

Chapter 19

Nested Classifications

C. R. Henderson

1984 - Guelph

The nested classification can be described as cross-classification with disconnectedness. For example, we could have a cross-classified design with the main factors being sires and dams. Often the design is such that a set of dams is mated to sire 1 a second set to sire 2, etc. Then σ_d^2 and σ_{ds}^2 , dams assumed random, cannot be estimated separately, and the sum of these is defined as $\sigma_{d/s}^2$. As is the case with cross-classified data, estimability and methods of analysis depend upon what factors are fixed versus random. We assume that the only possibilities are random within random, random within fixed, and fixed within fixed. Fixed within random is regarded as impossible from a sampling viewpoint.

1 Two Way Fixed Within Fixed

A linear model for fixed effects nested within fixed effects is

$$y_{ijk} = t_i + a_{ij} + e_{ijk}$$

with t_i and a_{ij} fixed. The j subscript has no meaning except in association with some i subscript. None of the t_i is estimable nor are differences among the t_i . So far as the a_{ij} are concerned

$$\sum_j \alpha_j a_{ij} \text{ for } \sum_j \alpha_j = 0 \text{ can be estimated.}$$

Thus we can estimate $2a_{i1} - a_{i2} - a_{i3}$. In contrast it is not possible to estimate differences between a_{ij} and a_{gh} ($i \neq g$) or between a_{ij} and a_{gh} ($i \neq g, j \neq h$). Obviously main effects can be defined only as some averaging over the nested factors. Thus we could define the mean of the i^{th} main factor as $\alpha_i = t_i + \sum_j k_j a_{ij}$ where $\sum_j k_j = 1$. Then the i^{th} main effect would be defined as $\alpha_i - \bar{\alpha}$. Tests of hypotheses of estimable linear functions can be effected in the usual way, that is, by utilizing the variance-covariance matrix of the estimable functions.

Let us illustrate with the following simple example

t	a	n_{ij}	y_{ij}	\bar{y}_{ij}
1	1	4	20	5
	2	5	15	3
2	3	1	8	8
	4	10	70	7
	5	2	12	6
3	6	5	45	9
	7	2	16	8

Assume that $Var(\mathbf{e}) = \mathbf{I}\sigma_e^2$.

Main effects	$\hat{\alpha}_i$	$Var(\hat{\alpha}_i)$
1	4.	$\sigma_e^2 (4^{-1} + 5^{-1})/4 = .1125 \sigma_e^2$
2	7.	$\sigma_e^2 (1 + 10^{-1} + 2^{-1})/9 = .177 \sigma_e^2$
3	8.5	$\sigma_e^2 (5^{-1} + 2^{-1})/4 = .175 \sigma_e^2$

Test

$$\begin{pmatrix} 1 & 0 & -1 \\ 0 & 1 & -1 \end{pmatrix} \boldsymbol{\alpha} = \mathbf{0}$$

$$\begin{pmatrix} 1 & 0 & -1 \\ 0 & 1 & -1 \end{pmatrix} \hat{\boldsymbol{\alpha}} = \begin{pmatrix} -3.5 \\ -.5 \end{pmatrix}$$

$$\sigma_e^{-2} \text{Var}(\hat{\boldsymbol{\alpha}}) = \text{dg}(.1125, .177, \dots, .175)$$

$$\text{Var}(\mathbf{K}'\hat{\boldsymbol{\alpha}})\sigma_e^{-2} = \begin{pmatrix} .2875 & .175 \\ .175 & .35278 \end{pmatrix}$$

with inverse

$$\begin{pmatrix} 4.98283 & -2.47180 \\ -2.47180 & 4.06081 \end{pmatrix}.$$

Then the numerator MS is

$$(-3.5 \quad -.5) \begin{pmatrix} 4.98283 & -2.47180 \\ -2.47180 & 4.06081 \end{pmatrix} \begin{pmatrix} -3.5 \\ -.5 \end{pmatrix} / 2 = 26.70$$

Estimate σ_e^2 as $\hat{\sigma}_e^2 =$ within subclass mean square. Then the test is numerator MS/ $\hat{\sigma}_e^2$ with 2,26 d.f. A possible test of differences among a_{ij} could be

$$\begin{pmatrix} 1 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 1 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & -1 \end{pmatrix} \mathbf{a},$$

the estimate of which is (2 2 1 1)' with

$$Var = \begin{pmatrix} .45 & 0 & 0 & 0 \\ 0 & 1.5 & .5 & 0 \\ 0 & .5 & .6 & 0 \\ 0 & 0 & 0 & .7 \end{pmatrix},$$

the inverse of which is

$$\begin{pmatrix} 2.22222 & 0 & 0 & 0 \\ 0 & .92308 & -.76923 & 0 \\ 0 & -.76923 & 2.30769 & 0 \\ 0 & 0 & 0 & 1.42857 \end{pmatrix}.$$

This gives the numerator MS = 13.24.

