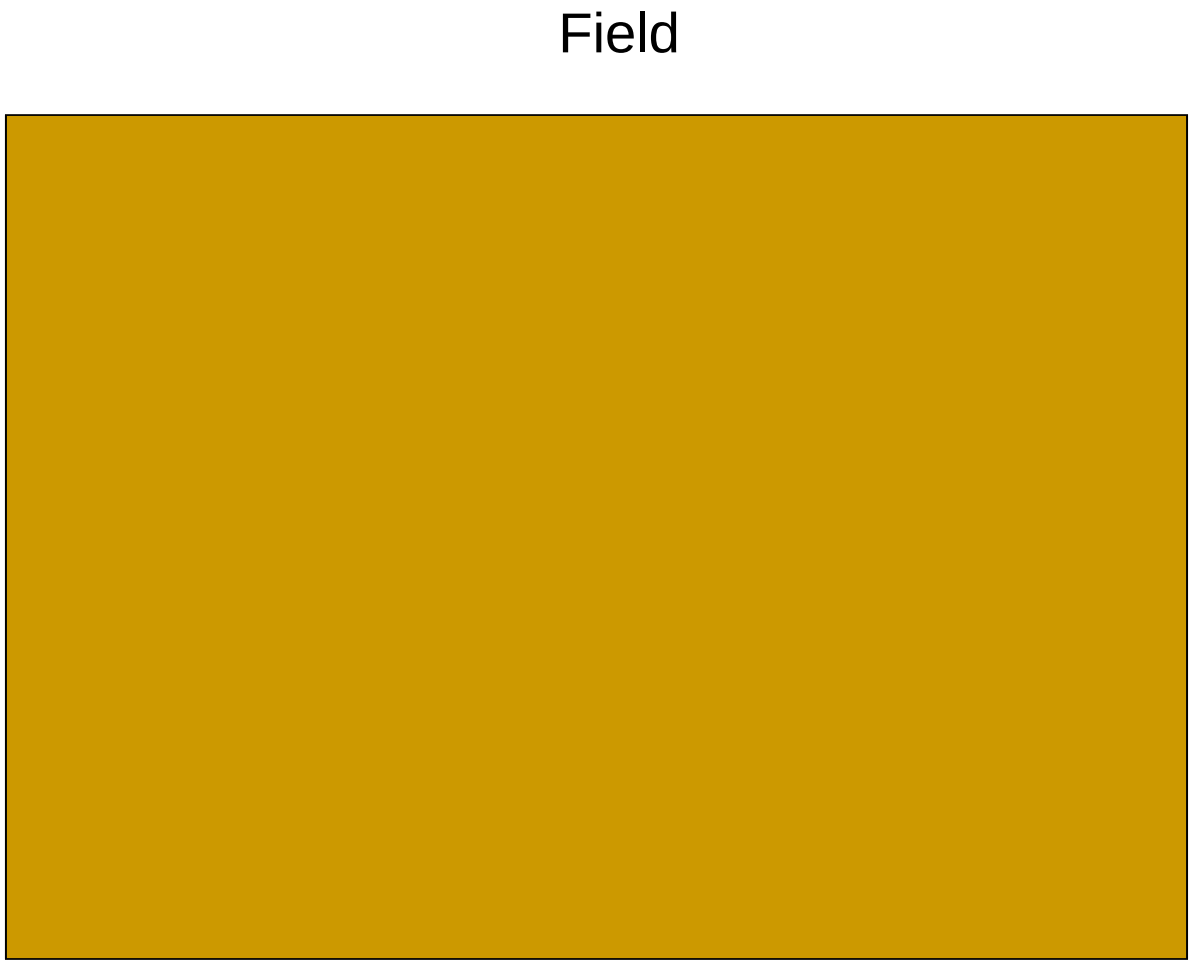
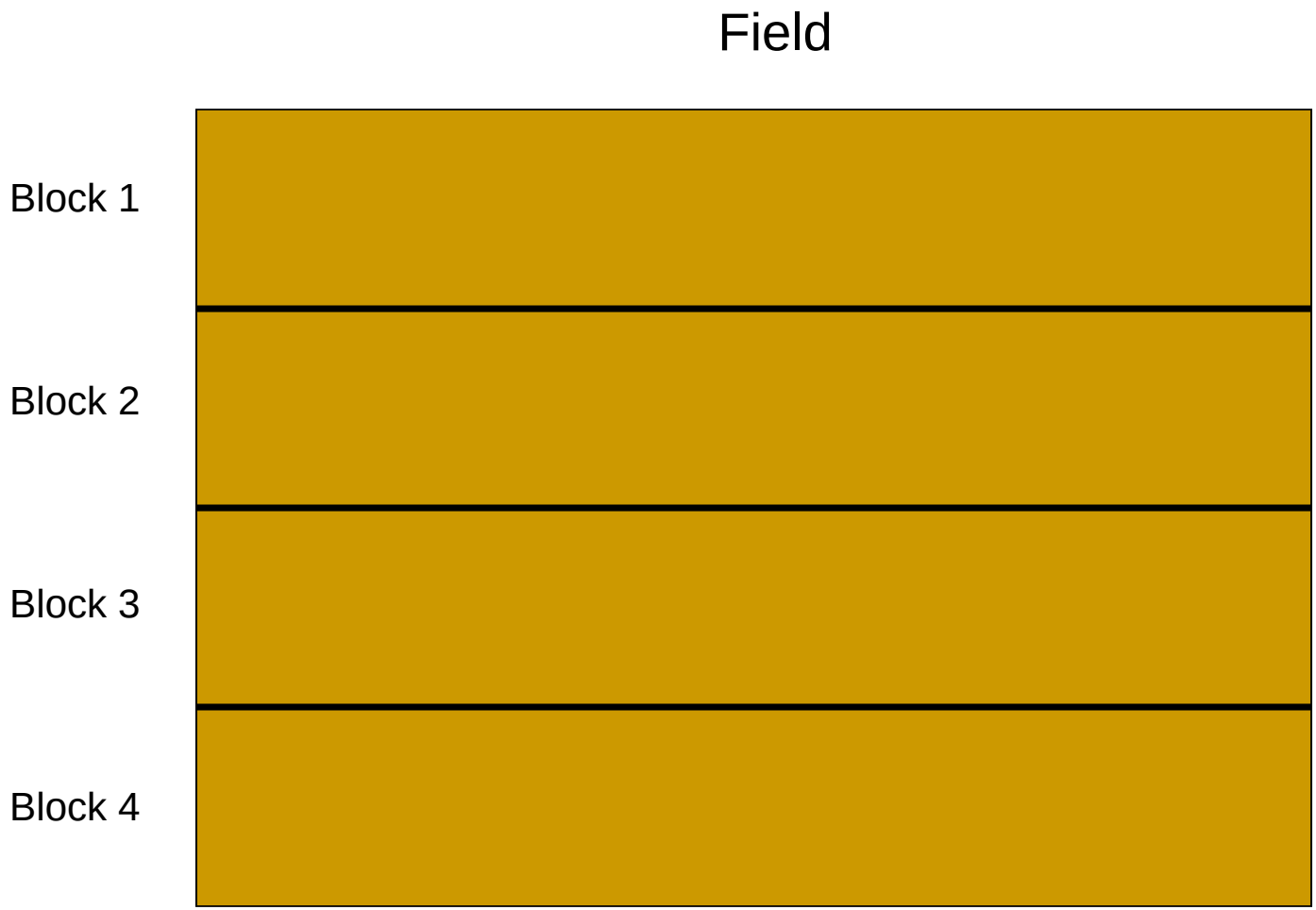
14. Linear Mixed-Effects Models for Data from Split-Plot Experiments

