

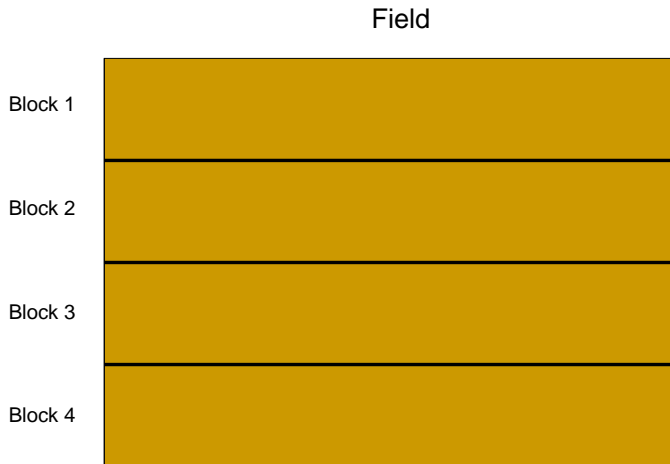
Linear Mixed-Effects Models for Data from Split-Plot Experiments

Start with a Field

Field



Partition the Field into Blocks



Partition Each Block into Plots

	Field		
Block 1			
Block 2			
Block 3			
Block 4			

Randomly Assign Genotypes to Plots within Blocks

	Field		
Block 1	Genotype C	Genotype A	Genotype B
Block 2	Genotype B	Genotype A	Genotype C
Block 3	Genotype A	Genotype B	Genotype C
Block 4	Genotype B	Genotype C	Genotype A

Partition Each Whole Plot into Split Plots

Field											
Block 1	Genotype C			Genotype A			Genotype B				
Block 2	Genotype B			Genotype A			Genotype C				
Block 3	Genotype A			Genotype B			Genotype C				
Block 4	Genotype B			Genotype C			Genotype A				

Randomly Assign Fertilizer Amounts within Split Plots

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

An Example Split-Plot Experiment

Field

*Whole Plot
or Main Plot*

*Split Plot
or Sub Plot*

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

- This experiment has two factors: genotype and fertilizer amount.
- Genotype has levels A, B, and C.
- Fertilizer has levels 0, 50, 100, 150 lbs. N / acre.
- Genotype is called the *whole-plot* (or *main-plot*) factor because its levels are randomly assigned to whole plots (main plots).
- Fertilizer is called the *split-plot* factor because its levels are randomly assigned to split plots within each whole plot.

Experimental Units in Split-Plot Designs

- Whole plots are the *whole-plot experimental units* because the levels of the whole-plot factor (genotype) are randomly assigned to whole plots.
- The split-plots are the *split-plot experimental units* because the levels of the split-plot factor (amount of fertilizer) are randomly assigned to split plots within each whole plot.
- Thus, we have two different sizes of experimental units in split-plot experimental designs.

Same Treatment Structure in an RCBD

Field

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

Same Treatment Structure in an CRD

Field

B 50	B 0	A 150	B 100	A 100	C 150	A 50	B 0	A 50	C 100	C 0	C 100
A 50	A 0	C 50	B 50	B 150	B 50	A 0	C 0	A 100	C 50	B 150	B 0
C 0	A 0	A 100	A 150	A 0	B 0	A 150	B 150	A 50	B 150	C 100	A 100
B 50	B 100	B 100	C 150	C 100	C 50	A 150	C 50	C 150	C 0	C 150	B 100

Why Use a Split-Plot Design?

- Split-plot designs usually arise because logistical constraints make a CRD or RCBD impractical.
- For example, it may be easier to change from one fertilizer level to another as a tractor drives through a field, while it may be more difficult to change from planting one genotype to planting another.
- In the engineering literature, split-plot designs are sometimes called designs with *hard-to-change* factors.

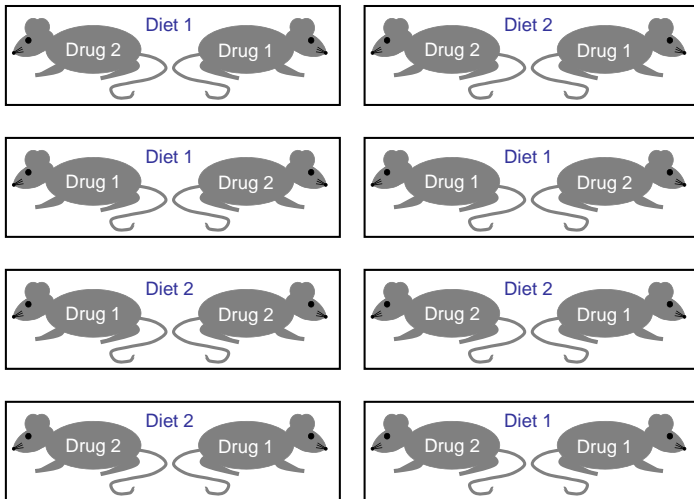
Recognizing Designs with Split-Plot Structures

- Many variations on split-plot designs are used for practical reasons.
- Examples include split-split-plot designs and split-block designs, but the names of these designs are not so important.
- Pay close attention to the experimental unit to which the levels of each factor are randomly assigned to recognize split-plot-like design structures.

Split-plot designs may not involve plots of land.

- Suppose eight pairs of mice from eight litters are housed in eight cages so that each cage holds two mice from the same litter.
- Suppose diets 1 and 2 are randomly assigned to the litters with four litters per diet.
- Within each cage, suppose drugs 1 and 2 are randomly assigned to the mice with one mouse per drug.

A Split-Plot Experimental Design



- Diet is the whole-plot treatment factor.
- Litters are the whole-plot experiment units.
- Drug is the split-plot treatment factor.
- Mice are the split-plot experiment units.

Diet $i = 1, 2$, Drug $j = 1, 2$, Litter $k = 1, 2, 3, 4$ (within each Diet i)

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \ell_{ik} + e_{ijk} \quad (i = 1, 2; j = 1, 2; k = 1, \dots, 4)$$

$\mu + \alpha_i + \beta_j + \gamma_{ij}$ = mean for Diet i and Drug j

ℓ_{ik} = random effect for k th litter that received Diet i

e_{ijk} = random error effect for Diet i , Drug j , Litter k

$$\mathbf{y} = \begin{bmatrix} y_{111} \\ y_{121} \\ y_{112} \\ y_{122} \\ y_{113} \\ y_{123} \\ y_{114} \\ y_{124} \\ y_{211} \\ y_{221} \\ y_{212} \\ y_{222} \\ y_{213} \\ y_{223} \\ y_{214} \\ y_{224} \end{bmatrix} \quad \boldsymbol{\beta} = \begin{bmatrix} \mu \\ \alpha_1 \\ \alpha_2 \\ \beta_1 \\ \beta_2 \\ \gamma_{11} \\ \gamma_{12} \\ \gamma_{21} \\ \gamma_{22} \end{bmatrix} \quad \mathbf{u} = \begin{bmatrix} \ell_{11} \\ \ell_{12} \\ \ell_{13} \\ \ell_{14} \\ \ell_{21} \\ \ell_{22} \\ \ell_{23} \\ \ell_{24} \end{bmatrix} \quad \mathbf{e} = \begin{bmatrix} e_{111} \\ e_{121} \\ e_{112} \\ e_{122} \\ e_{113} \\ e_{123} \\ e_{114} \\ e_{124} \\ e_{211} \\ e_{221} \\ e_{212} \\ e_{222} \\ e_{213} \\ e_{223} \\ e_{214} \\ e_{224} \end{bmatrix}$$

$$\mathbf{X} = \left[\mathbf{1}_{16 \times 1}, \mathbf{I}_{2 \times 2} \otimes \mathbf{1}_{8 \times 1}, \mathbf{1}_{8 \times 1} \otimes \mathbf{I}_{2 \times 2}, \mathbf{I}_{2 \times 2} \otimes \mathbf{1}_{4 \times 1}, \mathbf{1}_{4 \times 1} \otimes \mathbf{I}_{2 \times 2} \right]$$

