Math 362: Mathmatical Statistics II

Le Chen
le.chen@emory.edu

Emory University
Atlanta, GA

Last updated on March 24, 2020

2020 Spring

Chapter 13. Randomized Block Designs

Plan

§ 13.1 Introduction

§ 13.2 The *F* Test for a Randomized Block Design

Chapter 13. Randomized Block Designs

§ 13.1 Introduction

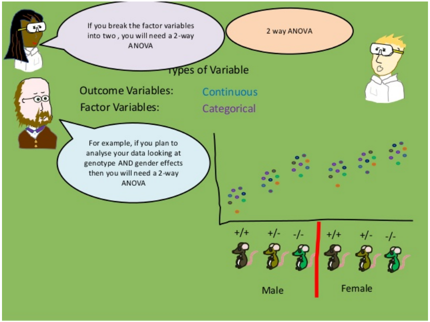
§ 13.2 The *F* Test for a Randomized Block Design

§ 13.1 Introduction

Rationale:

Reducing variability by blocking[†]

[†] *Blocking* is the arranging of experimental units in groups (blocks) that are similar to one another.



`https://www.slideshare.net/KevinHamill2/experimental-design-cartoon-part-5-sample-size`

FIGURE 2: Addressing Field Variability with Blocking

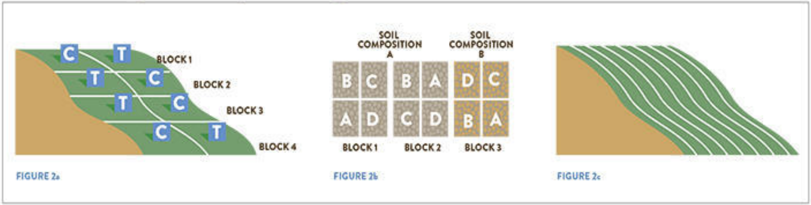


FIGURE 2a FIGURE 2b FIGURE 2c

Goal Reducing variability caused by

a *elevation.*
b *soil types.* } One-way ANOVA

v.s.

c *complete randomized design* Two-way ANOVA

https://www.sare.org/Learning-Center/Bulletins/How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/Basics-of-Experimental-Design

FIGURE 2: Addressing Field Variability with Blocking

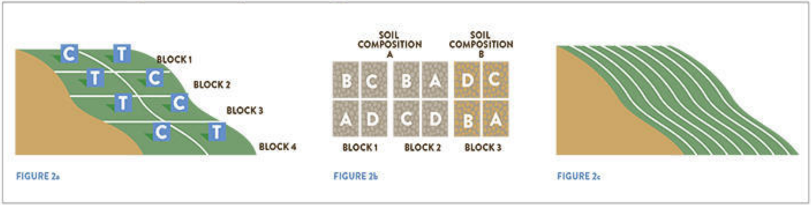


FIGURE 2a FIGURE 2b FIGURE 2c

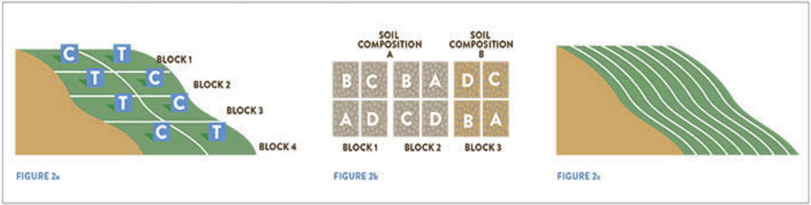
- Goal Reducing variability caused by
  - a *elevation.*
  - b *soil types.* } One-way ANOVA

v.s.

- c *complete randomized design* Two-way ANOVA

`https://www.sare.org/Learning-Center/Bulletins/How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/Basics-of-Experimental-Design`

FIGURE 2: Addressing Field Variability with Blocking



Goal Reducing variability caused by

a *elevation*.

b *soil types*.

} One-way ANOVA

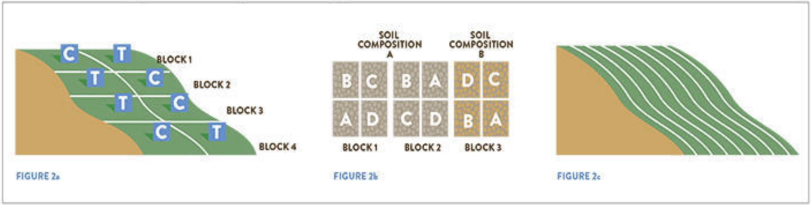
v.s.

c *complete randomized design*

Two-way ANOVA

`https://www.sare.org/Learning-Center/Bulletins/How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/Basics-of-Experimental-Design`

FIGURE 2: Addressing Field Variability with Blocking



Goal Reducing variability caused by

- a *elevation*.
- b *soil types*.

v.s.

