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Comparative Analyses of Twin Data *

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The biometrical genetical method of analysis of continuously varying human traits is described and shown to unify a number of common approaches to the analysis of twin data. The method, which is based on the analysis of variance, goes beyond alternative approaches by providing tests of basic assumptions and by investigating the possibility of assortative mating and dominant gene action.

Twins form an indispensable group for the application of the biometrical genetical method but the value of including other groups, often more easily collected, is demonstrated.

The techniques are illustrated through the reanalysis of data on the behavioural measures, *neuroticism* and *intelligence quotient* (I.Q.). For both measures fundamental assumptions are met. The results suggest the absence of dominant gene action for *neuroticism*, indicating an evolutionary history of stabilising selection, and directional dominance for high I.Q., indicating an evolutionary history of strong directional selection. Both these findings seem reasonable in view of psychological knowledge concerning the two measures.

The quantitative methods used give the following estimates. For *neuroticism* both broad and narrow heritability are 54% ± 9%. For I.Q. broad heritability is 86% ± 1% and narrow heritability 71% ± 1%. The number of genes controlling I.Q. is in excess of 100 and the level of dominance 0.74. Increasing and decreasing genes are, on average, equally frequent.

Other measures are analysed, including *extraversion*, *educational attainment* and two cognitive measures but basic assumptions are not met. Effects of genotype-environment interaction, correlated genotype and environment and sampling bias are demonstrated for these measures.

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* The full paper has been published in Psychol. Bull., **73**: 311-349, 1970.

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Acta Genet. Med. Gemellol. (1970), **19**: 140