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ABSTRACT

The estimation of genetic models reported by J. L. Jinks and L. J. Eaves in a recent review are critically examined. A number of errors in procedure and interpretation are found. It is concluded that the evidence, provided by kinship correlations, for the proposition that intelligence is highly heritable, is not persuasive. (Author/BJG)

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STATISTICAL INFERENCE IN THE GREAT IQ DEBATE

Arthur S. Goldberger

1. INTRODUCTION

In the great IQ debate, evidence that intelligence is a highly heritable trait has been offered to support the position that observed differences in IQ scores (e.g., between races or between socioeconomic groups) are largely genetic in origin and hence can neither be accounted for nor eliminated by environmental changes. To suggest the curious form that this evidence takes, one example from the recent literature will be examined here. For criticisms of other aspects of the hereditarian literature see, inter alia, Lewontin (1970), Bronfenbrenner (1972), Goldberger (1974a, b), and especially Kamin (1974).

2. THE GENETIC MODELS

In the classical genetic model, an individual's observed phenotype y (= IQ test score, say) is determined as the sum of three unobserved components: his additive genotypic value x, his dominance deviation d, and his environment u. That is,

$$y = x + d + u.$$

The three components are independently distributed, so that the phenotypic variance is given by

$$\sigma_y^2 = \sigma_x^2 + \sigma_d^2 + \sigma_u^2 .$$

It is assumed that marriage is assortative on the basis of phenotype, that relatives do not share common environments, and that the system is in equilibrium. The model then leads to a simple set of predicted correlations between the IQ test scores of relatives, in terms of only three parameters; see Fisher (1918), Burt & Howard (1956), and Burt (1971). These predictions, or expected correlations, are displayed in the center column of Table 1, the kinships being labelled with respect to an individual.

The three parameters are

$c_1 = (\sigma_x^2 + \sigma_d^2)/\sigma_y^2$ = ratio of total genotypic variance to phenotypic variance,

$c_2 = \sigma_x^2/(\sigma_x^2 + \sigma_d^2)$ = ratio of additive genotypic variance to total genotypic variance,

$m = \sigma_{yy*}/\sigma_y^2$ = correlation of phenotypes of spouses (where y* denotes spouse's phenotype).

The parameters are referred to as: broad heritability, c_1; the ratio of narrow heritability to broad heritability, c_2; and the marital correlation, m. The fourth symbol, A, is simply the product of the other three:

$$A = c_1 c_2 m.$$

In the model A gives the correlation between the additive genotypic values of spouses.

TABLE 1. ALTERNATIVE GENETIC MODELS FOR KINSHIP CORRELATIONS

Kinship	Classical Model	Neoclassical Models M1	Neoclassical Models M2
PT = PARENT together	$c_1c_2(\frac{1+m}{2})$	0	+f
PA = PARENT apart	same	0	0
GP = GRANDPARENT	$c_1c_2(\frac{1+m}{2})(\frac{1+A}{2})$	0	0
MZT = MZ TWIN together	c_1	+e	+f
MZA = MZ TWIN apart	same	0	0
DZT1 = DZ TWIN together (same sex)	$c_1c_2(\frac{1+A}{2}) + (c_1/4)(1-c_2)$	+e	+f
DZT2 = DZ TWIN together (opposite sex)	same	+e	+f
ST = SIBLING together	same	+e	+f
SA = SIBLING apart	same	0	0
UNC = UNCLE	$c_1c_2(\frac{1+A}{2})^2 + (c_1/4)(1-c_2)(\frac{A}{2})$	0	0
CF = FIRST COUSIN	$c_1c_2(\frac{1+A}{2})^3 + (c_1/4)(1-c_2)(\frac{A}{2})^2$	0	0
CS = SECOND COUSIN	$c_1c_2(\frac{1+A}{2})^5 + (c_1/4)(1-c_2)(\frac{A}{2})^4$	0	0
ADP = ADOPTIVE PARENT	0	0	+f
ADS = ADOPTIVE SIBLING	0	+e	+f
SPS = SPOUSE	m	0	0

In the classical model, members of a household do not share a common environment. (Exception: the assortative mating scheme induces a correlation, retroactively, between the childhood environments of husbands and wives.) This makes the model empirically inadequate, because observed kinship data show higher IQ correlations for kin raised together than for those raised apart (e.g. MZT vs. MZA, ST vs. SA) and also show positive IQ correlations for genetically unrelated persons living together (i.e., ADP and ADS). Therefore two extensions, which I label neoclassical genetic models, have been introduced in the literature.

