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# Statistical Design

## *Solutions to Odd-Numbered Exercises*

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## Preface

This manual provides the solutions to the odd numbered problems only. However, I am sure that it is only a matter of time until the solutions to the even numbered problems are somewhere on the web.

But—do the problems! The only way to truly understand any subject is to be able to solve the problems. Use the solutions as a guide and a learning tool after you have made a serious attempt to solve the problem. If you just copy the solution you are only fooling yourself.

Most of the calculations are done with **R**. We have not provided complete programs (data entry, etc.) but have provided the key **R** code to generate the correct anova.

Thanks to the students at Cornell - Stat 604- and at UF - Stat 6209 - for their interest and questions, and thanks to all of my colleagues and consulting clients who sometimes (unknowingly) provided examples and data sets.

Many people have contributed to solving these problems, although I alone am responsible for errors and omissions. Special thanks to Jamie Jarabek, Mihai Giurcanu, and Ruitao Liu, who proved many solution sets for the problems.

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September 1, 2009



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## Contents

<b>1</b>	<b>Basics</b>	5
	Exercise 1.1	5
	Exercise 1.3	5
	Exercise 1.5	6
	Exercise 1.7	6
	Exercise 1.9	7
	Exercise 1.11	7
	Exercise 1.13	7
	Exercise 1.15	8
	Exercise 1.17	9
	Exercise 1.19	10
	Exercise 1.21	12
	Exercise 1.23	12
	Exercise 1.25	12
<b>2</b>	<b>Completely Randomized Designs</b>	15
	Exercise 2.1	15
	Exercise 2.3	15
	Exercise 2.5	16
	Exercise 2.7	17
	Exercise 2.9	17
	Exercise 2.11	18
	Exercise 2.13	18
	Exercise 2.15	19
	Exercise 2.17	20
	Exercise 2.19	21
	Exercise 2.21	21
	Exercise 2.23	21
	Exercise 2.25	22
	Exercise 2.27	22
	Exercise 2.29	23

	Exercise 2.31 .....	24
<b>3</b>	<b>Complete Block Designs .....</b>	<b>25</b>
	Exercise 3.1 .....	25
	Exercise 3.3 .....	26
	Exercise 3.5 .....	26
	Exercise 3.7 .....	27
	Exercise 3.9 .....	28
	Exercise 3.11 .....	29
	Exercise 3.13 .....	29
	Exercise 3.15 .....	30
	Exercise 3.17 .....	30
	Exercise 3.19 .....	31
	Exercise 3.21 .....	32
	Exercise 3.23 .....	32
	Exercise 3.25 .....	33
	Exercise 3.27 .....	33
	Exercise 3.29 .....	35
	Exercise 3.31 .....	35
	Exercise 3.33 .....	35
	Exercise 3.35 .....	35
<b>4</b>	<b>Interlude: Assessing the Effects of Blocking .....</b>	<b>37</b>
	Exercise 4.1 .....	37
	Exercise 4.3 .....	38
	Exercise 4.5 .....	39
	Exercise 4.7 .....	40
	Exercise 4.9 .....	41
	Exercise 4.11 .....	42
	Exercise 4.13 .....	42
	Exercise 4.15 .....	43
	Exercise 4.17 .....	43
	Exercise 4.19 .....	44
<b>5</b>	<b>Split Plot Designs .....</b>	<b>47</b>
	Exercise 5.1 .....	47
	Exercise 5.3 .....	48
	Exercise 5.5 .....	49
	Exercise 5.7 .....	51
	Exercise 5.9 .....	51
	Exercise 5.11 .....	53
	Exercise 5.13 .....	54
	Exercise 5.15 .....	54
	Exercise 5.17 .....	55
	Exercise 5.19 .....	56

Exercise 5.21 .....	57
Exercise 5.23 .....	58
Exercise 5.25 .....	58
Exercise 5.27 .....	59
Exercise 5.29 .....	60
Exercise 5.31 .....	63
Exercise 5.33 .....	64
Exercise 5.35 .....	65
Exercise 5.37 .....	66
Exercise 5.39 .....	66
Exercise 5.41 .....	66
<b>6 Confounding in Blocks .....</b>	<b>69</b>
Exercise 6.1 .....	69
Exercise 6.3 .....	70
Exercise 6.5 .....	71
Exercise 6.7 .....	71
Exercise 6.9 .....	72
Exercise 6.11 .....	73
Exercise 6.13 .....	75
Exercise 6.15 .....	77
Exercise 6.17 .....	78
Exercise 6.19 .....	80
Exercise 6.21 .....	81
Exercise 6.23 .....	82
Exercise 6.25 .....	83
Exercise 6.27 .....	85
Exercise 6.29 .....	85
Exercise 6.31 .....	86
Exercise 6.33 .....	87
Exercise 6.35 .....	88





## Basics

### Essential

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#### Exercise 1.1

Suppose that, in a greenhouse, each table has six pots, each with different varieties. There are three plants for each pot. The anova is

Source	df
Blocks	3
Varieties	5
$T \times V$	15
Within	48
Total	71

The experimental unit is the pot, which is where the treatment is applied. The plants in the plot are subsamples. Depending on what the experimenter is willing to assume, the Within error may or may not be available to test the  $T \times B$  interaction. See Section 3.5.

Note also that we can remove a sum of squares for Pots (in Blocks) with 20 df, but this is then split into  $SS(\text{Varieties})$  and  $SS(V \times B)$ .

#### Exercise 1.3

- (1) The above example is a twoway CRD. We satisfy this exercise if we take two plants per pot.
- (2) We can modify the experiment in Exercise 1.1 to be a CRD in the following way. Instead of having four tables, we can have one table. If it is a big table and we could put all 24 pots in it, then the anova would be

Source	df
Varieties	5
Pots (In Varieties)	18
Within(Plants in Pots)	48
Total	71

where here the test on Varieties is with the 18 df for Pots in Varieties. The within is wasted.

### Exercise 1.5

If all of the resources can be used we run all tanks and fish. Eight tanks per diet and 6 fish per tank

Source	df
Diets	2
Tanks (in Diets)	21
Fish (in Tanks)	120

If all tanks and fish cannot be run, to address (1) we need to have a reasonable number of fish per tank, and can do with fewer tanks. In contrast, (2) would want the number of tanks maximized, and the remaining funds to be spent on fish per tank. Taking a stand, my feeling is that the number of tanks should be maximized, but try to have at least 2-3 fish per tank.

### Exercise 1.7

- (a) Equation (1.4) follows directly from the two displays above it, and the fact that the expectation of the difference is the difference of the expectations.  
 (b) (i) Since variance is unaffected by a constant,

$$\text{Var}(\bar{Y}_{i\cdot} - \bar{\bar{Y}}) = \text{Var}(\bar{Y}_{i\cdot} - \bar{\bar{Y}} - (\tau_i - \bar{\tau})) = \text{E} \left[ (\bar{Y}_{i\cdot} - \tau_i) - (\bar{\bar{Y}} - \bar{\tau}) \right]^2,$$

and expanding the square gives the expression.

- (ii) From the model,  $\text{Var}(Y_{ij}) = \sigma^2$ . The two expressions follow since these are means of independent observations.  
 (iii) Using properties of covariance and the definition of  $\bar{\bar{Y}}$ ,

$$\text{Cov}(\bar{Y}_{i\cdot}, \bar{\bar{Y}}) = \frac{1}{t} \sum_{i'=1}^t \text{Cov}(\bar{Y}_{i\cdot}, \bar{Y}_{i'\cdot})$$

where the fact that  $\sum_i \tau_i = 0$  allows use to change the mean. By independence all the terms are zero except when  $i = i'$ , which gives the variance.

- (c) Equation (1.6) follows directly from the display above it, and unbiasedness follows by dividing by the df.

**Exercise 1.9**

- (a) The cross term is

$$E([Y - E(Y|X)][E(Y|X) - E(Y)]) = E\{E([Y - E(Y|X)][E(Y|X) - E(Y)] | X)\}$$

and evaluating the inner expectation gives

$$[E(Y|X) - E(Y|X)][E(Y|X) - E(Y)] = 0.$$

- (b) Iterate the expectation in the first term to see that it is the variance of  $E(Y|X)$ . Iterating the expectation in the second term shows that it is the expected value of  $\text{Var}(Y|X)$ .
- (c) Using the given probability model  $E(Y|X) = \bar{y}_{i\cdot}$  and  $E(Y) = \bar{\bar{y}}$  and we can write

$$\begin{aligned}\text{Var}(Y) &= \frac{1}{rt} \sum_{i=1}^t \sum_{j=1}^r (y_{ij} - \bar{\bar{y}})^2 \\ \text{Var}[E(Y|X)] &= \frac{1}{t} \sum_{i=1}^t (\bar{y}_{i\cdot} - \bar{\bar{y}})^2 \\ E[\text{Var}(Y|X)] &= \frac{1}{rt} \sum_{i=1}^t \sum_{j=1}^r (y_{ij} - \bar{y}_{i\cdot})^2.\end{aligned}$$

**Exercise 1.11**

- (a) Yes  
(b) No  
(c) (0, 0, 0, 0, 1, -1)

**Exercise 1.13**

Contrasts.

- (a) The R program is on the web.
- (b) The original Helmert contrasts are not uncorrelated because they do not satisfy  $\sum_i a_i b_i / r_i = 0$ , where the  $r_i$  are in Example 1.15. The variation in the example satisfies this condition. Note that there is a typo in the first printing and the contrasts should be (the middle one is changed)

$\mu_1$	$\mu_2$	$\mu_3$	$\mu_4$
1	-8/19	-7/19	-4/19
0	1	-7/11	-4/11
0	0	1	-1

The treatment sum of squares in `RehabTime2` can be partitioned with the R code

```

summary(aov(RehabTime~ConditionCode,data=aovdata))
#-----Treatment means - Be careful about the ordering
Rmean<-tapply(RehabTime, ConditionCode, mean)
nmean<-tapply(RehabTime, ConditionCode, length) #observations in each mean
#-----Contrast sums of squares\\
C1<-c(1,-8/19,-7/19,-4/19)\\
C2<-c(0,1,-7/11,-4/11)\\
C3<-c(0,0,1,-1)\\
SS1<-(Rmean%*%C1)^2/(sum((C1^2)/nmean))\\
SS2<-(Rmean%*%C2)^2/(sum((C2^2)/nmean))\\
SS3<-(Rmean%*%C3)^2/(sum((C3^2)/nmean))\\
print(c(SS1, SS2, SS3, SS1+SS2+SS3))

```

which produces the R output

```

Df          Sum Sq   Mean Sq  F value  Pr(>F)
ConditionCode 3      830.37   276.79   21.488   1.816e-06 ***
Residuals    20      257.63   12.88
---
467.1158 147.1388 216.1169 830.3714

```

- (c) Multiplication verifies that they are uncorrelated. The three sums of squares are

```
577.47929    16.05982    236.83232,
```

which can be obtained from the same R code as above.

In no situation would I advise an experimenter to use the uncorrelated contrasts. They are an artifact of the unequal number of observations, and provide no meaningful inference. The original Helmert contrasts should be used.

### Exercise 1.15

The data for the experiment described in Exercise 1.16 can be found in dataset **FishTissueMass**. Using these data, complete the anova table that was started in the exercise. Note that the data are unbalanced, so orthogonal contrasts are not uncorrelated.

- (a) Here is the R code for the anova and the contrasts.

```

aovdata <- data.frame(Y,Tissue,hCG)
#-----This gives the anova table-----
summary(aov(Y~Tissue*hCG,data=aovdata))

```

```
#-----Main Effect Polynomial Contrasts-----
Tmean<-tapply(Y,Tissue,mean)
n<-tapply(Y,Tissue,length)
PC<-contr.poly(4,score=1:4)      #polynomial contrasts
SS1=(sum(Tmean*PC[,1]))^2/sum(PC[,1]^2/n)
SS2=(sum(Tmean*PC[,2]))^2/sum(PC[,2]^2/n)
SS3=(sum(Tmean*PC[,3]))^2/sum(PC[,3]^2/n)
print(c(SS1, SS2, SS3, SS1+SS2+SS3))
#-----Cell means and observation numbers-----
aov1<-subset(aovdata,hCG=="N")
mean1<-tapply(aov1[,1],aov1[,2],mean)
n1<-tapply(aov1[,1],aov1[,2],length)
aov2<-subset(aovdata,hCG=="Y")
mean2<-tapply(aov2[,1],aov2[,2],mean)
n2<-tapply(aov2[,1],aov2[,2],length)
#-----Interaction Polynomial Contrasts-----
SS1=(sum(mean1*PC[,1]-mean2*PC[,1]))^2/(sum(PC[,1]^2/n1)+sum(PC[,1]^2/n2))
SS2=(sum(mean1*PC[,2]-mean2*PC[,2]))^2/(sum(PC[,2]^2/n1)+sum(PC[,2]^2/n2))
SS3=(sum(mean1*PC[,3]-mean2*PC[,3]))^2/(sum(PC[,3]^2/n1)+sum(PC[,3]^2/n2))
print(c(SS1, SS2, SS3, SS1+SS2+SS3))
```

Which gives the output

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Tissue	3	1.67479	0.55826	0.7910	0.5589
hCG	1	0.43426	0.43426	0.6153	0.4767
Tissue:hCG	3	1.49048	0.49683	0.7039	0.5975
Residuals	4	2.82319	0.70580		
		0.12627	1.54825	0.00027	1.67479
		0.33326	0.41810	0.73912	1.49048

The main effect contrasts have equal cell sizes, so there is no problem with uncorrelated.

- (b) It turns out (to my surprise) that with this pattern of unequal  $n$  all of the polynomial contrasts remain uncorrelated, so we don't need another set.
- (c) Again, we want to use the orthogonal contrasts, even if the sum of squares is not partitioned.

### Exercise 1.17

- (1) The first randomization is throughout. So for the first experiment, we choose a variety and a treatment at random, and put them on a plot.

For the other experiment, we choose a weight class and an age class at random, and take the measure.

- (2) Here the Fertilizer can be applied to a plot, and three levels of Variety are randomized. Or we choose an age class at random, and measure three people of different weights.
- (3) Fertilizer is applied in one direction, and Varieties are planted in the other. This is problematic for the other experiment, as the treatments are not “applied”.

### Exercise 1.19

- (a) This R statement

```
summary(aov(Y~Block+Shipping+Storage+Shipping:Storage,data=aovdata))
```

will produce the “wrong” anova table

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	2483.3	1241.7	9.8014	0.0001935 ***
Shipping	2	156.3	78.2	0.6170	0.5427454
Storage	1	703.2	703.2	5.5509	0.0215459 *
Shipping:Storage	2	3.8	1.9	0.0151	0.9850328
Residuals	64	8107.6	126.7		

- (b) This R statement

```
summary(aov(Y~Block*Shipping*Storage),data=aovdata))
```

will produce an anova table with all of the block  $\times$  treatment interactions. The tests have to be done by hand.

- (c) This R statement

```
summary(aov(Y~Block+Shipping+Storage+Shipping:Storage
+Error(Block/Block:Shipping:Storage),data=aovdata))
```

will produce an anova where the treatment tests are done against the pooled treatment  $\times$  block interaction. The output is

Error: Block

	Df	Sum Sq	Mean Sq
Block	2	2483.3	1241.7

Error: Block:Shipping:Storage

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Shipping	2	156.3	78.2	0.1095	0.8974
Storage	1	703.2	703.2	0.9849	0.3444
Shipping:Storage	2	3.8	1.9	0.0027	0.9973
Residuals	10	7139.7	714.0		

Error: Within

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Residuals	54	967.82	17.92		

Probably the best thing to do in this case is to pool the interactions into one error term with 10 df - the individual errors have too few df.

- (d) With 6 Shipments and the same number of crates we have

Anova	
Source	df
Blocks (Shipments)	5
Shipping Method	2
Storage	1
Shipping $\times$ Storage	2
Blocks $\times$ Trts	25
Residual	36
Total	71

and we can break the  $B \times T$  term into its components. This is a much better design as we now have adequate df for the important tests.

With 3 Shipments and half the number of crates we have

Anova	
Source	df
Blocks (Shipments)	2
Shipping Method	2
Storage	1
Shipping $\times$ Storage	2
Blocks $\times$ Trts	10
Residual	18
Total	35

which, as far as the treatment tests, is as good as the original design but uses half the number of crates.

**Exercise 1.21**

- (a) The three cases are
- a)  $r = 4, p = 1, s = 1$ , variance = .3125, power = .812
  - b)  $r = 2, p = 1, s = 2$ , variance = .5625, power = .312
  - c)  $r = 4, p = 2, s = 1$ , variance = .15625, power = .973
- If we assume known variances, the power is (ignoring the lower tail)

$$P\left(Z \geq 1.645 - \frac{\sqrt{r/2}}{\sigma}\right),$$

where  $Z$  is standard normal and  $\sigma$  is as above. Note that only  $r$  appears in the expression, with both  $p$  and  $s$  being absorbed into  $\sigma$ .

- (b) Clearly the subsampling is useless. Pooling does the best, but it did have more experimental units. The advice is to replicate the EU as much as possible, first through  $r$  and then through  $p$ . Especially in plant and animal experiments, increasing  $p$  may be a plausible alternative.
- (c) As the subsampling only replicates  $\sigma_W^2$  but either  $r$  or  $p$  replicates  $\sigma_B^2 + \sigma_W^2$ , the equation follows.

**Accompaniment**

---

**Exercise 1.23**

- (a) The likelihood function can be written

$$\frac{1}{\sqrt{2\pi}\sigma} \exp\left\{\sum_{ij} [y_{ij} - (\mu + \tau_i)]^2\right\}.$$

Add  $\pm \bar{y}_{i\cdot}$  inside the square brackets, and the cross term is zero, giving (1.14).

- (b) From (1.14) it is clear that setting  $\bar{y}_{i\cdot} = \mu + \tau_i$  maximizes the function, as it minimizes the exponent. Differentiating (with respect to  $\mu + \tau_i$ ) will give the same results, but then the second derivative needs to be checked.
- (c) Starting from  $\bar{y}_{i\cdot} = \mu + \tau_i$ , add over  $i$  to get this.

**Exercise 1.25**

- (a) As the contrasts are written
- Helmert: The first contrast tests the difference of two treatments, and the second contrasts the average of these two against a third treatment.
  - Step: The first contrast tests the average of three against the remaining treatment, and the second compares two sets of averages.
  - Basin: The first basin contrast is a linear trend, and the others compare the average of treatments to a linear trend.



- (b) The Helmert contrasts are orthogonal, step and basin are not.
- (c)  $H_2$  is most appropriate for the threshold dose problem
- (d) Although Ruberg (1989) presents these three hypotheses and the three sets of contrasts, the correspondence is not obvious. We could use the Helmert contrasts for  $H_1$  and the step contrasts for  $H_2$ . The basin contrasts do not seem to cover  $H_3$ , however.
- (e) The data of Ruberg has 12 observations per group. His Table 4 gives the calculations. (Note that the examples in this Exercise were based on four groups, but the example has five groups.) The Ruberg table is

<i>t</i> -statistics for contrasts			
p	Helmert	Step	Basin
1	-.06	1.52	1.43
2	.42	2.55	3.64
3	1.65	3.36	3.74
4	3.36	3.36	3.36
Critical Value	2.294	2.268	2.225

The critical values are the Ruberg experimentwise values.



## Completely Randomized Designs

### Essential

---

#### Exercise 2.1

Referring to Example 2.1

- (a) A temperature is selected at random and set, and a random forage sample is assigned to the temperature. Note that the temperature needs to be reset after every sample. If more than one sample is run for one temperature setting, then the temperature becomes a block.
- (b) Complete the anova table:

Source	df	SS	MS	$F$
Temp	3	5.86	1.95	12.95
Within	12	1.81	.151	
Total	15	7.67		

The  $p$ -value is 0.00045.

- (c) Contrast (i) tests whether the effect of  $17^\circ$  is the same as the average of the other three. Contrast (ii) tests for a linear trend in temperature.
- (d) We can use the Helmert contrasts. Two orthogonal ones are  $(0, -2, 1, 1)$  and  $(0, 0, 1, -1)$ .
- (e) The data are in IVD. The  $t$  statistic is 5.142 with two-sided  $p$ -value .0002. The contrast sum of squares is 4.005, so the percent of variance not explained is  $(5.86 - 4.005)/5.86 \approx 32\%$ .

#### Exercise 2.3

- (a) The low temperatures have a similar effect, as do the high temperatures. However, there is a significant difference between the effect of the low and high temperatures.
- (b) The anova table is in Exercise 2.1

(i) The three contrast sums of squares are

$$0.211250, \quad 0.005000, \quad 5.6406255.856875$$

which sum to 5.86.

(ii)	$t$ -statistics	-1.1808	-0.1817	6.1018
	$p$ -value (two-sided)	0.2605	0.8589	5.3216e-05

(iii) The average of the squares of the  $t$  statistics is the  $F$ -statistic.

(c) The three contrast sums of squares are

Linear	Quadratic	Cubic
4.005125	0.140625	1.711125

with

$t$ -statistics	5.1416	0.9634	-3.3607
$p$ -value (two-sided)	0.0002	0.3543	0.0057

There is clearly a strong linear trend. The significant cubic term seems to be more of a data artifact - look at a plot of the means.

### Exercise 2.5

(a) This is essentially Exercise 1.23, where the likelihood estimates are derived. They are the same as the least squares estimates.

$$\begin{aligned} \text{Var}(\hat{\tau}_i) &= \text{Var}(\bar{y}_{i\cdot} - \bar{\bar{y}}) \\ &= \text{Var}(\bar{y}_{i\cdot}) - 2\text{Cov}(\bar{y}_{i\cdot}, \bar{\bar{y}}) + \text{Var}(\bar{\bar{y}}), \end{aligned}$$

where  $\text{Var}(\bar{y}_{i\cdot}) = \sigma^2/r$  and  $\text{Var}(\bar{\bar{y}}) = \sigma^2/(rt)$ . The covariance is

$$\begin{aligned} \text{Cov}(\bar{y}_{i\cdot}, \bar{\bar{y}}) &= \frac{1}{t} \sum_{i'=1}^t \text{E}(\bar{y}_{i\cdot} \bar{y}_{i'\cdot}) - \mu(\mu + \tau_i) \\ &= \frac{1}{t} \left[ \sum_{i'=1}^t (\mu + \tau_i)(\mu + \tau_{i'}) + \frac{\sigma^2}{r} \right] - \mu(\mu + \tau_i) \end{aligned}$$

Summing over  $i'$  cancels  $\mu(\mu + \tau_i)$  because the  $\tau_{i'}$  sum to zero. Gathering terms gives

$$\text{Var}(\hat{\tau}_i) = \frac{t-1}{rt} \sigma^2.$$

By independence,  $\text{Var}(\hat{\tau}_i - \hat{\tau}_{i'}) = 2 \frac{t-1}{rt} \sigma^2$ .

