

to  $y_i$  is applied so that

$$d \cdot \chi'^2 = \sum_{i=1}^{k-1} y_i^2,$$

where  $d$  is determined later by equating the coefficients of  $\chi'^2$ . Certain rectangles  $r(v)$  with  $(y_1, \dots, y_{k-1})$  as a mid-point are non-overlapping and cover the entire space  $R_{k-1}$  for  $v_i = 0, \pm 1, \pm 2, \dots$ . If  $\chi'^2 \leq c$ , then bounds on  $T$  in terms of the integral of the  $(k-1)$  dimensional normal frequency function over the rectangle  $r(v)$  are obtained. Prob.  $\{\chi'^2 \leq c\}$  is the sum of  $T$  over  $\chi'^2 \leq c$ , so the integral over the sum of rectangles whose mid-points lie within the hypersphere  $\chi'^2 \leq c$  is considered. Two hyperspheres, one which contains the sum of those rectangles, and one which is contained in it are used for the bounds, giving

$$\lambda_2 \cdot F_{k-1}(c_2) \leq \text{Prob. } \{\chi'^2 \leq c\} \leq \lambda_1 \cdot F_{k-1}(c_1),$$

where  $F_{k-1}(x)$  is a chi-square distribution function with  $(k-1)$  degrees of freedom and  $\lambda_1, \lambda_2, c_1, c_2$  are functions of  $c, n, k$  and  $p_1, \dots, p_k$ . As  $n \rightarrow \infty$ , both bounds tend to  $F_{k-1}(c)$ . Bounds of the same form are obtained for Prob.  $\{\chi^2 \leq C\}$ . Closer bounds for Prob.  $\{\chi^2 \leq C\}$  are given in terms of a non-central chi-square distribution.

**21. Estimation of Genetic Parameters.** C. R. HENDERSON, Cornell University.

Many applications of genetics and statistics to the improvement of plants and animals deal with experimental data for which the underlying model is assumed to be

$$y_\alpha = \sum_{i=1}^p b_i x_{i\alpha} + \sum_{i=1}^q u_i z_{i\alpha} + e_\alpha,$$

where  $b_i$  are unknown fixed parameters,  $x_{i\alpha}$  and  $z_{i\alpha}$  are observable parameters, the  $u_i$  are a random sample from a multivariate normal distribution with means zero and covariance matrix  $\|\sigma_{ij}\|$ , and the  $e_\alpha$  are normally and independently distributed with means zero and variances  $\sigma_\alpha^2$ . If  $\sigma_{ij} = 0$  when  $i \neq j$  and if  $\sigma_\alpha^2 = \sigma_\alpha^2$ , the model is the one usually assumed when components of variance are estimated.

Three different estimation problems are involved, (1) estimation of  $b_i$  under the assumptions of the model, (2) estimation of  $u_i$  and (3) estimation of  $\sigma_{ij}$ . The first two problems are not solved satisfactorily by the least squares procedure in which the  $u_i$  are regarded as fixed, but the maximum likelihood solution does lead to a satisfactory estimation procedure.

Assuming that the  $\sigma_{ij}$  and  $\sigma_\alpha^2$  are known, the joint maximum likelihood estimates of  $b_i$  and  $u_i$  are the solution to the set of linear equations

$$\sum_{i=1}^p b_i (\sum_\alpha x_{h\alpha} x_{i\alpha} / \sigma_\alpha^2) + \sum_{i=1}^q u_i (\sum_\alpha x_{h\alpha} z_{i\alpha} / \sigma_\alpha^2) = \sum_\alpha x_{h\alpha} y_\alpha / \sigma_\alpha^2, \quad h = 1, \dots, p,$$

$$\sum_{i=1}^p b_i (\sum_\alpha x_{i\alpha} z_{h\alpha} / \sigma_\alpha^2) + \sum_{i=1}^q u_i (\sigma^{ih} + \sum_\alpha z_{i\alpha} z_{h\alpha} / \sigma_\alpha^2) = \sum_\alpha z_{h\alpha} y_\alpha / \sigma_\alpha^2, \quad h = 1, \dots, q.$$

Some important applications of this estimation procedure to genetic studies are described and certain computational short-cuts are suggested.

