

Analysis of Quantitative Genetic Variation by
Nested Analysis of Variance and Offspring-Parent Regression
A Program Package - NESREG

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This package computes a complete analysis of variance (AOV) and covariance (AOCOV) table for a nested classification of up to six levels (the lowest three levels being sires, dams, and progeny) on balanced or unbalanced (see Table 1) data. From this analysis of full- and half-sibs all commonly applied quantitative genetic parameters are estimated. By providing parent data and combining the appropriate sum of squares (products) estimates from the AOV's and AOCOV's of parent and progeny data, offspring on parent regression (O-P) and correlation analyses are possible and are produced on request. Three versions of the package are currently available.

(a) Version 1

Written in FØRTRAN IV for an IBM 7040 computer with 32K store. It is divided into two programs (NESRG1 - with the subroutines FULSIB & READX, & NESRG2 with the subroutines ØPREG & PRØUT) to overcome memory restraints. The restrictions in using Version 1 are

(i) Maximum number of variables (Il) is:

nested problem analysis only - 12;

complete problem analysis - 6 parent and 6 progeny;
or 3 sire, 3 dam, 3 male and 3 female progeny

O-P analysis only - as for complete.

(ii) Unbalanced data of Types 1 and 2 may be analysed.

(iii) The number of observations within a single cell of the highest level must be $\leq 99,999$.

(iv) The following must be satisfied

$2 * \underline{N5} * (1 + \underline{N6}) \leq 12,000$. (see Appendix 1 for N5 and N6).

(v) The user must provide a subroutine (READX) to the first program for reading data into the machine.

(b) Version 2

Written in FØRTRAN Extended language for a CDC6600 computer with 96K store. It consists of a main program (NESREG) and eight subroutines (STEP1, FULSIB, STEP2, MIXTUR, ØPREG, PRØUT, READX, and GETFL). In Version 2 array storage is allocated dynamically at execution time - the maximum capacity is thus data dependent but is considerably greater than Version 1 (see Appendix 2). Unbalanced data of Types 1 and 2 may be analysed and the user must supply subroutine READX.

(c) Version 3

Written in FØRTRAN Extended for a CDC6600. It consists of a main program (NESREG) and ten subroutines (ADDRES, STEPS, STEP1, FULSIB, STEP2, MIXTUR, ØPREG, PRØUT, READX, and GETFL). With Version 3 unbalanced data of Types 1, 2 and 3 may be analysed and there is no limit (with respect to computer store) to the number of variables which may be included. The user must supply subroutine READX.

Table 1. Types of Unbalanced Data and the Appropriate Versions of NESREG to use in their Analysis

Type	Description	Version
1	Unequal class numbers, eg. dams per sire, in one or more levels of nesting	1, 2, 3
2	<u>All</u> observations for one or more relatives are missing, eg. offspring-sire regression only, offspring-dam regression only, paternal half-sib data, etc.	1, 2, 3
3	Varying numbers of observations between variables for some or all relatives	3
4	Varying numbers of variables between relatives, i.e. IS \neq ID \neq IM \neq IF (see Appendix 1 for IS, ID, IM, IF)	Not possible

Operating procedures for Versions 1, 2 and 3 are given in Appendices 1, 2 and 3, respectively. Versions 2 and 3 are readily convertible to a CDC3600 computer, and could be readily adapted to any computer for which fixed and floating point word lengths are equal.

II OUTPUT

The output for Versions 1 and 2 consists of $p(2p + 1)$ analyses where $2p$ is the number of offspring variables per observation set in the problem (see Appendix 3 for layout of the output for Version 3). The following discussion will assume the complete problem analysis is requested; portions of this will not be given if the nested problem analysis only, or the O-P problem only, is requested, or if the data to be analysed contains unequal numbers of parent and/or progeny variables across sexes.

Variables i and j

i = j: the table will be an AOV and will include variation due to regression and deviations therefrom. Variable means are given as are variance components for the parent and progeny levels; the phenotypic, genetic and environmental variances; all heritability estimates and their standard errors, for the sib analysis, offspring-parent regression (together with corrections when applied), and offspring-parent correlation; an indication of the influence of natural selection; the common environmental variance and the within-full-sib environmental variance; the k coefficients (for the lower three levels only); and finally some partitioning of the phenotypic variance is performed where possible. The parent-parent correlation is also given (expected to be zero with random mating).

i \neq j: the table will be an AOCOV for the offspring data only. Covariance components for the parent and progeny levels of the offspring analysis are given as are phenotypic, genetic and environmental covariances; the corrected phenotypic and genetic variances of the differences between i and j and the resultant heritability estimate for the sires level only; the genetic, environmental and phenotypic correlations and standardized correlated responses, and their standard errors for the sib analysis; the genetic correlations, their standard errors and the average coefficient of variation of the denominator covariances of these genetic correlations together with the appropriate standardized correlated responses and their standard errors for the O-P analysis; and the common-environmental and within-full-sib environmental covariances.

III METHODS

(a) Models

The basic nested model is of the form which is applied in the general (balanced or not) case, a complete description of which is given by Gates and Shine (1962). The program is designed basically for full-sib data, that is where the lowest three levels are between sires (within other levels), between dams within sires, and within dams.

(i) Observation sets

Each observation set consists of an array

$$\{x_1^s, x_2^s, \dots, x_p^s, | x_1^d, x_2^d, \dots, x_p^d, | x_1^m, x_2^m, \dots, x_p^m, | x_1^f, x_2^f, \dots, x_p^f\} = x_q^r$$

for $q = 1$ to p and $r = s, d, m$, or f , where p is the number of variables per relative, relatives being sires ($r=s$), dams ($r=d$), male progeny ($r=m$), and female progeny ($r=f$).

In the description which follows, the concept of "pseudo-variable" is used extensively. A pseudo-variable is defined by specifying both the variable and the relative on which it is measured. An observation set thus consists of an array of pseudo-variables, and the observation set previously defined may be rewritten

$$\{x_1, x_2, \dots, x_{4p}\} = x_q \text{ for } q = 1 \text{ to } 4p,$$

ignoring the partitioning into sire, dam, male, and female, for the purposes of AOV and AOCOV.

(ii) Model for nested AOV

The data is an array of observation sets, together with their "identifications", i.e. coding for classes within each level of the hierarchy to which the observations belong. Each parent observation is thus repeated over all its progeny in the data set. Ignoring any higher level than "between sires", the model for AOV of the q th pseudo-variable is

$$x_{qijl} = \mu_q + S_{qi} + D_{qij} + E_{qijl}$$

where

x_{qijl} is the observation for the q th pseudo-variable within the observation set having the "identification" l th progeny of j th dam mated to the i th sire;

μ_q is the population mean;

S_{qi} is the effect of the i th sire;

D_{qij} is the effect of the j th dam mated to the i th sire, and

E_{qijl} is the uncontrolled environmental and genetic deviations attributable to individuals;

$i = 1, 2, \dots, s_q$ is the "identification" for the between sires level;

$j = 1, 2, \dots, d_{qi}$ is the "identification" for the between dams level;

$\ell = 1, 2, \dots, n_{qij}$ is the "identification" for the lowest level, and

$$\sum_j n_{qij} = n_{qi}.$$

$$\sum_{ij} n_{qij} = \sum_i n_{qi} = n_{q..}$$

$$\sum_i d_{qi} = d_q.$$

Only Version 3 can carry out analyses where s_q , d_{qi} , and n_{qij} are not the same for all q (unbalanced data of Type 3), except for the special case in which all observations are missing for one or more relatives (unbalanced data of Type 2).

The AOV ($q = r$) or AOOCOV ($q \neq r$) is shown in Table 2, for the pair of pseudo-variables q and r .

(iii) SS and SCP matrices from nested AOV

After performing the analyses shown in Table 2 for all pairs of pseudo-variables, matrices (A, B, and C) of sums of squares and cross products (SS and SCP) or (U, V, and W) of mean squares and cross products (MS and MCP), are assembled.

The matrices A, B, and C can be partitioned as follows:

$$\underline{A} = \begin{bmatrix} \underline{A}^s & \underline{A}^{sd} & \underline{A}^{so} \\ & \underline{A}^d & \underline{A}^{do} \\ & & \underline{A}^o \end{bmatrix}$$

and similarly for B and C, the superscripts s , d , and o referring to observations on sires, dams, and progeny, respectively. The partitions correspond to those in the original notation for an observation set, except that male

Table 2. Analysis of Variance (Covariance) of a Pair of Pseudo-Variables for the Unbalanced Two-fold Nested Classification

SOURCE	D.F.	SS or SCP*	MC or MCP*	E(MS) or E(MCP)*
Sires (S)	s-1=u	$\sum_i \frac{(X_{qi..})(X_{ri..})}{n_i} - \frac{(\sum_q (X_{q...})(X_{r...}))}{n..} = A_{qr}$	U_{qr}	$E'_{qr} + k_2 D_{qr} + k_3 S_{qr}$
Dams (D)/S	d.-s=v	$\sum_{ij} \frac{(X_{qij.})(X_{rij.})}{n_{ij}} - \sum_i \frac{(\sum_q (X_{qi..})(X_{ri..}))}{n_i} = B_{qr}$	V_{qr}	$E'_{qr} + k_1 D_{qr}$
Offspring/D/S	n.-d.=w	$\sum_{ijl} (X_{qijl})(X_{rijl}) - \sum_{ij} \frac{(\sum_q (X_{qij.})(X_{rij.}))}{n_{ij}} = C_{qr}$	W_{qr}	E'_{qr}
Total	n.-1	$\sum_{ijl} (X_{qijl})(X_{rijl}) - \frac{(\sum_q (X_{q...})(X_{r...}))}{n..}$		

* q and r denote two variables, and for mean square etc., q = r.

and female offspring are not separated. Where the need⁷ arises, male and female offspring will be distinguished by further partitioning. Using the \underline{A} matrix again for example

$$\begin{aligned}\underline{A}^{so} &= \begin{bmatrix} \underline{A}^{sm} & \underline{A}^{sf} \\ \underline{A}^{dm} & \underline{A}^{df} \\ \underline{A}^m & \underline{A}^{mf} \\ \hline & \underline{A}^f \end{bmatrix} \\ \underline{A}^{do} &= \begin{bmatrix} \underline{A}^{dm} & \underline{A}^{df} \\ \underline{A}^m & \underline{A}^{mf} \\ \hline & \underline{A}^f \end{bmatrix} \\ \underline{A}^o &= \begin{bmatrix} \underline{A}^m & \underline{A}^{mf} \\ \hline & \underline{A}^f \end{bmatrix}\end{aligned}$$

The matrices \underline{U} , \underline{V} , and \underline{W} can be similarly partitioned. The interpretation of each partition and its use in subsequent analyses is given in Table 3. The notation for SS and SCP matrices is summarized in Table 4, using the \underline{A} matrix again for example.

(iv) Models for O-P regression

In the offspring-parent analyses, consider pseudo-variables q in the parent and r in the offspring, r being the same variable as q .

The offspring-sire regression coefficient, β_r^s , is defined by the model*

$$x_{rij}^o = \mu_r + \beta_r^s (x_{qij}^s - \bar{x}_{q..}^s) + e_{rij}$$

where

μ_r is the offspring population mean;

x_{rij}^o is the observation of the r th pseudo-variable on the j th offspring of the i th sire;

x_{qij}^s is the observation of the q th pseudo-variable on the i th sire repeated over j ;

\bar{x}_{qij}^s is the phenotypic mean of the q th pseudo-variable

and

e_{rij} is random error.

*See Sokal & Rohlf (1969), Section 14.6, for a description of the method and interpretation of the F tests.

