

HW3: Randomized Blocks, Latin Squares, and Related Designs

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Homework Guidelines

Please submit your answers on Gradescope as a PDF with pages matched to question answers.

One way to prepare your solutions to this homework is with R Markdown, which provides a way to include mathematical notation, text, code, and figures in a single document. A template .Rmd file is available through D2L.

Make sure all solutions are clearly labeled, and please utilize the question pairing tool on Gradescope. You are encouraged to work together, but your solutions, code, plots, and wording should always be your own. Come and see me during office hours or schedule an appointment when you get stuck and can't get unstuck.

I. Mathematical Foundations [13 pts]

- (1) [10 pts] The goal of the following questions is to demonstrate that a RCBD has higher power than a BIBD with the same number of treatment levels and total observations. Consider two potential experimental designs used to detect a treatment effect across three levels, A, B, and C while accounting for a nuisance blocking factor:

Randomized Complete Block Design

Block 1	Block 2
A	B
B	C
C	A

Balanced Incomplete Block Design

Block 1	Block 2	Block 3
A	A	-
B	-	B
-	C	C

- (a) [3 pts] Fill in the blanks in the following R code (or write your own from scratch) to simulate a single data set from each design assuming $\mu_A = -1$, $\mu_B = 0$, $\mu_C = 1$, $\beta_1 = 1$, $\beta_2 = 2$, $\beta_3 = 3$, and $\sigma = 1/2$.

```

set.seed(66)
mus <- c(A = -1, B = 0, C = 1)
betas <- c("1" = 1, "2" = 2, "3" = 3)
sigma <- 1/2
dat_RCBd <- data.frame(trt = c("A", "B", "C", "B", "C", "A"),
                      grp = c("1", "1", "1", "2", "2", "2"))
dat_BIBd <- data.frame(trt = c("A", "A", "B", "B", "C", "C"),
                      grp = c("1", "2", "1", "3", "2", "3"))
dat_RCBd$y <- mus[dat_RCBd$trt] + betas[dat_RCBd$grp] + rnorm(6, sd = sigma)
dat_BIBd$y <- mus[dat_BIBd$trt] + betas[dat_BIBd$grp] + rnorm(6, sd = sigma)

```

- (b) [2 pts] Perform an ANOVA and report the appropriate p -value for the test $H_0 : \mu_A = \mu_B = \mu_C$ for each design. RCBd p -value is 0.1555779 and BIBd p -value is 0.3462278.

```

set.seed(66)
mus <- c(A = -1, B = 0, C = 1)
betas <- c("1" = 1, "2" = 2, "3" = 3)
sigma <- 1/2
dat_RCBd <- data.frame(trt = c("A", "B", "C", "B", "C", "A"),
                      grp = c("1", "1", "1", "2", "2", "2"))
dat_BIBd <- data.frame(trt = c("A", "A", "B", "B", "C", "C"),
                      grp = c("1", "2", "1", "3", "2", "3"))
dat_RCBd$y <- mus[dat_RCBd$trt] + betas[dat_RCBd$grp] + rnorm(6, sd = sigma)
dat_BIBd$y <- mus[dat_BIBd$trt] + betas[dat_BIBd$grp] + rnorm(6, sd = sigma)

RCBd_aov <- aov(y ~ grp + trt, data = dat_RCBd)
BIBd_aov <- aov(y ~ grp + trt, data = dat_BIBd)

summary(RCBd_aov)[[1]]$`Pr(>F)`[2]

```

```
## [1] 0.1555779
```

```
summary(BIBd_aov)[[1]]$`Pr(>F)`[2]
```

```
## [1] 0.3462278
```

- (c) [3 pts] Re-run your code from (a)–(b) at least 10 times and report p -values for each design (you can use a for loop, an `*apply()` function, or just carry this out manually). Which design results in more rejections of the null hypothesis at the $\alpha = 0.05$ level? **We get the exact same values as earlier. Since blocking has been considered as a separate variable, it does not affect the p -value of the treatment when there is no difference in blocking.**

Trial	Design	p -value	reject H_0 ?	Design	p -value	reject H_0 ?
1	RCBD	0.15557790	NO	BIBD	0.34622782	NO
2	RCBD	0.02426753	YES	BIBD	0.22083558	NO
3	RCBD	0.07677549	NO	BIBD	0.19602235	NO
4	RCBD	0.01520752	YES	BIBD	0.05905391	NO
5	RCBD	0.27094347	NO	BIBD	0.49005577	NO
6	RCBD	0.09384457	NO	BIBD	0.08000487	NO

Trial	Design	p-value	reject H_0 ?	Design	p-value	reject H_0 ?
7	RCBD	0.09217056	NO	BIBD	0.08487576	NO
8	RCBD	0.06383738	NO	BIBD	0.09540772	NO
9	RCBD	0.02352167	YES	BIBD	0.19959121	NO
10	RCBD	0.07817043	NO	BIBD	0.14538601	NO
TOTAL	RCBD	0.8943165	3	BIBD	1.917461	0

```

set.seed(66)
RCBD_pvals <- rep(0,10)
BIBD_pvals <- rep(0,10)

for (i in 1:10) {
  # generate data
  mus <- c(A = -1, B = 0, C = 1)
  betas <- c("1" = 1, "2" = 2, "3" = 3)
  sigma <- 1/2
  dat_RCBD <- data.frame(trt = c("A", "B", "C", "B", "C", "A"),
                        grp = c("1", "1", "1", "2", "2", "2"))
  dat_BIBD <- data.frame(trt = c("A", "A", "B", "B", "C", "C"),
                        grp = c("1", "2", "1", "3", "2", "3"))
  dat_RCBD$y <- mus[dat_RCBD$trt] + betas[dat_RCBD$grp] + rnorm(6, sd = sigma)
  dat_BIBD$y <- mus[dat_BIBD$trt] + betas[dat_BIBD$grp] + rnorm(6, sd = sigma)

  # perform anova
  RCBD_aov <- aov(y ~ grp + trt, data = dat_RCBD)
  BIBD_aov <- aov(y ~ grp + trt, data = dat_BIBD)

  # get p-values
  RCBD_pvals[i] <- summary(RCBD_aov)[[1]]$`Pr(>F)`[2]
  BIBD_pvals[i] <- summary(BIBD_aov)[[1]]$`Pr(>F)`[2]
}
RCBD_pvals

