15. ANOVA for Balanced Split-Plot Experiments

A Traditional Split-Plot Experiment

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

Table of Means and Marginal Means

| | Fertilizer Amount | | | | |
Genotype	0	50	100	150	
A	μ_{11}	μ_{12}	μ_{13}	μ_{14}	$\bar{\mu}_{1\cdot}$
B	μ_{21}	μ_{22}	μ_{23}	μ_{24}	$\bar{\mu}_{2\cdot}$
C	μ_{31}	μ_{32}	μ_{33}	μ_{34}	$\bar{\mu}_{3\cdot}$
	$\bar{\mu}_{\cdot 1}$	$\bar{\mu}_{\cdot 2}$	$\bar{\mu}_{\cdot 3}$	$\bar{\mu}_{\cdot 4}$	$\bar{\mu}_{\cdot\cdot}$

Best Linear Unbiased Estimators

Because the experiment is balanced, the GLS estimator is equal to the OLS estimator for any estimable $C\beta$:

$$C\hat{\beta}_{\Sigma} = C(X'\Sigma^{-1}X)^{-}X'\Sigma^{-1}y = C(X'X)^{-}X'y = C\hat{\beta}.$$

Because the elements of $E(y)$ are $\{\mu_{ij} : i = 1, 2, 3; \ j = 1, 2, 3, 4\}$, the estimable quantities are all linear combinations of the cell means $\{\mu_{ij} : i = 1, 2, 3; \ j = 1, 2, 3, 4\}$.

The BLUE of $\sum_{i=1}^{3} \sum_{j=1}^{4} c_{ij}\mu_{ij}$ is $\sum_{i=1}^{3} \sum_{j=1}^{4} c_{ij}\bar{y}_{ij\cdot}$.

Table of Best Linear Unbiased Estimates

	Fertilizer Amount				
Genotype	0	50	100	150	
A	$\bar{y}_{11\cdot}$	$\bar{y}_{12\cdot}$	$\bar{y}_{13\cdot}$	$\bar{y}_{14\cdot}$	$\bar{y}_{1\cdot\cdot}$
B	$\bar{y}_{21\cdot}$	$\bar{y}_{22\cdot}$	$\bar{y}_{23\cdot}$	$\bar{y}_{24\cdot}$	$\bar{y}_{2\cdot\cdot}$
C	$\bar{y}_{31\cdot}$	$\bar{y}_{32\cdot}$	$\bar{y}_{33\cdot}$	$\bar{y}_{34\cdot}$	$\bar{y}_{3\cdot\cdot}$
	$\bar{y}_{\cdot1\cdot}$	$\bar{y}_{\cdot2\cdot}$	$\bar{y}_{\cdot3\cdot}$	$\bar{y}_{\cdot4\cdot}$	$\bar{y}_{\cdot\cdot\cdot}$

ANOVA Table for the Traditional Split-Plot Design

Source	DF		
Blocks	$4 - 1$	$=$	3
Genotypes	$3 - 1$	$=$	2
Blocks $\times$ Geno	$(4 - 1)(3 - 1)$	$=$	6
Fert	$4 - 1$	$=$	3
Geno $\times$ Fert	$(3 - 1)(4 - 1)$	$=$	6
Blocks $\times$ Fert	$(4 - 1)(4 - 1)$		
+Blocks $\times$ Geno $\times$ Fert	$+(4 - 1)(3 - 1)(4 - 1)$	$=$	27
C.Total	$48 - 1$	$=$	47

ANOVA Table for the Traditional Split-Plot Design

Source	DF		
Blocks	$4 - 1$	$=$	3
Genotypes	$3 - 1$	$=$	2
Blocks $\times$ *Geno*	$(4 - 1)(3 - 1)$	$=$	6
Fert	$4 - 1$	$=$	3
Geno $\times$ *Fert*	$(3 - 1)(4 - 1)$	$=$	6
Error	$3(4 - 1)(4 - 1)$	$=$	27
C.Total	$48 - 1$	$=$	47

Why does $SS_{Blocks \times Fert} + SS_{Blocks \times Geno \times Fert} = SS_{Error}$?

- There are no terms in our model corresponding to $Block \times Fert$ combinations; thus, there is no reason to devote a separate line of our ANOVA table to $Block \times Fert$.