Table 3. Matrices of SS and SCP used for further analyses

Matrix	Interpretation	Use
\underline{A}^s	Sire variances (diagonal elements) Sire-offspring covariances	offspring-sire regression and correlation
\underline{A}^{so}		
\underline{B}^d	Dam variances (diagonal elements) Dam-offspring covariances	intra-sire offspring-dam regression and correlation
\underline{B}^{do}		
\underline{A}^{sd}	Sire x dam covariances for same variable (diagonal elements)	sire-dam correlation
\underline{A}^o	sires dams/sires within dams	Partitioning of offspring variances and covariances by nested AOV & AOCOV
\underline{B}^o		
\underline{C}^o		
\underline{A}^d	Dam variances and covariances among the means for all dams mated to each sire	unused
\underline{A}^{do}	Dam-offspring covariances among the means for all dams mated to each sire and all offspring of each sire	unused
$\underline{B}^s, \underline{B}^{sd}, \underline{B}^{so}, \underline{C}^s, \underline{C}^{sd}, \underline{C}^{so}, \underline{C}^d, \underline{C}^{do}, \underline{C}^{so}, \underline{C}^o$	Null matrices	unused

Table 4. Notation used for SS and SCP Matrices

Symbol	Usage
\underline{A}	whole SS and SCP matrix
\underline{A}^s	partition of \underline{A} corresponding to SS and SCP's among $\{x_1^s, x_2^s, \dots, x_p^s\}$, the observations on sires
\underline{A}_{qr}	a particular element of \underline{A} containing the SS or SCP between pseudo-variables q and r
\underline{A}_{qr}^s	as for \underline{A}_{qr} but q and r both being observations on sires
\underline{A}_{qr}^{do}	as for \underline{A}_{qr} but q being an observation on dams and r being an observation on offspring

The intra-sire offspring-dam regression coefficient β_r^d , is defined by the model

$$x_{rijl}^o - S_{ri} = \mu_r + \beta_r^d (x_{qijl}^d - \bar{x}_q^d \dots) + e_{rijl}$$

where

μ_r is the offspring population mean;

x_{rijl}^o is the observation of the r th pseudo-variable on the l th offspring from a mating of the i th sire to the j th dam;

S_{ri} is the effect of the i th sire;

x_{qijl}^d is the observation of the q th pseudo-variable on the j th dam mated to the i th sire and repeated over l progeny;

$\bar{x}_q^d \dots$ is the phenotypic mean of the q th pseudo-variable

and

e_{rijl} is random error.

The O-P regression coefficients are estimated by

$$b_r^s = A_{qr}^{so}/A_{qq}^s, \quad \text{and} \quad b_r^d = B_{qr}^{do}/B_{qq}^d.$$

The AOV's for the two O-P analyses are given in Table 5. The deviations of individuals from linear regression are not printed but may be obtained by combining the appropriate levels.

The standard errors of O-P regression coefficients are

$$S.E.(b_r^s) = (M_{qr}^s/A_{qq}^s)^{1/2},$$

$$\text{and} \quad S.E.(b_r^d) = (M_{qr}^d/B_{qq}^d)^{1/2}.$$

Note that these standard errors are computed using the mean squares for deviations of individuals from regression, i.e. the deviations of the means from regression are assumed to be not significant.

(b) Estimates of Genetic Parameters

The following discussion uses, as an example, a problem where 2 variables were measured in each sex of the

¹⁰ Table 5. Analyses of Variance for Offspring-Sire and Intra-Sire Offspring-Dam Regressions

SOURCE	D.F.	SS	MS
Sire-Offspring			
Regression	1	$b_{rqr}^{sAsO} = R_{qr}^s$	
Deviations (means)	$u - 1$	$A_{rr}^O - R_{qr}^s$	M_{qr}^s
Deviations (individuals)	$u+v+w-1$	$A_{rr}^O + B_{rr}^O + C_{rr}^O - R_{qr}^s$	M_{qr}^s
Dam-Offspring			
Regression	1	$b_{rqr}^{dBdO} = R_{qr}^d$	
Deviations (means)	$v - 1$	$B_{rr}^O - R_{qr}^d$	\bar{M}_{qr}^d
Deviations (individuals)	$v+ w - 1$	$B_{rr}^O + C_{rr}^O - R_{qr}^d$	M_{qr}^d

parents and offspring, i.e. pseudo-variables 1 and 2 in sires, 3 and 4 in dams, 5 and 6 in male and 7 and 8 in female offspring.

No allowance has been made for relatedness of parents (see for example, Hinklemann 1971) or for in-breeding of unrelated parents in any estimates. When one is interested in estimates of genetic parameters for the present population then the parents are not inbred although throughout the literature we find a correction being applied in situations where estimates for the present population rather than for past generations of this population, are of concern.

(i) Variance and covariance components

The methods of computing estimates of phenotypic, genetic and environmental variances (covariances) utilizing the progeny mean square in combination with the sire, dam and sire plus dam mean squares (P_{qr} , G_{qr}^s , E_{qr}^s , G_{qr}^d , E_{qr}^d , G_{qr}^{sd} and E_{qr}^{sd} respectively), are given by Hammond and Nicholas (1972). The appropriate values to be substituted for f , ℓ ,

a, b and c in the general equation, given by them,

$$\hat{\theta} = f[aU_{qr} + bV_{qr} + cW_{qr}]/\ell,$$

are given in Table 6.

Table 6. Values for the Coefficients used in Computing θ Estimates

$\hat{\theta}_{qr}$	Coefficients				
	f	ℓ	a	b	c
Phenotypic:					
P	1	$k_1 k_3$	k_1	$k_3 - k_2$	$k_2 - k_1 + k_3 (k_1 - 1)$
Genetic:					
G^S	4	k_3	1	$-k_2/k_1$	$(k_2 - k_1)/k_1$
G^d	4	k_1	0	1	-1
G^{sd}	2	$k_1 k_3$	k_1	$k_3 - k_2$	$k_2 - k_1 - k_3$
Environmental:					
E^S	1	k_3	-2	$2k_2/k_1$	$((k_1 - k_2)/k_1) + k_3$
E^d	1	k_1	0	-2	$k_1 + 2$
E^{sd}	1	$k_1 k_3$	$-k_1$	$k_2 - k_3$	$k_1 - k_2 + k_3 (k_1 + 1)$

(ii) Heritabilities

1. Sib estimates: e.g. for $q=r=5$, from the sire, dam and sire plus dam θ values together with standard errors (approximate method - see Becker (1964)) are

$$H_5^S = G_{55}^S/P_{55}, \quad S.E.(H_5^S) = 4\text{Var}(S)^{1/2}/P_{55},$$

$$H_5^d = G_{55}^d/P_{55}, \quad S.E.(H_5^d) = 4\text{Var}(D)^{1/2}/P_{55},$$

$$H_5^{sd} = G_{55}^{sd}/P_{55}, \quad S.E.(H_5^{sd}) = 2[\text{Var}(S) + \text{Var}(D) + 2\text{Cov}(S, D)]^{1/2}/P_{55},$$

where

$$\text{Var}(S) = 2[U_{55}^2/(u+2) + V_{55}^2/(v+2)]/k_3^2,$$

$$\text{Var}(D) = 2[V_{55}^2/(v+2) + W_{55}^2/(w+2)]/k_1^2, \text{ and}$$

$$\text{Cov}(S,D) = -k_2[\text{Var}(D) - 2W_{55}^2/k_1^2(w+2)]/k_3.$$

2. O-P estimates: for the trait represented by variables 1-3-5-7 four separate O-P estimates are possible: (i) Male offspring on sire (51), (ii) female offspring on sire (71), (iii) male offspring on dam (53), and (iv) female offspring on dam (73). Heritability is given by, for example, male-sire

$$HB_{(M-S)} \equiv HB_{51} = 2b_{51}^s, \text{ S.E.}(HB_{51}) = 2[\text{S.E.}(b_{51}^s)].$$

Estimates (ii) and (iii) are corrected for assumed inequality of variances between the sexes so that

$$HB_{71} = 2b_{71}^s (U_{55}/U_{77})^{1/2},$$

and $HB_{53} = 2b_{53}^d (V_{77}/V_{55})^{1/2},$

and these corrections are also applied to the standard errors. N.B. When the data comprises both male and female observations the correction is a ratio of progeny mean squares but when only female progeny are measured it is a ratio of sire and female mean squares. The corrections are printed out alongside the respective corrected estimates.

With random mating one expects a zero correlation between sire and dam measurements and an estimate of the offspring on midparent heritability is given by $b^s + b^d$. When the correlation is not zero this heritability estimate would differ from that derived from the regression of offspring on mid-parent means and its variances would be biased down.

Heritabilities computed by offspring-parent correlation are also given, for example a female-sire estimate,

$$HR_{71} = 2A_{71}/[A_{11}(A_{77} + B_{77} + C_{77})]^{1/2}.$$

3. The heritability of the difference of two characters: (see Frankham (1968) for discussion on this parameter when the two characters are the same trait in different sexes) is estimated using P_{qr} in combination with G_{qr}^S only. For traits 5 and 7 the sire estimate of this heritability is

$$HD_{57}^S = \frac{G_{57}^S}{P_{57}} = \frac{G_{77}^S + G_{55}^S - 2G_{75}^S}{P_{77} + P_{55} - 2P_{57}},$$

but with heterogeneity of the genetic and phenotypic variances between the traits this estimate is corrected by

$$\begin{aligned} &= \frac{G_{57}^S - (\sqrt{G_{55}^S} - \sqrt{G_{77}^S})^2}{P_{57} - (\sqrt{P_{55}} - \sqrt{P_{77}})^2} \\ &= \frac{(G_{55}^S G_{77}^S)^{\frac{1}{2}} - G_{57}^S}{(P_{55} P_{77})^{\frac{1}{2}} - P_{57}}, \end{aligned}$$

and only the corrected estimates are printed out.

4. Influence of natural selection: it is possible that some of the difference between heritabilities estimated by sib analysis and those estimated by O-P is due to the differential effect of natural selection on the half-sib covariances ($Cov(HS)$) and the O-P covariances ($Cov(OP)$). For an additive situation James (1966) showed that

$$Cov(HS) \approx \frac{1}{2}(1 - \bar{S}) Cov(OP),$$

where \bar{S} is the coefficient of homeostatic strength. \bar{S} is estimated here from the paternal half-brother and sire-son heritability estimates and will therefore only be printed on a page where an analysis involves one male trait.

(iii) Correlations

1. Sib estimates: of the phenotypic, genetic and environmental correlations (\hat{r}_θ) are computed as the product moment correlation, e.g. those of traits 5 and 7 are given by

$$14 \quad \hat{r}_\theta = \hat{\theta}_{57} / (\hat{\theta}_{55} \hat{\theta}_{77})^{1/2}.$$

The respective standard errors are then

$$\begin{aligned} \text{S.E.}(\hat{r}_{\theta_{57}}) &= \left\{ 2f^2 \hat{r}_{\theta_{57}}^2 \left[J_{\theta_{57}} \right. \right. \\ &+ \frac{a^2 (U_{55} U_{77} + U_{57}^2) / u' + b^2 (V_{55} V_{77} + V_{57}^2) / v' + c^2 (W_{55} W_{77} + W_{57}^2) / w'}{2\hat{\theta}_{57}^2} \\ &- \frac{a^2 U_{55} U_{57} / u' + b^2 V_{55} V_{57} / v' + c^2 W_{55} W_{57} / w'}{\hat{\theta}_{55} \hat{\theta}_{57}} \\ &\left. \left. - \frac{a^2 U_{57} U_{77} / u' + b^2 V_{57} V_{77} / v' + c^2 W_{57} W_{77} / w'}{\hat{\theta}_{57} \hat{\theta}_{77}} \right] / \ell^2 \right\}^{1/2} \end{aligned}$$

where

$$\begin{aligned} J_{\theta_{57}} &= \frac{a^2 U_{55}^2 / u' + b^2 V_{55}^2 / v' + c^2 W_{55}^2 / w'}{4\hat{\theta}_{55}^2} + \frac{a^2 U_{77}^2 / u' + b^2 V_{77}^2 / v' + c^2 W_{77}^2 / w'}{4\hat{\theta}_{77}^2} \\ &+ \frac{a^2 U_{57}^2 / u' + b^2 V_{57}^2 / v' + c^2 W_{57}^2 / w'}{2\hat{\theta}_{55} \hat{\theta}_{77}}, \end{aligned}$$

and where $u' = u+2$, $v' = v+2$ and $w' = w+2$ and f , ℓ , a , b and c are given in Table 6 for the seven $\hat{\theta}$ estimates. When either of the θ variances ($\hat{\theta}_{55}$ and $\hat{\theta}_{77}$ in the above example) are negative or zero the correlation and its standard error are set equal to zero and a statement will be printed out immediately after the listing of the variable names for the problem.

