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Path analysis under generalized assortative mating

II. American I.Q.

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SUMMARY

Rice, Cloninger & Reich (1980) showed that correlational data on American I.Q. is consistent with a rather low genetic heritability. Here we confirm their general results with a more parsimonious model. From phenotypic data alone, the estimates of genetic and cultural heritability are 0·31 and 0·42, respectively. Using environmental indices, the parsimonious estimates become 0·34 and 0·26, respectively.

INTRODUCTION

A linear model incorporating generalized assortative mating, cultural inheritance, specific maternal effects, intergenerational differences in heritabilities, and sibship common environment was presented earlier (Rao, Morton & Cloninger, 1979*a*). In this paper we present an application of the model to correlational data on American I.Q., henceforth referred to as I.Q.

Although data on family resemblance for I.Q. are old and flawed, they have stimulated recent advances in path analysis. Rice *et al.* (1980) have shown that the evidence is consistent with a lower heritability than was previously inferred. Their argument depends on recognition of determinacy in a subset of the data, separation of paternal and maternal correlations for indices, novel treatment of SES as an index of I.Q., and different assumptions about the nature of assortative mating. By application to an extended data set of the generalized assortative mating model (Rao *et al.* 1979*a*), called *mixed homogamy*, we here confirm the general results of Rice *et al.* (1980) and examine the nature of assortative mating for I.Q.

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BACKGROUND

Correlational analysis of family resemblance has passed through two stages, which Haldane (1964) called the Halieutic (from Greek *halieutes*, a Fisher) and the Tectonic (from Greek *tekton*, a Wright). Both were characterized by use of pre-existing data collected for other purposes and by reliance of hand calculation, rather than a computer program. The Halieutic was exploratory, following the

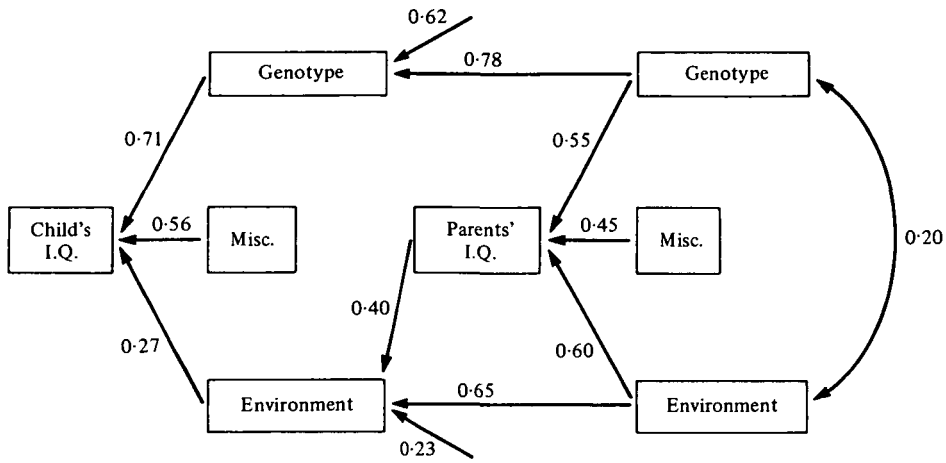

Fig. 1. Wright's interpretation of Burks' data.

brilliant synthesis of biometrical and Mendelian genetics by Fisher (1918). His interest was to show that familial correlations may be consistent with Mendelian expectations. For lack of experimental data he chose observations of Pearson & Lee (1903) as an illustration of this principle, without questioning their assumption that familial environment was negligible.

The Tectonic school tried seriously to model family environment, but was plagued by statistical indeterminacy. Wright (1931) fitted the path diagram of Fig. 1 to I.Q. data of Burks. His treatment was sophisticated in taking parents' I.Q. and environment as joint causes of child's environment, but much simplified in assuming that a score for material and cultural advantages of the home is a perfect measure of child's environment. Therefore his estimate of genetic heritability for children, $h^2 = 0{\cdot}71^2 = 0{\cdot}50$, is biased upward. We shall see that his estimate for adults, $h^2 = 0{\cdot}55^2 = 0{\cdot}30$, is remarkably accurate.