- c *complete randomized design*

} One-way ANOVA

Two-way ANOVA

`https://www.sare.org/Learning-Center/Bulletins/How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/Basics-of-Experimental-Design`

FIGURE 2: Addressing Field Variability with Blocking

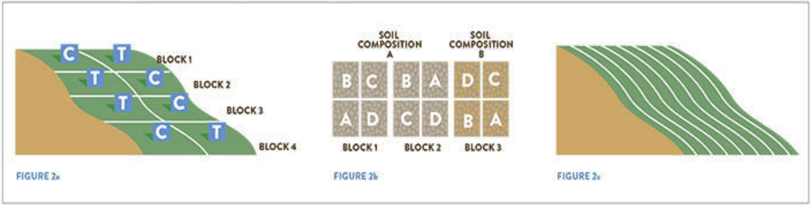


FIGURE 2a

FIGURE 2b

FIGURE 2c

Goal Reducing variability caused by

a *elevation*.

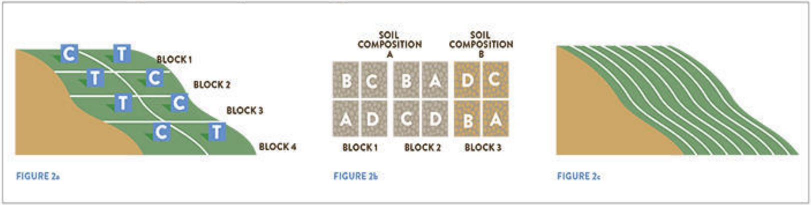
b *soil types*. } One-way ANOVA

v.s.

c *complete randomized design* Two-way ANOVA

https://www.sare.org/Learning-Center/Bulletins/How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/Basics-of-Experimental-Design

FIGURE 2: Addressing Field Variability with Blocking



Goal Reducing variability caused by

a *elevation*.

b *soil types*.

v.s.

c *complete randomized design*

} One-way ANOVA

Two-way ANOVA

https://www.sare.org/Learning-Center/Bulletins/How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/Basics-of-Experimental-Design

FIGURE 2: Addressing Field Variability with Blocking

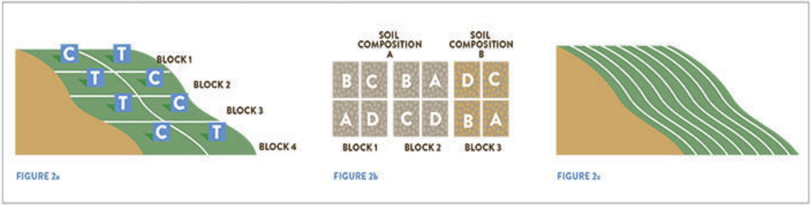


FIGURE 2a FIGURE 2b FIGURE 2c

Goal Reducing variability caused by

a *elevation*.

b *soil types*. } One-way ANOVA

v.s.

c *complete randomized design* Two-way ANOVA

`https://www.sare.org/Learning-Center/Bulletins/How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/Basics-of-Experimental-Design`

FIGURE 2: Addressing Field Variability with Blocking

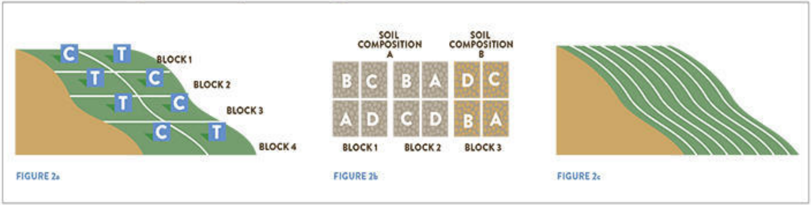


FIGURE 2a FIGURE 2b FIGURE 2c

Goal Reducing variability caused by

a *elevation*.
b *soil types*. } One-way ANOVA

v.s.

c *complete randomized design* Two-way ANOVA

`https://www.sare.org/Learning-Center/Bulletins/How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/Basics-of-Experimental-Design`

Plan

§ 13.1 Introduction

§ 13.2 The *F* Test for a Randomized Block Design

Chapter 13. Randomized Block Designs

§ 13.1 Introduction

§ 13.2 The *F* Test for a Randomized Block Design

§ 13.2 The F Test for a Randomized Block Design

Setup Y_{ij} indep. $\sim N(\mu_j + \beta_i, \sigma^2)$, i.e., $Y_{ij} = \mu_j + \beta_i + \epsilon_{ij}$, ϵ_{ij} i.i.d. $\sim N(0, \sigma^2)$

§ 13.2 The F Test for a Randomized Block Design

Setup Y_{ij} indep. $\sim N(\mu_j + \beta_i, \sigma^2)$, i.e., $Y_{ij} = \mu_j + \beta_i + \epsilon_{ij}$, ϵ_{ij} i.i.d. $\sim N(0, \sigma^2)$