2. The O-P genetic correlation: is computed by the method employing the arithmetic mean of the offspring-parent covariances. No estimate is calculated for variables 5 and 7 as these are the same trait in different sexes. For variables 5 and 6 the sire correlation, for example, is given by

$$\hat{r}_{56}^s = (A_{61} + A_{52}) / 2(A_{51} A_{62})^{1/2}.$$

The standard error for either the sire or dam estimate of the O-P genetic correlation is given by equation (12) of Hammond and Nicholas (1972) and with their $p = 2$ this becomes

$$S.E.(\hat{f}_{56}) = \{R[(k_3 R/2) + (k_3 + k_1 - 1)(1/D' - \hat{f}_{P_{56}} \hat{f}_{56}/C')/2] + (4(\hat{f}_{56}/D' - \hat{f}_{P_{56}}/C')/R) + 2(1 - \hat{f}_{P_{56}}^2/C'^2)]/k_3 d\}^{1/2},$$

where $d = (u-1)$ for the sire estimate, and $d = (v-1)$ for the dam estimate, the appropriate sire or dam estimates of heritabilities or correlations are substituted and $R = 1 - \hat{f}_{56}^2$, $1/D = [(1/HB_5) + (1/HB_6)]/2$ and $C' = (HB_5 \cdot HB_6)^{1/2}$.

When only the O-P analysis option is utilized then

$$S.E.(\hat{f}_{56}) = R[(SE(HB_5) \cdot SE(HB_6))/(HB_5 HB_6)]^{1/2} / 2^{1/2}.$$

Further explanation of the standard errors of all the above correlations and discussion of their usefulness is given by Hammond and Nicholas (1972).

Van Vleck and Henderson (1961) suggest that both \hat{f} and $Var(\hat{f})$ will be biased upwards if the average coefficient of variation of the denominator covariances of \hat{f} is > 0.20 . The estimate of this coefficient of variation is printed out and is computed as, e.g. for traits 5 and 6

$$CV_{56} = [((4 + HB_5^2)/HB_5^2)^{1/2} + ((4 + HB_6^2)/HB_6^2)^{1/2}] / 2u^{1/2}.$$

(iv) Standardized correlated response (SCR)

1. Sib estimates: of SCR utilising sire, dam, and sire plus dam genetic covariances and phenotypic variances are computed. For example, the sire estimate for variables 5 and 6 is given by

$$SCR_{56}^S = (H_{56}^{S H^S})^{1/2} \hat{f}_{G_{56}}^S = G_{56}^S / (P_{55} P_{66})^{1/2},$$

with standard error

$$S.E.(SCR_{56}^S) = \left\{ 2(SCR_{56}^S)^2 \left[\frac{J_{P_{56}}}{\ell_P^2} + (f_G^S)^2 \left[\frac{(a_G^S)^2 (U_{55} U_{66} + U_{56}^2)/u' + (b_G^S)^2 (V_{55} V_{66} + V_{56}^2)/v' + (c_G^S)^2 (W_{55} W_{66} + W_{56}^2)/w'}{2(G_{56}^S)^2 (\ell_G^S)^2} \right] - f_G^S \left[\frac{a_{GP}^S U_{55} U_{56}/u' + b_{GP}^S V_{55} V_{56}/v' + c_{GP}^S W_{55} W_{56}/w'}{P_{55} G_{56}^S \ell_{GP}^S} + \frac{a_{GP}^S U_{56} U_{66}/u' + b_{GP}^S V_{56} V_{66}/v' + c_{GP}^S W_{56} W_{66}/w'}{P_{66} G_{56}^S \ell_{GP}^S} \right] \right\}^{1/2}.$$

2. The O-P estimate: of SCR_{56}^S is

$$SCR_{56}^S = (HB_{51}HB_{61})^{\frac{1}{2}} \hat{f}_{56}^S = (A_{16}+A_{25})/(A_{11}A_{22})^{\frac{1}{2}},$$

and its standard error is

$$S.E.(SCR_{56}^S) = \{[(S^2+2/k_3)(1+\hat{f}_{P56}^2) + ((k_3+k_1-2)(C'^2/D'+S\hat{f}_{P56}^2)/2k_3) + (C'^2(1-4\hat{f}_{P56}^2 S/D')-3S^2)/2]d\}^{\frac{1}{2}},$$

where $S = SCR_{56}^S$ and d , C' and $1/D'$ are as previously defined. This standard error is computed only when a complete analysis is called. The development of the standard errors of the SCR estimates is given by Nicholas (1972).

(c) Partitioning the Phenotypic Variance

Expectations for the heritability estimates have been compiled utilizing Dickerson (1969), Bohidar (1964) and James (1972) and assuming males are the heterogametic sex. These are given in Table 7. Obviously the best estimates of the variance components will be obtained by solving a complete set of simultaneous equations. However, the options available in the program would introduce some difficulties in implementing this procedure, although it is possible to incorporate this for both variance and covariance components. Thus the method used to estimate the relative contributions of each of the components leads to somewhat inefficient estimates, the sum of which is likely to differ from unity. Heritabilities are used in preference to θ 's in partitioning the variance as only the heritabilities have been corrected for inequality of male and female variances. The expectations of the partitioned components are given in Table 8. When options other than the complete analysis with IS=ID=IM=IF are selected some of these components will not be given or will be set equal to ± 99.999999 .

The common (V_{EC}) and within full-sib (V_{EW}) environmental variance (covariance) components, Falconer (1960), p.174, are computed for all analyses from the variance (covariance) components as

$$\begin{aligned} V_{EC} &= \hat{D}_{qr} - \hat{S}_{qr} \\ V_{EW} &= \hat{E}'_{qr} - 2\hat{S}_{qr} \end{aligned}$$

Table 7. Expectations* for the Heritability Estimates

Estimate	Component (V_C) [†]														
	A	D	AA	AD	DD	M	EC	AS	AAS	ASAS	DAS	DS	ADS	DDS	DSDS
1.Sire-son	1		.5												
2.Sire-daughter	1		.5					1.41		1					
3.Dam-son	1		.5			1		1.41		1					
4.Dam-daughter	1		.5			1		1	.5	.5					
5.Paternal $\frac{1}{2}$ brother	1		> .25												
6.Paternal $\frac{1}{2}$ sister	1		> .25					2	.5	1					
7.Dams/S-males	1	1	> .75	> .5	> .25	4	4	2	1	1	.5				
8.Dams/S-females	1	1	> .75	> .5	> .25	4	4	1	1	1.25	.75	2	1	.5	1

* Assuming: Males are the heterogametic sex and the variances are equal in the 2 sexes; only 2 -locus interactions are important; no genotype X environment interaction; no genetic covariance between transmitted and direct maternal effects.

[†] Where subscript C is a combination of: A - additive
D - dominance
M - maternal
S - sex linkage
EC - common environmental

Table 8. Method of Computing Components and their Expectations

Component	Computed as*	Component (V_C) [†]														
		A	D	AA	AD	DD	M	EC	AS	AAS	ASAS	DAS	DS	ADS	DDS	DSDS
a.Additive	$\underline{5} - c/4$	1		$[\underline{.25}]^2$												
b.Dominance	$\underline{7} - (a + .75c + 2di + 4ei)$		1	$[\underline{.5}]$	$\underline{.5}$	$\underline{.25}$	$(4)^3$	4		$\underline{.5}$		$\underline{.5}$				
c.Add.xAdd. ¹	$4(\underline{1} - \underline{5})$			$\underline{1}$												
di Sex linkage	$(\underline{6} - \underline{5})/2$								$\underline{1}$	$\underline{.25}$	$\underline{.5}$					
ii "	$\underline{7} - \underline{8}$								$\underline{1}$							
iii "	$(\underline{3} - \underline{1} - ei)0.707$						$(.71)$		$\underline{1}$		$-.25$	$-.25$	-2	-1	$-.5$	-1
ei Maternal ¹	$\underline{3} - \underline{2}$						$\underline{1}$				$.71$					
ii "	$\underline{4} - \underline{2}$						$\underline{1}$		$-.41$	$\underline{.5}$	$-.5$					

* Underlined digits are from first column of Table 7.

† See Table 7 for explanation.

1 = Set equal to 0.0 if negative.

2 = When no O-P analysis performed estimates will include bracketed value.

3 = When no female offspring estimate will include values in parentheses.

(d) Binomially Distributed Data

Allowance is made in the program for the analysis of binomially distributed data although further development of the program to handle this data would be desirable by those using the option. The binomial variance components for the within dams, dams and sires levels are

$$E'B = [(\sum_{ijl} C/r_{ijl}) + (\sum_{ij} (\sum_l C/r_{ijl})/n_{ij})]/w$$

$$DB = [(\sum_{ij} (\sum_l C/r_{ijl})/n_{ij}) + (\sum_i (\sum_{ij} C/r_{ijl})/n_{i.})]/v$$

$$SB = [(\sum_i (\sum_{ij} C/r_{ijl})/n_{i.}) + ((\sum_{ijl} C/r_{ijl})/n_{...})]/u,$$

where r_{ijl} is the number of events from which the percentage calculated for cell ijl and $C = 0.25$. The variance components are then computed (but not the covariance components) as

$$\hat{E}'_{qr} = W_{qr} - E'B$$

$$\hat{D}_{qr} = (V_{qr} - DB - E'_{qr})/k_1$$

$$\hat{S}_{qr} = (U_{qr} - SB - k_2 D_{qr} - E'_{qr})/k_3.$$

H^s , H^d and H^{sd} are calculated as given previously except 0.25 is added to P_{qr} . See Boggy & Becker (1965) for derivation of the binomial variance components.

- Becker, W.A. (1964) - Manual of Procedures in Quantitative Genetics. Washington State University.
- Bogyo, T.P. & Becker, W.A. (1965) - Estimates of heritability from transformed percentage sib data with unequal subclass numbers. Biometrics, 21: 1001-7.
- Bohidar, N.R. (1964) - Derivation and estimation of variance and covariance components associated with covariance between relatives under sexlinked transmission. Biometrics, 20: 505-21.
- Dickerson, G.E. (1969) - Techniques for research in quantitative animal genetics. In: Techniques and Procedures in Animal Science Research, pp.36-79. American Society of Animal Production publication.
- Falconer, D.S. (1960) - Introduction of Quantitative Genetics. Oliver and Boyd, Edinburgh.
- Frankham, R. (1968) - Sex and selection for a quantitative character in *Drosophila*. II. The sex dimorphism. Aust.J. biol.Sci., 21: 1225-37.
- Gates, C.E. and Shine, C. (1962) - The analysis of variance of the s-stage hierarchal classification. Biometrics, 18: 529-36.
- Hammond, K. and Nicholas, F.W. (1972) - The sampling variance of the correlation coefficients estimated from two-fold nested and offspring-parent regression analyses. Theoret. Appld. Genet., [In Press].
- Hinkleman, K. (1971) - Estimation of heritability from experiments with inbred and related individuals. Biometrics, 27: 183-90.
- James, J.W. (1966) - Correlations between relatives when intermediates are fittest. Aust.J.biol.Sci., 19: 301-6.
- James, J.W. (1972) - Covariances between relatives due to sex-linked genes. Biometrics, [In Press].
- Nadler, J. (1967) - Bivariate samples with missing values. Technometrics, 9: 679-82.
- Nicholas, F.W. (1972) - The sampling variance of the standardized correlated response. [In Preparation].

Sokal, R.R. and Rohlf, F.J. (1969) - Biometry. The Principles and Practice of Statistics in Biological Research. Freeman, San Francisco.

Van Vleck, L.D. and Henderson, C.R. (1961) - Empirical sampling estimates of genetic correlations, Biometrics, 17: 359-71.

