

15. ANOVA for Balanced Split-Plot Experiments

A Traditional Split-Plot Experiment

block x fert

Field

Whole Plot
or Main 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

A Model for Data from the Traditional Split-Plot Experiment

Genotype $i = 1, 2, 3$, Fertilizer $j = 1, 2, 3, 4$, Block $k = 1, 2, 3, 4$

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

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

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

Best Linear Unbiased Estimators

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

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

Because the elements of $E(\mathbf{y})$ 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

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

due to the 4
blocks we have
4 replications
for each of the 12
treatments

ANOVA Table for the Traditional Split-Plot Design

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

Source	DF	
Blocks <i>random</i>	4 - 1	= <u>3</u>
Genotypes <i>fixed</i>	3 - 1	= <u>2</u>
Blocks × Geno <i>random</i>	(4 - 1)(3 - 1)	= <u>6</u>
<i>fixed</i> { Fert <i>not for split plot units</i>	4 - 1	= 3
Geno × Fert	(3 - 1)(4 - 1)	= 6
Blocks × Fert	(4 - 1)(4 - 1)	
<i>SSE</i> { + Blocks × Geno × Fert	+(4 - 1)(3 - 1)(4 - 1)	= 27
C.Total	48 - 1	= 47

not part of the model ⇒ SSE

ANOVA Table for the Traditional Split-Plot Design

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

Why does $SS_{Blocks \times Fert} + SS_{Blocks \times Geno \times Fert} = SS_{Error}$?
End lecture 29
04-07-25

- 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: