

## IQ and inequality

*I.Q. In the Meritocracy.* By R. J. Herrnstein. Pp. x+193. (Allen Lane: London, November 1973.) £2.50.

*Inequality: A Reassessment of the Effect of Family and Schooling in America.* By C. Jencks. Pp. xii+399. (Allen Lane: London, 1973.) £5.00.

JENCKS and Herrnstein present two interpretations of the problem of inequality. Whereas Jencks is primarily concerned with the sources of individual differences in access to the educational, social and economic benefits of American culture, Herrnstein is more concerned about the less immediate consequences of biological inequality for social structure in a meritocracy. Both authors base part of their work on what they regard, individually, as acceptable models for variability in intelligence. To some extent their models differ, consequently their overall assessments of the role of intelligence also differ. Herrnstein, partly because he has adopted a model in which there is considerable genetical variability for IQ, affirms the social relevance of IQ measurements. Jencks, partly by his acceptance of a model in which genetical differences are less important, suggests that the contribution of genetical variation in IQ to traits that have social consequences is proportionately less than is sometimes supposed, although more than many would admit. The authors seem to differ in their interpretation of data, the veracity of which they both seem to accept. Such disagreement as exists therefore, stems not from differences in their attitude to the data, but from differences in analytical procedure.

Herrnstein does not attempt to analyse data. He has accepted a model based on

Jinks and Fulker's biometrical genetical reanalysis of some of Burt's correlations for IQ. Although on this model some 80% of the variation in IQ may be attributed to genetical variation, a substantial part of this is due to the non-fixable contribution of dominance and to the increase in genetical variability arising from assortative mating. Jencks, on the other hand, provides a detailed reanalysis using the method of path coefficients and argues that the heritability of IQ is nearer 45%. In addition, he claims that different estimates of 'heritability' are obtained from different degrees of relationship and that there may be positive covariation between genotypic and environmental deviations: the so-called 'double advantage' phenomenon. Although Jencks suspects the presence of dominance, he does not treat the matter analytically, an omission which, as we shall see, could explain some of his unusual conclusions.

A fundamental weakness of Jencks's approach is his failure to make explicit the mathematical relationships between genetical paths in different pedigrees (path diagrams) and between different paths of the same pedigree. For example, not all the numerically feasible solutions given by Jencks in Table A-5 for the relationships between his paths  $g$  (between parental and offspring genotype) and  $h^2$  (broad heritability) are genetically sensible. Genetical theory indicates that only solutions in which  $g \leq \frac{1}{2}h^2$  for the parent-offspring covariation are genetically sensible. His failure to specify these restraints means that equal weight is given to sense and nonsense answers. When we consider the amount of assortative mating and make allowance for the possibility of dominance the only estimates of  $h^2$  consistent with a genetical model lie between 0.59

and 0.76 corresponding with Jencks's estimates of  $g$  of 0.25 and 0.30. Rather than supporting a lower heritability, therefore, on this basis alone Jencks's data are consistent with the value obtained by fitting a biometrical genetical model to all the data simultaneously (see Tables 1 and 2).

A further weakness of Jencks's approach is his failure to deal systematically with dominance. This can be seriously misleading for a trait such as IQ for which there seems to be considerable non-additive genetical variation. Dominance could account for much of the apparent heterogeneity between estimates of heritability obtained from different degrees of relationship. The ratios given by Jencks do not estimate the broad (or narrow) heritability in the presence of dominance and the inconsistencies to which he refers do not reflect haphazard inconsistencies in the data but the ordered departures from simple additivity which, within the limits of sampling variation, depend on the presence of a considerable amount of dominance (see Table 2).

Analytically, Jencks's procedure is inefficient. He estimates parameters from one set of data and uses these to correct estimates from other sets. This is not merely inelegant, it also yields the poorest approximations of the parameter estimates and could lead to the rejection of an otherwise acceptable model. Jencks may have been wise in eschewing statistics in a tentative analysis of heterogeneous data, but some attempt to use statistical criteria could have led to a more objective assessment of the confidence which others could place on his conclusions.