(b) We can use the R code

```
summary(aov(Y~Protein,data=aovdata))
Ymean<-tapply(Y,Protein,mean)
Ymean-mean(Y)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Protein	2	1228.27	614.14	110.43	1.873e-08
Residuals	12	66.74	5.56		

High	Low	Medium
12.3567	-9.0614	-3.2954

wit variance  $(2/15) * 5.56 = 0.741$ .

### Exercise 2.7

- (a) After reducing to  $\bar{y}_{ij.}$ , the minimizer is clearly  $\bar{y}_{ij.} = \mu + \tau_i + \gamma_j + (\tau\gamma)_{ij}$ . Display (2.5) follows.
- (b) The variance calculation is similar to that in Exercise 2.5. We have

$$\begin{aligned}\text{Var}(y_{i..} - \bar{y}) &= \left(\frac{t-1}{t}\right) \frac{\sigma^2}{tgr} \\ \text{Var}(y_{.j.} - \bar{y}) &= \left(\frac{g-1}{g}\right) \frac{\sigma^2}{tgr} \\ \text{Var}(y_{ij.} - \bar{y}) &= (tg-1) \frac{\sigma^2}{tgr}\end{aligned}$$

Cell means:

	Sulphur				
	0	3	6	9	
Nitrogen	0	4.5433	4.6400	5.24	5.9133
	20	5.7533	7.0467	5.81	6.2967

$$\text{Variance} = (8-1) * (0.0036)/(24) = 0.00105$$

Sulphur means

0	3	6	9
5.1483	5.8434	5.5251	6.1051

$$\text{Variance} = ((4-1)/4) * (0.0036)/(24) = 0.0001125$$

Nitrogen means

0	20
5.0842	6.2267

$$\text{Variance} = ((2-1)/2) * (0.0036)/(24) = 7.5e-05$$

### Exercise 2.9

- (i) We can use model (2.2) with  $\tau=\text{Tube}$ .
- (ii) Anova:

Source	df	EMS
Tube	2	$\sigma^2 + (8/2) \sum_i \tau_i^2$
Within	21	$\sigma^2$
Total	23	

- (iii) Depending on the meaning of “A, B, C” we could use pairwise differences, Helmert, or Polynomial. Helmert would be  $(2, -1, -1)$  and  $(0, 1, -1)$ . We can use the contrast test in the Inference subsection of Section 2.4.

### Exercise 2.11

- (a) The cross term is zero because the  $\tau_i$  are fixed, so the expectation is zero. Lemma 2.16 is then applied to the last term.  
 (b) Lemma 2.16 again.  
 (c) For part (a) this results in changing  $r$  to  $r_i$ . For (b) the Within EMS is  $(\sum_i r_i - t)\sigma^2$ . Note the typo in the first printing where the within EMS should be  $t(r - 1)\sigma^2$ .

### Exercise 2.13

- (a) The contrast coefficients are the linear, quadratic and cubic multiplied by 1 and  $-1$  for the two levels of hCG. For example, for the linear interaction we have

	Tissue			
hCG	-3	-1	1	3
	3	1	-1	3

- (b) The contrast SS is calculated using Definition 1.14. Note that the unbalance here does not affect the orthogonality.

	Lin	Quad	Cubic
SS	0.3333	0.4181	0.7391
F	0.4722	0.5924	1.0472
p	0.5298	0.4844	0.3640

- (c) For the main effect of tissue:

	Lin	Quad	Cubic
SS	0.1263	1.5482	0.0003
F	0.1789	2.1936	0.0004
p	0.6941	0.2127	0.9853

- (d) Although the picture is pretty, there is really not much going on here. Neither factor, nor any contrast, has a significant effect.

**Exercise 2.15**

- (a) The six contrasts are obtained by multiplication of each of the three  $A$  contrasts by each of the two  $B$  contrasts. For example,  $(1, -1/2, -1/2) \times (1, -1/3, -1/3, -1/3)$  gives

$$\begin{array}{c}
 A \\
 \begin{array}{|c|c|c|c|} \hline 1 & -1/3 & -1/3 & -1/3 \\ \hline \end{array}
 \end{array}
 \begin{array}{c}
 B \\
 \begin{array}{|c|c|c|c|} \hline -1/2 & 1/6 & 1/6 & 1/6 \\ \hline -1/2 & 1/6 & 1/6 & 1/6 \\ \hline \end{array}
 \end{array}
 \begin{array}{c}
 1 \quad 0 \\
 -1/2 \quad 1 \\
 -1/2 \quad -1 \\
 1 \quad -1/3 \quad -1/3 \quad -1/3 \\
 0 \quad 1 \quad -1/2 \quad -1/2 \\
 0 \quad 0 \quad 1 \quad -1
 \end{array}$$

- (b) Again we have six multiplications. Here is  $(-1, 0, 1) \times (-3, -1, 1, 3)$ .

$$\begin{array}{c}
 A \\
 \begin{array}{|c|c|c|c|} \hline 3 & 1 & -1 & -3 \\ \hline \end{array}
 \end{array}
 \begin{array}{c}
 B \\
 \begin{array}{|c|c|c|c|} \hline 0 & 0 & 0 & 0 \\ \hline -3 & -1 & 1 & 3 \\ \hline \end{array}
 \end{array}
 \begin{array}{c}
 -1 \quad 1 \\
 0 \quad -2 \\
 1 \quad 1 \\
 -3 \quad -1 \quad 1 \quad 3 \\
 1 \quad -1 \quad -1 \quad 1 \\
 1 \quad -3 \quad 3 \quad -1
 \end{array}$$

- (c) Denote the cell means by  $\bar{y}_{ij}$ ,  $i = 1, 3$ ,  $j = 1, 4$ . The contrast is

$$\begin{array}{c}
 A \\
 \begin{array}{|c|c|c|c|} \hline \bar{y}_{11} & (-1/3)\bar{y}_{12} & (-1/3)\bar{y}_{13} & (-1/3)\bar{y}_{14} \\ \hline \end{array}
 \end{array}
 \begin{array}{c}
 B \\
 \begin{array}{|c|c|c|c|} \hline (-1/2)\bar{y}_{21} & (1/6)\bar{y}_{22} & (1/6)\bar{y}_{23} & (1/6)\bar{y}_{24} \\ \hline (-1/2)\bar{y}_{31} & (1/6)\bar{y}_{32} & (1/6)\bar{y}_{33} & (1/6)\bar{y}_{34} \\ \hline \end{array}
 \end{array}$$

and collapsing the table gives

$$\begin{array}{c}
 A \\
 \begin{array}{|c|c|} \hline \text{Level 1} & \text{Average of Levels 2-4} \\ \hline \end{array}
 \end{array}
 \begin{array}{c}
 B \\
 \begin{array}{|c|c|} \hline \text{Level 1} & \begin{array}{|c|c|} \hline \bar{y}_{11} & (-1/3)(\bar{y}_{12} + \bar{y}_{13} + \bar{y}_{14}) \\ \hline \end{array} \\ \hline \text{Average of Levels 2-3} & \begin{array}{|c|c|} \hline (-1/2)(\bar{y}_{21} + \bar{y}_{31}) & (1/6)(\bar{y}_{22} + \bar{y}_{23} + \bar{y}_{24}) \\ \hline \end{array} \\ \hline \end{array}
 \end{array}$$

showing that we have a contrast in the collapsed means.

- (d) The contrast is

		C							
		-1		0		1			
		A				A			
B	1				1	1			
	-1	$\frac{1}{3}$	$\frac{1}{3}$	$\frac{1}{3}$		0	0	0	0
	$\frac{1}{2}$	$-\frac{1}{6}$	$-\frac{1}{6}$	$-\frac{1}{6}$		0	0	0	0
	$\frac{1}{2}$	$-\frac{1}{6}$	$-\frac{1}{6}$	$-\frac{1}{6}$		0	0	0	0
		1	$-\frac{1}{3}$	$-\frac{1}{3}$	$-\frac{1}{3}$	1	$-\frac{1}{3}$	$-\frac{1}{3}$	$-\frac{1}{3}$

This contrast asks if the piece of the  $A \times B$  interaction, that looks at the mean differences of part (c), increases linearly in the levels of C.

### Exercise 2.17

Referring to Example 2.13:

- The program for the ancova is on the web (Corn.R). The variances are calculated using (2.18).
- and (c). We test the unadjusted means using the MSE from the anova, which gives the standard error in the table in Example 2.13. For the ancova means we can pool the standard errors in the table, use them without pooling (which means we don't assume equal variances and should get the df with the Satterthwaite approximation - we won't do that here) or we can use the average variance from (2.23), which gives standard error of the difference as

$$0.534 = \sqrt{\frac{21.318}{6} \left( 1 + \frac{1}{3} \frac{75.792}{117.833} \right)}$$

where the  $X$  sums of squares can be obtained with the R statement `summary(aov(Yield Trt,data=aovdata))`

We summarize in the following table

	Two-sided $t$ -statistics					
	(360) -(K-24)	(360) -(M-15)	(360) -(M-4)	(K-24) -(M-15)	(K-24) -(M-4)	(M-15) -(M-4)
Unadjusted Mean	$\frac{ 10.617-11.733 }{\sqrt{2 \times .624}} = 1.265$	2.153	0.189	3.418	1.454	1.964
Adjusted Mean (Pooled)	$\frac{ 11.447-12.384 }{\sqrt{2 \times .255}} = 1.312$	6.053	1.239	7.365	2.551	4.814
Adjusted Mean (2.23)	$\frac{ 11.447-12.384 }{.534} = 1.755$	8.096	1.657	9.85	3.412	6.438

The pooled error is  $((0.496)^2 + (0.486)^2 + (0.563)^2 + (0.469)^2)/4 = 0.255$ .



The ancova certainly paid off, highlighting the differences from M-15. The 1% two-sided  $t$  cutoff with 19 df is 2.86, so the ancova will have more significant findings than the anova. The simultaneous inference can be formalized with Bonferroni, FDR, or some other method.

### Accompaniment

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#### Exercise 2.19

- (a) Expand the square as  $[(x_{ij} - \bar{x}_i) - (\bar{x}_j - \bar{x})]^2$  so the cross term is zero. Then just multiply out.  
 (b) Follows directly

#### Exercise 2.21

- (a) Let  $\mathcal{A}$  be a set of orthogonal contrasts.

$$\sum_{\mathcal{A}} \left( \sum_i a_i (\bar{y}_i - \bar{y}) \right)^2 = (\bar{\mathbf{y}} - \bar{y} \mathbf{1})' \left( \sum_{\mathcal{A}} \mathbf{a} \mathbf{a}' \right) (\bar{\mathbf{y}} - \bar{y} \mathbf{1}) = (\bar{\mathbf{y}} - \bar{y} \mathbf{1})' (\bar{\mathbf{y}} - \bar{y} \mathbf{1})$$

since  $\sum_{\mathcal{A}} \mathbf{a} \mathbf{a}'$  is the identity matrix (see Section 1.8.2). The result follows.

- (b) (i) If all  $\mu_i = \mu$ ,  $\sum_i a_i \mu_i = \mu \sum_i a_i = 0$  by the definition of contrast. If  $\sum_i a_i \mu_i \neq 0$  for some contrast, there is one nonzero term which implies one nonzero  $\mu_i$ , a contradiction.  
 (ii) This follows directly.  
 (iii) If any are rejected, clearly the biggest will be rejected. The maximization follows from Lemma 11.2.7 in Casella and Berger *Statistical Inference, Second Edition* 2001. Define  $b_i = a_i / (\sum_i a_i^2 / n_i)^{1/2}$  so we need to maximize  $(\sum_i b_i \bar{y}_i)^2$ . Using Cauchy-Schwarz,

$$\begin{aligned} \left( \sum_i b_i \bar{y}_i \right)^2 &= \left( \sum_i \frac{b_i}{\sqrt{n_i}} \sqrt{n_i} (\bar{y}_i - \bar{y}) \right)^2 \\ &\leq \sum_i \frac{b_i^2}{n_i} \sum_i n_i (\bar{y}_i - \bar{y})^2 = \sum_i n_i (\bar{y}_i - \bar{y})^2, \end{aligned}$$

since  $\sum_i b_i^2 / n_i = 1$ . Equality is obtained when

$$b_i = \sqrt{n_i} (\bar{y}_i - \bar{y}) / \left[ \sum_i n_i (\bar{y}_i - \bar{y})^2 \right]^{1/2}.$$

#### Exercise 2.23

- (a) The restrictions on the parameters result in

$$\sum_{tbc} (\bar{y}_i - \bar{y})^2 = \sum_{tbc} (\alpha_i + \bar{\varepsilon}_i - \bar{\varepsilon})^2$$

and the result follows from Lemma 2.16. Note a typo in the first printing, we should have

$$E(\text{MS}(\text{A})) = \sigma^2 + \frac{bcr}{(t-1)(b-1)} \sum_{i=1}^t \alpha_i^2.$$

(b) Similar to part (a). There is also a typo here (First Printing)

$$E(\text{MS}(\text{A} \times \text{B})) = \sigma^2 + \frac{cr}{(t-1)(b-1)} \sum_{i=1}^t \sum_{j=1}^b (\overline{\alpha\delta})_{ij}^2.$$

Source	df	EMS
Treatment A	$t - 1$	$\sigma^2 + \frac{bcr}{t-1} \sum_i \tau_i^2$
Treatment B	$b - 1$	$\sigma^2 + \frac{tcr}{b-1} \sum_j \delta_j^2$
Treatment C	$c - 1$	$\sigma^2 + \frac{tbr}{c-1} \sum_j \gamma_j^2$
(c) A $\times$ B	$(t-1)(b-1)$	$\sigma^2 + \frac{cr}{(t-1)(b-1)} \sum_{ij} (\alpha\delta)_{ij}^2$
A $\times$ C	$(t-1)(cb-1)$	$\sigma^2 + \frac{br}{(t-1)(c-1)} \sum_{ik} (\alpha\gamma)_{ik}^2$
B $\times$ C	$(b-1)(c-1)$	$\sigma^2 + \frac{tr}{(b-1)(c-1)} \sum_{jk} (\delta\gamma)_{jk}^2$
A $\times$ B $\times$ C	$(t-1)(b-1)(c-1)$	$\sigma^2 + \frac{r}{(t-1)(b-1)(c-1)} \sum_{ijk} (\alpha\delta\gamma)_{ijk}^2$
Within	$tbc(r-1)$	$\sigma^2$

(d)

$$H_0 : \sum_j \delta_j^2 = 0 \text{ and } H_0 : \sum_{jk} (\delta\gamma)_{jk}^2 = 0.$$

### Exercise 2.25

- (a)  $(\mathbf{a}\mathbf{a}')^2 = \mathbf{a}(\mathbf{a}'\mathbf{a})\mathbf{a}' = \mathbf{a}\mathbf{a}'$ , since  $\mathbf{a}'\mathbf{a}$  is the identity matrix.  
 (b) Part (a) is actually not needed. The result follows since  $\sum_i a_i Y_i / (\sigma^2 \sum_i a_i^2)^{1/2}$  is  $N(0,1)$ .

### Exercise 2.27

This is easiest done with a modification of the matrices  $B_1 - B_4$  of Technical Note 3.8.2. Write the  $Y$  vector in the order

$$\begin{aligned} \mathbf{Y}' &= \{Y_{ijk}\}' \\ &= (Y_{111}, \dots, Y_{11r}, \dots, Y_{t11}, \dots, Y_{t1r}, \dots, Y_{1g1}, \dots, Y_{1gr}, \dots, Y_{tg1}, \dots, Y_{tbr}), \end{aligned}$$

Define the matrices

$$\begin{aligned}
 B_1 &= \frac{1}{g} \begin{pmatrix} I_t \\ \vdots \\ I_t \end{pmatrix}_{tg \times t} (I_t \cdots I_t)_{t \times tg}, \\
 B_2 &= \frac{1}{t} \begin{pmatrix} \mathbf{1}_{t \times 1} & 0 & \cdots & 0 \\ 0 & \mathbf{1}_{t \times 1} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mathbf{1}_{t \times 1} \end{pmatrix}_{tg \times g} \begin{pmatrix} \mathbf{1}'_{1 \times t} & 0 & \cdots & 0 \\ 0 & \mathbf{1}'_{1 \times t} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mathbf{1}'_{1 \times t} \end{pmatrix}_{g \times tg}, \quad B_3 = \frac{1}{tg} J_{tg}, \\
 B_4 &= \begin{pmatrix} \mathbf{1}_{1 \times r} & 0 & \cdots & 0 \\ 0 & \mathbf{1}_{1 \times r} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mathbf{1}_{1 \times r} \end{pmatrix}_{tg \times tgr}.
 \end{aligned}$$

The sums of squares are all of the form  $\mathbf{Y}'A\mathbf{Y}$  using the matrices

$$\begin{aligned}
 A_1 &= (1/r)B'_4(B_1 - B_3)(1/r)B_4 \quad (\text{for SST}) \\
 A_2 &= (1/r)B'_4(B_2 - B_3)(1/r)B_4 \quad (\text{for SSG}) \\
 A_3 &= (1/r)B'_4(I - B_1 - B_2 + B_3)(1/r)B_4 \quad (\text{for SS T} \times \text{G}),
 \end{aligned}$$

and take  $A_4 = \text{Block Diagonal}(I - (1/r)J)$ , where there are  $tg$  replications of  $I - (1/r)J$ , so  $\mathbf{Y}'A_4\mathbf{Y}$  is the within SS. Then matrix multiplication shows that  $A_1 - A_4$  satisfy Cochran's Theorem, and the  $F$ -tests of Theorem 2.22 follow.

### Exercise 2.29

Referring to Section 2.6:

- (a) We need to minimize the residual sum of squares  $\sum_{ij} [y_{ij} - \theta_i - \beta(x_{ij} - \bar{x})]^2$ , where  $\theta_i = \mu + \tau_i$ . Differentiate with respect to  $\theta_i$  to get  $\theta_i = \bar{y}_i - \beta(\bar{x}_i - \bar{x})$ , and substitute this back into the residual sum of squares, which now becomes  $\sum_{ij} [(y_{ij} - \bar{y}_i) - \beta(x_{ij} - \bar{x}_i)]^2$ . This is minimized by the LS estimate given after (2.17), and substitution gives  $\hat{\theta}_i = \bar{y}_i - \hat{\beta}(\bar{x}_i - \bar{x})$ , which is clearly unbiased.
- (b) Since  $E\hat{\theta}_i = \mu + \tau_i$  and  $E\sum_i \hat{\theta}_i = t\mu + \sum_i \tau_i$ , if  $\sum_i \tau_i = 0$  then  $E\hat{\theta}_i - (1/t)\sum_i \hat{\theta}_i = \tau_i$ , and  $\hat{\theta}_i - (1/t)\sum_i \hat{\theta}_i = y_i - \bar{y} - \hat{\beta}(\bar{x}_i - \bar{x})$ . If the  $r_i$  are unequal, the least squares estimates of  $\hat{\theta}_i$  and  $\beta$  are the same, but now  $E\sum_i \hat{\theta}_i$  does not produce an unbiased estimate of  $\mu$ . However,  $E\sum \hat{\theta}_i = \mu \sum_i r_i - \beta \sum_i (\bar{x}_i - \bar{x})$ . From this we can construct the estimator

$$\bar{y}_i - \frac{\sum_i \bar{y}_i}{\sum_i r_i} - \hat{\beta} \left[ (\bar{x}_i - \bar{x}) - \frac{\sum_i (\bar{x}_i - \bar{x})}{\sum_i r_i} \right],$$

which is an unbiased estimator of  $\tau_i$ .

- (c) Same as (2.18) except replace  $r$  with  $r_i$ .

### Exercise 2.31

The following data are measurements on the strength index of three varieties of cotton, where the treatments are pounds of potassium oxide per acre (dataset **Imbalance**). Here we want to see the effect of imbalance on the anova.

Strength Index of Cotton			
Varieties			
Treatment	1	2	3
36	7.06	7.75, 8.22	7.95, 8.59
60	7.51, 7.5	8.08, 8.18	8.69, 8.39
84	7.27, 7.49	7.9	8.04
108	6.55, 6.47	7.26, 7.06	7.35
132	6.97, 7.14	7.52, 7.83	7.63, 7.2

- (a) Verify the anova tables in Miscellanea 2.9.3. The anova tables can be produced with the R commands  
`summary(aov(Strength Trt+Variety,data=aovdata))`  
 and  
`summary(aov(Strength Variety+Trt,data=aovdata))`
- (b) Produce one anova table that contains the partial sums of squares. (You can do this by combining the two tables from part (a) or by using the R command `drop1`.)  
 Combine the tables as indicated or use the R commands  
`imb1<-aov(Strength Variety+Trt,data=aovdata)`  
`drop1(imb1,test="F")`
- (c) In terms of the analysis of these data, explain why the table in part (b) is most appropriate.  
 The partial SS measures the effect of a treatment after all of the other treatments have been fit. This is most appropriate in a twoway, where both treatments are of interest. For example, fitting Variety before Treatment could mistakenly ascribe variation explained by Treatment to Variety. This is different from a RCB, where we would always fit Blocks first.
- (d) Calculate the contrast sum of squares for the linear effect of potassium oxide and test its significance.
- (e) Estimate the contrast and its standard error, and give a 95% confidence interval.

## Complete Block Designs

### Essential

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#### Exercise 3.1

Referring to Example 3.3:

- (a) The anova table is created with the R statement  
`summary(aov(yield ~ block + trt, strawdata)).`  
 To do the  $t$ -tests use `t.test(A-B)` and `t.test(.5*A+.5*B-C)`

- (b) (c) and (d) The two component anova tables are created with

