

ANOVA ANALYSIS OF A
BALANCED SPLIT-LOT
EXPERIMENT

Split-Plot Experimental Designs

	Field								Plot			
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

Split Plot or Sub Plot

$$Y_{ijk} = \mu_{ij} + b_k + W_{ik} + e_{ijk}$$

Genotype $i = 1, 2, 3$

Fertilizer $j = 1, 2, 3, 4$

Block $k = 1, 2, 3, 4$

μ_{ij} = Mean for
Genotype i
Fertilizer j

$$\tilde{u} = \begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \\ w_{11} \\ w_{21} \\ \vdots \\ w_{34} \end{bmatrix} = \begin{bmatrix} \mu \\ \omega \end{bmatrix} \sim N \left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_b^2 I & 0 \\ 0 & \sigma_w^2 I \end{bmatrix} \right)$$

$$\begin{bmatrix} \tilde{u} \\ \tilde{e} \end{bmatrix} \sim N \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} G & 0 \\ 0 & \sigma_e^2 I \end{bmatrix} \right)$$

<u>Source</u>	<u>DF</u>		
Blocks	$4-1$	$=$	3
Genotypes	$3-1$	$=$	2
Blocks x Geno	$(4-1)(3-1)$	$=$	6 whole plot x u
Fert	$4-1$	$=$	3
Geno x Fert	$(3-1)(4-1)$	$=$	6
Block x Fert + Blocks x Geno x Fert	$(4-1)(4-1)$ $+ (4-1)(3-1)(4-1)$	$=$	27 split plot x u
<hr/> C. Total	<hr/> $48-1$		<hr/> 47

Source

Sum of Squares

Blocks

$$\sum_{i=1}^3 \sum_{j=1}^4 \sum_{k=1}^4 (\bar{y}_{\cdot\cdot k} - \bar{y}_{\cdot\cdot\cdot})^2$$

Geno

$$\sum_{i=1}^3 \sum_{j=1}^4 \sum_{k=1}^4 (\bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot\cdot\cdot})^2$$

Blocks x Geno

$$\sum_{i=1}^3 \sum_{j=1}^4 \sum_{k=1}^4 (\bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot\cdot k} + \bar{y}_{\cdot\cdot\cdot})^2$$

Fert

$$\sum_{i=1}^3 \sum_{j=1}^4 \sum_{k=1}^4 (\bar{y}_{\cdot j \cdot} - \bar{y}_{\cdot\cdot\cdot})^2$$

Geno x Fert

$$\sum_{i=1}^3 \sum_{j=1}^4 \sum_{k=1}^4 (\bar{y}_{ij\cdot} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot j \cdot} + \bar{y}_{\cdot\cdot\cdot})^2$$

error

$$\sum_{i=1}^3 \sum_{j=1}^4 \sum_{k=1}^4 (y_{ijk} - \bar{y}_{i\cdot k} - \bar{y}_{ij\cdot} + \bar{y}_{i\cdot\cdot})^2$$

c. Total

$$\sum_{i=1}^3 \sum_{j=1}^4 \sum_{k=1}^4 (y_{ijk} - \bar{y}_{\cdot\cdot\cdot})^2$$

$$E(MS_{GENO}) = \frac{FB}{G-1} \sum_{i=1}^G E(\bar{Y}_{i..} - \bar{Y}_{...})^2$$

$$= \frac{FB}{G-1} \sum_{i=1}^G E(\bar{\mu}_{i.} - \bar{\mu}_{..} + \bar{w}_{i.} - \bar{w}_{..} + \bar{e}_{i..} - \bar{e}_{...})^2$$

$$= FB \frac{\sum_{i=1}^G (\bar{\mu}_{i.} - \bar{\mu}_{..})^2}{G-1} + FB E \left[\frac{\sum_{i=1}^G (\bar{w}_{i.} - \bar{w}_{..})^2}{G-1} \right]$$

$$+ FB E \left[\frac{\sum_{i=1}^G (\bar{e}_{i..} - \bar{e}_{...})^2}{G-1} \right]$$

$$= FB \sum_{i=1}^G \frac{(\bar{\mu}_{i.} - \bar{\mu}_{..})^2}{G-1} + FB \sigma_w^2 / B + FB \sigma_e^2 / FB$$

$$= FB \sum_{i=1}^G \frac{(\bar{\mu}_{i.} - \bar{\mu}_{..})^2}{G-1} + F \sigma_w^2 + \sigma_e^2$$

$$E(MS_{\text{BLOCK} \times \text{GENO}}) = \frac{F}{(B-1)(G-1)} \sum_{i=1}^G \sum_{k=1}^B E(\bar{y}_{i \cdot k} - \bar{y}_{i \cdot \cdot} - \bar{y}_{\cdot \cdot k} + \bar{y}_{\cdot \cdot \cdot})^2$$

$$= \frac{F}{(B-1)(G-1)} \sum_{i=1}^G \sum_{k=1}^B E(w_{ik} - \bar{w}_{i \cdot} - \bar{w}_{\cdot k} + \bar{w}_{\cdot \cdot} + e_{i \cdot k} - \bar{e}_{i \cdot \cdot} - \bar{e}_{\cdot \cdot k} + \bar{e}_{\cdot \cdot \cdot})^2$$

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

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

$$= \frac{F}{(B-1)(G-1)} \left[G(B-1)\sigma_w^2 - G(B-1)\sigma_w^2/G + e \text{ terms} \right]$$

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

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

$$H_0: \bar{\mu}_{1.} = \bar{\mu}_{2.} = \bar{\mu}_{3.} \iff H_0: \frac{FB}{G-1} \sum_{i=1}^G (\bar{\mu}_{i.} - \bar{\mu}_{..})^2 = 0,$$

compare $\frac{MS_{GENO}}{MS_{BLOCK \times GENO}}$ to an

F distribution with $G-1$ and $(B-1)(G-1)$ d.f.