- Also, it can be shown that

$$E(MS_{Blocks \times Fert}) = E(MS_{Blocks \times Geno \times Fert}) = \sigma_e^2$$

Thus, it makes sense to estimate σ_e^2 with an inverse variance weighted average of independent unbiased estimators:

For this slide only, let

$$1 = Blocks \times Fert \text{ and } 2 = Blocks \times Geno \times Fert.$$

For $\ell = 1, 2$, $MS_\ell \sim \dfrac{E(MS_\ell)}{df_\ell} \chi^2_{df_\ell} \implies \text{Var}(MS_\ell) = 2\sigma_e^4/df_\ell$.

$$
\begin{aligned}
\frac{\text{Var}^{-1}(MS_1)MS_1 + \text{Var}^{-1}(MS_2)MS_2}{\text{Var}^{-1}(MS_1) + \text{Var}^{-1}(MS_2)} &= \frac{\frac{df_1}{2\sigma_e^4}MS_1 + \frac{df_2}{2\sigma_e^4}MS_2}{\frac{df_1}{2\sigma_e^4} + \frac{df_2}{2\sigma_e^4}} \\
&= \frac{df_1 MS_1 + df_2 MS_2}{df_1 + df_2} \\
&= \frac{SS_1 + SS_2}{df_1 + df_2}
\end{aligned}
$$

Thus, we combine the *Blocks × Fert* and *Blocks × Geno × Fert* lines of the ANOVA table and label the resulting line as *Error*.

$$SS_{Blocks \times Fert} + SS_{Blocks \times Geno \times Fert} = SS_{Error}$$

$$df_{Blocks \times Fert} + df_{Blocks \times Geno \times Fert} = df_{Error}$$

$$MS_{Error} = SS_{Error}/df_{Error}$$

$$E(MS_{Error}) = \sigma_e^2$$

Now let's look at the ANOVA table and the analyses that can be done with it in more detail.

For greater generality, let

- $w =$ the number of levels of the whole-plot treatment factor,

- $s =$ the number of levels of the split-plot treatment factor, and

- $b =$ the number of blocks.

ANOVA Table for the Traditional Split-Plot Design

Source	DF
Blocks	$b-1$
Genotypes	$w-1$
Blocks $\times$ *Geno*	$(b-1)(w-1)$
Fert	$s-1$
Geno $\times$ *Fert*	$(w-1)(s-1)$
Blocks $\times$ *Fert*	$(b-1)(s-1)$
$+Blocks \times Geno \times Fert$	$+(b-1)(w-1)(s-1)$
C.Total	$bws-1$

ANOVA Table for the Traditional Split-Plot Design

Source	DF
Blocks	$b - 1$
Genotypes	$w - 1$
Blocks $\times$ *Geno*	$(b-1)(w-1)$
Fert	$s - 1$
Geno $\times$ *Fert*	$(w-1)(s-1)$
Error	$w(b-1)(s-1)$
C.Total	$bws - 1$

ANOVA Table Sums of Squares

Source	Sum of Squares
Block	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (\bar{y}_{\cdot\cdot k} - \bar{y}_{\cdots})^2$
Geno	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (\bar{y}_{i\cdot\cdot} - \bar{y}_{\cdots})^2$
Block $\times$ Geno	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (\bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot\cdot k} + \bar{y}_{\cdots})^2$
Fert	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (\bar{y}_{\cdot j\cdot} - \bar{y}_{\cdots})^2$
Geno $\times$ Fert	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (\bar{y}_{ij\cdot} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot j\cdot} + \bar{y}_{\cdots})^2$
Error	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (y_{ijk} - \bar{y}_{i\cdot k} - \bar{y}_{ij\cdot} + \bar{y}_{i\cdot\cdot})^2$
C.Total	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (y_{ijk} - \bar{y}_{\cdots})^2$

Simplified ANOVA Table Sums of Squares

Source	Sum of Squares
Block	$ws \sum_{k=1}^{b} (\bar{y}_{\cdot\cdot k} - \bar{y}_{\cdots})^2$
Geno	$sb \sum_{i=1}^{w} (\bar{y}_{i\cdot\cdot} - \bar{y}_{\cdots})^2$
Block $\times$ *Geno*	$s \sum_{i=1}^{w} \sum_{k=1}^{b} (\bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot\cdot k} + \bar{y}_{\cdots})^2$
Fert	$wb \sum_{j=1}^{s} (\bar{y}_{\cdot j\cdot} - \bar{y}_{\cdots})^2$
Geno $\times$ *Fert*	$b \sum_{i=1}^{w} \sum_{j=1}^{s} (\bar{y}_{ij\cdot} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot j\cdot} + \bar{y}_{\cdots})^2$
Error	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (y_{ijk} - \bar{y}_{i\cdot k} - \bar{y}_{ij\cdot} + \bar{y}_{i\cdot\cdot})^2$
C.Total	$\sum_{i=1}^{w} \sum_{j=1}^{s} \sum_{k=1}^{b} (y_{ijk} - \bar{y}_{\cdots})^2$

$$E(MS_{Geno}) = \frac{sb}{w-1} \sum_{i=1}^{w} E(\bar{y}_{i\cdot\cdot} - \bar{y}_{\cdots})^2$$

