	0.15	0.15
	E ₂	-	0.25	0.10	0.40
2	E ₁	1	-	0.01	-0.05
	D _R	-	1	0.48	1.18
3	E ₁	1	-	0.02	-0.11
	E ₂	-	-	-0.11	0.13
	D _R	-	1	0.49	1.04
4	E ₁	1	-	-	0.01
	D _R	-	1	-	3.11
	H _R	-	-	1	-4.06
5	E ₁	1	-	0.01	-0.03
	D _R	-	1	0.48	1.05
	D _R '	-	-	0.02	0.03
	D _R ''	-	-	-0.02	0.16
6	E ₁	1	-	0.01	-
	D _R	-	1	0.64	-
	M	-	-	-0.14	1
7	E ₁	1	-	-	-0.03
	E ₂	-	-	-	0.09
	D _R	-	1	-	2.85
	H _R	-	-	1	-3.71
8	E ₁	1	-	0.01	-0.02
	E ₂	-	-	-0.03	0.30
	D _R	-	1	0.48	1.19
	I	-	-	0.06	-0.67
9	E ₁	1	-	0.00	-
	E ₂	-	-	0.01	-
	D _R	-	1	0.65	-
	M	-	-	-0.15	1

TABLE 5B.1

MODEL	TRUE PARAMETER VALUES				SAMPLE SIZES		
	E ₁	D _R	H _R	M	E ₁	E ₂	D _R
1a	112.50	150.00	150.00	30.00	84	621	-
b	22.50	270.00	270.00	115.71	91	171	-
c	112.50	200.00	50.00	57.14	85	482	-
d	22.50	360.00	90.00	240.00	91	136	-
2a	112.50	150.00	150.00	30.00	120	-	164
b	22.50	270.00	270.00	115.71	142	-	38
c	112.50	200.00	50.00	57.14	121	-	139
d	22.50	360.00	90.00	240.00	144	-	37
3a	112.50	150.00	150.00	30.00	164	∞	219
b	22.50	270.00	270.00	115.71	276	∞	39
c	112.50	200.00	50.00	57.14	172	72130	189
d	22.50	360.00	90.00	240.00	280	88286	38
4a	112.50	150.00	150.00	30.00	135	-	3934
b	22.50	270.00	270.00	115.71	144	-	537
c	112.50	200.00	50.00	57.14	136	-	1673
d	22.50	360.00	90.00	240.00	144	-	207
5a	112.50	150.00	150.00	30.00	124	-	290
b	22.50	270.00	270.00	115.71	142	-	86
c	112.50	200.00	50.00	57.14	126	-	255
d	22.50	360.00	90.00	240.00	142	-	84

NEEDED TO DETECT:	R	h_N^2	h_B^2	
H_R	D_R^{II}	D_R^I		
-	-	-	508	-
-	-	-	137	-
-	-	-	440	-
-	-	-	117	-
-	-	-	∞	0.53
-	-	-	9788	0.92
-	-	-	25339	0.57
-	-	-	1633	0.94
-	-	-	∞	0.53
-	-	-	9646	0.92
-	-	-	31059	0.55
-	-	-	1589	0.93
∞	-	-	∞	0.50
14413 ^x	-	-	14266	1.12
28605 ^x	-	-	44801	0.74
854 ^x	-	-	5148	1.61
-	∞	∞	∞	0.53
-	∞	19183	14960	0.92
-	∞	66275	32335	0.56
-	68734	2730	2264	0.93

TABLE 5B.2

MODEL	TRUE PARAMETER VALUES				SAMPLE SIZES		
	E ₁	D _R	H _R	M	E ₁	E ₂	D _R
6a	112.50	150.00	150.00	30.00	126	-	935
b	22.50	270.00	270.00	115.71	142	-	174
c	112.50	200.00	50.00	57.14	128	-	1107
d	22.50	360.00	90.00	240.00	144	-	196
7a	112.50	150.00	150.00	30.00	194	∞	4670
b	22.50	270.00	270.00	115.71	279	∞	546
c	112.50	200.00	50.00	57.14	199	∞	2006
d	22.50	360.00	90.00	240.00	280	∞	211
8a	112.50	150.00	150.00	30.00	242	∞	255
b	22.50	270.00	270.00	115.71	285	11721	39
c	112.50	200.00	50.00	57.14	247	31126	208
d	22.50	360.00	90.00	240.00	286	2343	39
9a	112.50	150.00	150.00	30.00	199	∞	956
b	22.50	270.00	270.00	115.71	280	∞	174
c	112.50	200.00	50.00	57.14	202	∞	1128
d	22.50	360.00	90.00	240.00	281	∞	196
10a*	112.50	150.00	150.00	30.00	135	-	45299
b*	22.50	270.00	270.00	115.71	144	-	23333
c*	112.50	200.00	50.00	57.14	136	-	30348
d*	22.50	360.00	90.00	240.00	144	-	23054

NEEDED TO DETECT:	R	h_N^2	h_B^2	
H_R	I	M		
-	-	∞	∞	0.53
-	-	6729	73152	0.92
-	-	14779	∞	0.56
-	-	747	∞	0.94
∞	-	-	∞	0.49
14849 ^x	-	-	13933	1.11
36882 ^x	-	-	53920	0.71
865 ^x	-	-	5006	1.61
∞	∞ ^x	-	∞	0.53
-	12174 ^x	-	1976	0.92
-	53037 ^x	-	46728	0.57
-	2416 ^x	-	2552	0.94
-	-	∞	∞	0.53
-	-	6861	70488	0.92
-	-	18131	∞	0.56
-	-	754	∞	0.94
∞	-	91133	-	0.38
45341	-	10874	-	0.68
∞	-	30560	-	0.51
∞	-	4643	-	0.87

TABLE 6A.1

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E_1	E_2	D_R	H_R	M
1	E_1	1	-	0.25	0.15	0.16
	E_2	-	1	0.25	0.10	0.38
2	E_1	1	0.46	-	0.01	-0.03
	D_R	-	1.04	1	0.49	1.14
3	E_1	1	-	-	0.01	-0.05
	E_2	-	1	-	-0.01	0.09
	D_R	-	-	1	0.51	0.95
4	E_1	1	0.50	-	-	0.00
	D_R	-	3	1	-	3.19
	H_R	-	-4	-	1	-4.17
5	E_1	1	-	-	-	-0.01
	E_2	-	1	-	-	0.05
	D_R	-	-	1	-	2.97
	H_R	-	-	-	1	-3.94
6	E_1	1	-	-	0.01	-0.01
	E_2	-	1	-	-0.04	0.27
	D_R	-	-	1	0.48	1.18
	I	-	-	-	0.09	-0.61
7	E_1	1	0.49	-	-	-
	D_R	-	-4.12	1	-	-
	H_R	-	5.33	-	1	-
	M	-	2.24	-	-	1
8	E_1	1	-	-	-	0.00
	E_2	-	1	-	-	0.14
	D_R	-	-	1	-	2.83
	H_R	-	-	-	1	-3.45
	I	-	-	-	-	-0.29

TABLE 6A.2

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E ₁	E ₂	D _R	H _R	M
9	E ₁	1	-	-	0.00	-
	E ₂	-	1	-	0.02	-
	D _R	-	-	1	0.72	-
	I	-	-	-	-0.03	-
	M	-	-	-	-0.20	1
10	E ₁	1	0.51	-	0.00	-
	D _R	-	-0.49	1	0.68	-
	M	-	1.33	-	-0.17	1
11	E ₁	1	-	-	0.00	-
	E ₂	-	1	-	0.01	-
	D _R	-	-	1	0.69	-
	M	-	-	-	-0.19	1
12	E ₁	1	0.52	-	0.01	-0.03
	D _R	-	0.81	1	0.49	1.03
	D _R '	-	-0.47	-	0.02	0.07
	D _R ''	-	0.85	-	-0.02	0.16
	D _R '''	-	-	-	-	-
13	E ₁	1	-	-	0.00	-0.02
	E ₂	-	1	-	0.01	0.00
	D _R	-	-	1	0.48	1.03
	D _R '	-	-	-	0.03	-0.01
	D _R ''	-	-	-	-0.03	0.17
14	E ₁	1	0.53	-	0.00	-
	D _R	-	0.48	1	0.68	-
	M	-	0.33	-	-0.18	1
	D _R '	-	-0.52	-	0.03	-
	D _R ''	-	0.80	-	0.01	-

TABLE 6B.1

MODEL	TRUE PARAMETER VALUES					SAM
	E ₁	E ₂	D _R	H _R	M	E ₁
1a	56.25	56.25	150.00	150.00	30.00	91
b	56.25	56.25	200.00	50.00	57.14	91
c	11.25	11.25	270.00	270.00	115.71	91
d	11.25	11.25	360.00	90.00	240.00	92
2a	56.25	56.25	150.00	150.00	30.00	128
b	56.25	56.25	200.00	50.00	57.14	130
c	11.25	11.25	270.00	270.00	115.71	142
d	11.25	11.25	360.00	90.00	240.00	142
3a	56.25	56.25	150.00	150.00	30.00	227
b	56.25	56.25	200.00	50.00	57.14	232
c	11.25	11.25	270.00	270.00	115.71	284
d	11.25	11.25	360.00	90.00	240.00	285
4a	56.25	56.25	150.00	150.00	30.00	139
b	56.25	56.25	200.00	50.00	57.14	140
c	11.25	11.25	270.00	270.00	115.71	144
d	11.25	11.25	360.00	90.00	240.00	144
5a	56.25	56.25	150.00	150.00	30.00	253
b	56.25	56.25	200.00	50.00	57.14	255
c	11.25	11.25	270.00	270.00	115.71	285
d	11.15	11.25	360.00	90.00	240.00	285

PLE SIZES NEEDED TO DETECT:

R h_N^2 h_B^2

E_2 D_R H_R

160	-	-	401	-	-	
147	-	-	342	-	-	
144	-	-	127	-	-	
120	-	-	108	-	-	
-	96	-	1095	0.66	-	6
-	87	-	977	0.68	-	6
-	37	-	1677	0.94	-	0
-	36	-	860	0.95	-	0
658	181	-	∞	0.53	-	
616	163	-	26913	0.55	-	
1291	39	-	9739	0.92	-	
1234	37	-	1540	0.93	-	
-	1154	19256 ^x	1095	0.86	0.65	
-	667	4409 ^x	1056	1.08	0.67	
-	468	9346 ^x	1789	1.18	0.94	
-	190	737 ^x	1447	1.66	0.95	
674	3475	∞	∞	0.50	0.53	
669	1474	22190 ^x	71793	0.73	0.55	
1314	522	13711 ^x	14774	1.12	0.92	
1294	202	813	5240	1.61	0.94	

TABLE 6B.2

MODEL	TRUE PARAMETER VALUES					SAMPLE SIZES NEEDED TO DETECT:					R	h_N^2	h_B^2	
	E_1	E_2	D_R	H_R	M	E_1	E_2	D_R	H_R	I	M			
6a	56.25	56.25	150.00	150.00	30.00	270	1541	260	-	∞^x	-	∞	0.53	0.52
b	56.25	56.25	200.00	50.00	57.14	272	1190	213	-	46023 ^x	-	39218	0.57	0.51
c	11.25	11.25	270.00	270.00	115.71	286	5688	41	-	12216 ^x	-	19746	0.92	0.84
d	11.25	11.25	360.00	90.00	240.00	286	1648	39	-	2269 ^x	-	2454	0.94	0.74
7a	56.25	56.25	150.00	150.00	30.00	139	-	∞^x	13492	-	4874	1281	0.18	0.64
b	56.25	56.25	200.00	50.00	57.14	140	-	∞^x	24197	-	4157	1291	0.30	0.66
c	11.25	11.25	270.00	270.00	115.71	144	-	36775	30414	-	7740	2112	0.64	0.94
d	11.25	11.25	360.00	90.00	240.00	144	-	32614	∞	-	3960	2112	0.84	0.95
8a	56.25	56.25	150.00	150.00	30.00	278	1762	3801	∞	∞^x	-	∞	0.49	0.52
b	56.25	56.25	200.00	50.00	57.14	278	1732	1639	37755 ^x	∞^x	-	92737	0.71	0.53
c	11.25	11.25	270.00	270.00	115.71	286	9759	683	42360 ^x	25094 ^x	-	25051	1.05	0.86
d	11.25	11.25	360.00	90.00	240.00	286	6090	272	1503 ^x	11107 ^x	-	8585	1.50	0.85
9a*	56.25	56.25	150.00	150.00	30.00	255	817	62001	∞	-	∞	-	0.38	0.53
b*	56.25	56.25	200.00	50.00	57.14	256	831	40438	∞	-	48123	-	0.51	0.56
c*	11.25	11.25	270.00	270.00	115.71	285	1397	24480	47107	-	11619	-	0.68	0.92
d**	11.25	11.25	360.00	90.00	240.00	285	1397	23916	∞	-	4872	-	0.87	0.93
10a	56.26	56.25	150.00	150.00	30.00	274	2557	1295	-	∞^x	∞^x	∞	0.53	0.52
b	56.25	56.25	200.00	50.00	57.14	275	3041	1565	-	∞^x	23495	∞	0.56	0.55
c	11.25	11.25	270.00	270.00	115.71	286	42039	276	-	∞^x	15022	80955	0.92	0.90
d	11.25	11.25	360.00	90.00	240.00	286	98327	322	-	∞^x	1132	∞	0.94	0.93