```

```

## [1] 0.15557790 0.02426753 0.07677549 0.01520752 0.27094347 0.09384457
## [7] 0.09217056 0.06383738 0.02352167 0.07817043

```

```
sum(RCBD_pvals)
```

```
## [1] 0.8943165
```

```
BIBD_pvals
```

```

## [1] 0.34622782 0.22083558 0.19602235 0.05905391 0.49005577 0.08000487
## [7] 0.08487576 0.09540772 0.19959121 0.14538601

```

```
sum(BIBD_pvals)
```

```
## [1] 1.917461
```

- (d) [2 pts] Repeat your analysis in (a)–(c) for the situation with zero block effects (i.e., $\beta_j = 0, j = 1, 2, 3$). You do not need to report p-values or rejection rates. How do your overall findings change? RCBD experiment resulted in 3 rejections and BIBD resulted in 0 rejections. Once blocking did not explain any significant variation, it was easier to detect explained variation by the treatment.

```
set.seed(66)
RCBD_pvals <- rep(0,10)
BIBD_pvals <- rep(0,10)

for (i in 1:10) {
  # generate data
  mus <- c(A = -1, B = 0, C = 1)
  sigma <- 1/2
  dat_RCBD <- data.frame(trt = c("A", "B", "C", "B", "C", "A"),
                        grp = c("1", "1", "1", "2", "2", "2"))
  dat_BIBD <- data.frame(trt = c("A", "A", "B", "B", "C", "C"),
                        grp = c("1", "2", "1", "3", "2", "3"))
  dat_RCBD$y <- mus[dat_RCBD$trt] + rnorm(6, sd = sigma)
  dat_BIBD$y <- mus[dat_BIBD$trt] + rnorm(6, sd = sigma)

  # perform anova
  RCBD_aov <- aov(y ~ grp + trt, data = dat_RCBD)
  BIBD_aov <- aov(y ~ grp + trt, data = dat_BIBD)

  # get p-values
  RCBD_pvals[i] <- summary(RCBD_aov)[[1]]$`Pr(>F)`[2]
  BIBD_pvals[i] <- summary(BIBD_aov)[[1]]$`Pr(>F)`[2]
}
RCBD_pvals
```

```
## [1] 0.15557790 0.02426753 0.07677549 0.01520752 0.27094347 0.09384457
## [7] 0.09217056 0.06383738 0.02352167 0.07817043
```

```
sum(RCBD_pvals)
```

```
## [1] 0.8943165
```

```
BIBD_pvals
```

```
## [1] 0.34622782 0.22083558 0.19602235 0.05905391 0.49005577 0.08000487
## [7] 0.08487576 0.09540772 0.19959121 0.14538601
```

```
sum(BIBD_pvals)
```

```
## [1] 1.917461
```

- (2) [3 pts] (DAE 4.45) An experimenter wishes to compare four treatments in blocks of two runs. Find a BIBD for this experiment with six blocks. $a=4, b=6, k=2, r=12/4=3, \lambda = 3*1/3=1$ each pair of treatments is seen only once per block

table	Block 1	Block 2	Block 3	Block 4	Block 5	Block 6
TRT1	X	X	X			
TRT2	X			X	X	
TRT3		X		X		X
TRT4			X		X	X

II. Applications [27 pts]

(3) [4 pts] (DAE 4.1) *See text.*

(a) [2 pts] Left-Right Top-Bottom:

Treatment MS = $1010.56/4 = 252.64$

Treatment p-value = $\text{pf}(29.84, 4, 20, \text{lower.tail} = \text{F}) = 3.544848\text{e-}08$

Block DF = $29-24 = 5$

Block SS = $1503.71 - (1010.56+169.33) = 323.82$ (randomized complete = orthogonal)

Block F = $64.765/8.4665 = 7.64956$

Block p-value = $\text{pf}(7.64956, 5, 20, \text{lower.tail} = \text{F}) = 0.0003688504$

Error MS = $169.33/20 = 8.4665$

(b) [1 pts] There are 6 blocks

(c) [1 pts] At least one treatment has a significant effect on the outcome, and at least one block is significantly different from the other blocks.