The two classical stages were dominated by single individuals. By contrast the current phase is synarchic (from Greek *synarchia*, joint rule). We take tests of hypotheses from Fisher and path analysis from Wright. The phenotype is jointly determined by genes, family environment, and random environment. Correlation of marital phenotypes is jointly determined by phenotypic and social homogamy. Environment is estimated by an imperfect index, as described later. An investigator is free to pursue two strategies: analysis of familial correlations on multiple

relationships, testing that they do not involve unique parameters: and analysis of phenotype and index, testing a model which specifies their joint determination. Here we will investigate both strategies for the analysis of I.Q. data.

AMERICAN I.Q.

Rao & Morton (1978) compiled 65 estimates of 16 relevant correlations in samples which appeared representative of the predominantly white, non-farm American population. Here we separate dizygous twins from other sibs, distinguish

Table 1. *Heterogeneity* χ^2 among multiple estimates

Relation	r	N	χ^2	D.F.
Marital phenotypes	0·5126	1118	17·85	7
Parent-child	0·4847	1310	6·23	4
Sibs	0·5132	2261	32·04	8
Ego as child and adult	0·8300	40	0	0
Child's phenotype with self index	0·3046	4717	10·21	3
Adult's phenotype with self index	0·3480	887	0	0
Father's phenotype with child's index	0·5709	1272	10·47	3
Marital indices	0·2260	1165	0	0
Father-child indices	0·3486	16267	16·49	4
Mother-child indices	0·2600	1165	0	0
Foster sibs together	0·3622	421	9·10	5
Natural-adopted sibs	0·2835	228	2·07	3
Sibs apart	0·2500	125	0	0
Parent and child adopted out	0·4100	63	0	0
Foster parent-child	0·2285	1181	10·49	5
Phenotype and index of a foster child	0·2862	774	8·34	2
MZ twins together	0·8427	421	11·25	2
Adult *MZ* twins apart	0·6900	19	0	0
DZ twins together	0·5632	206	0·71	1
Parents as children	0·3300	1016	0	0
Child and parent as child	0·4400	2032	0	0
Index of child and phentoype of father as child	0·3630	4386	0	0
Total				
Only phenotypes			89·74	35
Including indices			45·51	12
All data			135·25	47

father-child and mother-child correlations for indices, and add 4 additional correlations as described below, generating 69 estimates of correlations on 22 types of relationships:

(*a*) Childhood and adulthood IQs of the same person, $r = 0{\cdot}83$, $N = 40$ (Bayley, 1949).

(*b*) Childhood I.Q.'s of parents, $r = 0{\cdot}33$, $N = 1016$ (Higgins, Reed & Reed, 1962).

(*c*) I.Q. of a child and the childhood I.Q. of a parent, $r = 0{\cdot}44$, $N = 2032$ (Higgins *et al.* 1962).

(*d*) Index of a child and childhood I.Q. of father , $r = 0{\cdot}363$, $N = 4386$ (Duncan, Featherman & Duncan, 1972).

There is clear heterogeneity among estimates of the same correlations, especially with indices (Table 1). This is not surprising, since there was some variation in the measures of I.Q. (mostly Stanford–Binet or Wechsler), and of the index (mostly the Duncan occupational scale), and correlations are as spatiotemporally limited as gene frequencies. Total heterogeneity among multiple estimates is divided into two parts: one dealing with the 14 phenotype correlations ($\chi^2_{35} = 89{\cdot}745$), and the other 8 involving indices ($\chi^2_{12} = 45{\cdot}504$), both of which are highly significant. To accommodate significant heterogeneity as well as possible, we scale the sample sizes and take the new 'scaled sample sizes' as $n = N/V$, where V is the ratio of heterogeneity χ^2 to its degrees of freedom. As shown by McGue, Gottesman & Rao (1981), the expected value of V can be approximated by $1+\sigma^2_h$, where σ^2_h denotes heterogeneity variance among multiple studies. Also, under significant heterogeneity, the variance of a pooled z-transformation is given by $(1+\sigma^2_h)/N$, and not $1/N$ (McGue *et al.* 1981). Therefore, we take the estimated variance of a pooled z-transformation as $V/N = 1/n$, which gives $n = N/V$ as done here. For these data, $V = 89{\cdot}745/35 = 2{\cdot}564$ for phenotypic correlations, and $V = 45{\cdot}504/12 = 3{\cdot}792$ for correlations involving indices. Sample sizes are scaled separately for the two types.

