STAT 5309

Lab 4-B

****CONTENTS: 1 BLOCKING FACTOR – 2 BLOCKING FACTORS (LATIN SQUARES)**

-OTHERS

****Due: ___________**

A. PRACTICE

##----------------------------One Treatment Factor-One Blocking Factor-------------------

##---------------------- 1-**Quantitative factor + 1 blocking factor------**

Data: drug. Rat Behavior. 50 observations.

Rat: There are 10 rats. A factor with levels 1, 2, 3, 4, 5, 6, 7, 8, 9, 10.

Dose: a factor with 5 levels: 0.0, 0.5, 1.0, 1.5, 2.0.

Rate: a numeric vector

head(drug)

```
> drug
   rat dose rate
1    1    0 0.60
2    1  0.5 0.80
3    1    1 0.82
4    1  1.5 0.81
13   3    1 0.83
14   3  1.5 0.80
15   3    2 0.52
16   4    0 0.60
47  10  0.5 1.20
48  10    1 1.18
49  10  1.5 1.23
50  10    2 1.05
```

attach(drug)

\# **rat** used as a one block factor

drug.mod<- aov(rate ~ rat +dose, data=drug) #Suppose **no interaction** between rat and dose

summary.aov(drug.mod)

```
            Df Sum Sq Mean Sq F value   Pr(>F)
rat          9 1.6685 0.18538   22.20 3.75e-12 ***
dose         4 0.4602 0.11505   13.78 6.53e-07 ***
Residuals   36 0.3006 0.00835
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Note: Rat means are significiant different.
Dose means are significant different.

#---------------Power/Sample size: power.anova.test()-------------------------------
trt.means <- tapply(rate, dose, mean)
trt.means

```
    0   0.5     1   1.5     2
0.764 0.934 1.014 1.009 0.850
```

MSE <- 0.00835

```
      > power.anova.test(groups=5, between.var=var
(trt.means), within.var=MSE, sig.level=.05,power=.
90)

     Balanced one-way analysis of variance power c
alculation

         groups = 5
              n = 3.804702
    between.var = 0.0115052
     within.var = 0.0081
      sig.level = 0.05
          power = 0.9

NOTE: n is number in each group
```

Note: n = 4, to have a power of 0.9

------------- **Effects** ------------------------------------

```
> model.tables(drug.mod, type="effects")
Tables of effects

 rat
rat
      1       2       3       4       5       6       7       8       9      10
-0.2082 -0.2222 -0.1962 -0.0922  0.0738 -0.0802 -0.0062  0.2318  0.2918  0.2078

 dose
dose
      0     0.5       1     1.5       2
-0.1502  0.0198  0.0998  0.0948 -0.0642
```

```
effect_dose<- c(-0.1502,  0.0198 , 0.0998 , 0.0948, -0.0642)
sum_effect_dose_sq <- sum ( (effect_dose)^2)

[1] 0.0460208
```

#-----------------------------   Number of Blocks [Optional]-----------------

#------------------------------- Fpower(alpha, nu1, nu2, nc), package daewr---------------------

$$\boldsymbol{\lambda} = \frac{b\,\Sigma\tau_i^2}{\sigma^2}$$ (noncentrality parameter)

```
alpha <- .05
a <-5                              # 5 treatment levels
bmin <- 1
bmax<- 15
sigma2 <- .00834                   #σ^2 ,  from summary.aov()
sum_effect_dose_sq <- .04602       #Σ τ_i^2
b <- c(bmin:bmax)
nu1 <- a-1                         #ν_1,  ν_2
nu2 <- (b -1)*(a-1)
nc <- (b*sum_effect_dose_sq)/sigma2
power <- Fpower(alpha, nu1, nu2, nc)

data.frame(b, nu1, nu2, nc, power)
```

	b	nu1	nu2	nc	power
1	1	4	0	5.517986	NaN
2	2	4	4	11.035971	0.3210692
3	3	4	8	16.553957	0.6832522
4	4	4	12	22.071942	0.8881262
5	5	4	16	27.589928	0.9672684
6	6	4	20	33.107914	0.9916474
7	7	4	24	38.625899	0.9980807
8	8	4	28	44.143885	0.9995944
9	9	4	32	49.661871	0.9999200
10	10	4	36	55.179856	0.9999851
11	11	4	40	60.697842	0.9999974
12	12	4	44	66.215827	0.9999996
13	13	4	48	71.733813	0.9999999
14	14	4	52	77.251799	1.0000000
15	15	4	56	82.769784	1.0000000

Note: b= 10 (rats) is a reasonable number of blocks

##--------------------------**2-Factor and 1-Block Design**-------------------------

data: bha: mouse liver enzyme experiment. **Description:** Data from the mouse liver enzyme experiment . 16 observations.

Block: a factor with 2 levels: 1, 2.

Strain: a factor with 4 levels: A/J, 129O1a, NIH, BALB/c.

Treat: a factor with levels: treated. Control. Y : a numeric vector

1 Block and 2 Factors. A data frame with 16 observations

library(daewr)

data(bha)

