



USE OF BIOMETRICAL TECHNIQUES IN
QUANTITATIVE GENETICS

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in the University of Adelaide

by

Trevor William Hancock, B. Ag. Sci.

Biometry Section,
Waite Agricultural Research Institute,
GLEN OSMOND,
South Australia 5064.

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SUMMARY

While the existing theory of quantitative genetics has much to offer the plant or animal breeder it is recognised that many of the statistics used are difficult to understand and interpret. In this thesis several biometrical techniques are investigated which can be used by the breeder. The suitability of these techniques is illustrated using the data from the Roseworthy selection trial. This trial was designed to compare the efficiency of selection for clean fleece weight by direct measurement to the conventional method of visual appraisal.

When analysing such breeding data two aspects are of interest, firstly, what changes have occurred between the populations as a result of the different selection criteria, and secondly, what changes can be expected if a particular method of selection is subsequently employed? In Chapters I, II, III and IV the former aspect is considered while the latter is investigated in Chapters II, V and VI.

The conventional methods of analysing breeding experiments are detailed in Chapters I and II. Thus the two flocks are initially compared using both parametric and non-parametric univariate tests. Genetic parameters (i.e. heritability, genetic, phenotypic and environmental correlations) are subsequently calculated for the various subsets of the data.

In view of the problems encountered in applying these correlations, it is proposed in Chapter III that Hotelling's T^2 (a multivariate technique) provides a simpler, but comprehensive, comparison of the two populations. On applying it to the Roseworthy data it can be seen that the two populations have diverged. In particular, it can be seen

from the simultaneous confidence intervals that staple length, clean scoured yield and secondary follicle number are positively associated with the increase in clean fleece weight while crimps per inch and body weight are negatively associated.

In Chapter IV the analysis of discrete variates such as reproductive performance is considered. An "improved" FORTRAN algorithm for the Exact Test of R x C contingency tables is developed. As this test does not require approximation to a known distribution it can be applied to contingency data irrespective of the minimum size of the expected cell frequencies.

Several methods for recognising the important factors among a multivariate data set are considered in Chapter V. Principal Component Analysis is observed to provide the most effective method, especially from the point of consistency. Using its orthogonal components the breeder can predict the changes which would occur following a particular method of selection. Unlike the genetic parameters of Chapter II which are often used for this purpose, the above method remains manageable as the number of variates increases.

In Chapter VI the effects of a major gene on the frequency distribution of a metric character are investigated. As the segregation of a major gene can be expected to result in non-normality of the frequency distribution, it is proposed that a normality test can be used to screen data. When non-normality is identified, the method of moments (Hawkins, 1975) can be used to estimate the means and variances for the general population and for those carrying the major gene respectively.

DECLARATION

I declare that this thesis contains no material which has been accepted for the award of any other degree or diploma in any university and that, to the best of my knowledge and belief, this thesis contains no material previously published or written by another person, except where due reference has been made in the text of the thesis.

T. W. Hancock

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