$$= \frac{sb}{w-1} \sum_{i=1}^{w} E(\bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot\cdot} + \bar{w}_{i\cdot} - \bar{w}_{\cdot\cdot} + \bar{e}_{i\cdot\cdot} - \bar{e}_{\cdots})^2$$

$$= sb \left\{ \frac{\sum_{i=1}^{w} (\bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot\cdot})^2}{w-1} + E\left[\frac{\sum_{i=1}^{w} (\bar{w}_{i\cdot} - \bar{w}_{\cdot\cdot})^2}{w-1} \right] + E\left[\frac{\sum_{i=1}^{w} (\bar{e}_{i\cdot\cdot} - \bar{e}_{\cdots})^2}{w-1} \right] \right\}$$

$$= sb \frac{\sum_{i=1}^{w} (\bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot\cdot})^2}{w-1} + sb \frac{\sigma_w^2}{b} + sb \frac{\sigma_e^2}{sb}$$

$$= sb \frac{\sum_{i=1}^{w} (\bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot\cdot})^2}{w-1} + s\sigma_w^2 + \sigma_e^2$$

$$E(MS_{Block \times Geno}) = \frac{s}{(w-1)(b-1)} \sum_{i=1}^{w} \sum_{k=1}^{b} E(\bar{y}_{i \cdot k} - \bar{y}_{i \cdot \cdot} - \bar{y}_{\cdot \cdot k} + \bar{y}_{\cdots})^2$$

$$= \frac{s}{(w-1)(b-1)} \sum_{i=1}^{w} \sum_{k=1}^{b} E(w_{ik} - \bar{w}_{i \cdot} - \bar{w}_{\cdot k} + \bar{w}_{\cdot \cdot} + \bar{e}_{i \cdot k} - \bar{e}_{i \cdot \cdot} - \bar{e}_{\cdot \cdot k} + \bar{e}_{\cdots})^2$$

$$= \frac{s}{(w-1)(b-1)} E \left[\sum_{i=1}^{w} \sum_{k=1}^{b} (w_{ik} - \bar{w}_{i \cdot})^2 - 2 \sum_{i=1}^{w} \sum_{k=1}^{b} (w_{ik} - \bar{w}_{i \cdot})(\bar{w}_{\cdot k} - \bar{w}_{\cdot \cdot}) \right.$$
$$\left. + \sum_{i=1}^{w} \sum_{k=1}^{b} (\bar{w}_{\cdot k} - \bar{w}_{\cdot \cdot})^2 + e^2 \text{ sum} \right]$$

$$= \frac{s}{(w-1)(b-1)} E \left[\sum_{i=1}^{w} \sum_{k=1}^{b} (w_{ik} - \bar{w}_{i \cdot})^2 - w \sum_{k=1}^{b} (\bar{w}_{\cdot k} - \bar{w}_{\cdot \cdot})^2 + e^2 \text{ sum} \right]$$

$$= \frac{s}{(w-1)(b-1)} [w(b-1)\sigma_w^2 - w(b-1)\sigma_w^2/w + E(e^2 \text{ sum})]$$

It can be shown that

$$
\begin{aligned}
E(e^2 \text{ sum}) &= E\left[\sum_{i=1}^{w}\sum_{k=1}^{b}(\bar{e}_{i\cdot k} - \bar{e}_{i\cdot\cdot} - \bar{e}_{\cdot\cdot k} + \bar{e}_{\cdots})^2\right] \\
&= \frac{(w-1)(b-1)}{s}\sigma_e^2.
\end{aligned}
$$

Putting it all together yields

$$
E(MS_{Block \times Geno}) = s\sigma_w^2 + \sigma_e^2.
$$

Source	Expected Mean Squares
Block	
Geno	$s\sigma_w^2 + \sigma_e^2 + \frac{sb}{w-1} \sum_{i=1}^{w} (\bar{\mu}_{i \cdot} - \bar{\mu}_{\cdot \cdot})^2$
Block $\times$ *Geno*	$s\sigma_w^2 + \sigma_e^2$
Fert	
Geno $\times$ *Fert*	
Error	

The Test for Whole-Plot Factor Main Effects

To test for genotype main effects, i.e.,

$$H_0 : \bar{\mu}_{1.} = \cdots = \bar{\mu}_{w.} \iff H_0 : \frac{sb}{w-1} \sum_{i=1}^{w} (\bar{\mu}_{i.} - \bar{\mu}_{..})^2 = 0,$$

compare $\frac{MS_{Geno}}{MS_{Block \times Geno}}$ to a central F distribution with $w - 1$ and $(w - 1)(b - 1)$ degrees of freedom.