The problem of estimating  $\sigma_{ij}$  has not been solved satisfactory although under certain quite general assumptions the equations for the joint estimation of  $b_i, u_i, \sigma_{ij}$ , and  $\sigma_\alpha^2$  can easily be written. The solution to the equations, however, is too difficult to make the procedure practical. Nevertheless unbiased estimates of  $\sigma_{ij}$  can be obtained by equating to their expected values the differences between certain reductions in sums of squares computed by least squares and solving for the  $\sigma_{ij}$ . In general, the expectation of the reduction due to  $b_1, \dots, b_p, u_1, \dots, u_k (k \leq q)$  is  $\sum_{gh} d^{gh} E(Y_g Y_h)$ , where  $d^{gh}$  are the elements

of the matrix which is the inverse of the  $(p + k)^2$  matrix of coefficients and the  $Y_0$  are the right members of the least squares equations.

**22. Estimating the Mean and Standard Deviation of Normal Populations from Double Truncated Samples.** A. C. COHEN, JR., University of Georgia.

The method of maximum likelihood is employed to obtain estimates of the mean and standard deviation of a normally distributed population from double truncated random samples. Two cases are considered. In the first, the number of missing variates is assumed to be unknown. In the second, the number of missing (unmeasured) variates in each tail is known. Variances for the estimates involved in each case are obtained from the maximum likelihood information matrices. A numerical example is given to illustrate the practical application of the estimating equations obtained for each of the two cases considered.

**23. Minimax Estimates of Location and Scale Parameters.** GOPINATH KALLIANPUR, University of North Carolina.

If the joint fr. f. of the random variables  $X_1, \dots, X_N$  contains only a scale parameter and is of the form

$$\frac{1}{\alpha^N} p\left(\frac{x_1}{\alpha}, \dots, \frac{x_N}{\alpha}\right),$$

then under mild restrictions the following theorem is proved:

**THEOREM 1:** *If the loss function is of the form  $W\left(\frac{\alpha - \bar{\alpha}}{\alpha}\right)$ , the best or minimax estimate  $\bar{\alpha}_0(x)$  of  $\alpha$  minimizes*

$$\int_0^\infty W\left(\frac{\alpha - \bar{\alpha}}{\alpha}\right) \frac{1}{\alpha^N} p\left(\frac{x_1}{\alpha}, \dots, \frac{x_N}{\alpha}\right) d\alpha$$

w.r.t.  $\bar{\alpha}$  and further,

$$\bar{\alpha}_0(\mu x_1, \dots, \mu x_N) = \mu \bar{\alpha}_0(x_1, \dots, x_N), \quad \mu > 0.$$

When both location and scale parameters are present and the joint fr. f. is of the form

$$\frac{1}{\alpha^N} p\left(\frac{x_1 - \theta}{\alpha}, \dots, \frac{x_N - \theta}{\alpha}\right),$$

(under conditions similar to those in Theorem 1) we obtain two results for the estimation of  $\theta$  and  $\alpha$ , respectively, one of which is:

**THEOREM 2:** *If the loss function is of the form  $W\left(\frac{\theta - \hat{\theta}}{\alpha}\right)$ , the best estimate  $\hat{\theta}_0(x)$  of  $\theta$  minimizes*

$$\int_{-\infty}^{\infty} \int_0^{\infty} W\left(\frac{\theta - \hat{\theta}}{\alpha}\right) \frac{1}{\alpha^N} p\left(\frac{x_1 - \theta}{\alpha}, \dots, \frac{x_N - \theta}{\alpha}\right) d\theta d\alpha$$

$$\text{and } \hat{\theta}_0\left(\frac{x_1 + \lambda}{\mu}, \dots, \frac{x_N + \lambda}{\mu}\right) = \frac{\hat{\theta}_0(x_1, \dots, x_N) + \lambda}{\mu}.$$

These theorems have been applied to derive minimax estimates in the case of standard distributions. Finally, the problem of estimating the difference between the location parameters of two populations is briefly considered. The results obtained in this paper are a continuation of the line of approach suggested in Theorem 5 of Wald's, "Contributions