THE MODEL

Original development of mixed homogamy (Morton & Rao, 1979; Rao *et al.* 1979*b*) is refined in terms of a *copath* which is designated by a headless bar (Cloninger, 1980). The revised path model, as appropriate for I.Q., is shown in Fig. 2 where phenotypic homogamy is treated in terms of a copath (p) which can be traced in either direction in deriving expected correlations, and social homogamy is represented by a simple correlation between parental environments (u). Indices are most useful when they are merely estimates of the environment, as has been validated for physiological phenotypes by nonsignificant goodness of fit tests (Rao *et al.* 1979*b*; Morton *et al.* 1980; Gulbrandsen *et al.* 1979; Krieger *et al.* 1980). Adopting father's occupation on the Duncan scale as index for child's I.Q. is much more questionable (Wright, 1931; Goldberger, 1978, and Rice *et al.* 1980). Following Rice *et al.* (1980), we therefore introduce a path j from father's I.Q. to his occupation as an index for his children. Apart from this new path shown in Fig. 2, and another parameter designating environmental effect unique to *MZ* twins reared together (t), the model is given in Rao *et al.* (1972*a*). All the 12 relevant parameters are defined in Table 2. Statistical analysis is based on the overall log-likelihood for m pooled correlations.

$$\ln L = -\chi^2/2 + \text{constant},$$
$$\chi^2 = \sum_{i=1}^{m} n_i (z_i - \bar{z}_i)^2.$$

Where, n_i is the total scaled sample size for the i^{th} correlation, z_i is the z-transform

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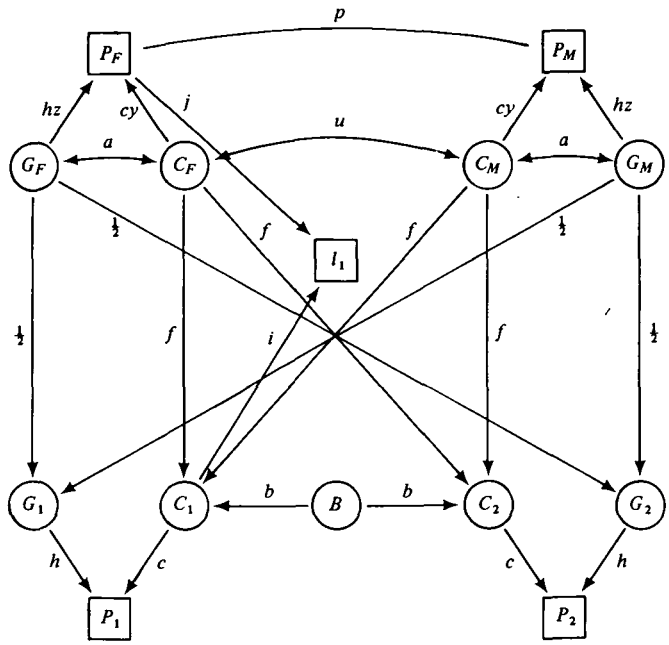

Fig. 2. Mixed homogamy model for American I.Q. Variables *P*, *G*, *C*, *I*, *B* denote phenotype, genotype, transmissible environment, index, and non-transmitted sibling common environments. Subscripts F, M, 1, 2 denote father, mother and two children. See Table 2 for definition of the parameters. For simplicity only the index of the first child is shown.

Table 2. Parameters of the path model

Symbol	Definition
General	
h	Effect of genotype on child's phenotype (square root of heritability)
hz	Effect of genotype on adult's phenotype
c	Effect of child's indexed environment on the child's phenotype
cy	Effect of adult's indexed environment on the adult's phenotype
p	Primary correlation between parental phenotypes, not due to secondary resemblance through social homogamy (Copath; Cloninger, 1980)
u	Correlation between parental indexed environments through social homogamy
f	Effect of parent's indexed environment on child's indexed environment
b	Effect of non-transmitted common sibship environment on child's indexed environment
i	Effect of child's indexed environment on child's index
iv	Effect of adult's indexed environment on adult's index
t	Effect of environment specific to *MZ* twins reared together, which adds t^2 to the expected correlation
j	Effect of father's phenotype on child's index
derived	
a	Correlation between genotype and environment as a function of other parameters (Rao *et al.* 1979*a*)

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of the pooled sample correlation, and z_i is the z-transform of the corresponding expected correlation derived as a function of the path coefficients ($m \leqslant 22$).

