

Math 362: Mathematical Statistics II

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Chapter 13. Randomized Block Designs

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§ 13.1 Introduction

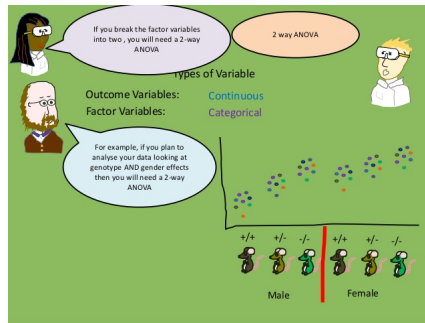
§ 13.2 The F Test for a Randomized Block Design

§ 13.1 Introduction

Rationale:

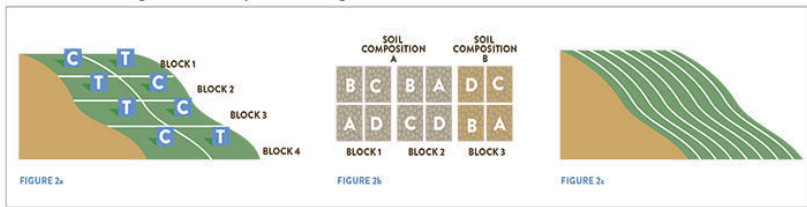
Reducing variability by blocking[†]

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



<https://www.slideshare.net/KevinHamill12/experimental-design-cartoon-part-5-sample-size>

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

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. $\sim N(0, \sigma^2)$

Table 13.2.1								
	Treatment Level					<i>Block Totals</i>	<i>Block Means</i>	<i>True Block Effects</i>
		<i>1</i>	<i>2</i>	...	<i>k</i>			
<i>Blocks</i>	1	Y_{11}	Y_{12}	...	Y_{1k}	$T_{1.}$	$\bar{Y}_{1.}$	β_1
	2	Y_{21}	Y_{22}		Y_{2k}	$T_{2.}$	$\bar{Y}_{2.}$	β_2
	$\vdots$	$\vdots$			$\vdots$	$\vdots$	$\vdots$	$\vdots$
	<i>b</i>	Y_{b1}	Y_{b2}		Y_{bk}	$T_{b.}$	$\bar{Y}_{b.}$	β_b
Sample totals		$T_{.1}$	$T_{.2}$		$T_{.k}$	$T_{..}$		
Sample means		$\bar{Y}_{.1}$	$\bar{Y}_{.2}$	...	$\bar{Y}_{.k}$		$\bar{Y}_{..}$	
True means		μ_1	μ_2		μ_k			

Recall For one-way ANOVA,

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

$\Downarrow$

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

$$SSTOT = SSE + SSTR$$

$$\Downarrow$$

$$\frac{SSTOT}{\sigma^2} = \frac{SSE}{\sigma^2} + \frac{SSTR}{\sigma^2}$$

 $\downarrow$
 $\downarrow$
 $\downarrow$

$$\chi^2(bk - 1) \quad \chi^2(bk - k) \quad \perp \quad \chi^2(k - 1)$$

Under H_0

✓

Under H_0

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

Symmetry If

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

$\Downarrow$

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

$$SSTOT = SSE + SSB$$

$$\Downarrow$$

$$\frac{SSTOT}{\sigma^2} = \frac{SSE}{\sigma^2} + \frac{SSB}{\sigma^2}$$

$$\wr$$

$$\wr$$

$$\wr$$

$$\chi^2(bk - 1) \quad \chi^2(bk - b) \quad \perp \quad \chi^2(b - 1)$$

Under $\tilde{H}_0$

✓

Under $\tilde{H}_0$

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

Similarly If

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

$\Downarrow$

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

$$SSTOT = SSE + SSB + SSTR$$

$\Downarrow$

$$\frac{SSTOT}{\sigma^2} = \frac{SSE}{\sigma^2} + \frac{SSB}{\sigma^2} + \frac{SSTR}{\sigma^2}$$

}

}

}

}

$$\chi^2(bk - 1) \quad \chi^2((k - 1)(b - 1)) \quad \perp \quad \chi^2(b - 1) \quad \perp \quad \chi^2(k - 1)$$

Under H_0 or $\tilde{H}_0$

✓

under $\tilde{H}_0$

under H_0

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

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

↓

Table 13.2.2					
Source	df	<i>SS</i>	<i>MS</i>	<i>F</i>	<i>P</i>
Treatments	$k - 1$	<i>SSTR</i>	$SSTR/(k - 1)$	$\frac{SSTR/(k - 1)}{SSE/(b - 1)(k - 1)}$	$P[F_{k-1, (b-1)(k-1)} \geq \text{obs. } F]$
Blocks	$b - 1$	<i>SSB</i>	$SSB/(b - 1)$	$\frac{SSB/(b - 1)}{SSE/(b - 1)(k - 1)}$	$P[F_{b-1, (b-1)(k-1)} \geq \text{obs. } F]$
Error	$(b - 1)(k - 1)$	<i>SSE</i>	$SSE/(b - 1)(k - 1)$		
Total	$n - 1$	<i>SSTOT</i>			

↑

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

Computing formulas

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

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

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

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

$$SSE = SSTOT - SSTR - SSB$$

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

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


```

1 > # Case Study 13.2.1
2 > # install .packages("ggpubr")
3 > DIRS <- c(112.9, 123.1, 135.2, 140.2)
4 > STD <- c(115.1, 125.6, 132.4, 143.7)
5 > Wines <- c("W1", "W2", "R1", "R2")
6 > # Create a data frame
7 > my_data <- data.frame(
8 +   method = rep(c("DIRS", "STD"), each =4),
9 +   types = c(Wines,Wines),
10 +   concentration = c(DIRS, STD)
11 + )
12 > # Show data
13 > print(my_data)
14   method types concentration
15 1  DIRS   W1      112.9
16 2  DIRS   W2      123.1
17 3  DIRS   R1      135.2
18 4  DIRS   R2      140.2
19 5   STD   W1      115.1
20 6   STD   W2      125.6
21 7   STD   R1      132.4
22 8   STD   R2      143.7

```

```

1 > # Compute t—test with equal variances
2 > res <- t.test(concentration ~ method,
3 +               data = my_data,
4 +               var.equal = TRUE)
5 > res

```

Two Sample t—test

```

9 data: concentration by method
10 t = -0.15721, df = 6, p—value = 0.8802
11 alternative hypothesis: true difference in
    means is not equal to 0
12 95 percent confidence interval:
13  -22.362 19.662
14 sample estimates:
15 mean in group DIRS mean in group STD
16      127.85      129.20

```

```

1 > # Compute t—test with unequal variances
2 > res <- t.test(concentration ~ method,
3 +               data = my_data,
4 +               var.equal = FALSE)
5 > res

```

Welch Two Sample t—test

```

9 data: concentration by method
10 t = -0.15721, df = 5.9968, p—value = 0.8802
11 alternative hypothesis: true difference in
    means is not equal to 0
12 95 percent confidence interval:
13  -22.3647 19.6647
14 sample estimates:
15 mean in group DIRS mean in group STD
16      127.85      129.20

```

```

1 > # The following one—way ANOVA is
    equivalent
2 > # to the two—sample t test
3 > library(car)
4 > model3 = lm(concentration ~ method,
5 +             data=my_data)
6 > Anova(model3)
7 Anova Table (Type II tests)

```

```

9 Response: concentration
10      Sum Sq Df F value Pr(>F)
11 method    3.64  1  0.0247 0.8802
12 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

```

1 > # Now let's carry out two-way ANOVA
2 > library(car)
3 > model = lm(concentration ~ method + types,
4 +           data=my_data)
5 > Anova(model)
6 Anova Table (Type II tests)
7
8 Response: concentration
9             Sum Sq Df F value  Pr(>F)
10 method      3.65   1  0.9154 0.409258
11 types      872.92   3 73.0787 0.002652 **
12 Residuals   11.94   3

```

```

1 > # Now let's try one-way ANOVA
2 > model2 = lm(concentration ~ types,
3 +           data=my_data)
4 > Anova(model2)
5 Anova Table (Type II tests)
6
7 Response: concentration
8             Sum Sq Df F value  Pr(>F)
9 types      872.92   3 74.657 0.0005739 ***
10 Residuals  15.59   4
11 ---
12 Signif. codes:  0 '***' 0.001 '**' 0.01 '*'
                  0.05 '.' 0.1 ' ' 1

```

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

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 $\alpha = 0.05$

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

and

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