(a) Appendix 1

Operating Procedures and Listing for Version 1

(i) Deck structure

Order of control cards, program, and data decks is:-

```

$ID (or as required by system)
$PAUSE DIAL UNITS 0, 1, 2, 3, 4
$IJBØB (or as required by system)
--
--
Source deck NESRG1
--
--
Data deck
--
--
$IJBØB (or as required by system)
--
--
Source deck NESRG2
--
--
$IBSYS (return to system)

```

(ii) Data Deck

Structure of data deck is:-

```

Parameter card type 1 (number of problems)
Parameter card type 2 for problem No.1 (size
of problem and type of analysis)
Parameter card type 3 for problem No.1 (title)
Parameter card(s) type 4 for problem No.1
(variable names)
Data cards for problem No.1
Blank trailer card

Parameter card type 2 for problem No.2
Parameter card type 3 for problem No.2
Parameter card type 4 for problem No.2
Blank trailer card
--
-- etc.

```

(iii) Punching Schedule for Parameter Cards

23

<u>Columns</u>	<u>Symbol</u>	<u>Information</u>
<u>Parameter card type 1</u>		
1-4	NPRØB	Number of problems
<u>Parameter card type 2</u>		
1-6	CHECK(1)	START (sixth column blank)
7-9	I1	Number of pseudo-variables (limit 12)
10	I2	Number of fold (=number of levels -1) (maximum is five-fold, minimum is two-fold)
11	N3	Analysis required 1 = complete problem 2 = nested problem only 3 = O-P problem only
12	N4	On-line debugging option 1 = first observation set will be printed on line for inspection; if correct the program will proceed if the "start" button is pressed 2 = no debugging pause
13-16	N5	Maximum number of sires
17-19	N6	Maximum number of dams per sire
NB: $2 \cdot N5 \cdot (1 + N6) \leq 12,000$		
20	IS	Number of sire variables)
21	ID	Number of dam variables)
22	IM	Number of male offspring) per obser- variables) vation set
23	IF	Number of female offspring) variables)
NB: $\underline{IS} + \underline{ID} + \underline{IM} + \underline{IF} = \underline{I1}$		

All information to be punched right adjustedParameter card type 3

1-72	TITLE(I)	Problem title (alphameric)
------	----------	----------------------------

Operating Procedures and Listing for Version 2

(i) Deck structure

Order of control cards, program, and data decks
is:-

JØBNAM (CM60000, CL100000, T--, P-)

FTN.

RFL (100000)

REDUCE.

LGØ.

7/8/9

--

--

Source deck

--

--

7/8/9

--

--

Data deck

--

--

7/8/9

6/7/8/9

(ii) Data deck

Structure of the data deck is as for Version 1.

(iii) Punching schedule for parameter cards

<u>Columns</u>	<u>Symbol</u>	<u>Information</u>
<u>Parameter card type 1</u>		
1-4	NPRØB	Number of problems
<u>Parameter card type 2</u>		
1-5	ICHEK	START
6	-	Blank column
7-9	I1	Number of pseudo-variables
10	I2	Number of fold (maximum 5-fold, minimum is two-fold)
11	N3	Analysis required 1 = complete problem 2 = nested problem only 3 = O-P problem only

<u>Columns</u>	<u>Symbol</u>	<u>Information</u>
12	N4	Data listing option 1 = listing of all observation sets required 2 = no listing
13-16	N5	Maximum number of sires
17-20	N6	Maximum number of dams per sire
21-23	IS	Number of sire variables)
24-26	ID	Number of dam variables)
27-29	IM	Number of male offspring)per obser- variables)vation set
30-32	IF	Number of female offspring) variables)

Parameter card type 3

1-72	ITLE	Problem title (alphanumeric)
------	------	------------------------------

Parameter card type 4

1-8	NAMVAR(1)	Alphanumeric name of first pseudo- variable
9-16	NAMVAR(2)	Alphanumeric name of second pseudo- variable
17-24	--	--
25-32	etc.	Continue up to column 72 of first card, and as many subsequent cards as required.

(iv) Input of data cards

Subroutine READX is slightly different to that for Version 1. Communication between READX and the calling program is partly via formal parameters in the call statement

```
CALL READX (XID, X)
```

and partly via labelled `COMMON`

```
COMMON/CMBLK1/I1, I2, N3, N4, N5, N6, IS, ID,  
IM, IF, N1, ITLE(9), Y, KPUT
```

(v) Array storage allocation

In Version 2 all variable-length arrays are equivalenced (by means of formal parameter lists in subroutine calls) to a single array in the main program, which is in blank `COMMON`. When the program deck is

compiled and loaded into store, only one word of blank CØMMØN is dimensioned. After control is passed to the program and it has read the parameter cards, the number of words of blank CØMMØN required for STEP1 (originally program NESRG1 of Version 1) is calculated, and the amount of central store occupied by the program is increased sufficiently to allow all arrays used by STEP1 to occupy blank CØMMØN. When STEP1 is completed, the number of words of blank CØMMØN required for STEP2 (originally program NESRG2 of Version 1) is calculated, and central store limit is again changed.

Either STEP1 or STEP2 may require the greater amount of store, depending on the data structure. There are thus two restrictions on problem size

$$\text{LPRØG} + 48 + \underline{\text{I1}}(4 + \underline{\text{I2}}) + 6\underline{\text{I2}} + \underline{\text{I1}}^2(45 + 3\underline{\text{I2}}) + 2(\underline{\text{N5}} + \underline{\text{N5}} * \underline{\text{N6}}) \leq 98304$$

and

$$\text{LPRØG} + 54 + \underline{\text{I1}} + 2\underline{\text{I2}} + \underline{\text{I1}}^2(114 + 3\underline{\text{I2}}) \leq 98304$$

where LPRØG is the field length of the program up to first word of blank CØMMØN. LPRØG will be approximately 16200, but will vary depending on the length of the user-supplied READX subroutine.

Subroutine GETFL is used to determine LPRØG and to vary the field length of the program during execution.
A

CALL GETFL (LPRØG)

statement returns to the calling program the field length of the executing program up to the first word of blank CØMMØN. A

CALL SETFL (LFIELD)

statement (SETFL is a multiple entry point to GETFL) changes the field length of the executing program to LFIELD (in the same way as an RFL control card under SCØPE).

(vi) Compatibility

Users wishing to convert Version 2 of NESREG to other computers should note that subroutine GETFL will not be transferrable. If the proposed computer is time-shared a facility equivalent to GETFL should be available, and should be used, since the user pays for number of store cells occupied as well as time of occupancy, in such a machine. If the proposed computer is not time-shared, array A(1) in blank CØMMØN in the main program should be re-dimensioned to use all the store available, and a dummy subroutine GETFL

which does nothing, should be substituted. In either case Version 2 will only be readily transferrable to a computer in which fixed and floating point word lengths are equal, since both integer and real arrays in the subroutines are equivalenced to a single real array A(1) in the main program.

Listing of Version 2

(c) Appendix 3

Operating Procedures and Listing for Version 3

(i) Deck structure

Order of control cards, program, and data decks is as for Version 2.

(ii) Data deck

Structure of the data deck is as for Versions 1 and 2, except that the data cards and blank trailer card may be either in the data deck, as before, or stored on a separate logical unit such as a magnetic tape.

(iii) Punching schedule for parameter cards

As for Version 2, with the addition of three extra parameters on parameter card type 2:

<u>Columns</u>	<u>Symbol</u>	<u>Information</u>
33-34	ICYC	Single pass or cyclic operation 1 = single pass, all variables and pairs of variables 2 = cyclic, single variables only, <u>i.e.</u> only heritabilities required 3 = cyclic, single variables and pairs 4 = cyclic, pairs of variables only, <u>i.e.</u> only correlations required (see section (vii) of this appendix)
35-36	LUI	Logical unit number for input of data, Punch 05 for card input, or 07 otherwise
37-38	LUS	Logical unit number of scratch unit used to store data during cyclic operation. Unit LUS is rewound every cycle. Punch 04 for cyclic mode, or 00 for single pass mode

(iv) Input of data cards or tape

30

In cyclic mode Version 3 copies the data cards (LUI=05) or tape (LUI=07) onto scratch unit LUS=04 so that they may be rewound during cyclic operation. Thus, in cyclic mode, subroutine READX must be written to read from unit LUS. In single pass mode, Version 3 reads the data directly from cards (LUI=05) or tape (LUI=07). Thus, in single pass mode, subroutine READX must be written to read from unit LUI. Subroutine READX must supply different observation sets to the main program, depending on which cycle (which trait or pair of traits) is currently being analysed. This information is communicated to READX via a labelled COMMON block

```
COMMON/CMBLK7/M11, MIS, MID, MIM, MIF, M1, M2,  
ICYC, LUI, LUS
```

where

```
M11 = maximum number pseudo-variables (total over  
      all cycles)  
MIS = maximum number of sire variables  
MID = maximum number of dam variables  
MIM = maximum number of male offspring variables  
MIF = maximum number of female offspring variables  
M1  = variable number for first variable of a pair  
M2  = variable number for second variable of a pair
```

```
if M1 = M2 supply 4 data items - sire, dam,  
male and female
```

```
if M1 ≠ M2 supply 8 data items - 2 sire, 2  
dam, 2 male and 2 female
```

```
ICYC = cycling option  
LUI  = unit number for input of data  
LUS  = unit number for scratch unit
```

Subroutine READX must also be programmed to check for missing observations, and to supply only complete observation sets, with sire, dam, male, and female observations all present for the pair of traits specified by M1 and M2 of the current cycle. Or, if an analysis is to be performed on Type 2 unbalanced data, READX must supply observation sets which are as complete as the analysis requires.

(v) Array storage allocation

As for Version 2 when in single pass mode. In cyclic mode field length is set once, before cycling starts, to

the greater of the two requirements given for Version 2, taking $I1 = 1$ if $ICYC = 2$ and $I1 = 2$ if $ICYC = 3$ or 4 .

(vi) Compatibility

As for Version 2. A 32K machine should handle any size of problem if cyclic mode is used.

(vii) Single pass or cyclic mode

Single pass mode ($ICYC = 1$) does exactly the same calculations as Version 2.

Cyclic mode allows large sets of Type 3 unbalanced data to be processed, and the degrees of freedom for any trait or pair of traits may be different to that for every other trait or pair of traits. Therefore, every trait or pair of traits must be analysed by a separate run, the same data set being re-read each run and the appropriate trait or pair of traits extracted. In the notation of section III (iii), this is the case where every element of the A , B , and C (or U , V and W) matrices is estimated with different number of degrees of freedom. It is not advisable (Nadler, 1967) to use the elements of such matrices to estimate correlation coefficients. The degrees of freedom for the covariance in the numerator of a correlation coefficient should be the same as those of the variances in the denominator. The only way to achieve this is to re-estimate subsets of the A , B and C matrices for each pair of traits, using only those observation sets where the observation for both traits of the pair is present. This is done automatically by the cyclic mode option, if the user supplies an appropriate READX subroutine (see section (iv) of this appendix).

As $ICYC = 2$ or 4 produces subsets of the output produced by $ICYC = 3$, only the latter will be described. The output will appear as if a number of single variable problems ($I1 = 4$, $IS = ID = IM = IF = 1$) were processed, followed by a number of two variable problems ($I1 = 8$, $IS = ID = IM = IF = 2$). Each single variable problem will furnish the appropriate heritability and variance component estimates, for a variable, based on all the observation sets complete for that variable. Each two variable problem will furnish the appropriate correlations and covariance component estimates, for a pair of variables based on all observation sets complete for both variables. Heritability and variance component estimates appearing in the two-variable problems will be based on the same or fewer degrees of freedom as those furnished by the single-variable problems.

Version 3 allows very heterogeneous data to be processed almost automatically. The dangers of misinterpretation should be appreciated. If missing observations are caused by some systematic event (such as death or culling of animals) genetic parameter estimates could be greatly biased.

Listing of Version 3

Fortran listings omitted

Neville Jackson

20 Oct 2021

1 Note on acces to program code

The listings of fortran program code have been onitted from this document.
The code for versions 2 and 3 of nesreg is available at

<https://github.com/nevillejackson>

Go to the *Fortran* repository and look in the *nesreg2* and *nesreg3* subdirectories.

(d) Appendix 4

Listing of Test Data and its Analysis

The test data has been taken from a *Drosophila* experiment. Three traits, fourth, fifth and total abdominal chaeta number are given for sires, dams, male and female progeny respectively, and the data has been arranged into a five-fold nested problem. Only two traits, the fourth and total abdominal chaeta number, have been used in the test problem. The READX subroutines listed in Appendices 1, 2 and 3 have been written for this test problem.

```

1
START 008512.101 32222
***** TEST DATA OF NESREG *****
SIRE 4TH SIRE ABD DAM 4TH DAM ABD MALE 4TH MALE ABD
FEML 4TH FEML ABD
111246737070714111021091019101121 TSD10001
111246737070714111021091120121729 TSD10002
111246736070714091019070714111021 TSD10003
111246736070714091019070714111021 TSD10004
111246736070714091019080816111425 TSD10005
111246736070714091019090918071219 TSD10006
111247739070714091221060612111122 TSD10007
111247739070714091221070613101222 TSD10008
111247739070714091221060814091422 TSD10009
111247740070714111021050712071118 TSD10010
111247740070714111021060612091221 TSD10011
111247740070714111021091019071116 TSD10012
111247741070714091120070916071219 TSD10013
111247741070714091120060713101121 TSD10014
111247741070714091120090716081018 TSD10015
111247741070714091120090716081018 TSD10016
11124874200611070714070512081119 TSD10017
11124874200611070714060511060915 TSD10018
11124874200611070714080614111223 TSD10019
11124874300611101222060713110020 TSD10020
11124874300611101222060612121022 TSD10021
11124874300611101222050712111223 TSD10022
1112487440061111021080816101121 TSD10023
1112487440061111021060612071118 TSD10024
1112487440061111021080614131427 TSD10025
11124974500614091221060612090918 TSD10026
11124974500614091221090716131225 TSD10027
11124974500614091221080715101222 TSD10028
11124974600614111223090716141024 TSD10029
11124974600614111223100919121224 TSD10030
11124974600614111223090615141024 TSD10031
11124974700614141327060511081321 TSD10032
11124974700614141327090716110020 TSD10033
11124974700614141327060715111324 TSD10034
123250746060713111223060715090918 TSD10035
123250746060713111223060614070613 TSD10036
123250746060713111223080816111324 TSD10037
123250749060713101222060713070815 TSD10038
123250749060713101222070411101121 TSD10039
123250749060713101222070510111122 TSD10040
123250750060713121123060511101121 TSD10041
123250750060713121123050611100919 TSD10042
1232507500607131211230506111091221 TSD10043
123251751060612101020080513080816 TSD10044
123251751060612101020061016421127 TSD10045
123251751060612101020070512111021 TSD10046
123251752060612151631070714101121 TSD10047
123251752060612151631080715091221 TSD10048
123251752060612151631080917101626 TSD10049
123251753060612081220050611081018 TSD10050
123251753060612081220060612100919 TSD10051
123251753060612081220070613101121 TSD10052
124252754080816091019110815131225 TSD10053
124252754080816091019060614091019 TSD10054
124252754080816091019120921100919 TSD10055
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124253758050712121325070815081018 TSD10067
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124253759050712121325070815111223 TSD10069
TSD10070
TSD10071
TSD10072

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 235255763070714121022060713060915
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 TSD10102
 TSD10103
 TSD10104
 TSD10105
 TSD10106
 TSD10107

1
 START 008511 101 3 2 2 2 2
 ***** TEST DATA OF NESREG *****
 SIRE 1STSIRE 2ND DAM 1ST DAM 2NDMALE 1STMALE 2NDFEML 1STFEML 2ND
 111246737070714111021091019101121
 111246737070714111021091120121729

DATA AS FOR VERSION 1

236257770090918091019060713091019
 236257770090918091019070815091120

TSD20001
 TSD20002
 TSD20003
 TSD20004
 TSD20005
 TSD20006

TSD20104
 TSD20105
 TSD20106

1
 START 012513 101 3 3 3 3 3 3 5 4
 ***** TEST DATA OF NESREG *****
 SIRE 1STSIRE 2ND SIRE 3RD DAM 1ST DAM 2ND DAM 3RDMALE 1STMALE 2NDMALE 3RDTSD030004
 FEML 1STFEML 2NDFEML 3RD
 111246737070714111021091019101121
 111246737070714111021091120121729

DATA AS FOR VERSION 1

236257770090918091019060713091019
 236257770090918091019070815091120

TSD30001
 TSD30002
 TSD30003
 TSD30004
 TSD30005
 TSD30006
 TSD30007

TSD30105
 TSD30106
 TSD30107

PROGRAM NESREG
ANALYSIS OF QUANTITATIVE VARIATION BY NESTED ADV AND/OR Q-P REGRESSION

NUMBER OF PROBLEMS = 1

PROBLEM NO 1
ERRORS AND/OR COMMENTS FOR NESRG1
MERIT. OF DIF. FOR CHARS. SAND TCANNOT BE CALCULATED
CORRELATION NO 1 FOR CHARACTERS SAND TCANNOT BE CALCULATED
CORRELATION NO 2 FOR CHARACTERS SAND SCANNOT BE CALCULATED
CORRELATION NO 3 FOR CHARACTERS SAND SCANNOT BE CALCULATED
MERIT. OF DIF. FOR CHARS. SAND TCANNOT BE CALCULATED
CORRELATION NO 1 FOR CHARACTERS SAND TCANNOT BE CALCULATED
CORRELATION NO 2 FOR CHARACTERS SAND SCANNOT BE CALCULATED
CORRELATION NO 3 FOR CHARACTERS SAND SCANNOT BE CALCULATED
MERIT. OF DIF. FOR CHARS. TAND SCANNOT BE CALCULATED
CORRELATION NO 1 FOR CHARACTERS TAND SCANNOT BE CALCULATED
CORRELATION NO 2 FOR CHARACTERS TAND SCANNOT BE CALCULATED
CORRELATION NO 3 FOR CHARACTERS TAND SCANNOT BE CALCULATED

PROBLEM NO 1 ***** TEST DATA OF NESREG *****
NO. OF VARIABLES = 8
NO. OF LEVELS = 5
THE VARIABLES ARE THE FOLLOWING
VARIABLE NO. 1 IS STRE 4TH
VARIABLE NO. 2 IS STRE ABD
VARIABLE NO. 3 IS DAM 4TH
VARIABLE NO. 4 IS DAM ABD
VARIABLE NO. 5 IS PALE 4TH
VARIABLE NO. 6 IS PALE ABD
VARIABLE NO. 7 IS FEPL 4TH
VARIABLE NO. 8 IS FEPL ABD
ERRORS AND/OR COMMENTS FOR NESRG2

PROBLEM NO. 1
VARIABLES 5 AND 5

PARENT MEAN = 0.676238E 01 P-P CORLN. = 0.0104
PROGENY MEAN = 0.735644E 01

ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	0.47180176E 00	0.47180176E 00	0.82234042E 00
2	1	0.57373047E 00	0.57373047E 00	0.23988363E 00
3	3	0.71751098E 01	0.23917033E 01	0.36506889E 00
4	6	0.39525330E 02	0.65875550E 01	0.29725178E 01
5	22	0.48755371E 02	0.22161532E 01	0.13178861E 01
6	67	0.11266699E 03	0.16615969E 01	0.
SIRES REGRESSION DEVIATIONS	1	0.17246244E 02	0.17246244E 02	0.38705007E 01
	5	0.22279086E 02	0.44558172E 01	0.20106089E 01
DAMS/REGRESSION DEVIATIONS	1	0.12110015E 00	0.12110015E 00	0.52290353E-01
	21	0.48634271E 02	0.23159177E 01	0.13772133E 01
TOTAL	100	0.20916833E 03		

VARIANCE (COVARIANCE)

	PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.16815969E 01	0.14010302E 01	0.98108176E 00 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.17982017E 00	0.71928067E 00	0.13219565E 01 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.52069494E 00	0.20827798E 01	0.63971584E 00 (SIRE)

HERITABILITIES AND STD. ERRORS

(SIRE)	(DAM)	(S+D)
0.87434167E 00	0.67091212E 00	0.30195082E 00
0.87991012E 00	0.29619889E 00	0.58814623E 00
0.58591652E 00		0.35869111E 00

OF O-P REGRESSION

HOMEOSTATIC COEF. (=0.0 IF NO NAT. SEL.) = 0.63284263E-02

O-P CORLN. 0.58591652E 00

O-P CORLN. 0.54779805E-01

COMMON ENVIR. VAR. (CCVAR.) -0.34087478E 00

W/IN FS ENVIR. VAR. (COVAR.) 0.64020701E 00

COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS. (1) = 2.97273 (2) = 2.96544 (3) = 8.39784

PROBLEM NO. 1
VARIABLES 5 AND 6
ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	0.24339600E 01	0.24339600E 01	0.18582479E 01
2	1	0.13098145E 01	0.13098145E 01	0.24504803E 00
3	3	0.16035401E 02	0.53451334E 01	0.50857451E 00
4	6	0.63060181E 02	0.10510030E 02	0.32474834E 01
5	22	0.71199951E 02	0.32363614E 01	0.15058032E 01
6	67	0.14400037E 03	0.21492592E 01	0.
TOTAL	100	0.29803967E 03		

VARIANCE (COVARIANCE)

	PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.21492592E 01	0.24642901E 01	0.91711410E 00 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.36569189E 00	0.14627675E 01	0.14178754E 01 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.86645316E 00	0.34658127E 01	0.41572511E 00 (SIRE)
DIFFERENCE OF VARIABLES 5 AND 6	HERIT. SIRE 0.19009729E 00	0.11955624E 01	0.22727317E 00

CORRELATIONS AND STD. ERRORS

(SIRE) (DAM) (S+D)

OF SIB ANALYSIS

GENETIC	0.96825305E 00	0.56223709E-01	0.11282636E 01	0.24701069E 00	0.10103749E 01	0.53047761E-01
ENVIRONMENTAL	0.43198033E 00	0.81760722E 00	0.67311360E 00	0.16994922E 00	0.59732984E 00	0.24329095E 00
PHENOTYPIC					0.84977297E 00	0.34386782E-01
S-C-R.	0.67098546E 00	0.54019868E 00	0.36760477E 00	0.36861198E 00	0.61929511E 00	0.26360715E 00

OF O-P REGRESSION

SIRE GENETIC	0.10530582E 01	0.51755604E-01	C-V.(DEN.COVS.) = 0.87774108E 00
S-C-R.	0.11342653E 01	0.24819926E 00	
DAMS GENETIC		0.13188431E 01	0.10141945E 01 C-V.(DEN.COVS.) = 0.47313591E 01
S-C-R.		0.13895352E 00	0.15969530E 00

COMMON ENVIR. VAR. (COVAR.) -0.50076128E 00
W/IN FS ENVIR. VAR. (COVAR.) 0.41635286E 00

COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 2.97273 (2) = 2.96544 (3) = 8.39784

PROBLEM NO. 1
VARIABLES 5 AND 7
ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	-0.16491699E 01	-0.16491699E 01	-0.90680269E 00
2	1	0.18186646E 01	0.18186646E 01	-0.47657408E 01
3	3	-0.11448364E 01	-0.38161214E 00	-0.13437257E 00
4	6	0.17039734E 02	0.28399557E 01	0.32242871E 01
5	22	0.19377625E 02	0.88080111E 00	0.23924207E 01
6	67	0.24666931E 02	0.36816315E 00	0.
TOTAL	100	0.60108948E 02		

VARIANCE (COVARIANCE)

	GENETIC	PHENOTYPIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.36816315E 00	0.77405256E 00	-0.37726273E-01 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.17244702E 00		0.68978807E 00 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.23344239E 00		0.93376957E 00 -0.98829165E-01 (SIRE)
DIFFERENCE OF VARIABLES 5 AND 7	HERIT. SIRE 0.	0.35576163E 01	0.

CORRELATIONS AND STD. ERRORS

	(SIRE)	(DAM)	(S+D)
GENETIC	0.	0.74341162E 00	0.95432118E 00
ENVIRONMENTAL	-0.77243971E-01	0.45321832E 00	-0.25566711E-01
PHENOTYPIC		0.14763554E-01	0.30320987E 00
S.C.R.	0.36577380E 00	0.27020200E 00	0.31798791E 00

OF SIB ANALYSIS

COMMON ENVIR. VAR. (CCVAR.)	-0.60995374E-01
W/IN FS ENVIR. VAR. (COVAR.)	-0.98721638E-01
COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) =	2.97273
(2) =	2.96544
(3) =	8.39784

PROBLEM NO. 1
VARIABLES 5 AND 8
ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	-0.29721680E 01	-0.29721680E 01	-0.66159447E 00
2	1	0.44924317E 01	0.44924317E 01	0.14381399E 02
3	3	0.9313379E 00	0.31044597E 00	0.78692263E-01
4	6	0.23817383E 02	0.39695638E 01	0.42031039E 01
5	22	0.20777588E 02	0.94443581E 00	0.26003763E 01
6	67	0.24333863E 02	0.36319198E 00	0.
TOTAL	100	0.71386231E 02		

VARIANCE (COVARIANCE)			
	PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.36319198E 00	0.11116442E 01	-0.19273016E 00 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.19552545E 00	0.78210180E 00	-0.27858936E-01 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.36039668E 00	0.14415867E 01	-0.35770746E 00 (SIRE)
DIFFERENCE OF VARIABLES 5 AND 8	HERIT. SIRE -0.10155898E 00	0.64223175E 01	-0.65224403E 00

CORRELATIONS AND STD. ERRORS

	(SIRE)	(DAM)	(S+D)
OF SIB ANALYSIS			
GENETIC	0.12923642E 01	0.16274239E 01	0.
ENVIRONMENTAL	-0.16746683E 00	0.46508071E 00	-0.70101614E-01
PHENOTYPIC			0.25902514E 00
S.C.R.	0.34702941E 00	0.31751110E 00	0.22253108E 00
		0.18935838E 00	0.26919390E 00
		0.28877527E 00	0.17996106E 00

COMMON ENVIR. VAR. (CCVAR.) -0.16487122E 00
W/IN FS ENVIR. VAR. (COVAR.) -0.35760137E 00
COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 2.97273 (2) = 2.96544 (3) = 8.39784

PROBLEM NO. 1
VARIABLES 6 AND 6

PARENT MEAN = 0.138812E 02
PROGENY MEAN = 0.145545E 02
P-P CORLN. = 0.0386

ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	0.12556889E 02	0.12556889E 02	0.41989550E 01
2	1	0.29904789E 01	0.29904789E 01	0.16180479E 00
3	3	0.55446045E 02	0.18482015E 02	0.96399049E 00
4	6	0.11503442E 03	0.19172404E 02	0.30619033E 01
5	22	0.13775513E 03	0.62615967E 01	0.13838115E 01
6	67	0.30316773E 03	0.45248914E 01	0.
SIRE REGRESSION DEVIATIONS	1	0.58674073E 02	0.58674073E 02	0.52052616E 01
	5	0.56360351E 02	0.11272070E 02	0.18001910E 01
DAMS/S REGRESSION DEVIATIONS	1	0.10877763E 02	0.10877763E 02	0.18004239E 01
	21	0.12687738E 03	0.60417791E 01	0.13352319E 01
TOTAL	100	0.62695068E 03		

VARIANCE (COVARIANCE)

	PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.45248914E 01	0.42442324E 01	0.24027751E 01 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.58421279E 00	0.23368512E 01	0.33564657E 01 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.15379034E 01	0.61316137E 01	0.14477629E 01 (SIRE)

HERITABILITIES AND STD. ERRORS

(SIRE)	(DAM)	(S+D)
0.92547114E 00	0.69903561E 00	0.39775492E 00
0.13185185E 01	0.39591420E 00	0.63851776E 00
0.64972923E 00		0.37158510E 00
HOMEOSTATIC COEF. (+0.0 IF NO NAT. SEL.) = 0.29809773E 00		
O-P CORLN. 0.24591897E 00		
O-P CORLN. 0.31413657E 00		
COMMON ENVIR. VAR. (COVAR.)		
W/IN FS ENVIR. VAR. (COVAR.)		
COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 2.97273 (2) = 2.96544 (3) = 8.39784		
CORRECTION APPLD. = 0.99340376E 00		

PROBLEM NO. 1
VARIABLES 6 AND 7
ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	-0.85079346E 01	-0.85079346E 01	-0.20491283E 01
2	1	0.41519776E 01	0.41519776E 01	-0.69046507E 00
3	3	-0.18039917E 02	-0.60133056E 01	-0.12432478E 01
4	6	0.29020630E 02	0.48367716E 01	0.25142770E 01
5	22	0.42321900E 02	0.19237227E 01	0.40701190E 01
6	67	0.31667237E 02	0.47264532E 00	0.
TOTAL	100	0.80613892E 02		

VARIANCE (COVARIANCE)

	GENETIC	PHENOTYPIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.47264532E 00	0.13080798E 01	-0.36278923E 00 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.48813001E 00		0.19525200E 01 -0.50361470E 00 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.34730453E 00		0.13892181E 01 -0.22210179E 00 (SIRE)
DIFFERENCE OF VARIABLES 6 AND 7	HERIT. SIRE 0.	0.59126636E 01	0.

CORRELATIONS AND STD. ERRORS

	(SIRE)	(DAM)	(S+D)
GENETIC	0.	0.11674622E 01	0.11285568E 01
ENVIRONMENTAL	-0.11539218E 00	0.54051392E 00	-0.15710188E 00
PHENOTYPIC		-0.20052899E 00	0.30674333E 00
S-C-R.	0.32577017E 00	0.35120924E 00	0.39181702E 00

COMMON ENVIR. VAR. (COVAR.) 0.14082548E 00
W/IN FS ENVIR. VAR. (COVAR.) -0.22196374E 00
COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS {1} = 2.97273 {2} = 2.96544 {3} = 8.39784

PROBLEM NO. 1
VARIABLES 6 AND 8
ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	-0.15333496E 02	-0.15333496E 02	-0.14950250E 01
2	1	0.10256348E 02	0.10256348E 02	-0.48679027E 02
3	3	-0.63208008E 00	-0.21069336E 00	-0.27629852E-01
4	6	0.45753418E 02	0.76255696E 01	0.28979956E 01
5	22	0.57889161E 02	0.26313255E 01	0.29712956E 01
6	67	0.59333985E 02	0.88558185E 00	0.
TOTAL	100	0.15726733E 03		
VARIANCE (COVARIANCE)				
		PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)		0.88558185E 00	0.23649377E 01	-0.29688702E 00 (S+D)
VARIANCE COMPONENT 2 (DAM)		0.58725321E 00		0.23490128E 01 -0.28892457E 00 (DAM)
VARIANCE COMPONENT 1 (SIRE)		0.59521566E 00		0.23808626E 01 -0.30510814E 00 (SIRE)
DIFFERENCE OF VARIABLES 6 AND 8		HERIT. SIRE -0.96005177E-01	0.96626802E 01	-0.92766732E 00

CORRELATIONS AND STD. ERRORS

	(SIRE)	(DAM)	(S+D)
OF SIB ANALYSIS			
GENETIC	0.12419544E 01	0.14306459E 01	0.
ENVIRONMENTAL	-0.94950974E-01	0.50421508E 00	-0.54823875E-01
PHENOTYPIC			0.29310288E 00
S.C.R.	0.34508302E 00	0.33396986E 00	-0.69002622E-01
			0.28175997E 00
			0.29974396E 00
			0.96316405E-01
		0.34046670E 00	0.34277486E 00
		0.29921708E 00	0.18123036E 00

COMMON ENVIR. VAR. (COVAR.) -0.79624578E-02
W/IN FS ENVIR. VAR. (COVAR.) -0.30484948E 00
COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 2.97273 (2) = 2.96544 (3) = 8.39784

PROBLEM NO. 1
VARIABLES 7 AND 7

PARENT MEAN = 0.106436E 02
PROGENY MEAN = 0.952475E 01
P-P CORLN. = 0.0104

ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	0.57644043E 01	0.57644043E 01	0.99995764E 00
2	1	0.57644043E 01	0.57644043E 01	0.88881081E 00
3	3	0.19457398E 02	0.64857991E 01	0.21471678E 01
4	6	0.18123780E 02	0.30206299E 01	0.89708393E 00
5	22	0.74077637E 02	0.33671653E 01	0.13590336E 01
6	67	0.16600037E 03	0.24776174E 01	0.
SIRE REGRESSION DEVIATIONS	1	0.31676939E 01	0.31676939E 01	0.10589983E 01
	5	0.14956085E 02	0.29912171E 01	0.88834874E 00
DAMS/S REGRESSION DEVIATIONS	1	0.10020263E 01	0.10020263E 01	0.28795589E 00
	21	0.73075610E 02	0.34797910E 01	0.14044908E 01
TOTAL	100	0.28918824E 03		

VARIANCE (COVARIANCE)

	PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.24776174E 01	0.51646252E 00	0.22193861E 01 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.29923631E 00	0.11969452E 01	0.18791447E 01 (DAM)
VARIANCE COMPONENT 1 (SIRE)	-0.41005038E-01	-0.16402014E 00	0.25589038E 01 (SIRE)

HERITABILITIES AND STD. ERRORS

(SIRE)	(DAM)	(S+D)
-0.59952196E-01	0.31269696E 00	0.52113926E 00
0.55689847E 00	0.51539430E 00	0.18877599E 00
0.22152461E 00	0.51539430E 00	0.22801194E 00
	0.51539430E 00	0.14767717E 01
	0.51539430E 00	0.14767717E 01

O-P CORLN. 0.22152461E 00
O-P CORLN. 0.12901531E 00
O-P CORLN. 0.12920918E 00

PRELIMINARY PARTITIONING OF PHEN. VARIANCE

ADDITIVE	0.86877323E 00
DOMINANCE	-0.58352774E 00
ADD. * ADD.	0.22273779E-01
SEX LINK.	0.
MAT. EFFECT	0.
	-0.135555336E 00
	-0.58301004E 00

COMMON ENVIR. VAR. (CCVAR.) 0.34024134E 00
W/IN FS ENVIR. VAR. (COVAR.) 0.25596275E 01

COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 2.97273 (2) = 2.96544 (3) = 8.39784

PROBLEM NO. 1
VARIABLES 7 AND 8
ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	0.10388916E 02	0.10388916E 02	0.72954670E 00
2	1	0.14240234E 02	0.14240234E 02	0.42257480E 01
3	3	0.10109619E 02	0.33698731E 01	0.74974199E 00
4	6	0.26968262E 02	0.44947103E 01	0.13049192E 01
5	22	0.75777588E 02	0.34444358E 01	0.10489838E 01
6	67	0.22000073E 03	0.32835930E 01	0.
TOTAL	100	0.35748535E 03		

VARIANCE (COVARIANCE)

	GENETIC	PHENOTYPIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.32835930E 01	0.34628109E 01	0.31043750E 01 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.54106143E-01		0.21642457E 00 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.12511180E 00		0.50044725E 00 (SIRE)
DIFFERENCE OF VARIABLES 7 AND 8	HERIT. SIRE 0.	0.19270361E 01	0.

CORRELATIONS AND STD. ERRORS

	(SIRE)	(DAM)	(S+D)
GENETIC	0.	0.	0.
ENVIRONMENTAL	0.70983162E 00	0.71359840E-01	0.75073850E 00
PHENOTYPIC			0.75988618E-01
S-C.R.	0.11306147E 00	0.27527367E 00	0.78232118E 00
		0.48894823E-01	0.80978138E-01
		0.40602148E 00	0.19424157E 00

OF O-P REGRESSION

	C.V. (DEN.COVS.)	C.V. (DEN.COVS.)
SIRE GENETIC	0.12605357E 01	0.48039624E 00
S.C.R.	0.28265448E 00	0.35225616E 00
DAMS GENETIC	0.13424729E 01	0.45729084E 00
S.C.R.	0.34423944E 00	0.16711558E 00
		C.V. (DEN.COVS.) = 0.20876565E 01

COMMON ENVIR. VAR. (CCVAR.) -0.71005642E-01
W/IN FS ENVIR. VAR. (COVAR.) 0.30333694E 01

COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 2.97273 (2) = 2.96544 (3) = 8.39784

PROBLEM NO. 1
VARIABLES 8 AND 8
PARENT MEAN = 0.220099E 02
PROGENY MEAN = 0.204059E 02
P-P CORLN. = 0.0386

ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	1	0.18723145E 02	0.18723145E 02	0.53225896E 00
2	1	0.35176758E 02	0.35176758E 02	0.10745053E 02
3	3	0.98212890E 01	0.32737630E 01	0.44007833E 00
4	6	0.44634277E 02	0.74390462E 01	0.12033881E 01
5	22	0.1359854E 03	0.61817516E 01	0.83167735E 00
6	67	0.49800244E 03	0.74328722E 01	0.
SIRE REGRESSION DEVIATIONS	1	0.59999999E 00	0.59999999E 00	0.68128744E-01
	5	0.44034277E 02	0.88068553E 01	0.14246537E 01
DAMS/S REGRESSION DEVIATIONS	1	0.46123243E 02	0.46123243E 02	0.10777023E 02
	21	0.89875292E 02	0.42797758E 01	0.57579031E 00
TOTAL	100	0.74235644E 03		

VARIANCE (COVARIANCE)

	PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.74328722E 01	-0.54303049E 00	0.77043875E 01 (S+D)
VARIANCE COMPONENT 2 (DAM)	-0.42086629E 00	-0.16834651E 01	0.82746045E 01 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.14935105E 00	0.59740423E 00	0.71319992E 01 (SIRE)

HERITABILITIES AND STD. ERRORS

(SIRE)	(DAM)	(S+D)
0.83420534E-01	0.27439024E 00	-0.75827875E-01
0.21405156E 00	-0.23507628E 00	0.20300896E 00
0.59468558E-01	0.74217270E 00	

OF SIB ANALYSIS
OF O-P REGRESSION
CORRECTION APPLD. = 0.16053867E 01

O-P CORLN. 0.59468558E-01
O-P CORLN. 0.53944224E 00

PRELIMINARY PARTITIONING OF PHEN. VARIANCE

ADDITIVE	0.53242378E 00
DOMINANCE	-0.14874711E 01
ADD. * ADD.	0.15721895E 01
SEX LINK.	0.
MAT. EFFECT	0.31867411E-01
	0.29559479E 00

COMMON ENVIR. VAR. (CCVAR.) -0.57021733E 00
W/IN FS ENVIR. VAR. (CCVAR.) 0.71341701E 01
COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 2.97273 (2) = 2.96544 (3) = 8.39784

(e) Appendix 5

Some Examples for Type 2 (See Table 1,
p.2) Unbalanced Data

There are a number of possible types of type 2 unbalanced data and the program has been checked for only some of these combinations. Five examples from Becker (1964) were tested. NESREG gives correct values for every parameter that can be estimated from these examples, but several misleading values are also printed (a line has been ruled through these in the following listing). The user is urged to gain experience from the Becker examples. A listing of the required parameter cards, data cards, and READX subroutine, together with the output given by NESREG, is included in this Appendix. A brief comment on the method of setting up each example follows.

NB: I2 should never be less than 2.

(i) Paternal half-sib analysis (Becker, p.5)

Data punched with dam and progeny identifications the same. Note that I2 = 2 (3 levels). A dummy dam identification is included to make up 3 levels. Set N3 = 2.

Coding the problem this way, implies that every progeny has a separate dam. This is a basic assumption of "half-sib" analysis. The method of coding for NESREG highlights this assumption, and discourages use of half-sib analysis in inappropriate cases or where the dams are simply not identified.

(ii) Full-sib analysis - one sex of progeny (Becker, p.10)

No difficulties in coding this problem.

Set N3 = 2.

Standard errors of heritability estimates given by NESREG for (full or half) sib analyses do not agree with Becker (1964), because Becker's formulae use the degrees of freedom of a mean square, while NESREG adds 2 to the same, to allow for using an estimate in place of a known mean square.

(iii) Regression of offspring mean on sire (Becker, p.27)

Data punched with sire and dam identifications the same. Use can punch progeny means or write READX to read individual progeny data and calculate means. Set N3 =

3 (O-P problem only) - sib analysis is misleading when both dam and progeny degrees of freedom are zero. ³⁵

- (iv) Intra-sire regression of offspring mean on dam
(Becker, p.30)

Data punched with dam and progeny identifications the same. Can punch progeny means or write READX to calculate means from individual data. Set N3 = 1 or 3. This problem is coded in a similar way to the half-sib problem.

- (v) Intra-sire regression of offspring on repeated dam (Becker, p.33)

This problem is coded in a similar way to the full-sib problem. Set N3 = 1 or 3.

Listing of test examples from
Becker (1964)

5-1