(4) [6 pts] (DAE 4.9) *See text.*

(a) [2 pts] the truck type and oil type both seem to have at least one level that is significantly different from the others.

```
trucks <- read.csv("./HW3_data/Q4-9.csv")
#head(trucks)
trucks_aov <- aov(Consumption ~ as.factor(Truck) + as.factor(Oil), data = trucks)
summary(trucks_aov)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## as.factor(Truck)  4 0.09210  0.023025   43.626 1.78e-05 ***
## as.factor(Oil)    2 0.00671  0.003353    6.353  0.0223 *
## Residuals        8 0.00422  0.000528
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(b) [2 pts] Use Tukey's Honest Significant Difference method at a level of $\alpha = 0.05$ instead.

Provide a grouping of the treatment levels.

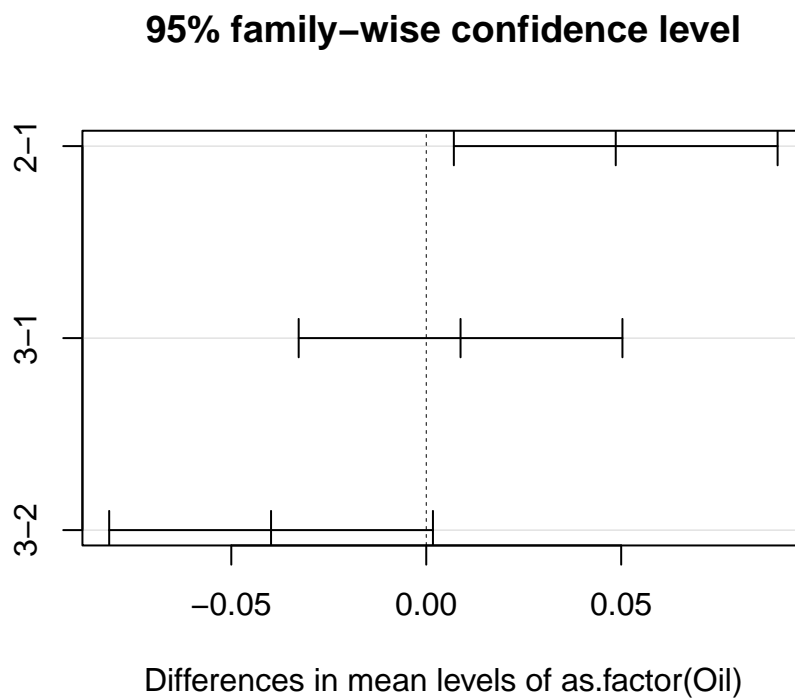
2 and 1 are significantly different, so we group (2) and (1,3).

```
trucks_HSD <- TukeyHSD(trucks_aov,
                      which = "as.factor(Oil)")
trucks_HSD
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Consumption ~ as.factor(Truck) + as.factor(Oil), data = trucks)
##
## $'as.factor(Oil)'
```

	diff	lwr	upr	p adj
2-1	0.0486	0.007082078	0.090117922	0.0245809
3-1	0.0088	-0.032717922	0.050317922	0.8210970
3-2	-0.0398	-0.081317922	0.001717922	0.0594979

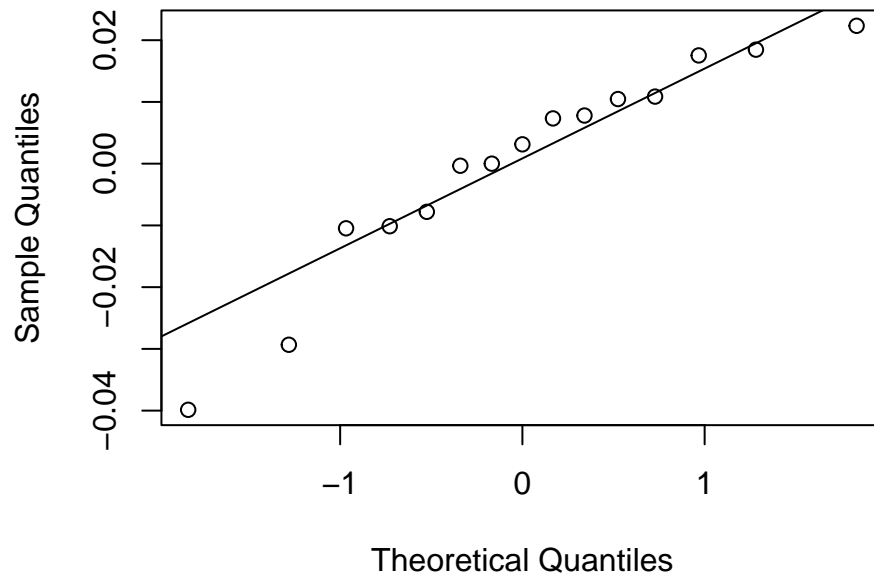
```
plot(trucks_HSD)
```



- (c) [2 pts] The QQ plot shows normal residuals. The Residuals v. Fitted plot shows slight variation in the residuals (middle values have slightly lower variance in residuals) but overall the residuals appear pretty even. The Residuals v. Oil and Residuals v. Truck both have residuals that appear to have constant variance.

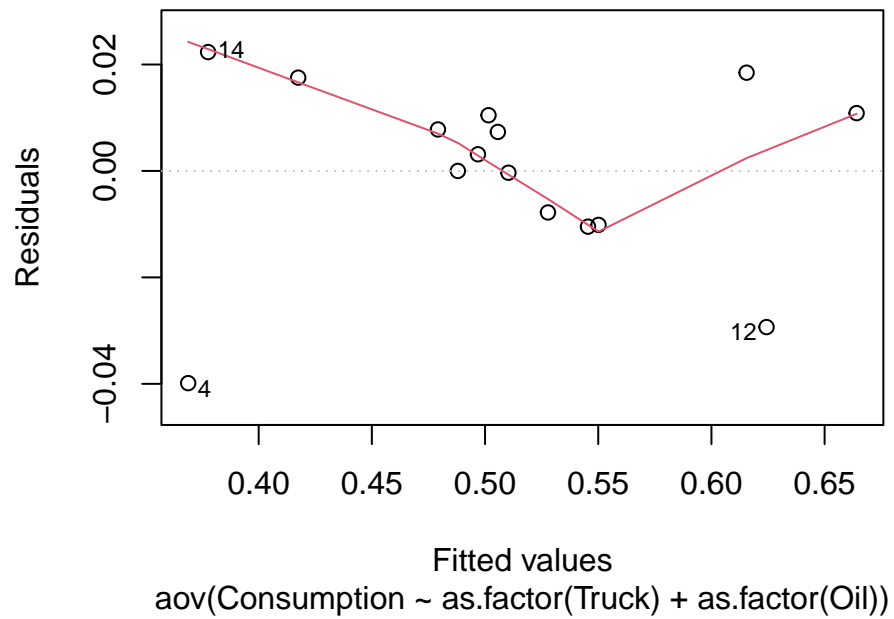
```
qqnorm(resid(trucks_aov))
qqline(resid(trucks_aov))
```

Normal Q-Q Plot

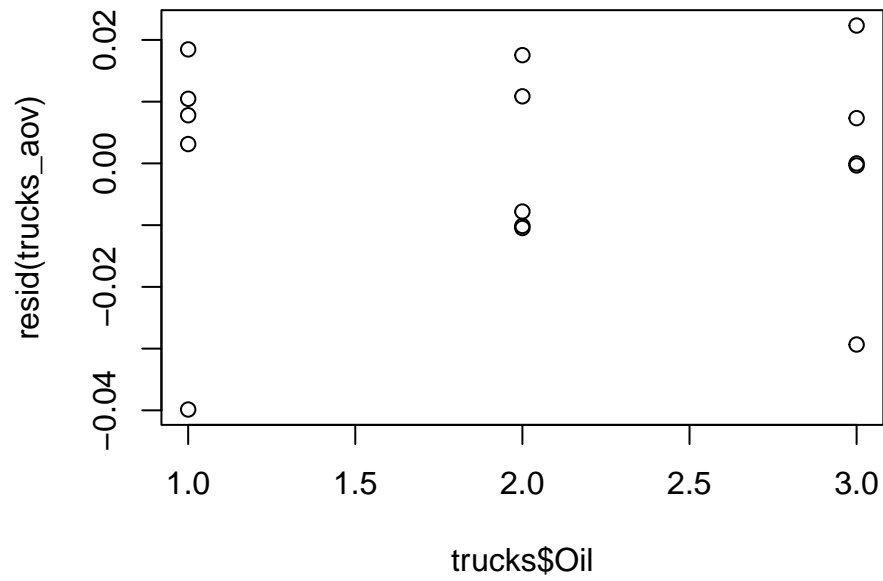