The “usual” ANOVA described in many text books is as follows.

$$\begin{aligned} \text{S.S. for T} &= \sum_i y_{i..}^2/n_{i.} - y_{...}^2/n_{..} \\ \text{S.S. for A} &= \sum_i \sum_j y_{ij.}^2/n_{ij} - \sum_i y_{i..}^2/n_{i.} \end{aligned}$$

In our example,

$$\begin{aligned} \text{MST} &= (1290.759 - 1192.966)/2 = 48.897. \\ \text{MSA} &= (1304 - 1290.759)/1 = 13.24. \end{aligned}$$

Note that the latter is the same as in the previous method. They do in fact test the same hypothesis. But MST is different from the result above which tests treatments averaged equally over the **a** nested within it. The second method tests differences among **t** weighted over **a** according to the number of observations. Thus the weights for t_1 are (4,5)/9.

To illustrate this test,

$$\mathbf{K}' = \begin{pmatrix} .444444 & .555555 & 0 & 0 & 0 & -.71429 & -.28572 \\ 0 & 0 & .07692 & .76923 & .15385 & -.71429 & -.28572 \end{pmatrix}$$

$$Var(\mathbf{K}'\bar{y}_{ij})/\sigma_e^2 = \begin{pmatrix} .253968 & .142857 \\ .142857 & .219780 \end{pmatrix}$$

$$\text{with inverse} = \begin{pmatrix} 6.20690 & -4.03448 \\ -4.03448 & 7.17242 \end{pmatrix}$$

Then the MS is

$$(-4.82540 \quad -1.79122) \begin{pmatrix} 6.20690 & -4.03448 \\ -4.03448 & 7.17242 \end{pmatrix} \begin{pmatrix} -4.82540 \\ -1.79122 \end{pmatrix} / 2 = 48.897$$

as in the regular ANOVA. Thus ANOVA weights according to the n_{ij} . This does not appear to be a particularly interesting test.

2 Two Way Random Within Fixed

There are two different sampling schemes that can be envisioned in the random nested within fixed model. In one case, the random elements associated with every fixed factor are assumed to be a sample from the same population. A different situation is one in which the elements within each fixed factor are assumed to be from separate populations. The first type could involve treatments as the fixed factors and then a random sample of sires is drawn from a common population to assign to a particular treatment. In contrast, if the main factors are breeds, then the sires sampled would be from separate populations, namely the particular breeds. In the first design we can estimate the difference among treatments, each averaged over the same population of sires. In the second case we would compare breeds defined as the average of all sires in each of the respective breeds.

2.1 Sires within treatments

We illustrate this design with a simple example

	n_{ij}			y_{ij}		
	Treatments			Treatments		
Sires	1	2	3	1	2	3
1	5	0	0	7	-	-
2	2	0	0	6	-	-
3	0	3	0	-	7	-
4	0	8	0	-	9	-
5	0	0	5	-	-	8

Let us treat this first as a multiple trait problem with $Var(\mathbf{e}) = 40\mathbf{I}$,

$$Var \begin{pmatrix} s_{i1} \\ s_{i2} \\ s_{i3} \end{pmatrix} = \begin{pmatrix} 3 & 2 & 1 \\ 2 & 4 & 2 \\ 1 & 2 & 5 \end{pmatrix},$$

where s_{ij} refers to the value of the i^{th} sire with respect to the j^{th} treatment. Assume that the sires are unrelated. The inverse is

$$\begin{pmatrix} 3 & 2 & 1 \\ 2 & 4 & 2 \\ 1 & 2 & 5 \end{pmatrix}^{-1} = \begin{pmatrix} .5 & -.25 & 0 \\ -.25 & .4375 & -.125 \\ 0 & -.125 & .25 \end{pmatrix}.$$

Then the mixed model equations are (19.1).

$$80^{-1} \begin{pmatrix} 50 & -20 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -20 & 35 & -10 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -10 & 20 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 44 & -20 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -20 & 35 & -10 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -10 & 20 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 40 & -20 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -20 & 41 & -10 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -10 & 20 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 40 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -20 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 10 & 0 & 0 & 4 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 6 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 10 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 4 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 0 & 6 & 0 \\ & & & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & -20 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 51 & -10 & 0 & 0 & 0 & 0 & 16 & 0 \\ & & & -10 & 20 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & 40 & -20 & 0 & 0 & 0 & 0 \\ & & & 0 & 0 & -20 & 35 & -10 & 0 & 0 & 0 \\ & & & 0 & 0 & 0 & -10 & 30 & 0 & 0 & 10 \\ & & & 0 & 0 & 0 & 0 & 0 & 14 & 0 & 0 \\ & & & 16 & 0 & 0 & 0 & 0 & 0 & 22 & 0 \\ & & & 0 & 0 & 0 & 0 & 10 & 0 & 0 & 10 \end{pmatrix}$$

$$\begin{aligned} & (s_{11}, s_{12}, s_{13}, s_{21}, s_{22}, s_{23}, s_{31}, s_{32}, s_{33}, \\ & \quad s_{41}, s_{42}, s_{43}, s_{51}, s_{52}, s_{53}, t_1, t_2, t_3)' \\ & = [.175, 0, 0, .15, 0, 0, 0, .175, 0, 0, .225, \\ & \quad 0, 0, 0, .2, .325, .4, .2]'. \end{aligned}$$

