STAT 425 Assignment 7

Due Tuesday, May 4, 11:59 pm. Submit through Moodle.

Name: (insert your name here)

Netid: (insert)

Submit your computational work both as an R markdown (*.Rmd) document and as a pdf, along with any files needed to run the code. Embed your answers to each problem in the document below after the question statement. If you have hand-written work, please scan or take pictures of it and include in a pdf file, ideally combined with your pdf output file from R Markdown.

Most relevant class notes: 10.1.TwoWayAnova1, 10.2.TwoWayAnova2, 11.1.ExperimentalDesign1, 11.2.ExperimentalDesign2

Problem 1

The data set `ctsib` in `faraway` comes from an experiment described in the documentation as follows:

> An experiment was conducted to study the effects of surface and vision on balance. The balance of subjects were observed for two different surfaces and for restricted and unrestricted vision. Balance was assessed qualitatively on an ordinal four-point scale based on observation by the experimenter. Forty subjects were studied ... while standing on foam or a normal surface and with their eyes closed or open or with a dome placed over their head. Each subject was tested twice in each of the surface and eye combinations for a total of 12 measures per subject.

In this problem, we will ignore the subject effects, and perform the two-way ANOVA analysis of the response score `CTSIB` as a function of `Surface` and `Vision` as if the experiment had completely randomized design. In Problem 2, for comparison, we will perform the more proper analysis that accounts for the subject as a blocking variable.

a) Here is a way to count how many observations fall in each combination of the two treatment factors:

```
library(faraway)
xtabs(~Surface+Vision, data=ctsib)

##        Vision
## Surface closed dome open
```

```
##     foam      80    80    80
##     norm      80    80    80
```

Because the design is balanced across all 6 factor combinations, we can do the balanced two-way ANOVA analysis. Here is the ANOVA table for the model with main effects and interactions.

```
modCRD = lm(CTSIB~Surface*Vision, data=ctsib)
summary(aov(modCRD))
```

```
##                  Df Sum Sq Mean Sq F value Pr(>F)
## Surface           1  58.10   58.10 297.132 <2e-16 ***
## Vision            2  36.84   18.42  94.193 <2e-16 ***
## Surface:Vision    2   0.20    0.10   0.522  0.594
## Residuals       474  92.69    0.20
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Are there significant interactions? Explain.

Answer:

The p-value for the interaction term is 0.594 which is far above any reasonable alpha. We do not have enough evidence to conclude that the interaction term is significant.

b) Here is how we can get one of the two possible interaction plots for these data.