The first neoclassical model (M1) adds a parameter, e, to the expected IQ correlation of a child with a sib with whom he is raised, be the sib natural or adoptive. Thus,

$$e = \sigma_{uu'}/\sigma_y^2 = \text{common environmental component of children living together,}$$

where u' denotes the environment of a sib with whom the child is raised. (The correlation between their environments is $\rho_{uu'} = e/(1-c_1)$.) The second neoclassical model (M2) instead adds a parameter, f, to the expected IQ correlation of a child with a sib with whom he is raised (be the sib natural or adoptive) and to the expected IQ correlation of a child with a parent who raises him (be the parent natural or adoptive). Thus

$$f = \sigma_{uu''}/\sigma_y^2 = \text{common environmental component of children and parents living together,}$$

where u'' denotes the environment of a sib with whom the child is raised or of a parent who raises him. (The environmental correlation is here $\rho_{uu''} = f/(1-c_1)$.) These alternative neoclassical amendments are shown in the last two columns of Table 1. For example, in M2 the predicted correlation for MZT -- identical twins raised together -- is $c_1 + f$.

3. THE EMPIRICAL PICTURE

Several scholars have used selected kinship correlations to estimate parameters of the genetic models, and occasionally to test the models: Burt (1966, 1971), Jinks and Fulker (1970), Jensen (1971, pp. 121-128, 294-326; 1973, pp. 161-173). What emerged from their analyses was a rather neat picture: IQ was a trait whose variation is well accounted for by one or another of the simple genetic models; furthermore, IQ was a very highly heritable trait. With c_1 repeatedly estimated to be around .8, it was said that 80% of the variation in IQ scores was attributable to genes and only 20% to environments.

This neat picture was disturbed by the publication of Christopher Jencks's Inequality. Using an assortment of American kinship correlations, Jencks (1972) arrived at the following allocation of IQ variance: genes 45%, environment 35%, gene-environment covariance 20%. Jencks's model was not of the classical/neoclassical type: he permitted correlation between the genetic and environmental components of an individual's IQ, and did not handle dominance deviations in a rigorous manner. Nor was the model fitted systematically. Jencks pieced together estimates obtained from separate kinship comparisons rather than fitting the full set of parameters to the full set of data. In doing so, he detected inconsistencies, remarking that some of the comparisons yielded "drastically different estimates of heritability." His estimation procedure was informal, following the path analysis tradition; thus, no standard errors or formal test statistics were obtained.

In a critical review of the Jencks book, Professor John L. Jinks and Dr. Lindon J. Eaves of the University of Birmingham's Department of Genetics set out to show that the "American data do not in fact give a picture for the genetics of intelligence which differs in principle from that which has long been apparent from British studies."

4. JINKS-EAVES CRITICISMS OF JENCKS

The core of the Jinks-Eaves (1974) review is devoted to their own fits of the second neoclassical model to a set of 14 British kinship correlations given by Burt (1966) and to a set of 9 American kinship correlations taken from Jencks (1972). Before turning to the core, some comments on their treatment of Jencks's approach are in order. They wish to show that Jencks mishandled the data and that the inconsistencies which he found will vanish when the data are properly handled by the methods of biometrical genetics.

Now the inconsistencies noted by Jencks (1972, Appendix A) all concern adopted children. He found the PA correlation to be too high relative to the PT correlation, and the ADS correlation to be too high relative to the ST correlation. These problems do not vanish in Jinks-Eaves's analysis; their residuals for PA and ADS are also high. Among ADS, two types may be distinguished: adopted-adopted pairs and adopted-natural pairs; Jencks found the former too high relative to the latter. This problem does vanish in Jinks-Eaves's analysis, but only because they pooled the two types together.

Jencks's emphasis on gene-environment covariance is reduced to an apparent absurdity by Jinks-Eaves when they note that a negative (and non-significant) estimate for the covariance is obtained when their model is extended to allow for it. Buc their extension, which is not spelled out in their article, appears to involve a wholly arbitrary specification.