TABLE 6B.3

MODEL	TRUE PARAMETER VALUES					SA
	E ₁	E ₂	D _R	H _R	M	E ₁
11a	56.25	56.25	150.00	150.00	30.00	133
b	56.25	56.25	200.00	50.00	57.14	134
c	11.25	11.25	270.00	270.00	115.71	144
d	11.25	11.25	360.00	90.00	240.00	144
12a	56.25	56.25	150.00	150.00	30.00	254
b	56.25	56.25	200.00	50.00	57.14	255
c	11.25	11.25	270.00	270.00	115.71	285
d	11.25	11.25	360.00	90.00	240.00	285
13a	56.25	56.25	150.00	150.00	30.00	129
b	56.25	56.25	200.00	50.00	57.14	130
c	11.25	11.25	270.00	270.00	115.71	142
d	11.25	11.25	360.00	90.00	240.00	142
14a	56.25	56.25	150.00	150.00	30.00	276
b	56.25	56.25	200.00	50.00	57.14	276
c	11.25	11.25	270.00	270.00	115.71	286
d	11.25	11.25	360.00	90.00	240.00	286
15a	56.25	56.25	150.00	150.00	30.00	130
b	56.25	56.25	200.00	50.00	57.14	135
c	11.25	11.25	270.00	270.00	115.71	144
d	11.25	11.25	360.00	90.00	240.00	144

AMPLE SIZES NEEDED TO DETECT:

 R b_N^2

E_2	D_R	M	D_R	D_R	R	b_N^2
-	886	4580	-	-	1271	0.64
-	1016	182	-	-	1315	0.66
-	162	4594	-	-	2112	0.94
-	180	645	-	-	2190	0.95
752	652	∞	-	-	∞	0.53
785	756	15156	-	-	∞	0.56
1369	160	6838	-	-	72839	0.92
1389	178	720	-	-	∞	0.93
-	195	-	55151 ^x	1264	1833	0.64
-	178	-	62491 ^x	1070	1682	0.66
-	81	-	∞	6789	1848	0.94
-	80	-	∞	1796	1066	0.95
1103	345	-	∞	∞ ^x	∞	0.53
1128	300	-	∞	83606	30257	0.56
1406	87	-	∞	18709	14642	0.92
1437	84	-	81073	2586	2097	0.93
-	754	83246	41673 ^x	1987	1799	0.63
-	848	10200	29555 ^x	2191	1853	0.66
-	235	11182	∞ ^x	53305	1980	0.94
-	278	1140	∞ ^x	77210	2048	0.95

TABLE 7A

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS			
		E ₁	E ₂	D _R	I
1	E ₁	1	-	0.25	0.25
	E ₂	-	1	0.25	0.25
2	E ₁	1	0.45	-	0.25
	D _R	-	1.07	1	0.25
3	E ₁	1	-	-	0.07
	E ₂	-	1	-	0.25
	D _R	-	-	1	0.43
4	E ₁	1	0.50	-	0.25
	D _R	-	3	1	0.50
	H _R	-	-4	-	-
5	E ₁	1	0.53	-	0.26
	D _R	-	0.77	1	0.40
	D _R '	-	-0.44	-	0.10
	D _R ''	-	0.84	-	0.08
6	E ₁	1	0.51	-	0.25
	D _R	-	-0.53	1	0.50
	M	-	1.36	-	-
7	E ₁	1	-	-	0.05
	E ₂	-	1	-	0.27
	D _R	-	-	1	-0.40
	H _R	-	-	-	1.62
8	E ₁	1	-	-	0.04
	E ₂	-	1	-	0.30
	D _R	-	-	1	0.91
	M	-	-	-	-0.50
9	E ₁	1	0.48	-	0.25
	D _R	-	-4.07	1	0.50
	H _R	-	5.27	-	-
	M	-	2.23	-	-

TABLE 7B.1

MODEL	TRUE PARAMETER VALUES				SAMPLE	
	E_1	E_2	D_R	I	E_1	E_2
1a	56.25	56.25	180.00	45.00	91	160
	11.25	11.25	360.00	45.00	91	160
	56.25	56.25	135.00	90.00	91	160
	11.25	11.25	315.00	90.00	91	160
2a	56.25	56.25	180.00	45.00	123	-
	11.25	11.25	360.00	45.00	141	-
	56.25	56.25	135.00	90.00	120	-
	11.25	11.25	315.00	90.00	139	-
3a	56.25	56.25	180.00	45.00	215	477
	11.25	11.25	360.00	45.00	281	489
	56.25	56.25	135.00	90.00	213	395
	11.25	11.25	315.00	90.00	282	354
4a	56.25	56.25	180.00	45.00	136	-
	11.25	11.25	360.00	45.00	142	-
	56.25	56.25	135.00	90.00	135	-
	11.25	11.25	315.00	90.00	142	-
5a	56.25	56.25	180.00	45.00	124	-
	11.25	11.25	360.00	45.00	141	-
	56.25	56.25	135.00	90.00	121	-
	11.25	11.25	315.00	90.00	140	-

SIZES NEEDED TO DETECT:				R	h_N^2	h_B^2
D_R	H_R	D_R''	D_R'			
-	-	-	-	215	-	-
-	-	-	-	152	-	-
-	-	-	-	665	-	-
-	-	-	-	171	-	-
120	-	-	-	802	0.59	-
44	-	-	-	689	0.88	-
159	-	-	-	636	0.54	-
51	-	-	-	479	0.83	-
269	-	-	-	31323	0.44	-
55	-	-	-	17844	0.81	-
352	-	-	-	8252	0.39	-
68	-	-	-	4805	0.74	-
1308	14413 ^x	-	-	807	0.83	0.58
868	∞ ^x	-	-	670	0.93	0.88
1545	15398 ^x	-	-	636	0.76	0.53
1011	∞ ^x	-	-	464	0.88	0.83
262	-	55006 ^x	1023	1252	0.55	-
96	-	∞ ^x	14785	665	0.87	-
336	-	∞ ^x	920	944	0.49	-
110	-	∞ ^x	9286	464	0.82	-

TABLE 7B.2

MODEL	TRUE PARAMETER VALUES				SAMPLE	
	E ₁	E ₂	D _R	I	E ₁	E ₂
6a	56.25	56.25	180.00	45.00	128	-
b	11.25	11.25	360.00	45.00	142	-
c	56.25	56.25	135.00	90.00	126	-
d	11.25	11.25	315.00	90.00	141	-
7a	56.25	56.25	180.00	45.00	247	487
b	11.25	11.25	360.00	45.00	284	488
c	56.25	56.25	135.00	90.00	248	397
d	11.25	11.25	315.00	90.00	285	354
8a*	56.25	56.25	180.00	45.00	269	1459
b*	11.25	11.25	360.00	45.00	286	37714
c*	56.25	56.25	135.00	90.00	269	1456
d*	11.25	11.25	315.00	90.00	286	37702
9a	56.25	56.25	180.00	45.00	248	524
b	11.25	11.25	360.00	45.00	284	493
c	56.25	56.25	135.00	90.00	249	418
d	11.25	11.25	315.00	90.00	285	357
10a	56.25	56.25	180.00	45.00	136	-
b	11.25	11.25	360.00	45.00	142	-
c	56.25	56.25	135.00	90.00	135	-
d	11.25	11.25	315.00	90.00	142	-

SIZES NEEDED TO DETECT:

R	h_N^2	h_B^2
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D_R	H_R	I	M	R	h_N^2	h_B^2
1472	-	-	4637	875	0.56	-
195	-	-	91307	674	0.87	-
2141	-	-	4726	680	0.51	-
243	-	-	92973	469	0.82	-
6704	∞	-	-	3510	0.36	0.44
1471	53345	-	-	21540	0.70	0.81
16347	33355	-	-	9069	0.23	0.39
2744	13703	-	-	5906	0.52	0.74
559	-	18666	-	-	0.40	0.50
66	-	10628	-	-	0.80	0.90
1109	-	5029	-	-	0.30	0.50
108	-	2958	-	-	0.70	0.90
808	-	-	61755 ^x	41878	0.44	-
174	-	-	22883 ^x	30609	0.81	-
865	-	-	17630 ^x	10501	0.38	-
185	-	-	6254 ^x	57113	0.73	-
∞^x	26501	-	6157	846	0.23	0.57
7949 ^x	∞	-	∞	645	0.80	0.87
∞^x	27475	-	6175	650	0.18	0.52
9078	∞	-	∞	450	0.75	0.82

TABLE 8A.1

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E ₁	E ₂	D _R	I	M
1	E ₁	1	-	0.25	0.25	0.16
	E ₂	-	1	0.25	0.25	0.38
2	E ₁	1	0.46	-	0.25	-0.04
	D _R	-	1.05	1	0.50	1.15
3	E ₁	1	-	-	0.06	-0.05
	E ₂	-	1	-	0.27	0.10
	D _R	-	-	1	0.43	0.93
4	E ₁	1	0.50	-	0.25	0.01
	D _R	-	3	1	0.50	3.21
	H _R	-	-4	-	-	-4.22
5	E ₁	1	-	-	0.40	-0.01
	E ₂	-	1	-	0.29	0.53
	D _R	-	-	1	-0.44	2.97
	H _R	-	-	-	1.69	-3.95
6	E ₁	1	-	-	-	-0.01
	E ₂	-	1	-	-	0.26
	D _R	-	-	1	-	1.19
	I	-	-	-	1	-0.61
7	E ₁	1	0.49	-	0.25	-
	D _R	-	-4.17	1	0.50	-
	H _R	-	5.43	-	-	-
	M	-	2.24	-	-	1
8	E ₁	1	-	-	-	0.00
	E ₂	-	1	-	-	0.14
	D _R	-	-	1	-	2.83
	H _R	-	-	-	-	-3.46
	I	-	-	-	1	-0.28

TABLE 8A.2

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E_1	E_2	D_R	I	M
9	E_1	1	-	-	0.03	-
	E_2	-	1	-	0.33	-
	D_R	-	-	1	1.88	-
	H_R	-	-	-	-1.41	-
	M	-	-	-	-0.78	1
10	E_1	1	0.51	-	0.25	-
	D_R	-	-0.45	1	0.50	-
	M	-	1.28	-	-	1
11	E_1	1	-	-	0.03	-
	E_2	-	1	-	0.32	-
	D_R	-	-	1	0.90	-
	M	-	-	-	0.51	1
12	E_1	1	0.52	-	0.25	-0.04
	D_R	-	0.80	1	0.41	1.04
	D_R'	-	-0.45	-	0.08	0.07
	D_R''	-	0.85	-	0.08	0.16
13	E_1	1	-	-	0.00	-0.02
	E_2	-	1	-	0.45	0.00
	D_R	-	-	1	0.07	1.05
	D_R'	-	-	-	0.33	-0.03
	D_R''	-	-	-	-0.30	0.16
14	E_1	1	0.54	-	0.25	-
	D_R	-	0.50	1	0.52	-
	M	-	0.32	-	-0.09	1
	D_R'	-	-0.55	-	0.07	-
	D_R''	-	0.80	-	0.10	-

TABLE 8B.1.

