twins, (b) that some of the cases are of the translocation mode, (c) that another mode of twinning exists (uniovular dispermatic twins), and (d) that an assumption of the test is violated. It is shown that explanation (c) is an equally likely predictor of the test result.

If uniovular dispermatic twins exist, it is estimated that they would constitute only about 1% of a random sample of twins, and their incidence in the general population is estimated to be about 9.6×10^{-5}. It is suggested that this alleged form of twinning be considered as a mutational event, rather than as a " mode " of twinning.

These estimations suggest that twin methodology would not be appreciably biased if alleged uniovular dispermatic twins were included in the test sample.

Dr. Larry L. Mai, Department of Anthropology, University of California, Los Angeles, California 90024, USA

THE PROBLEM OF GENOTYPE × ENVIRONMENT COVARIANCE IN THE ESTIMATION OF HERITABILITY FROM MZ AND DZ TWINS

ARTHUR R. JENSEN

Institute of Human Learning, University of California, Berkeley, California, USA

It is commonly, but incorrectly, assumed that the presence of genotype × environment covariance must necessarily reduce the heritability (h^2) as estimated from twin data, when the formula used to obtain h^2 makes no assumption about G × E covariance or assumes that it is zero. But, in fact, G × E covariance does not always reduce the genetic variance, and it can be shown under some conditions, an increase in the G × E covariance implies a greater genetic variance. The effect of G × E covariance on h^2, as estimated from data on MZ and DZ twins, depends jointly upon the degree of assortative mating and the degree of environmental correlation between MZ twins and between DZ twins. A method, based on the solution of a pair of simultaneous quadratic equations, is proposed for estima-

ting the range of h^2 from twin data under varying assumed values for assortative mating, the environmental correlations between MZ and DZ twins, and the G × E covariance. The solution of three simultaneous equations permits direct estimation of the genetic variance, environmental variance, and G × E covariance, under varying reasonable assumed values for assortative mating and the MZ and DZ environmental correlations. Examples of the method are based on intelligence test scores of MZ and DZ twins.

Dr. Arthur Jensen, Institute of Human Learning, University of California, Berkeley, California 94720, USA

ANALYSIS OF TWIN DATA AND ESTIMATION OF HERITABILITY EFFECTS

RONALD S. WILSON

Louisville Twin Study, School of Medicine, University of Louisville, Kentucky, USA

In a statistical sense, the objective of twin research is to partition the variance on some criterion measure among genetic and environmental factors. Although certain elaborate models have been developed, these models do not supply a convenient test statistic to show which factors make a significant contribution. Consequently several procedures drawn from analysis of variance have been adapted for use with twin data. The general case is illustrated below.
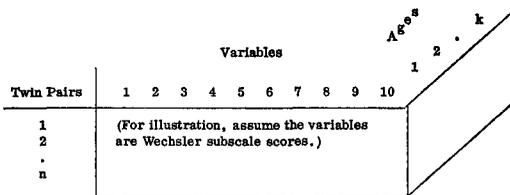
This design provides for the analysis of data that has been collected at successive ages, as in longitudinal studies; and it also pro-

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vides for the analysis of a series of scores obtained at a single visit, such as the subtest 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.

Ronald S. Wilson, Ph.D., Medical-Dental Research Bldg. Rm. 111H, P.O. Box 1055, Louisville, Kentucky 40201, USA

GENETIC STUDIES OF THE OFFSPRING OF IDENTICAL TWINS

A Model for the Analysis of Quantitative Inheritance in Man

W. E. NANCE

Department of Medical Genetics, Indiana University School of Medicine, Indianapolis, Indiana, USA

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.

Dr. Walter E. Nance, Department of Medical Genetics, 1100 West Michigan Street, Indianapolis, Indiana 46202, USA