Table A-5 in Jencks (p. 281) presents various combinations of values for h^2 (heritability) and g (the path coefficient from parent's genotype to child's genotype). Jinks-Eaves devote a full paragraph in their review to explaining that this table gives equal weight to sense and nonsense because it overlooks the fact that "Genetical theory indicates that only solutions in which $g \leq h^2/2$ ... are genetically sensible." But genetical theory indicates nothing of the kind, as can be seen directly in the case in which gene-environment covariance is absent. There $h^2 = c_1$ and $g = c_2/2$, so that their inequality reads $c_2 \leq c_1$, which is hardly a requirement of genetical theory.

On the other hand, Jinks-Eaves overlook an error in Jencks's specification of the adoptive parent-child correlation. According to Loehlin, Lindzey, & Spulber (1975, pp. 300-302), correcting this error would bring Jencks's estimates more into line with the traditional ones.

5. JINKS-EAVES MODEL-FITTING

The two data sets to which Jinks-Eaves fit the genetic models are given in the left-hand panels of Tables 2 and 3. Here r_j denotes the correlation observed for the j-th kinship in a sample of n_j pairs.

Their fitting procedure, iterative weighted least squares, may be sketched as follows. The expected correlation for the j-th kinship is

$$\rho_j = \rho_j(\underline{\theta})$$

where $\underline{\theta}$ is the vector of K unknown parameters and the $\rho_j(\cdot)$ functions are generally nonlinear (as we have seen in Table 1). The r_j's are taken to be independent and normally distributed with

$$E(r_j) = \rho_j, \qquad V(r_j) = (1 - \rho_j^2)^2/n_j = \sigma_j^2.$$

For a data set with j = 1,...,N, a pure weighted least squares procedure would choose $\underline{\theta}$ to minimize the criterion

$$\Sigma_{j=1}^{N} (r_j - \rho_j(\theta))^2/\sigma_j^2 .$$

But σ_j^2 is itself unknown, so the criterion is modified to

$$\Sigma_{j=1}^{N}(r_j - \rho_j(\underline{\theta}))^2/\hat{\sigma}_j^2 ,$$

where $\hat{\sigma}_j^2 = (1 - \hat{\rho}_j^2)^2/n_j$ with $\hat{\rho}_j = \rho_j(\hat{\underline{\theta}})$. The calculation proceeds iteratively until convergence is attained, at which point the value of the criterion is referred to a chi-square distribution with N-K degrees of freedom as a test of the model, and asymptotic standard errors are obtained.

In reworking their analyses, I followed their estimation procedure. In retrospect, it would have been better to fit not the correlation coefficients but rather their z-transforms:

TABLE 2. ALTERNATIVE MODELS FITTED TO BURT'S DATA SET

Kin	Observation r_j	Observation n_j	M2*	M2	M1*	M1
			Predicted Correlations			
PT	.49	374	.48	.53	.47	.49
GP	.33	132	.28	.29	.32	.32
MZT	.92	95	.92	.92	.92	.92
MZA	.87	53	.83	.85	.85	.85
DZT1	.55	71	.57	.53	.56	.56
DZT2	.52	56	.57	.53	.56	.56
ST	.53	264	.57	.53	.56	.56
SA	.44	151	.47	.47	.50	.49
UNC	.34	161	.32	.27	.31	.29
CF	.28	215	.22	.17	.21	.19
CS	.16	127	.12	.07	.09	.08
ADP	.19	88	.09	.07	0	0
ADS	.27	136	.09	.07	.07	.07
SPS	.39	100	.41	.41	.42	.42
			Parameter Estimates (± standard errors)			
			M2*	M2	M1*	M1
		c_1	.83 ± .03	.85 ± .03	.85 ± .04	.85 ± .03
		c_2	.65 ± .08	.76 ± 08	.78 ± .10	.82 ± .08
		m	.41 ± .08	.41 ± .10	.42 ± .10	.42 ± .10
		A	.48 ± .11	-	.35 ± .11	-
		e	-	-	.07 ± .04	.07 ± .03
		f	.09 ± .03	.07 ± .03	-	-
Chi-square (deg. of free.)			9.05 (9)	13.65 (10)	13.13 (9)	13.49 (10)

TABLE 3. ALTERNATIVE MODELS FITTED TO JENCKS'S DATA SET

Kin	Observation r_j	Observation n_j	M2*	M2	M1*	M1
			Predicted Correlations			
PT	.55	1250	.56	.56	.55	.51
PA	.45	63	.27	.27	.55	.51
MZT	.97	50	.97	.97	.97	.97
MZA	.75	19	.68	.68	.61	.84
DZT1	.70	50	.59	.58	.59	.62
ST	.59	1951	.59	.58	.59	.62
ADP	.28	1181	.29	.29	0	0
ADS	.38	259	.29	.29	.36	.13
SPS	.57	887	.57	.57	.57	.57
			Parameter Estimates (± standard errors)			
			M2*	M2	M1*	M1
		c_1	.68 ± .03	.68 ± .03	.61 ± .25	.84 ± .13
		c_2	.50 ± .06	.51 ± .05	1.14 ± .51	.77 ± .12
		m	.57 ± .03	.57 ± .03	.57 ± .11	.57 ± .11
		A	.29 ± .14	-	-.27 ± .57	-
		e	-	-	.36 ± .25	.13 ± .12
		f	.29 ± .03	.29 ± .03	-	-
Chi-square (deg. of free.)			6.92 (4)	7.63 (5)	96.29 (4)	120.74 (5)

$$z_j = (1/2) \log ((1+r_j)/(1-r_j)).$$

These are asymptotically normal with

$$E(z_j) = (1/2) \log ((1+\rho_j)/(1-\rho_j)), \quad V(z_j) = 1/n_j.$$

Not only is the normal approximation better for the z's than for the r's, but the dependence of variances on parameters is eliminated, thus obviating the need for iteration. (See Rao, Morton, & Yee (1974)).

Jinks-Eaves report parameter estimates, standard errors, chi-squares, and predicted values for their fit of the M2 to Burt's and Jencks's data sets. Their parameterization differs from that used here, the translation being as follows:

$$E_c \to f, \quad \mu \to m, \quad D_R \to 2(1-A)c_1c_2, \quad H_R \to 4c_1(1-c_2).$$

Taking their reported parameter estimates, translating into c_1, c_2, m, f, and inserting into the M2 formulary of Table 1, I obtained their predicted values with one exception. Their prediction was off for Burt's UNC. It turns out that the biometrical geneticists had accidentally misspecified the genetic component of this correlation, in effect dividing $c_1(1-c_2)$ by 2 instead of by 8, and had proceeded to fit this misspecified model. After correcting this error, I refitted this model, obtaining the results given in the M2*-columns of Tables 2 and 3. These results are virtually identical to those published by Jinks-Eaves, the error in the UNC formula having been an isolated one with little impact. Note the good fit of the model, the small standard errors, and the high estimates of broad heritability.

Their second misspecification, however, was more substantial and not accidental. Jinks-Eaves treat A (the correlation between the additive genotypic values of husband and wife) as a free parameter despite the fact that their genetic model requires that $A = c_1c_2m$. (There are, to be sure, alternative specifications of the assortative mating process which remove that requirement, but then the formulary of Table 1 does not apply). This constraint was not imposed in fitting and is violated by their estimates: e.g., for Burt's data, $c_1c_2m = .22$ while $A = .47$. Imposing the constraint, I fitted the proper model, obtaining the results given in the M2-columns of Tables 2 and 3. For the Burt data set, the parameter estimates change somewhat, and the fit worsens: the increment to chi-square is 4.60, which with 1 degree of freedom is significant at the 5% level. (For the Jencks data set, little change occurs.) Thus there is, after all, some evidence against the genetic model.

Jinks-Eaves did touch on this problem of the second neoclassical model, remarking that "A small anomaly in the results of our analysis of Burt's data is that A is numerically (though not significantly) greater than μ." "This anomaly is removed," they went on to say, "by stipulating that parents and offspring do not share developmentally important environmental features" -- that is by adopting the first neoclassical model instead. They stated, however, that doing so "results in a slightly poorer fit to Jencks's data." To investigate this, I fitted the first model, in two versions: M1*, in which A is a free parameter, and M1, in which $A = c_1c_2m$ is imposed. My results are given in the right-hand columns of Tables 2 and 3. For Burt's data, the "anomaly" is indeed removed: in M1*, we have $A = .35 < .42 = m$, and furthermore

the constraint $A = c_1 c_2 m$ is acceptable by the chi-square test. For Jencks's data, on the other hand, the results are quite startling. Rather than giving "a slightly poorer fit," the first neoclassical model is strongly rejected. In particular, M1* (which is presumably the version they fitted) is simply untenable: it fails to fit the data, and its parameter values lie outside the admissible range.