We have, therefore, subjected the correlations used by Jencks to a biometrical genetical analysis in which the

TABLE 1 Observed and expected correlations for IQ

Relationship	Burt			Jencks*		
	$r_{obs}$	$r_{exp}$	$N$	$r_{obs}$	$r_{exp}$	$N$
Parent-child T	0.49	0.48	374	0.55	0.55	1250
Parent-child A	—	—	—	0.45	0.27	63
Grandparent-grandchild	0.33	0.28	132	—	—	—
Monozygotic twins T	0.92	0.92	95	0.97	0.97	50
Monozygotic twins A	0.87	0.83	53	0.75	0.68	19
Like-sex dizygotic twins T	0.55	0.56	71	0.70	0.59	50
Unlike-sex dizygotic twins T	0.52	0.56	56	—	—	—
Full sibs T	0.53	0.56	264	0.59	0.59	1951
Full sibs A	0.44	0.47	151	—	—	—
Uncle-niece etc	0.34	0.36	161	—	—	—
1st cousins	0.28	0.22	215	—	—	—
2nd cousins	0.16	0.11	127	—	—	—
Fosterparent-fosterchild T	0.19	0.10	88	0.28	0.29	1181
Unrelated T	0.27	0.10	136	0.38	0.29	259
Marital	0.3875	0.4133	(100)†	0.57	0.57	887

\* correlated for unreliability and differences between sample means.

† Actual sample size not known.

T = living together; A = living apart.

TABLE 2 Results of model fitting

Parameter	Burt			Jencks						
	$\hat{\theta}$	$\sigma\hat{\theta}$	$\chi^2$	d.f.	$P$	$\hat{\theta}$	$\sigma\hat{\theta}$	$\chi^2$	d.f.	$P$
$D_R$	0.57	0.17	11.12	1	†	0.48	0.10	24.86	1	†
$H_R$	1.15	0.25	21.66	1	†	1.37	0.11	159.65	1	†
$E_c$	0.10	0.03	8.99	1	*	0.29	0.02	152.40	1	†
$A$	0.47	0.10	21.98	1	†	0.30	0.11	6.86	1	*
$\mu$	0.41	0.08	17.28	1	†	0.57	0.02	630.87	1	†
$E_1$	0.08	—	—	—	—	0.03	—	—	—	—
Residual	—	—	8.96	9	0.5-0.3	—	—	6.63	4	0.2-0.1
Broad heritability	0.83	—	—	—	—	0.68	—	—	—	—

\* significant at the 0.01 level

† significant at the 0.001 level

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 agreement between the observed and expected statistics after fitting the model can be tested. A parallel analysis of the full table of correlations given by Burt, only part of which has been hitherto analysed by these methods, has been carried out for comparison.

The data are given in Table 1. Normally we prefer to work with raw variances and covariances rather than correlations because the latter are far from normally distributed even in quite large samples and because valuable information is lost by standardisation to unit variance. A weighted least squares analysis of the two sets of correlations was conducted which has the advantage of efficiency and provides (given normality) a test of goodness of fit of the model. Because of assortative mating the model is non-linear and a more complete discussion of the method and the model will be published elsewhere. 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 monozygotic twins reared apart, which have been criticised on several grounds, play a relatively small part in our analysis. In fitting the model simultaneously to a wide range of relationships we have evaluated its predictive validity in a broad context. Our model involves five parameters: an additive genetical component ( $D_R$ ), a dominance component ( $H_R$ ), a common environmental component ( $E_c$ ), the marital correlation ( $\mu$ ) and the correlation between the additive genetical deviations of spouses ( $A$ ). A sixth component, the specific environmental component ( $E_1$ ), is obtained by difference at the end of the analysis.