PHENOTYPIC CORRELATIONS

We first analysed the 14 phenotypic correlations not involving indices. This analysis requires only 9 of the 12 parameters. Tests of hypotheses and estimates of parameters are summarized in Table 3. The general model fits very well ($\chi^2_5 = 3{\cdot}60$, $P > 0{\cdot}6$). The data can be 'explained' by either social homogamy ($\chi^2_1 = 4{\cdot}39 - 3{\cdot}60 = 0{\cdot}79$) or phenotypic homogamy ($\chi^2_1 = 3{\cdot}81 - 3{\cdot}60 = 0{\cdot}21$). Intergenerational differences ($\chi^2_2 = 4{\cdot}50 - 3{\cdot}60 = 0{\cdot}9$) and environment unique to MZ twins ($\chi^2_1 = 7{\cdot}16 - 3{\cdot}6 = 3{\cdot}56$) are not significant. However, both cultural inheritance ($\chi^2_5 = 71{\cdot}38 - 3{\cdot}60 = 67{\cdot}78$, $P < 0{\cdot}0001$) and genetic inheritance ($\chi^2_2 = 51{\cdot}95 - 3{\cdot}60 = 48{\cdot}35$, $P < 0{\cdot}0001$) are highly significant. Nontransmitted sibling common environment (b) is also significant ($\chi^2_1 = 8{\cdot}42 - 3{\cdot}60 = 4{\cdot}82$, $P < 0{\cdot}03$). This analysis arrives at two alternative parsimonious models: phenotypic homogamy without intergenerational differences ($y = z = 1$, $u = 0$), and social homogamy with no intergenerational difference for genetic heritability($z = 1$, $p = 0$). Under the phenotypic homogamy model, genetic heritability is $h^2 = 0{\cdot}31$ and cultural heritability is $c^2 = 0{\cdot}42$. The social homogamy model nearly reverses these heritabilities in children ($h^2 = 0{\cdot}44$, $c^2 = 0{\cdot}33$), with greater cultural heritability in adults ($c^2y^2 = 0{\cdot}48$). Even if heterogeneity among replicates were ignored, neither residual χ^2 would be significant. Goodness-of-fit of both models is shown in Table 4. For phenotypic homogamy these results are in close agreement with those of Rice *et al.* (1980).

I.Q. AND INDICES

Here we analyse all the 22 pooled correlations on I.Q. and indices. Tests of hypotheses and estimates of parameters are summarized in Table 5. The general model in 12 parameters gives a conventionally acceptable fit, even though the scale χ^2 value is uncomfortably large ($\chi^2_{10} = 16{\cdot}99$, $P > 0{\cdot}07$). It must be possible to improve the fit by adding other paths to the index, as done by Rice *et al.* 1980. However, having decided on the general model in 9 parameters for the I.Q. correlations (Table 3), our inclination was to expand such a 9-parameter model by adding only the minimum number of interpretable paths required to make the residual χ^2 nonsignificant. This consideration resulted in the 12-parameter general model for I.Q. and indices. A remarkable outcome under such a model is that whereas the cultural heritability remains the same, the genetic heritability is halved compared to the general model fitted to the phenotypic correlations (Table 3). Neither social homogamy ($\chi^2_1 = 24{\cdot}41 - 16{\cdot}99 = 7{\cdot}42$, $P < 0{\cdot}007$) nor phenotypic homogamy ($\chi^2_1 = 33{\cdot}35 - 16{\cdot}99 = 16{\cdot}36$, $P < 0{\cdot}0001$) alone fits the data, implicating mixed homogamy. I.Q. data alone did not resolve the two models for homogamy, perhaps due to reduced power. Intergenerational differences are not significant