MODEL	TRUE PARAMETER VALUES					SAM
	E ₁	E ₂	D _R	I	M	
1a	56.25	56.25	180.00	45.00	45.00	91
b	56.25	56.25	135.00	90.00	23.82	91
c	11.25	11.25	360.00	45.00	240.00	92
d	11.25	11.25	315.00	90.00	169.62	92
2a	56.25	56.25	180.00	45.00	45.00	127
b	56.25	56.25	135.00	90.00	23.82	122
c	11.25	11.25	360.00	45.00	240.00	142
d	11.25	11.25	315.00	90.00	169.62	141
3a	56.25	56.25	180.00	45.00	45.00	229
b	56.25	56.25	135.00	90.00	23.82	220
c	11.25	11.25	360.00	45.00	240.00	285
d	11.25	11.25	315.00	90.00	169.62	285
4a	56.25	56.25	180.00	45.00	45.00	138
b	56.25	56.25	135.00	90.00	23.82	135
c	11.25	11.25	360.00	45.00	240.00	144
d	11.25	11.25	315.00	90.00	169.62	142
5a	56.25	56.25	180.00	45.00	45.00	253
b	56.25	56.25	135.00	90.00	23.82	251
c	11.25	11.25	360.00	45.00	240.00	285
d	11.25	11.25	315.00	90.00	169.62	285

IPLE SIZES NEEDED TO DETECT: R h_N^2 h_B^2

E_2 D_R H_R

147	-	-	418	-	-
153	-	-	564	-	-
117	-	-	113	-	-
124	-	-	131	-	-
-	107	-	749	0.63	-
-	140	-	623	0.57	-
-	38	-	442	0.92	-
-	44	-	381	0.88	-
464	213	-	36593	0.48	-
388	299	-	11227	0.41	-
482	45	-	1770	0.87	-
358	59	-	4038	0.79	-
-	761	4576 ^x	795	1.03	0.62
-	1111	7732 ^x	637	0.89	0.55
-	183	626 ^x	585	1.69	0.92
-	262	1188 ^x	439	1.49	0.88
497	2290	66744 ^x	50540	0.59	0.48
401	6436	∞	10969	0.36	0.41
486	221	839 ^x	8221	1.53	0.87
358	395	2608 ^x	12024	1.20	0.80

TABLE 8B.2

MODEL	TRUE PARAMETER VALUES										SAMPLE SIZES NEEDED TO DETECT:				R^2	χ^2_N	b_B^2
	E_1	E_2	D_R	I	H	E_1	E_2	D_R	H_R	I	H						
6a	56.25	56.25	180.00	45.00	45.00	271	1174	370	-	∞	-	42973	0.47	0.50	0.50	0.50	0.50
	b	56.25	135.00	90.00	23.82	270	1290	804	-	7623 ^x	-	-	0.34	0.34	0.34	0.34	0.34
	c	11.25	360.00	45.00	240.00	286	1464	49	-	4157 ^x	-	2163	0.88	0.88	0.88	0.88	0.88
	d	11.25	315.00	90.00	169.62	286	2094	69	-	∞	-	3901	0.79	0.79	0.79	0.79	0.79
7a	56.25	56.25	180.00	45.00	45.00	138	-	∞ ^x	31736	-	4449	885	0.29	0.61	0.61	0.61	0.61
	b	56.25	135.00	90.00	23.82	137	-	∞ ^x	30221	-	5103	665	0.22	0.54	0.54	0.54	0.54
	c	11.25	360.00	45.00	240.00	142	-	28246	∞	-	3958	649	0.87	0.92	0.92	0.92	0.92
	d	11.25	315.00	90.00	169.62	142	-	24001	∞	-	5350	452	0.82	0.87	0.87	0.87	0.87
8a	56.25	56.25	180.00	45.00	45.00	278	1748	2221	34925 ^x	49761	-	∞	0.62	0.62	0.52	0.52	0.52
	b	56.25	135.00	90.00	23.82	278	1775	4956	∞ ^x	7676 ^x	-	∞	0.42	0.42	0.51	0.51	0.51
	c	11.25	360.00	45.00	240.00	286	6048	278	1289 ^x	∞ ^x	-	8649	1.49	1.49	0.84	0.84	0.84
	d	11.25	315.00	90.00	169.62	286	7523	432	2633 ^x	37488	-	14286	1.26	1.26	0.85	0.85	0.85
9a	56.25	56.25	180.00	45.00	45.00	279	584	21785	∞ ^x	∞ ^x	-	49159	0.55	0.48	0.48	0.48	0.48
	b	56.25	135.00	90.00	23.82	254	457	16037	∞ ^x	∞ ^x	-	83342 ^x	11372	0.52	0.41	0.41	0.41
	c	11.25	360.00	45.00	240.00	284	510	13492	∞ ^x	∞ ^x	-	7894	59452	0.96	0.87	0.87	0.87
	d	11.25	315.00	90.00	169.62	284	377	7868	96952 ^x	∞ ^x	-	41873	14060	0.97	0.80	0.80	0.80
10a	56.25	56.25	180.00	45.00	45.00	276	3040	2878	-	32054	25303	-	0.45	0.55	0.55	0.55	0.55
	b	56.25	135.00	90.00	23.82	276	2813	5257	-	8036	88731	-	0.34	0.53	0.53	0.53	0.53
	c	11.25	360.00	45.00	240.00	286	∞	517	-	35010	1003	-	0.87	0.93	0.93	0.93	0.93
	d	11.25	315.00	90.00	169.62	286	∞	779	-	8762	2005	-	0.55	0.55	0.55	0.55	0.55

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TABLE 8B.

MODEL TRUE PARAMETER VALUES

	E_1	E_2	D_R	I	M
11a	56.25	56.25	180.00	45.00	45.00
	b	56.25	135.00	90.00	23.82
	c	11.25	360.00	45.00	240.00
	d	11.25	315.00	90.00	169.62
12a	56.25	56.25	180.00	45.00	45.00
	b	56.25	135.00	90.00	23.82
	c	11.25	360.00	45.00	240.00
	d	11.25	315.00	90.00	169.62
13a	56.25	56.25	180.00	45.00	45.00
	b	56.25	135.00	90.00	23.82
	c	11.25	360.00	45.00	240.00
	d	11.25	315.00	90.00	169.62
14a	56.25	56.25	180.00	45.00	45.00
	b	56.25	135.00	90.00	23.82
	c	11.25	360.00	45.00	240.00
	d	11.25	315.00	90.00	169.62
15a	56.25	56.25	180.00	45.00	45.00
	b	56.25	135.00	90.00	23.82
	c	11.25	360.00	45.00	240.00
	d	11.25	315.00	90.00	169.62

SAMPLES SIZE NEEDED TO DETECT:

 R
 h_N^2

E_1	E_2	D_R	M	D_R''	D_R'	R	h_N^2
132	-	1527	2261	-	-	917	0.60
127	-	2186	3135	-	-	695	0.54
142	-	231	562	-	-	677	0.92
142	-	285	997	-	-	471	0.87
253	556	868	70188 ^x	-	-	49336	0.49
251	432	901	86566 ^x	-	-	11509	0.41
285	506	211	779	-	-	57113	0.87
285	371	225	2559	-	-	13470	0.80
127	-	218	-	80412 ^x	955	1164	0.60
122	-	293	-	∞ ^x	900	921	0.52
142	-	86	-	∞	1491	481	0.92
141	-	97	-	∞	1879	398	0.87
275	758	451	-	∞	∞ ^x	47033	0.47
275	565	803	-	28648	11383 ^x	51661	0.36
286	536	101	-	67476	4672	1978	0.87
286	403	130	-	49634	∞	3886	0.79
133	-	1157	11882	35382 ^x	1740	1224	0.60
129	-	1545	30768	70865 ^x	1376	914	0.52
142	-	339	∞	28432	1038	633	0.92
142	-	379	∞	13750	2077	444	0.87

TABLE 9A.1

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E ₁	E ₂	D _R	H _R	I
1	E ₁	1	-	0.25	0.15	0.25
	E ₂	-	1	0.25	0.10	0.25
2	E ₁	1	0.45	-	0.01	0.25
	D _R	-	1.07	1	0.48	0.50
3	E ₁	1	-	-	0.03	0.18
	E ₂	-	1	-	-0.01	0.18
	D _R	-	-	1	0.46	0.29
4	E ₁	1	0.50	-	-	0.25
	D _R	-	3	1	-	0.50
	H _R	-	-4	-	1	-
5	E ₁	1	-	-	-	0.05
	E ₂	-	1	-	-	0.27
	D _R	-	-	1	-	-0.40
	H _R	-	-	-	1	1.64
6	E ₁	1	-	-	0.01	-
	E ₂	-	1	-	-0.04	-
	D _R	-	-	1	0.47	-
	I	-	-	-	0.10	1
7	E ₁	1	0.48	-	-	0.25
	D _R	-	-4.01	1	-	0.50
	H _R	-	5.17	-	1	-
	M	-	2.23	-	-	-
8	E ₁	1	-	-	-	0.04
	E ₂	-	1	-	-	0.31
	D _R	-	-	1	-	1.76
	H _R	-	-	-	1	-1.22
	M	-	-	-	-	-0.74

TABLE 9A.2

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E_1	E_2	D_R	H_R	I
9	E_1	1	-	-	0.00	-
	E_2	-	1	-	0.02	-
	D_R	-	-	1	0.71	-
	I	-	-	-	-0.03	1
	M	-	-	-	-0.20	-
10	E_1	1	0.52	-	0.01	0.25
	D_R	-	-0.57	1	0.66	0.50
	M	-	1.40	-	-0.16	-
11	E_1	1	-	-	0.00	0.04
	E_2	-	1	-	0.01	0.30
	D_R	-	-	1	0.68	0.92
	M	-	-	-	-0.18	-0.51
12	E_1	1	0.53	-	0.01	0.26
	D_R	-	0.77	1	0.48	0.40
	$D_R^{(1)}$	-	-0.44	-	0.02	0.10
	$D_R^{(2)}$	-	0.84	-	-0.02	0.08
13	E_1	1	-	-	0.00	0.01
	E_2	-	1	-	0.01	0.44
	D_R	-	-	1	0.47	0.08
	$D_R^{(1)}$	-	-	-	0.04	0.33
	$D_R^{(2)}$	-	-	-	-0.04	-0.29
14	E_1	1	0.55	-	0.01	0.25
	D_R	-	0.34	1	0.66	0.51
	M	-	0.40	-	-0.17	-0.11
	$D_R^{(1)}$	-	-0.46	-	0.03	0.11
	$D_R^{(2)}$	-	0.78	-	0.01	0.09

TABLE 9

MODEL

TRUE PARAMETER VALUES

	E_1	E_2	D_R	H_R	I
1a	56.25	56.25	120.00	120.00	45.00
b	56.25	56.25	90.00	90.00	90.00
c	56.25	56.25	160.00	40.00	45.00
d	56.25	56.25	120.00	30.00	90.00
e	11.25	11.25	240.00	240.00	45.00
f	11.25	11.25	210.00	210.00	90.00
g	11.25	11.25	320.00	80.00	45.00
h	11.25	11.25	280.00	70.00	90.00
2a	56.25	56.25	120.00	120.00	45.00
b	56.25	56.25	90.00	90.00	90.00
c	56.25	56.25	160.00	40.00	45.00
d	56.25	56.25	120.00	30.00	90.00
e	11.25	11.25	240.00	240.00	45.00
f	11.25	11.25	210.00	210.00	90.00
g	11.25	11.25	320.00	80.00	45.00
h	11.25	11.25	280.00	70.00	90.00
3a	56.25	56.25	120.00	120.00	45.00
b	56.25	56.25	90.00	90.00	90.00
c	56.25	56.25	160.00	40.00	45.00
d	56.25	56.25	120.00	30.00	90.00
e	11.25	11.25	240.00	240.00	45.00
f	11.25	11.25	210.00	210.00	90.00
g	11.25	11.25	320.00	80.00	45.00
h	11.25	11.25	280.00	70.00	90.00

B.1

SAMPLE SIZE NEEDED	R	h_N^2
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E ₁	E ₂	D _R		
91	170	-	568	-
91	168	-	689	-
91	164	-	552	-
91	163	-	623	-
90	178	-	163	-
90	176	-	182	-
91	166	-	156	-
91	166	-	175	-
123	-	133	838	0.58
120	-	163	655	0.53
123	-	130	816	0.58
120	-	160	643	0.54
141	-	44	694	0.87
139	-	51	490	0.82
141	-	44	609	0.88
139	-	51	485	0.82
211	501	269	16628	0.44
212	410	357	6737	0.39
214	485	269	25972	0.44
212	400	353	7762	0.39
282	504	55	5781	0.82
282	361	68	2856	0.75
282	497	55	12406	0.81
282	357	68	4084	0.74