```

SUBROUTINE READX
C-----VERSION.1
C-----READX FOR BECKER PROBLEMS
COMMON XID(5),X(12),Y,N1,N3,N4,11,12,15,10,1M,1F
GO TO (10,10,10,10,10),N1
10 READ(5,1) (XID(J),J=1,12),(X(J),J=1,11)
1 FORMAT(2F2.0,2X,2F4.0)
RETURN
END

```

RXB10001
RXB10002
RXB10003
RXB10004
RXB10005
RXB10006
RXB10007
RXB10008
RXB10009

```

5
START 1222 5 60010
BECKER P5,NESTED ANALYSIS,SIRE GROUPS ONLY,MALE OFFSPRING ONLY
MALE 1ST

```

1 1 687
1 2 691
1 3 793
1 4 675
1 5 700
1 6 753
1 7 704
1 8 717
2 1 618
2 2 680
2 3 592
2 4 683
2 5 631
2 6 691
2 7 694
2 8 732
3 1 618
3 2 687
3 3 763
3 4 747
3 5 678
3 6 737
3 7 731
3 8 603
4 1 600
4 2 657
4 3 669
4 4 606
4 5 718
4 6 693
4 7 669
4 8 648
5 1 717
5 2 658
5 3 674
5 4 611
5 5 678
5 6 788
5 7 650
5 8 690

BKD10001
BKD10002
BKD10003
BKD10004
BKD10005
BKD10006
BKD10007
BKD10008
BKD10009
BKD10010
BKD10011
BKD10012
BKD10013
BKD10014
BKD10015
BKD10016
BKD10017
BKD10018
BKD10019
BKD10020
BKD10021
BKD10022
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BKD10049
BKD10050
BKD10051
BKD10052
BKD10053
BKD10054
BKD10055
BKD10056
BKD10057
BKD10058
BKD10059
BKD10060
BKD10061
BKD10062
BKD10063