```
1. yield<-(sqrt(2)/sqrt(2))*c(A,B)
   trt<-rep(c("A","B"),each=4)
   block <- rep(c("1","2","3","4"),each=1,times=2)
2. yield<-(sqrt(2)/sqrt(1.5))*c(.5*A+.5*B,C)
   trt<-rep(c(".5*A+.5*B","C"),each=4)
   block <- rep(c("1","2","3","4"),each=1,times=2)
```

The residuals from these tables will add as in part (c), and the respective  $F$ -tests will match the  $t$ -tests.

- (e) For example

$$\begin{aligned} E\left([ (Y_{1j} - Y_{2j}) - (\bar{Y}_{1\cdot} - \bar{Y}_{2\cdot}) ]^2\right) &= \text{Var}(Y_{1j} - \bar{Y}_{1\cdot}) + \text{Var}(Y_{2j} - \bar{Y}_{2\cdot}) \\ &\quad - 2\text{Cov}(Y_{1j} - \bar{Y}_{1\cdot}, Y_{2j} - \bar{Y}_{2\cdot}). \end{aligned}$$

Now compute

$$\text{Var}(Y_{1j} - \bar{Y}_{1\cdot}) = \text{Var}(Y_{2j} - \bar{Y}_{2\cdot}) = \left(1 - \frac{1}{b}\right) (\sigma^2 + \sigma_\beta^2)$$

and

$$\begin{aligned} \text{Cov}(Y_{1j} - \bar{Y}_{1\cdot}, Y_{2j} - \bar{Y}_{2\cdot}) &= E\left([(\beta_j - \bar{\beta}) + (\varepsilon_{1j} - \bar{\varepsilon}_{1\cdot})][(\beta_j - \bar{\beta}) + (\varepsilon_{2j} - \bar{\varepsilon}_{2\cdot})]\right) \\ &= \left(1 - \frac{1}{b}\right) \sigma_\beta^2, \end{aligned}$$

and put these together to get that

$$\frac{1}{2} \sum_{j=1}^b E \left( [(Y_{1j} - Y_{2j}) - (\bar{Y}_{1.} - \bar{Y}_{2.})]^2 \right) = (b-1)\sigma^2.$$

A similar, but more involved calculation (with three covariances) will show that the second sum of squares has the same expectation.

### Exercise 3.3

- (a) This gives the full anova table, wrong tests  
`summary(aov(Yield Variety+Block+Block:Variety,data=aovdata))`  
 This gives the correct test on Variety  
`summary(aov(Yield Variety+Block+Error(Variety/Block:Variety),data=aovdata))`
- (b) Looking at the SS formulas in Table 3.3 will show that the test on Variety only uses cell means.
- (c) The 4 block experiment is in the example, the other two anovas follow; note that the 8 block anova is unbalanced in the cells. The best design is the 12 block experiment, giving the most df for the Variety test. The eight block experiment could be appropriate if there is a lot of concern about interaction. The 4 block experiment is a waste of effort.

Eight Blocks		Twelve Blocks	
Source	df	Source	df
Block	7	Block	11
Variety	3	Variety	3
V × B	21	V × B	33
Within	16	Within	0

### Exercise 3.5

- (a) This gives the correct anova table with pooled error:  
`aov(Yield Block+Shading*Stage,data=aovdata)`

Source	df	SS	MS	F	p-value
Block	3	86.22	28.74	1.2400	0.3171054
Shading	2	622.89	311.44	13.4369	0.0001215
Stage	2	684.06	342.03	14.7564	6.623e-05
Shading:Stage	4	126.11	31.53	1.3602	0.2771167
Residuals	24	556.28	23.18		

Of course, the test on blocks is nonsense.

The EMS table (calculations are easier using Exercise 2.19) is based on the model

$$Y_{ijk}\mu + \tau_i + \beta_j + \gamma_k + (\tau\gamma)_{ik} + (\tau\beta)_{ij} + (\beta\gamma)_{jk} + (\beta\tau\gamma)_{ijk} + \varepsilon_{ijk},$$

with  $\tau$  = Shade and  $\gamma$  = Stage.

Source	df	EMS
Blocks	$b - 1$	$\sigma_\varepsilon^2 + \sigma_{\beta\tau\gamma}^2 + t\sigma_{\beta\gamma}^2 + g\sigma_{\beta\tau}^2 + tg\sigma_\beta^2$
Shade	$t - 1$	$\sigma_\varepsilon^2 + \sigma_{\beta\tau\gamma}^2 + g\sigma_{\tau\beta}^2 + \frac{bg}{t-1} \sum_i \tau_i^2$
Stage	$g - 1$	$\sigma_\varepsilon^2 + \sigma_{\beta\tau\gamma}^2 + t\sigma_{\beta\gamma}^2 + \frac{bt}{g-1} \sum_k \gamma_k^2$
Shade $\times$ Stage	$(t-1)(g-1)$	$\sigma_\varepsilon^2 + \sigma_{\beta\tau\gamma}^2 + \frac{b}{(t-1)(g-1)} \sum_{ik} \tau\gamma_{ik}^2$
B $\times$ Shade	$(b-1)(t-1)$	$\sigma_\varepsilon^2 + \sigma_{\beta\tau\gamma}^2 + g\sigma_{\beta\tau}^2$
B $\times$ Stage	$(b-1)(g-1)$	$\sigma_\varepsilon^2 + \sigma_{\beta\tau\gamma}^2 + t\sigma_{\beta\gamma}^2$
B $\times$ Shade $\times$ Stage	$(b-1)(t-1)(g-1)$	$\sigma_\varepsilon^2 + \sigma_{\beta\tau\gamma}^2$

The tests of the treatments are against the respective interaction with Blocks. In the analysis we pooled the Block interactions, which makes the assumption that the twoway Block  $\times$  Treatment interactions are zero.

- (b) Because of the ordering on the treatments, polynomial contrasts are suggested.

Contrast	Linear Shade	Quadratic Shade	Linear Stage	Quadratic Stage
$F$ -statistic	26.756	0.117	16.914	12.599
$p$ -value	0.00003	0.73480	0.00040	0.00163

Here is the R code

```

MSE<-sum((ShadeAov$residuals)^2)/ShadeAov$df.residual #Mean Square
Residual
df<-ShadeAov$df.residual #df residual
A<- contr.poly(3, scores = 1:3, contrasts = TRUE)
YShade<-tapply(Yield, Shading, mean)
YStage<-tapply(Yield, Stage, mean)
nShade<-tapply(Yield,Shading,length) #number of obs in each mean
nStage<-tapply(Yield,Stage,length) #number of obs in each mean
LinShade<-(sum(A[,1]*YShade))^2/(MSE*sum(A[,1]^2/nShade))
QuadShade<-(sum(A[,2]*YShade))^2/(MSE*sum(A[,2]^2/nShade))
LinStage<-(sum(A[,1]*YStage))^2/(MSE*sum(A[,1]^2/nStage))
QuadStage<-(sum(A[,2]*YStage))^2/(MSE*sum(A[,2]^2/nStage))

```

### Exercise 3.7

- (a) The nested anova is

Source	df
Category	3
Art (in Category)	36
Judges (in Art $\times$ Category)	440
Total	479

In the nested design each factor is tested by the one below it. But all of the anova assumptions are violated due to correlation in the cells - the response of a Judge across the different pieces of Art are correlated.

- (b) Whenever there are correlated observations, this suggests a blocking design. The RCB anova is

Source	df
Judges (Blocks)	11
Category	3
Art (in Category)	36
Category $\times$ Judge	33
Art (in Category) $\times$ Judge	396
Total	479

Note that both Category and Art (in Category) are crossed with Judges. The tests are against the respective interaction with Judges.

- (c) Numerically, we have

$$\begin{aligned} \text{SS}(\text{Judges (in Art} \times \text{Category)}) &= \text{SS}(\text{Judges}) + \text{SS}(\text{Category} \times \text{Judge}) \\ &\quad + \text{SS}(\text{Art (in Category)} \times \text{Judge}), \end{aligned}$$

where the left side is from the nested anova and the right side is from the RCB anova. So we see that in the nested anova the error term contains extraneous variation due to Judges, and is not tailored to the individual components (and is, in fact, wrong because of the correlation).

### Exercise 3.9

- (a) Although the locations (edge of a dropoff, etc.) can be thought of as random, it is probably best to model them as fixed and thus infer only to the three subreefs. Then traps are nested in location and time is crossed. Since the traps are reset there is no correlation across time.
- (b) The anova table for the analysis is

Source	df
Location	2
Traps (in Loc.)	12
Time	3
Time $\times$ Loc	6
Time $\times$ Trap (in Loc.)	36
Total	59

and we can get the EMS from Table 3.10 if we identify Location with Rep, Traps with Blocks, and Time with Treatments. In that table Replications are random, and have no test on Replication. If we model Locations as fixed, the Location EMS will not have the  $\sigma_{\tau R}^2$  term (the correlation with



a fixed effect is zero), and can be tested with Traps (in Location). Time is tested with Time  $\times$  Loc and Time  $\times$  Loc is tested with Time  $\times$  Trap (in Loc.)

- (c) This variance comes from Traps (in Loc.), and is estimated by  $MS(\text{Traps (in Loc.)})/20$ .  
 (d) Doubling the number of cages.

### Exercise 3.11

The solution here is contained in that of Exercise 3.5.

### Exercise 3.13

- (a) For each gene, this is a paired  $t$  test on Pre-Post, which is and RCB with subjects as blocks. Thus a model is

$$\log(Y_{ij}) = \mu + \tau_i + \beta_j + \varepsilon_{ij},$$

with  $\tau$  = Pre-Post and  $\beta$  = Blocks.

- (b) The anova from R is

Source	df	SS	MS	F	$p$ -value
Block	4	0.199322	0.049831	0.7598	0.6017
Treatment	1	0.191240	0.191240	2.9161	0.1629
Residuals	4	0.262323	0.065581		

There is no evidence that this gene has different expression levels. Of course the test on Blocks is again nonsense.

- (c) To loop the anova over the genes use
- ```
for(i in 1:nGene)
{GeneAov<-aov(log(ExpLevel[,i]) ~ Block+Treatment,data=aovdata)
Pvalue[i]<-summary(GeneAov)[[1]][[5]][[2]]
}
```

The sorted  $p$ -values can be obtained with `op<-order(Pvalue);Pvalue[op]`. After calculating the Q-values, they cross at the 99<sup>th</sup> sorted gene. The significant genes at the .05 FDR are `sort(op[1:99])`

10 14 46 48 49 53 54 55 56 57 58 61 63 71 80 82 83 85 88  
 90 93 96 99 100 104 105 106 107 110 117 119 120 123 125 126 128 131 133  
 134 135 136 137 138 141 142 146 147 148 149 150 152 156 157 162 164 165 167  
 168 169 171 172 176 177 178 180 181 187 188 189 190 192 194 195 197 200 201  
 205 206 208 212 214 215 216 217 221 222 224 225 228 230 231 232 235 237 240  
 241 248 249 250

**Exercise 3.15**

- (a) The R code

```
summary(aov(Yield ~ Year*Block+Variety*Block+Variety*Year,data=aovdata))
```

will give the following anova table

| Source        | df | SS      | MS      | F       | p-value   |
|---------------|----|---------|---------|---------|-----------|
| Year          | 2  | 0.2624  | 0.1312  | 0.2942  | 0.74868   |
| Block         | 3  | 4.3587  | 1.4529  | 3.2579  | 0.04578   |
| Variety       | 3  | 31.2318 | 10.4106 | 23.3439 | 1.989e-06 |
| Year:Block    | 6  | 5.9003  | 0.9834  | 2.2051  | 0.09046   |
| Block:Variety | 9  | 3.1190  | 0.3466  | 0.7771  | 0.63955   |
| Year:Variety  | 6  | 2.6702  | 0.4450  | 0.9979  | 0.45642   |
| Residuals     | 18 | 8.0274  | 0.4460  |         |           |

where the “Residuals” are the threeway interaction.

- (b) From Table 3.11 we know that the tests on the interaction with Variety are valid (the Year  $\times$  Block test is nonsense), but we must assume that the interactions are zero to get a valid test on Variety. Since both tests are very non-significant, we are comfortable in doing this.
- (c) If the interactions with Variety are not zero, then the F-test numerator is inflated and the test is anti-conservative, that is, you could make the mistake of declaring significance falsely.
- (d) The Variety means are

|         |         |       |        |
|---------|---------|-------|--------|
| DuPuits | Flamand | Ladak | Narrag |
| 6.080   | 5.992   | 4.076 | 5.162  |

with standard error  $\sqrt{.446/12} = .193$ . This leads us to conclude that Ladak is worst, Narrag is next, and DuPuits and Flamand are best, and equivalent.

**Exercise 3.17**

- (a) (i) The anova R command is

```
summary(aov(Yield ~ Row+Column+Treatment,data=aovdata)).
```

- (ii) The treatment means are

|        |        |        |        |
|--------|--------|--------|--------|
| 1      | 2      | 3      | 4      |
| 24.700 | 27.775 | 25.525 | 24.975 |

with standard error  $\sqrt{3.997/4} = .999$ . Treatment 2 seems to have a significantly higher yield than the control. The  $t$ -statistic is  $(27.775 - 24.7)/\sqrt{3.997/2} = 2.175$  with a  $p$ -value of 0.036.

- (iii) With standard error
- $\approx 1$
- , the power is approximately

$$P(Z > 1.645 - \sqrt{n/2}\delta),$$

and for  $\delta = .5$  and  $n = 4$  this is .174. To increase the power using Latin squares we would need to replicate the squares. However, to get a power of .9 we would need  $n \approx 70$ , which is unrealistic.

- (b) The anova table is produced with  
`summary(aov(Yield ~ Rep*Row+Column+Treatment,data=aovdata))`  
 and note how the data are coded to reflect the nesting.

| Source    | df | SS     | MS    | F      | p-value   |
|-----------|----|--------|-------|--------|-----------|
| Rep       | 2  | 15.83  | 7.92  | 0.9828 | 0.38884   |
| Row       | 9  | 66.12  | 7.35  | 0.9121 | 0.53110   |
| Column    | 9  | 530.76 | 58.97 | 7.3210 | 4.553e-05 |
| Treatment | 3  | 95.75  | 31.92 | 3.9620 | 0.01992   |
| Residuals | 24 | 193.33 | 8.06  |        |           |

The means are

| 1      | 2      | 3      | 4      |
|--------|--------|--------|--------|
| 24.458 | 27.825 | 24.958 | 24.392 |

With 12 observations in each mean, the standard error of a difference is  $\sqrt{2 \times 8.06/12} = 1.159$ . This leads us to believe that Treatment 2 is significantly better.

It should be clear that this is a nested design, as the Rows and Columns are in different locations - they are not crossed with locations.

- (c) This is a consequence of the fact that  $SS(A) + SS(A \times B) = SS(A \text{ (in B)})$ .

### Exercise 3.19

- (a) The anova table comes from  
`Height=as.character(c("B","M","T","B","M","T","B","M","T"))`  
`Depth=as.character(c("F","F","F","M","M","M","T","T","T"))`  
`Trt=as.character(c("M","H","L","H","L","M","L","M","H"))`  
`Intake=c(96,81,106,94,116,114,100,91,89)`  
`aovdata <- data.frame(Intake,Height,Depth,Trt)`  
`#-----Latin Square ANOVA -----`  
`LSAov<-aov(Intake ~ Height+Depth+Trt,data=aovdata)`  
`summary(LSAov)`

| Source    | df | SS     | MS     | F       | p-value |
|-----------|----|--------|--------|---------|---------|
| Height    | 2  | 89.56  | 44.78  | 5.3026  | 0.15866 |
| Depth     | 2  | 402.89 | 201.44 | 23.8553 | 0.04023 |
| Trt       | 2  | 574.89 | 287.44 | 34.0395 | 0.02854 |
| Residuals | 2  | 16.89  | 8.44   |         |         |

- (b) This is tested with the Treatment test in the anova. We see that the intakes are significantly different after controlling for location

- (c) The contrasts can be estimated using similar R code to Exercise 3.5. For example
- ```
MSE<-sum((LSAov$residuals)^2)/LSAov$df.residual #Mean Square Residual
df<-LSAov$df.residual
HL=c(-1,.5,.5)
HLMean=sum(HL*YIntake)
HLSD=sqrt(MSE*sum(HL^2/nIntake))
```

Linear Trend:  $8.721 \pm 2 \times 1.678$

Low vs. Average of M and H:  $15.833 \pm 2 \times 2.055$

### Accompaniment

---

#### Exercise 3.21

Show details for the following calculations in Section 3.2.

- (a) These follow directly from the model (3.5).  
 (b) If we condition on the  $\beta$ s, then the only random variables left in the covariance are the  $\varepsilon$ s.  
 (c)  $\text{Cov}(\beta_j + \varepsilon_{ij}, \beta_j + \varepsilon_{i'j}) = E[(\beta_j + \varepsilon_{ij})(\beta_j + \varepsilon_{i'j})]$ , and then expand the product.  
 (d) Verify the EMS calculations in Table 3.6. The EMS for blocks is given in (3.11). The calculation for treatments is similar

$$\begin{aligned} \text{ESS}(\text{Trts}) &= E \sum_i b(\bar{Y}_i - \bar{Y})^2 = bE \sum_i [\tau_i + \bar{\varepsilon}_i - \bar{\varepsilon}]^2 \\ &= b \sum_i \tau_i^2 + bE \sum_i (\bar{\varepsilon}_i - \bar{\varepsilon})^2 \\ &= b \sum_i \tau_i^2 + b(t-1) \frac{\sigma_\varepsilon^2}{b}, \end{aligned}$$

where the  $\bar{\beta}$  terms cancel,  $\bar{\tau} = 0$  and the last equality is from Lemma 3.16.

The calculations for the interaction term are the same as in Exercise 3.23.

#### Exercise 3.23

The equality

$$\sum_{ij} (\varepsilon_{ij} - \bar{\varepsilon}_{i.} - \bar{\varepsilon}_{.j} + \bar{\varepsilon})^2 = \sum_{ij} \varepsilon_{ij}^2 - b \sum_i \bar{\varepsilon}_{i.}^2 - t \sum_j \bar{\varepsilon}_{.j}^2 + bt \bar{\varepsilon}^2$$

is a direct consequence of Exercise 2.19. The expectations

$$E \varepsilon_{ij}^2 = \sigma_\varepsilon^2, \quad E \bar{\varepsilon}_{i.}^2 = \frac{\sigma_\varepsilon^2}{b}, \quad E \bar{\varepsilon}_{.j}^2 = \frac{\sigma_\varepsilon^2}{t}, \quad E \bar{\varepsilon}^2 = \frac{\sigma_\varepsilon^2}{bt},$$

are the variances of the respective random variables.

**Exercise 3.25**

Here we will prove Theorem 3.18.

- (a) Note that  $\mathbf{Y}$  is *block diagonal* with  $b \times t$  blocks  $\sigma_\varepsilon^2 I + \sigma_\beta^2 J$ . The vector  $\mathbf{Y}$  is clearly multivariate normal, and from (3.5), in each block

$$\begin{aligned}\text{Var}(Y_{ij}) &= \sigma_\beta^2 + \sigma^2 \\ \text{Cov}(Y_{ij}, Y_{i'j}) &= \text{Cov}(\beta_j + \varepsilon_{ij}, \beta_j + \varepsilon_{i'j}) = \sigma_\beta^2.\end{aligned}$$

- (b) Matrix multiplication will establish that  $B_1$ ,  $B_2$ , and  $B_3$  are all idempotent, and  $B_1 B_3 = B_2 B_3 = B_1 B_2 = B_3$ . The idempotency of  $I - B_1 - B_2 + B_3$  and  $B_1 - B_3$  now follows. The sums of squares formulas can be obtained from the idempotency and  $\bar{Y}_{i\cdot} = B_1 Y$ ,  $\bar{Y}_{\cdot j} = B_2 Y$ ,  $\bar{Y} = B_3 Y$ , which also can be obtained from matrix multiplication.
- (c) This is again matrix multiplication.
- (d) Now that we have all of the matrices straight, we can use Theorem 2.20. We can assume that  $\mu = 0$  because the  $A$  matrices mean center  $Y$ .

**Exercise 3.27**

- (a) Recall that  $\hat{\varepsilon}_{ij} = \varepsilon_{ij} - \bar{\varepsilon}_{i\cdot} - \bar{\varepsilon}_{\cdot j} + \bar{\varepsilon}$ . Clearly  $T_{lm}$  has mean zero. Its variance is

$$\text{Var}(T_{lm}) = E \left( \sum_{i=1}^t \sum_{j=1}^r a_{ij}^{lm} \hat{\varepsilon}_{ij} \right)^2 = \sum_{i=1}^t \sum_{j=1}^r \sum_{i'=1}^t \sum_{j'=1}^r a_{ij}^{lm} a_{i'j'}^{lm} E(\hat{\varepsilon}_{ij} \hat{\varepsilon}_{i'j'}).$$

To evaluate the expectation we need to be careful about whether  $i = i'$ , etc. First, for all  $i$  and  $j$

$$E(\varepsilon_{ij} \bar{\varepsilon}) = E(\bar{\varepsilon}_{i\cdot} \bar{\varepsilon}) = E(\bar{\varepsilon}_{\cdot j} \bar{\varepsilon}) = E(\bar{\varepsilon} \bar{\varepsilon}) = \sigma^2 / bt.$$

Next,

$$E(\bar{\varepsilon}_i^2) = \sigma^2 / b, \quad E(\bar{\varepsilon}_j^2) = \sigma^2 / t, \quad E(\bar{\varepsilon}_i \bar{\varepsilon}_j) = \sigma^2 / bt,$$

the last for  $i \neq j$ . Finally,

$$E(\varepsilon_{ij} \bar{\varepsilon}_i) = \sigma^2 / b, \quad E(\varepsilon_{ij} \bar{\varepsilon}_j) = \sigma^2 / t,$$

and all other expectations are zero (these are mostly with  $\varepsilon_{ij}$ ). To summarize,

$$E(\hat{\varepsilon}_{ij} \hat{\varepsilon}_{i'j'}) = \frac{\sigma^2}{bt} - \frac{\sigma^2}{b} I(i = i') - \frac{\sigma^2}{t} I(j = j') + \sigma^2 I(i = i', j = j').$$

When we now substitute this into  $\text{Var}(T_{lm})$  and use the fact that the  $a_{ij}^{lm}$  sum to zero over either index, the first three terms in the expectation are zero. For example,

$$\sum_{i=1}^t \sum_{j=1}^r \sum_{i'=1}^t \sum_{j'=1}^r a_{ij}^{lm} a_{i'j'}^{lm} \frac{\sigma^2}{b} I(i=i') = \frac{\sigma^2}{b} \sum_{i=1}^t \sum_{j=1}^r a_{ij}^{lm} \sum_{j'=1}^r a_{ij'}^{lm} = 0,$$

and hence

$$\text{Var}(T_{lm}) = \sum_{i=1}^t \sum_{j=1}^r \sum_{i'=1}^t \sum_{j'=1}^r a_{ij}^{lm} a_{i'j'}^{lm} \sigma^2 I(i=i', j=j') = \sigma^2 \sum_{i=1}^t \sum_{j=1}^r (a_{ij}^{lm})^2 = \sigma^2.$$

- (b) This calculation is almost the same as in part (a), except that the last piece is

$$\sigma^2 \sum_{i=1}^t \sum_{j=1}^r a_{ij}^{lm} a_{ij}^{l'm'} = 0,$$

since the two contrasts are orthogonal.

- (c)

$$\begin{aligned} \sum_{l=1}^{t-1} \sum_{m=1}^{r-1} (T_{lm})^2 &= \sum_{l=1}^{t-1} \sum_{m=1}^{r-1} \left( \sum_{i=1}^t \sum_{j=1}^r a_{ij}^{lm} \hat{\varepsilon}_{ij} \right)^2 \\ &= \sum_{i,j,i',j'} \left( \sum_{l=1}^{t-1} \sum_{m=1}^{r-1} a_{ij}^{lm} a_{i'j'}^{lm} \right) \hat{\varepsilon}_{ij} \hat{\varepsilon}_{i'j'}. \end{aligned}$$

Now we use the product construction of the  $a_{ij}^{lm}$  to evaluate the inner sum. From Table 3.14, the  $a_{ij}^{lm}$  are constructed by taking products of rows from the first set of contrasts in Table 3.14 with columns from the second set. Specifically, let  $c^\ell$  be the  $\ell^{\text{th}}$  row in the first set of contrasts, and  $d^m$  be the  $m^{\text{th}}$  column in the second set. Then  $a_{ij}^{lm} = c_i^\ell d_j^m$ , where we are picking out the elements from the  $c$  row and  $d$  column. Then

$$\begin{aligned} \sum_{l=1}^{t-1} \sum_{m=1}^{r-1} a_{ij}^{lm} a_{i'j'}^{lm} &= \sum_{l=1}^{t-1} \sum_{m=1}^{r-1} c_i^\ell c_{i'}^\ell d_j^m d_{j'}^m \\ &= \left( \sum_{l=1}^{t-1} c_i^\ell c_{i'}^\ell \right) \left( \sum_{m=1}^{r-1} d_j^m d_{j'}^m \right) \end{aligned}$$

Within each of the parentheses, the quantity is the inner product of two rows (for the  $c$ s) or columns (for the  $d$ s). By construction, each of these sets are orthogonal contrasts, so the sum is zero unless  $i = i'$  or  $j = j'$ . If  $i = i'$  and  $j = j'$  the sum is 1, so we have

$$\sum_{l=1}^{t-1} \sum_{m=1}^{r-1} (T_{lm})^2 = \sum_{i=1}^t \sum_{j=1}^r \hat{\varepsilon}_{ij}^2.$$

Note that this proof works for any set of contrasts obtained from a product construction.

- (d) Since  $T_{lm}/\sigma$  are iid  $N(0, 1)$ , their squares are  $\chi_1^2$  and the sum is  $\chi_{(r-1)(t-1)}^2$ . Formally, we can use Theorem 2.18 or Theorem 2.20

**Exercise 3.29**

- (a) Matrix multiplication will establish (i)-(v). For (ii), note that  $(1/r)B_4Y = \{\bar{Y}_{ij}\}$  (Section 3.8.3).  
 (b) This follows from (iv) and (v).  
 (c) Lemma 3.20 is established by verifying the multiplication. Theorem 3.21 (1) and (2) follow from Theorem 2.20, and (3) is from the properties of the  $F$  distribution.

**Exercise 3.31**

- (a) Since  $\sum_i \gamma_{ij} = 0$ ,

$$\text{Var}(\sum_i \gamma_{ij}) = t\sigma_m^2 + t(t-1)\rho\sigma_m^2 = 0 \Rightarrow \rho = -1/(t-1).$$

- (b) Similarly

$$\text{Var}(\sum_i (\tau\beta)_{ij}) = t\sigma_{\tau\beta}^2 + t(t-1)\rho_{\tau\beta}\sigma_{\tau\beta}^2 = 0 \Rightarrow \rho_{\tau\beta} = -1/(t-1).$$

**Exercise 3.33**

- (a) The matrix  $ZZ'$  is block diagonal with blocks  $J_t$ , the  $t \times t$  matrix of ones, so the result follows.  
 (b) This is straightforward matrix multiplication. Use the fact that  $V^{*-1}$  is block diagonal with  $t \times t$  blocks

$$\frac{1}{\sigma^2} \left( I - \frac{\sigma_\beta^2}{\sigma^2 + t\sigma_\beta^2} J \right)$$

- (c) Matrix multiplication again.  
 (d)

$$\text{Cov}(Y, \beta) = EY\beta' = E[E(Y|\beta)\beta'] = E[(X\theta + Z\beta)\beta'] = ZE[\beta\beta'] = \sigma_\beta^2 Z.$$

**Exercise 3.35**

- (a) From Table 3.6

$$\begin{aligned} E\hat{\sigma}_\varepsilon^2 &= E[\text{MS}(\text{T} \times \text{B})] = \sigma_\varepsilon^2 \\ E\hat{\sigma}_\beta^2 &= \frac{1}{t}E[\text{MS}(\text{Blocks}) - \text{MS}(\text{T} \times \text{B})] = \frac{1}{t}[\sigma_\varepsilon^2 + t\sigma_\beta^2 - \sigma_\varepsilon^2] = \sigma_\beta^2. \end{aligned}$$

- (b)  $\hat{\sigma}_\varepsilon^2 = .476$ ,  $\hat{\sigma}_\beta^2 = (1/4)(1.327 - .476) = 0.213$ .

- (c) Unfortunately, this is not straightforward because of the replication. If you just read in the data, the REML estimates don't match the anova estimates (at least I can't get them to match). Here is what works: After reading in the data, use the following R