Comparison of Whole-Plot Factor Marginal Means

The BLUE of $\bar{\mu}_{1\cdot} - \bar{\mu}_{2\cdot}$ is $\bar{y}_{1\cdot\cdot} - \bar{y}_{2\cdot\cdot}$.

$$
\begin{aligned}
\mathrm{Var}(\bar{y}_{1\cdot\cdot} - \bar{y}_{2\cdot\cdot}) &= \mathrm{Var}(\bar{\mu}_{1\cdot} - \bar{\mu}_{2\cdot} + \bar{w}_{1\cdot} - \bar{w}_{2\cdot} + \bar{e}_{1\cdot\cdot} - \bar{e}_{2\cdot\cdot}) \\[2mm]
&= \frac{2\sigma_w^2}{b} + \frac{2\sigma_e^2}{sb} \\[2mm]
&= \frac{2}{sb}(s\sigma_w^2 + \sigma_e^2) = \frac{2}{sb}E(MS_{Block \times Geno})
\end{aligned}
$$

$$
\widehat{\mathrm{Var}}(\bar{y}_{1\cdot\cdot} - \bar{y}_{2\cdot\cdot}) = \frac{2}{sb}MS_{Block \times Geno}
$$

We can use

$$t = \frac{\bar{y}_{1..} - \bar{y}_{2..} - (\bar{\mu}_{1.} - \bar{\mu}_{2.})}{\sqrt{\frac{2}{sb}MS_{Block \times Geno}}} \sim t_{(w-1)(b-1)}$$

to get tests of $H_0 : \bar{\mu}_{1.} = \bar{\mu}_{2.}$

or construct confidence intervals for $\bar{\mu}_{1.} - \bar{\mu}_{2.}$.

Furthermore, suppose C is a matrix whose rows are contrast vectors so that $C\mathbf{1} = \mathbf{0}$. Then

$$
\text{Var}\left(C \begin{bmatrix} \bar{y}_{1..} \\ \vdots \\ \bar{y}_{w..} \end{bmatrix} \right) = \text{Var}\left(C \begin{bmatrix} \bar{b}_{.} & + & \bar{w}_{1.} & + & \bar{e}_{1..} \\ & & & \vdots & \\ \bar{b}_{.} & + & \bar{w}_{w.} & + & \bar{e}_{w..} \end{bmatrix} \right)
$$

$$
= \text{Var}\left(C\mathbf{1}\bar{b}_{.} + C \begin{bmatrix} \bar{w}_{1.} & + & \bar{e}_{1..} \\ & \vdots & \\ \bar{w}_{w.} & + & \bar{e}_{w..} \end{bmatrix} \right) = C\, \text{Var}\left(\begin{bmatrix} \bar{w}_{1.} & + & \bar{e}_{1..} \\ & \vdots & \\ \bar{w}_{w.} & + & \bar{e}_{w..} \end{bmatrix} \right) C'
$$

$$
= C \left(\frac{\sigma_w^2}{b} + \frac{\sigma_e^2}{sb} \right) IC' = \left(\frac{\sigma_w^2}{b} + \frac{\sigma_e^2}{sb} \right) CC' = \frac{E(MS_{Block \times Geno})}{sb} CC'
$$

An F statistic, with q and $(w-1)(b-1)$ degrees of freedom, for testing

$$H_0 : \boldsymbol{C} \begin{bmatrix} \bar{\mu}_{1\cdot} \\ \vdots \\ \bar{\mu}_{w\cdot} \end{bmatrix} = \boldsymbol{0}, \text{ is}$$

$$F = \frac{\left(\boldsymbol{C} \begin{bmatrix} \bar{y}_{1\cdot} \\ \vdots \\ \bar{y}_{w\cdot} \end{bmatrix} \right)' \left[\frac{MS_{Block \times Geno}}{sb} \boldsymbol{C}\boldsymbol{C}' \right]^{-1} \left(\boldsymbol{C} \begin{bmatrix} \bar{y}_{1\cdot\cdot} \\ \vdots \\ \bar{y}_{w\cdot\cdot} \end{bmatrix} \right)}{q},$$

where q is the number of rows of $\boldsymbol{C}$ (which must have full row rank to ensure that the hypothesis is testable).

Inference for the Split-Plot Factor

$$
\begin{aligned}
E(MS_{Fert}) &= \frac{wb}{s-1} \sum_{j=1}^{s} E(\bar{y}_{\cdot j \cdot} - \bar{y}_{\cdots})^2 \\
&= \frac{wb}{s-1} \sum_{j=1}^{s} E(\bar{\mu}_{\cdot j} - \bar{\mu}_{\cdot \cdot} + \bar{e}_{\cdot j \cdot} - \bar{e}_{\cdots})^2 \\
&= \frac{wb}{s-1} \sum_{j=1}^{s} (\bar{\mu}_{\cdot j} - \bar{\mu}_{\cdot \cdot})^2 + \sigma_e^2.
\end{aligned}
$$