```
> bha
   block strain   treat    y
1      1    A/J treated 18.7
2      1    A/J control  7.7
3      2    A/J treated 16.7
4      2    A/J control  6.4
5      1 129Ola treated 17.9
6      1 129Ola control  8.4
7      2 129Ola treated 14.4
8      2 129Ola control  6.7
9      1    NIH treated 19.2
10     1    NIH control  9.8
11     2    NIH treated 12.0
12     2    NIH control  8.1
13     1 BALB/c treated 26.3
14     1 BALB/c control  9.7
15     2 BALB/c treated 19.8
16     2 BALB/c control  6.0
```

attach(bha)

bha.mod <- aov(y ~ block +strain *treat, data=bha) # interaction between strain and treat

summary.aov(bha.mod)

```
             Df Sum Sq Mean Sq F value   Pr(>F)
block         1   47.6    47.6  18.372  0.00363 **
strain        3   33.0    11.0   4.240  0.05274 .
treat         1  422.3   422.3 162.961 4.19e-06 ***
strain:treat  3   40.3    13.4   5.189  0.03368 *
Residuals     7   18.1     2.6
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Note: Block means are significant different; Strain, Treat (main effects) means are significant different ; Interaction is significant different.

#---------------------Suppose we don't use block

bha.mod1 <- aov(y ~ strain*treat, data=bha)

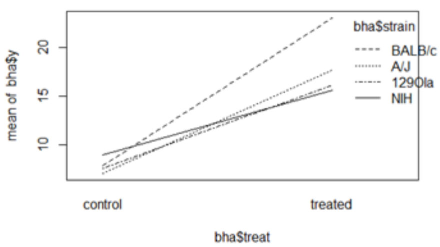
anova(bha.mod1)

```
Analysis of Variance Table

Response: y
             Df Sum Sq Mean Sq F value    Pr(>F)    
strain        3  32.96   10.99  1.3369    0.3290    
treat         1 422.30  422.30 51.3828 9.538e-05 ***
strain:treat  3  40.34   13.45  1.6362    0.2566    
Residuals     8  65.75    8.22                      
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#--------------Interaction --------------------------

interaction.plot(treat, strain, y)   #interaction plot between treat and strain



##-------------------- 4 by 4-LATIN SQUARE--------------

library(agricolae)
str(design.lsd)
treat <- c("A", "B", "C", "D")
design.lsd <- design.lsd(treat, seed=543, serie=2)

lsd.book <- design.lsd$book

```
> design.lsd$book
  plots row col treat
1   101   1   1     C
2   102   1   2     A
3   103   1   3     B
4   104   1   4     D
5   201   2   1     D
6   202   2   2     B
7   203   2   3     C
```

```
8      204    2    4    A
9      301    3    1    B
10     302    3    2    D
11     303    3    3    A
12     304    3    4    C
13     401    4    1    A
14     402    4    2    C
15     403    4    3    D
16     404    4    4    B
```

names(lsd.book)

[1] "plots" "row"   "col"   "treat"

levels(lsd.book$row) <- c("Week1", "Week2","Week3", "Week4")

levels(lsd.book$col) <- c("Store1", "Store2", "Store3", "Store4")

sales <- c(10,12,15,12,8,16,8,11,15,10,13,8,14,7,10,14)

```
> data <- data.frame(lsd.book,sales )
> data
   plots   row    col treat sales
1    101 Week1 Store1     C    10
2    102 Week1 Store2     A    12
3    103 Week1 Store3     B    15
4    104 Week1 Store4     D    12
5    201 Week2 Store1     D     8
6    202 Week2 Store2     B    16
7    203 Week2 Store3     C     8
8    204 Week2 Store4     A    11
9    301 Week3 Store1     B    15
10   302 Week3 Store2     D    10
11   303 Week3 Store3     A    13
12   304 Week3 Store4     C     8
13   401 Week4 Store1     A    14
14   402 Week4 Store2     C     7
15   403 Week4 Store3     D    10
16   404 Week4 Store4     B    14
```

```
> sales.aov <- aov(sales ~ row +col +treat, data=data)
> summary.aov(sales.aov)
            Df Sum Sq Mean Sq F value  Pr(>F)
row          3   4.69    1.56   0.652 0.61011
col          3   0.69    0.23   0.096 0.95964
treat        3 104.19   34.73  14.496 0.00372 **
Residuals    6  14.37    2.40
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

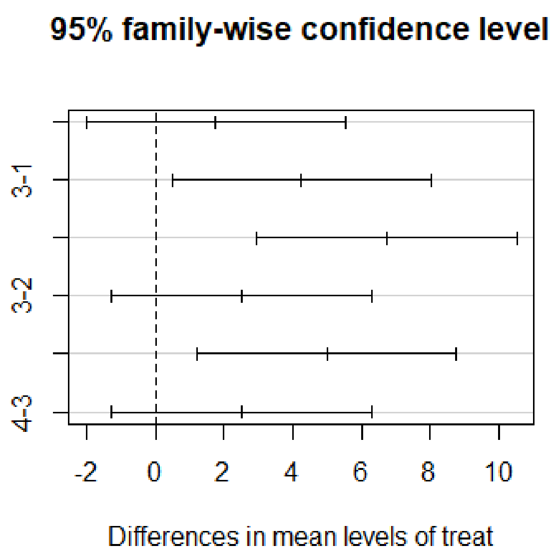
Note: the row and col means are NOT significant different [which are not of interest]

The trt means are significant different.

```
> sales.Tukey <- TukeyHSD(sales.aov, "treat")
> sales.Tukey
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = sales ~ row + col + treat, data = data)

$treat
    diff        lwr       upr     p adj
2-1 1.75 -2.0388216  5.538822 0.4445573
3-1 4.25  0.4611784  8.038822 0.0310526
4-1 6.75  2.9611784 10.538822 0.0033922
3-2 2.50 -1.2888216  6.288822 0.2037456
4-2 5.00  1.2111784  8.788822 0.0149758
4-3 2.50 -1.2888216  6.288822 0.2037456
```



##--------------Other Blocking designs-------------
#-----------------Graeco-Latin Square-----------------

```
str(design.graeco)
trt <- c("A", "B", "C", "D")
trt2 <- 1:4
design.graeco <- design.graeco(trt, trt2,seed=543, serie=2)
design.graeco$book
```

```
  plots row col trt trt2
1   101   1   1   A    1
2   102   1   2   D    4
3   103   1   3   B    3
4   104   1   4   C    2
5   201   2   1   D    3
```

```
6     202   2   2   A    2
7     203   2   3   C    1
8     204   2   4   B    4
9     301   3   1   B    2
10    302   3   2   C    3
11    303   3   3   A    4
12    304   3   4   D    1
13    401   4   1   C    4
14    402   4   2   B    1
15    403   4   3   D    2
16    404   4   4   A    3
```

##--------------------Balanced Incomplete Block--------------------

```
str(design.bib)
trt <- c("A", "B", "C", "D")
k<- 4                #4 treatments allowed in each block    - Balanced Blocking
design.bib <- design.bib(trt, k, seed=543, serie=2)
```

```
Parameters BIB
==============
Lambda     : 2
treatmeans : 4
Block size : 4
Blocks     : 2
Replication: 2

Efficiency factor 1
```

```
> design.bib$statistics
       lambda treatmeans blockSize blocks r Efficiency
values      2          4         4      2 2          1
```

```
trt1 <- c("A", "B", "C", "D", "E")   #Suppose there ae 5 treatment levels

k <- 3               #only 2 treatments allowed in each block
design.bib.2 <- design.bib(trt1, k, seed=543, serie=2)
```

```
Parameters BIB
==============
Lambda     : 3
treatmeans : 5
Block size : 3
Blocks     : 10
Replication: 6
```

10 blocks, block size is 3 (treatment), replicate is 6.

```
> design.bib.2$book
   plots block trt1
1     101     1    D
2     102     1    E
3     103     1    C
4     201     2    D
5     202     2    A
6     203     2    C
7     301     3    B
8     302     3    D
9     303     3    C
10    401     4    E
11    402     4    A
12    403     4    D
13    501     5    E
14    502     5    C
15    503     5    A
16    601     6    A
17    602     6    C
18    603     6    B
19    701     7    E
20    702     7    B
21    703     7    A
22    801     8    D
23    802     8    B
24    803     8    E
25    901     9    B
26    902     9    C
27    903     9    E
28   1001    10    B
29   1002    10    D
30   1003    10    A
```

##--------------------FACTORIAL[NO BLOCKING]----------------

```
str(design.ab)
trt <- c(4,2,3)  #  3  factors,  4,2,3- level
trt
trt <- c(3,2)       # 2 factors, 3 and 2 levels
design.ab <- design.ab(trt, r=3, serie=2)
design.ab$book
```

```
> design.ab$book
   plots block A B
1    101     1 2 2
2    102     1 3 2
3    103     1 2 1
4    104     1 1 2
5    105     1 3 1
6    106     1 1 1
7    107     2 2 2
8    108     2 3 1
9    109     2 2 1
10   110     2 3 2
11   111     2 1 2
12   112     2 1 1
13   113     3 1 1
14   114     3 2 1
15   115     3 3 2
16   116     3 3 1
17   117     3 1 2
18   118     3 2 2
```

B. EXERCISE

1.

