

Thus, the covariance between two observations from the same litter is σ_ℓ^2 and the correlation is $\frac{\sigma_\ell^2}{\sigma_\ell^2 + \sigma_e^2}$.

These computations can also be done using the non-matrix expression of the model.

$$\forall i, j, \text{Var}(y_{ijk}) = \text{Var}(\mu + \alpha_i + \beta_j + \gamma_{ij} + \ell_{ik} + e_{ijk})$$

ℓ_{ik} & e_{ijk}
are independent

$$\begin{aligned} &= \text{Var}(\ell_{ik} + e_{ijk}) \\ &= \sigma_\ell^2 + \sigma_e^2. \end{aligned}$$

2 mice within the same litter

$$\begin{aligned}\text{Cov}(y_{i1k}, y_{i2k}) &= \text{Cov}(\mu + \alpha_i + \beta_1 + \gamma_{i1} + \cancel{l_{ik}} + e_{i1k}, \\ &\quad \mu + \alpha_i + \beta_2 + \gamma_{i2} + \cancel{l_{ik}} + e_{i2k}) \\ &= \text{Cov}(\cancel{l_{ik}} + e_{i1k}, \cancel{l_{ik}} + e_{i2k}) \\ &= \text{Cov}(\cancel{l_{ik}}, \cancel{l_{ik}}) + \text{Cov}(\cancel{l_{ik}}, e_{i2k}) \\ &\quad + \text{Cov}(e_{i1k}, \cancel{l_{ik}}) + \text{Cov}(e_{i1k}, e_{i2k}) \\ &= \text{Cov}(\cancel{l_{ik}}, \cancel{l_{ik}}) + 0 + 0 + 0 \\ &= \text{Var}(\cancel{l_{ik}}) = \sigma_\ell^2.\end{aligned}$$

= 0
due to
independ.
assumptions

Back to the Traditional Split-Plot Experimental Design

Field												
Block 1	Genotype C				Genotype A				Genotype B			
	0	100	150	50	50	100	150	0	150	100	50	0
Block 2	Genotype B				Genotype A				Genotype C			
	150	100	50	0	0	50	150	100	100	50	150	0
Block 3	Genotype A				Genotype B				Genotype C			
	100	50	0	150	0	100	150	50	50	100	150	0
Block 4	Genotype B				Genotype C				Genotype A			
	0	50	100	150	150	100	50	0	50	150	100	0

A Model for Data from the Traditional Split-Plot Experiment

Genotype $i = 1, 2, 3$, Fertilizer $j = 1, 2, 3, 4$, Block $k = 1, 2, 3, 4$

$$y_{ijk} = \mu_{ij} + b_k + w_{ik} + e_{ijk}$$

μ_{ij} = mean for Genotype i , Fertilizer j

b_k = random block effect

w_{ik} = random whole-plot exp. unit effect

e_{ijk} = random error = random split-plot exp. unit effect

Some statisticians
could treat blocks as fixed
due to the small
number

To express the model precisely in vector and matrix form as $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e}$, we will sort the data first by Block, then Genotype, and then Fertilizer:

$$N = 48$$

$$\mathbf{y} = [y_{111}, y_{121}, y_{131}, y_{141}, y_{211}, y_{221}, y_{231}, y_{241}, \dots, y_{314}, y_{324}, y_{334}, y_{344}]^T$$

$$\mathbf{e} = [e_{111}, e_{121}, e_{131}, e_{141}, e_{211}, e_{221}, e_{231}, e_{241}, \dots, e_{314}, e_{324}, e_{334}, e_{344}]^T$$

$$\mathbf{X} = \begin{matrix} \boxed{1}_{4 \times 1} \otimes \boxed{\mathbf{I}}_{12 \times 12} \end{matrix} \quad \begin{matrix} \text{12 whole plot exp. units} \\ \text{4 fertilizer levels} \end{matrix}$$

$$\boldsymbol{\beta} = [\mu_{11}, \mu_{12}, \mu_{13}, \mu_{14}, \mu_{21}, \mu_{22}, \mu_{23}, \mu_{24}, \mu_{31}, \mu_{32}, \mu_{33}, \mu_{34}]^T$$

$$\underline{Z} = \left[\begin{array}{cc} \mathbf{I}_{4 \times 4} \otimes \mathbf{1}_{12 \times 1} & \mathbf{I}_{12 \times 12} \otimes \mathbf{1}_{4 \times 1} \end{array} \right]$$

12 whole-plot experimental units, each having 4 subplots

blocks — within each block we have 12 split-plot experimental units

$$\underline{u} = \begin{bmatrix} \mathbf{b} \\ \mathbf{w} \end{bmatrix} = \begin{bmatrix} b_1 \\ \vdots \\ b_4 \\ w_{11} \\ w_{21} \\ \vdots \\ w_{34} \end{bmatrix} \sim \mathcal{N} \left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \sigma_b^2 \mathbf{I} & \mathbf{0} \\ \mathbf{0} & \sigma_w^2 \mathbf{I} \end{bmatrix} \right)$$

random block

effect & random whole-plot effect are indep.

$$\begin{bmatrix} b \\ w \\ e \end{bmatrix} \sim \mathcal{N} \left(\begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_b^2 I & 0 & 0 \\ 0 & \sigma_w^2 I & 0 \\ 0 & 0 & \sigma_e^2 I \end{bmatrix} \right)$$

or

$$\begin{bmatrix} u \\ e \end{bmatrix} \sim \mathcal{N} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix} \right)$$