```
plot(trucks_aov, which = 1)
```

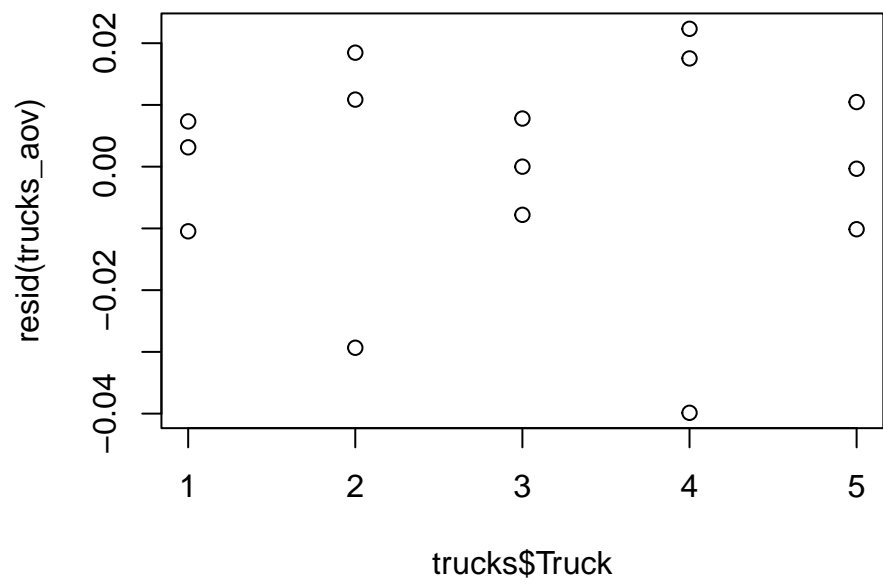
Residuals vs Fitted



```
plot(trucks$Oil, resid(trucks_aov))
```



```
plot(trucks$Truck, resid(trucks_aov))
```

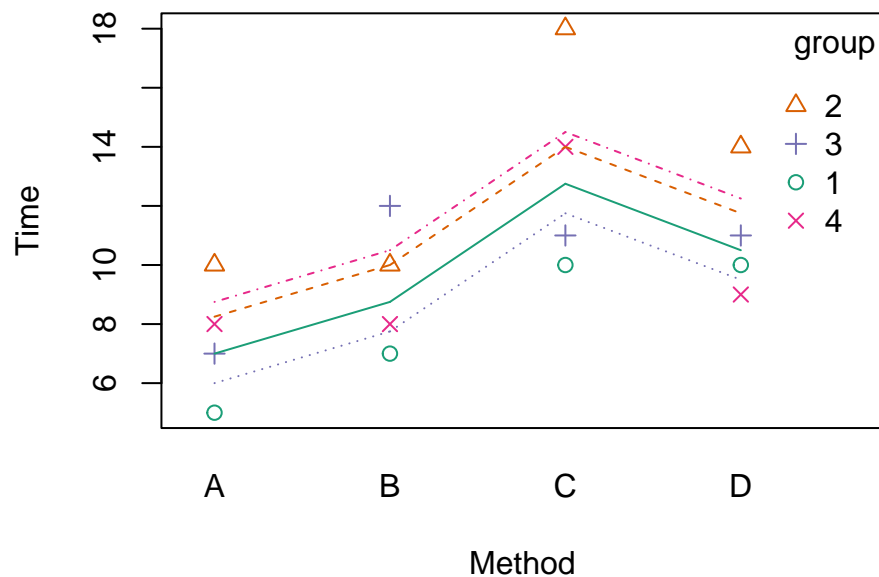


- (5) [4 pts] (DAE 4.23) See text. In addition, create pairwise interaction plots to check the additivity assumption. Do you see any gross violations of additivity?

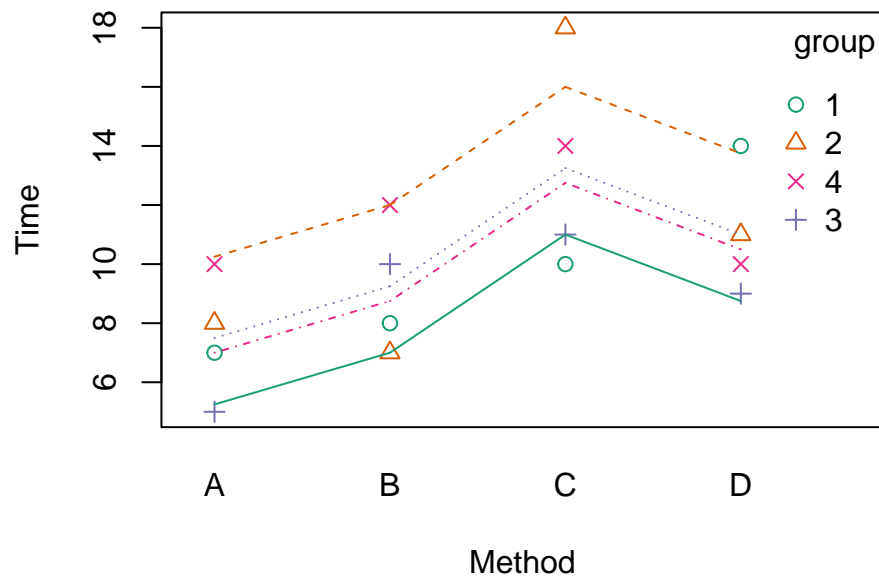
In plots 2, 3, 4 we can see violations of additivity in operator 1, method B, and order 4, respectively.

```
source('interaction_plot.R')
assembly <- read.csv("./HW3_data/Q4-23.csv")
#head(assembly)

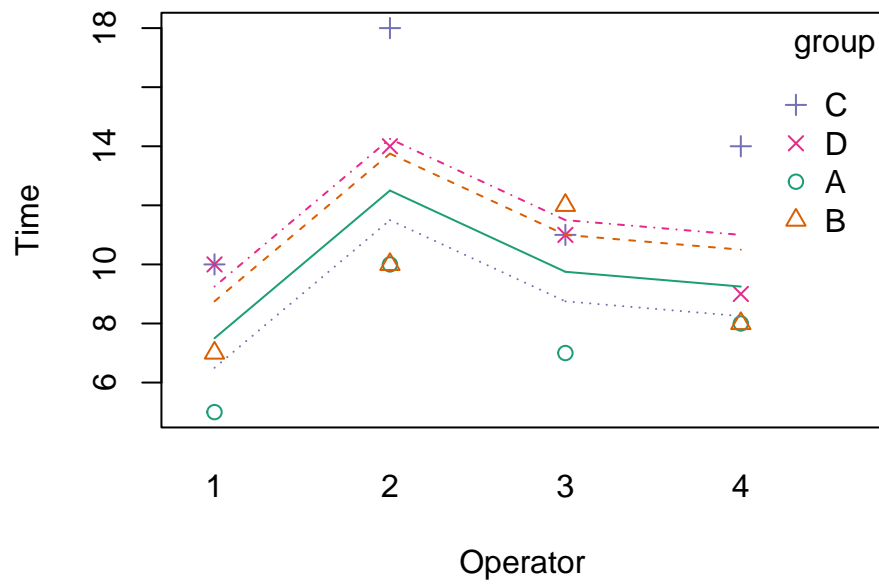
interaction_plot(aov(Time ~ Method + as.factor(Operator) + as.factor(Order), data = assembly))
```



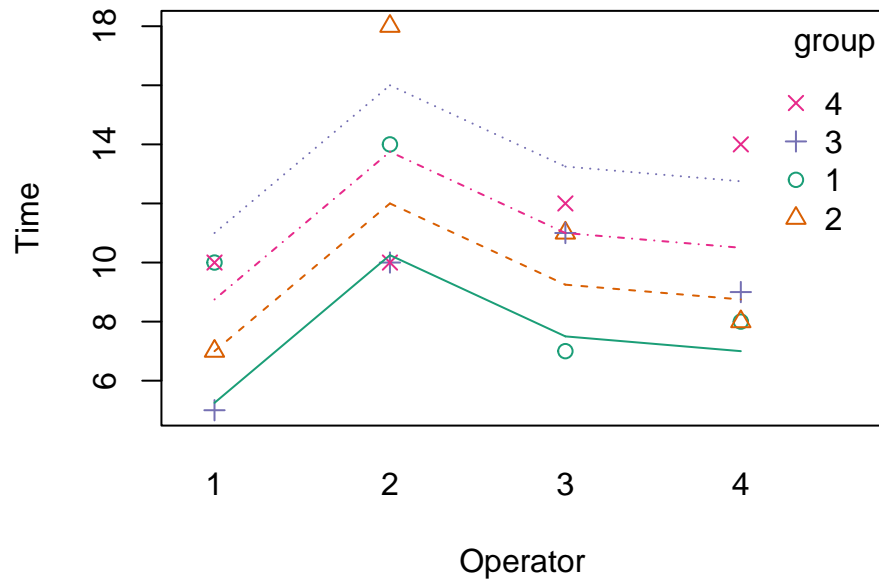
```
# Operator 1 violates
interaction_plot(aov(Time ~ Method + as.factor(Order) + as.factor(Operator), data = assembly))
```



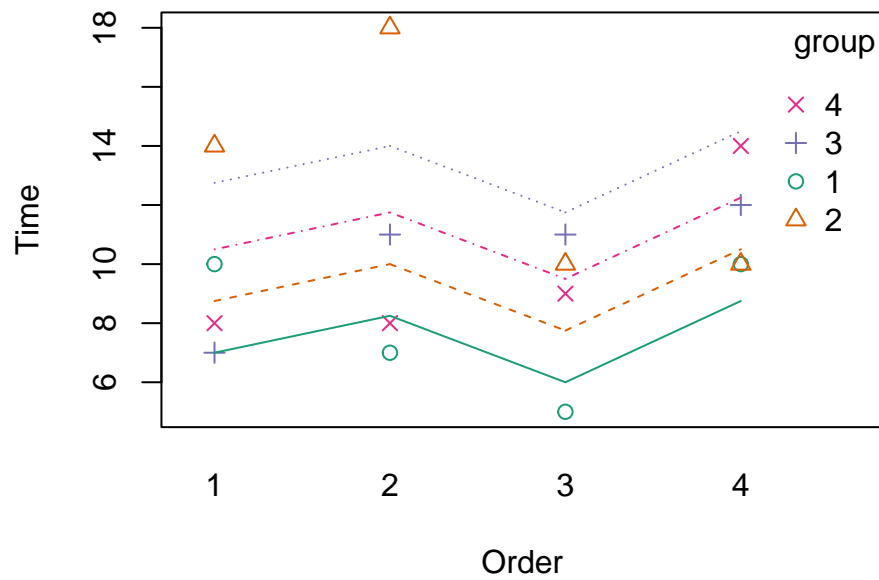
```
# Method B violates
interaction_plot(aov(Time ~ as.factor(Operator) + Method + as.factor(Order), data = assembly))
```



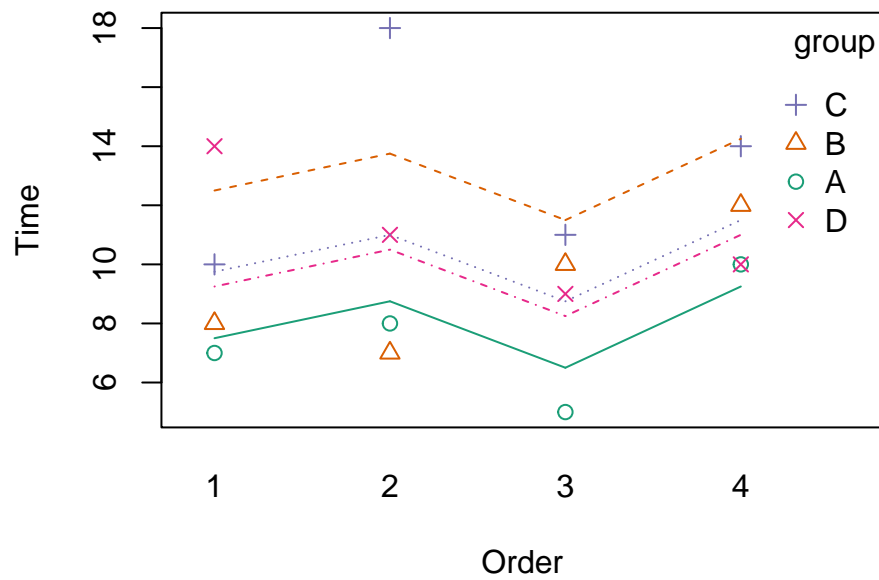
```
# Order 4 violates
interaction_plot(aov(Time ~ as.factor(Operator) + as.factor(Order) + Method, data = assembly))
```