```

START 1222 5 30010
BECKER P10,NESTED ANALYSIS,S AND D GROUPS,MALE OFFSPRING ONLY
MALE 1ST

```

1 1 1 965
1 1 2 813
1 1 3 765
1 2 4 803
1 2 5 640
1 2 6 714
1 3 7 644
1 3 8 753
1 3 9 705
2 410 740
2 411 798
2 412 941
2 513 701
2 514 847
2 515 909

2 616 907
 2 617 800
 2 618 853
 3 719 696
 3 720 807
 3 721 800
 3 822 752
 3 823 863
 3 824 739
 3 925 686
 3 926 832
 3 927 796
 41028 979
 41029 798
 41030 788
 41131 905
 41132 880
 41133 770
 41234 797
 41235 721
 41236 765
 51337 809
 51338 756
 51339 775
 51440 887
 51441 935
 51442 937
 51543 872
 51544 811
 51545 925

START 2232 17 11010

BECKER P27-O-P ANALYSIS-SIRE AND MALE OFFSPRING ONLY

SIRE 1ST MALE 1ST

1 1 601 910
 2 2 733 983
 3 3 793 976
 4 4 7951050
 5 5 8181080
 6 6 8381040
 7 7 8541040
 8 8 8801025
 9 9 882 994
 1010 8951030
 1111 9521021
 1212 9531078
 1313 961 964
 1414 979 976
 1515 9951110
 1616 9971041
 1717 10401035

START 2232 6 30101

BECKER P30-O-P ANALYSIS-DAM AND FEML OFFSPR ONLY-OFFSPRING MEAN OBS.

DAM 1ST FEML 1ST

1 1 1 754 808
 1 2 2 648 700
 1 3 3 861 720
 2 4 4 740 725
 2 5 5 712 840
 2 6 6 812 800
 3 7 7 765 780
 3 8 8 807 840
 4 9 9 969 850
 41010 849 802
 41111 732 830
 51212 740 805
 51313 741 835
 61414 831 830
 61515 639 800
 61616 733 504

START 2232 6 30101

BKD10064
 BKD10065
 BKD10066
 BKD10067
 BKD10068
 BKD10069
 BKD10070
 BKD10071
 BKD10072
 BKD10073
 BKD10074
 BKD10075
 BKD10076
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 BKD10099
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 BKD10101
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 BKD10128
 BKD10129
 BKD10130
 BKD10131
 BKD10132
 BKD10133
 BKD10134
 BKD10135
 BKD10136

BECKER P33.0-P ANALYSIS.DAM AND FEML OFFSPR ONLY.REPEATED PARENT OFS.

DAM 1ST FEML 1ST

1 1 1 754 772
 1 1 2 754 781
 1 1 3 754 871
 1 2 4 648 627
 1 2 5 648 653
 1 2 6 648 694
 1 2 7 648 826
 1 3 8 881 786
 1 3 9 881 653
 1 310 881 851
 1 311 881 588
 2 412 740 782
 2 413 740 668
 2 514 712 665
 2 515 712 977
 2 516 712 878
 2 617 812 936
 2 618 812 779
 2 619 812 685
 3 720 765 666
 3 721 765 871
 3 722 765 817
 3 723 765 766
 3 824 807 916
 3 825 807 657
 3 826 807 962
 3 827 807 825
 4 928 969 962
 4 929 969 738
 41030 849 909
 41031 849 699
 41132 732 747
 41133 732 666
 41134 732 656
 41135 732 878
 41136 732 1003
 51237 740 877
 51238 740 807
 51239 740 797
 51240 740 743
 51341 741 695
 51342 741 829
 51343 741 936
 51344 741 856
 51345 741 796
 51346 741 700
 61447 831 822
 61448 831 832
 61449 831 887
 61450 831 696
 61451 831 911
 61552 639 802
 61553 639 798
 61654 733 607
 61655 733 545
 61656 733 477
 61657 733 387

SUBROUTINE READX(XID,X)

C-----VERSION 2

C-----READX FOR BECKER PROBLEMS

DIMENSION XID(1),X(1)

COMMON/CPBLK1/ I1,I2,N3,N4,N5,N6,I5,I0,IM,IF,N1,ITL(9),Y,KPUT

REAL(8) XID(J),J=1,I2,X(J),J=1,I1

1 FORMAT(2F2.0,2X,2F4.0)

RETURN

END

5

START 1221 5 8 0 0 1 0

BECKER P5.NESTED ANALYSIS.SIRE GROUPS ONLY.MALE OFFSPRING ONLY

BKD10137
 BKD10138
 BKD10139
 BKD10140
 BKD10141
 BKD10142
 BKD10143
 BKD10144
 BKD10145
 BKD10146
 BKD10147
 BKD10148
 BKD10149
 BKD10150
 BKD10151
 BKD10152
 BKD10153
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 BKD10189
 BKD10190
 BKD10191
 BKD10192
 BKD10193
 BKD10194
 BKD10195
 BKD10196
 RXB20001
 RXB20002
 RXB20003
 RXB20004
 RXB20005
 RXB20006
 RXB20007
 RXB20008
 RXB20009
 BKD20001
 BKD20002
 BKD20003

MALE 1ST
1 1 687
1 2 691

BKD20004
BKD20005
BKD20006

DATA AS FOR VERSION 1

5 7 650
5 8 690

BKD20043
BKD20044
BKD20045
BKD20046
BKD20047
BKD20048
BKD20049
BKD20050

START 1221 5 3 0 0 1 0

BECKER P10-NESTED ANALYSIS.S AND D GROUPS.MALE OFFSPRING ONLY

MALE 1ST
1 1 985
1 2 813

BKD20048
BKD20049
BKD20050

DATA AS FOR VERSION 1

51544 811
51545 925

BKD20092
BKD20093
BKD20094
BKD20095

START 2211 17 1 1 0 1 0

BECKER P27-O-P ANALYSIS.SIRE AND MALE OFFSPRING ONLY

SIRE 1STMALE 1ST
1 1 601 910
2 2 733 983

BKD20096
BKD20097
BKD20098
BKD20099

DATA AS FOR VERSION 1

1616 9971041
1717 10401035

BKD20113
BKD20114
BKD20115
BKD20116

START 2211 6 3 0 1 0 1

BECKER P30-O-P ANALYSIS.DAM AND FEML OFFSPR ONLY.OFFSPRING MEAN OBS

DAM 1STFEML 1ST
1 1 1 754 800
1 2 2 648 700

BKD20117
BKD20118
BKD20119
BKD20120

DATA AS FOR VERSION 1

61515 639 800
61616 733 504

BKD20133
BKD20134
BKD20135
BKD20136

START 2211 6 3 0 1 0 1

BECKER P33-O-P ANALYSIS.DAM AND FEML OFFSPR ONLY.REPEATED PARENT OBS

DAM 1STFEML 1ST
1 1 1 754 772
1 1 2 754 781

BKD20137
BKD20138
BKD20139
BKD20140

DATA AS FOR VERSION 1

61656 733 477
61657 733 387

BKD20194
BKD20195
BKD20196

SUBROUTINE READX(XID,X)

C-----VERSION 3

C-----READX FOR BECKER PROBLEMS

DIMENSION XID(1),X(1)

COMMON/CMBLK1/ I1,I2,N3,N4,N5,N6,IS,ID,IP,IF,N1,ITL(9),Y,KPUT

COMMON/CMBLK7/ M11,M15,M16,M17,M18,M19,M20,M21,M22,ICYC,LUT,LLS

READ(5,1)(XID(J),J=1,12),IX(J),J=1,11)

1 FORMAT(2F2.0,2X,2F4.0)

RETURN

END

FXB30001
RXB30002
RXB30003
RXB30004
RXB30005
RXB30006
RXB30007
RXB30008
RXB30009
RXB30010

START 1221 5 3 0 0 1 0 1 0

BECKER P5-NESTED ANALYSIS.SIRE GROUPS ONLY.MALE OFFSPRING ONLY

MALE 1ST
1 1 687
1 2 691

BKD30001
BKD30002
BKD30003
BKD30004
BKD30005
BKD30006

DATA AS FOR VERSION 1

5-5

5 7 650
5 8 690

START 1221 5 3 0 0 1 0 1 5 0
BECKER P10-NESTED ANALYSIS-S AND D GROUPS-MALE OFFSPRING ONLY
MALE 1ST
1 1 1 965
1 1 2 813

DATA AS FOR VERSION 1

51544 811
51545 925

START 2211 17 1 1 0 1 0 1 5 0
BECKER P27-O-P ANALYSIS-SIRE AND MALE OFFSPRING ONLY
SIRE 1ST MALE 1ST
1 1 601 910
2 2 733 983

DATA AS FOR VERSION 1

1616 9971041
1717 10401035

START 2211 6 3 0 1 0 1 1 5 0
BECKER P30-O-P ANALYSIS-DAM AND FEMLE OFFSPR ONLY-OFFSPRING MEAN OBS.
DAM 1ST FEMLE 1ST
1 1 1 754 808
1 2 2 648 700

DATA AS FOR VERSION 1

61515 639 800
61616 733 504

START 2211 6 3 0 1 0 1 1 5 0
BECKER P33-O-P ANALYSIS-DAM AND FEMLE OFFSPR ONLY-REPEATED PARENT OBS.
DAM 1ST FEMLE 1ST
1 1 1 754 772
1 1 2 754 781

DATA AS FOR VERSION 1

61656 733 477
61657 733 387

BKD30043
BKD30044
BKD30045
BKD30046
BKD30047
BKD30048
BKD30049
BKD30050

BKD30092
BKD30093
BKD30094
BKD30095
BKD30096
BKD30097
BKD30098
BKD30099

BKD30113
BKD30114
BKD30115
BKD30116
BKD30117
BKD30118
BKD30119
BKD30120

BKD30133
BKD30134
BKD30135
BKD30136
BKD30137
BKD30138
BKD30139
BKD30140

BKD30194
BKD30195
BKD30196

PROGRAM NESREG

ANALYSIS OF QUANTITATIVE VARIATION BY NESTED ADV AND/OR O-P REGRESSION

NUMBER OF PROBLEMS = 5

PROBLEM NO 1

ERRORS AND/OR COMMENTS FOR NESRG1

HERIT. OF OIF. FOR CHARS. 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 1 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 2 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 3 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 4 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 5 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 6 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 7 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

PROBLEM NO 1 BECKER P5, NESTED ANALYSIS, SIRE GROUPS ONLY, MALE OFFSPRING ONLY

NO. OF VARIABLES = 1

NO. OF LEVELS = 2

THE VARIABLES ARE THE FOLLOWING

VARIABLE NO. 1 IS MALE 1ST

ERRORS AND/OR COMMENTS FOR NESRG2

PROBLEM NO. 1
VARIABLES 1 AND 1
PROGENY MEAN = 0.683275E 03

ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	4	0.17197500E 05	0.42993750E 04	0.18421419E 01
2	35	0.81686500E 05	0.23339000E 04	0.
3	0	0.	0.	0.
TOTAL	39	0.98884000E 05		

	VARIANCE (COVARIANCE)	PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.	0.25795844E 04	0.	0.
VARIANCE COMPONENT 2 (DAM)	0.23339000E 04		0.	0.
VARIANCE COMPONENT 1 (SIRE)	0.24568439E 03		0.98273758E 03	0.15968468E 04 (SIRE)

HERITABILITIES AND STD. ERRORS

(SIRE) (DAM) (S+D)

0.38096741E 00 0.49249442E 00 0. ~~0.00000000E 00~~ 0. ~~0.00000000E 00~~

OF SIB ANALYSIS

PRELIMINARY PARTITIONING OF PHEN. VARIANCE

ADDITIVE 0.99999999E 02
DOMINANCE 0.99999999E 02
ADD. * ADD. 0.99999999E 02 (2)
SEX LINK 0.99999999E 02 0.99999999E 02 (3)
MAT. EFFECT -0.99999999E 02 -0.99999999E 02

COMMON ENVIR. VAR. (COVAR.) 0.
W/IN ES ENVIR. VAR. (COVAR.) 0.
COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 1.00000 (2) = 1.00000 (3) = 8.00000

PROBLEM NO 2

ERRORS AND/OR COMMENTS FOR NESRG1

HERIT. OF DIF. FOR CHARS. 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 1 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 2 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 3 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 4 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 5 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 6 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

CORRELATION NO 7 FOR CHARACTERS 1 AND 2 CANNOT BE CALCULATED

PROBLEM NO 2 BECKER PIO, NESTED ANALYSIS, S AND D GROUPS, MALE OFFSPRING ONLY

NO. OF VARIABLES = 1

NO. OF LEVELS = 2

THE VARIABLES ARE THE FOLLOWING

VARIABLE NO. 1 IS MALE 1ST

ERRORS AND/OR COMMENTS FOR NESRG2

PROBLEM NO. 2
VARIABLES 1 AND 1 PROGENY MEAN = 0.808467E 03

ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	4	0.63208500E 05	0.15802125E 05	0.17934084E 01
2	10	0.88112250E 05	0.88112250E 04	0.15949378E 01
3	30	0.16573275E 06	0.55244250E 04	0.
TOTAL	44	0.31705350E 06		

VARIANCE (COVARIANCE)

	PHENOTYPIC	GENETIC	ENVIRONMENTAL
VARIANCE COMPONENT 3 (ERROR)	0.55244250E 04	0.37447334E 04	0.36520583E 04 (S+D)
VARIANCE COMPONENT 2 (DAM)	0.10956000E 04	0.43824000E 04	0.33332249E 04 (DAM)
VARIANCE COMPONENT 1 (SIRE)	0.77676669E 03	0.31070668E 04	0.39708915E 04 (SIRE)

HERITABILITIES AND STD. ERRORS

(DAM)

(SIRE)

(S+D)

OF SIB ANALYSIS

0.42005601E 00	0.58925862E 00	0.59247309E 00	0.69456949E 00	0.50626455E 00	0.37059210E 00
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PRELIMINARY PARTITIONING OF PHEN. VARIANCE

ADDITIVE	0.42005601E 00		
DOMINANCE	0.99999999E 02		
ADD. * ADD.	0.99999999E 02	(2)	(3)
SEX LINK.	0.99999999E 02	0.99999999E 02	0.99999999E 02
MAT. EFFECT	-0.99999999E 02	-0.99999999E 02	

COMMON ENVIR. VAR. (COVAR.)

W/TIN FS ENVIR. VAR. (COVAR.)

COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 3.00000 (2) = 3.00000 (3) = 9.00000

PROBLEM NO 4

ERRORS AND/OR COMMENTS FOR NESRG1

HERIT. OF DIF. FOR CHARS. 2AND 3CANNOT BE CALCULATED

CORRELATION NO 1 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 2 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 3 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 4 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 5 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 6 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 7 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

PROBLEM NO 4 BECKER P30,O-P ANALYSIS,DAM AND FEML OFFSPR ONLY,OFFSPRING MEAN OBS.

NO. OF VARIABLES = 2

NO. OF LEVELS = 2

THE VARIABLES ARE THE FOLLOWING

VARIABLE NO. 1 IS DAM 1ST

VARIABLE NO. 2 IS FEML 1ST

ERRORS AND/OR COMMENTS FOR NESRG2

PROBLEM NO. 4
VARIABLES 2 AND 2

PARENT MEAN = 0.772053E 03
PROGENY MEAN = 0.779375E 03
P-P CORLV. = 0.0000

ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	5	0.30330500E 05	0.60661000E 04	0.74218265E 00
2	10	0.81733250E 05	0.81733250E 04	0.
3	0	0.	0.	0.
DAMS/S REGRESSION DEVIATIONS	1	0.80349137E 03	0.80349137E 03	0.893346305E-01
	9	0.80929758E 05	0.89921933E 04	0.
TOTAL	15	0.11206375E 06		

HERITABILITIES AND STD. ERRORS

(SIRE) (DAM)
(S+D)
OF O-P REGRESSION

0.20050629E 00 0.67076480E 00
O-P CORLN. 0.19829932E 00

COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 1.00000 (2) = 1.00000 (3) = 2.65000

PROBLEM NO 5

ERRORS AND/OR COMMENTS FOR NESRG1

HERIT. OF DIF. FOR CHARS. 2AND 3CANNOT BE CALCULATED

CORRELATION NO 1 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 2 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 3 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 4 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 5 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 6 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

CORRELATION NO 7 FOR CHARACTERS 2AND 3CANNOT BE CALCULATED

PROBLEM NO 5 BECKER P33-O-P ANALYSIS,DAM AND FEML OFFSPR ONLY,REPEATED PARENT OBS.

NO. OF VARIABLES = 2

NO. OF LEVELS = 2

THE VARIABLES ARE THE FOLLOWING

VARIABLE NO. 1 IS DAM 1ST

VARIABLE NO. 2 IS FEML 1ST

ERRORS AND/OR COMMENTS FOR NESRG2

PROBLEM NO. 5
VARIABLES 2 AND 2

PARENT MEAN = 0.768158E 03
PROGENY MEAN = 0.779088E 03
P-P CORLN. = 0.0000

ANALYSIS OF VARIANCE (COVARIANCE)

LEVEL NO. (SOURCE)	DEGREES OF FREEDOM	SUM OF SQUARES	MEAN SQUARE	COMPUTED F-VALUES
1	5	0.12986300E 06	0.25972600E 05	0.84596343E 00
2	10	0.30701800E 06	0.30701800E 05	0.27892298E 01
3	41	0.45129800E 06	0.11007268E 05	0.
DAMS/S REGRESSION DEVIATIONS	1	0.11884916E 05	0.11884916E 05	0.36242717E 00
	9	0.29513308E 06	0.32792564E 05	0.29791738E 01
TOTAL	56	0.88617900E 06		

HERITABILITIES AND STD. ERRORS

(SIRE)

(DAM)

OF O-P REGRESSION

0.42000252E 00
O-P CORLN. 0.25038191E 00
0.47072113E 00

COEFFICIENTS OF VARIANCE (COVARIANCE) COMPONENTS (1) = 3.35652 (2) = 3.89750 (3) = 9.46667