```
tab<-list(Block,Variety)
Yield<-sqrt(3)*c(tapply(Yield,tab,mean))
Block<-as.character(c("1", "2", "3", "4" ,"1", "2", "3", "4",
"1", "2", "3" ,"4", "1", "2", "3" ,"4"))
Variety<-as.character(c("L","L","L","L","N","N","N",
"N","D","D","D","D","F","F","F","F"))
aovdata <- data.frame(Yield,Variety,Block)
summary(aov(Yield ~ Variety+Block,data=aovdata))
library(nlme)
alfmodel<-lme(Yield ~ 1+Variety,aovdata,random=~1|Block)
summary(alfmodel)
VarCorr(alfmodel)
(The  $\sqrt{3}$  makes the sums of squares match Example 3.4. The last part of
the R output is
```

	Variance	StdDev
(Intercept)	0.2129218	0.4614345
Residual	0.4756873	0.6897008

and the variances match part (a).

- (d)

$$\begin{aligned}\hat{\sigma}_\varepsilon^2 &= .253 \\ \hat{\sigma}_{\tau\beta}^2 &= (1/3)(.476 - .253) = 0.0743 \\ \hat{\sigma}_\beta^2 &= (1/12)(1.327 - .476) = 0.0709\end{aligned}$$

- (e) Since the anova estimates are positive, they will match the REML estimates. At this time I can't produce the R code to get the REML estimates!



## Interlude: Assessing the Effects of Blocking

### Essential

---

#### Exercise 4.1

Referring to Example 4.2:

- (a) The fertilizer is applied to the pot, so the pot is the experimental unit.
- (b) To get the correct test use the R code  
`aov(Height ~ Bench+Fertilizer, data=aovdata)`  
and “Residuals” is the interaction term.
- (c) There are three observations for each treatment, so the variance of a difference is estimated with

$$\hat{\text{Var}}(\hat{\tau}_i - \hat{\tau}_{i'}) = 2 \times \sqrt{\frac{32.10}{3}} = 6.542.$$

- (d) The contrasts can be calculated with `contr.helmert` or you can just type them in.

```
> TrtMean=tapply(Height,Fertilizer,mean)
> A=c(3,-1,-1,-1,0,2,-1,-1,0,0,1,-1)
> A=matrix(A,nrow=4)
> A\%*\%TrtMean
```

gives the vector of contrast estimates 37.180, −5.917, −28.823.

- (e) The relevant R code is

```
> Tstat=(t(A)\%*\%TrtMean)^2/(32.10*apply(A^2,2,sum))
> 1-pf(Tstat,1,6)
```

gives the  $p$ -values 0.818, 0.130, 0.0450. This tells us, somewhat surprisingly, that the average of Fertilizers 2-4 is not different from the control. The only significant difference is between Fertilizers 3 and 4. It is obvious that 4 is a winner.

- (f) If we assume known variances, the power is (ignoring the lower tail)

$$P\left(Z \geq Z_\alpha - \frac{1.5}{\sqrt{2\sigma^2/n}}\right) = P\left(Z \geq 1.645 - \frac{1.5}{\sqrt{2 \times 32.10/3}}\right) = 0.0933,$$

where  $Z$  is standard normal. This is rotten power. Either the size of the desired difference needs to be bigger, or the number of blocks needs to be increased.

### Exercise 4.3

- (a) The anova table is

Source	df
Brand	2
Power	1
Time	2
Power $\times$ Time	2
Brand $\times$ Power	2
Brand $\times$ Time	4
Brand $\times$ Power $\times$ Time	4
Within	18

The following R code produces an anova table with the treatments tested against the pooled interaction.

```
> aov(Texture~Brand+Power*Time+Error(Brand/Brand:Power:Time))
```

Source	df	SS	MS	F	<i>p</i> -value
Brand	2	819.71	409.85		
Power	1	495.88	495.88	3.2786	0.10029
Time	2	1460.68	730.34	4.8289	0.03407
Power:Time	2	63.72	31.86	0.2107	0.81356
Residuals (Interactions)	10	1512.45	151.24		
Residuals (Within)	18	1823.86	101.33		

R calls everything “Residuals”.

- (b) The following R code produces an anova table with everything tested against within error.

```
> aov(Texture~Brand*Power*Time,data=aovdata)
```

Source	df	SS	MS	F	p-value
Brand	2	819.71	409.85	4.0449	0.035417
Power	1	495.88	495.88	4.8939	0.040119
Time	2	1460.68	730.34	7.2079	0.005019
Brand:Power	2	163.29	81.65	0.8058	0.462210
Brand:Time	4	1321.37	330.34	3.2602	0.035447
Power:Time	2	63.72	31.86	0.3144	0.734130
Brand:Power:Time	4	27.79	6.95	0.0686	0.990646
Residuals (Within)	18	1823.86	101.33		

An interesting difference is that here the factor Power becomes significant. This is clearly a case of using too small an error term. In the RCB the error term takes the Brand variation into account and, when that is done, the differences due to Power are too small to be significant.

- (c) (i) and (ii). If we consider the six treatment combinations to be "Samples" within the brands, then we get the anova table

Source	df	SS
Brand	2	819.71
Sample(in Brands)	15	3532.73
Residuals (Within)	18	1823.86

where

$$\begin{aligned} \text{SS}(\text{Samples in Brands}) &= \text{SS}(\text{Samples}) + \text{SS}(\text{Samples} \times \text{Brands}) \\ &= \text{SS}(\text{Trts}) + \text{SS}(\text{Trts} \times \text{Brands}). \end{aligned}$$

In the anova table in part (b), if you sum all of the degrees of freedom for the factors involving Power or Time, they add to 15. We could pull out of this the sums of squares for Power in Brands, Time in Brands, and Power  $\times$  Time in Brands, but this is an inferior (and incorrect) analysis. This is a fully nested design so the tests should be clear. In particular, things like "Power in Brands" are tested against within error.

#### Exercise 4.5

Continuing from Exercise 4.4:

- (a) The least square estimate for  $\tau_i - \bar{\tau}$  is  $y_{i\cdot} - y_{\cdot\cdot}$ . Since  $y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}$ , we have

$$y_{i\cdot} = \mu + \tau_i + \bar{\beta} + \bar{\epsilon}_{i\cdot} \text{ and } y_{\cdot\cdot} = \mu + \bar{\tau} + \bar{\beta} + \bar{\epsilon}_{\cdot\cdot}.$$

Therefore

$$E(y_{i\cdot} - y_{\cdot\cdot}) = E((\tau_i - \bar{\tau}) + (\bar{\epsilon}_{i\cdot} - \bar{\epsilon}_{\cdot\cdot})) = \tau_i - \bar{\tau}.$$

Similarly, The least square estimate for  $\beta_j - \bar{\beta}$  is  $y_{\cdot j} - y_{\cdot\cdot}$ , and  $y_{\cdot j} = \mu + \bar{\tau} + \beta_j + \bar{\epsilon}_{\cdot j}$ . Therefore

$$E(y_{.j} - y_{..}) = E((\beta_j - \bar{\beta}) + (\bar{\epsilon}_{.j} - \bar{\epsilon}_{..})) = \beta_j - \bar{\beta}.$$

Finally,

$$E(y_{..}) = E(\mu + \bar{\tau} + \bar{\beta} + \bar{\epsilon}_{..}) = \mu + \bar{\tau} + \bar{\beta}.$$

(b) Because of the correlation structure, we know

$$\text{Var}\left(\sum_i a_i \hat{\tau}_i\right) = \frac{\sigma^2}{b} \sum_i a_i^2 + \frac{2\rho\sigma^2}{b} \sum_{i>i'} a_i a_{i'}$$

Therefore, we have

$$\begin{aligned} \text{Var}(y_{i.} - y_{..}) &= \frac{(1-\rho)\sigma^2}{b} \left( \left(\frac{t-1}{t}\right)^2 + (t-1) \left(\frac{1}{t}\right)^2 \right) \\ &= \frac{(1-\rho)\sigma^2}{b} \frac{t-1}{t}, \\ \text{Var}(y_{.j} - y_{..}) &= \text{Var}(\bar{\epsilon}_{.j} - \bar{\epsilon}_{..}) = \frac{(b-1)\sigma^2}{bt} [1 + (t-1)\rho], \\ \text{Var}(y_{..}) &= \text{Var}(\bar{\epsilon}_{..}) = \text{Var}\left(\sum_i \frac{\bar{\epsilon}_{i.}}{t}\right) \\ &= \frac{(1-\rho)\sigma^2}{b} \sum_i \left(\frac{1}{t}\right)^2 + \frac{\rho\sigma^2}{b} = \frac{(1-\rho+t\rho)\sigma^2}{bt}. \end{aligned}$$

#### Exercise 4.7

(a) As stated this is a terrible experiment:

Ozone Level			
1	2	3	4
$x$ $x$	$x$ $x$	$x$ $x$	$x$ $x$
$x$ $x$	$x$ $x$	$x$ $x$	$x$ $x$
$x$ $x$	$x$ $x$	$x$ $x$	$x$ $x$
$x$ $x$	$x$ $x$	$x$ $x$	$x$ $x$
$x$ $x$	$x$ $x$	$x$ $x$	$x$ $x$
$x$ $x$	$x$ $x$	$x$ $x$	$x$ $x$

Ozone level and chamber are completely confounded, so the only hope is to ignore chamber and treat this as a oneway anova. If the experiment could be re-run four times then we could do 12 observations at each time: Put 3 observations in each of the four chambers, having the chambers at the four levels of ozone. This is an RCB (because of the correlation in the chambers) with three subsamples.

(b) The experimental unit is the chamber, which is where the treatment is applied. We could argue for either fixed or random chambers, but if we account for the correlation as in Section 4.2 the tests will be the same.

- (c) It is better to analyze plants from all four chambers on each day. This would unconfound any day-to-day bias with the chamber effect.

### Exercise 4.9

We can understand the treatments in the following table:

	Before	Now
A	Wheat	Wheat
B	Soy	Wheat
C	Wheat or Triticale	Triticale
D	Soy	Triticale

- (a) Reasonable contrasts are

	$\mu_A$	$\mu_B$	$\mu_C$	$\mu_D$
1)	1	1	-1	-1
2)	1	-1	0	0
3)	0	0	1	-1

where

- 1) Wheat v. Triticale Now
  - 2) The effect of previous planting on Wheat
  - 3) The effect of previous planting on Triticale
- (b) We can get the correct anova table with the R command

```
summary(aov(Meas~Lab+Material+Error(Lab/Lab:Material)))
```

and the contrasts can be obtained with

```
MSE<-0.80418/6 #Mean Square Residual
df<-6          #df residual
YMat=tapply(Meas,Material,mean)
nMat=tapply(Meas,Material,length)
C1<- c(1,1,-1,-1)
F1= (sum(C1*YMat))^2/(MSE*sum(C1^2/nMat))
```

This can be summarized in the anova table

Source	df	SS	MS	<i>p</i> -value
Lab	2	0.43251	0.21625	
Material	3	219.020	73.007	1.070e-07
C1	1	184.10	184.10	0.00000
C2	1	34.39	34.39	0.00000
C3	1	0.53	0.53	0.09379
Residuals	6	0.804	0.134	
(L × M)				
Within	24	1.02587	0.04274	

- (c) With the usual formulas for contrasts and their standard errors

Contrast	Mean	SE
C1	-9.0456	0.2441
C2	-2.7644	0.1725
C3	-0.3433	0.17258

So we see that there is a big effect of Wheat vs. Triticale (C1), and a big effect of the previous planting before Wheat (C2), but no effect of the previous planting before Triticale.

**Exercise 4.11**

- (a) We calculate

$$\text{Cov}(\bar{\varepsilon}_{ij}, \bar{\varepsilon}_{i'j}) = \rho_B \sigma^2, \quad \text{Var}(\bar{\varepsilon}_{ij}) = \frac{\sigma^2}{r} [1 + (r-1)\rho_\varepsilon].$$

Now, since  $\text{Corr}(\bar{\varepsilon}_{ij}, \bar{\varepsilon}_{i'j}) \leq 1$ , the inequality follows.

- (b) From the variance in part (a) we must have
- $1 + (r-1)\rho_\varepsilon \geq 0$
- , and so
- $1 + (r-1)\rho_\varepsilon + r(t-1)\rho_B \geq 0$
- as long as

$$\frac{1 + (r-1)\rho_\varepsilon}{r(t-1)} \geq \rho_B.$$

The left side is a decreasing function of  $r$ , and we have for all  $r$

$$\frac{\rho_\varepsilon}{t-1} \leq \frac{1 + (r-1)\rho_\varepsilon}{r(t-1)} \leq \frac{1}{t-1},$$

so  $\rho_B \geq -1/(t-1)$ , which could only happen if  $\rho_\varepsilon = 1$ .

**Accompaniment**

---

**Exercise 4.13**

- (a) In text.
- (b) As noted in the text, the argument is virtually the same used to verify Theorem 3.18. Details of that are in the solution to Exercise 3.25
- (c) Under the null hypothesis in (4.10), both mean squares have the same expectation so, from Cochran, we have a valid  $F$ -test.
- (d) From (4.20) we know that (4.21) has the form of a  $N(0, 1)$  divided by the square root of a chi-square over its degrees of freedom. The fact that it has Student's  $t$  will follow if the numerator and denominator are independent, that is, if we verify condition (3) in Lemma 3.17. If  $\mathbf{a}$  denotes the contrast vector in the numerator of (4.21), then apply Lemma 3.17 with (ignoring the  $\sigma$ s)  $A_1^* = \mathbf{a}\mathbf{a}'$  and  $A_2^* = I - B_1 - B_2 + B_3$ , the latter being the matrix for  $\text{MS}(\text{T} \times \text{B})$ . For  $\Sigma$  of the form  $(1-\rho)I + \rho J$  direct matrix multiplication shows that  $\mathbf{a}\mathbf{a}'\Sigma(I - B_1 - B_2 + B_3) = 0$  for any contrast  $\mathbf{a}$ , which then shows that (4.21) is Student's  $t$ .

**Exercise 4.15**

(a) For example

$$\begin{aligned}\text{Var}(\bar{\varepsilon}_{ij}) &= \text{Var}\left(\frac{1}{r} \sum_k \varepsilon_{ijk}\right) = \frac{1}{r^2}(r\sigma^2 + r(r-1)\rho_\varepsilon\sigma^2) \\ &= \frac{\sigma^2}{r}(1 + (r-1)\rho_\varepsilon)\end{aligned}$$

$$\begin{aligned}\text{Var}(\bar{\varepsilon}_i) &= \text{Var}\left(\frac{1}{b} \sum_j \bar{\varepsilon}_{ij}\right) = \frac{1}{b^2} \left[ b(\sigma^2/r)(1 + (r-1)\rho_\varepsilon) + 2 \sum_{j>j'} \text{E}(\bar{\varepsilon}_{ij}\bar{\varepsilon}_{ij'}) \right] \\ &= \frac{\sigma^2}{rb}(1 + (r-1)\rho_\varepsilon),\end{aligned}$$

since  $\text{E}(\bar{\varepsilon}_{ij}\bar{\varepsilon}_{ij'}) = 0$  for  $j \neq j'$ .

(b) Analogous to the calculations for Table 4.1.

**Exercise 4.17**

- (a) All row sums are equal to  $1 + (t-1)\rho$ .  
 (b) The matrices are block diagonal, so we only need do the calculations for one block. So, suppressing  $\sigma^2$ , which cancels itself,

$$X = I_t, \quad V = (1-\rho)I_t + \rho J_t, \quad V^{-1} = \frac{1}{1-\rho} \left( I_t - \frac{\rho}{1+(t-1)\rho} J_t \right)$$

where the inverse can be directly verified. Next, matrix multiplication shows

$$\begin{aligned}X'V^{-1}X &= \frac{1}{1-\rho} \left( I_t - \frac{\rho}{1+(t-1)\rho} J_t \right), \\ (X'V^{-1}X)^{-1} &= (1-\rho) \left( I_t + \frac{\rho}{1+\rho} J_t \right),\end{aligned}$$

and finally,  $(X'V^{-1}X)^{-1}X'V^{-1} = I_t$ , implying the equality of the least squares and generalized least squares estimates.

(c) The same thing happens here. For  $Z = \mathbf{1}_t$ ,

$$\begin{aligned}Z'V^{-1}Z &= \frac{t}{1+(t-1)\rho}, \\ (Z'V^{-1}Z)^{-1} &= \frac{1+(t-1)\rho}{t} \frac{1}{1-\rho} \left( \mathbf{1}' - \frac{\rho}{1+(t-1)\rho} \mathbf{1}' J_t \right) \\ &= \frac{1}{t} \mathbf{1}' = (Z'Z)^{-1} Z'\end{aligned}$$

- (d) The definition of  $V^*$  is in Section 3.8.4. We have, just looking at one block of the block diagonal matrix,

$$V^* = \sigma_\varepsilon^2 I + \sigma_\beta^2 J$$

$$V = (1 - \rho)\sigma^2 I + \rho\sigma^2 J_t.$$

The relationship in (4.9) equates  $\sigma_\varepsilon^2 = (1 - \rho)\sigma^2$  and  $\sigma_\beta^2 = \rho\sigma^2$ . Direct multiplication verifies the estimate of  $\beta$ .

#### Exercise 4.19

- (a) (i) Here is R code that will generate the  $F$ -statistics