Table 3. *Estimates and tests of hypotheses for phenotypic correlations*

Hypothesis	Scaled n											Derived parameter
	χ^2	D.F.	h^2	c^2	t^2	y	z	p	u	f	b	a
General	3·60	5	0·439	0·278	0·106	1·215	1·026	0·116	0·950	0·325	0·760	0·026
$t = 0$	7·16	6	0·547	0·308	0	1·285	0·948	0·000	1·000	0·292	0·739	0·000
$b = 0$	8·42*	6	0·215	0·267	0·262	0·494	1·662	0·475	0·526	0·558	0	0·203
$p = 0$	4·39	6	0·469	0·327	0·077	1·240	0·946	0	1·000	0·310	0·715	0
$u = 0$	3·81	6	0·281	0·438	0·204	0·841	1·205	0·515	0	0·324	0·613	0·108
$y = z = 1$	4·50	7	0·311	0·425	0·193	1	1	0·504	0·016	0·308	0·623	0·099
$c = y = f = u = b = 0$	71·38**	10	0·705	0	0·138	0	0·991	0·514	0	0	0	0
$h = z = 0$	51·95**	7	0	0·651	0·349	0·813	0	0·350	0·368	0·427	0·443	0
$y = z = 1$, $u = 0$	4·50	8	0·310	0·424	0·193	1	1	0·511	0	0·308	0·624	0·100
$y = z = 1$, $p = 0$	15·04*	8	0·432	0·426	0·104	1	1	0	1·000	0·281	0·636	0
$z = 1$, $p = 0$	5·12	7	0·438	0·334	0·080	1·202	1	0	1·000	0·320	0·727	0

Note. The parameter 'a' is functionally dependent on the other parameters, evaluated from a quadratic equation as discussed in Rao *et al.* (1979*a*).

* The likelihood ratio χ^2 is significant at 5% level.

** The likelihood ratio χ^2 is significant at 0·01% level.

($\chi^2_2 = 19{\cdot}57 - 16{\cdot}99 = 2{\cdot}58$, $P > 0{\cdot}25$). Environment unique to *MZ* twins (t) is now highly significant ($\chi^2_1 = 29{\cdot}54 - 16{\cdot}99 = 12{\cdot}55$, $P < 0{\cdot}0004$), consistent with the results of Rice *et al.* (1980). Nontransmitted sibling environment (b) is not significant ($\chi^2_1 = 17{\cdot}37 - 16{\cdot}99 = 0{\cdot}38$, $P > 0{\cdot}5$).

As inferred by Rice *et al.*, father's I.Q. has a profound effect on the child's index ($\chi^2_1 = 33{\cdot}24 - 16{\cdot}99 = 16{\cdot}25$, $P < 0{\cdot}00006$). The parsimonious model of phenotypic

Table 4. *Goodness of fit of the two parsimonious models to the* 14 *phenotypic correlations*

Relation	r	$y = z = 1, u = 0$		$z = 1, p = 0$	
		ρ	χ^2	ρ	χ^2
Marital	0·513	0·511	0·00	0·482	0·72
Parent–child	0·485	0·477	0·06	0·476	0·07
Sibs	0·513	0·525	0·23	0·532	0·60
Ego as child and adult	0·830	0·807*	0·07	0·839	0·01
Foster sibs together	0·362	0·288	1·15	0·313	0·50
Natural-adopted sibs	0·283	0·315	0·10	0·313	0·10
Sibs apart	0·250	0·200	0·13	0·219	0·05
Parent–child adopted out	0·410	0·272	0·60	0·219	1·12
Foster parent–child	0·228	0·223	0·02	0·257	0·42
MZ twins together	0·843	0·842	0·00	0·831	0·24
Adult *MZ* twins apart	0·690	0·334	1·85	0·438	1·06
DZ twins together	0·563	0·525	0·24	0·532	0·16
Parents as children	0·330	0·333	0·01	0·334	0·01
Child and parent as child	0·440	0·445	0·04	0·433	0·06
Totals			4·50		5·12

homogamy without intergenerational differences ($y = z = 1$, $u = 0$) does not fit ($\chi^2_3 = 34{\cdot}10 - 16{\cdot}99 = 17{\cdot}11$, $P < 0{\cdot}0007$). The parameter estimates are remarkably similar to those of column C, table II of Rice *et al.* (1980).