Likewise, it can be shown that

$$
E(MS_{Error}) = \sigma_e^2.
$$

Source	Expected Mean Squares
Block	
Geno	$s\sigma_w^2 + \sigma_e^2 + \frac{sb}{w-1}\sum_{i=1}^{w}(\bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot\cdot})^2$
Block $\times$ *Geno*	$s\sigma_w^2 + \sigma_e^2$
Fert	$\sigma_e^2 + \frac{wb}{s-1}\sum_{j=1}^{s}(\bar{\mu}_{\cdot j} - \bar{\mu}_{\cdot\cdot})^2$
Geno $\times$ *Fert*	
Error	σ_e^2

The Test for Split-Plot Factor Main Effects

To test for fertilizer main effects, i.e.,

$$H_0 : \bar{\mu}_{\cdot 1} = \cdots = \bar{\mu}_{\cdot s} \Longleftrightarrow H_0 : \frac{wb}{s-1} \sum_{j=1}^{s} (\bar{\mu}_{\cdot j} - \bar{\mu}_{\cdot \cdot})^2 = 0,$$

compare $\frac{MS_{Fert}}{MS_{Error}}$ to a central F distribution with $s - 1$ and $w(s - 1)(b - 1)$ degrees of freedom.

Comparison of Split-Plot Factor Marginal Means

The BLUE of $\bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 2}$ is $\bar{y}_{\cdot 1 \cdot} - \bar{y}_{\cdot 2 \cdot}$.

$$\bar{y}_{\cdot 1 \cdot} - \bar{y}_{\cdot 2 \cdot} = (\bar{\mu}_{\cdot 1} + \bar{b}_{\cdot} + \bar{w}_{\cdot \cdot} + \bar{e}_{\cdot 1 \cdot}) - (\bar{\mu}_{\cdot 2} + \bar{b}_{\cdot} + \bar{w}_{\cdot \cdot} + \bar{e}_{\cdot 2 \cdot})$$

$$\mathrm{Var}(\bar{y}_{\cdot 1 \cdot} - \bar{y}_{\cdot 2 \cdot}) = \mathrm{Var}(\bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 2} + \bar{e}_{\cdot 1 \cdot} - \bar{e}_{\cdot 2 \cdot})$$

$$= \tfrac{2}{wb}\sigma_e^2 = \tfrac{2}{wb}E(MS_{Error})$$

$$\widehat{\mathrm{Var}}(\bar{y}_{\cdot 1 \cdot} - \bar{y}_{\cdot 2 \cdot}) = \tfrac{2}{wb}MS_{Error}$$

We can use

$$t = \frac{\bar{y}_{\cdot 1 \cdot} - \bar{y}_{\cdot 2 \cdot} - (\bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 2})}{\sqrt{\frac{2}{wb}MS_{Error}}} \ \sim \ t_{w(s-1)(b-1)}$$

to get tests of $H_0 : \bar{\mu}_{\cdot 1} = \bar{\mu}_{\cdot 2}$

or to construct confidence intervals for $\bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 2}$.

Furthermore, suppose C is a matrix with rows that are contrast vectors so that $C\mathbf{1} = \mathbf{0}$. Then

$$\mathrm{Var}\left(C \left[\begin{array}{c} \bar{y}_{\cdot 1 \cdot} \\ \vdots \\ \bar{y}_{\cdot s \cdot} \end{array} \right] \right) = \mathrm{Var}\left(C \left[\begin{array}{ccccc} \bar{b}_{\cdot} & + & \bar{w}_{\cdot\cdot} & + & \bar{e}_{\cdot 1 \cdot} \\ & & & \vdots & \\ \bar{b}_{\cdot} & + & \bar{w}_{\cdot\cdot} & + & \bar{e}_{\cdot s \cdot} \end{array} \right] \right)$$

$$= \mathrm{Var}\left(C\mathbf{1}\bar{b}_{\cdot} + C\mathbf{1}\bar{w}_{\cdot\cdot} + C \left[\begin{array}{c} \bar{e}_{\cdot 1 \cdot} \\ \vdots \\ \bar{e}_{\cdot s \cdot} \end{array} \right] \right) = C\, \mathrm{Var}\left(\left[\begin{array}{c} \bar{e}_{\cdot 1 \cdot} \\ \vdots \\ \bar{e}_{\cdot s \cdot} \end{array} \right] \right)\, C'$$

$$= C \left(\frac{\sigma_e^2}{wb} \right) I C' = \frac{E(MS_{Error})}{wb} CC'$$

An F statistic, with q and $w(s-1)(b-1)$ degrees of freedom, for testing

$$H_0 : \boldsymbol{C} \left[\begin{array}{c} \bar{\mu}_{\cdot 1} \\ \vdots \\ \bar{\mu}_{\cdot s} \end{array} \right] = \boldsymbol{0}, \text{ is}$$

$$F = \frac{\left(\boldsymbol{C} \left[\begin{array}{c} \bar{y}_{\cdot 1 \cdot} \\ \vdots \\ \bar{y}_{\cdot s \cdot} \end{array} \right] \right)' \left[\frac{MS_{Error}}{wb} \boldsymbol{C} \boldsymbol{C}' \right]^{-1} \left(\boldsymbol{C} \left[\begin{array}{c} \bar{y}_{\cdot 1 \cdot} \\ \vdots \\ \bar{y}_{\cdot s \cdot} \end{array} \right] \right)}{q}$$

where q is the number of rows of $\boldsymbol{C}$ (which must have full row rank to ensure that the hypothesis is testable).