(1)

The solution is

$$\begin{aligned} &(-.1412, -.0941, -.0471, .1412, .0941, .0471, .0918, .1835, \\ &.0918, -.0918, -.1835, -.0918, 0, 0, 0, 1.9176, 1.5380, 1.600)' \end{aligned} \quad (2)$$

Now if we treat this as a nested model, $\mathbf{G} = \text{diag}(3,3,4,4,5)$. Then the mixed model equations are in (19.3).

$$120^{-1} \begin{pmatrix} 55 & 0 & 0 & 0 & 0 & 15 & 0 & 0 \\ & 46 & 0 & 0 & 0 & 6 & 0 & 0 \\ & & 39 & 0 & 0 & 0 & 9 & 0 \\ & & & 54 & 0 & 0 & 24 & 0 \\ & & & & 39 & 0 & 0 & 15 \\ & & & & & 21 & 0 & 0 \\ & & & & & & 33 & 0 \\ & & & & & & & 15 \end{pmatrix} \begin{pmatrix} \hat{s}_1 \\ \hat{s}_2 \\ \hat{s}_3 \\ \hat{s}_4 \\ \hat{s}_5 \\ \hat{t}_1 \\ \hat{t}_2 \\ \hat{t}_3 \end{pmatrix} = 120^{-1} \begin{pmatrix} 21 \\ 18 \\ 21 \\ 27 \\ 24 \\ 39 \\ 48 \\ 24 \end{pmatrix} \quad (3)$$

The solution is

$$(-.1412, .1412, .1835, -.1835, 0, 1.9176, 1.5380, 1.6000)' \quad (4)$$

Note that $\hat{s}_{11} = \hat{s}_1$, $\hat{s}_{21} = \hat{s}_2$, $\hat{s}_{32} = \hat{s}_3$, $\hat{s}_{42} = \hat{s}_4$, $\hat{s}_{53} = \hat{s}_5$ from the solution in (19.2) and (19.4). Also note that t_j are equal in the two solutions. The second method is certainly easier than the first but it does not predict values of sires for treatments in which they had no progeny.

2.2 Sires within breeds

Now we assume that we have a population of sires unique to each breed. Then the first model of Section 19.2.1 would be useless. The second method illustrated would be appropriate if sires were unrelated and $\sigma_s^2 = 3,4,5$ for the 3 breeds. If σ_s^2 were the same for all breeds $\mathbf{G} = \mathbf{I}_5\sigma_s^2$.

3 Random Within Random

Let us illustrate this model by dams within sires. Suppose the model is

$$y_{ijk} = \mu + s_i + d_{ij} + e_{ijk}.$$

$$\text{Var} \begin{pmatrix} \mathbf{s} \\ \mathbf{d} \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{I}\sigma_s^2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I}\sigma_d^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_e^2 \end{pmatrix}.$$

Let us use the data of Section 19.2.1 but now let \mathbf{t} refer to sires and \mathbf{s} to dams. Suppose $\sigma_e^2/\sigma_s^2 = 12$, $\sigma_e^2/\sigma_d^2 = 10$. Then the mixed model equations are in (19.5).

$$\begin{pmatrix} 23 & 7 & 11 & 5 & 5 & 2 & 3 & 8 & 5 \\ & 19 & 0 & 0 & 5 & 2 & 0 & 0 & 0 \\ & & 23 & 0 & 0 & 0 & 3 & 8 & 0 \\ & & & 17 & 0 & 0 & 0 & 0 & 5 \\ & & & & 15 & 0 & 0 & 0 & 0 \\ & & & & & 12 & 0 & 0 & 0 \\ & & & & & & 13 & 0 & 0 \\ & & & & & & & 18 & 0 \\ & & & & & & & & 15 \end{pmatrix} \begin{pmatrix} \hat{\mu}_1 \\ \hat{s}_1 \\ \hat{s}_2 \\ \hat{s}_3 \\ \hat{d}_1 \\ \hat{d}_2 \\ \hat{d}_3 \\ \hat{d}_4 \\ \hat{d}_5 \end{pmatrix} = \begin{pmatrix} 37 \\ 13 \\ 16 \\ 8 \\ 7 \\ 6 \\ 7 \\ 9 \\ 8 \end{pmatrix} \quad (5)$$

The solution is $(1.6869, .0725, -.0536, -.0189, -.1198, .2068, .1616, -.2259, -.0227)'$. Note that $\sum \hat{s}_i = 0$ and that 10 (Sum of \hat{d} within i^{th} sire)/ $12 = \hat{s}_i$.