

The Test for Whole-Plot Factor Main Effects

end lecture 30
4-9-25

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

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

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

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

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

$$\begin{aligned} &= \frac{2\sigma_w^2}{b} + \frac{2\sigma_e^2}{sb} \quad \text{Var}(\bar{w}_{i.}) = \frac{5\sigma_w^2}{b} \\ &\quad \text{Var}(\bar{e}_{i..}) = \frac{5\sigma_e^2}{sb} \\ &= \frac{2}{sb} (\boxed{s\sigma_w^2 + \sigma_e^2}) = \frac{2}{sb} E(MS_{Block \times Geno}) \end{aligned}$$

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

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 $C1 = 0$. Then

$$\begin{aligned}
 \text{Var} \left(C \begin{bmatrix} \bar{y}_{1..} \\ \vdots \\ \bar{y}_{w..} \end{bmatrix} \right) &= \text{Var} \left(C \begin{bmatrix} \bar{b}. & + & \bar{w}_1. & + & \bar{e}_{1..} \\ & & \vdots & & \\ \bar{b}. & + & \bar{w}_w. & + & \bar{e}_{w..} \end{bmatrix} \right) \\
 &= \text{Var} \left(\begin{matrix} =0 \\ C1\bar{b}. \end{matrix} + C \begin{bmatrix} \bar{w}_1. & + & \bar{e}_{1..} \\ \vdots & & \\ \bar{w}_w. & + & \bar{e}_{w..} \end{bmatrix} \right) = C \text{Var} \left(\begin{bmatrix} \bar{w}_1. & + & \bar{e}_{1..} \\ \vdots & & \\ \bar{w}_w. & + & \bar{e}_{w..} \end{bmatrix} \right) C^\top \\
 &= C \left(\frac{\sigma_w^2}{b} + \frac{\sigma_e^2}{sb} \right) IC^\top = \left(\frac{\sigma_w^2}{b} + \frac{\sigma_e^2}{sb} \right) CC^\top = \frac{E(MS_{Block \times Geno})}{sb} CC^\top
 \end{aligned}$$

output

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

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

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


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

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

Likewise, it can be shown that

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

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

The Test for Split-Plot Factor Main Effects

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

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

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

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

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

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

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

interpretation: averaging over
blocks and genotype,
the average

We can use

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

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 $C\mathbf{1} = \mathbf{0}$. Then

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

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

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

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

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 Interactions

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

It can be shown that

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

is equivalent to

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

Thus,

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

is equivalent to no interactions between genotypes and fertilizers.

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

The Test for Whole \times Split Interaction Effects

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

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

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

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 $\bar{y}_{11\cdot} - \bar{y}_{12\cdot}$.

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

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

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

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

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

end
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