

CLUSTERING POPULATIONS BY MIXED LINEAR MODELS

JUN ZHU

*(Department of Agronomy, Zhejiang Agricultural University, Hangzhou
310029, Zhejiang, CHINA)*

BRUCE S. WEIR

*(Department of Statistics, North Carolina State University, Raleigh,
NC 27695-8203, USA)*

ABSTRACT

Two mixed linear models are proposed for grouping populations by a dissimilarity coefficient which has two parameters for squared difference of marginal mean and variance component of interaction. Cluster trees can be constructed by the mixed linear model approaches for experimental data with sampling errors within populations or with some missing values. Unweighted pair-group method (UPGM) is suggested as fusion method. Sampling variances of estimated dissimilarity coefficient can be obtained by the jackknife procedure. A one-tail t -test is applicable for detecting significance of dissimilarity of populations within specific group. Unbiasedness and efficiency for estimation of dissimilarity coefficients are proved by Monte Carlo simulations. Worked example from cotton yield data is given for demonstration of the use of these cluster methods.

Key Words: Cluster method, Mixed linear models, Monte carlo simulation, Genotype \times environment interaction.

coefficient and its two components. The observed sampling variances for estimates are also much larger than those obtained by UPGM method.

ACKNOWLEDGMENT

This research was supported in part by NIH Grant of USA (GM32519) and by National Natural Science Foundation of China (39170417).

LITERATURE CITED

- [1] About-El-Fittouh, H. A., J. O. Rawling, and P. A. Miller. 1969. Classification of environments to control genotype by environment interaction with an application to cotton. *Crop Sci.* 9: 135-140.
- [1] Brown, M. M., E. M. Prager, A. Wand A. C. Wilson. 1982. Mitochondrial DNA sequences of primates: Tempo and mode of evolution. *J. Mol. Evol.* 18: 225-239.
- [3] Edwards, A. W. F. and L. L. Cavalli-sforza, 1963. The reconstruction of evolution. *Heredity* 18: 553.
- [4] Efron, B. 1982. *The Jackknife, the Bootstrap and other Resampling Plans*. Society for Industrial and Applied Mathematics, Philadelphia, PA.
- [5] Everitt, B. S. 1993. *Cluster Analysis*. Edward Arnold, London.
- [6] Felsenstein, J. 1981. Evolutionary trees from DNA sequences. A maximum likelihood approach. *J. Mol. Evol.* 17: 368-376.
- [7] Gauch, E. G. and R. W. Zobel. 1988. Predictive and postdictive success of statistical analysis of yield trials. *Theor. Appl. Genet.* 76: 1-10.
- [8] Hu, B. M. and S. Geng. 1993. *Analysis Methods for Crop Stability*. Science Press, Beijing.
- [9] Lin, C. S. 1982. Grouping genotypes by a cluster method directly related to genotype-environment interaction mean square. *Theor. Appl. Genet.* 62: 277-280.
- [10] Lin, C. S. and B. Thompson. 1975. An empirical method of grouping genotypes based on a linear function of the genotype-environment interaction. *Heredity* 34: 255-263.
- [11] Miller, R. G. 1974. The jackknife-a review.