By publishing one portion of their results and inaccurately describing the other portion, Jinks and Eaves have given a misleading picture of the success with which simple genetic models account for variation in IQ scores. Nevertheless, the M2 model gives a good fit to both data sets, with sharp estimates of parameters, and high values for broad heritability c_1.

6. SENSITIVITY ANALYSIS

Jinks-Eaves emphasize the virtues of their "biometrical genetical analysis in which the expectations in terms of a model are fitted to all the statistics simultaneously so that the parameters are estimated from the full data set and the ... model can be tested." Without disputing the merits of formal model-fitting, we may still wish to determine whether the parameter estimates are in fact sensitive to all of the observations.

To explore this, I undertook some calculations along the following lines. Suppose that a linear regression model were applicable to the correlations, that is,

$$E(r_j) = \rho_j(\underline{\theta}) = \underline{x}_j'\underline{\theta} , \qquad V(r_j) = \sigma^2.$$

The least squares estimator of $\underline{\theta}$ would be

$$\underline{\hat{\theta}} = (X'X)^{-1}X'\underline{r} = W\underline{r}, \text{ where } W = (X'X)^{-1}X', \quad \underline{r} = (r_1, \ldots, r_N)'.$$

Then

$$\hat{\theta}_i = \Sigma_{j=1}^{N} w_{ij} r_j,$$

so that $w_{ij} = \partial\hat{\theta}_i/\partial r_j$ would give the change in the i-th parameter estimate resulting from a unit change in the j-th observed correlation. The present nonlinear iterative weighted least squares situation is of course more complicated, but we can obtain an approximate answer. If $\underline{\hat{\theta}}^o$ is the estimate when the observed correlation vector is $\underline{r}^o$, then

$$\hat{\theta}_i - \hat{\theta}_i^o \doteq \Sigma_{j=1}^{N} \hat{w}_{ij} (r_j - r_j^o) ,$$

where

$$\hat{W} = \{\hat{w}_{ij}\} = (F'S^{-1}F)^{-1}F'S^{-1} ,$$

$$F = \{\partial\rho_j/\partial\theta_i\} \quad \text{evaluated at } \underline{\hat{\theta}}^o ,$$

$$S = \text{diag } \{\sigma_j^2\} \quad \text{evaluated at } \underline{\hat{\theta}}^o.$$

The $\hat{w}_{ij}$ then provide local approximations to the $\partial\hat{\theta}_i/\partial r_j$.

Some results of this calculation for the M2 model are given in Table 4. They indicate for example that the broad heritability estimate is sensitive to only a few of the observed correlations. In particular, the c_1 estimate for the British data is heavily dependent on the MZT and MZA observations, while that for the American data set is heavily dependent on the MZT and ADP observations. To illustrate this point: if Burt had reported .82 and .77 as the MZT and

TABLE 4. PARTIAL DERIVATIVES OF M2 PARAMETER ESTIMATES WITH RESPECT TO OBSERVED CORRELATIONS

Burt Data Set			Jencks Data Set	
c_1	f		c_1	f
-.16	.16	PT = PARENT together	.10	-.13
-	-	PA = PARENT apart	.04	-.05
.06	-.07	GP = GRANDPARENT	-	-
.43	.50	MZT = MZ TWIN together	1.02	-.04
.57	-.50	MZA = MZ TWIN apart	.04	-.03
-.02	.03	DZT1 = DZ TWIN together (same sex)	-.01	.01
-.02	.02	DZT2 = DZ TWIN together (opp. sex)	-	-
-.07	.11	ST = SIBLING together	-.24	.29
.13	-.15	SA = SIBLING apart	-	-
.07	-.09	UNC = UNCLE	-	-
.06	-.07	CF = FIRST COUSIN	-	-
.02	-.02	CS = SECOND COUSIN	-	-
-.06	.07	ADP = ADOPTIVE PARENT	-.72	.72
-.09	.11	ADS = ADOPTIVE SIBLING	-.16	.16
-.01	.02	SPS = SPOUSE	-.01	.01

MZA correlations (rather than .92 and .87), the broad heritability estimate would have been about .73 (rather than .83).