TABLE 9B.2

MODEL	TRUE PARAMETER VALUES					SAM
	E ₁	E ₂	D _R	H _R	I	E ₁
4a	56.25	56.25	120.00	120.00	45.00	136
b	56.25	56.25	90.00	90.00	90.00	135
c	56.25	56.25	160.00	40.00	45.00	136
d	56.25	56.25	120.00	30.00	90.00	135
e	11.25	11.25	240.00	240.00	45.00	142
f	11.25	11.25	210.00	210.00	90.00	142
g	11.25	11.25	320.00	80.00	45.00	142
h	11.25	11.25	280.00	70.00	90.00	142
5a	56.25	56.25	120.00	120.00	45.00	248
b	56.25	56.25	90.00	90.00	90.00	249
c	56.25	56.25	160.00	40.00	45.00	247
d	56.25	56.25	120.00	30.00	90.00	248
e	11.25	11.25	240.00	240.00	45.00	284
f	11.25	11.25	210.00	210.00	90.00	285
g	11.25	11.25	320.00	80.00	45.00	284
h	11.25	11.25	280.00	70.00	90.00	285
6a	56.25	56.25	120.00	120.00	45.00	268
b	56.25	56.25	90.00	90.00	90.00	269
c	56.25	56.25	160.00	40.00	45.00	269
d	56.25	56.25	120.00	30.00	90.00	269
e	11.25	11.25	240.00	240.00	45.00	286
f	11.25	11.25	210.00	210.00	90.00	286
g	11.25	11.25	320.00	80.00	45.00	286
h	11.25	11.25	280.00	70.00	90.00	286

AMPLE SIZES NEEDED TO DETECT:

R h_N^2 h_B^2

E_2	D_R	H_R	I	R	h_N^2	h_B^2
-	1942	69803 ^x	-	819	0.69	0.56
-	2099	44365 ^x	-	643	0.68	0.53
-	1485	21709 ^x	-	811	0.78	0.58
-	1704	20754 ^x	-	638	0.74	0.53
-	1898	16024	-	673	0.66	0.88
-	2051	23422	-	468	0.64	0.83
-	1100	∞	-	671	0.84	0.88
-	1255	∞	-	467	0.80	0.83
493	17845	18319	-	35104	0.23	0.44
401	53109	12906	-	8930	0.13	0.39
489	8883	51400	-	35104	0.31	0.44
399	22637	22947	-	9070	0.20	0.39
492	4203	5206	-	22018	0.44	0.81
357	9627	3679	-	5977	0.29	0.74
489	1994	17020	-	21718	0.61	0.81
355	3890	7829	-	5933	0.44	0.74
1746	592	-	11892	95600	0.39	0.52
1667	1181	-	4180	∞	0.29	0.51
1547	570	-	15875	∞	0.40	0.51
1523	1132	-	4719	∞	0.30	0.50
∞	67	-	5074	19418	0.80	0.94
∞	109	-	2014	26768	0.69	0.94
76563	66	-	7984	∞	0.80	0.91
69540	109	-	2579	∞	0.70	0.91

TABLE 9B.3

MODEL	TRUE PARAMETER VALUES					SAMPLE SIZES	
	E ₁	E ₂	D _R	H _R	I	E ₁	E ₂
7a	56.25	56.25	120.00	120.00	45.00	137	-
b	56.25	56.25	90.00	90.00	90.00	136	-
c	56.25	56.25	160.00	40.00	45.00	137	-
d	56.25	56.25	120.00	30.00	90.00	136	-
e	11.25	11.25	240.00	240.00	45.00	142	-
f	11.25	11.25	210.00	210.00	90.00	142	-
g	11.25	11.25	320.00	80.00	45.00	142	-
h	11.25	11.25	280.00	70.00	90.00	142	-
8a*	56.25	56.25	120.00	120.00	45.00	277	1795
b*	56.25	56.25	90.00	90.00	90.00	277	1802
c*	56.25	56.25	160.00	40.00	45.00	277	1787
d*	56.25	56.25	120.00	30.00	90.00	277	1797
e*	11.25	11.25	240.00	240.00	45.00	286	47911
f*	11.25	11.25	210.00	210.00	90.00	286	48366
g*	11.25	11.25	320.00	80.00	45.00	286	46995
h*	11.25	11.25	280.00	70.00	90.00	286	47664
9a	56.25	56.25	120.00	120.00	45.00	251	563
b	56.25	56.25	90.00	90.00	90.00	252	449
c	56.25	56.25	160.00	40.00	45.00	251	559
d	56.25	56.25	120.00	30.00	90.00	252	446
e	11.25	11.25	240.00	240.00	45.00	284	506
f	11.25	11.25	210.00	210.00	90.00	284	370
g	11.25	11.25	320.00	80.00	45.00	284	504
h	11.25	11.25	280.00	70.00	90.00	284	368

NEEDED TO DETECT:

D_R	H_R	I	M	R	b_N^2	b_B^2
∞ x	13866	-	6164	896	0.10	0.57
∞ x	16526	-	6181	656	0.08	0.52
∞ x	20848	-	6160	851	0.18	0.57
∞ x	22846	-	6177	651	0.15	0.52
19087	20240	-	∞	647	0.54	0.87
20349	25326	-	∞	450	0.52	0.82
10222	89373	-	∞	646	0.72	0.87
11478	∞	-	∞	448	0.68	0.82
13487	56484	22439	-	-	0.27	0.50
23978	∞	6127	-	-	0.20	0.50
7363	∞	22439	-	-	0.36	0.50
13207	∞	6127	-	-	0.27	0.50
3322	12508	13538	-	-	0.53	0.90
4425	17077	3836	-	-	0.47	0.90
1761	∞	13346	-	-	0.71	0.90
2369	∞	3807	-	-	0.62	0.90
29656	∞	-	∞ x	41473	0.36	0.44
20652	∞ x	-	31199 x	10334	0.39	0.38
20476	∞ x	-	∞	41473	0.45	0.44
16203	∞ x	-	31173 x	10337	0.45	0.38
7227	∞	-	30196 x	34448	0.66	0.81
5016	∞	-	8452 x	8698	0.71	0.73
4791	∞ x	-	30286 x	33650	0.84	0.81
3687	∞ x	-	8484 x	8595	0.87	0.73

TABLE 9B.4

MODEL	TRUE PARAMETER VALUES					SAM
	E ₁	E ₂	D _R	H _R	I	E ₁
10a	56.25	56.25	120.00	120.00	45.00	272
b	56.25	56.25	90.00	90.00	90.00	273
c	56.25	56.25	160.00	40.00	45.00	272
d	56.25	56.25	120.00	30.00	90.00	273
e	11.25	11.25	240.00	240.00	45.00	286
f	11.25	11.25	210.00	210.00	90.00	286
g	11.25	11.25	320.00	80.00	45.00	286
h	11.25	11.25	280.00	70.00	90.00	286
11a	56.25	56.25	120.00	120.00	45.00	128
b	56.25	56.25	90.00	90.00	90.00	124
c	56.25	56.25	160.00	40.00	45.00	128
d	56.25	56.25	120.00	30.00	90.00	126
e	11.25	11.25	240.00	240.00	45.00	142
f	11.25	11.25	210.00	210.00	90.00	141
g	11.25	11.25	320.00	80.00	45.00	142
h	11.25	11.25	280.00	70.00	90.00	141
12a	56.25	56.25	120.00	120.00	45.00	249
b	56.25	56.25	90.00	90.00	90.00	249
c	56.25	56.25	160.00	40.00	45.00	248
d	56.25	56.25	120.00	30.00	90.00	249
e	11.25	11.25	240.00	240.00	45.00	285
f	11.25	11.25	210.00	210.00	90.00	285
g	11.25	11.25	320.00	80.00	45.00	285
h	11.25	11.25	280.00	70.00	90.00	285

IPLE SIZES NEEDED TO DETECT:

E_2	D_R	I	M	R	h_N^2	h_B^2
2302	2082	31684	83719 ^x	∞	0.40	0.49
2377	3922	7671	∞ ^x	∞	0.30	0.49
2415	2407	28683	∞ ^x	∞	0.40	0.50
2462	4547	7449	∞ ^x	∞	0.30	0.50
28630	358	40202	18859 ^x	55713	0.80	0.87
33438	536	7378	26490 ^x	72603	0.70	0.88
50751	397	24318	∞ ^x	∞	0.80	0.90
55611	606	6169	∞ ^x	∞	0.70	0.89
-	1243	-	7769	880	0.56	-
-	1847	-	6806	682	0.51	-
-	1387	-	5457	879	0.56	-
-	2032	-	5307 ^x	679	0.51	-
-	175	-	47237 ^x	669	0.88	-
-	217	-	86178 ^x	470	0.83	-
-	188	-	∞	673	0.87	-
-	233	-	∞	469	0.82	-
519	694	-	16079 ^x	43405	0.43	-
416	767	-	9257 ^x	10817	0.38	-
523	766	-	34963 ^x	43275	0.44	-
418	829	-	13821 ^x	10656	0.38	-
491	157	-	4541 ^x	29923	0.81	-
354	169	-	2574 ^x	9111	0.73	-
493	168	-	11088 ^x	34875	0.81	-
355	180	-	4368 ^x	8571	0.73	-

TABLE 9B.5

MODEL	TRUE PARAMETER VALUES					SAMPLE
	E_1	E_2	D_R	H_R	I	E_1
13a	56.25	56.25	120.00	120.00	45.00	125
	b	56.25	56.25	90.00	90.00	120
	c	56.25	56.25	160.00	40.00	125
	d	56.25	56.25	120.00	30.00	120
	e	11.25	11.25	240.00	240.00	45.00
	f	11.25	11.25	210.00	210.00	90.00
	g	11.25	11.25	320.00	80.00	45.00
	h	11.25	11.25	280.00	70.00	90.00
14a	56.25	56.25	120.00	120.00	45.00	275
	b	56.25	56.25	90.00	90.00	275
	c	56.25	56.25	160.00	40.00	45.00
	d	56.25	56.25	120.00	30.00	90.00
	e	11.25	11.25	240.00	240.00	45.00
	f	11.25	11.25	210.00	210.00	90.00
	g	11.25	11.25	320.00	80.00	45.00
	h	11.25	11.25	280.00	70.00	90.00
15a	56.25	56.25	120.00	120.00	45.00	130
	b	56.25	56.25	90.00	90.00	127
	c	56.25	56.25	160.00	40.00	45.00
	d	56.25	56.25	120.00	30.00	90.00
	e	11.25	11.25	240.00	240.00	45.00
	f	11.25	11.25	210.00	210.00	90.00
	g	11.25	11.25	320.00	80.00	45.00
	h	11.25	11.25	280.00	70.00	90.00

SIZES NEEDED TO DETECT:

R h_N^2

E_2	D_R	M	D_R''	D_R'	R	h_N^2
-	269	-	67652 ^x	1148	1268	0.55
-	346	-	∞ ^x	991	960	0.48
-	265	-	58736 ^x	1062	1262	0.55
-	340	-	∞ ^x	943	951	0.49
-	96	-	∞ ^x	86473	648	0.87
-	110	-	∞ ^x	24557	484	0.82
-	96	-	∞ ^x	23011	663	0.87
-	110	-	∞ ^x	12217	467	0.82
731	622	-	59149	16812 ^x	47777	0.40
550	1043	-	18111	6494 ^x	25206	0.31
740	606	-	83375	23104 ^x	∞	0.41
554	1011	-	21056	7506 ^x	31117	0.32
508	125	-	65972	5631 ^x	16538	0.80
374	173	-	20180	2501 ^x	12729	0.70
512	124	-	∞	9693 ^x	62007	0.80
379	171	-	27348	3375 ^x	22595	0.71
-	976	∞ ^x	71673 ^x	1477	1210	0.55
-	1352	∞ ^x	∞ ^x	1262	916	0.48
-	1059	∞	50566 ^x	1476	1360	0.55
-	1456	∞	∞ ^x	1261	914	0.49
-	230	15889 ^x	∞	17914	628	0.87
-	272	15107 ^x	∞	10468	445	0.82
-	257	83792 ^x	∞ ^x	18436	633	0.87
-	292	61664 ^x	∞ ^x	10507	440	0.82

TABLE 10A

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS			
		E ₁	E ₂	D _R	C
1	E ₁	1	0.25	-	-0.02
	E ₂	-	0.25	1	0.44
2	E ₁	1	-	0.47	-0.03
	D _R	-	1	1.00	0.90
3	E ₁	1	-	-	-0.04
	E ₂	-	-	1	0.20
	D _R	-	1	-	0.43
4	E ₁	1	-	0.50	-0.00
	D _R	-	1	3	2.73
	H _R	-	-	-4	-3.68
5	E ₁	1	-	0.51	-0.00
	D _R "	-	1	0.85	0.47
	D _R "'	-	-	-0.46	0.35
	D _R '	-	-	0.85	0.41
6	E ₁	1	-	-	-0.02
	E ₂	-	-	1	0.15
	D _R	-	1	-	1.79
	H _R	-	-	-	-2.48
7	E ₁	1	-	0.51	-0.02
	D _R	-	1	-0.37	0.41
	M	-	-	1.22	0.46
8	E ₁	1	-	-	-0.02
	E ₂	-	-	1	0.37
	D _R	-	1	-	0.73
	I	-	-	-	-0.60
9	E ₁	1	-	-	-0.03
	E ₂	-	-	1	0.18
	D _R	-	1	-	0.24
	M	-	-	-	0.23

TABLE 10A contd.