Inference for Interactions

$$E(MS_{Geno \times Fert}) = \frac{b}{(w-1)(s-1)} \sum_{i=1}^{w} \sum_{j=1}^{s} E(\bar{y}_{ij\cdot} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot j\cdot} + \bar{y}_{\cdots})^2$$

$$= \frac{b}{(w-1)(s-1)} \sum_{i=1}^{w} \sum_{j=1}^{s} E(\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot} + \bar{e}_{ij\cdot} - \bar{e}_{i\cdot\cdot} - \bar{e}_{\cdot j\cdot} + \bar{e}_{\cdots})^2$$

$$= \cdots$$

$$= \frac{b}{(w-1)(s-1)} \sum_{i=1}^{w} \sum_{j=1}^{s} (\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot})^2 + \sigma_e^2.$$

It can be shown that

$$\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot} = 0 \ \forall \ i, j$$

is equivalent to

$$\mu_{ij} - \mu_{ij^*} - \mu_{i^*j} + \mu_{i^*j^*} = 0 \ \forall \ i \neq i^*, \ j \neq j^*.$$

Thus, $\qquad \dfrac{b}{(w-1)(s-1)} \sum_{i=1}^{w} \sum_{j=1}^{s} (\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot})^2 = 0$

is equivalent to no interactions between genotypes and fertilizers.

Source	Expected Mean Squares
Block	
Geno	$s\sigma_w^2 + \sigma_e^2 + \frac{sb}{w-1}\sum_{i=1}^{w}(\bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot\cdot})^2$
Block $\times$ *Geno*	$s\sigma_w^2 + \sigma_e^2$
Fert	$\sigma_e^2 + \frac{wb}{s-1}\sum_{j=1}^{s}(\bar{\mu}_{\cdot j} - \bar{\mu}_{\cdot\cdot})^2$
Geno $\times$ *Fert*	$\sigma_e^2 + \frac{b}{(w-1)(s-1)}\sum_{i=1}^{w}\sum_{j=1}^{s}(\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot})^2$
Error	σ_e^2

The Test for Whole $\times$ Split Interaction Effects

To test for genotype $\times$ fertilizer interaction effects, i.e.,

$$H_0 : \mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot} = 0 \ \forall \ i,j \iff$$

$$H_0 : \frac{b}{(w-1)(s-1)} \sum_{i=1}^{w} \sum_{j=1}^{s} (\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot})^2 = 0,$$

compare $\frac{MS_{Geno \times Fert}}{MS_{Error}}$ to a central F distribution with $(w-1)(s-1)$ and $w(s-1)(b-1)$ degrees of freedom.

Inference for Simple Effects

Consider the difference between two fertilizer means within a genotype, e.g., $\mu_{11} - \mu_{12}$ whose BLUE is $\bar{y}_{11\cdot} - \bar{y}_{12\cdot}$.

$$
\begin{aligned}
\mathrm{Var}(\bar{y}_{11\cdot} - \bar{y}_{12\cdot}) &= \mathrm{Var}(\mu_{11} - \mu_{12} + \bar{b}_\cdot - \bar{b}_\cdot + \bar{w}_{1\cdot} - \bar{w}_{1\cdot} + \bar{e}_{11\cdot} - \bar{e}_{12\cdot}) \\[2mm]
&= \tfrac{2}{b}\sigma_e^2 \\[2mm]
\widehat{\mathrm{Var}}(\bar{y}_{11\cdot} - \bar{y}_{12\cdot}) &= \tfrac{2}{b}MS_{Error}
\end{aligned}
$$

We can use

$$t = \frac{\bar{y}_{11\cdot} - \bar{y}_{12\cdot} - (\mu_{11} - \mu_{12})}{\sqrt{\frac{2}{b}MS_{Error}}} \sim t_{w(s-1)(b-1)}$$

to get tests of $H_0 : \mu_{11} = \mu_{12}$

or construct confidence intervals for $\mu_{11} - \mu_{12}$.