This sort of arithmetic casts some doubt on Jinks-Eaves's contention that "By adopting a weighted least squares approach we have ensured that statistics based on small samples are given proportionately less weight in determining the final solution. As a result, the small samples of MZA's which have been criticized on several grounds, play a relatively small part in our analysis."

7. DATA PROBLEMS

Jinks-Eaves assert that "whatever else may be said about the quality of the data, their quantity is such that our estimates are fairly precise and our test of the model fairly sensitive." Sceptical readers may be less sanguine about the empirical material.

There are good grounds for believing that Burt's IQ correlations are spurious. He provided virtually no documentation of the tests used, of the sampling frame, of the age and sex of the subjects, nor are his sample means and variances published. The figures for various kinship correlations in his series of articles contain numerous inconsistencies; see Jensen (1974), Kamin (1974, pp. 33-44). Furthermore, he provided many clues that his test scores were adjusted in a manner that should make them unsuitable for the estimation of heritability. For example:

"To assess intelligence as we have defined the term, it will be unwise to rely exclusively on formal tests of the usual type... the only way to be sure that no distorting influences have affected the results is to submit the marks to some competent observer who has enjoyed a first-hand knowledge of the testees. With children this will usually be the school teacher; and whenever discrepancies appear between the teacher's verdict and that of the test, the child must be re-examined individually... The interview, the use of non-verbal tests, and the information available about the child's home circumstances usually made it practicable to allow for the influence of an exceptionally favorable or unfavorable cultural environment." -- Burt & Howard (1956, pp. 121-122).

"... having satisfied ourselves that by these means we can reduce the disturbing effects of environment to relatively slight proportions...." -- Burt and Howard (1957, p. 39).

"Nor were we concerned with any specific observable trait, but with differences in a hypothetical innate general factor. Indeed, our primary aim was to assess the relative accuracy of different methods of assessing this hypothetical factor...." -- Burt (1971, p. 15).

It seems that Burt's observations are not correlations of IQ test scores, but rather estimated correlations of the genetic component of IQ test scores.

If so, they are hardly suitable for estimating the relative contributions of heredity and environment to variation in IQ test scores. (We might say that the 17% (= 100 $(1-c_1)$%) that is left to environment in Burt's data reflects only his failure to completely purify his figures.)

Such objections do not apply to the Jencks data set, which was assembled from a dozen well-documented American studies. But this data may not be suitable for present purposes either. All of the studies were published in the 1920s, 1930s, and 1940s. One-third of the total of 5710 pairs come from three studies of adoptive families and matched control families; these are surely a highly selected group. All 119 twins come from a single study. The ADP figure reported as .29 with sample size 1181 is in fact an adjusted average of 6 separate correlations ranging from .07 to .37 each from a sample of about 200. Furthermore, all the raw correlations reported in the original studies were adjusted upward by Jencks to correct for unreliability and nonrepresentativeness, the latter adjustment being quite arbitrary.

8. CONCLUSION

This critical examination of the Jinks-Eaves review leads me to the conclusion that the evidence for the high heritability of intelligence is by no means overwhelming.

Whatever the weight of the evidence may be, it must be recognized that within-group heritability carries no implications for between-group heritability and, furthermore, that high heritability carries no implications

for the effectiveness of environmental policies. These points were clearly stated by Lewontin (1970).

9. A POSTSCRIPT

After completing the first version of this paper, I learnt that some of the material had already been covered by Jinks and Eaves.

A "Corrigendum" in Nature, Vol. 24, April 12, 1974, p. 622, indicates that fitting the first neoclassical model gave "a significantly poorer fit" rather than "a slightly poorer fit."

A subsequent article by Eaves (1975) presents the models and estimation procedure in more detail than was possible in the earlier review. The objection to Jencks's violation of genetical theory is withdrawn, the equation for the avuncular correlation (UNC) is corrected, and the constraint $A = c_1 c_2 m$ is imposed. Eaves's parameter estimates and chi-square values for M2 (in his Table 2) and for M1 (in his Table 3) correspond closely (after translation) to those in my Tables 2 and 3.

Eaves does not discuss the sensitivity of estimates to particular observations nor does he discuss the quality of the data except to say that "The data may still be questioned." He maintains that

> "Successive improvements in the procedure by which biometrical-genetical models are fitted to correlations between relatives for IQ make little substantive

difference to earlier conclusions about the statistical significance and biological importance of the various genetical and environmental determinants of individual differences in measured intelligence."

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