

vides for the analysis of a series of scores obtained at a single visit, such as the sub-test scores on the Wechsler Intelligence Scale.

The analysis provides within-pair correlation which express the degree of the similarity in twins for their profile of scores. It also provides within-pair correlations for the stability of the profile over ages and for the concordance among twins on the overall score (summing across variables).

In some cases, the variables dimension would collapse to a single variable, such as the Bayley Scale of Infant Development. If the Scale were administered at periodic occasions during infancy, the profile of scores for each twin over occasions would represent his pattern of acceleration or lag in mental development from one age to the next. The analysis then calculates how closely the twins match one another in the course of mental development, which is expressed by within-pair correlations for profile similarity and overall level. And when the analysis is performed for groups of MZ pairs, DZ pairs, and sibling pairs, the evidence for heritability effects comes from tests of the differences between groups in the size of the correlations. Finally, by referring to the expected values of the variance components in the model, the contribution of genetic and environmental factors can be estimated.

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GENETIC STUDIES OF THE OFFSPRING OF IDENTICAL TWINS

A Model for the Analysis of Quantitative Inheritance in Man

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The value of half-sib studies for the analysis of quantitative inheritance has long been recognized. In conjunction with full-sib

and parental observations, half-sib analysis permits an estimation of the genetic and environmental variance as well as a partitioning of the genetic variance into its additive, dominance and epistatic components. The offspring of identical twins are a unique class of human half-sibs who provide an unusual opportunity to resolve and measure several additional potentially important sources of human variation including maternal effects, the influences of common environmental factors and assortative mating. From the genetic relationships within the families of male and female identical twins, it is possible to derive as many as 16 different equations of estimation which can be used to estimate some or all of the following variance components: V_A , the additive component of variance; V_D , the dominance component of variance; V_M , the component of variance resulting from maternal effects; and V_{AA} , V_{AD} , and V_{DD} , the epistatic components of variance. In addition to these genetic variance components, the model permits the identification of the source of environmental variance on the trait in question. Since the parent-twin, spouse, and their offspring, live in the same home and are exposed to similar geographic, socioeconomic, and dietary influences, while all of the children of the other twin (i.e., the "half-sibs") live in a different home, a clear separation of genetic and environmental effects is possible. The environmental variation may be further partitioned into: among half-sibships, between sibship, within half-sibship, and within-half-sibship components. Overall estimates of the parameters of interest can be obtained by the least squares method using either a weighted or an unweighted estimation procedure. The model has been used to study dermatoglyphic data from the families of 19 MZ female and 20 MZ male twins including a total of 196 offspring. In agreement with previous results, the analysis shows that most of the observed variation in total ridge count is genetic in origin. However, in addition to additive and dominance components of variance there was evidence for a previously unreported maternal effect on total ridge count.

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