§ 13.2 The F Test for a Randomized Block Design

Setup Y_{ij} indep. $\sim N(\mu_j + \beta_i, \sigma^2)$, i.e., $Y_{ij} = \mu_j + \beta_i + \epsilon_{ij}$, ϵ_{ij} i.i.d. $\sim N(0, \sigma^2)$

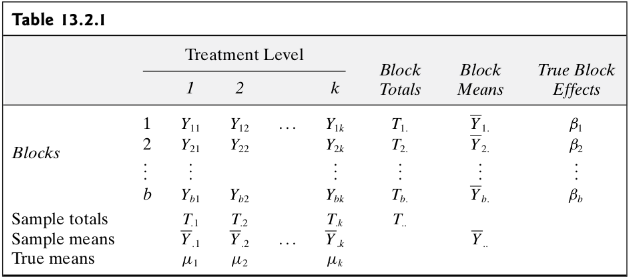


Table 13.2.1

		Treatment Level						
		1	*2*		*k*	*Block Totals*	*Block Means*	*True Block Effects*
Blocks	1	Y_{11}	Y_{12}	$\dots$	Y_{1k}	$T_{1.}$	$\overline{Y}_{1.}$	β_1
	2	Y_{21}	Y_{22}		Y_{2k}	$T_{2.}$	$\overline{Y}_{2.}$	β_2
	$\vdots$	$\vdots$			$\vdots$	$\vdots$	$\vdots$	$\vdots$
	b	Y_{b1}	Y_{b2}		Y_{bk}	$T_{b.}$	$\overline{Y}_{b.}$	β_b
Sample totals		$T_{.1}$	$T_{.2}$		$T_{.k}$	$T_{..}$		
Sample means		$\overline{Y}_{.1}$	$\overline{Y}_{.2}$	$\dots$	$\overline{Y}_{.k}$		$\overline{Y}_{..}$	
True means		μ_1	μ_2		μ_k			

Recall For one-way ANOVA,

$$Y_{ij} = \mu_j + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{..} \right)^2 \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left[\left(Y_{ij} - \overline{Y}_{.j} \right) + \left(\overline{Y}_{.j} - \overline{Y}_{..} \right) \right]^2 \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{.j} \right)^2 + \text{zero cross term} + \sum_{i=1}^{b} \sum_{j=1}^{k} \left(\overline{Y}_{.j} - \overline{Y}_{..} \right)^2 \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{.j} \right)^2 + b \sum_{j=1}^{k} \left(\overline{Y}_{.j} - \overline{Y}_{..} \right)^2 \\
&= SSE + SSTR
\end{aligned}$$

Recall For one-way ANOVA,

$$Y_{ij} = \mu_j + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{..}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left[\left(Y_{ij} - \overline{Y}_{.j}\right) + \left(\overline{Y}_{.j} - \overline{Y}_{..}\right)\right]^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{.j}\right)^2 + \text{zero cross term} + \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{.j} - \overline{Y}_{..}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{.j}\right)^2 + b\sum_{j=1}^{k}\left(\overline{Y}_{.j} - \overline{Y}_{..}\right)^2 \\
&= SSE + SSTR
\end{aligned}$$

Recall For one-way ANOVA,

$$Y_{ij} = \mu_j + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{\cdot\cdot} \right)^2 \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left[\left(Y_{ij} - \overline{Y}_{\cdot j} \right) + \left(\overline{Y}_{\cdot j} - \overline{Y}_{\cdot\cdot} \right) \right]^2 \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{\cdot j} \right)^2 + \text{zero cross term} + \sum_{i=1}^{b} \sum_{j=1}^{k} \left(\overline{Y}_{\cdot j} - \overline{Y}_{\cdot\cdot} \right)^2 \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{\cdot j} \right)^2 + b \sum_{j=1}^{k} \left(\overline{Y}_{\cdot j} - \overline{Y}_{\cdot\cdot} \right)^2 \\
&= SSE + SSTR
\end{aligned}$$

$$\begin{array}{ccccc}
SSTOT & = & SSE & + & SSTR \\
 & \Downarrow & & & \\
\frac{SSTOT}{\sigma^2} & = & \frac{SSE}{\sigma^2} & + & \frac{SSTR}{\sigma^2} \\
\wr & & \wr & & \wr \\
\chi^2(bk-1) & & \chi^2(bk-k) & \perp & \chi^2(k-1) \\
\text{Under } H_0 & & \checkmark & & \text{Under } H_0
\end{array}$$

$$H_0 : \mu_1 = \cdots = \mu_k$$

Symmetry If

$$Y_{ij} = \beta_i + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{..}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left[\left(Y_{ij} - \overline{Y}_{i.}\right) + \left(\overline{Y}_{i.} - \overline{Y}_{..}\right)\right]^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i.}\right)^2 + \text{zero cross term} + \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{i.} - \overline{Y}_{..}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i.}\right)^2 + k\sum_{i=1}^{b}\left(\overline{Y}_{i.} - \overline{Y}_{..}\right)^2 \\
&= SSE + SSB
\end{aligned}$$