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS			
		E_1	E_2	D_R	C
10	E_1	1	-	0.49	-
	D_R	-	1	-4.37	6.00
	H_R	-	-	5.74	-8.00
	M	-	-	2.26	-1.00

TABLE 10B.1

MODEL	TRUE PARAMETER VALUES				SAMPLE	
	E ₁	E ₂	D _R	C	E ₁	E ₂
1a	56.25	61.61	225.00	150.00	93	95
b	11.25	98.04	405.00	270.00	95	66
c	56.25	6.76	225.00	50.00	90	209
d	11.25	10.33	405.00	90.00	92	114
2a	56.25	61.61	225.00	150.00	133	-
b	11.25	98.04	405.00	270.00	140	-
c	56.25	6.76	225.00	50.00	132	-
d	11.25	10.33	405.00	90.00	142	-
3a	56.25	61.61	225.00	150.00	245	354
b	11.25	98.04	405.00	270.00	285	215
c	56.25	6.76	225.00	50.00	217	6416
d	11.25	10.33	405.00	90.00	284	1359
4a	56.25	61.61	225.00	150.00	140	-
b	11.25	98.04	405.00	270.00	142	-
c	56.25	6.76	225.00	50.00	140	-
d	11.25	10.33	405.00	90.00	144	-
5a	56.25	61.61	225.00	150.00	130	-
b	11.25	98.04	405.00	270.00	139	-
c	56.25	6.76	225.00	50.00	133	-
d	11.25	10.33	405.00	90.00	142	-
6a	56.25	61.61	225.00	150.00	263	415
b	11.25	98.04	405.00	270.00	286	233
c	56.25	6.76	225.00	50.00	235	8632
d	11.25	10.33	405.00	90.00	284	1412

SIZES NEEDED TO DETECT:

D_R	H_R	D_R''	D_R'	R	h_N^2	h_B^2
-	-	-	-	308	-	-
-	-	-	-	152	-	-
-	-	-	-	301	-	-
-	-	-	-	136	-	-
74	-	-	-	353	0.72	-
45	-	-	-	162	0.86	-
79	-	-	-	2408	0.71	-
37	-	-	-	930	0.94	-
180	-	-	-	765	0.50	-
85	-	-	-	456	0.65	-
110	-	-	-	2967	0.67	-
39	-	-	-	1608	0.91	-
349	1297 ^x	-	-	420	1.38	0.71
119	644 ^x	-	-	190	1.65	0.86
836	9952 ^x	-	-	2785	0.97	0.70
373	3955 ^x	-	-	1073	1.29	0.94
177	-	58581	346	744	0.66	-
105	-	80	251	249	0.84	-
168	-	86949	3311	4381	0.68	-
83	-	89165	1905	1271	0.93	-
930	5268 ^x	-	-	829	0.85	0.53
388	1685 ^x	-	-	554	1.14	0.69
1124	17943 ^x	-	-	3235	0.87	0.67
416	5232 ^x	-	-	1981	1.22	0.92

TABLE 10B.2

MODEL	TRUE PARAMETER VALUES				SAMPLE	
	E ₁	E ₂	D _R	C	E ₁	E ₂
7a	56.25	61.61	225.00	150.00	136	-
	11.25	98.04	405.00	270.00	142	-
	56.25	6.76	225.00	50.00	136	-
	11.25	10.33	405.00	90.00	143	-
8a	56.25	61.61	225.00	150.00	274	473
	11.25	98.04	405.00	270.00	286	275
	56.25	6.76	225.00	50.00	269	9767
	11.25	10.33	405.00	90.00	286	4460
9a	56.25	61.61	225.00	150.00	265	421
	11.25	98.04	405.00	270.00	286	240
	56.25	6.76	225.00	50.00	244	7614
	11.25	10.33	405.00	90.00	284	1409
10a	56.25	61.61	225.00	150.00	141	-
	11.25	98.04	405.00	270.00	142	-
	56.25	6.76	225.00	50.00	140	-
	11.25	10.33	405.00	90.00	143	-
11a	56.25	61.61	225.00	150.00	233	634
	11.25	98.04	405.00	270.00	260	284
	56.25	6.76	255.00	50.00	212	25332
	11.25	10.33	405.00	90.00	283	1521

SIZES NEEDED TO DETECT:

	R	h_N^2	h_B^2
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D_R	H_R	I	M	C			
767	-	-	1814	-	379	0.71	-
331	-	-	831	-	175	0.86	-
136	-	-	36445	-	2424	0.70	-
159	-	-	9114	-	960	0.94	-
213	-	5582 ^x	-	-	831	0.57	0.42
97	-	1417 ^x	-	-	584	0.73	0.50
120	-	69316 ^x	-	-	2964	0.67	0.63
42	-	8987 ^x	-	-	1769	0.92	0.82
686	-	-	34013	-	752	0.51	-
263	-	-	3238	-	491	0.68	-
445	-	-	∞	-	2860	0.67	-
158	-	-	16976	-	1658	0.92	-
1944	4055 ^x	-	∞ ^x	-	404	1.42	0.71
1169	2272 ^x	-	∞ ^x	-	184	1.77	0.86
2382	9585 ^x	-	36120 ^x	-	2840	1.66	0.70
1265	4642 ^x	-	16865 ^x	-	1082	1.80	0.94
247	-	-	-	631	-	0.30	0.69
100	-	-	-	461	-	0.35	0.81
163	-	-	-	2000	-	0.50	0.72
60	-	-	-	1232	-	0.64	0.93

TABLE 11A.1

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS			
		E_1	D_R	D_R''	D_R'
1	E_1	1	0.25	0.23	-0.52
	E_2	-	0.25	-0.01	0.74
2	E_1	1	-	0.00	-0.06
	D_R	-	1	0.55	0.54
3	E_1	1	-	0.04	-0.17
	E_2	-	-	0.11	0.89
	D_R	-	1	0.65	-1.10
4	E_1	1	-	0.00	-0.02
	D_R	-	1	0.65	3.43
	H_R	-	-	-0.19	-5.81
5	E_1	1	-	0.01	-0.02
	D_R	-	1	0.43	-1.00
	M	-	-	0.09	1.37
6	E_1	1	-	-0.07	-0.73
	E_2	-	-	0.19	1.00
	D_R	-	1	-0.06	-
	H_R	-	-	0.75	-
7	E_1	1	-	-0.01	-0.05
	E_2	-	-	-0.24	1.22
	D_R	-	1	0.45	0.45
	I	-	-	0.54	-2.32
8	E_1	1	-	0.03	-0.14
	E_2	-	-	-0.09	0.65
	D_R	-	1	0.71	-1.53
	M	-	-	-0.08	0.80
9	E_1	1	-	-	-0.03
	D_R	-	1	-1.00	-2.17
	H_R	-	-	2.00	1.63
	M	-	-	0.50	1.71

TABLE 11A.2

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS			
		E_1	D_R	$D_R^{(1)}$	$-D_R^{(1)}$
1	E_1	1	0.25	-0.21	-0.96
	E_2	-	0.25	0.45	1.20
2	E_1	1	-	0.01	-0.23
	D_R	-	1	0.52	0.99
3	E_1	1	-	-0.22	-0.84
	E_2	-	-	0.24	0.82
	D_R	-	1	0.51	0.63
4	E_1	1	-	0.01	-0.06
	D_R	-	1	0.42	3.34
	H_R	-	-	0.24	-5.38
5	E_1	1	-	0.03	-0.08
	D_R	-	1	0.02	-1.10
	M	-	-	0.43	1.62
6	E_1	1	-	-0.22	-0.78
	E_2	-	-	0.24	0.81
	D_R	-	1	0.64	1.43
	H_R	-	-	-0.32	-1.80
7	E_1	1	-	-0.37	-1.17
	E_2	-	-	0.21	0.77
	D_R	-	1	0.43	0.45
	I	-	-	0.44	0.89
8	E_1	1	-	-0.30	-1.10
	E_2	-	-	0.29	1.06
	D_R	-	1	0.64	1.27
	M	-	-	-0.07	-0.58
9	E_1	1	-	-	-0.08
	D_R	-	1	-1.00	-1.29
	H_R	-	-	2.00	0.31
	M	-	-	0.50	1.65

TABLE 11B.1

POPULATION		TRUE PARAMETER VALUES			
h_N^2	ρ	E_1	D_R	D_R^{II}	D_R^{III}
0.5	1.0	112.50	225.00	225.00	225.00
	1.0	112.50	225.00	112.50	159.10
	0.5	112.50	225.00	225.00	112.50
	0.5	112.50	225.00	112.50	79.55
	-1.0	112.50	225.00	225.00	-225.00
	-1.0	112.50	225.00	112.50	-159.10
	-0.5	112.50	225.00	225.00	-112.50
	-0.5	112.50	225.00	112.50	-79.55
0.9	1.0	22.50	405.00	405.00	405.00
	1.0	22.50	405.00	202.50	286.38
	0.5	22.50	405.00	405.00	202.50
	0.5	22.50	405.00	202.50	143.19
	-1.0	22.50	405.00	405.00	-405.00
	-1.0	22.50	405.00	202.50	-286.38
	-0.5	22.50	405.00	405.00	-202.50
	-0.5	22.50	405.00	202.50	-143.19

SAMPLE SIZE: R

E ₁	E ₂	R
85	72	305
85	90	452
83	143	322
82	173 ^x	466
47	147 ^x	343
51	42 ^x	386
67	∞	328
68	∞	416

6
6
4

88	36	149
88	39	188
85	71	116
85	72 ^x	143
35	39 ^x	136
38	56 ^x	135
68	∞ ^x	121
69	41603	135

TABLE 11B.2

POPULATION		TRUE PARAMETER VALUES			
h_N^2	ρ	E_1	D_R	D_R''	D_R'
0.5	1.0	112.50	225.00	225.00	225.00
0.5	1.0	112.50	225.00	112.50	159.10
0.5	0.5	112.50	225.00	225.00	112.50
0.5	0.5	112.50	225.00	112.50	79.55
0.5	-1.0	112.50	225.00	225.00	-225.00
0.5	-1.0	112.50	225.00	112.50	-159.10
0.5	-0.5	112.50	225.00	225.00	-112.50
0.5	-0.5	112.50	225.00	112.50	-79.55
0.9	1.0	22.50	405.00	405.00	405.00
0.9	1.0	22.50	405.00	202.50	286.38
0.9	0.5	22.50	405.00	405.00	202.50
0.9	0.5	22.50	405.00	202.50	143.19
0.9	-1.0	22.50	405.00	405.00	-405.00
0.9	-1.0	22.50	405.00	202.50	-286.38
0.9	-0.5	22.50	405.00	405.00	-202.50
0.9	-0.5	22.50	405.00	202.50	-143.19

SAMPLE SIZE: R h_N^2

E_1 D_R

132	80	185	0.70
128	98	306	0.65
129	93	443	0.66
126	114	835	0.61
101	769	132	0.27
104	542	227	0.31
117	185	578	0.50
115	218	1091	0.47

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142	36	82	0.94
142	37	119	0.93
142	37	207	0.94
142	38	342	0.93
142	39	51	0.91
141	42	77	0.89
142	38	205	0.92
142	39	338	0.91

TABLE 11B.3

POPULATION		TRUE PARAMETER VALUES			
h_N^2	ρ	E_1	D_R	D_R''	D_R'
0.5	1.0	112.50	225.00	225.00	225.00
0.5	1.0	112.50	225.00	112.50	159.10
0.5	0.5	112.50	225.00	225.00	112.50
0.5	0.5	112.50	225.00	112.50	79.55
0.5	-1.0	112.50	225.00	225.00	-225.00
0.5	-1.0	112.50	225.00	112.50	-159.10
0.5	-0.5	112.50	225.00	225.00	-112.50
0.5	-0.5	112.50	225.00	112.50	-79.55
0.9	1.0	22.50	405.00	405.00	405.00
0.9	1.0	22.50	405.00	202.50	286.38
0.9	0.5	22.50	405.00	405.00	202.50
0.9	0.5	22.50	405.00	202.50	143.19
0.9	-1.0	22.50	405.00	405.00	-405.00
0.9	-1.0	22.50	405.00	202.50	-286.38
0.9	0.5	22.50	405.00	405.00	-202.50
0.9	0.5	22.50	405.00	202.50	-143.19

