

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				Split Plot or Sub Plot	
		0	100	150	50	50	100	150	0	150	100	50	0		
Block 2	2	Genotype B				Genotype A				Genotype C					
Block 3	3	150	100	50	0	0	50	150	100	100	50	150	0		
Block 4	4	Genotype A				Genotype B				Genotype C					
		100	50	0	150	0	100	150	50	50	100	150	0		
		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 $k = 1, 2, 3, 4$

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

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				$\bar{\mu}_{..}$
	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}	$\bar{\mu}_{3..}$
	$\bar{\mu}_{.1}$	$\bar{\mu}_{.2}$	$\bar{\mu}_{.3}$	$\bar{\mu}_{.4}$	

Best Linear Unbiased Estimators

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

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

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 $\sum_{i=1}^3 \sum_{j=1}^4 c_{ij}\bar{y}_{ij}$.

Table of Best Linear Unbiased Estimates

Genotype	Fertilizer Amount				$\bar{y}_{1..}$
	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	random	DF	looks like an RCBID
Blocks	fixed	4 - 1	= 3
Genotypes		3 - 1	= 2
Blocks × Geno	random	(4 - 1)(3 - 1)	= 6
Fert	†† for split plot units		
Geno × Fert		(3 - 1)(4 - 1)	= 6
Blocks × Fert		(4 - 1)(4 - 1)	
+Blocks × Geno × Fert		+(4 - 1)(3 - 1)(4 - 1)	= 27
C.Total		48 - 1	= 47
not part of the model \Rightarrow 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 $SS_{Blocks \times Fert} + SS_{Blocks \times Geno \times Fert} = SS_{Error}$?

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- 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: