

# Math 362: Mathematical Statistics II

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# Chapter 13. Randomized Block Designs

§ 13.1 Introduction

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

§ 13.A Appendix: Some Discussions and Extensions

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§ 13.1 Introduction

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

§ 13.A Appendix: Some Discussions and Extensions

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

<b>Table 13.2.1</b>								
		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>	<i>1</i>	$Y_{11}$	$Y_{12}$	...	$Y_{1k}$	$T_{1.}$	$\bar{Y}_{.1}$	$\beta_1$
	<i>2</i>	$Y_{21}$	$Y_{22}$		$Y_{2k}$	$T_{2.}$	$\bar{Y}_{.2}$	$\beta_2$
	$\vdots$	$\vdots$			$\vdots$	$\vdots$	$\vdots$	$\vdots$
	<i>b</i>	$Y_{b1}$	$Y_{b2}$		$Y_{bk}$	$T_{b.}$	$\bar{Y}_{.b}$	$\beta_b$
<i>Sample totals</i>		$T_{.1}$	$T_{.2}$		$T_{.k}$	$T_{..}$		
<i>Sample means</i>		$\bar{Y}_{.1}$	$\bar{Y}_{.2}$	...	$\bar{Y}_{.k}$		$\bar{Y}_{..}$	
<i>True means</i>		$\mu_1$	$\mu_2$		$\mu_k$			

Recall For one-way ANOVA,

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

↓

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

$$SSTOT = SSE + SSTR$$

↓

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

∝

∝

∝

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

Under  $H_0$

✓

Under  $H_0$

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

Symmetry If

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

↓

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

$$SSTOT = SSE + SSB$$

↓

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

∝

∝

∝

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

Under  $\tilde{H}_0$

✓

Under  $\tilde{H}_0$

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



Similarly If

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

↓

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

$$SSTOT = SSE + SSB + SSTR$$

↓

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

∝

∝

∝

∝

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

Under  $H_0$  or  $\tilde{H}_0$

✓

under  $\tilde{H}_0$

under  $H_0$

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

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



<b>Table 13.2.2</b>					
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

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

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

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

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

$$SSE = SSTOT - SSTR - SSB$$

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"),
9 +               each =4),
10 +  types = c(Wines,Wines),
11 +  concentration = c(DIRS, STD)
12 + )
13 > # Show data
14 > print(my_data)
15   method types concentration
16 1  DIRS  W1      112.9
17 2  DIRS  W2      123.1
18 3  DIRS  R1      135.2
19 4  DIRS  R2      140.2
20 5   STD  W1      115.1
21 6   STD  W2      125.6
22 7   STD  R1      132.4
23 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
6
7 Two Sample t-test
8
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 > # 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)
8
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 > # Compute t-test with unequal
  variances
2 > res <- t.test(concentration ~ method,
3 +               data = my_data,
4 +               var.equal = FALSE)
5 > res
6
7 Welch Two Sample t-test
8
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. 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](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",
5   ordered = TRUE)
6   Tukey multiple comparisons of means
7   95% family-wise confidence level
8   factor levels have been ordered
9 Fit: aov(formula = Activity ~ Genotype,
10  data = Data)
11 $Genotype
12      diff      lwr      upr      p
13      adj
14 fs-ff 0.05483333 -0.8100204 0.919687
15      0.9867505
16 ss-ff 0.20741667 -0.6574370 1.072270
17      0.8272105
18 ss-fs 0.15258333 -0.7122704 1.017437
19      0.9021607
```

```
1 > # Tukey's pairwise comparison (Two-way)
2 > model2 = aov(Activity ~ Sex +
3   Genotype,
4 +           data=Data)
5 > TukeyHSD(model2, "Genotype",
6   ordered = TRUE)
7   Tukey multiple comparisons of means
8   95% family-wise confidence level
9   factor levels have been ordered
10 Fit: aov(formula = Activity ~ Sex +
11  Genotype, data = Data)
12 $Genotype
13      diff      lwr      upr      p
14      adj
15 fs-ff 0.05483333 -0.8234920 0.9331586
16      0.987114
17 ss-ff 0.20741667 -0.6709086 1.0857420
18      0.831554
19 ss-fs 0.15258333 -0.7257420 1.0309086
20      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.