```
m<-1000
Fstat<-array(0,dim=c(m,1))
for(i in 1:m)
{
  Yp<-sample(Y)
  Yi<-tapply(Yp,Trt,mean)
  MStrts <- 4*sum((Yi-mY)^2)/2
  MSWithin <-sum((Yp-rep(Yi,times=4))^2)/9
  Fstat[i] <-MStrts/MSWithin
}
```

You then find the  $p$ -value by counting how many of these  $F$ -statistics are greater than the observed  $F$ -statistic.

- (ii) Since the randomization is throughout the table, and the table has  $rt$  entries, the probability is  $1/rt$ . Of course, since we are sampling with replacement this probability changes for the next  $y_k$ , since there are only  $rt - 1$  slots left.
- (b) Repeat part (a) for the RCB of Example 4.4 of Miscellanea 4.9.1. Remember that here the permutation must respect the blocks, and with  $t$  treatments and  $b$  blocks we will have  $P(\delta_{ijk} = 1) = 1/t$ . The usual anova is

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	3	102.00	34.00	1.3645	0.34030
Trt	2	408.50	204.25	8.1973	0.01923 *
Residuals	6	149.50	24.92		

The randomization is similar to the above; here is the relevant R code:

```
for(i in 1:m)
{
  Yp=sample(Y[1:3]);for(j in 1:3)Yp=c(Yp,sample(Y[(3*j+1):(3*j+3)]))
}
```



```

Yi<-tapply(Yp,Trt,mean)
Yj<-tapply(Yp,Block,mean)
SSB=3*sum((Yj-mY)^2)
SST=4*sum((Yi-mY)^2)
SSResid<-SSTot-SSB-SST
Fstat[i]<-(SST/2)/(SSResid/6)
}

```

We can find the randomization  $p$ -value with the R statement

```
mean((Fstat>8.1973))
```

which gives a value of 0.0391.

The randomization variable picks the first observation with probability  $1/t$ , then  $1/(t-1)$ , etc.

- (c) The R code is similar to that of part (b), with the randomization  $p$ -value of 0.0288. For this experiment the randomization test seems reasonable, and the fact that the  $p$  values are similar is always nice - less to worry about.



## Split Plot Designs

### Essential

---

#### Exercise 5.1

(a) The anova table is:

Source	df	SS	MS	F	<i>p</i> -value
A(WP Trt)	1	4.083	4.083	0.6125	0.4776
WP Error	4	26.667	6.667		
B(SP Trt)	1	10.083	10.083	30.25	0.0053
A × B (WP Trt × SP Trt)	1	0.083	0.083	0.25	0.6433
SP Error	4	1.333	0.333		

So there appears to be an effect for  $B$ , but not for  $A$  or for the  $A \times B$  interaction.

(b) Test for effect of  $A$ :

Two sample  $t$  test,  $A = 0$  vs.  $A = 1$ , using the whole plot means as observations.  $t = 0.7826$ ,  $p$ -value=0.4776. (This test assumes equal variance for the two groups).

Test for effect of  $B$ :

Paired  $t$  test, six observations, consisting of each whole plot's  $B = 1$  measurement minus its  $B = 0$  measurement.  $t = -5.9656$ ,  $p$ -value=0.0019. (This test assumes equal variance for the two groups).

(c) The  $t$  test for the effect of  $A$  yields exactly the same value as the  $F$  test. However, the  $t$  test for the effect of  $B$  does not yield the same value as the

$F$  test. This is because the split plot ANOVA is able to partition out the variability due to a possible  $A \times B$  interaction, while the paired  $t$  test cannot.

To see this, we can run an RCB on  $B$  only, with the six reps being the blocks. This yields

Source	df	SS	MS	F	$p$ -value
Rep	5	30.7500	6.1500	21.706	
B	1	10.0833	10.0833	35.588	0.001894
Residuals	5	1.4167	0.2833		

The interesting thing is that  $B$  is more significant here than in the Split Plot. This is because there is almost no variability in  $A \times B$ , and losing the degree of freedom cost us.

### Exercise 5.3

- (a) The split plot anova can be done with the R command

```
aov(Y ~ Trt+Error(Subject/Trt)+Time*Trt)
```

and yields the anova table

Source	df	SS	MS	F	$p$ -value
Trt	1	847.5	847.5	3.6266	0.07212
Residuals (Subjects in Trt)	19	4440.0	233.7		
Time	1	542.88	542.88	15.142	0.0009823
Trt $\times$ Time	1	407.41	407.41	11.363	0.0032085
Residuals (Sub $\times$ Time in Trt)	19	681.21	35.85		

The assumptions for the design seem plausible; we might be suspect of the normality assumption since the response is a maximum. Some diagnostics, and maybe a log or other transformation should be considered.

- (b) (i) The R code is

```
Y1=Y[Trt=="Sel" & Time=="Post"]+Y[Trt=="Sel" & Time=="Pre"]
Y2=Y[Trt=="Nsel" & Time=="Post"]+Y[Trt=="Nsel" & Time=="Pre"]
t.test(Y1,Y2,var.equal=T)
```

which gives output

```
t = 1.9044, df = 19, p-value = 0.07212
```

- (ii) Similar to part (i), the R  $t$ -test output is

```
t = 3.3709, df = 19, p-value = 0.003209
```

- (iii)  $t = -2.9767$ ,  $df = 19$ ,  $p$ -value = 0.00775

In the unbalanced case the anova sums of squares are gotten by subtraction, so the direct formulas do not apply.

**Exercise 5.5**

Let  $O$  denote the Organ duct,  $C$  the Catheter type,  $S$  the Sensor location and  $P$  the patient.

- (a) In design (1), the randomization is throughout the 8 treatment combinations, and  $P$  acts as blocks. Therefore (1) is a randomized complete block (RCB) design.

The randomization in design (2) is throughout the  $C \times S$  combinations in  $O$ . This implies a split plot design with whole plots in an RCB, where  $P$  acts as blocks. Therefore  $O$  is the whole plot treatment, and  $C \times S$  is the split plot treatment.

Design (3) is a split split plot design with whole plots in an RCB, where  $P$  acts as blocks. It can be seen that  $C$  is the whole plot treatment,  $O$  is the split plot treatment, and  $S$  is the split split plot treatment.

- (b) Design (1) is an RCB, and the anova table is

Source	df
$P$	29
$O$	1
$C$	1
$S$	1
$O \times C$	1
$O \times S$	1
$C \times S$	1
$O \times C \times S$	1
$P \times O$	29
$P \times C$	29
$P \times S$	29
$P \times O \times C$	29
$P \times O \times S$	29
$P \times C \times S$	29
$P \times O \times C \times S$	29

In an RCB, all treatment effects are tested against their respective interaction with blocks ( $P$ ). Since there are 30 blocks there does not seem to be any need for pooling the interaction terms.

Design (2) is split plot design with whole plot treatment in blocks  $P$ . The anova table is

Source	df
$P$	29
$O$	1
$P \times O$	29
$C$	1
$S$	1
$C \times S$	1
$C \times O$	1
$S \times O$	1
$C \times S \times O$	1
$P \times C$	29
$P \times S$	29
$P \times C \times S$	29
$P \times C \times O$	29
$P \times S \times O$	29
$P \times C \times S \times O$	29

Above the line  $O$  is tested against  $P \times O$ . Below the line each effect is tested against its interaction with  $P$ . Again, with 30 blocks there is no need to pool interactions.

Design (3) is split split plot with whole plot in blocks  $P$ . The anova table is

Source	df
$P$	29
$C$	1
$P \times C$	29
$O$	1
$O \times C$	1
$O \times P$	29
$O \times C \times P$	29
$S$	1
$S \times C$	1
$S \times O$	1
$S \times O \times C$	1
$S \times P$	29
$S \times C \times P$	29
$S \times O \times P$	29
$S \times O \times C \times P$	29

As before, everything is tested against its interaction with  $P$ .

- (c) If the experimenter is interested in all treatments equally, then design (1) is recommended, as there is equal information on all treatments
- (d) If the experimenter is interested in the sensor effects most, then design (3) is recommended. Sensor location is the split split plot treatment and hence gets the best precision

- (e) It is not recommended to use design (3) if the experimenter is interested in testing catheters. One should still use split split plot design but put catheters as the split split plot treatment as that will get better precision.

### Exercise 5.7

- (a) If  $j \neq j'$  then the observations are in different blocks, and they are independent observations.  
 (b) Same SP, different WP:

$$\begin{aligned} \text{Cov}(Y_{ijk}, Y_{i'jk}) &= \text{Cov}(\beta_j + \varepsilon_{ij} + (\beta\gamma)_{jk} + \delta_{ijk}, \beta_j + \varepsilon_{i'j} + (\beta\gamma)_{jk} + \delta_{i'jk}) \\ &= \sigma_\beta^2 + \sigma_{\beta\gamma}^2 \end{aligned}$$

Different SP, Same WP:

$$\begin{aligned} \text{Cov}(Y_{ijk}, Y_{ijk'}) &= \text{Cov}(\beta_j + \varepsilon_{ij} + (\beta\gamma)_{jk} + \delta_{ijk}, \beta_j + \varepsilon_{ij} + (\beta\gamma)_{jk'} + \delta_{ijk'}) \\ &= \sigma_\beta^2 + \sigma_\varepsilon^2 \end{aligned}$$

Different SP, Different WP:

$$\begin{aligned} \text{Cov}(Y_{ijk}, Y_{i'jk'}) &= \text{Cov}(\beta_j + \varepsilon_{ij} + (\beta\gamma)_{jk} + \delta_{ijk}, \beta_j + \varepsilon_{i'j} + (\beta\gamma)_{jk'} + \delta_{i'jk'}) \\ &= \sigma_\beta^2 \end{aligned}$$

The whole plot error is typically greater, so we expect  $\sigma_\beta^2 + \sigma_\varepsilon^2$  to be the greatest.

### Exercise 5.9

- (a) If the experiment design is CRD, then different oven temperatures and baking times must be randomly selected and assigned to each electronic component. After any observation is obtained, the temperature must be reset to the original setting and restarted under the same conditions as the previous ones. This is time-consuming, so it may not be a good way to run this experiment.  
 (b) If this is a RCB, then the experiments are run individually two times, with Rep 1 and Rep 2 as blocks. Within blocks the oven temperatures and baking time are crossed.

If this is split plot, then it means either oven temperature or baking time is set to be the whole plot treatment, and the levels of other one, the split plot treatment, are randomized within. From a practical standpoint, taking Temperature as the whole plot treatment is most sensible; it avoids much heating and cooling of the ovens.

Source	df
$T$	1
$B$	1
$T \times B$	1
Within	4

Source	df
$R$	1
$T$	2
$B$	2
$T \times B$ (in $R$ )	2

- (c) Here we call  $T$  the temperature,  $B$  the baking time and  $R$  the replicates.  
 The anova table for the CRD case is  
 The anova table for the RCB case is  
 The anova table for the split plot case with  $T$  as whole plot treatment is

Source	df
Blocks(Reps)	1
WP Trt( $T$ )	1
Reps $\times$ T (WP Err)	1
SP Trt( $B$ )	1
Temp $\times$ B	1
Rep $\times$ B	1
Reps $\times$ B $\times$ T	1

The split plot design is the most practical, and only the experimenter can tell us if it is appropriate. Also, below the line we would typically pool the two interactions with Reps.

- (d) (i) Same time, different temp:  
 (1) CRD:  $\rho = 0$ .  
 (2) RCB: different blocks  $\Rightarrow \rho = 0$ .  
 (3) Split Plot: Use model in Section 5.3.1 of the text.  
 Case 1. Same block(rep).

$$\text{Cov}(Y_{ijk}, Y_{i'jk}) = \sigma_\beta^2 + \sigma_{\beta\gamma}^2, \quad \rho = \frac{\sigma_\beta^2 + \sigma_{\beta\gamma}^2}{\sigma_\beta^2 + \sigma_{\beta\gamma}^2 + \sigma_\epsilon^2 + \sigma_\delta^2}.$$

Case 2. Different block(rep).



$$Cov(Y_{ijk}, Y_{i'j'k}) = 0, \quad \rho = 0.$$

(ii) Same temp, different time:

(1) CRD:  $\rho = 0$ .

(2) RCB: same blocks  $\Rightarrow \rho = \frac{\sigma_\beta^2}{\sigma_\beta^2 + \sigma_\epsilon^2}$ .

(3) Split Plot: Use model in Section 5.3.1 of the text.

Case 1. Same block(rep).

$$Cov(Y_{ijk}, Y_{ijk'}) = \sigma_\beta^2 + \sigma_\epsilon^2, \quad \rho = \frac{\sigma_\beta^2 + \sigma_\epsilon^2}{\sigma_\beta^2 + \sigma_{\beta\gamma}^2 + \sigma_\epsilon^2 + \sigma_\delta^2}.$$

Case 2. Different block(rep).

$$Cov(Y_{ijk}, Y_{ij'k'}) = 0, \quad \rho = 0.$$

This information will not change the answer in (b).

### Exercise 5.11

- (a) For estimating  $\mu$ ,  $\tau_i$ , or  $\gamma_k$ , the contrast will always zero out the subtracted mean. For example, the  $i^{\text{th}}$  cell mean is estimated with  $\bar{y}_i$ , and the effect is  $\bar{y}_i - \bar{y}$ . If  $(a_1, \dots, a_t)$  is a contrast, then  $\sum_i a_i(\bar{y}_i - \bar{y}) = \sum_i a_i \bar{y}_i$ .
- (b) For all comparisons except the third one, we are in Case (3) of the split plot comparisons, so we use (5.10). For the third contrast we are in Case (4), so we use (5.12). For the effects we use (5.24). We have

Contrast	Variance-Cell Means	Variance - Effects
1	$\frac{16.17}{3} \times (1^2 + (-1)^2) = 10.78$	$\frac{16.17}{3} \times ((3/4)^2 + (-3/4)^2) = 6.064$
2	$\frac{16.17}{3} \times (4 \times 1^2) = 21.56$	$\frac{16.17}{3} \times (4 \times (1/2)^2) = 5.39$
3	$\frac{16.17}{3} \times (2 \times 1^2) + \frac{7.33}{3} \times (2 \times 1^2) = 6.064$	$\frac{16.17}{3} \times (2 \times 1^2) = 2.70$
4	$\frac{16.17}{3} \times (4 \times 1^2) = 21.56$	$\frac{16.17}{3} \times (4 \times 1^2) = 21.56$

- (c) Note that the full contrast specification for the first contrast is

Main Effect of K vs. A and G				
	pk	pK	Pk	PK
A	1	-1	1	-1
G	1	-1	1	-1
K	0	0	0	0
N	0	0	0	0
O	0	0	0	0
R	0	0	0	0

and we are in Case (4). The second contrast is also Case (4), but has a smaller variance since the column sums are all zero. For the cell means contrast variances we use (5.19) and (5.21).

Contrast	Variance
1-Cell Means	$\frac{.170}{2} \times (2 \times 4 \times (2/3)^2 + 4 \times 4 \times (1/3)^2) + \frac{.249}{2 \times 6} \times (4 \times 2^2) = 0.785$
1-Effects	$\frac{.170}{2} \times (2 \times 4 \times (2/3)^2 + 4 \times 4 \times (1/3)^2) = 0.453$
2-Cell Means	$\frac{.170}{2} \times (2 \times 4 \times 1^2) = 0.68$
2-Effects	$\frac{.170}{2} \times (2 \times 4 \times 1^2) = 0.68$

### Exercise 5.13

- (a) The test of Variety  $V$  should be against the whole plot error. The test of Gene  $G$  should be against the split plot error  $G \times A$  (in  $V$ ). The test of Probe  $P$  should be against the split split plot error,  $(P \text{ in } G) \times (A \text{ in } V)$ .
- (b) The R code to produce the anova for this Array split split plot design is

```
aovdata <- data.frame(logY, Gene, Variety, Array, Probe)
aov( logY ~ Variety*Gene*Probe + Error(Array/Gene))
```

where we took logs of the data. The output verifies the anova table.

- (c) To estimate the variance of  $V \times P$  interaction contrast, that is, the interaction of whole plot treatment and split split plot treatment, we use the formula from Section 5.5,

$$\text{Var} \left( \sum_{i\ell} a_{i\ell} \bar{Y}_{i\ell} \right) = \frac{\sigma_\omega^2}{rg} \sum_{i\ell} a_{i\ell}^2 + \frac{\sigma_\delta^2 + g\sigma_\epsilon^2}{rg} \sum_i \left( \sum_\ell a_{i\ell} \right)^2,$$

where we can estimate  $\sigma_\omega^2$  with the SSP error and  $\sigma_\delta^2 + g\sigma_\epsilon^2$  with the WP error.

- (d) The anova table:

Source	df	EMS
Variety	$(v-1)$	$\sigma_\xi^2 + p\sigma_\delta^2 + gp\sigma_\epsilon^2 + \frac{rgp}{v-1} \sum_i V_i^2$
WP Err	$v(r-1)$	$\sigma_\xi^2 + p\sigma_\delta^2 + gp\sigma_\epsilon^2$
Gene	$(g-1)$	$\sigma_\xi^2 + p\sigma_\delta^2 + \frac{vrp}{g-1} \sum_k G_k^2$
$V \times G$	$(g-1)(v-1)$	$\sigma_\xi^2 + p\sigma_\delta^2 + \frac{rp}{(g-1)(v-1)} \sum_{ik} (VG)_{ik}^2$
SP Err	$(g-1)(r-1)v$	$\sigma_\xi^2 + p\sigma_\delta^2$
Probe	$(p-1)g$	$\sigma_\xi^2 + \frac{vr}{(p-1)g} \sum_{kl} P_{kl}^2$
$V \times P$	$(p-1)(v-1)g$	$\sigma_\xi^2 + \frac{r}{(p-1)(v-1)g} \sum_{ikl} (VP)_{ikl}^2$
SSP Err	$(p-1)(r-1)gv$	$\sigma_\xi^2$

### Exercise 5.15

- (a) The model equation is (5.26) with Lab as Blocks, Solution as the WP treatment, Day as the SP treatment, and Assay as the SSP treatment.

- (b) The relevant R code to produce all of the correct error terms is

```
aov( Y ~ Solution*Day*Assay + Error(Lab/Solution/Day))
```

- (c) The relevant R code is

```
aov( Y ~ Lab*Solution*Day*Assay + Error(Lab/Solution/Day))
```

This gives all the mean squares but no  $F$  tests or  $p$ -values - it just groups the treatments. You can also use

```
aov( Y ~ Lab*Solution*Day*Assay)
```

since you have to do the  $F$ -ratios and  $p$ -values yourself.

The test of the interaction  $S \times L$  is  $9.29/19.33 = 0.48 < 3.00 = F_{6,12}$ , so it is not significant which indicates that pooling to get one split plot error is not a terrible thing to do.

Similarly, it can be shown that the interactions  $A \times L$ ,  $A \times S \times L$  and  $A \times D \times L$  are all non-significant when tested against  $A \times S \times D \times L$ . Again, pooling to get one split plot error is not terrible.

### Exercise 5.17

- (a) Clearly, if one of the treatments is ignored, the other is completely randomized in each block.  
 (b) The relevant R code is

```
summary(aov(Y~K*P+Error(Block/(K:Block+P:Block))))
```

and the anova table is

Source	df	SS	MS	F	$p$ -value
Blocks	2	85.778	42.889		
K	2	925.78	462.89	21.811	0.007055
K $\times$ B	4	84.89	21.22		
P	1	162	162	0.4426	0.5743
P $\times$ B	2	7	732	366	
K $\times$ P	2	49.333	24.667	1.3962	0.3468
K $\times$ P $\times$ B	4	70.667	17.667		

From the output we can see that the only significant treatment is Potassium  $K$ .

- (c) The cell means are

P/K	25	50
0	41.333	50.000
25	54.000	62.000
50	62.000	63.333

with standard error of a difference

$$\sqrt{2 \times \frac{17.667}{3}} = 3.432.$$

You can run your favorite multiple comparisons procedure now. But consider that two standard deviations is about 7, which suggest that the three highest means are similar to each other and different from the others.

- (d) The split plot anova can be obtained with

```
summary(aov(Y ~K+Error(Block/K)+P*K))
```

or realize that the anova will be the same as above with the exception that the split plot error is  $P \times B + K \times P \times B$ . The conclusions are the same.

### Exercise 5.19

- (a) The R code

```
summary(aov( UrRibo ~ Order + Error(Order/Subject) +Order*Period))
```

produces the anova table in Example 5.14. If we run the oneway anova

```
summary(aov( UrRibo ~ Treatment, data=aovdata ))
```

we get the output

```

              Df  Sum Sq Mean Sq F value    Pr(>F)
Treatment      1   835.44   835.44   8.0827 0.009462 **

Residuals    22  2273.96   103.36

---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
```

which shows that the treatment sum of squares is 835.44, and equals the  $P \times O$  interaction sum of squares.

- (b) The effect of Order is not significant, suggesting that there is no carryover.  
 (c) No evidence of a time trend = Period is not significant.  
 (d) Since treatment is significant, there is an effect of exercise on urinary riboflavin. The test for carryover is not significant, which says that, in particular, the effect of exercise does not carry over - one needs to continue exercise to maintain the effect.  
 (e) The following R code does the anova for Period 1:

```
aovdata1 <- subset(aovdata, Period=="1")
summary(aov( UrRibo ~ Treatment, data=aovdata1 ))
```

with output

```

      Df Sum Sq Mean Sq F value Pr(>F)
Treatment    1  952.30   952.30   5.7853 0.03698 *

Residuals   10 1646.07   164.61
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

So the difference is significant.

