

The Test for Whole-Plot Factor Main Effects

~~end lecture 30
4-9-25~~

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

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

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 $\bar{\mu}_{1..} - \bar{\mu}_{2..}$ is $\bar{y}_{1..} - \bar{y}_{2..}$

(write out $\bar{y}_{1..}$ & $\bar{y}_{2..}$
in terms of the model)

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

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

$$\text{Var}(\bar{w}_{i..}) = \frac{\sigma_w^2}{b}$$

$$\text{Var}(\bar{e}_{i..}) = \frac{\sigma_e^2}{sb}$$

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

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

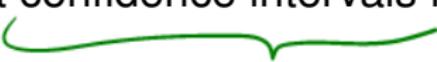
from the
output

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
 $\bar{\mu}_{1.} - \bar{\mu}_{2..}$

Practical vs.
statistical
significance

 give us an estimate
of the effect size

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

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

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

$$= C \left(\left(\frac{\sigma_w^2}{b} \right) + \left(\frac{\sigma_e^2}{sb} \right) \right) I C^\top = \boxed{\left(\frac{\sigma_w^2}{b} + \frac{\sigma_e^2}{sb} \right) C C^\top} = \frac{\text{E}(MS_{Block \times Geno})}{sb} C C^\top$$

output

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

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

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

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

Inference for the Split-Plot Factor

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

Likewise, it can be shown that

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

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

The Test for Split-Plot Factor Main Effects

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

$$H_0 : \bar{\mu}_{.1} = \dots = \bar{\mu}_{.s} \iff H_0 : \frac{wb}{s-1} \sum_{j=1}^s (\bar{\mu}_{.j} - \bar{\mu}_{..})^2 = 0,$$

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 $\bar{\mu}_{.1} - \bar{\mu}_{.2}$ is $\bar{y}_{.1.} - \bar{y}_{.2.}$

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

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

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

$$\widehat{\text{Var}}(\bar{y}_{.1.} - \bar{y}_{.2.}) = \underbrace{\frac{2}{wb}MS_{Error}}$$

interpretation: averaging over
blocks and genotype,

We can use

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

the average difference
between fertilizer level 1

to get tests of $H_0 : \bar{\mu}_{\cdot 1} = \bar{\mu}_{\cdot 2}$ or to construct confidence intervals
for $\bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 2}$.

and 2 is . . .

Furthermore, suppose C is a matrix with rows that are contrast vectors so that $\underline{C1} = \underline{0}$. Then

$$\begin{aligned} \text{Var} \left(\mathbf{C} \begin{bmatrix} \bar{y}_{.1.} \\ \vdots \\ \bar{y}_{.s.} \end{bmatrix} \right) &= \text{Var} \left(\mathbf{C} \begin{bmatrix} \bar{b}_{.} + \bar{w}_{..} + \bar{e}_{.1.} \\ \vdots \\ \bar{b}_{.} + \bar{w}_{..} + \bar{e}_{.s.} \end{bmatrix} \right) \\ &= \text{Var} \left(\mathbf{C1}\bar{b}_{.} + \mathbf{C1}\bar{w}_{..} + \mathbf{C} \begin{bmatrix} \bar{e}_{.1.} \\ \vdots \\ \bar{e}_{.s.} \end{bmatrix} \right) = \mathbf{C} \text{Var} \begin{pmatrix} \bar{e}_{.1.} \\ \vdots \\ \bar{e}_{.s.} \end{pmatrix} \mathbf{C}^{\top} \\ &= \mathbf{C} \left(\frac{\sigma_e^2}{wb} \right) \mathbf{I} \mathbf{C}^{\top} = \frac{\text{E}(MS_{Error})}{wb} \mathbf{C} \mathbf{C}^{\top} \end{aligned}$$

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

$$H_0 : C \begin{bmatrix} \bar{\mu}_{.1} \\ \vdots \\ \bar{\mu}_{.s} \end{bmatrix} = \mathbf{0}, \text{ is}$$

$$F = \frac{\left(C \begin{bmatrix} \bar{y}_{.1} \\ \vdots \\ \bar{y}_{.s} \end{bmatrix} \right)^\top \left[\frac{MS_{Error}}{wb} CC^\top \right]^{-1} \left(C \begin{bmatrix} \bar{y}_{.1} \\ \vdots \\ \bar{y}_{.s} \end{bmatrix} \right)}{q}$$

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

Inference for Interactions

$$\begin{aligned}\underline{\underline{\mathbb{E}(MS_{Geno \times Fert})}} &= \frac{b}{(w-1)(s-1)} \sum_{i=1}^w \sum_{j=1}^s \mathbb{E}(\bar{y}_{ij\cdot} - \bar{y}_{i..} - \bar{y}_{\cdot j\cdot} + \bar{y}_{...})^2 \\ &= \frac{b}{(w-1)(s-1)} \sum_{i=1}^w \sum_{j=1}^s \mathbb{E}(\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{...} + \bar{e}_{ij\cdot} - \bar{e}_{i..} - \bar{e}_{\cdot j\cdot} + \bar{e}_{...})^2 \\ &= \dots \\ &= \frac{b}{(w-1)(s-1)} \sum_{i=1}^w \sum_{j=1}^s (\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{...})^2 + \sigma_e^2.\end{aligned}$$

It can be shown that

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

is equivalent to

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

Thus,

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

is equivalent to no interactions between genotypes and fertilizers.

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

The Test for Whole \times Split Interaction Effects

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

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

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

compare $\boxed{\frac{MS_{Geno \times Fert}}{MS_{Error}}}$ 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 $\bar{y}_{11\cdot} - \bar{y}_{12\cdot}$.

$$\begin{aligned}\text{Var}(\bar{y}_{11\cdot} - \bar{y}_{12\cdot}) &= \text{Var}(\mu_{11} - \mu_{12} + \cancel{\bar{b}_1} - \cancel{\bar{b}_2} + \cancel{\bar{w}_{11\cdot}} - \cancel{\bar{w}_{12\cdot}} + \cancel{\bar{e}_{11\cdot}} - \cancel{\bar{e}_{12\cdot}}) \\ &= \frac{2}{b} \sigma_e^2\end{aligned}$$

$$\widehat{\text{Var}}(\bar{y}_{11\cdot} - \bar{y}_{12\cdot}) = \frac{2}{b} MS_{Error}$$

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 $\bar{y}_{11\cdot} - \bar{y}_{21\cdot}$.

$$\begin{aligned}\text{Var}(\bar{y}_{11\cdot} - \bar{y}_{21\cdot}) &= \text{Var}(\mu_{11} - \mu_{21} + \bar{w}_{1\cdot} - \bar{w}_{2\cdot} + \bar{e}_{11\cdot} - \bar{e}_{21\cdot}) \\ &= \frac{2\sigma_w^2}{b} + \frac{2\sigma_e^2}{b} \\ &= \frac{2}{b}(\underline{\sigma_w^2 + \sigma_e^2}).\end{aligned}$$

need to identify
an unbiased estimator

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

identify an appropriate
linear combin.
of available MS

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

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

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

Thus,

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

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

bad
lecture 31
04-11-25