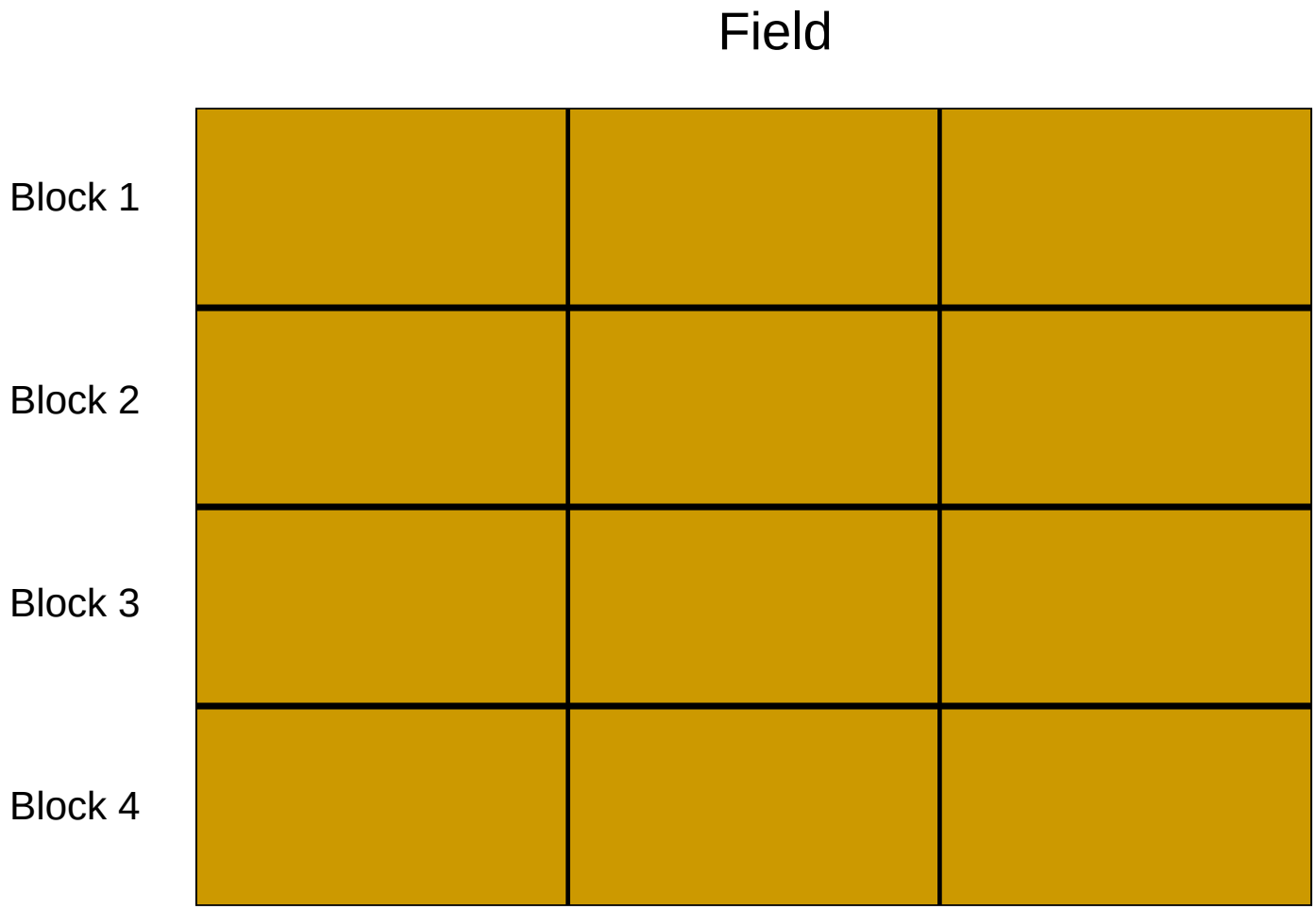
Start with a Field



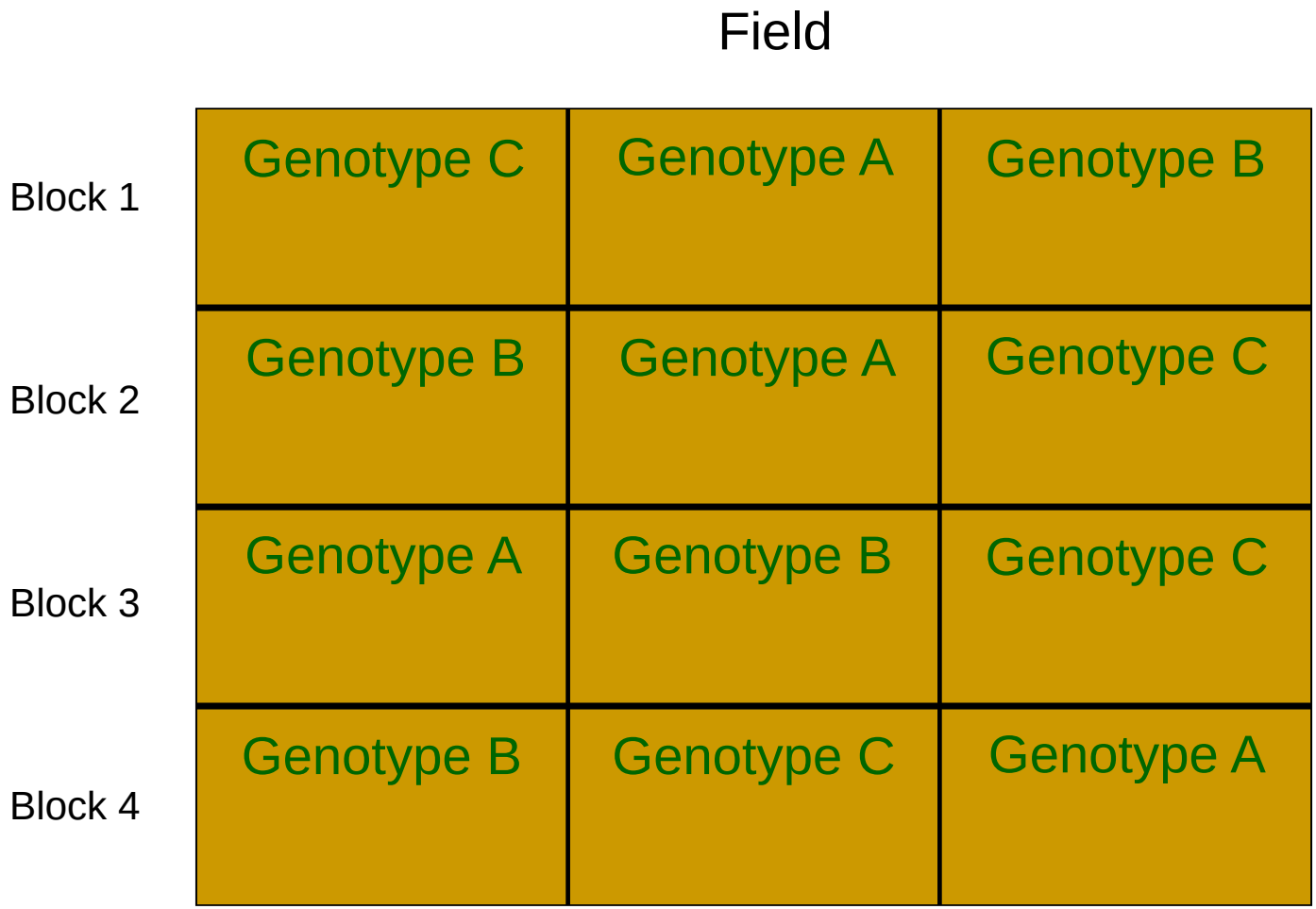
Partition the Field into Blocks



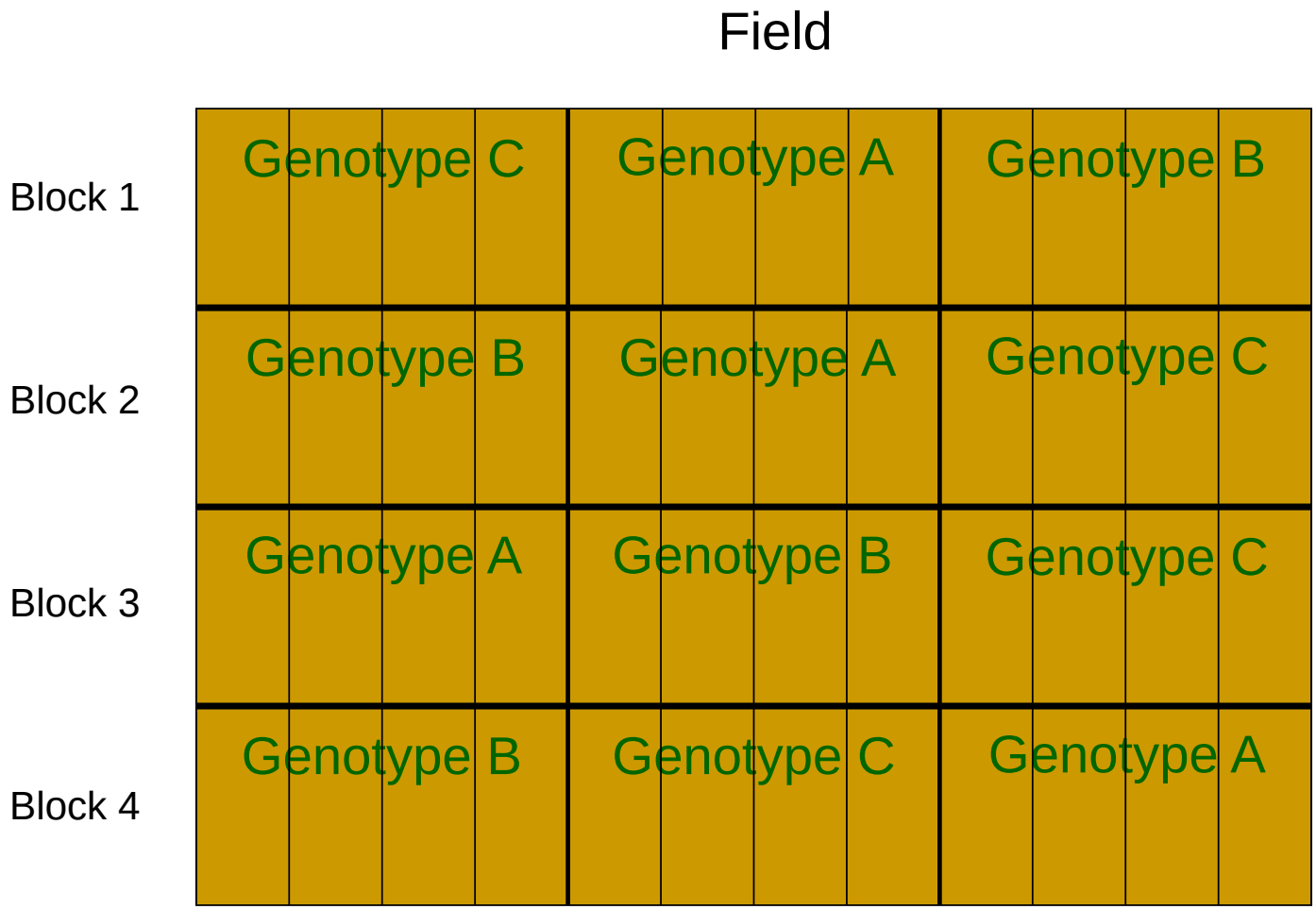
Partition Each Block into Plots



Randomly Assign Genotypes to Plots within Blocks



Partition Each Whole Plot into Split Plots

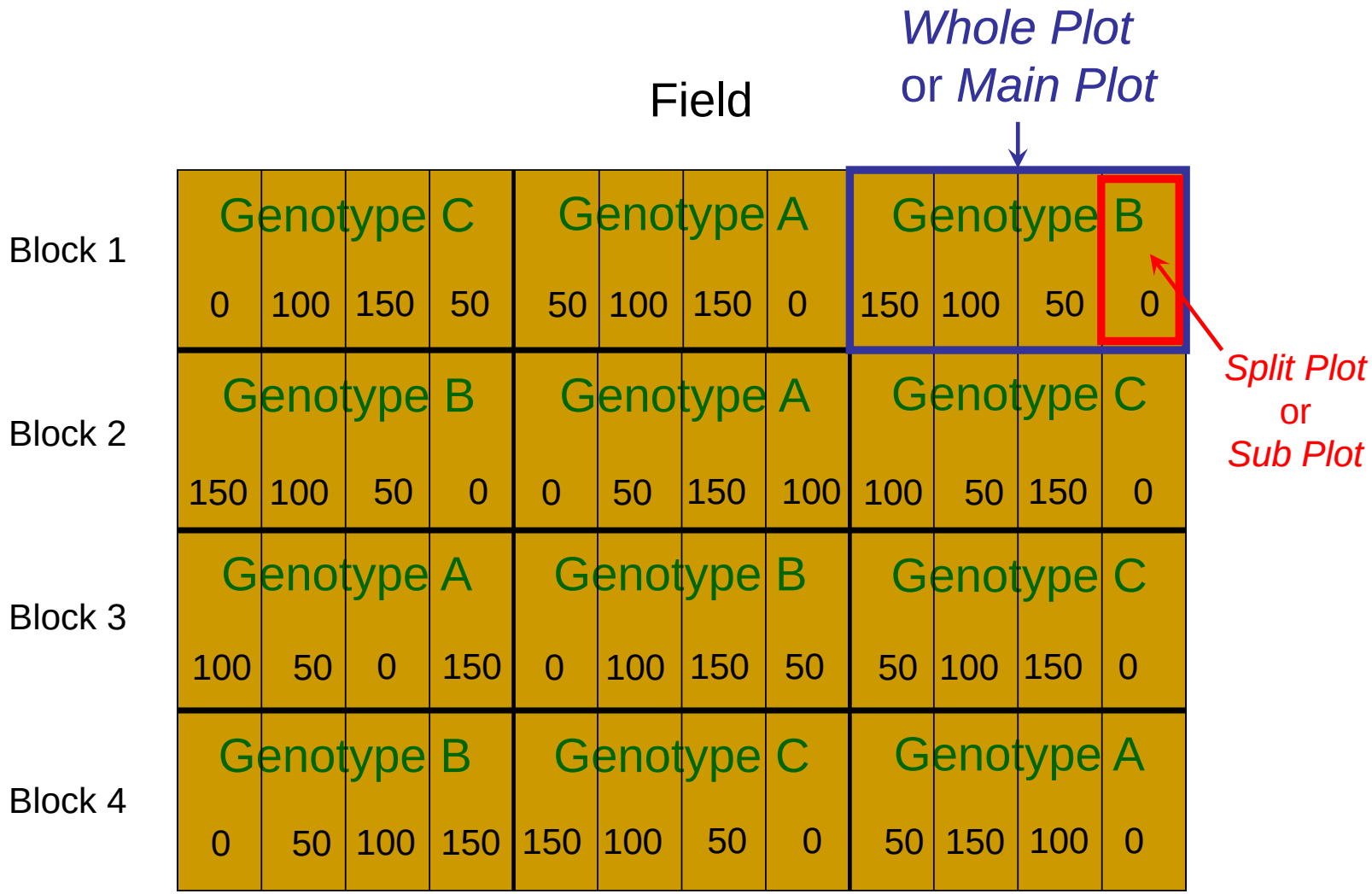


Randomly Assign Fertilizer Amounts within Split Plots

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



- 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.

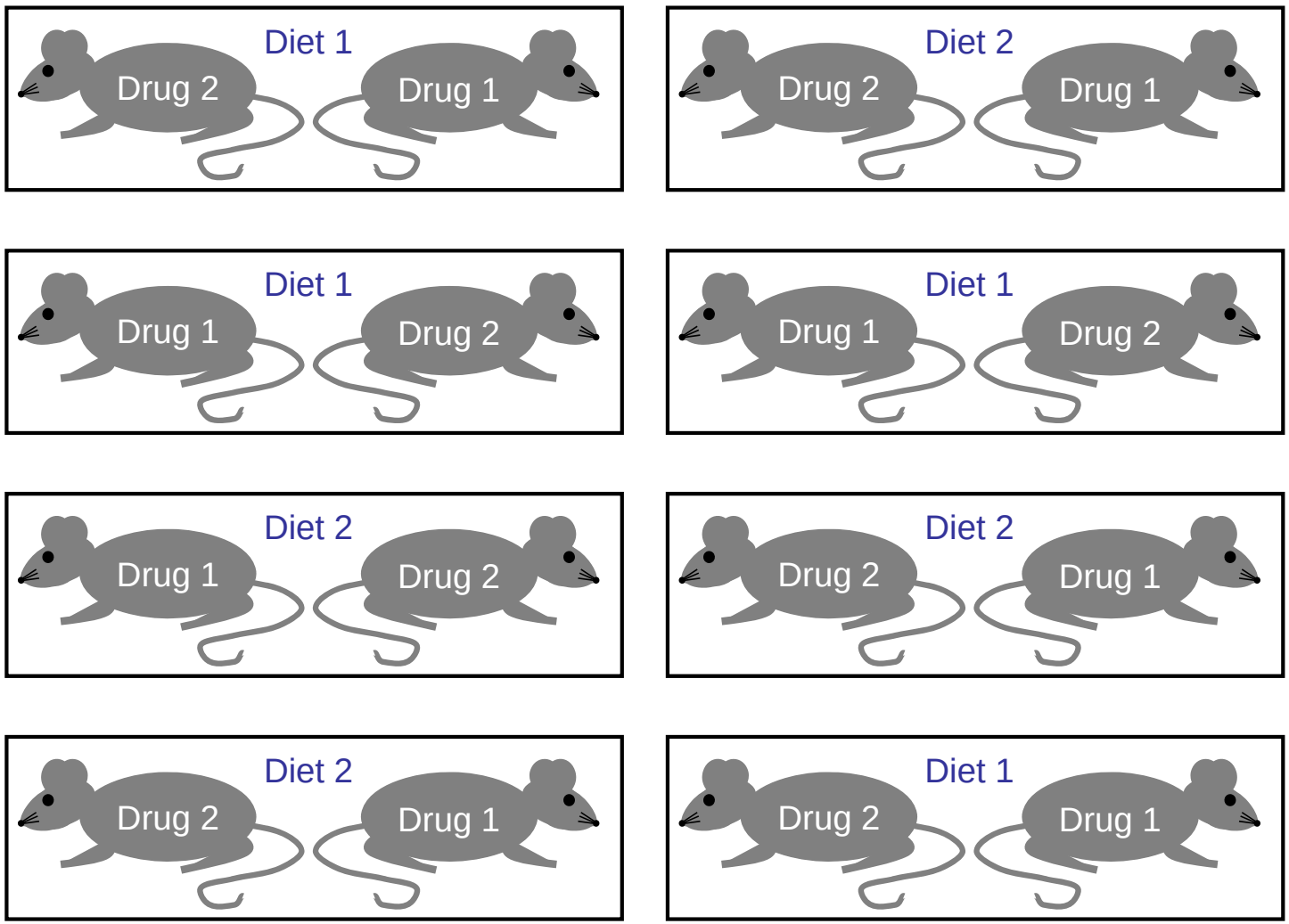
Recognizing Designs with Split-Plot Structures

- 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)

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

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

$\ell_{ik} =$ random litter effect $=$ whole-plot exp. unit random effect

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

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

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

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

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

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

$$\begin{aligned} \mathrm{Var}(\boldsymbol{Zu}) &= \boldsymbol{ZGZ}' = \sigma_\ell^2 \boldsymbol{ZZ}' \\ &= \sigma_\ell^2 \left[\underset{8\times 8}{\boldsymbol{I}} \otimes \underset{2\times 1}{\boldsymbol{1}} \right] \left[\underset{8\times 8}{\boldsymbol{I}} \otimes \underset{2\times 1}{\boldsymbol{1}} \right]' \\ &= \sigma_\ell^2 \left[\underset{8\times 8}{\boldsymbol{I}} \otimes \underset{2\times 2}{\boldsymbol{1}\boldsymbol{1}'} \right] \\ &= \text{Block Diagonal with blocks } \begin{bmatrix} \sigma_\ell^2 & \sigma_\ell^2 \\ \sigma_\ell^2 & \sigma_\ell^2 \end{bmatrix} \end{aligned}$$

$$\begin{aligned}
\text{Var}(\boldsymbol{y}) &= \boldsymbol{ZGZ'} + \boldsymbol{R} = \sigma^2_\ell \underset{8\times 8}{\boldsymbol{I}} \otimes \underset{2\times 2}{\mathbf{1}\mathbf{1}'} + \sigma^2_e \boldsymbol{I} \\
&= \text{Block Diagonal with blocks} \\
&\begin{bmatrix} \sigma^2_\ell + \sigma^2_e & \sigma^2_\ell \\ \sigma^2_\ell & \sigma^2_\ell + \sigma^2_e \end{bmatrix}
\end{aligned}$$

Thus, the covariance between two observations from the same litter is σ^2_ℓ and the correlation is $\frac{\sigma^2_\ell}{\sigma^2_\ell+\sigma^2_e}$.

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

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

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

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 $k = 1, 2, 3, 4$

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

$\mu_{ij} =$ 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

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

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

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

$$\boldsymbol{X} = \underset{4\times 1}{\mathbf{1}} \otimes \underset{12\times 12}{\boldsymbol{I}}, \qquad \boldsymbol{\beta} = \begin{bmatrix} \mu_{11} \\ \mu_{12} \\ \mu_{13} \\ \mu_{14} \\ \mu_{21} \\ \mu_{22} \\ \mu_{23} \\ \mu_{24} \\ \mu_{31} \\ \mu_{32} \\ \mu_{33} \\ \mu_{34} \end{bmatrix}$$

$$\boldsymbol{Z} = \left[\underset{4\times4}{\boldsymbol{I}} \otimes \underset{12\times1}{\mathbf{1}}, \quad \underset{12\times12}{\boldsymbol{I}} \otimes \underset{4\times1}{\mathbf{1}} \right]$$

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

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

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