$$\mathbf{Z} = \mathbf{I}_{8 \times 8} \otimes \mathbf{1}_{2 \times 1}$$

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

$$\begin{bmatrix} \mathbf{u} \\ \mathbf{e} \end{bmatrix} \sim N \left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \sigma_\ell^2 \mathbf{I} & \mathbf{0} \\ \mathbf{0} & \sigma_e^2 \mathbf{I} \end{bmatrix} = \begin{bmatrix} \mathbf{G} & \mathbf{0} \\ \mathbf{0} & \mathbf{R} \end{bmatrix} \right)$$

$$\begin{aligned} \text{Var}(\mathbf{Zu}) &= \mathbf{ZGZ}' = \sigma_\ell^2 \mathbf{ZZ}' \\ &= \sigma_\ell^2 \begin{bmatrix} \mathbf{I}_{8 \times 8} & \mathbf{1}_{2 \times 1} \\ \mathbf{1}_{8 \times 8} & \mathbf{1}_{2 \times 1} \end{bmatrix} \begin{bmatrix} \mathbf{I}_{8 \times 8} & \mathbf{1}_{2 \times 1} \\ \mathbf{1}_{8 \times 8} & \mathbf{1}_{2 \times 1} \end{bmatrix}' \\ &= \sigma_\ell^2 \begin{bmatrix} \mathbf{I}_{8 \times 8} & \mathbf{11}' \\ \mathbf{11}' & \mathbf{11}' \end{bmatrix} \\ &= \text{Block Diagonal with blocks} \begin{bmatrix} \sigma_\ell^2 & \sigma_\ell^2 \\ \sigma_\ell^2 & \sigma_\ell^2 \end{bmatrix} \end{aligned}$$

$$\text{Var}(\mathbf{y}) = \mathbf{ZGZ}' + \mathbf{R} = \sigma_{\ell}^2 \mathbf{I}_{8 \times 8} \otimes \mathbf{1}\mathbf{1}'_{2 \times 2} + \sigma_e^2 \mathbf{I}$$

= Block Diagonal with blocks

$$\begin{bmatrix} \sigma_{\ell}^2 + \sigma_e^2 & \sigma_{\ell}^2 \\ \sigma_{\ell}^2 & \sigma_{\ell}^2 + \sigma_e^2 \end{bmatrix}$$

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.

$$\begin{aligned}\forall i, j, \text{Var}(y_{ijk}) &= \text{Var}(\mu + \alpha_i + \beta_j + \gamma_{ij} + \ell_{ik} + e_{ijk}) \\ &= \text{Var}(\ell_{ik} + e_{ijk}) \\ &= \sigma_\ell^2 + \sigma_e^2.\end{aligned}$$

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

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 effect for Block k

w_{ik} = random effect for Genotype i whole plot in Block k

e_{ijk} random error effect for Genotype i , Fertilizer j , Block k

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:

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

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

$$\mathbf{X} = \underset{4 \times 1}{\mathbf{1}} \otimes \underset{12 \times 12}{\mathbf{I}},$$

$$\boldsymbol{\beta} = \begin{bmatrix} \mu_{11} \\ \mu_{12} \\ \mu_{13} \\ \mu_{14} \\ \mu_{21} \\ \mu_{22} \\ \mu_{23} \\ \mu_{24} \\ \mu_{31} \\ \mu_{32} \\ \mu_{33} \\ \mu_{34} \end{bmatrix}$$

$$\mathbf{Z} = \left[\underset{4 \times 4}{\mathbf{I}} \otimes \underset{12 \times 1}{\mathbf{1}}, \underset{12 \times 12}{\mathbf{I}} \otimes \underset{4 \times 1}{\mathbf{1}} \right]$$

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

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

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