Reject H_0 at level α iff

$$\frac{MS_{GENO}}{MS_{BLOCK \times GENO}} \geq F_{G-1, (B-1)(G-1)}^{\alpha}.$$

Contrasts among genotype means:

$$\text{Var}(\bar{Y}_{1..} - \bar{Y}_{2..}) = \text{Var}(\bar{\mu}_{1.} - \bar{\mu}_{2.} + \bar{w}_{1.} - \bar{w}_{2.} + \bar{e}_{1..} - \bar{e}_{2..})$$

$$= \frac{2\sigma_w^2}{B} + \frac{2\sigma_e^2}{FB}$$

$$= \frac{2}{FB} (F\sigma_w^2 + \sigma_e^2)$$

$$= \frac{2}{FB} E(MS_{\text{BLOCK} \times \text{GENO}})$$

$$\hat{\text{Var}}(\bar{Y}_{1..} - \bar{Y}_{2..}) = \frac{2}{FB} MS_{\text{BLOCK} \times \text{GENO}}$$

Can use

$$t = \frac{\bar{y}_{1..} - \bar{y}_{2..} - (\bar{\mu}_{1.} - \bar{\mu}_{2.})}{\sqrt{\frac{2}{FB} MS_{\text{BLOCK} \times \text{GENO}}} \sim t_{(B-1)(G-1)}$$

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

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

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

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

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

$$= C \operatorname{Var} \begin{pmatrix} \bar{w}_{1..} + \bar{e}_{1..} \\ \vdots \\ \bar{w}_{a..} + \bar{e}_{a..} \end{pmatrix} C'$$

$$= C \left(\frac{\sigma_w^2}{B} + \frac{\sigma_e^2}{FB} \right) I C'$$

$$= \left(\frac{\sigma_w^2}{B} + \frac{\sigma_e^2}{FB} \right) CC' = \frac{E(MS_{\text{BLOCK} \times \text{GENO}})}{FB} CC'$$

An F statistic for testing

$$H_0: C \begin{bmatrix} \bar{\mu}_{1.} \\ \vdots \\ \bar{\mu}_{a.} \end{bmatrix} = \underline{0}, \text{ with } df = q, (B-1)(a-1), \text{ is}$$

$$\frac{\left(C \begin{bmatrix} \bar{y}_{1..} \\ \vdots \\ \bar{y}_{a..} \end{bmatrix} \right)' \left[\frac{MS_{\text{BLOCK} \times \text{GENO}}}{FB} CC' \right]^{-1} C \begin{bmatrix} \bar{y}_{1..} \\ \vdots \\ \bar{y}_{a..} \end{bmatrix}}{q},$$

where q is the number of rows of C
 (which must be linearly independent to ensure
 that the hypothesis is testable).

What if we want to compare the first two genotypes in the absence of fertilizer, i.e., what if we want to test

$$H_0: \mu_{11} = \mu_{21} \quad ?$$

$$\begin{aligned} \text{Var}(\bar{Y}_{11\cdot} - \bar{Y}_{21\cdot}) &= \text{Var}(\mu_{11} - \mu_{21} + \bar{W}_{1\cdot} - \bar{W}_{2\cdot} + \bar{e}_{11\cdot} - \bar{e}_{21\cdot}) \\ &= 2\sigma_w^2/B + 2\sigma_e^2/B \\ &= \frac{2}{B} (\sigma_w^2 + \sigma_e^2). \end{aligned}$$

We can estimate $F\sigma_w^2 + \sigma_e^2$ with $MS_{\text{BLOCK} \times \text{GENO}}$, but what about $\sigma_w^2 + \sigma_e^2$?

$$E(MS_{\text{ERROR}}) = \sigma_e^2 \quad \text{so}$$

$$\begin{aligned} E\left(\frac{MS_{\text{BLOCK} \times \text{GENO}}}{F} + \frac{F-1}{F} MS_{\text{ERROR}}\right) \\ = \sigma_w^2 + \sigma_e^2/F + (F-1)\sigma_e^2/F = \sigma_w^2 + \sigma_e^2. \end{aligned}$$

Thus,

$$\hat{\text{Var}}(\bar{Y}_{11.} - \bar{Y}_{21.}) \equiv \frac{2}{BF} MS_{\text{BLOCK} \times \text{GENO}} + \frac{2(F-1)}{BF} MS_{\text{ERROR}}$$

is an unbiased estimate of $\text{Var}(\bar{Y}_{11.} - \bar{Y}_{21.})$.

$$\frac{\bar{Y}_{11.} - \bar{Y}_{21.} - (\mu_{11} - \mu_{21})}{\sqrt{\hat{\text{Var}}(\bar{Y}_{11.} - \bar{Y}_{21.})}} \sim t \text{ with df.}$$

determined by the Cochran-Satterthwaite approximation.