Symmetry If

$$Y_{ij} = \beta_i + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{\cdot\cdot}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left[\left(Y_{ij} - \overline{Y}_{i\cdot}\right) + \left(\overline{Y}_{i\cdot} - \overline{Y}_{\cdot\cdot}\right)\right]^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i\cdot}\right)^2 + \text{zero cross term} + \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{i\cdot} - \overline{Y}_{\cdot\cdot}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i\cdot}\right)^2 + k\sum_{i=1}^{b}\left(\overline{Y}_{i\cdot} - \overline{Y}_{\cdot\cdot}\right)^2 \\
&= SSE + SSB
\end{aligned}$$

Symmetry If

$$Y_{ij} = \beta_i + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{..}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left[\left(Y_{ij} - \overline{Y}_{i.}\right) + \left(\overline{Y}_{i.} - \overline{Y}_{..}\right)\right]^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i.}\right)^2 + \text{zero cross term} + \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{i.} - \overline{Y}_{..}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i.}\right)^2 + k\sum_{i=1}^{b}\left(\overline{Y}_{i.} - \overline{Y}_{..}\right)^2 \\
&= SSE + SSB
\end{aligned}$$

$$\begin{array}{ccccc}
SSTOT & = & SSE & + & SSB \\
 & \Downarrow & & & \\
\dfrac{SSTOT}{\sigma^2} & = & \dfrac{SSE}{\sigma^2} & + & \dfrac{SSB}{\sigma^2} \\
\wr & & \wr & & \wr \\
\chi^2(bk-1) & & \chi^2(bk-b) & \perp & \chi^2(b-1) \\
\text{Under } \widetilde{H}_0 & & \checkmark & & \text{Under } \widetilde{H}_0
\end{array}$$

$$\widetilde{H}_0 : \beta_1 = \cdots = \beta_b$$

Similarly If

$$Y_{ij} = \mu_j + \beta_i + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{..} \right)^2 \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left[\left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..} \right) + \left(\overline{Y}_{i.} - \overline{Y}_{..} \right) + \left(\overline{Y}_{.j} - \overline{Y}_{..} \right) \right]^2 \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..} \right)^2 + \sum_{i=1}^{b} \sum_{j=1}^{k} \left(\overline{Y}_{i.} - \overline{Y}_{..} \right)^2 \\
&\quad + \sum_{i=1}^{b} \sum_{j=1}^{k} \left(\overline{Y}_{.j} - \overline{Y}_{..} \right)^2 + \text{zero cross terms} \\
&= \sum_{i=1}^{b} \sum_{j=1}^{k} \left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} - \overline{Y}_{..} \right)^2 + k \sum_{i=1}^{b} \left(\overline{Y}_{i.} - \overline{Y}_{..} \right)^2 + b \sum_{j=1}^{k} \left(\overline{Y}_{.j} - \overline{Y}_{..} \right)^2 \\
&= SSE + SSB + SSTR
\end{aligned}$$

Similarly

If

$$Y_{ij} = \mu_j + \beta_i + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{..}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left[\left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..}\right) + \left(\overline{Y}_{i.} - \overline{Y}_{..}\right) + \left(\overline{Y}_{.j} - \overline{Y}_{..}\right)\right]^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..}\right)^2 + \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{i.} - \overline{Y}_{..}\right)^2 \\
&\quad + \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{.j} - \overline{Y}_{..}\right)^2 + \text{zero cross terms} \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} - \overline{Y}_{..}\right)^2 + k\sum_{i=1}^{b}\left(\overline{Y}_{i.} - \overline{Y}_{..}\right)^2 + b\sum_{j=1}^{k}\left(\overline{Y}_{.j} - \overline{Y}_{..}\right)^2 \\
&= SSE + SSB + SSTR
\end{aligned}$$

Similarly

If

$$Y_{ij} = \mu_j + \beta_i + \epsilon_{ij}$$

$$\Downarrow$$

$$\begin{aligned}
SSTOT &= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{..}\right)^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left[\left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..}\right) + \left(\overline{Y}_{i.} - \overline{Y}_{..}\right) + \left(\overline{Y}_{.j} - \overline{Y}_{..}\right)\right]^2 \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..}\right)^2 + \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{i.} - \overline{Y}_{..}\right)^2 \\
&\quad + \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{.j} - \overline{Y}_{..}\right)^2 + \text{zero cross terms} \\
&= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} - \overline{Y}_{..}\right)^2 + k\sum_{i=1}^{b}\left(\overline{Y}_{i.} - \overline{Y}_{..}\right)^2 + b\sum_{j=1}^{k}\left(\overline{Y}_{.j} - \overline{Y}_{..}\right)^2 \\
&= SSE + SSB + SSTR
\end{aligned}$$