Now consider the difference between two genotype means within a fertilizer, e.g., $\mu_{11} - \mu_{21}$ whose BLUE is $\bar{y}_{11.} - \bar{y}_{21.}$.

$$\text{Var}(\bar{y}_{11.} - \bar{y}_{21.}) = \text{Var}(\mu_{11} - \mu_{21} + \bar{w}_{1.} - \bar{w}_{2.} + \bar{e}_{11.} - \bar{e}_{21.})$$

$$= \frac{2\sigma_w^2}{b} + \frac{2\sigma_e^2}{b}$$

$$= \frac{2}{b}(\sigma_w^2 + \sigma_e^2).$$

This variance is not a constant times any expected mean square from our ANOVA table.

We need an estimator of $\sigma_w^2 + \sigma_e^2$. We have

$$E(MS_{Block \times Geno}) = s\sigma_w^2 + \sigma_e^2, \qquad E(MS_{Error}) = \sigma_e^2, \qquad \text{and}$$

$$E\left(\frac{1}{s}MS_{Block \times Geno} + \frac{s-1}{s}MS_{Error}\right) = \sigma_w^2 + \frac{\sigma_e^2}{s} + \frac{(s-1)\sigma_e^2}{s}$$

$$= \sigma_w^2 + \sigma_e^2.$$

Thus,

$$\frac{1}{s}MS_{Block \times Geno} + \frac{s-1}{s}MS_{Error}$$

is an unbiased estimator of $\sigma_w^2 + \sigma_e^2$.

It follows that

$$\widehat{\mathrm{Var}}(\bar{y}_{11\cdot} - \bar{y}_{21\cdot}) \equiv \frac{2}{sb}MS_{Block \times Geno} + \frac{2(s-1)}{sb}MS_{Error}$$

is an unbiased estimator of $\mathrm{Var}(\bar{y}_{11\cdot} - \bar{y}_{21\cdot})$.

We can use

$$\frac{\bar{y}_{11\cdot} - \bar{y}_{21\cdot} - (\mu_{11} - \mu_{21})}{\sqrt{\widehat{\mathrm{Var}}(\bar{y}_{11\cdot} - \bar{y}_{21\cdot})}} \stackrel{\cdot}{\sim} t_d, \text{ with } d \text{ degrees of freedom}$$

computed by Cochran-Satterthwaite to get approximate tests of $H_0 : \mu_{11} = \mu_{21}$ or to construct approximate confidence intervals for $\mu_{11} - \mu_{21}$.

Full Table of Expected Mean Squares

Source	Expected Mean Squares
Block	$ws\sigma_b^2 + s\sigma_w^2 + \sigma_e^2$
Geno	$s\sigma_w^2 + \sigma_e^2 + \frac{sb}{w-1}\sum_{i=1}^{w}(\bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot\cdot})^2$
Block $\times$ Geno	$s\sigma_w^2 + \sigma_e^2$
Fert	$\sigma_e^2 + \frac{wb}{s-1}\sum_{j=1}^{s}(\bar{\mu}_{\cdot j} - \bar{\mu}_{\cdot\cdot})^2$
Geno $\times$ Fert	$\sigma_e^2 + \frac{b}{(w-1)(s-1)}\sum_{i=1}^{w}\sum_{j=1}^{s}(\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot})^2$
Error	σ_e^2

Inferences for Cell Mean μ_{ij}

$$
\begin{aligned}
\text{Var}(\bar{y}_{ij\cdot}) &= \text{Var}(\mu_{ij} + \bar{b}_\cdot + \bar{w}_{i\cdot} + \bar{e}_{ij\cdot}) \\
&= \frac{\sigma_b^2}{b} + \frac{\sigma_w^2}{b} + \frac{\sigma_e^2}{b}
\end{aligned}
$$

We can construct the unbiased estimator

$$
\widehat{\text{Var}}(\bar{y}_{ij\cdot}) = \frac{1}{wbs}\left[MS_{Block} + (w-1)\,MS_{Block \times Geno} + w(s-1)\,MS_{Error}\right]
$$

with approximate degrees of freedom from
Cochran-Satterthwaite.

Inferences for Whole-Plot-Factor Means $\bar{\mu}_{i\cdot}$

$$
\begin{aligned}
\text{Var}(\bar{y}_{i\cdot\cdot}) &= \text{Var}(\bar{\mu}_{i\cdot} + \bar{b}_{\cdot} + \bar{w}_{i\cdot} + \bar{e}_{i\cdot\cdot}) \\
&= \frac{\sigma_b^2}{b} + \frac{\sigma_w^2}{b} + \frac{\sigma_e^2}{sb}
\end{aligned}
$$

This can be estimated with a linear combination of mean squares.

