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

Plan

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

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Table 13.2.1

		Treatment Level				*Block Totals*	*Block Means*	*True Block Effects*
		1	*2*		*k*			
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,

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

$$\Downarrow$$

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

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SSTOT & = & SSE & + & SSTR \\
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\dfrac{SSTOT}{\sigma^2} & = & \dfrac{SSE}{\sigma^2} & + & \dfrac{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

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

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\dfrac{SSTOT}{\sigma^2} & = & \dfrac{SSE}{\sigma^2} & + & \dfrac{SSB}{\sigma^2} \\
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\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}
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$$\widetilde{H}_0 : \beta_1 = \cdots = \beta_b$$

Similarly If

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

$$\Downarrow$$

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

$$= \sum_{i=1}^{b}\sum_{j=1}^{k}\left[\left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..}\right) + \left(\overline{Y}_{i.} - \overline{Y}_{..}\right) + \left(\overline{Y}_{.j} - \overline{Y}_{..}\right)\right]^2$$

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

$$+ \sum_{i=1}^{b}\sum_{j=1}^{k}\left(\overline{Y}_{.j} - \overline{Y}_{..}\right)^2 + \text{zero cross terms}$$

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

$$= SSE + SSB + SSTR$$

Similarly If

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SSTOT &= \sum_{i=1}^{b}\sum_{j=1}^{k}\left(Y_{ij} - \overline{Y}_{..}\right)^2 \\
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&= \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 \\
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Similarly If

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

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\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

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

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```
> # 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
```

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> # Compute t-test with unequal variances
> res <- t.test(concentration ~ method,
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  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
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```
> # 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

$\Downarrow$

The same answer (p-value)

Concl. Fail to reject H_0

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> 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

$\Downarrow$

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.

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