$$
\begin{array}{ccccccc}
SSTOT & = & SSE & + & SSB & + & SSTR \\
 & \Downarrow & & & & & \\
\dfrac{SSTOT}{\sigma^2} & = & \dfrac{SSE}{\sigma^2} & + & \dfrac{SSB}{\sigma^2} & + & \dfrac{SSTR}{\sigma^2} \\
\wr & & \wr & & \wr & & \wr \\
\chi^2(bk-1) & & \chi^2((k-1)(b-1)) & \perp & \chi^2(b-1) & \perp & \chi^2(k-1) \\
\text{Under } H_0 \text{ or } \widetilde{H}_0 & & \checkmark & & \text{under } \widetilde{H}_0 & & \text{under } H_0
\end{array}
$$

$$
\widetilde{H}_0 : \beta_1 = \cdots = \beta_b \qquad \text{and} \qquad H_0 : \mu_1 \cdots = \mu_k
$$

$$H_0 : \mu_1 \cdots = \mu_k$$

$$\Downarrow$$

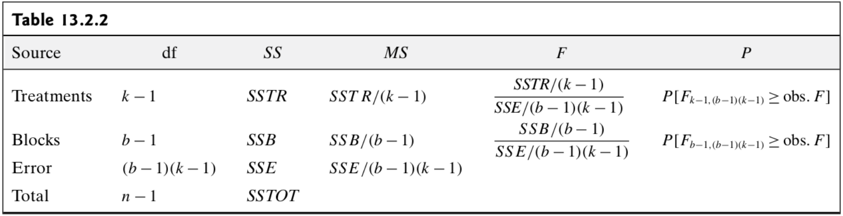


Table 13.2.2

Source	df	SS	MS	F	P
Treatments	$k-1$	$SSTR$	$SSTR/(k-1)$	$\dfrac{SSTR/(k-1)}{SSE/(b-1)(k-1)}$	$P[F_{k-1,(b-1)(k-1)} \geq \text{obs. } F]$
Blocks	$b-1$	SSB	$SSB/(b-1)$	$\dfrac{SSB/(b-1)}{SSE/(b-1)(k-1)}$	$P[F_{b-1,(b-1)(k-1)} \geq \text{obs. } F]$
Error	$(b-1)(k-1)$	SSE	$SSE/(b-1)(k-1)$		
Total	$n-1$	$SSTOT$			

$$\Uparrow$$

$$\widetilde{H}_0 : \beta_1 = \cdots = \beta_b$$

Computing formulas

$$C = \frac{T_{\cdot\cdot}^2}{bk}$$

$$SSTR = b\sum_{j=1}^{k}\left(\overline{Y}_{\cdot j} - \overline{Y}_{\cdot\cdot}\right)^2 = b\sum_{j=1}^{k}\overline{Y}_{\cdot j}^2 - bk\overline{Y}_{\cdot\cdot}^2 = \frac{1}{b}\sum_{j=1}^{k}\overline{T}_{\cdot j}^2 - C.$$

$$SSB = k\sum_{i=1}^{b}\left(\overline{Y}_{i\cdot} - \overline{Y}_{\cdot\cdot}\right)^2 = k\sum_{i=1}^{b}\overline{Y}_{i\cdot}^2 - bk\overline{Y}_{\cdot\cdot}^2 = \frac{1}{k}\sum_{j=1}^{k}\overline{T}_{i\cdot}^2 - C.$$

$$SSTOT = \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{\cdot\cdot}\right)^2 = \sum_{i=1}^{b}\sum_{j=1}^{k}Y_{ij}^2 - bk\overline{Y}_{\cdot\cdot}^2 = \sum_{i=1}^{b}\sum_{j=1}^{k}Y_{ij}^2 - C.$$

$$SSE = SSTOT - SSTR - SSB$$

E.g. Two methods to test wines: whether these two procedures produce the same measurements?

	DRS-FTIR	Standard
White wine 1	112.9	115.1
White wine 2	123.1	125.6
Red wine 1	135.2	132.4
Red wine 2	140.2	143.7

Test at $\alpha = 0.05$

$$H_0 : \mu_{DRS} = \mu_{STD} \quad \text{v.s.} \quad H_1 : \mu_{DRS} \neq \mu_{STD}$$

and

$$\widetilde{H}_0 : \mu_{W1} = \mu_{W2} = \mu_{R1} = \mu_{R2} \quad \text{v.s.} \quad \widetilde{H}_1 : \text{not equal}$$

E.g. Two methods to test wines: whether these two procedures produce the same measurements?