If block effects are considered fixed rather than random,

$$
\begin{aligned}
\text{Var}(\bar{y}_{i\cdot\cdot}) &= \text{Var}(\bar{\mu}_{i\cdot} + \bar{b}_{\cdot} + \bar{w}_{i\cdot} + \bar{e}_{i\cdot\cdot}) \\
&= \frac{\sigma_w^2}{b} + \frac{\sigma_e^2}{sb} \\
&= \frac{1}{sb}\left(s\sigma_w^2 + \sigma_e^2\right)
\end{aligned}
$$

We can estimate this variance by $\frac{1}{sb}MS_{Block \times Geno}$ with $(w-1)(b-1)$ degrees of freedom.

Inferences for Split-Plot-Factor Means $\bar{\mu}_{\cdot j}$
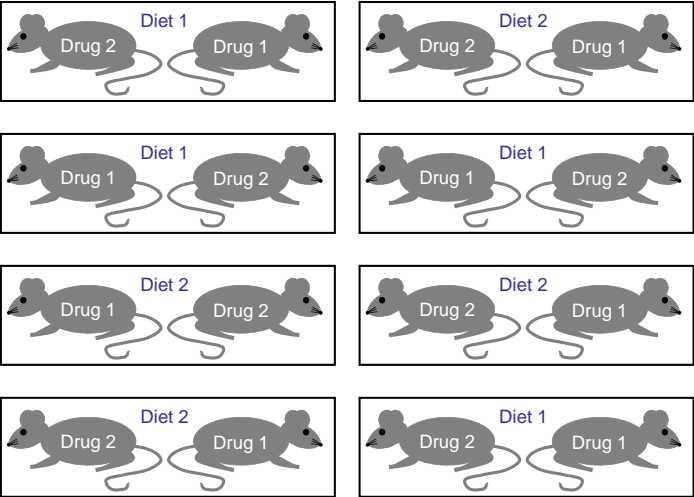
If block effects are considered random,

$$
\begin{aligned}
\text{Var}(\bar{y}_{\cdot j\cdot}) &= \text{Var}(\bar{\mu}_{\cdot j} + \bar{b}_{\cdot} + \bar{w}_{\cdot\cdot} + \bar{e}_{\cdot j\cdot}) \\
&= \frac{\sigma_b^2}{b} + \frac{\sigma_w^2}{wb} + \frac{\sigma_e^2}{wb}
\end{aligned}
$$

If block effects are considered fixed,

$$
\begin{aligned}
\text{Var}(\bar{y}_{\cdot j\cdot}) &= \text{Var}(\bar{\mu}_{\cdot j} + \bar{b}_{\cdot} + \bar{w}_{\cdot\cdot} + \bar{e}_{\cdot j\cdot}) \\
&= \frac{\sigma_w^2}{wb} + \frac{\sigma_e^2}{wb}.
\end{aligned}
$$

Both can be estimated by linear combinations of mean squares.

Diet and Drug Split-Plot Experiment

Linear Mixed-Effects Model

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

$\ell_{ik} \overset{iid}{\sim} N(0, \sigma_\ell^2)$ independent of $e_{ijk} \overset{iid}{\sim} N(0, \sigma_e^2)$

Start of the ANOVA Table

With v = # of whole-plot experimental units per level of the whole-plot factor...

Source	DF
Diet	$w - 1$
Litter(Diet)	$(v - 1)w$
Drug	$s - 1$
Diet $\times$ *Drug*	$(w - 1)(s - 1)$
Drug $\times$ *Litter(Diet)*	$(s - 1)(v - 1)w$
C.Total	$wvs - 1$

Start of the ANOVA Table

With $v =$ # of whole-plot experimental units per level of the whole-plot factor...

Source	DF
Diet	$w - 1$
Whole Plot Error	$(v - 1)w$
Drug	$s - 1$
Diet $\times$ Drug	$(w - 1)(s - 1)$
Split Plot Error	$(s - 1)(v - 1)w$
C.Total	$wvs - 1$

Completing the ANOVA Table and Additional Analyses

- The techniques used in the previous slides can be applied to find expressions for the sums of squares, mean squares, expected mean squares, and F statistics.

- Because of balance, $\bar{y}_{ij\cdot}$ is the BLUE of $\mu + \alpha_i + \beta_j + \gamma_{ij}$.

- The reasoning in the previous slides can be used to determine appropriate standard errors, tests, and confidence intervals.

Summary of ANOVA for a Balanced Split-Plot

- Use whole-plot-error mean square for inferences on
  - contrasts among whole-plot-factor marginal means
- Use split-plot-error mean square for inferences on
  - contrasts among split-plot-factor marginal means
  - whole$\times$ split interactions
  - comparison of split-plot levels within a whole-plot level
- Construct a linear combination of mean squares for inferences on
  - comparison of whole-plot levels within a split-plot level
  - a comparison within neither whole-plot nor split-plot levels (e.g., $\mu_{11} - \mu_{22}$)
  - most means