This model differs from that quoted by Herrnstein by making  $E_c$  an environmental component shared by parents as well as offspring. This may lead to underestimation of  $D_R$  and consequent overestimation of  $H_R$  and  $A$  if unjustified. Making  $E_c$  applicable

purely to offspring results in a significantly poorer fit to Jencks's data. Our model differs from Jencks's in assuming that placement effects and the covariation of genotype and environment are negligible. The former assumption will lead to the overestimation of  $E_c$  in the event of placement correlations being significant, the latter assumption to failure of the model in the event of genotype-environment covariation being substantial. Such covariation is most easily detected by the analysis of raw variances. Jinks and Fulker were unable to detect it in their analysis of variances but the relevant sample sizes were small. Any analysis which does not make provision for an adequate test of the model may well discount some dominance variation as positive genotype-environment covariance and *vice versa*.

Burt's correlations are for final assessments and those given by Jencks include his corrections for unreliability and for differences between sample means. We have retained these corrections in order to yield results which are more directly comparable with those of Jencks. By treating such estimates as raw correlations we have, among other things, overestimated their precision and consequently regarded the analysis as more sensitive than is really the case. But 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.

Table 2 gives the weighted least squares estimates of the parameters. The standard errors are approximate and assume that the deviations between observed and expected are small enough to be ignored. The expected values obtained by fitting the model to the data are given alongside the corresponding observed values in Table 1. Although individual deviations are sometimes large, the overall weighted sum of squared deviations, which is  $\chi^2$  if the observations are normal, is small in relation to the total weighted sum of squares of the observations.

Although the two data sets differ with respect to  $\mu$  and  $E_c$  they are con-

sistent for the estimates of  $D_R$ ,  $H_R$  and  $A$ . There is some support for Jencks's conclusion that the heritability of IQ is apparently lower in the American studies than in Burt's British study. The best estimate of the broad heritability of IQ scores, however, for Jencks's data, is 68% which is 50% higher than the estimate Jencks has accepted. Since the model fits his data we cannot support his conclusion that the data give a heterogeneous picture of the genetics of IQ. Neither can we conclude that the data provide any evidence of genotype-environment covariation when proper allowance is made for dominance. On the contrary, when we allow for such covariation in the simplest way by adding to our five-parameter model one further parameter,  $r_{ge}$ , to specify the contribution of this covariation, no significant improvement in fit of the model to the data set is achieved. Furthermore, the weighted least squares estimate of  $r_{ge}$  is  $-0.31$  with an approximate standard error of 0.20. This is not only non-significantly different from zero but in so far as it is negative it has the opposite sign to the covariation postulated by Jencks in his model.

A small anomaly in the results of our analysis of Burt's data is that  $A$  is numerically (though not significantly) greater than  $\mu$ . This anomaly is removed by stipulating that parents and offspring do not share developmentally important environmental features. The correlation between foster parent and adopted children then has to be accounted for partly by placement.

The analyses strikingly confirm Jinks and Fulker's conclusion regarding the importance of dominance variation. Even if we make allowance for possible overestimation this can best be explained only if dominance deviations at individual gene loci are large or if increasing dominant alleles are more frequent than their recessive counterparts. Coupled with the evidence for inbreeding depression, this suggests that IQ displays the pattern of genetical variation associated with a fitness character, that is, a trait which has been subject to a history of directional selection for increasing IQ score. What-

ever else may be said about its social significance, IQ is clearly a trait of biological relevance.

Because much has already been made of the relatively low estimate of heritability argued for by Jencks, we have concentrated on the small part of his book devoted to this subject. We felt that it was important for the continuing discussion to establish that Jencks's 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. In so doing we have not

done justice to the scholarly presentation and thought-provoking discussions contained in both Herrnstein's and Jencks's books, which have more in common than perhaps either author would admit to, and little that we would wish to dissent from. We are agreed that there are individual differences for IQ, that only a proportion of these differences might be removed by environmental manipulation, and that the features of the environment that would require modification to achieve this have still to be identified. Those concerned with inequalities in our society might

just as well resign themselves therefore to the fact that individual differences for IQ at more or less their present level will continue to be an important factor. In these circumstances, those who wish to see progress towards a more equitable society should turn their attention to the means of ensuring that the greater social and financial rewards of our society are not reserved for those who, whether through their genotype or environment, have a higher than average IQ.

J. L. JINKS  
L. J. EAVES