	DRS-FTIR	Standard
White wine 1	112.9	115.1
White wine 2	123.1	125.6
Red wine 1	135.2	132.4
Red wine 2	140.2	143.7

Test at $\alpha = 0.05$

$$H_0 : \mu_{DRS} = \mu_{STD} \quad \text{v.s.} \quad H_1 : \mu_{DRS} \neq \mu_{STD}$$

and

$$\widetilde{H}_0 : \mu_{W1} = \mu_{W2} = \mu_{R1} = \mu_{R2} \quad \text{v.s.} \quad \widetilde{H}_1 : \text{not equal}$$

```
> # Case Study 13.2.1
> #  install .packages("ggpubr")
> DIRS <- c(112.9, 123.1, 135.2, 140.2)
> STD <- c(115.1, 125.6, 132.4, 143.7)
> Wines <- c("W1", "W2", "R1", "R2")
> # Create a data frame
> my_data <- data.frame(
+   method = rep(c("DIRS", "STD"), each =4),
+   types = c(Wines,Wines),
+   concentration = c(DIRS,  STD)
+ )
> # Show data
>  print (my_data)
  method types concentration
1   DIRS    W1         112.9
2   DIRS    W2         123.1
3   DIRS    R1         135.2
4   DIRS    R2         140.2
5    STD    W1         115.1
6    STD    W2         125.6
7    STD    R1         132.4
8    STD    R2         143.7
```

```
> # Compute t-test with equal variances
> res <- t.test(concentration ~ method,
+                data = my_data,
+                var.equal = TRUE)
> res

  Two Sample t-test

data:  concentration by method
t = -0.15721, df = 6, p-value = 0.8802
alternative hypothesis: true difference in
        means is not equal to 0
95 percent confidence interval:
 -22.362 19.662
sample estimates:
mean in group DIRS mean in group STD
            127.85            129.20
```

```
> # Compute t-test with unequal variances
> res <- t.test(concentration ~ method,
+                data = my_data,
+                var.equal = FALSE)
> res

  Welch Two Sample t-test

data:  concentration by method
t = -0.15721, df = 5.9968, p-value = 0.8802
alternative hypothesis: true difference in
        means is not equal to 0
95 percent confidence interval:
 -22.3647 19.6647
sample estimates:
mean in group DIRS mean in group STD
            127.85            129.20
```

```
> # The following one-way ANOVA is
        equivalent
> # to the two-sample t test
> library(car)
> model3 = lm(concentration ~ method,
+              data=my_data)
> Anova(model3)
Anova Table (Type II tests)

Response: concentration
          Sum Sq Df F value Pr(>F)
method      3.64  1  0.0247 0.8802
Residuals 884.87  6
```

1. Classical method
2. Welch approximation
3. one-way ANOVA

⇓

The same answer
(p-value)

Concl. Fail to reject H_0

```
> # Compute t−test with equal variances
> res <− t.test(concentration ~ method,
+                 data = my_data,
+                 var.equal = TRUE)
> res

  Two Sample t−test

data:   concentration by method
t  = −0.15721, df = 6, p−value = 0.8802
 alternative  hypothesis: true  difference  in
        means is not equal to  0
95 percent confidence interval :
  −22.362 19.662
sample estimates:
mean in group DIRS mean in group STD
              127.85             129.20
```

```
> # Compute t−test with unequal variances
> res <− t.test(concentration ~ method,
+                 data = my_data,
+                 var.equal = FALSE)
> res

  Welch Two Sample t−test

data:   concentration by method
t  = −0.15721, df = 5.9968, p−value = 0.8802
 alternative  hypothesis: true  difference  in
        means is not equal to  0
95 percent confidence interval :
  −22.3647 19.6647
sample estimates:
mean in group DIRS mean in group STD
              127.85             129.20
```

```
> # The following  one−way ANOVA is
        equivalent
> # to  the  two−sample t test
>  library (car)
> model3 = lm(concentration ~ method,
+                data=my_data)
> Anova(model3)
Anova Table (Type II  tests)

Response: concentration
             Sum Sq Df F value Pr(>F)
method       3.64   1   0.0247 0.8802
Residuals 884.87  6
```

1. Classical method
2. Welch approximation
3. one-way ANOVA

⇓

The same answer
(p-value)

Concl. Fail to reject H_0

```
> # Compute t-test with equal variances
> res <- t.test(concentration ~ method,
+               data = my_data,
+               var.equal = TRUE)
> res

  Two Sample t-test

data:  concentration by method
t = -0.15721, df = 6, p-value = 0.8802
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -22.362 19.662
sample estimates:
mean in group DIRS mean in group STD
            127.85            129.20
```

```
> # Compute t-test with unequal variances
> res <- t.test(concentration ~ method,
+               data = my_data,
+               var.equal = FALSE)
> res

  Welch Two Sample t-test

data:  concentration by method
t = -0.15721, df = 5.9968, p-value = 0.8802
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -22.3647 19.6647
sample estimates:
mean in group DIRS mean in group STD
            127.85            129.20
```

```
> # The following one-way ANOVA is equivalent
> # to the two-sample t test
> library(car)
> model3 = lm(concentration ~ method,
+             data=my_data)
> Anova(model3)
Anova Table (Type II tests)

Response: concentration
          Sum Sq Df F value Pr(>F)
method      3.64  1  0.0247 0.8802
Residuals 884.87  6
```

1. Classical method
2. Welch approximation
3. one-way ANOVA

⇓

The same answer
(p-value)

Concl. Fail to reject H_0

```
> # Compute t-test with equal variances
> res <- t.test(concentration ~ method,
+               data = my_data,
+               var.equal = TRUE)
> res

  Two Sample t-test

data:   concentration by method
t  = -0.15721, df = 6, p-value = 0.8802
alternative  hypothesis: true  difference  in
        means is not equal to  0
95 percent confidence interval:
 -22.362 19.662
sample estimates:
mean in group DIRS mean in group STD
            127.85            129.20
```

```
> # Compute t-test with unequal variances
> res <- t.test(concentration ~ method,
+               data = my_data,
+               var.equal = FALSE)
> res

  Welch Two Sample t-test

data:   concentration by method
t  = -0.15721, df = 5.9968, p-value = 0.8802
alternative  hypothesis: true  difference  in
        means is not equal to  0
95 percent confidence interval:
 -22.3647 19.6647
sample estimates:
mean in group DIRS mean in group STD
            127.85            129.20
```

```
> # The following  one-way ANOVA is
        equivalent
> # to  the  two-sample t test
>  library (car)
> model3 = lm(concentration ~ method,
+             data=my_data)
> Anova(model3)
Anova Table (Type II  tests)

Response: concentration
          Sum Sq Df F value Pr(>F)
method      3.64  1   0.0247 0.8802
Residuals 884.87  6
```

1. Classical method
2. Welch approximation
3. one-way ANOVA

⇓

The same answer
(p-value)

Concl. Fail to reject H_0

```
> # Now let's carry out two-way ANOVA
> library (car)
> model = lm(concentration ~ method + types,
+                data=my_data)
> Anova(model)
Anova Table (Type II tests)

Response: concentration
          Sum Sq Df F value  Pr(>F)
method      3.65  1  0.9154 0.409258
types     872.92  3 73.0787 0.002652 **
Residuals  11.94  3
```

```
> # Now let's try one-way ANOVA
> model2 = lm(concentration ~ types,
+               data=my_data)
> Anova(model2)
Anova Table (Type II tests)

Response: concentration
          Sum Sq Df F value    Pr(>F)
types     872.92  3  74.657 0.0005739 ***
Residuals  15.59  4
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*'
        0.05 '.' 0.1 ' ' 1
```

1. Fail to reject H_0
2. Reject $\widetilde{H}_0$

```
> # Now let's carry out two-way ANOVA
> library(car)
> model = lm(concentration ~ method + types,
+                data=my_data)
> Anova(model)
Anova Table (Type II tests)

Response: concentration
           Sum Sq Df F value  Pr(>F)
method       3.65  1  0.9154 0.409258
types      872.92  3 73.0787 0.002652 **
Residuals   11.94  3
```

```
> # Now let's try one-way ANOVA
> model2 = lm(concentration ~ types,
+                data=my_data)
> Anova(model2)
Anova Table (Type II tests)

Response: concentration
           Sum Sq Df F value    Pr(>F)
types      872.92  3  74.657 0.0005739 ***
Residuals   15.59  4
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*'
      0.05 '.' 0.1 ' ' 1
```

1. Fail to reject H_0
2. Reject $\widetilde{H}_0$

E.g. 2 `https://rcompanion.org/rcompanion/d_08.html`

Test at $\alpha = 0.05$

$$H_0 : \mu_F = \mu_M \quad v.s. \quad H_1 : \mu_F \neq \mu_F$$

and

$$\widetilde{H}_0 : \mu_{FF} = \mu_S = \mu_{SS} \quad v.s. \quad \widetilde{H}_1 : \text{not all equal}$$

E.g. 2 `https://rcompanion.org/rcompanion/d_08.html`

Genotype	Female	Male
FF	2.838	1.884
	4.216	2.283
	2.889	4.939
	4.198	3.486
FS	3.550	2.396
	4.556	2.956
	3.087	3.105
	1.943	2.649
SS	3.620	2.801
	3.079	3.421
	3.586	4.275
	2.669	3.110