SAMPLE SIZE NEEDED: R $\frac{2}{h_N}$

E_1 E_2 D_R

214	157	1136	286	0.19
208	275	621	476	0.29
208	1017	217	568	0.50
196	1416	248	1185	0.48
68	150 ^x	298	513	0.45
78	220 ^x	285	832	0.47
129	1146 ^x	165	1193	0.60
128	1488 ^x	200	3912	0.55

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245	41	17341	143	0.01
267	51	734	188	0.09
281	8675	38	202	0.93
279	7816	41	335	0.91
37	42 ^x	47	119	0.87
47	57 ^x	47	195	0.87
266	1450 ^x	38	215	0.93
261	2393 ^x	39	365	0.92

TABLE

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	D_R	D_R''
0.5	1.0	112.50	225.00	225.00
0.5	1.0	112.50	225.00	112.50
0.5	0.5	112.50	225.00	225.00
0.5	0.5	112.50	225.00	112.50
0.5	-1.0	112.50	225.00	225.00
0.5	-1.0	112.50	225.00	112.50
0.5	-0.5	112.50	225.00	225.00
0.5	-0.5	112.50	225.00	112.50
0.9	1.0	22.50	405.00	405.00
0.9	1.0	22.50	405.00	202.50
0.9	-0.5	22.50	405.00	405.00
0.9	-0.5	22.50	405.00	202.50
0.9	1.0	22.50	405.00	405.00
0.9	1.0	22.50	405.00	202.50
0.9	-0.5	22.50	405.00	405.00
0.9	-0.5	22.50	405.00	202.50

11B.4

SAMPLE SIZES NEEDED: R h_N^2 h_B^2

D_R'	E_1	D_R	H_R	R	h_N^2	h_B^2
225.00	140	214	524 ^x	223	1.67	0.68
159.10	139	337	1002 ^x	354	1.43	0.63
112.50	139	527	2392 ^x	497	1.19	0.65
79.55	138	779	4431 ^x	922	1.03	0.60
-225.00	130	1358 ^x	741	146	-0.95	0.44
-159.10	129	3420 ^x	1347	245	-0.60	0.42
-112.50	135	∞ ^x	3060	661	-0.09	0.54
-79.55	133	∞	1088	1231	0.03	0.50
						6 2
405.00	144	71	104 ^x	104	2.37	0.95
286.38	144	90	163 ^x	146	2.17	0.94
202.50	144	160	504 ^x	276	1.76	0.94
143.19	144	202	792 ^x	446	1.63	0.93
-405.00	144	342 ^x	184	54	-1.88	0.91
-286.38	144	790 ^x	297	81	-1.24	0.89
-202.50	144	48622 ^x	907	257	-0.15	0.92
-143.19	144	∞	1288	422	0.04	0.91

TABLE 11B.5

POPULATION		TRUE PARAMETER VALUES				SAMP.
h_N^2	ρ	E_1	D_R	D_R''	D_R'	E_1
0.5	1.0	112.50	225.00	225.00	225.00	135
0.5	1.0	112.50	225.00	112.50	159.10	133
0.5	0.5	112.50	225.00	225.00	112.50	133
0.5	0.5	112.50	225.00	112.50	79.55	130
0.5	-1.0	112.50	225.00	225.00	-225.00	118
0.5	-1.0	112.50	225.00	112.50	-159.10	117
0.5	0.5	112.50	225.00	225.00	-112.50	126
0.5	0.5	112.50	225.00	112.50	-79.55	123
0.9	1.0	22.50	405.00	405.00	405.00	144
0.9	1.0	22.50	405.00	202.50	286.38	144
0.9	0.5	22.50	405.00	405.00	202.50	144
0.9	0.5	22.50	405.00	202.50	143.19	142
0.9	1.0	22.50	405.00	405.00	-405.00	142
0.9	1.0	22.50	405.00	202.50	-286.38	142
0.9	-0.5	22.50	405.00	405.00	-202.50	142
0.9	-0.5	22.50	405.00	202.50	-143.19	142

LE SIZE NEEDED

R

 h_N^2 D_R

M

5969	395	243	0.66
4391	689	392	0.62
1738	1258	566	0.63
1776	2213 ^x	1064	0.59
189	251 ^x	176	0.43
254	421 ^x	230	0.43
415	2836 ^x	680	0.54
499	3565 ^x	1335	0.51

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333	103	11	0.94
308	154	154	0.93
212	394	319	0.94
217	595 ^x	527	0.93
42	43 ^x	74	0.91
49	60 ^x	115	0.90
103	765 ^x	273	0.93
108	825 ^x	478	0.91

TABLE 11B.6

POPULATION		TRUE PARAMETER VALUES				SAN
$\frac{h^2}{N}$	P	E_1	D_R	D_R''	D_R'	E_1
0.5	1.0	112.50	225.00	225.00	225.00	118
0.5	1.0	112.50	225.00	112.50	159.10	120
0.5	0.5	112.50	225.00	225.00	112.50	124
0.5	0.5	112.50	225.00	112.50	79.55	123
0.5	-1.0	112.50	225.00	225.00	-225.00	117
0.5	-1.0	112.50	225.00	112.50	-159.10	118
0.5	-0.5	112.50	225.00	225.50	-112.50	126
0.5	-0.5	112.50	225.00	112.50	-79.55	124
0.9	1.0	22.50	405.00	405.00	405.00	129
0.9	1.0	22.50	405.00	202.50	286.38	136
0.9	0.5	22.50	405.00	405.00	202.50	142
0.9	0.5	22.50	405.00	202.50	143.19	142
0.9	-1.0	22.50	405.00	405.00	-405.00	128
0.9	-1.0	22.50	405.00	202.50	-286.38	139
0.9	-0.5	22.50	405.00	405.00	-202.50	142
0.9	-0.5	22.50	405.00	202.50	-143.19	142

AMPLE SIZES NEEDED TO DETECT:

R

h_N^2

D_R	D_R^{II}	D_R^I	R	h_N^2
322	835	148	-	0.50
323	2513	194	-	0.50
326	778	539	-	0.50
326	2463	753	-	0.50
322	1319	272 ^x	-	0.50
322	3743	351 ^x	-	0.50
327	1020	783 ^x	-	0.50
326	3080	1066 ^x	-	0.50

629

90	487	99	-	0.90
90	1218	108	-	0.90
90	364	275	-	0.90
90	984	316	-	0.90
90	711	156 ^x	-	0.90
90	1715	170 ^x	-	0.90
90	475	388 ^x	-	0.90
90	1233	440 ^x	-	0.90

TABLE 11B.7

POPULATION		TRUE PARAMETER VALUES				SAM
h_N^2	ρ	E_1	D_R	D_R''	D_R'	E_1
0.5	1.0	112.50	225.00	225.00	225.00	251
0.5	1.0	112.50	225.00	112.50	159.10	112
0.5	0.5	112.50	225.00	225.00	112.50	232
0.5	0.5	112.50	225.00	112.50	79.55	221
0.5	-1.0	112.50	225.00	225.00	-225.00	81
0.5	-1.0	112.50	225.00	112.50	-159.10	93
0.5	-0.5	112.50	225.00	225.00	-112.50	159
0.5	-0.5	112.50	225.00	112.50	-79.55	157
0.9	1.0	22.50	405.00	405.00	405.00	285
0.9	1.0	22.50	405.00	202.50	286.38	280
0.9	0.5	22.50	405.00	405.00	202.50	281
0.9	0.5	22.50	405.00	202.50	143.19	280
0.9	-1.0	22.50	405.00	405.00	-405.00	39
0.9	-1.0	22.50	405.00	202.50	-286.38	50
0.9	-0.5	22.50	405.00	405.00	-202.50	279
0.9	-0.5	22.50	405.00	202.50	-143.19	275

SAMPLE SIZE NEEDED TO DETECT: R h_N^2 h_B^2

E_2 D_R H_R

234	1430	3484 ^x	276	0.64	0.27
378	1313	3777 ^x	489	0.75	0.33
1334	1242	8696 ^x	578	0.82	0.52
1759	1714	14354 ^x	1215	0.73	0.49
164 ^x	79594	7558	505	0.11	0.49
243 ^x	27826	13822	811	0.20	0.50
1454 ^x	11400	16014	1158	0.33	0.60
1811 ^x	10144	26836	2622	0.35	0.56

42	38977	∞ ^x	137	0.03	0.01
266	99	126 ^x	150	1.98	0.72
16211	166	527 ^x	265	1.74	0.93
11072	211	832 ^x	435	1.60	0.92
45 ^x	237 ^x	91	138	-0.78	0.89
61 ^x	7673 ^x	454	198	-0.26	0.88
5653 ^x	∞ ^x	1018	256	-0.08	0.93
5323 ^x	83458	1488	430	0.11	0.92

TABLE 11B.8

POPULATION		TRUE PARAMETER VALUES				SAM
h_N^2	ρ	E_1	D_R	D_R''	D_R'	E_1
0.5	1.0	112.50	225.00	225.00	225.00	238
0.5	1.0	112.50	225.00	112.50	159.10	241
0.5	0.5	112.50	225.00	225.00	112.50	257
0.5	0.5	112.50	225.00	112.50	79.55	250
0.5	-1.0	112.50	225.00	225.00	-225.00	91
0.5	-1.0	112.50	225.00	112.50	-159.10	138
0.5	-0.5	112.50	225.00	225.00	-112.50	242
0.5	-0.5	112.50	225.00	112.50	-79.55	233
0.9	1.0	22.50	405.00	405.00	405.00	241
0.9	1.0	22.50	405.00	202.50	286.38	263
0.9	0.5	22.50	405.00	405.00	202.50	285
0.9	0.5	22.50	405.00	202.50	143.19	284
0.9	-1.0	22.50	405.00	405.00	-405.00	284
0.9	-1.0	22.50	405.00	202.50	-286.38	284
0.9	-0.5	22.50	405.00	405.00	-202.50	285
0.9	-0.5	22.50	405.00	202.50	-143.19	285

AMPLE SIZE NEEDED TO DETECT: R h_N^2 h_B^2

E_2 D_R I

122	152	321 ^x	386	0.64	0.04
187	193	546 ^x	714	0.59	0.08
848	168	2433 ^x	656	0.61	0.35
1136	213	3640 ^x	1433	0.57	0.34
197 ^x	317	3986 ^x	551	0.49	0.26
292 ^x	346	∞	787	0.48	0.49
1031 ^x	236	2866	467	0.55	0.82
1394 ^x	280	4784	3613	0.51	0.74

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45	45	48 ^x	209	0.94	0.00
54	47	59 ^x	357	0.93	0.05
349	41	367 ^x	338	0.94	0.50
371	43	397 ^x	675	0.93	0.50
50 ^x	51	60 ^x	268	0.90	0.01
59 ^x	48	73	226	0.89	1.71
404 ^x	39	431	547	0.92	1.37
452 ^x	42	489	1190	0.91	1.33

TABLE 11B.9

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	D_R	D_R''	D_R'
0.5	1.0	112.50	225.00	225.00	225.00
0.5	1.0	112.50	225.00	112.50	159.10
0.5	0.5	112.50	225.00	225.00	112.50
0.5	0.5	112.50	225.00	112.50	79.55
0.5	-1.0	112.50	225.00	225.00	-225.00
0.5	-1.0	112.50	225.00	112.50	-159.10
0.5	-0.5	112.50	225.00	225.00	-112.50
0.5	-0.5	112.50	225.00	112.50	-79.55
0.9	1.0	22.50	405.00	405.00	405.00
0.9	1.0	22.50	405.00	202.50	286.38
0.9	0.5	22.50	405.00	405.00	202.50
0.9	0.5	22.50	405.00	202.50	143.19
0.9	-1.0	22.50	405.00	405.00	-405.00
0.9	-1.0	22.50	405.00	202.50	-286.38
0.9	-0.5	22.50	405.00	405.00	-202.50
0.9	-0.5	22.50	405.00	405.00	-143.19

SAMPLE SIZES NEEDED TO DETECT: R $\frac{h^2}{N}$

E_1	E_2	D_R	M	R	$\frac{h^2}{N}$
242	230	36918	1818	271	0.32
232	516	10469	2604	486	0.36
229	2387	1758	3123	606	0.54
48	63	260	224	1262	0.50
73	185 ^x	3604	1649	688	0.46
91	290 ^x	1778	5987	924	0.47
166	1485 ^x	719	∞ ^x	1155	0.59
165	2140 ^x	778	∞ ^x	2537	0.56
					69
					66
					65
284	127	∞	225	95	0.40
278	369	1265	112	150	0.12
280	34712	213	407	307	0.93
280	7417	219	621	510	0.92
45	65 ^x	5741	117	202	0.69
77	96 ^x	250	554 ^x	221	0.85
281	8755 ^x	105	907 ^x	268	0.93
280	9432 ^x	111	993 ^x	475	0.92