A special case of our present model that corresponds to the social homogamy model of Rao & Morton (1978), given by $j = t = p = 0$, does not fit the data ($\chi^2_3 = 39{\cdot}05 - 16{\cdot}99 = 22{\cdot}06$, $P < 0{\cdot}00007$). Parameter estimates obtained under this unacceptable model are in close agreement with those of Rao & Morton (1978).

It is of some incidental interest that the correlation for MZ twins reared together is inflated by common environment, measured by t^2. This cannot plausibly be attributed to dominance, since adding t^2 to both *MZ* correlations, $t^2/4$ to both sibling correlations, and $t^2/4$ to the *DZ* correlation gives a poorer fit ($\chi^2_{10} = 24{\cdot}22$, $P < 0{\cdot}008$). This result is presented in the last line of Table 5. Details of goodness-of-fit of the general model and the special case of $y = z = 1$ are presented in Table 6.

Table 5. *Analysis of American I.Q. with indices*

Hypothesis	Scaled n χ^2	D.F.	h^2	c^2	t^2	y	z	p	u	f	b	i	v	j	Derived parameter a
General	16·99	10	0·228	0·292	0·250	0·573	1·440	0·453	0·570	0·510	0·379	0·201	2·633	0·476	0·140
$p = 0$	24·41*	11	0·473	0·276	0·093	1·329	0·767	0	1·000	0·381	0·647	0·356	1·269	0·334	0
$u = 0$	33·35**	11	0·250	0·334	0·229	0·660	1·293	0·540	0	0·474	0·535	0·147	3·880	0·511	0·170
$j = 0$	33·24**	11	0·511	0·176	0·121	1·510	0·804	0·145	0·935	0·500	0·000	0·747	0·618	0	0·059
$y = z = 1$	19·59	12	0·344	0·260	0·191	1	1	0·310	0·740	0·422	0·589	0·252	1·908	0·424	0·079
$y = z = 1$, $u = 0$	34·10**	13	0·302	0·248	0·198	1	1	0·538	0	0·469	0·671	0·183	2·699	0·485	0·182
$j_1 = t = p = 0$	39·05**	13	0·628	0·191	0	1·619	0·674	0	1·000	0·500	0·000	0·764	0·592	0	0
$b = 0$	17·37	11	0·209	0·285	0·267	0·506	1·556	0·465	0·587	0·549	0	0·198	2·607	0·474	0·166
$y = z = 1$, $b = 0$	30·34*	13	0·346	0·175	0·217	1	1	0·434	0·394	0·573	0	0·294	1·483	0·381	0·215
$t = 0$	29·54**	11	0·601	0·218	0	1·492	0·684	0·032	0·984	0·372	0·668	0·397	1·017	0·342	0·007
General with dominance†	24·22	10	0·409	0·212	0·186	1·279	0·856	0·234	0·794	0·422	0·572	0·316	1·228	0·398	0·062

Note. The parameter 'a' is functionally dependent on the other parameters, evaluated from a quadratic equation as done in Rao *et al.* (1979*a*).

* The likelihood ratio χ^2 is significant at 1 % level.

** The likelihood ratio χ^2 is significant at 0·1 % level.

† For this entry, t^2 corresponds to dominance (*MZ*-specific environment is ignored).

