

Thus, the covariance between two observations from the same litter is  $\sigma_\ell^2$  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.

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

$\ell_{ik}$  &  $e_{ijk}$   
are independent

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

2 mice within the same litter

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

$\Rightarrow 0$   
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  $k = 1, 2, 3, 4$

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

$\mu_{ij}$  = 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

would 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:

$$N = 48$$

$$\mathbf{y} = [y_{011}, y_{012}, y_{013}, y_{014}, y_{121}, y_{122}, y_{123}, y_{124}, \dots, y_{314}, y_{324}, y_{334}, y_{344}]^\top$$

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

$$\mathbf{X} = \underbrace{\mathbf{1}_{4 \times 1}}_{\text{4 fertilizer levels}} \otimes \underbrace{\mathbf{I}_{12 \times 12}}_{\text{12 whole plot exp. units}}$$

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

$$\underline{Z} = \begin{bmatrix} I_{4 \times 4} \otimes \begin{smallmatrix} 1 \\ 12 \times 1 \end{smallmatrix}, & I_{12 \times 12} \otimes \begin{smallmatrix} 1 \\ 4 \times 1 \end{smallmatrix} \end{bmatrix}$$

12 whole-plot experimental units, each having 4 subplots

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

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

random block effect & random whole-plot effect are indep.

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

or

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