TABLE 11B.10

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	D_R	D_R''	D_R'
0.5	1.0	112.50	225.00	225.00	225.00
0.5	1.0	112.50	225.00	112.50	159.10
0.5	0.5	112.50	225.00	225.00	112.50
0.5	0.5	112.50	225.00	112.50	79.55
0.5	-1.0	112.50	225.00	225.00	-225.00
0.5	-1.0	112.50	225.00	112.50	-159.10
0.5	-0.5	112.50	225.00	225.00	-112.50
0.5	-0.5	112.50	225.00	112.50	79.55
0.9	1.0	22.50	405.00	405.00	405.00
0.9	1.0	22.50	405.00	202.50	286.38
0.9	0.5	22.50	405.00	405.00	202.50
0.9	0.5	22.50	405.00	202.50	143.19
0.9	-1.0	22.50	405.00	405.00	-405.00
0.9	-1.0	22.50	405.00	202.50	-286.38
0.9	-0.5	22.50	405.00	405.00	-202.50
0.9	-0.5	22.50	405.00	202.50	-143.19

SAMPLE SIZE NEEDED TO DETECT: R h_N^2 h_B^2

E ₁	D _R	H _R	M	R	h_N^2	h_B^2
140	16205 ^x	10910	1532	225	0.01	0.66
139	53021 ^x	22159	2204	369	0.20	0.62
139	50996 ^x	14062	2667	531	0.13	0.64
138	∞ ^x	33277	4406	1012	0.13	0.59
133	4762	9589	327 ^x	171	0.07	0.46
132	3622	74013	555 ^x	287	0.29	0.44
135	29139	16872	12039 ^x	670	0.20	0.55
134	13090	75773	9474 ^x	1294	0.34	0.59
					6	6
					3	3

144	6477 ^x	4695	947	98	-0.25	0.94
144	14017 ^x	7448	1188	143	0.08	0.93
144	17855 ^x	5925	1501	290	0.06	0.94
144	∞ ^x	11042	2115	490	0.34	0.92
144	1734	882	45 ^x	71	-0.19	0.92
144	856	4174	62 ^x	108	0.37	0.90
144	7464	5815	3159 ^x	268	0.38	0.92
144	3236	23064	2195	462	0.64	0.91

TABLE 12 A1.1

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E_1	E_2	D_R	D_R''	D_R'''
1	E_1	1	-	0.25	0.23	-0.52
	E_2	-	1	0.25	0.00	0.75
2	E_1	1	0.48	-	0.00	-0.05
	D_R	-	0.99	1	0.55	0.49
3	E_1	1	-	-	0.01	-0.10
	E_2	-	1	-	-0.06	0.61
	D_R	-	-	1	0.63	-0.85
4	E_1	1	0.50	-	0.00	-0.01
	D_R	-	3	1	0.64	3.42
	H_R	-	-4	-	-0.17	-5.84
5	E_1	1	0.51	-	0.00	-0.01
	D_R	-	-0.25	1	0.43	-1.05
	M	-	1.10	-	0.10	1.39
6	E_1	1	0.52	-	-	-
	D_R	-	0.82	1	-	-
	D_R''	-	-0.44	-	1	-
	D_R'''	-	0.86	-	-	1
7	E_1	1	-	-	0.01	-0.07
	E_2	-	1	-	-0.05	0.51
	D_R	-	-	1	0.18	1.69
	H_R	-	-	-	0.87	-4.64
	I	-	-	-	0.46	-2.32
8	E_1	1	-	-	-0.00	-0.02
	E_2	-	1	-	-0.20	1.20
	D_R	-	-	1	0.45	0.40
	I	-	-	-	0.46	-2.32
	M	-	-	-	-0.08	1.15

TABLE 12A 1.2

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E ₁	E ₂	D _R	D _R ¹¹	D _R ¹
10	E ₁	1	0.49	-	-	-0.02
	D _R	-	-4.38	1	-1	-2.18
	H _R	-	5.75	-	2	1.58
	M	-	2.26	-	0.50	1.72
11	E ₁	1	0.52	-	-	-
	D _R	-	0.74	1	-	-
	M	-	0.08	-	-	-
	D _R ¹¹	-	-0.45	-	1	-
	D _R ¹	-	0.85	-	-	1
12	E ₁	1	-	-	-0.04	-0.60
	E ₂	-	1	-	-0.20	1.17
	D _R	-	-	1	0.47	0.69
	H _R	-	-	-	-0.04	-0.60
	I	-	-	-	0.46	-2.26
13	E ₁	1	-	-	0.01	-0.07
	E ₂	-	1	-	-0.08	0.44
	D _R	-	-	1	-1.84	-0.91
	H _R	-	-	-	3.52	-1.10
	M	-	-	-	0.68	0.92
14	E ₁	1	-	-	0.00	-0.02
	E ₂	-	1	-	-0.26	1.21
	D _R	-	-	1	0.21	0.44
	I	-	-	-	0.57	-2.34
	M	-	-	-	0.21	-0.03

TABLE 12A 2.1

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E_1	E_2	D_R	$D_R^{''}$	$D_R^{'''}$
1	E_1	1	-	0.25	-0.10	-0.85
	E_2	-	1	0.25	0.36	1.11
2	E_1	1	0.44	-	0.00	-0.12
	D_R	-	1.10	1	0.54	0.73
3	E_1	1	-	-	-0.12	-0.66
	E_2	-	1	-	0.15	0.76
	D_R	-	-	1	0.50	0.40
4	E_1	1	0.50	-	0.00	-0.03
	D_R	-	3	1	0.46	3.45
	H_R	-	-4	-	0.18	-5.78
5	E_1	1	0.52	-	0.01	-0.04
	D_R	-	-1.09	1	0.15	-1.22
	M	-	1.88	-	0.35	1.62
6	E_1	1	0.56	-	-	-
	D_R	-	0.71	1	-	-
	$D_R^{''}$	-	-0.58	-	1	-
	$D_R^{'''}$	-	0.88	-	-	1
7	E_1	1	-	-	-0.11	-0.58
	E_2	-	1	-	0.15	0.72
	D_R	-	-	1	0.52	1.43
	H_R	-	-	-	-0.07	-2.20
8	E_1	1	-	-	-0.01	-0.09
	E_2	-	1	-	0.17	0.91
	D_R	-	-	1	0.44	0.39
	I	-	-	-	-0.22	-1.57
9	E_1	1	-	-	-0.10	-0.68
	E_2	-	1	-	0.12	0.76
	D_R	-	-	1	0.31	0.36
	M	-	-	-	0.20	0.07

TABLE 12A 2.2

MODEL	ESTIMATED PARAMETERS	TRUE PARAMETERS				
		E ₁	E ₂	D _R	D _R ¹¹	D _R ¹
10	E ₁	1	0.49	-	-	-0.04
	D _R	-	-3.47	1	-1	-1.42
	H _R	-	4.10	-	2	0.29
	M	-	2.22	-	0.50	1.67
11	E ₁	1	0.58	-	-	-
	D _R	-	0.04	1	-	-
	M	-	0.72	-	-	-
	D _R ¹¹	-	-0.62	-	1	-
	D _R ¹	-	0.74	-	-	1
12	E ₁	1	-	-	-0.02	-0.06
	E ₂	-	1	-	0.19	0.89
	D _R	-	-	1	0.33	1.89
	H _R	-	-	-	0.18	-3.16
	I	-	-	-	-0.24	-1.48
13	E ₁	1	-	-	-0.12	-0.68
	E ₂	-	1	-	0.14	0.79
	D _R	-	-	1	0.21	1.85
	H _R	-	-	-	0.22	-2.52
	M	-	-	-	0.17	-0.20
14	E ₁	1	-	-	-0.01	-0.09
	E ₂	-	1	-	-0.04	0.93
	D _R	-	-	1	-0.18	0.49
	I	-	-	-	0.27	-1.61
	M	-	-	-	0.50	-0.07

TABLE 12B.1

POPULATION		TRUE PARAMETER VALUES				
b_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE

R

E₁ E₂

95	51	315
93	87	278
95	56	468
93	90	394
62	728 ^x	272
81	1373	260
69	5084 ^x	301
84	753	318

369
33

96	37	150
95	72	108
96	39	174
95	71	131
39	49 ^x	132
75	57	118
44	73 ^x	131
77	8598	130

TABLE 12B.2

POPULATION

TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE

R

 h_N^2 E_1 D_R

135	62	124	0.77
134	68	249	0.75
133	71	172	0.74
132	78	341	0.71
120	109	201	0.53
128	98	797	0.65
120	160	404	0.54
126	110	1512	0.62

66

144	35	73	0.96
142	36	179	0.95
142	36	105	0.95
142	36	271	0.95
142	37	53	0.93
142	36	203	0.94
142	38	81	0.92
142	37	332	0.93

TABLE 12B.3

POPULATION

TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R	D_R
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	22.500	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE

R

 h_N^2 E_1 E_2 D_R

236	63	4349	299	0.06
250	268	206	566	0.46
238	84	1418	474	0.13
244	276	238	1151	0.43
101	439 ^x	196	419	0.56
41	51	124	744	0.65
126	1284 ^x	196	598	0.56
196	7329	146	1453	0.61

200

243	38	66275	144	0.00
285	926	38	197	0.93
275	44	509	191	0.07
285	893 ^x	39	325	0.91
42	49	47	126	0.88
284	3752 ^x	37	197	0.94
55	68 ^x	45	197	0.88
282	3518	38	326	0.93

TABLE 12B.4

POPULATION

TRUE PARAMETER VALUES

σ_N^2	ρ	E_1	E_2	D_R	D_R^{II}	D_R^I
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE	R	h_N^2	h_B^2
E ₁	D _R	H _R	
141	138	284 ^x	1.92
141	294	1006 ^x	1.47
141	193	470 ^x	1.72
140	382	1488 ^x	1.34
138	3266 ^x	907	-0.60
139	16859	5933	0.25
136	22481 ^x	1894	-0.23
139	6697	16348	0.38
		1482	0.63
144	67	97 ^x	2.41
144	150	446 ^x	1.81
144	85	147 ^x	2.22
144	184	676 ^x	1.68
144	375 ^x	190	-1.80
144	∞ ^x	962	-0.08
144	909 ^x	310	-1.15
144	94401	1397	0.11
		396	0.93

TABLE 12B.5

POPULATION

TRUE PARAMETER VALUES

b_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'''
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE

R

 h_N^2 E_1 D_R M

139	4306	236	154	0.74
138	1316	622	334	0.72
138	3515	358	208	0.70
136	1474	860	439	0.68
129	221	728 ^x	244	0.60
133	397	27066 ^x	784	0.66
128	309	1636 ^x	462	0.58
132	510	∞ ^x	1456	0.63

2
0
n

144	274	97	92	0.96
144	190	358	270	0.95
144	258	141	127	0.95
144	194	519	396	0.94
142	44	50 ^x	76	0.94
144	102	899 ^x	256	0.94
142	50	73 ^x	117	0.93
142	107	1010 ^x	429	0.93

TABLE 12B.6

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R''
0.5	1.0	56.25	56.25	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00
0.5	1.0	56.25	56.25	225.00	112.50
0.5	0.5	56.25	56.25	225.00	112.50
0.5	-1.0	56.25	56.25	225.00	225.00
0.5	-0.5	56.25	56.25	225.00	225.00
0.5	-1.0	56.25	56.25	225.00	112.50
0.5	-0.5	56.25	56.25	225.00	112.50
0.9	1.0	11.25	11.25	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00
0.9	1.0	11.25	11.25	405.00	202.50
0.9	0.5	11.25	11.25	405.00	202.50
0.9	-1.0	11.25	11.25	405.00	405.00
0.9	-0.5	11.25	11.25	405.00	405.00
0.9	-1.0	11.25	11.25	405.00	202.50
0.9	-0.5	11.25	11.25	405.00	202.50

SAMPLE SIZE NEEDED TO DETECT: R χ^2_N

D_R'	E_1	D_R	D_R''	D_R'	
225.00	116	197	1054	109	1667 0.63
112.50	128	211	947	247	1950 0.61
159.10	118	200	3865	121	1705 0.62
79.55	127	209	3899	264 ^x	1906 0.61
-225.00	128	221	1479	343 ^x	1759 0.60
-112.50	132	215	1124	1937 ^x	1978 0.61
-159.10	129	220	5839	536 ^x	1787 0.60
-79.55	130	215	4614	5385 ^x	1937 0.61
					2 0 0
405.00	123	84	509	97	1732 0.93
202.50	142	85	377	249	2153 0.92
286.38	135	85	1318	103	1989 0.93
143.19	142	85	1055	274 ^x	2150 0.93
-405.00	139	85	716	157 ^x	1795 0.92
-202.50	142	85	476	412 ^x	2153 0.92
-286.38	141	85	1783	174 ^x	2016 0.92
-143.19	142	85	1278	482 ^x	2249 0.92

