Letters to the Editor

Programs for Pedigree Analysis: MENDEL, FISHER, and dGENE

To the Editor: We would like to announce the availability of our package, *Programs for Pedigree Analysis*. The first program in the package, MENDEL, is intended for gene mapping calculations, genetic counseling, segregation analysis, paternity testing, and related kinds of problems. The second program, FISHER, is designed for the analysis of classical biometric traits like blood pressure and total finger ridge count. The third program, dGENE, serves as an interface to the popular microcomputer data base management system dBASE III. Our documentation shows how to set up a genetic data base using dBASE III. dGENE can then be used to extract information from this data base in the correct format for input to the analysis programs MENDEL and FISHER. MENDEL and FISHER are written in FORTRAN 77; dGENE is written in the dBASE III programming language. At this time the program SEARCH described in John Hopper's review is not being distributed.

The bulk of MENDEL and FISHER will be supplied as object code. dGENE will be supplied as executable code for IBM PCs and compatibles. Source code is available in MENDEL to permit users to modify subroutines defining penetrances, prior probabilities of genotypes, and transmission probabilities from parental genotypes to gamete genotypes. In FISHER the source code defining trait means, variances, and covariances can likewise be modified. There are also subroutines for changing the likelihood of individual pedigrees, defining parameter specifications, and increasing program array dimensions. Both programs can be run in either interactive or batch mode. Full documentation is provided. This includes definition of all variables and a detailed description of the subroutines.

MENDEL has a number of attractive features. For instance, phenotype data can be character and need not be translated into integers. Unobserved phenotypes are coded as blanks. MENDEL incorporates an algorithm for automatic elimination of superfluous genotypes of an individual based on the phenotypes of surrounding pedigree members. Correct handling of inbreeding and other loops is done internally by MENDEL, and there is no need for users to split complicated pedigrees. Mono-

zygous (MZ) twin data is acceptable. Finally, maximum-likelihood parameter estimation is straightforward in MENDEL.

FISHER performs likelihood calculations under the assumption that measured traits within a pedigree conform to either a multivariate normal or a multivariate t distribution. The multivariate normal distribution is a plausible choice for traits determined by a large number of additive loci having comparable variances. The multivariate t distribution allows for departures from normality and provides a robust method for estimating mean and covariance parameters. One additional parameter characterizes the t distribution. As this parameter tends to infinity, one recovers the multivariate normal distribution. Other distinctive features of FISHER include ascertainment correction by conditioning on probands, the analysis of multivariate as well as univariate traits, prediction of an individual's traits based on the trait values of his relatives, a detailed outlier analysis for individuals and pedigrees, and systematic testing of the overall statistical validity of a model.

The program package is currently available at no charge in two IBM PC compatible versions and a VAX VMS version. The PC compatible versions are compiled under Ryan-McFarland Fortran V2.10 and Microsoft Fortran V4.10. Minimum requirements include 512K of RAM and a math coprocessor. Likewise, VMS Fortran must be available to VAX users. Versions of the package for other computers may be available at a later date.

For the Ryan-McFarland version contact Michael Boehnke. For the Microsoft and VAX versions contact Kenneth Lange or Daniel Weeks.

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