An industrial engineer is conducting an experiment on eye focus time. He is interested in the effect of the distance of the object from the eye on the focus time. Four different distances are of interest. He has five subjects available for the experiment. Because there may be differences among individuals, he decides to conduct the experiment in a randomized block design. The data obtained follow. Analyze the data from this experiment (use $\alpha = 0.05$) and draw appropriate conclusions.

	Subject				
Distance (ft)	1	2	3	4	5
4	10	6	6	6	6
6	7	6	6	1	6
8	5	3	3	2	5
10	6	4	4	2	3

(a) Set up the data frame, named “eye” , using “subject” as a blocking factor, “distance” as treatment factor. Time as response.
(b) Build a linear model, name “eye.mod” . Are the Subject means significant different? Are the Distance means significant different?
(c) Which distances bring the longest/ shortest focus time
(d) Calculate the sample size(number of treatment replicates) for power > .90

2. 5-by-5 Latin Square.

The effect of five different ingredients (A, B, C, D, E) on the reaction time of a chemical process is being studied. Each batch of new material is only large enough to permit five runs to be made. Furthermore, each run requires approximately $1\frac{1}{2}$ hours, so only five runs can be made in one day. The experimenter decides to run the experiment as a Latin square so that day and batch effects may be systematically controlled. She obtains the data that follow. Analyze the data from this experiment (use $\alpha = 0.05$) and draw conclusions.

	Day				
Batch	1	2	3	4	5
1	$A = 8$	$B = 7$	$D = 1$	$C = 7$	$E = 3$
2	$C = 11$	$E = 2$	$A = 7$	$D = 3$	$B = 8$
3	$B = 4$	$A = 9$	$C = 10$	$E = 1$	$D = 5$
4	$D = 6$	$C = 8$	$E = 6$	$B = 6$	$A = 10$
5	$E = 4$	$D = 2$	$B = 3$	$A = 8$	$C = 8$

(a) Set up a data frame.

Hint: Create a vector for 1st Blocking factor, named "Day"5 levels: 1,2,3,4,5 .

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

Create a vector for 2nd Blocking factor, named "Batch" 5 levels: 1,2,3,4,5

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

Create a vector for Treatment factor , named "Ingredient"

Ingredient A, B, D, C…[follow the patteren]

Create a vector for response , named "Time"

Time: 8,7, 1,7…..

Set up data frame, named "Chemical"

(b) Build a linear model, using aov(). Do the ingredients affect the reaction time?
Day means, Batch means, Ingredient means, are significant different?
Check interaction between Day and Batch.

(c) Find the lowest reaction time.

3.

An industrial engineer is investigating the effect of four assembly methods (A, B, C, D) on the assembly time for a color television component. Four operators are selected for the study. Furthermore, the engineer knows that each assembly method produces such fatigue that the time required for the last assembly may be greater than the time required for the first, regardless of the method. That is, a trend develops in the required assembly time. To account for this source of variability, the engineer uses the Latin square design shown below. Analyze the data from this experiment ($\alpha = 0.05$) and draw appropriate conclusions.

Order of Assembly	Operator			
	1	2	3	4
1	$C = 10$	$D = 14$	$A = 7$	$B = 8$
2	$B = 7$	$C = 18$	$D = 11$	$A = 8$
3	$A = 5$	$B = 10$	$C = 11$	$D = 9$
4	$D = 10$	$A = 10$	$B = 12$	$C = 14$

(a) Set up a data frame. [Similar to Prob 4]

Hint: Create a vector for 1st Blocking factor, named "Assembly" 4 levels: 1,2,3,4.

Create a vector for 2nd Blocking factor, named "Operator" 4 levels: 1,2,3,4.
Create a vector for Treatment factor , named "Treatment"
Create a vector of response, named: "time"

(a) Build a linear model, using aov(). Do the Treatment affect the assembly time?
Operator means, Assembly means, Treatment means, are they (their means) significant different?

(b) Find the lowest assembly time.