TABLE 12B.7

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.00
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE NEEDED TO DETECT: R h_N^2 h_B^2

E_1 E_2 D_R H_R

273	71	7315	18159 ^x	285	0.17	0.07
267	314	1109	6863 ^x	576	0.76	0.49
272	107	2240	5461 ^x	453	0.40	0.17
262	315 ^x	1398	9635 ^x	1196	0.69	0.45
129	582 ^x	∞	4514	389	0.05	0.59
236	9247	99812	3578	752	0.10	0.65
164	2196 ^x	∞	4756	546	0.06	0.59
233	4127	27339	6043	1535	0.20	0.61

286	38	∞	∞ ^x	138	0.01	0.00
285	1011	163	509 ^x	263	1.74	0.93
285	174	107	122 ^x	144	1.86	0.66
287	941	201	758 ^x	427	1.61	0.92
44	51 ^x	608 ^x	153	138	-0.66	0.89
285	2587	40484 ^x	866	246	-0.15	0.93
60	74 ^x	59038 ^x	762	194	-0.11	0.89
285	2635	∞	1230	406	0.05	0.92

TABLE 12B.8

POPULATION

TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	122.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-122.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE NEEDED TO DETECT: R h_N^2 h_B^2

E_1 E_2 D_R I

241	61	164	209 ^x	401	0.63	0.01
273	300	178	543 ^x	684	0.61	0.35
247	77	206	323 ^x	763	0.58	0.05
270	304	224	1044 ^x	1535	0.56	0.32
270	354 ^x	291	403	474	0.51	1.17
275	3122 ^x	232	1067	1431	0.55	0.95
268	687 ^x	324	591	858	0.49	1.06
273	9130 ^x	278	1600	3709	0.52	0.86

239	43	47	47 ^x	209	0.94	0.00
286	302	42	354 ^x	340	0.94	0.51
273	49	48	55 ^x	360	0.93	0.05
286	304	43	372 ^x	683	0.93	0.50
239	50 ^x	47	50	150	0.90	1.82
239	456 ^x	39	395	548	0.92	1.38
239	69 ^x	47	67	244	0.89	1.74
239	524 ^x	42	442	1201	0.91	1.35

TABLE 12B.9

POPULATION TRUE PARMATETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE NEEDED TO DETECT: R h_N^2

E_1	E_2	D_R	M		
270	75	∞	11993	282	0.08
266	396	1095	2973	603	0.51
272	122	21292	4111	446	0.19
261	378	1264	5330	1246	0.47
128	571 ^x	956	39973	431	0.55
242	9002	339	7509 ^x	719	0.65
180	3537 ^x	512	12017 ^x	535	0.57
241	3772	397	9176 ^x	1485	0.60
					2 C G
286	38	∞	∞	138	0.00
285	1111	191	400	304	0.93
285	209	1258	99	146	0.72
285	1017 ^x	196	583	503	0.92
50	69 ^x	1854	135 ^x	188	0.72
286	2243	98	749 ^x	261	0.93
285	4849	50	73 ^x	114	0.92
285	2215	103	829 ^x	455	0.92

TABLE 12B.10

POPULATION		TRUE PARAMETER VALUES				
h_N^2	ρ	E_1	E_2	D_R	D_R^{II}	D_R^{III}
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	122.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZES NEEDED TO DETECT: R h_N^2 h_B^2

E_1	D _R	H _R	M	R	h_N^2	h_B^2
141	7478 ^x	5838	1145	143	-0.24	0.74
141	13072 ^x	6600	1637	312	-0.10	0.72
140	12334 ^x	8229	1409	196	-0.07	0.70
140	24824 ^x	9668	2060	417	0.04	0.68
138	38320	4333	2069 ^x	236	-0.03	0.61
139	∞ ^x	6819	42735	780	0.05	0.66
138	25399	10585	6010 ^x	441	0.16	0.59
139	∞	12208	36286	1447	0.17	0.63
144	5884 ^x	4336	915	84	-0.31	0.95
144	14785 ^x	5358	1415	247	0.01	0.95
144	11604 ^x	6520	1126	118	0.02	0.95
144	2185 ^x	9204	1915 ^x	370	0.28	0.94
144	1997	895	53 ^x	72	-0.17	0.94
144	1486	5343	4886 ^x	251	0.36	0.94
144	978	4050	79 ^x	110	0.38	0.93
144	4025	17790	3475 ^x	414	0.62	0.93

TABLE 12B.11

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R^{11}	D_R^{19}
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE NEEDED TO DETECT:

 R η_N^2

E_1	E_2	D_R	D_R''	D_R'	R	η_N^2
238	1163	395	877	197	-	0.5
275	1190	394	752	676	-	0.5
245	1160	394	2590	280	-	0.5
272	1172	393	2349	1011	-	0.5
280	943	363	1087	239 ^x	-	0.5
282	1126	385	854	765 ^x	-	0.5
280	972	366	3053	320 ^x	-	0.5
281	1105	383	2578	1096 ^x	-	0.5
						2
						0
						65
239	1371	92	494	102	-	0.9
286	1418	92	364	278	-	0.9
273	1405	92	1239	111	-	0.9
286	1417	92	982	320 ^x	-	0.9
282	1042	91	687	150 ^x	-	0.9
286	1412	77	460	373 ^x	-	0.9
285	1253	91	1647	163 ^x	-	0.9
286	1409	77	1186	421 ^x	-	0.9

TABLE 12B.12

POPULATION

TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R^{II}	D_R^{III}
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE NEEDED TO DETECT:

 R h_N^2

E_1	D_R	M	D_R''	D_R'	R	h_N^2
139	716	15899	1164	116	1758	0.62
138	901	∞	962	296	1869	0.61
138	734	20170	4676	134	1769	0.62
136	862	∞	4051	334	1846	0.61
128	740	14729	1515	337 ^x	1829	0.60
134	920	∞	1132	2244 ^x	1898	0.61
128	759	18479	252	531 ^x	1833	0.60
133	880	∞	4804	5681 ^x	1875	0.61
						2
						3
						4
144	95	7326 ^x	517	98	2042	0.93
144	255	∞	379	291	2154	0.92
144	103	26655 ^x	1353	105	2043	0.93
144	224	∞ ^x	1067	340	2054	0.92
142	97	6623 ^x	720	454 ^x	2044	0.93
142	256	∞ ^x	479	408 ^x	2056	0.92
142	108	18049	1813	171 ^x	2045	0.93
142	229	∞	1290	573 ^x	2054	0.92

TABLE 12B.13

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'	E_1
0.5	1.0	56.25	56.25	225.00	225.00	225.00	281
0.5	0.5	56.25	56.25	225.00	225.00	112.50	281
0.5	1.0	56.25	56.25	225.00	112.50	159.10	279
0.5	0.5	56.25	56.25	225.00	112.50	79.55	286
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00	275
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50	279
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10	275
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55	284
0.9	1.0	11.25	11.25	405.00	405.00	405.00	286
0.9	0.5	11.25	11.25	405.00	405.00	202.50	286
0.9	1.0	11.25	11.25	405.00	202.50	286.38	286
0.9	0.5	11.25	11.25	405.00	202.50	143.19	286
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00	286
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50	286
0.9	-1.0	11.25	11.25	405.00	405.00	-286.38	286
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19	286

SAMPLE SIZE NEEDED TO DETECT: R h_N^2 h_B^2

E_2	D_R	H_R	I	R	h_N^2	h_B^2
63	537	∞ x	212 ^x	383	0.65	0.01
383	1364	∞ x	2237 ^x	657	0.67	0.36
80	839	∞ x	331 ^x	729	0.60	0.05
377 ^x	1729	∞ x	2785	1472	0.61	0.33
467 ^x	16223 ^x	1977	482	528	-0.28	1.15
4923 ^x	15229	14529	1441	1481	0.27	0.93
893 ^x	∞ x	4723	723	907	-0.01	1.04
15737 ^x	9845	32799	2146	3853	0.34	0.84
210						
43	53	∞ x	47 ^x	200	0.95	0.00
467	390	11320 ^x	555 ^x	333	1.12	0.55
50	77	∞ x	56 ^x	344	0.94	0.05
436	445	22593 ^x	539 ^x	669	1.06	0.53
55 ^x	165 ^x	108	54	143	-2.00	1.82
617 ^x	4179	5399	528	570	0.50	1.35
94 ^x	1649 ^x	402	73	234	-0.78	1.73
696 ^x	3200	7952	579	1274	0.57	1.33

TABLE

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'''
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.10
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.00
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

12B.14

SAMPLE SIZES NEEDED TO DETECT: R h_N^2 h_B^2

E_1	E_2	D_R	H_R	M	R	h_N^2	h_B^2
273	85	41101 ^x	38409	21710	264	-0.29	0.80
267	433	37767 ^x	13417	5621	568	-0.06	0.52
269	128	∞	∞	32193	428	0.04	0.18
262	409	∞	49280	11706	1182	0.19	0.47
132	540 ^x	26114 ^x	3766	7144	428	-0.13	0.57
243	11530	∞	7604	∞	718	0.07	0.65
181	2906 ^x	∞	7741	∞	521	0.06	0.59
241	4592	1081	1600	327 ^x	1468	0.23	0.61
2 1 1							
286	43	18552 ^x	18507	18277	128	-0.59	0.00
285	1131	15621 ^x	5550	1531	276	0.00	0.93
290	209	16881 ^x	14506	1702	134	0.02	0.68
285	1042 ^x	25443 ^x	10664	2191	466	0.30	0.91
62	72 ^x	1225 ^x	455	168	224	0.22	0.88
286	2313	2054	5625	3454 ^x	254	0.37	0.93
286	5561	899	4613	79 ^x	107	0.41	0.92
285	2276	3470	21638	2482 ^x	436	0.64	0.92

TABLE 12B.

POPULATION TRUE PARAMETER VALUES

h_N^2	ρ	E_1	E_2	D_R	D_R''	D_R'
0.5	1.0	56.25	56.25	225.00	225.00	225.00
0.5	0.5	56.25	56.25	225.00	225.00	112.50
0.5	1.0	56.25	56.25	225.00	112.50	159.19
0.5	0.5	56.25	56.25	225.00	112.50	79.55
0.5	-1.0	56.25	56.25	225.00	225.00	-225.00
0.5	-0.5	56.25	56.25	225.00	225.00	-112.50
0.5	-1.0	56.25	56.25	225.00	112.50	-159.10
0.5	-0.5	56.25	56.25	225.00	112.50	-79.55
0.9	1.0	11.25	11.25	405.00	405.00	405.00
0.9	0.5	11.25	11.25	405.00	405.00	202.50
0.9	1.0	11.25	11.25	405.00	202.50	286.38
0.9	0.5	11.25	11.25	405.00	202.50	143.19
0.9	-1.0	11.25	11.25	405.00	405.00	-405.00
0.9	-0.5	11.25	11.25	405.00	405.00	-202.50
0.9	-1.0	11.25	11.25	405.00	202.50	-286.38
0.9	-0.5	11.25	11.25	405.00	202.50	-143.19

SAMPLE SIZE NEEDED TO DETECT:

 R h_N^2 h_B^2

E_1	E_2	D_R	I	M			
279	66	306	214 ^x	∞	383	0.63	0.01
278	534	893	3346 ^x	26549	657	0.60	0.38
276	85	454	337 ^x	∞	728	0.58	0.05
276	480	994	3506 ^x	∞	1471	0.56	0.34
268	639 ^x	18700	602	3731	508	0.45	1.39
275	2264 ^x	4991	1150	5749	1680	0.52	1.11
267	1168 ^x	6946	894	9137	876	0.46	1.20
273	6332 ^x	3360	1918	16680	4220	0.50	0.95
286	43	48	107 ^x	∞	200	0.94	0.00
286	790	208	967 ^x	4003	332	0.94	0.61
286	50	55	56 ^x	∞	344	0.93	0.05
286	591 ^x	195	738 ^x	12643	666	0.93	0.56
286	194 ^x	457	184	3020	154	0.90	2.06
286	498 ^x	396	454	1988	650	0.92	1.63
286	278 ^x	430	260	8134	242	0.89	1.89
286	784 ^x	376	686	6548	1335	0.91	1.50

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