- (f) and (g) If we want to maintain the within subject comparison, there is not much that we can do other than a crossover with 12 per group. Otherwise, we could do a oneway CRD on E/NE. The increased number of subjects might overcome the fact that this is a between-subjects rather than within-subjects design. The anova and tests are straightforward.

### Exercise 5.21

- (a) There would be six squares, accounting for 5 df. Period is crossed with Squares, and crossed with Subjects within squares. The R code is

```
aov(Y ~Square+Error(Subject/Square)+Period*Square)
```

producing the anova table

Source	df	SS	MS	F	p-value
Square	5	545.88	109.18	0.5801	0.7167
Subject (in Square)	6	1129.26	188.21		
Period	1	3.53	3.53	0.0208	0.8900
Square $\times$ Period	5	415.21	83.04	0.4906	0.7741
SP Error	6	1015.51	169.25		

where the SP Error is Period  $\times$  Subjects in Square.

- (b) The easiest was to do this is to run the full crossed anova

```
summary(aov(Y ~Order*Period*Square))
```

resulting in

```

      Df Sum Sq Mean Sq
Order    1 217.20   217.20
Period    1   3.53    3.53
Square    5 545.88   109.18
Order:Period    1 835.44   835.44
Order:Square    5 912.06   182.41
Period:Square    5 415.21    83.04
Order:Period:Square    5 180.07    36.01

```

Now the relevant terms can be added together.

- (c) We note that nothing is gained, in either df or confounding, by running the experiment in Latin squares. The reason to do it is when it is difficult to keep the conditions the same for all of the subjects. By running the squares we only have to make sure that the pairs of subjects are under identical conditions, other than the treatment. This could be an advantage.

### Exercise 5.23

First note that you have to add a column to the dataset for the variable “Square”. Upon doing that, the R command

```
summary(aov(Y ~ Square+Error(Subject/Square)+Period+Drug+Period*Square))
```

produces the output

```
Error: Subject
      Df Sum Sq Mean Sq F value Pr(>F)
Square   1   18.0    18.0  0.0115 0.9196
Residuals 4 6234.4 1558.6

Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
Period   2 1053.8   526.9  0.5208 0.6186
Drug     2 2276.8  1138.4  1.1252 0.3846
Square:Period 2 4709.3 2354.7  2.3275 0.1786
Residuals 6 6070.1 1011.7
```

Above the line are the 5 df for Order, here broken in to Square and Residuals (WP error). Below the line we have Period and Drug as before, but now we have taken the Residual from the anova in Example 5.15 and broken it into two pieces, removing the Period  $\times$  Square variability from the Residual. This would be advantageous if the Period  $\times$  Square variability is large; here it doesn't make much of a difference. Note also that we can only do this anova if the experiment were actually run in Latin squares.

### Exercise 5.25

- (a) Here we are only interested in the treatments  $A$  and  $A + B$ , so we should choose among the orders  $A \rightarrow A + B \rightarrow A$  and  $A + B \rightarrow A \rightarrow A + B$ . With 4 subjects in each order, we have two groups with one order and one group with the other. Then the anova is

Source	df
Groups	2
Order (in Groups)	1
Subjects (in Groups)	9
Period	2
$P \times G$	4
Treatment	1
Residual	17

where the residual is the SP error with the treatment SS removed. The  $P \times O$  interaction will be a piece of  $P \times G$ .

The problem required a three-period crossover and 4 subjects per order. However, it seems that there are two better designs. First, we could do a two-period crossover with  $A \rightarrow A + B$  and  $A + B \rightarrow A$ . Or, if we do the three-period we could use 3 subjects per order and then balance the orders.

- (b) Now we are interested in all six orders, and we should choose three at random. The anova is

Source	df
Order	2
Subjects (in Order)	9
Period	2
$P \times O$	4
Treatment	1
Residual	17

### Exercise 5.27

- (a) The oneway analysis yields the same  $F$  statistic (1.5981) and  $p$ -value (0.2418) as the test on treatments in the original split plot design. Note that  $SS(\text{Trt})$  and  $SS(\text{Res})$  are equal to 1/3 of their values from the original analysis, since we have replaced the three time observations with their average.
- (b) Since this is a trend over time, it is reasonable to look at linear and quadratic trend. The anova is

Source	df	SS	MS	F	$p$ -value
Treatment	1	1153.2	1153.2	1.5981	0.2418
WP Err	8	5772.9	721.6		
Time	2	343.3	171.6		
Linear	1	211.3	211.3	1.9083	0.1861
Quadratic	1	132.0	132.0	1.1926	0.2910
Trt $\times$ Time	2	5028.2	2514.1		
SP Err	16	1771.9	110.7		

- (c) (i) To run the CRD we must treat the subjects in a totally random order, assigning a subject to a treatment and a time period. The anova is

Source	df
Trt	1
Time	2
Trt $\times$ Time	2
Within	24

- (ii) If you run the CRD in R the within SS is 7544.8. This is partitioned as

$$SS(\text{Within}) = 7544.8 = 5772.9 + 1771.9 = SS(\text{WP Err}) + SS(\text{SP Err}),$$

with the df also partitioning.

- (iii) The CRD might be preferable if we are interested in comparing the two treatments, since then we would have 24 df for the test.

### Accompaniment

---

#### Exercise 5.29

- (a) Under the identifiable condition that

$$\bar{\tau} = \bar{\gamma} = (\bar{\tau}\bar{\gamma})_{i\cdot} = (\bar{\tau}\bar{\gamma})_{\cdot k} = 0,$$

we have

$$\begin{aligned} Y_{ijk} &= \mu + \tau_i + \epsilon_{ij} + \gamma_k + (\tau\gamma)_{ik} + \delta_{ijk}, \\ Y_{ij\cdot} &= \mu + \tau_i + \epsilon_{ij} + (\tau\gamma)_{i\cdot} + \delta_{ij\cdot}, \\ Y_{i\cdot k} &= \mu + \tau_i + \epsilon_{i\cdot} + \gamma_k + (\tau\gamma)_{ik} + \delta_{i\cdot k}, \\ Y_{i\cdot\cdot} &= \mu + \tau_i + \epsilon_{i\cdot} + (\tau\gamma)_{i\cdot} + \delta_{i\cdot\cdot}, \\ Y_{\cdot k} &= \mu + \epsilon_{\cdot\cdot} + \gamma_k + (\tau\gamma)_{\cdot k} + \delta_{\cdot\cdot k}, \\ Y_{\cdot\cdot\cdot} &= \mu + \epsilon_{\cdot\cdot} + \delta_{\cdot\cdot\cdot}, \end{aligned}$$

and therefore the calculations for the expectations of the sum of squares are as follows

$$\begin{aligned} ESS(\text{WP}) &= rgE \sum_i (y_{i\cdot\cdot} - y_{\cdot\cdot\cdot})^2 = rgE \sum_i (\tau_i + \epsilon_i - \epsilon + \delta_i - \delta)^2 \\ &= rg \left( \sum_i \tau_i^2 + (t-1) \frac{\sigma_\epsilon^2}{r} + (t-1) \frac{\sigma_\delta^2}{gr} \right) \\ &= (t-1) \left( \frac{rg}{t-1} \sum_i \tau_i^2 + g\sigma_\epsilon^2 + \sigma_\delta^2 \right), \end{aligned}$$

$$\begin{aligned} ESS(\text{Reps in WP}) &= gE \sum_i (y_{ij\cdot} - y_{i\cdot\cdot})^2 = gE \sum_i (\epsilon_{ij} - \epsilon_i + \delta_{ij} - \delta_i)^2 \\ &= g \left( t(r-1) \sigma_\epsilon^2 + t(r-1) \frac{\sigma_\delta^2}{g} \right) \\ &= t(r-1) (g\sigma_\epsilon^2 + \sigma_\delta^2), \end{aligned}$$



$$\begin{aligned}
\text{ESS}(\text{SP}) &= rt \text{E} \sum_i (y_{.k.} - y_{...})^2 = g \text{E} \sum_i (\gamma_k + \delta_k - \delta)^2 \\
&= rt \left( \sum_k \gamma_k^2 + (g-1) \frac{\sigma_\delta^2}{rt} \right) \\
&= (g-1) \left( \frac{rt}{g-1} \sum_i \gamma_k^2 + \sigma_\delta^2 \right),
\end{aligned}$$

$$\begin{aligned}
\text{ESS}(\text{SP} \times \text{WP}) &= r \text{E} \sum_{ik} (y_{i.k} - y_{i..} - y_{..k} + \bar{y}_{...})^2 \\
&= r \text{E} \sum_{ik} ((\tau\gamma)_{ik} + \delta_{ik} - \delta_i - \delta_k + \delta)^2 \\
&= r \left( \sum_{ik} (\tau\gamma)_{ik}^2 + r(g-1)(t-1) \frac{\sigma_\delta^2}{r} \right) \\
&= (g-1)(t-1) \left( \frac{r}{(g-1)(t-1)} \sum_i (\tau\gamma)_{ik}^2 + \sigma_\delta^2 \right),
\end{aligned}$$

$$\begin{aligned}
\text{ESS}(\text{SP} \times \text{Rep in WP}) &= \text{E} \sum_{ijk} (y_{ijk} - y_{ij.} - y_{i.k} + y_{i..})^2 \\
&= \text{E} \sum_{ijk} (\delta_{ijk} - \delta_{ij.} - \delta_{i.k} + \delta)^2 \\
&= t(g-1)(r-1)\sigma_\delta^2.
\end{aligned}$$

By dividing their corresponding df, the anova table with *MS* can be easily verified.

(b) We start with

$$\begin{aligned}
Y_{ijk} &= \mu + \tau_i + \beta_j + \epsilon_{ij} + \gamma_k + (\tau\gamma)_{ik} + (\beta\gamma)_{jk} + \delta_{ijk}, \\
Y_{ij.} &= \mu + \tau_i + \beta_j + \epsilon_{ij} + (\beta\gamma)_{j.} + \delta_{ij.}, \\
Y_{.jk} &= \mu + \beta_j + \epsilon_{.j} + \gamma_k + (\beta\gamma)_{jk} + \delta_{.jk}, \\
Y_{ik.} &= \mu + \tau_i + \bar{\beta} + \epsilon_{i.} + \gamma_k + (\tau\gamma)_{i.} + (\beta\gamma)_{.k} + \delta_{i.k}, \\
Y_{i.} &= \mu + \tau_i + \bar{\beta} + \epsilon_{i.} + (\beta\gamma)_{..} + \delta_{i..}, \\
Y_{.j} &= \mu + \beta_j + \epsilon_{.j} + (\beta\gamma)_{j.} + \delta_{.j.}, \\
Y_{.k} &= \mu + \bar{\beta} + \epsilon_{..} + \gamma_k + (\beta\gamma)_{.k} + \delta_{..k}, \\
Y &= \mu + \bar{\beta} + \epsilon_{..} + (\beta\gamma)_{..} + \delta_{...},
\end{aligned}$$

and the calculation of the expectations of the sums of squares are

$$\begin{aligned}
\text{ESS}(\text{Blocks}) &= gt \text{E} \sum_j (y_j - \bar{y})^2 = gt \text{E} \sum_j (\beta_j - \bar{\beta} + \epsilon_{.j} - \epsilon_{..} + (\beta\gamma)_{j.} - (\beta\gamma)_{..} + \delta_j - \delta)^2 \\
&= gt \left( (b-1)\sigma_\beta^2 + (b-1)\frac{\sigma_\epsilon^2}{t} + (b-1)\frac{\sigma_{\beta\gamma}^2}{g} + (b-1)\frac{\sigma_\delta^2}{gt} \right) \\
&= (b-1) (gt\sigma_\beta^2 + g\sigma_\epsilon^2 + t\sigma_{\beta\gamma}^2 + \sigma_\delta^2),
\end{aligned}$$

$$\begin{aligned}
\text{ESS(WP)} &= bgE \sum_i (y_i - y)^2 = bgE \sum_j (\tau_i + \epsilon_{.i} - \epsilon_{..} + \delta_i - \delta)^2 \\
&= bg \left( \sum_i \tau_i^2 + (t-1) \frac{\sigma_\epsilon^2}{b} + (t-1) \frac{\sigma_\delta^2}{gb} \right) \\
&= (t-1) \left( \frac{bg}{t-1} \sum_i \tau_i^2 + g\sigma_\epsilon^2 + \sigma_\delta^2 \right),
\end{aligned}$$

$$\begin{aligned}
\text{ESS(B} \times \text{WP)} &= gE \sum_{ij} (y_{ij} - y_i - y_j + y)^2 \\
&= gE \sum_{ij} (\epsilon_{ij} - \epsilon_{i.} - \epsilon_{.j} + \epsilon_{..} + \delta_{ij} - \delta_i - \delta_j + \delta)^2 \\
&= g \left( (b-1)(t-1)\sigma_\epsilon^2 + (b-1)(t-1) \frac{\sigma_\delta^2}{g} \right) \\
&= (t-1)(b-1) (g\sigma_\epsilon^2 + \sigma_\delta^2),
\end{aligned}$$

$$\begin{aligned}
\text{ESS(SP)} &= btE \sum_k (y_k - y)^2 \\
&= btE \sum_k (\gamma_k + (\beta\gamma)_{.k} - (\beta\gamma)_{..} + \delta_k - \delta)^2 \\
&= bt \left( \sum_k \gamma_k^2 + (g-1) \frac{\sigma_{\beta\gamma}^2}{b} + (g-1) \frac{\sigma_\delta^2}{bt} \right) \\
&= (g-1) \left( \frac{bt}{g-1} \sum_k \gamma_k^2 + t\sigma_{\beta\gamma}^2 + \sigma_\delta^2 \right),
\end{aligned}$$

$$\begin{aligned}
\text{ESS(SP} \times \text{WP)} &= bE \sum_{ik} (y_{ik} - y_i - y_k + y)^2 \\
&= bE \sum_{ij} ((\tau\gamma)_{ik} + \delta_{ik} - \delta_i - \delta_k + \delta)^2 \\
&= b \left( \sum_{ik} (\tau\gamma)_{ik}^2 + (t-1)(g-1) \frac{\sigma_\delta^2}{b} \right) \\
&= (t-1)(g-1) \left( \frac{b}{(t-1)(g-1)} \sum_{ik} (\beta\gamma)_{ik}^2 + \sigma_\delta^2 \right),
\end{aligned}$$

$$\text{ESS(B} \times \text{SP)} = tE \sum_{jk} (y_{jk} - y_j - y_k + y)^2$$

$$\begin{aligned}
&= tE \sum_{jk} ((\beta\gamma)_{jk} - (\beta\gamma)_{j\cdot} - (\beta\gamma)_{\cdot k} + (\beta\gamma) + \delta_{jk} - \delta_j - \delta_k + \delta)^2 \\
&= t \left( (g-1)(b-1) \frac{\sigma_{\beta\gamma}^2}{t} + (g-1)(b-1) \sigma_\delta^2 \right) \\
&= (b-1)(g-1) (t\sigma_{\beta\gamma}^2 + \sigma_\delta^2),
\end{aligned}$$

$$\begin{aligned}
\text{ESS}(\text{B} \times \text{SP} \times \text{WP}) &= E \sum_{ijk} (y_{ijk} - y_{ij\cdot} - y_{j\cdot k} - y_{i\cdot k} + y_i + y_j + y_k - y)^2 \\
&= E \sum_{ijk} (\delta_{ijk} - \delta_{ij\cdot} - \delta_{j\cdot k} - \delta_{i\cdot k} + \delta_i + \delta_j + \delta_k - \delta)^2 \\
&= (t-1)(g-1)(b-1)\sigma_\delta^2,
\end{aligned}$$

By dividing by the corresponding df, the EMS table can be verified.

### Exercise 5.31

- (a) The microarray model is a split plot design with model equation

$$y_{ijk} = \mu + T_i + A_{ij} + G_k + (TG)_{ik} + \epsilon_{ijk},$$

where  $i = 1, \dots, t$ ,  $j = 1, \dots, r$  and  $k = 1, \dots, g$ . The least square estimate of  $(TG)_{ik}$  is

$$(\hat{TG})_{ik} = \bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot\cdot k} + \bar{y}_{\cdot\cdot\cdot}$$

and the least square estimate of  $(TG)_{i'k}$  is

$$(\hat{TG})_{i'k} = \bar{y}_{i'\cdot k} - \bar{y}_{i'\cdot\cdot} - \bar{y}_{\cdot\cdot k} + \bar{y}_{\cdot\cdot\cdot}$$

and hence the least square estimate of  $(TG)_{ik} - (TG)_{i'k}$  is

$$(\bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot}) - (\bar{y}_{i'\cdot k} - \bar{y}_{i'\cdot\cdot}).$$

- (b) We have

$$\text{Var}(\bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot}) = \text{Var}(\bar{\epsilon}_{i\cdot k} - \bar{\epsilon}_{i\cdot\cdot}) = \left(1 - \frac{1}{g}\right) \frac{\sigma^2}{r} = (g-1) \frac{\sigma^2}{gr}$$

for all  $i = 1, \dots, t$ , and  $\bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot}$  and  $\bar{y}_{i'\cdot k} - \bar{y}_{i'\cdot\cdot}$  are independent if  $i \neq i'$ , thus

$$\text{Var}((\bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot}) - (\bar{y}_{i'\cdot k} - \bar{y}_{i'\cdot\cdot})) = 2\text{Var}(\bar{y}_{i\cdot k} - \bar{y}_{i\cdot\cdot}) = \frac{g-1}{g} \left(\frac{2}{r}\right) \sigma^2.$$

**Exercise 5.33**

(a) First, we have

$$\sum_k a_{ik}^2 = \sum_k (a_{ik} - \bar{a}_i + \bar{a}_i)^2 = \sum_k (a_{ik} - \bar{a}_i)^2 + g\bar{a}_i^2.$$

Then (5.12) can be rewritten as

$$\begin{aligned} & \text{Var} \left( \sum_{ik} a_{ik} \bar{Y}_{ik} \right) \\ &= \frac{\sigma_\delta^2}{r} \sum_{ik} a_{ik}^2 + \frac{\sigma_\epsilon^2}{r} \sum_i \left( \sum_k a_{ik} \right)^2 \\ &= \frac{\sigma_\delta^2}{r} \sum_i \left( \sum_k (a_{ik} - \bar{a}_i)^2 + g\bar{a}_i^2 \right) + \frac{\sigma_\epsilon^2}{r} \sum_i \left( \sum_k a_{ik} \right)^2 \\ &= \frac{\sigma_\delta^2}{r} \sum_{ik} (a_{ik} - \bar{a}_i)^2 + \frac{g\sigma_\delta^2}{r} \sum_i \bar{a}_i^2 + \frac{\sigma_\epsilon^2}{r} \sum_i \left( \sum_k a_{ik} \right)^2 \\ &= \frac{\sigma_\delta^2}{r} \sum_{ik} (a_{ik} - \bar{a}_i)^2 + \frac{\sigma_\delta^2}{gr} \sum_i \left( \sum_k a_{ik} \right)^2 + \frac{\sigma_\epsilon^2}{r} \sum_i \left( \sum_k a_{ik} \right)^2 \\ &= \frac{\sigma_\delta^2}{r} \sum_{ik} (a_{ik} - \bar{a}_i)^2 + \frac{\sigma_\delta^2 + g\sigma_\epsilon^2}{gr} \sum_i \left( \sum_k a_{ik} \right)^2. \end{aligned}$$

(b) Since  $M_i$  are independent and

$$M_i \sim \frac{\chi_{\nu_i}^2}{\nu_i}, \quad i = 1, \dots, k,$$

we have  $E(M_i) = 1$  for all  $i = 1, \dots, k$ , and hence

$$E \left( \sum_i a_i M_i \right) = \sum_i a_i E(M_i) = \sum_i a_i.$$

(c)

$$E \left( \frac{\chi_\nu^2}{\nu} \right)^2 = \text{Var} \left( \frac{\chi_\nu^2}{\nu} \right) + \left( E \left( \frac{\chi_\nu^2}{\nu} \right) \right)^2 = \frac{1}{\nu^2} \cdot 2\nu + 1 = \frac{2}{\nu} + 1.$$

Equating second moments we have

$$E \left( \sum_i a_i M_i \right)^2 = E \left( \frac{\chi_\nu^2}{\nu} \right)^2 = \frac{2}{\nu} + 1,$$

and solving for  $\nu$  gives

$$\nu = \frac{2}{E(\sum_i a_i M_i)^2 - 1}.$$

We now substitute  $(\sum_{i=1}^k a_i Y_i)^2$  for the expected value above, to get  $\hat{\nu}$ , which could be negative.

### Exercise 5.35

- (a) This follows from the fact that

$$\bar{Y}_i = \bar{\beta} + \bar{\varepsilon}_i + (\bar{\tau}\bar{\beta}) + \bar{\delta}_i$$

- (b) This follows from the fact that

$$\bar{Y}_k = \bar{\beta} + \bar{\varepsilon} + (\bar{\tau}\bar{\beta})_k + \bar{\delta}_k$$

- (c) Similarly, write

$$\bar{Y}_{ik} = \bar{\beta} + \bar{\varepsilon}_i + (\bar{\tau}\bar{\beta})_k + \bar{\delta}_{ik}$$

to get variances and covariances. We then get

$$\text{Var}\left(\sum_k a_k \bar{Y}_{ik}\right) = \frac{\sigma_\delta^2 + \sigma_{\beta\gamma}^2}{b} \sum_k a_k^2 + \frac{1}{b}(\sigma_\varepsilon^2 + \sigma_\beta^2) \left(\sum_k a_{ik}\right)^2,$$

but the sum in the second term is zero because this is a within WP contrast.

- (d) Part (c) can be used for the first term since the different WP treatments have independent observations. To calculate the covariance write

$$\begin{aligned} & \text{Cov}\left(\sum_k a_{ik} \bar{Y}_{ik}, \sum_k a_{i'k} \bar{Y}_{i'k}\right) \\ &= E\left(\sum_k a_{ik} (\bar{\beta} + \bar{\varepsilon}_i + (\bar{\tau}\bar{\beta})_k + \bar{\delta}_{ik}) \sum_{k'} a_{i'k'} (\bar{\beta} + \bar{\varepsilon}_{i'} + (\bar{\tau}\bar{\beta})_{k'} + \bar{\delta}_{i'k'})\right) \\ &= E\left(\sum_k \sum_{k'} a_{ik} a_{i'k'} [\bar{\beta}^2 + (\bar{\beta}\bar{\gamma})_k (\bar{\beta}\bar{\gamma})_{k'}]\right) \\ &= \frac{\sigma_\beta^2}{b} \sum_{kk'} a_{ik} a_{i'k'} + \frac{\sigma_{\beta\gamma}^2}{b} \sum_k a_{ik} a_{i'k}. \end{aligned}$$

Now combining everything gives

$$\begin{aligned} \text{Var}\left(\sum_{ik} a_{ik} \bar{Y}_{ik}\right) &= \sum_i \left[ \frac{\sigma_\delta^2 + \sigma_{\beta\gamma}^2}{b} \sum_k a_{ik}^2 + \frac{\sigma_\varepsilon^2 + \sigma_\beta^2}{b} \left(\sum_k a_{ik}\right)^2 \right] \\ &\quad + \sum_{i>i'} \left[ \frac{\sigma_\beta^2}{b} \sum_k a_{ik} \sum_{k'} a_{i'k'} + \frac{\sigma_{\beta\gamma}^2}{b} \sum_k a_{ik} a_{i'k} \right]. \end{aligned}$$

Now doing the algebra to combine all of the  $a_{ik}$  will give (5.20).

### Exercise 5.37

Everything above the split split level is the same as in the split plot anova, Table 5.3. The only difference is that the calculations use  $\bar{Y}_{ijk}$ , where  $\text{Var}(\bar{Y}_{ijk}) = \sigma_\varepsilon^2 + \sigma_\delta^2 + \frac{1}{s}\sigma_\omega^2$ . The split split calculations are also reminiscent of previous ones. For example

$$\begin{aligned} \text{ESS}(\text{SSP Trt}) &= rgt \sum_{\ell} E(\bar{Y}_{\ell} - \bar{\bar{Y}})^2 = rgt \sum_{\ell} E(\psi_{\ell} + \bar{\omega}_{\ell} - \bar{\omega})^2 \\ &= rgt \sum_{\ell} \psi_{\ell}^2 + rgt(\ell - 1) \frac{\sigma_{\omega}^2}{rgt}, \end{aligned}$$

$$\begin{aligned} \text{ESS}(\text{SSP Trt} \times \text{WP Trt}) &= rg \sum_{i\ell} E((\tau\psi)_{i\ell} + \bar{\omega}_{i\ell} - \bar{\omega}_i - \bar{\omega}_{\ell} + \bar{\omega})^2 \\ &= rg \sum_{i\ell} (\tau\psi)_{i\ell}^2 + \sigma_{\omega}^2 \left[ \frac{1}{rg} - \frac{1}{srg} - \frac{1}{trg} + \frac{1}{tsrg} \right] \\ &= rg \sum_{i\ell} (\tau\psi)_{i\ell}^2 + \sigma_{\omega}^2 \frac{(t-1)(s-1)}{tsrg}. \end{aligned}$$

### Exercise 5.39

Referring to Technical Note 5.8.2:

- (a) Since the observations in different whole plots are independent, the covariance matrix must be in diagonal blocks. Within a whole plot we have equicorrelation, which results in blocks of the form  $\sigma_{\delta}^2 I + \sigma_{\varepsilon}^2 J$ .
- (b) All of the matrix properties are established by careful matrix multiplication. No tricks.
- (c) Application of Cochran's theorem is straightforward.

### Exercise 5.41

- (a) From (5.27), we see that

$$\begin{aligned} \text{Cov}(Y_{ijk}, Y_{i'j'k'}) &= \text{Cov}(\beta_j + (\beta\tau)_{ij} + (\beta\gamma)_{jk} + (\beta\tau\gamma)_{ijk} + \varepsilon_{ijk}, \beta_{j'} + (\beta\tau)_{i'j'} + (\beta\gamma)_{j'k'} + (\beta\tau\gamma)_{i'j'k'} + \varepsilon_{i'j'k'}). \end{aligned}$$

Unless  $j = j'$  the observations are in different blocks and are independent. Note that the covariance terms only come from variances, which only appear if the indices are the same. If  $i = i'$  but  $k \neq k'$ , we have

$$\text{Cov}(Y_{ijk}, Y_{ij'k'}) = \text{Cov}(\beta_j + (\beta\tau)_{ij}, \beta_{j'} + (\beta\tau)_{ij}) = \sigma_{\beta}^2 + \sigma_{\beta\tau}^2.$$

The other case, where  $i \neq i'$  but  $k = k'$  is similar.

- (b) Here all of the indices  $i, j, k$  match, so we get all variance components with those indices. The calculation is almost the same as in part (a).





## Confounding in Blocks

### Essential

#### Exercise 6.1

- (a) This is a balanced incomplete block design (BIBD), with 3 treatments  $A$ ,  $B$  and  $C$  and 2 blocks. The  $A \times B \times C$  interaction is completely confounded with the block effect. The R code used to generate the anova table is

```
summary(aov(Y ~ Block + A*B*C, data = aovdata))
```

which gives the anova table

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	1	97.5	97.5	2.4481	0.12330
A	1	8625.8	8625.8	216.5505	< 2e-16 ***
B	1	22312.9	22312.9	560.1667	< 2e-16 ***
C	1	10480.6	10480.6	263.1172	< 2e-16 ***
A:B	1	159.4	159.4	4.0015	0.05032 .
A:C	1	9.8	9.8	0.2452	0.62244
B:C	1	15.0	15.0	0.3770	0.54172
Residuals	56	2230.6	39.8		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

so everything is, by default, tested against “Residual”, which is a mixture of the Block  $\times$  Treatment interactions. We see that the A, B and C main effects are all significant, the A  $\times$  B interaction is borderline significant, and the other two interactions are not significant.

The 95% confidence interval for the B  $\times$  C interaction is  $(-8.26, 4.38)$ .

- (b) From the effects listed in Example 6.1, we see that the threeway interaction is completely comfounded with blocks, so we can just say “the sums of squares MUST be the same”, which is true. But lets see this precisely. The cell means are

Block	Trt. Comb	Effect							Cell Mean
		A	B	C	AB	AC	BC	ABC	
1	a	+	-	-	-	-	+	+	107.75
1	b	-	+	-	-	+	-	+	168.500
1	c	-	-	+	+	-	-	+	154.375
1	abc	+	+	+	+	+	+	+	166.750
2	(1)	-	-	-	+	+	+	-	129.50
2	ab	+	+	-	+	-	-	-	145.375
2	ac	+	-	+	-	+	-	-	136.000
2	bc	-	+	+	-	-	+	-	196.375

So the sum of squares for the threeway interaction contrast is

$$(107.75+168.50+154.375+166.750-129.5-145.375-136.0-196.375)^2 = 97.5,$$

which agrees with the anova table.

- (c) The anova table is given in Example 6.2

### Exercise 6.3

- (a) The easiest way to see this is to look at the effect table in Example 6.3, and make sure that the block pairs have two pluses and two minuses for each effect.

Effect	Block Pairs
A $\times$ Block	B, C, BC
B $\times$ Block	A, C, AC
C $\times$ Block	A, B, AB
AB $\times$ Block	C, AC, BC
AC $\times$ Block	B, AB, BC
BC $\times$ Block	A, AB, AC
ABC $\times$ Block	A, B, C

- (b)  $b = 14, t = 8, k = 4, r = 7, \lambda = 3$   
(c) With eight treatments we have  $8r = bk$  and  $7\lambda = r(k-1)$ . Eliminating  $r$  gives  $56\lambda = bk(k-1)$ . We now check this for  $k = 1, \dots, 7$  ( $k = 8$  is an RCB).

$k$	$\lambda$	$b$
2	1	28
3	3	28
4	3	14
5	5	14
7	3	4

There is no solution for  $k = 6$ . The most interesting is  $k = 7$ , where we only need 4 blocks and 28 observations.

### Exercise 6.5

(a) Specific case.

(i) 
$$\begin{array}{ccccccc} A & B & C & D & E & F & G \\ B & C & D & E & F & G & A \\ C & D & E & F & G & A & B \\ D & E & F & G & A & B & C \\ E & F & G & A & B & C & D \\ F & G & A & B & C & D & E \\ G & A & B & C & D & E & F \end{array}$$

(ii) 
$$\begin{array}{ccccccc} A & B & C & D & E & F & G \\ B & C & D & E & F & G & A \\ D & E & F & G & A & B & C \end{array}$$

Yes.  $b = 7, t = 7, k = 3, r = 3, \lambda = 1$

(iii) 
$$\begin{array}{ccccccc} C & D & E & F & G & A & B \\ E & F & G & A & B & C & D \\ F & G & A & B & C & D & E \\ G & A & B & C & D & E & F \end{array}$$

Yes.  $b = 7, t = 7, k = 4, r = 4, \lambda = 2$

(b) General case.

If you write out the standard cyclic square and drop any column, then clearly  $t = b = p - 1$ . We also have  $k = p - 1$  by construction, and  $r = p - 1$  because of the Latin square. Lastly,  $\lambda = p - 1$ .

### Exercise 6.7

(a)  $b = 4, t = 4, k = 3, r = 3, \lambda = 2$

(b) The following table gives the contrasts for the effects and the blocking structure. We see that no effect is confounded with blocks (there is never the same sign in a block). However, there is confounding with the  $\text{Trt} \times \text{Block}$  interactions.

Block	Trt. Comb	Effect		
		A	B	AB
1	(1)	-	-	+
1	a	+	-	-
1	b	-	+	-
2	(1)	-	-	+
2	a	+	-	-
2	ab	+	+	+
3	(1)	-	-	+
3	b	-	+	-
3	ab	+	+	+
4	a	+	-	-
4	b	-	+	-
4	ab	+	+	+

The anova table is

Source	df
Blocks	3
A	1
B	1
AB	1
Trts $\times$ Blocks	5

The full RCB would have 9 df for the Trts  $\times$  Blocks interaction. The confounding is here.

### Exercise 6.9

- (a) The easiest way to answer this question is to stare at the effect table in Example 6.1.

Rep	Confounded
1	AB
2	AC
3	BC
4	ABC

- (b) It was mean not to put the data online, but it is instructive to go from the data layout in the book to the data file `ABCdata`, which is online. The relevant R code is

```
summary(aov(Y ~Rep+Block+A*B*C,data=aovdata))
```

giving the anova

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Rep	3	123.750	41.250	5.9302	0.005845 **

Block	4	125.750	31.438	4.5196	0.011398	*
A	1	200.000	200.000	28.7526	5.174e-05	***
B	1	8.000	8.000	1.1501	0.298516	
C	1	4.500	4.500	0.6469	0.432316	
A:B	1	22.042	22.042	3.1688	0.092938	.
A:C	1	15.042	15.042	2.1624	0.159687	
B:C	1	1.500	1.500	0.2156	0.648270	
A:B:C	1	16.667	16.667	2.3961	0.140056	
Residuals	17	118.250	6.956			

Of course we only have partial information on the interactions, and the residual is a mixture of all of the  $\text{Trt} \times \text{Block}$  interactions.

- (c) The main effects can be estimated with

```
tapply(Y,A,mean)-mean(Y)
```

which gives

	0	1
A	-2.5	2.5
B	0.5	-0.5
C	0.375	-0.375

with variance estimate (1.5)

$$\frac{\hat{\sigma}^2}{r} \left(1 - \frac{1}{t}\right) = \frac{6.956}{16} \left(1 - \frac{1}{3}\right) = 0.2898.$$

This was probably not the right variance to ask for, the variance of a difference is more useful.

### Exercise 6.11

- (a) The parameters of the BIBB are  $b = 10, t = 5, k = 3, r = 6, \lambda = 3$ . The blocks are

1	1	1	1	1	1	2	2	2	3
2	2	2	3	3	4	3	3	4	4
3	4	5	4	5	5	4	5	5	5

- (b) The anova and treatment means come from the R code

```
summary(aov(Force~Block+Trt,data=aovdata))
tab<-list(Trt)
tapply(Force,tab,mean)
```

yielding

```

          Df Sum Sq Mean Sq F value    Pr(>F)
Block      9 1097669  121963   13.892 5.526e-06 ***
Trt        4 2033580  508395   57.906 2.577e-09 ***
Residuals 16  140474    8780
---
          1          2          3          4          5
1316.943 1503.112 1941.830 1928.415 2045.550

```

- (c) Using (6.2), the least squares means are

Treatment				
1	2	3	4	5
-505.263	-304.105	320.481	126.296	362.593

with estimated variance, from (6.5)

$$\frac{3}{15} \frac{4}{5} \times 8780 = 1404.8.$$

I don't know how to get these means out of R . Using the code

```

> bone=lm(Force~Block+Trt,data=aovdata)
> bone$coefficients

```

gives the output

(Intercept)	Block10	Block2	Block3	Block4	Block5
1476.7358	-68.7060	-184.5753	-117.3949	-472.4056	138.4482
Block6	Block7	Block8	Block9	Trt2	Trt3
-322.8271	-113.4076	-175.8038	-136.4391	147.6460	580.4067
Trt4	Trt5				
668.0727	682.6013				

which are not the above least squares means. They may be using a different normalization.

- (d) The standard deviation of a difference is  $\sqrt{2 * 1404.8} = 53.01$ , so it appears that treatments 3 and 5 are superior. The dip in treatment 4 is strange. The test for linear trend can be done with

```

(sum(contr.poly(5)[,1]*tapply(Force,Trt,mean)))^2
/sum(contr.poly(5)^2)/8780

```

giving a value of 10.09074 with a  $p$ -value of 0.00586, showing a significant linear trend.

- (e) This is a very strange plan. First, allocating observations based on the data results in a bias that is not controllable and, second, they are unbalancing the BIBD and thus introducing the block variation into the contrasts.

The BIBD eliminates the block variability from the contrasts, and they are putting it back!

A better strategy might be to run two experiments. After the first, using 30 observations, they can eliminate a treatment. With  $t = 4$  they only need 4 blocks ( $b = 4, t = 4, k = 3, r = 3, \lambda = 2$ ) taking 12 observations.

**Exercise 6.13**

Array	Effect			Confounded
	Trt.	Comb	P T PT	
1	(1) p	(1)	- - +	T
			+ - -	
2	p pt	(1)	+ - -	P
			+ + +	
3	(1) t	(1)	- - +	P
			- + -	
4	(1) pt	(1)	- - +	PT
			+ + +	

(b) The parameters in this case are

$$(t, b, k, r, \lambda) = (4, 6, 2, 3, 1).$$

We can add two blocks,  $(p, t)$  and  $(t, pt)$ , to get a BIBD.

Using the notation

Array	1	1	2	2	3	3	4	4	5	5	6	6
Trt	(1)	p	p	pt	(1)	t	(1)	pt	p	t	t	pt
Label	$y_{111}$	$y_{121}$	$y_{221}$	$y_{222}$	$y_{311}$	$y_{312}$	$y_{411}$	$y_{422}$	$y_{521}$	$y_{512}$	$y_{612}$	$y_{622}$

from (6.2) the treatment effect estimates are

$$\begin{aligned}\hat{\tau}_{(1)} &= \frac{1}{4}(y_{111} + y_{311} + y_{411} - y_{121} - y_{312} - y_{422}) \\ \hat{\tau}_p &= \frac{1}{4}(y_{121} + y_{221} + y_{521} - y_{111} - y_{222} - y_{512}), \\ \hat{\tau}_t &= \frac{1}{4}(y_{312} + y_{512} + y_{612} - y_{311} - y_{521} - y_{622}), \\ \hat{\tau}_{pt} &= \frac{1}{4}(y_{222} + y_{422} + y_{622} - y_{221} - y_{411} - y_{612}),\end{aligned}$$

and we can estimate the treatment effect differences with

$$\begin{aligned}\text{Effect of } P &: \frac{\hat{\tau}_p + \hat{\tau}_{pt}}{2} - \frac{\hat{\tau}_t + \hat{\tau}_{(1)}}{2} \\ \text{Effect of } T &: \frac{\hat{\tau}_t + \hat{\tau}_{pt}}{2} - \frac{\hat{\tau}_p + \hat{\tau}_{(1)}}{2} \\ \text{Effect of } PT &: \hat{\tau}_{pt} - \hat{\tau}_p - \hat{\tau}_t + \hat{\tau}_{(1)}.\end{aligned}$$

- (c) As there is no (assumed) interaction, and the model equation is

$$Y_{ijk} = \mu + A_i + P_j + T_k + \epsilon_{ijk},$$

we have

$$Y_{222} - Y_{221} = T_2 - T_1 + \epsilon_{222} - \epsilon_{221},$$

which is an estimate of  $T_2 - T_1$ , as is  $Y_{312} - Y_{311}$ . Also,  $Y_{121} - Y_{111}$  estimates  $P_2 - P_1$ . There are others to be found.

- (d) The anova comes from the R code

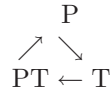
```
summary(aov(Y ~Rep*TrtComb+Array,data=aovdata))
```

and we can also get the individual sums of squares with

```
summary(aov(Y ~Rep*P*T+Array,data=aovdata))
```

For standard errors of the differences in part (c), it seems that the best that we can do is to estimate the variance of each mean with  $0.3626/3$ , and then use the variance of the difference.

- (e) The best design is a BIBD, and with 12 arrays we can only run two of them, as part (b) shows that we need six arrays. An alternative would be a loop such as



which could do all three tissues with nine arrays.

- (f) In the statement of the problem there may be some confusion between true replication (running the same experiment) and replicating the experiment for different tissues. In part (d) the reference is to true replication, but in part (f) the replication is actually different tissues. This was the experiment that was actually done. However, since these are different tissues, we should analyze each “replication” separately.

We do the analysis for Rep=1, one of the tissue types, using the R code

```
if(Rep==1)
{
  summary(aov(Y ~P*T+Error(Array/P:T)+Gene*P*T,data=aovdata))
}
```

This gives the output

```
Error: Array
      Df Sum Sq Mean Sq F value    Pr(>F)
P       1  22.041   22.041  183.71 8.434e-07 ***
```



```

T          1  31.577  31.577  263.19 2.096e-07 ***
P:T        1 144.573 144.573 1204.97 5.188e-10 ***
Residuals  8   0.960   0.120
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Error: Array:P:T

```

          Df Sum Sq Mean Sq F value    Pr(>F)
P          1 11.1882 11.1882 127.545 1.289e-06 ***
T          1  5.8985  5.8985  67.242 1.816e-05 ***
P:T        1  1.9551  1.9551  22.288 0.001088 **
Residuals  9  0.7895  0.0877
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Error: Within

```

          Df Sum Sq Mean Sq F value    Pr(>F)
Gene      149 5519.9    37.0 296.2086 < 2.2e-16 ***
P:Gene    149  49.7     0.3  2.6674 < 2.2e-16 ***
T:Gene    149  91.9     0.6  4.9333 < 2.2e-16 ***
P:T:Gene  149  27.5     0.2  1.4782 0.0002079 ***
Residuals 2980 372.7     0.1

```

which shows that all of the interactions are wildly significant. At this point there are many choices, but perhaps the easiest is to run an anova for each gene to get the individual interaction sum of squares. The question is then what to use for the denominator of the test. To use the overall split plot error .1 with 2980 degrees of freedom makes the strong assumption that there is homogeneity across genes. But not to pool at all, and do the individual tests, loses power. The best answer is still unknown, but is probably in the middle somewhere. See, for example, Cui *et al.* (2005).

### Exercise 6.15

$$\begin{array}{c}
 \text{A with } ABC \\
 \hline
 \begin{array}{cc|cc}
 x_2 + x_3 = 0 & & x_2 + x_3 = 1 & \\
 \hline
 \begin{array}{|c|} \hline 000 \\ \hline 011 \\ \hline 100 \\ \hline 111 \\ \hline \end{array} & = & \begin{array}{|c|} \hline (1) \\ \hline bc \\ \hline a \\ \hline abc \\ \hline \end{array} & & \begin{array}{|c|} \hline 001 \\ \hline 010 \\ \hline 101 \\ \hline 110 \\ \hline \end{array} & = & \begin{array}{|c|} \hline c \\ \hline b \\ \hline ac \\ \hline ab \\ \hline \end{array}
 \end{array}
 \end{array}
 \quad (a)$$

$C$ with $ABC$			
$x_1 + x_2 = 0$		$x_1 + x_2 = 1$	
000	=	010	b
001		011	bc
110		100	a
111		101	ac

- (b) We have seven effects to confound with blocks.  
 (c) There are 2 distinct fractions  
 (d) There are  $2^{p-q}$  distinct fractions

**Exercise 6.17**

- (a) The intrablock subgroup is

$x_1 + x_2 + x_3 + x_4 + x_5 = 0$ and $x_1 + x_2 + x_3 + x_4 = 0$	
00000	(1)
00110	cd
01010	bd
01100	bc
10010	ad
10100	ac
11000	ab
11110	abcd

Note that the subgroup given in the text is not this one; this is the correct one. The other three blocks are

$x_1 + x_2 + x_3 + x_4 + x_5 = 0$ and $x_1 + x_2 + x_3 + x_4 = 1$	
00001	e
00111	cde
01011	bde
01101	bce
10011	ade
10101	ace
11001	abe
11111	abcde

$$\begin{array}{l} x_1 + x_2 + x_3 + x_4 + x_5 = 0 \\ \text{and } x_1 + x_2 + x_3 + x_4 = 0 \end{array}$$


---

00011	de
00101	ce
01001	bc
01111	bcde
10001	ae
10111	acde
11011	abde
11101	abce

$$\begin{array}{l} x_1 + x_2 + x_3 + x_4 + x_5 = 0 \\ \text{and } x_1 + x_2 + x_3 + x_4 = 0 \end{array}$$


---

00010	d
00100	c
01000	b
01110	bcd
10000	a
10110	acd
11010	abd
11100	abc

(b) Write

$$0 = x_1 + x_2 + x_3 + x_4 + x_5 = x_1 + x_2 + x_3 + x_4 = x_5$$

and then successively add  $x_1, x_2, x_3, x_4, x_1 + x_2, x_1 + x_3, x_1 + x_4$  to all sides of the equation.

(c) The intrablock subgroup is

$$\begin{array}{l} x_1 + x_2 + x_3 + x_4 = 0 \\ \text{and } x_2 + x_3 + x_4 + x_5 = 0 \end{array}$$


---

00000	(1)
00110	cd
01010	bd
01100	bc
10011	ade
10101	ace
11001	ade
11111	abcde

For the alias sets write

$$0 = x_1 + x_2 + x_3 + x_4 = x_2 + x_3 + x_4 + x_5 = x_1 + x_5$$

and proceed as above to get

$$\begin{array}{ll}
\{(1), ABCD, BCDE, AE\} & \{A, BCD, ABCDE, E\} \\
\{B, ACD, CDE, ACE\} & \{C, ABD, BDE, ACE\} \\
\{D, ABC, BCE, ADE\} & \{AB, CD, ACDE, BE\} \\
\{AC, BD, ADE, CE\} & \{AD, BC, ABCE, DE\}.
\end{array}$$

This is probably a better set of aliases, as the main effects tend to be confounded with higher order terms, although we do confound  $A$  with  $E$ . However, with such a small fraction there is really no good way out - there will always be lots of confounding!

### Exercise 6.19

- (a) 
$$\begin{array}{llll}
\{(1), ABCDE\} & \{A, BCDE\} & \{B, ACDE\} & \{C, ABDE\} \\
\{D, ABCE\} & \{E, ABCD\} & \{AB, CDE\} & \{AC, BDE\} \\
\{AD, BCE\} & \{AE, BCD\} & \{BC, ADE\} & \{BD, ACE\} \\
\{BE, ACD\} & \{CD, ABE\} & \{CE, ABD\} & \{DE, ABC\}
\end{array}$$
- (b) If we assume that there are no threeway or higher interactions, we can write the data as (using the aliases)

c 26	b 25	(1) 36	ac 46
ab 29	be 35	cd 23	a 32
ce 40	ae 28	d 35	de 27
bd 22	e 21	ad 37	bc 39

We can estimate main effects like:

$$C \text{ effect: } (c - (1)) + (ce - e) + (cd - d) + (ac - a) + (bc - b)$$

and interactions such as

$$AC \text{ interaction: } (c - (1)) - (ac - a).$$

- (c) We can actually get out sums of squares for all main effects and twoway interactions, but then we would have no degrees of freedom for error. So we only get to specify some of the twoway interactions, and leave the rest for "residual". The R code

```
summary(aov(Y ~ A+B+C+D+E+A*B+A*C+A*D+A*E,data=aovdata))
```

gives the anova

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
A	1	3.06	3.06	0.0747	0.79373
B	1	33.06	33.06	0.8068	0.40367
C	1	27.56	27.56	0.6726	0.44350
D	1	351.56	351.56	8.5791	0.02632 *

E	1	1.56	1.56	0.0381	0.85163
A:B	1	45.56	45.56	1.1118	0.33228
A:C	1	3.06	3.06	0.0747	0.79373
A:D	1	18.06	18.06	0.4408	0.53142
A:E	1	68.06	68.06	1.6609	0.24494
Residuals	6	245.87	40.98		

- (d) For the model specified in (c), we can test all main effect differences, and differences involving the specified interactions. However we specify the model tells what assumptions that we are making about interactions - which ones we are assuming to be zero and which effects we will estimate.

### Exercise 6.21

- (a) If we ignore columns, then every treatment is in every row (block). As long as the randomization is properly done, this is an RCB.
- (b) Explain why, if we ignore rows, we have a BIBD. Identify the BIBD parameters.  
Without rows, the treatments are balanced with  $b = 4, t = 4, k = 3, r = 3, \lambda = 2$ .
- (c) The model is straightforward, but we have to be careful about the indices. The development of the Latin square model, see (3.30), is probably the most similar. Write

$$y_{ijk} = \mu + \tau_i + C_j + R_k + \varepsilon_{ijk},$$

where  $R$  and  $C$  are the row and column effects,  $j = 1, \dots, 4, k = 1, \dots, 3$ , and

$$i_{jk} \in I_i = \{(j, k)y_{ijk} \text{ is from treatment } i\}.$$

- (d) We can (naively) estimate  $\tau_i$  with

$$\begin{aligned} \tilde{\tau}_i &= \bar{y}_i - \{\text{mean of columns containing treatment } i\} \\ &= \bar{y}_i - \frac{1}{3 \times 3} \sum_{(j,k) \in I_i} y_{ijk}, \end{aligned}$$

where the  $3 \times 3$  comes from the fact that we know that treatment  $i$  is in 3 columns and 3 rows. We can calculate the expected value of  $\tilde{\tau}_i$  (make a table like the one after model (3.30) to be

$$E(\tilde{\tau}_i) = \left(1 - \frac{1}{9}\right) \tau_i,$$

showing us that  $\tilde{\tau}_i$  is biased, and  $\hat{\tau}_i = \frac{9}{8}\tilde{\tau}_i$  is unbiased and, in fact, must be the least squares estimator. For the general least squares estimator

see Dean and Voss (1999, Section 12.4.2) but be aware that they have swapped the definition of rows and columns.

Since  $\tilde{\tau}_i$  is free of  $R$  and  $C$  effects, as they cancel out, the only variability comes from the  $\varepsilon_{jk}$ , so all contrasts are free of row and column effects.

- (e) It is, in fact, a Latin square.

### Exercise 6.23

- (a) Here we have, in BIBD notation,  $k = 5$  and  $t = 25$ . Since  $rt = bk$  we get  $r = 6$ ,  $b = 30$ , and  $\lambda = 1$ . If we specify  $k$  and  $t = k^2$ , then algebra shows  $r = k + 1$ ,  $b = k(k + 1)$  and  $\lambda = 1$ .
- (b) The model is a variation on (6.12), and is also similar to the model in Exercise 6.21. Write

$$y_{i_{j\ell}} = \mu + \tau_i + R_j + \beta_{j\ell} + \varepsilon_{j\ell},$$

where  $R$  and  $\beta$  are the rep and block effects. Here the number of blocks is  $b = k(k + 1)$ , so  $j = 1, \dots, k + 1$ ,  $\ell = 1, \dots, k$ , and

$$i_{j\ell} \in I_i = \{(j, \ell) : y_{i_{j\ell}} \text{ is from treatment } i\}.$$

The anova table is

Source	df
Reps	$k$
Blocks (in Reps)	$(k + 1)(k - 1)$
Treatments	$k^2 - 1$
Residual	$(k + 1) \times (k - 1)^2$
Total	$k^2 \times (k + 1) - 1$

The residual term is pieces of the  $T \times R$  and  $T \times B$  interactions. Note that if this were and RCB nested in Reps, the error term for treatments would be  $T \times R$  (see Table 3.10 ).

- (c) This is a BIBD so the treatment contrasts are free of blocks. We can use the model (6.1) to see that the least squares estimates are

$$\hat{\tau}_i = \frac{1}{k} \left( (k + 1)\bar{y}_i - \sum_{j \in J_i} \bar{y}_j \right).$$

If we partition the blocks into Reps and Blocks in Reps, and use the model in part (b), we find

$$\bar{y}_i = \mu + \tau_i + \frac{1}{k + 1} \sum_{j=1}^{k+1} R_j + \sum_{(j,\ell) \in J_i} \beta_{j\ell}$$

$$\sum_{j \in J_i} \bar{y}_j = \sum_{j=1}^{k+1} \sum_{(j,\ell) \in J_i} \bar{y}_{j\ell}$$

$$= (k+1)\mu + (k+1)\tau_i + \sum_{i' \neq i} \tau_{i'} + \sum_{j=1}^{k+1} R_j + \sum_{j=1}^{k+1} \sum_{(j,\ell) \in J_i} \beta_{j\ell},$$

and we see the the  $R_j$  cancels out of  $\hat{\tau}_i$ .

- (d) The relevant R code is

```
aov(Yield ~ Rep+Block/Rep+Variety)
```

which produces the anova table

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Rep	5	3.2953	0.6591	4.5642	0.0008889 ***
Block	24	11.2118	0.4672	3.2353	2.410e-05 ***
Variety	24	10.7547	0.4481	3.1034	4.581e-05 ***
Residuals	96	13.8618	0.1444		

- (e) Our estimate of MSE is 0.1444, and the standard error of a treatment difference is  $\sqrt{2 \times 0.1444} = 0.537$ . The R command

```
sort(round(tapply(Yield,Variety,mean),3))
```

produces a sorted table of treatment means

7	23	1	9	11	15	21	16	25
3.963	3.973	4.002	4.005	4.053	4.082	4.127	4.130	4.255
5	20	3	19	6	13	12	2	
4.288	4.345	4.362	4.385	4.390	4.405	4.460	4.513	
10	8	18	24	14	22	17	4	
4.517	4.573	4.587	4.612	4.678	4.680	4.747	4.808	

and with 96 degrees of freedom we can use a normal cutoff. The LSD procedure would declare two means significantly different at  $\alpha = .05$  if their difference is greater than  $1.96 \times .537 = 1.053$ . Unfortunately, no pairs are significantly different.

### Exercise 6.25

- (a) The relevant R code is

```
aov(ExpLevel~Array+Tissue+Gene+Tissue*Gene)
```

The anova table is

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Array	1	0.874	0.874	62.601	3.701e-12 ***
Tissue	2	36.723	18.361	1315.790	< 2.2e-16 ***
Gene	99	129.949	1.313	94.063	< 2.2e-16 ***
Tissue:Gene	198	59.990	0.303	21.712	< 2.2e-16 ***
Residuals	99	1.382	0.014		

Note that we did not specify a split plot error - there are no degrees of freedom to estimate it. The tests on Array and Tissue are nonsense, but the interaction text is OK.

- (b) The Dye effect is the contrast

	Array	
Dye	1	2
Red	-1	-1
Green	1	1

and the treatment effect has 2 degrees of freedom, but is confounded with Array. We can partition the treatment effect into two orthogonal 1 df contrasts: (Liver + Muscle) - 2Placenta, which is given by

	Array	
Dye	1	2
Red	-1	-1
Green	1	1

and Liver - Muscle, which is given by

	Array	
Dye	1	2
Red	0	0
Green	1	-1

So we see that the Dye effect is confounded with the average effect of the treatment vs. the control.

If we use the R code

```
aov(ExpLevel~Array+Dye+Gene+Tissue*Gene)
```

we can get the SS for Dye. In fact, the anova is

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Array	1	0.874	0.874	62.601	3.701e-12 ***
Dye	1	32.493	32.493	2328.495	< 2.2e-16 ***
Gene	99	129.949	1.313	94.063	< 2.2e-16 ***
Tissue	1	4.229	4.229	303.086	< 2.2e-16 ***
Gene:Tissue	198	59.990	0.303	21.712	< 2.2e-16 ***
Residuals	99	1.382	0.014		

so we see that the Dye effect, or trt vs. control, is the big part of the treatment effect. The 1 df Tissue here is the difference between Muscle and Liver. Note also the the Tissue SS of the first anova has been partitioned

$$32.493 + 4.229 = 36.722.$$



- (c) This is just the least squares estimate  $(\tau\gamma)_{ij}$  expressed on the log scale. The variance is calculated according to Section 5.2.3, and is estimated with the Residual term in the anova.

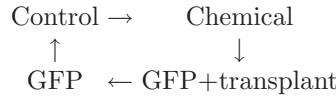
### Exercise 6.27

- (a) The original design was to divide each of the six mouse RNA into four, and run the treatments: Control, Chemical, GFP, and GFP+transplant. So the subject is a block and the treatments are in a CRD. To run the six pairs would mean splitting the RNA into six parts. So within each subject would be a BIBD with six arrays (blocks). The parameters of the BIBD are  $b = 6, k = 2, t = 4, r = 3, \lambda = 1$ . The anova on the six mice, using  $6 \times 6 = 36$  arrays is

Source	df
Subjects	5
Arrays (in Subjects)	30
Treatments	3
Residual	18
Total	71

where the residual contains the pieces of the  $T \times A$  interaction.

- (b) We can loop with



or some other arrangement of the treatments in the loop. This will take four arrays. To balance for dye swap would need eight arrays per subject.

- (c) Clearly the BIBD is preferred, as the treatment comparisons will be free of the array effects. The loop variance is given in (6.17), so the better comparisons are for the treatments on the same array, but they will never be as good as the BIBD.

### Accompaniment

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### Exercise 6.29

- (a) Differentiating

$$\frac{\partial}{\partial \mu} \sum_i \sum_{j \in J_i} (y_{ij} - \mu - \tau_i - \beta_j)^2 = 2 \left[ rt\bar{y} - rt\mu - \sum_i \sum_{j \in J_i} \tau_i - \sum_i \sum_{j \in J_i} \beta_j \right],$$

and we assume that both double sums are zero so  $\hat{\mu} = \bar{y}$ . Continuing,

$$\begin{aligned}\frac{\partial}{\partial \tau_i} \sum_i \sum_{j \in J_i} (y_{ij} - \mu - \tau_i - \beta_j)^2 &= 2 \left[ r\bar{y}_i - r\mu - r\tau_i - \sum_{j \in J_i} \beta_j \right], \\ \frac{\partial}{\partial \beta_j} \sum_j \sum_{i \in I_j} (y_{ij} - \mu - \tau_i - \beta_j)^2 &= 2 \left[ k\bar{y}_j - k\mu - \sum_{i \in I_j} \tau_i - \beta_j \right].\end{aligned}$$

Now substitute for  $\beta_j$  in the  $\tau_i$  derivative to get

$$r\bar{y}_i - r\bar{y} - r\tau_i - \sum_{j \in J_i} \left( \bar{y}_j - \bar{y} - \frac{1}{k} \sum_{i \in I_j} \tau_i \right) = 0.$$

Now the terms involving  $\bar{y}$  cancel, and the double sum is equal to  $(r - \lambda)\tau_i$ . Using the BIBD parameter relations results in (6.2).

(b) From the definition,

$$\begin{aligned}\mathbb{E}\bar{Y}_i &= \frac{1}{r} \sum_{j \in J_i} \mathbb{E}Y_{ij} = \mu + \tau_i \\ \mathbb{E}\bar{Y}_j &= \frac{1}{k} \sum_{i \in I_j} \mathbb{E}Y_{ij} = \mu + \frac{1}{k} \sum_{i \in I_j} \tau_i.\end{aligned}$$

Noting that the  $\mu$ s cancel,

$$\mathbb{E} \left( r\bar{Y}_i - \sum_{j \in J_i} \bar{Y}_j \right) = r\tau_i - \frac{1}{k} \sum_{j \in J_i} \sum_{i \in I_j} \tau_i = \tau_i \left( r - \frac{r - \lambda}{k} \right),$$

and rearrangement yields unbiasedness.

### Exercise 6.31

(a) The model (6.1) is

$$Y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij},$$

where  $i = 1, \dots, t$  and  $j = 1, \dots, J_i$ , or  $j = 1, \dots, b$  and  $i = 1, \dots, I_j$ . Therefore, we have

$$\begin{aligned}\sum_{j \in J_i} \text{Var} \left( Y_{ij} - \frac{1}{k} \sum_{i' \in I_j} Y_{i'j} \right) &= \sum_{j \in J_i} \text{Var} \left( \beta_j + \epsilon_{ij} - \frac{1}{k} \sum_{i' \in I_j} (\beta_{i'j} + \epsilon_{i'j}) \right) \\ &= \sum_{j \in J_i} \text{Var}(\beta_j + \epsilon_{ij} - \beta_j - \bar{\epsilon}_{\cdot j}) \\ &= \sum_{j \in J_i} \text{Var}(\epsilon_{ij} - \bar{\epsilon}_{\cdot j}).\end{aligned}$$

(b) Starting from

$$\text{Var}(\epsilon_{ij} - \bar{\epsilon}_{.j}) = \left(1 - \frac{1}{k}\right) \sigma_\epsilon^2,$$

using the fact that errors in different blocks are independent, we have

$$\sum_{j \in J_i} \text{Var}(\epsilon_{ij} - \bar{\epsilon}_{.j}) = r \left(1 - \frac{1}{k}\right) \sigma_\epsilon^2.$$

(c) Write

$$\begin{aligned} \text{Var}(\hat{\tau}_i) &= \left(\frac{k}{\lambda t}\right)^2 \sum_{j \in J_i} \text{Var}(\epsilon_{ij} - \bar{\epsilon}_{.j}) \\ &= \left(\frac{k}{\lambda t}\right)^2 r \left(1 - \frac{1}{k}\right) \sigma_\epsilon^2 \\ &= \frac{kr(k-1)}{\lambda^2 t^2} \sigma_\epsilon^2. \end{aligned}$$

Using  $\lambda(t-1) = r(k-1)$ , we have

$$\text{Var}(\hat{\tau}_i) = \frac{kr(k-1)}{\lambda^2 t^2} \sigma_\epsilon^2 = \frac{k}{\lambda t} \left(\frac{t-1}{t}\right) \sigma_\epsilon^2.$$

### Exercise 6.33

(a) The expectation of the first term is

$$\text{E}[(Y_{212} + Y_{221})/2] = \frac{1}{2} \text{E}[\tau_2 + \beta_1 + \gamma_2 + \varepsilon_{212} + \tau_2 + \beta_2 + \gamma_1 + \varepsilon_{221}].$$

The  $\gamma$ s sum to zero, and the  $\beta$ s and  $\varepsilon$ s have mean zero. Note that the  $\beta$ s do not cancel.

(b) The second term is

$$\text{E}[(Y_{111} + Y_{122})/2] = \frac{1}{2} \text{E}[\tau_1 + \beta_1 + \gamma_1 + \varepsilon_{111} + \tau_1 + \beta_2 + \gamma_2 + \varepsilon_{122}].$$

Comparing to the above shows that the  $\beta$ s now cancel, and we have an unbiased estimate of  $\tau_2 - \tau_1$ .

The estimate of the  $\gamma$  effect is

$$\frac{1}{2}(Y_{122} + Y_{221}) - \frac{1}{2}(Y_{111} + Y_{212}).$$

In expectation the  $\tau$ s sum to zero and the  $\beta$ s and  $\varepsilon$ s have mean zero. The expectation is  $\gamma_2 - \gamma_1$ .

- (c) Deviating from our usual notation, write the model as

$$y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + B_\ell + \varepsilon_{ijkl},$$

where  $B$  is the block effect and the rest are treatment effects. With this notation the data are

$(1) = y_{1111}$ $ab = y_{2211}$ $ac = y_{2121}$ $bc = y_{1221}$	$a = y_{2112}$ $b = y_{1212}$ $c = y_{1122}$ $abc = y_{2222}$
---	--

The expected value, keeping track of the blocks, is

$$\begin{aligned}
& \frac{1}{4}(\alpha_2 + \beta_1 + \gamma_1 + B_2 + \alpha_2 + \beta_2 + \gamma_1 + B_1) \\
& + \frac{1}{4}(\alpha_2 + \beta_1 + \gamma_2 + B_1 + \alpha_2 + \beta_2 + \gamma_2 + B_2) \\
& - \frac{1}{4}(\alpha_1 + \beta_1 + \gamma_1 + B_1 + \alpha_1 + \beta_2 + \gamma_1 + B_2) \\
& - \frac{1}{4}(\alpha_1 + \beta_1 + \gamma_2 + B_2 + \alpha_1 + \beta_2 + \gamma_2 + B_1) \\
& = \alpha_2 - \alpha_1,
\end{aligned}$$

since all of the  $\beta$ s,  $\gamma$ s, and  $B$ s cancel.

- (d) Here we add the term
- $(\alpha\gamma)_{ik}$
- to the model. The expected value of the contrast, again keeping track of the
- $B$
- s, is

$$\begin{aligned}
& \frac{1}{4}([\alpha_2 + \beta_2 + \gamma_2 + B_2 + (\alpha\gamma)_{22}] - [\alpha_1 + \beta_2 + \gamma_2 + B_1 + (\alpha\gamma)_{12}]) \\
& - \frac{1}{4}([\alpha_2 + \beta_2 + \gamma_1 + B_1 + (\alpha\gamma)_{21}] - [\alpha_1 + \beta_2 + \gamma_1 + B_2 + (\alpha\gamma)_{11}]) \\
& + \frac{1}{4}([\alpha_2 + \beta_1 + \gamma_2 + B_1 + (\alpha\gamma)_{22}] - [\alpha_1 + \beta_1 + \gamma_2 + B_2 + (\alpha\gamma)_{12}]) \\
& - \frac{1}{4}([\alpha_2 + \beta_1 + \gamma_1 + B_2 + (\alpha\gamma)_{21}] - [\alpha_1 + \beta_1 + \gamma_1 + B_1 + (\alpha\gamma)_{11}]) \\
& = \frac{1}{2}([( \alpha\gamma )_{22} - ( \alpha\gamma )_{12}] - [( \alpha\gamma )_{21} - ( \alpha\gamma )_{11}]),
\end{aligned}$$

since all of the  $\alpha$ s,  $\beta$ s,  $\gamma$ s, and  $B$ s cancel.

### Exercise 6.35

- (a) The  $R_k$  will always cancel since we would get a + contribution of  $R_k$  from  $\bar{y}_i$  and a - contribution from  $\bar{y}_{iR}$ . Similarly, in  $\bar{y}_{iC}$  we get the sum of the  $R_k$  with a - sign and in  $\bar{\bar{y}}$  we get the sum with a + sign.

- (b) Carefully substituting from (6.12) into the least squares estimator (6.13) will give the expression for  $\hat{\tau}_i$ . Then note that it is free of  $R$ , as we know, and that all of the  $\beta$ s and  $\gamma$ s cancel. So they make no contribution to the variance.
- (c) From part (b):
  - (i) The cancellation that occurs in the special case will persist in general, the structure of the design guarantees it.
  - (ii) Since all of the random effects cancel, and the  $\tau_i$  are fixed and do not contribute to the variance, we can ignore the  $i$  index and just have the variance of the residuals  $\varepsilon_{j\ell m}$ .



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