Test at $\alpha = 0.05$

$$H_0 : \mu_F = \mu_M \quad v.s. \quad H_1 : \mu_F \neq \mu_F$$

and

$$\widetilde{H}_0 : \mu_{FF} = \mu_S = \mu_{SS} \quad v.s. \quad \widetilde{H}_1 : \text{not all equal}$$

```
> Data
   id    Sex Genotype Activity
1   1   male       ff    1.884
2   2   male       ff    2.283
3   3   male       fs    2.396
4   4 female       ff    2.838
5   5   male       fs    2.956
6   6 female       ff    4.216
7   7 female       ss    3.620
8   8 female       ff    2.889
9   9 female       fs    3.550
10 10   male       fs    3.105
11 11 female       fs    4.556
12 12 female       fs    3.087
13 13   male       ff    4.939
14 14   male       ff    3.486
15 15 female       ss    3.079
16 16   male       fs    2.649
```

```
17 17 female       fs    1.943
18 19 female       ff    4.198
19 20 female       ff    2.473
20 22 female       ff    2.033
21 24 female       fs    2.200
22 25 female       fs    2.157
23 26   male       ss    2.801
24 28   male       ss    3.421
25 29 female       ff    1.811
26 30 female       fs    4.281
27 32 female       fs    4.772
28 34 female       ss    3.586
29 36 female       ff    3.944
30 38 female       ss    2.669
31 39 female       ss    3.050
32 41   male       ss    4.275
33 43 female       ss    2.963
34 46 female       ss    3.236
35 48 female       ss    3.673
36 49   male       ss    3.110
```

```
> # Two-way ANOVA
> model = lm(Activity  ~ Sex + Genotype,
+              data=Data)
> Anova(model, type="II")
Anova Table (Type II  tests)

Response: Activity
          Sum Sq Df F value Pr(>F)
Sex       0.0681  1  0.0888 0.7676
Genotype  0.2772  2  0.1808 0.8354
Residuals 24.5285 32
> # One-way ANOVA
> model_Sex = lm(Activity ~ Sex,
+                data=Data)
> Anova(model_Sex, type="II")
Anova Table (Type II  tests)

Response: Activity
          Sum Sq Df F value Pr(>F)
Sex       0.0681  1  0.0933 0.7619
Residuals 24.8057 34
> # One-way ANOVA
> model_Genotype = lm(Activity ~ Genotype,
+                data=Data)
> Anova(model_Genotype, type="II")
Anova Table (Type II  tests)

Response: Activity
          Sum Sq Df F value Pr(>F)
Genotype  0.2772  2   0.186 0.8312
Residuals 24.5965 33
```

Tuckey's pairwise comparison

Replace $Q_{\alpha,k,b(k-k)}$ by $Q_{\alpha,k,(b-1)(k-1)}$

```
> # Tukey's pairwise comparison (One-way)
> model1 = aov(Activity ~ Genotype,
+                          data=Data)
> TukeyHSD(model1, "Genotype", ordered =
     TRUE)
  Tukey multiple  comparisons of means
    95% family-wise confidence level
    factor  levels  have been ordered

Fit :  aov(formula =  Activity  ~ Genotype, data
     = Data)

$Genotype
             diff           lwr         upr       p
          adj
fs-ff 0.05483333 -0.8100204 0.919687
     0.9867505
ss-ff 0.20741667 -0.6574370 1.072270
     0.8272105
ss-fs 0.15258333 -0.7122704 1.017437
     0.9021607
```

```
> # Tukey's pairwise comparison (Two-way)
> model2 = aov(Activity ~ Sex + Genotype,
+                          data=Data)
> TukeyHSD(model2, "Genotype", ordered =
     TRUE)
  Tukey multiple  comparisons of means
    95% family-wise confidence level
    factor  levels  have been ordered

Fit :  aov(formula =  Activity  ~ Sex +
     Genotype, data = Data)

$Genotype
             diff           lwr         upr       p
          adj
fs-ff 0.05483333 -0.8234920 0.9331586
     0.987114
ss-ff 0.20741667 -0.6709086 1.0857420
     0.831554
ss-fs 0.15258333 -0.7257420 1.0309086
     0.904729
```

Remark By two-way ANOVA, or through blocking one factor, we obtain

1. larger p-values:
   more conservative to reject H_0.

2. wider C.I.'s:
   more conservative on our estimates.

Remark By two-way ANOVA, or through blocking one factor, we obtain

1. larger p-values:

   more conservative to reject H_0.

2. wider C.I.'s:

   more conservative on our estimates.

Remark By two-way ANOVA, or through blocking one factor, we obtain

1. larger *p*-values:
   more conservative to reject H_0.

2. wider C.I.'s:
   more conservative on our estimates.

Remark By two-way ANOVA, or through blocking one factor, we obtain

1. larger p-values:
   more conservative to reject H_0.

2. wider C.I.'s:
   more conservative on our estimates.

Remark By two-way ANOVA, or through blocking one factor, we obtain

1. larger p-values:
   more conservative to reject H_0.

2. wider C.I.'s:
   more conservative on our estimates.