```
interaction_plot(aov(Time ~ as.factor(Operator) + as.factor(Order) + Method, data = assembly))
```



```
interaction_plot(aov(Time ~ as.factor(Order) + Method + as.factor(Operator), data = assembly))
```



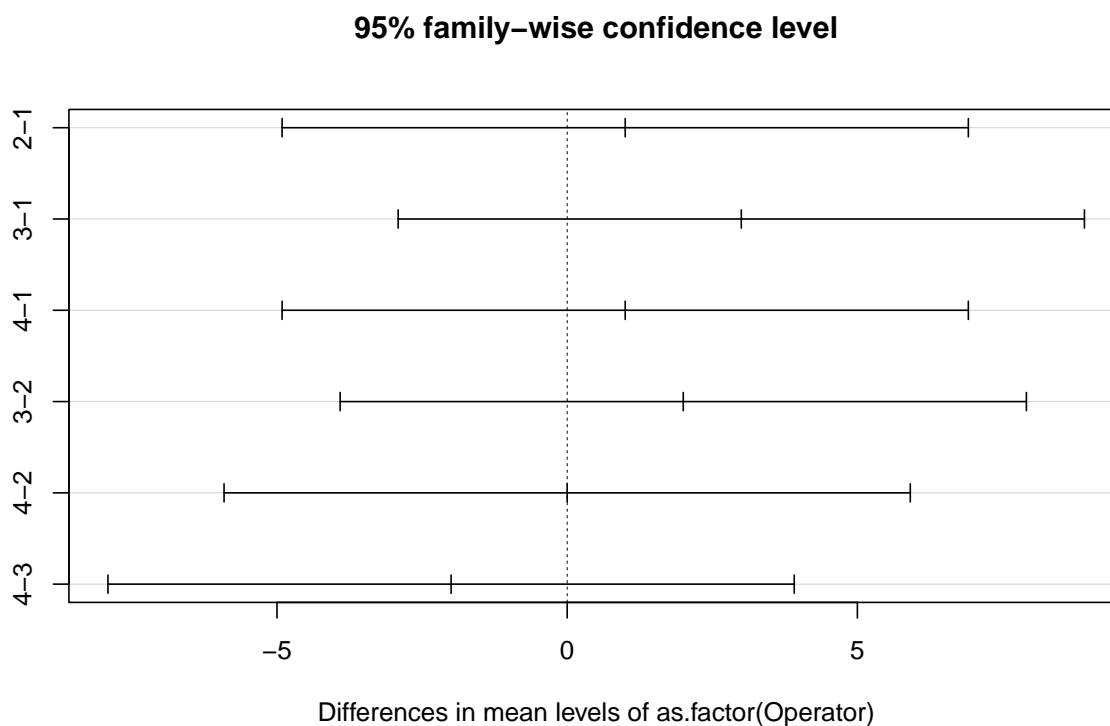
(6) [3 pts] (DAE 4.36) See *text*. At an alpha of .05, we see that the method block is significant. Looking at

the Tukey test, we can infer that within the method blocks, C and B are significantly different at a 0.05 alpha level. We can group the methods as (C,D) and (A,B).

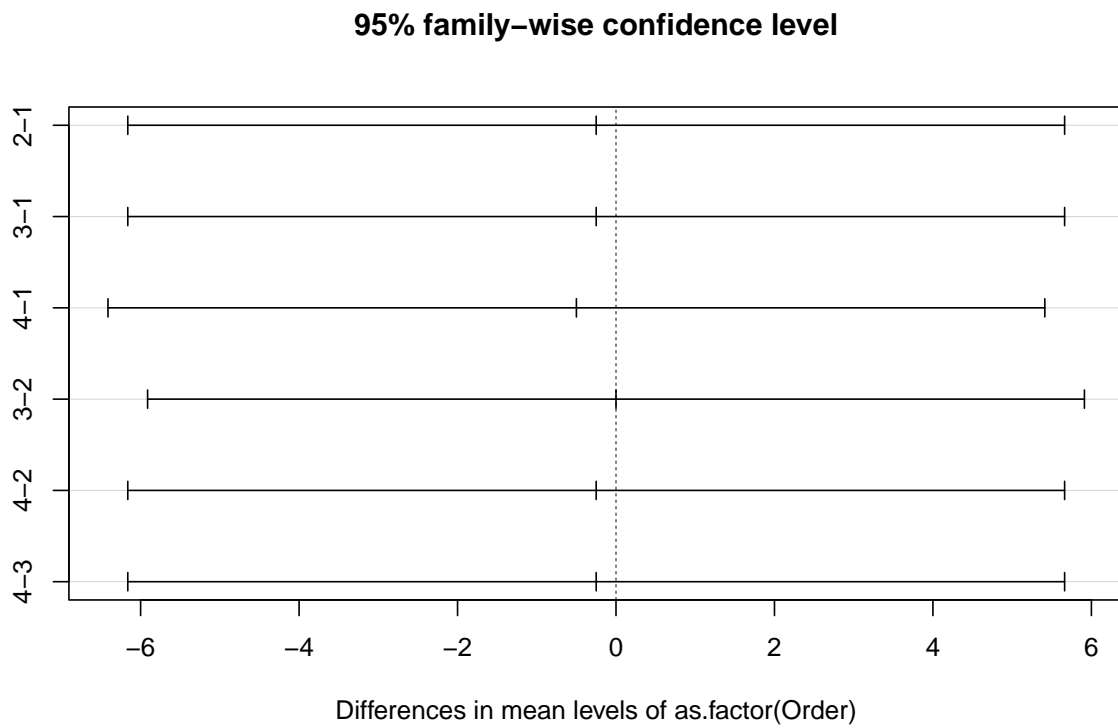
```
assembly_GL <- read.csv("./HW3_data/Q4-36.csv")
assembly_GL_aov <- aov(Time ~ as.factor(Order) + as.factor(Operator) + Method, data=assembly_GL)
summary(assembly_GL_aov)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(Order)    3    0.5    0.17  0.029 0.9928
## as.factor(Operator) 3   19.0    6.33  1.086 0.4240
## Method              3   95.5   31.83  5.457 0.0377 *
## Residuals          6   35.0    5.83
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

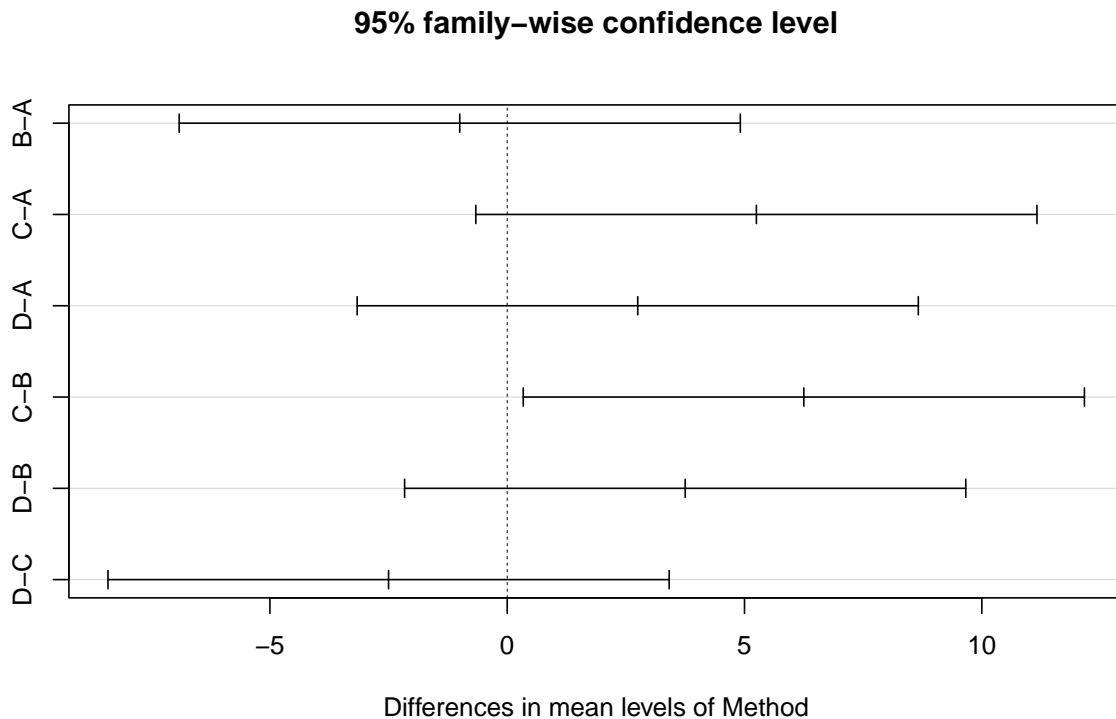
```
plot(TukeyHSD((assembly_GL_aov), which = "as.factor(Operator)"))
```



```
plot(TukeyHSD((assembly_GL_aov), which = "as.factor(Order)"))
```



```
plot(TukeyHSD((assembly_GL_aov), which = "Method"))
```



```
TukeyHSD(assembly_GL_aov, which = "Method")
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Time ~ as.factor(Order) + as.factor(Operator) + Method, data = assembly_GL)
##
## $Method
##      diff      lwr      upr    p adj
## B-A -1.00 -6.9119977  4.911998 0.9328804
## C-A  5.25 -0.6619977 11.161998 0.0787664
## D-A  2.75 -3.1619977  8.661998 0.4393220
## C-B  6.25  0.3380023 12.161998 0.0398761
## D-B  3.75 -2.1619977  9.661998 0.2264008
## D-C -2.50 -8.4119977  3.411998 0.5098871
```