```

1 > Data
2   id   Sex Genotype Activity
3 1 1 male      ff    1.884
4 2 2 male      ff    2.283
5 3 3 male      fs    2.396
6 4 4 female    ff    2.838
7 5 5 male      fs    2.956
8 6 6 female    ff    4.216
9 7 7 female    ss    3.620
10 8 8 female    ff    2.889
11 9 9 female    fs    3.550
12 10 10 male    fs    3.105
13 11 11 female  fs    4.556
14 12 12 female  fs    3.087
15 13 13 male    ff    4.939
16 14 14 male    ff    3.486
17 15 15 female  ss    3.079
18 16 16 male    fs    2.649

```

```

1 17 17 female   fs    1.943
2 18 19 female   ff    4.198
3 19 20 female   ff    2.473
4 20 22 female   ff    2.033
5 21 24 female   fs    2.200
6 22 25 female   fs    2.157
7 23 26 male     ss    2.801
8 24 28 male     ss    3.421
9 25 29 female   ff    1.811
10 26 30 female   fs    4.281
11 27 32 female   fs    4.772
12 28 34 female   ss    3.586
13 29 36 female   ff    3.944
14 30 38 female   ss    2.669
15 31 39 female   ss    3.050
16 32 41 male     ss    4.275
17 33 43 female   ss    2.963
18 34 46 female   ss    3.236
19 35 48 female   ss    3.673
20 36 49 male     ss    3.110

```

```

1 > # Two-way ANOVA
2 > model = lm(Activity ~ Sex + Genotype,
3 +           data=Data)
4 > Anova(model, type="II")
5 Anova Table (Type II tests)
6
7 Response: Activity
8           Sum Sq Df F value Pr(>F)
9 Sex          0.0681  1  0.0888 0.7676
10 Genotype    0.2772  2  0.1808 0.8354
11 Residuals 24.5285 32
12 > # One-way ANOVA
13 > model_Sex = lm(Activity ~ Sex,
14 +               data=Data)
15 > Anova(model_Sex, type="II")
16 Anova Table (Type II tests)
17
18 Response: Activity
19           Sum Sq Df F value Pr(>F)
20 Sex          0.0681  1  0.0933 0.7619
21 Residuals 24.8057 34
22 > # One-way ANOVA
23 > model_Genotype = lm(Activity ~ Genotype,
24 +                     data=Data)
25 > Anova(model_Genotype, type="II")
26 Anova Table (Type II tests)
27
28 Response: Activity
29           Sum Sq Df F value Pr(>F)
30 Genotype    0.2772  2  0.186 0.8312
31 Residuals 24.5965 33

```

Tukey's pairwise comparison

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

```

1 > # Tukey's pairwise comparison (One-way)
2 > model1 = aov(Activity ~ Genotype,
3 + data=Data)
4 > TukeyHSD(model1, "Genotype", ordered =
  TRUE)
5   Tukey multiple comparisons of means
6   95% family-wise confidence level
7   factor levels have been ordered
8
9   Fit: aov(formula = Activity ~ Genotype, data
  = Data)
10
11 $Genotype
12      diff      lwr      upr      p
      adj
13 fs-ff 0.05483333 -0.8100204 0.919687
      0.9867505
14 ss-ff 0.20741667 -0.6574370 1.072270
      0.8272105
15 ss-fs 0.15258333 -0.7122704 1.017437
      0.9021607
  
```

```

1 > # Tukey's pairwise comparison (Two-way)
2 > model2 = aov(Activity ~ Sex + Genotype,
3 + data=Data)
4 > TukeyHSD(model2, "Genotype", ordered =
  TRUE)
5   Tukey multiple comparisons of means
6   95% family-wise confidence level
7   factor levels have been ordered
8
9   Fit: aov(formula = Activity ~ Sex +
  Genotype, data = Data)
10
11 $Genotype
12      diff      lwr      upr      p
      adj
13 fs-ff 0.05483333 -0.8234920 0.9331586
      0.987114
14 ss-ff 0.20741667 -0.6709086 1.0857420
      0.831554
15 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.