Table 6. *Goodness-of-fit of two models to correlations on I.Q. and indices*

Relation	r	General ρ	General χ^2	$y = z = 1$ ρ	$y = z = 1$ χ^2
Marital	0·513	0·508	0·02	0·503	0·08
Parent–child	0·485	0·465	0·33	0·479	0·03
Sibs	0·513	0·506	0·08	0·500	0·26
Ego as child and adult	0·830	0·568	4·60	0·651	2·63
Child's phenotype with self index	0·305	0·344	2·36	0·343	2·30
Adult's phenotype with self index	0·348	0·446	3·21	0·470	5·07
Father's phenotype with childs index	0·571	0·555	0·18	0·542	0·60
Marital indices	0·226	0·250	0·20	0·239	0·06
Father–child indices	0·349	0·337	0·73	0·333	1·26
Mother–child indices	0·260	0·282	0·17	0·305	0·74
Foster sibs together	0·362	0·315	0·46	0·273	1·61
Natural-adopted sibs	0·283	0·341	0·36	0·291	0·01
Sibs apart	0·250	0·153	0·50	0·202	0·12
Parent–child adopted out	0·410	0·263	0·68	0·247	0·83
Foster parent–child	0·228	0·220	0·04	0·244	0·12
Phenotype-index of foster child	0·286	0·217	1·10	0·235	0·62
MZ twins together	0·843	0·843	0·00	0·843	0·00
Adult *MZ* twins apart	0·690	0·502	0·65	0·361	1·64
DZ twins together	0·563	0·506	0·51	0·500	0·62
Parents as children	0·330	0·313	0·14	0·324	0·02
Child and parent as child	0·440	0·458	0·43	0·446	0·04
Index of child-phenotype of father as child	0·363	0·375	0·24	0·387	0·93
Totals		$\chi^2_{10} = 16·99$		$\chi^2_{12} = 19·59$	

Table 7. *Relative variance components under most parsimonious models for phenotypic correlations*

Source	Phenotypic homogamy ($y = z = 1$, $u = 0$)	Social homogamy ($z = 1$, $p = 0$) Children	Social homogamy ($z = 1$, $p = 0$) Adults
Genetic	0·310 ± 0·050	0·438 ± 0·059	0·438 ± 0·019
Cultural	0·424 ± 0·073	0·334 ± 0·039	0·482 ± 0·035
Covariance	0·073 ± 0·012	0	0
Residual	0·193 ± 0·017	0·228 ± 0·019	0·080 ± 0·047
Goodness-of-fit χ^2_8	4·50	5·12	

Table 8. *Relative variance components under mixed homogamy with indices*

Source	General Children	General Adults	Most parsimonious ($y = z = 1$)
Genetic	0·228 ± 0·080	0·472 ± 0·034	0·344 ± 0·050
Cultural	0·292 ± 0·092	0·096 ± 0·009	0·260 ± 0·056
Covariance	0·072 ± 0·213	0·060 ± 0·189	0·047 ± 0·066
Residual	0·408 ± 0·242	0·372 ± 0·280	0·349 ± 0·070
Goodness-of-fit:	$\chi^2_{10} = 16·99$		$\chi^2_{12} = 19·57$

DISCUSSION

There are several paradoxes in the data. Genetic heritability is less than cultural heritability when estimated under phenotypic homogamy, but the difference is reversed under social homogamy (Tables 7 and 8). Environment common to *MZ* twins is suggestive but nonsignificant in phenotype data and highly significant with indices, but the converse is true for nontransmitted sibling environment. Gene-environment covariance is small but significant for phenotopic and mixed homogamy, but nil for social homogamy. Genetic heritability is less in adults for social homogamy but greater for phenotypic homogamy, and the converse is true for cultural heritability.

Because of these unresolved differences, there is considerable uncertainty in the estimates. Acceptable models give a genetic heritability as low as 0·228 and as high as 0·438 in children, compared with a low of 0·310 and a high of 0·472 in adults. Cultural heritability may be as low as 0·096 or as high as 0·482 (Tables 7 and 8). Residual variation may be as low as 0·080 or as high as 0·408.

Variable as they are, the estimates are strikingly consistent in implicating both genetic and cultural inheritance, with no clear preponderance of one over the other. There are no grounds for a strongly hereditarian or environmentalist position. Thus the conclusions as well as the methods are synarchic.

Rice *et al.* fitted a more complicated eclectic model which they emphasized was descriptive rather than causal. They used the raw χ^2 test, without allowance for highly significant heterogeneity among estimates of the same correlation, and obtained two negative paths, from maternal phenotype to child's index and from child's environment to the index. We prefer the alternative criterion of testing the residual variance against the variance among replicates, here represented as scaled chi-squares. The negative paths are no longer required, but the parsimonious model gives estimates of the primary variance components in reasonable agreement with Rice *et al.* In particular, all analyses appear to rule out high genetic heritability. Of course, agreement does not signify truth. Other data or truer models may modify these conclusions, as in all science.

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