- (7) [5 pts] (DAE 4.40) *See text. In addition, report the values of a , b , r , k , and λ for the design.* Based on the analysis, both the additives and the car blocking have significant effects at an $\alpha = 0.05$. Based on the Tukey HSD, Car 5 appears to have significantly lower mileage than Cars 1-4 (all similar). Additionally, car additives (1, 2) lead to significantly higher mileage than (3, 4, 5).

$a=5$, $b=5$, $r=4$, $k=4$, $\lambda=3$

```
mileage <- read.csv("./HW3_data/Q4-40.csv")
#head(mileage)

# order matters
```

```
mileage_aov <- aov(Mileage ~ as.factor(Car) + as.factor(Additive) , data = mileage)
summary(mileage_aov)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## as.factor(Car)      4   31.20     7.800    8.566 0.00216 **
## as.factor(Additive)  4   35.73     8.933    9.810 0.00125 **
## Residuals          11   10.02     0.911
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(mileage_aov, which = "as.factor(Car)")
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Mileage ~ as.factor(Car) + as.factor(Additive), data = mileage)
##
## $'as.factor(Car)'  
##      diff      lwr      upr      p adj  
## 2-1  1.000000e+00 -1.182193  3.18219269 0.5930409  
## 3-1 -5.000000e-01 -2.682193  1.68219269 0.9420551  
## 4-1  3.552714e-15 -2.182193  2.18219269 1.0000000  
## 5-1 -2.750000e+00 -4.932193 -0.56780731 0.0126554  
## 3-2 -1.500000e+00 -3.682193  0.68219269 0.2406188  
## 4-2 -1.000000e+00 -3.182193  1.18219269 0.5930409  
## 5-2 -3.750000e+00 -5.932193 -1.56780731 0.0012777  
## 4-3  5.000000e-01 -1.682193  2.68219269 0.9420551  
## 5-3 -2.250000e+00 -4.432193 -0.06780731 0.0424345  
## 5-4 -2.750000e+00 -4.932193 -0.56780731 0.0126554
```

```
TukeyHSD(mileage_aov, which = "as.factor(Additive)")
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Mileage ~ as.factor(Car) + as.factor(Additive), data = mileage)
##
## $'as.factor(Additive)'  
##      diff      lwr      upr      p adj  
## 2-1 -1.3750 -3.557193  0.80719269 0.3105946  
## 3-1 -2.2500 -4.432193 -0.06780731 0.0424345  
## 4-1 -2.9375 -5.119693 -0.75530731 0.0080952  
## 5-1 -3.7500 -5.932193 -1.56780731 0.0012777  
## 3-2 -0.8750 -3.057193  1.30719269 0.6985532  
## 4-2 -1.5625 -3.744693  0.61969269 0.2106293  
## 5-2 -2.3750 -4.557193 -0.19280731 0.0313345  
## 4-3 -0.6875 -2.869693  1.49469269 0.8416475  
## 5-3 -1.5000 -3.682193  0.68219269 0.2406188  
## 5-4 -0.8125 -2.994693  1.36969269 0.7494153
```

(8) [5 pts] (DAE 4.53) See text. Instead of bounds on the p -value for (g) and (h), report specific value.

- a) Factor SS = $108.63 - 37.75 = 70.88$
- b) Factor DF = $70.88 / 14.18 = 5$
- c) Error DF = $23 - 5 = 18$
- d) MSE = $37.75 / 18 = 2.097222$
- e) F value = $MS_{\text{Factor}} / MSE = 14.18 / 2.097222 = 6.761325$
- f) Reject null at $\alpha = 0.05$ with a p-value of 0.001037926
- g) and h) p-value = $\text{pf}(6.761325, 5, 18, \text{lower.tail} = F) = 0.001037926$
- h) no. factor levels = There are 6 factor levels
- i) replicates = $24 / 6 = 4$
- j) Reconstructed (Left-Right Top-Bottom) -

Block DF: 4

$\text{Block_DF} * \text{Factor_DF} = \text{Error_DF}$

$\text{Block_DF} + \text{Factor_DF} + \text{Error_DF} = \text{Total_DF}$

$\text{Block_DF} + \text{Factor_DF} + \text{Block_DF} * \text{Factor_DF} = \text{Total_DF}$ where $\text{Factor_DF} = 4$, $\text{Total_DF} = 23$

$\text{Block_DF} + 4 + 4 * \text{Block_DF} = 23$

$5 * \text{Block_DF} = 19$

Block = 4

Block SS: 12

Block MS: $12 / 4 = 3$

Block F-value: $\text{pf}(3 / 2.359375, 4, 16, \text{lower.tail} = F) = 0.322$

Factor DF: $58.88 / 14.18 = 4$

Factor SS: $108.63 - (37.75 + 12) = 58.88$

Factor F-value: $14.18 / 2.359375 = 6.010066$

Error DF: $4 * 4 = 16$

Error MS: $37.75 / 16 = 2.359375$

p-value: $\text{pf}(6.010066, 4, 16, \text{lower.tail} = F) = 0.003772708$

Comparing the p-values, we see that blocking increased the p-values from 0.0010 to 0.0037. However, in both cases, there is a significant p-value for the factor.