Math 362: Mathematical Statistics II

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Chapter 13. Randomized Block Designs

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								
		\multicolumn{4}{c}{Treatment Level}		*Block*	*Block*	*True Block*
		1	*2*		*k*	*Totals*	*Means*	*Effects*
Blocks	1	Y_{11}	Y_{12}	$\ldots$	Y_{1k}	$T_{1.}$	$\overline{Y}_{1.}$	β_1
	2	Y_{21}	Y_{22}		Y_{2k}	$T_{2.}$	$\overline{Y}_{2.}$	β_2
	$\vdots$	$\vdots$	$\vdots$		$\vdots$	$\vdots$	$\vdots$	$\vdots$
	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		$\overline{Y}_{.1}$	$\overline{Y}_{.2}$	$\ldots$	$\overline{Y}_{.k}$		$\overline{Y}_{..}$	
True means		μ_1	μ_2		μ_k			

Recall For one-way ANOVA,

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

$$\Downarrow$$

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

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

$$\wr \qquad\qquad \wr \qquad\qquad \wr$$

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

Under H_0 $\qquad\qquad \checkmark \qquad\qquad$ Under H_0

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

Symmetry If

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

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

Under $\widetilde{H}_0$ $\qquad\qquad \checkmark \qquad\qquad$ Under $\widetilde{H}_0$

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Similarly If

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

Under H_0 or $\widetilde{H}_0$ $\qquad\qquad$ $\checkmark$ $\qquad\qquad$ under $\widetilde{H}_0$ $\qquad$ under H_0

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

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

$$\Downarrow$$

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	$n-1$	$SSTOT$			

$$\Uparrow$$

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

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

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

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

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

$$SSE = SSTOT - \textcolor{cyan}{SSTR} - \textcolor{red}{SSB}$$

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

```
> # 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
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> # Compute t−test with unequal
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  Welch Two Sample t−test

data: concentration by method
t = −0.15721, df = 5.9968, p−value =
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alternative hypothesis: true difference in
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 −22.3647 19.6647
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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

⇓

The same answer
(p-value)

Concl. Fail to reject H_0

19

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```
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 $\widetilde{H}_0$

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

Test at $\alpha = 0.05$

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

and

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

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 $\alpha = 0.05$

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

and

$\widetilde{H}_0 : \mu_{FF} = \mu_S = \mu_{SS}$ v.s. $\widetilde{H}_1 :$ 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 $Q_{\alpha,k,(b-1)(k-1)}$

```
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.

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