```
with(ctsib, interaction.plot(x.factor=Surface, trace.factor=Vision, response=CTSIB))
```
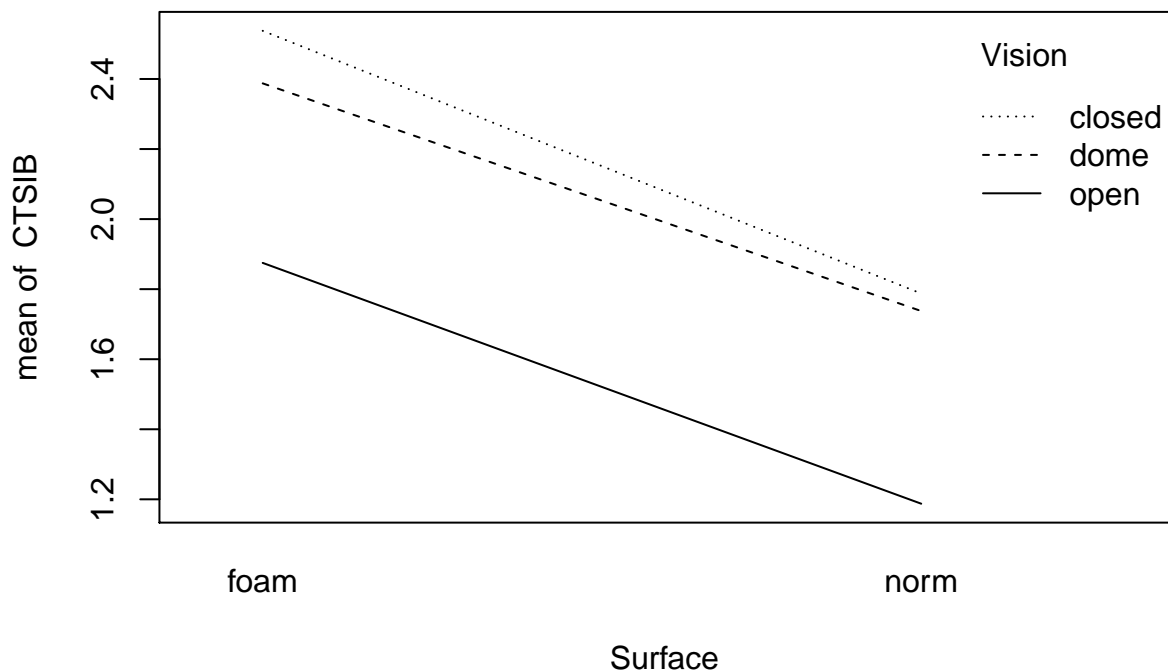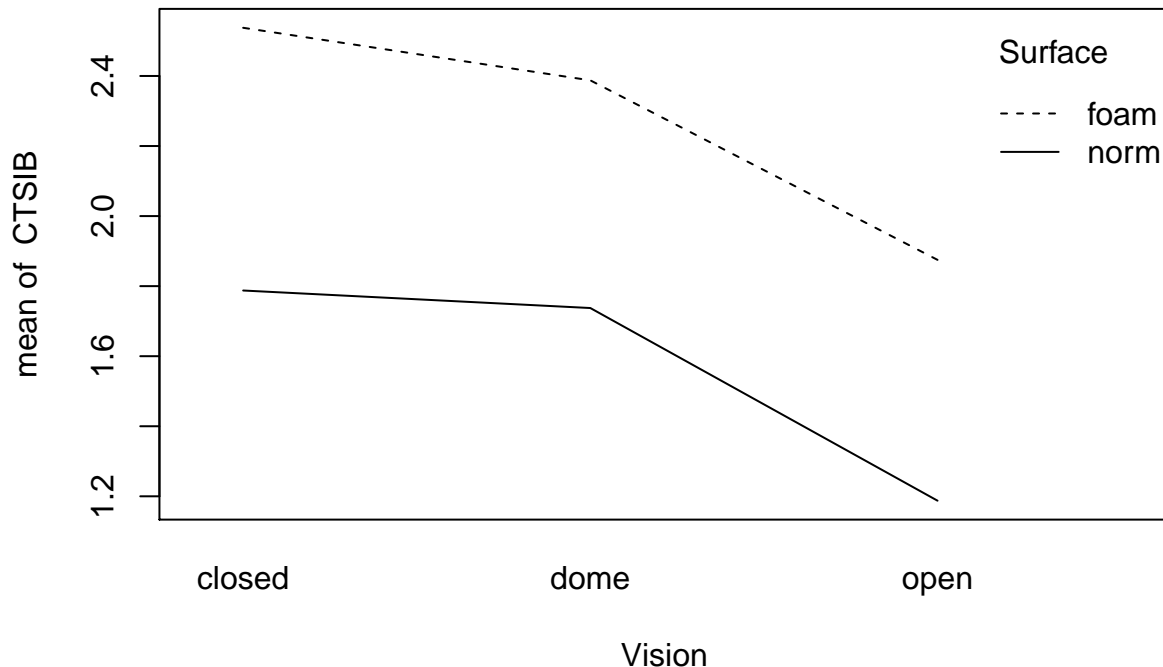

Provide the other interaction plot, with `Vision` on the x-axis, and describe what the plots suggest about how the mean balance scores vary across the different combinations of Vision

and Surface.

Answer:

```r
with(ctsib, interaction.plot(x.factor = Vision, trace.factor = Surface, response = CTSI
```


The traces across varying levels of Vision are fairly parallel in the first plot. This is also true for the two levels of Surface in the second plot. The mean balance score seems to respond more to the individual Vision and Surface levels. This makes sense because the interaction term in part a was insiginificant.

c) Fit the additive model (main effects only for `Surface` and `Vision`), and show the corresponding analysis of variance table. Are the main effects significant?

Answer:

```r
fit_1c = lm(CTSIB ~ Surface + Vision, data = ctsib)
summary(aov(fit_1c))
```

```
##               Df Sum Sq Mean Sq F value Pr(>F)
## Surface        1  58.10   58.10  297.73 <2e-16 ***
## Vision         2  36.84   18.42   94.38 <2e-16 ***
## Residuals    476  92.89    0.20
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

With p-values of 0, both main effects are significant.

d) Display the additive model summary that includes the coefficient estimates and standard errors. What are the reference categories for `Surface` and `Vision`?

Answer:

```r
summary(fit_1c)
```

```
##
## Call:
## lm(formula = CTSIB ~ Surface + Vision, data = ctsib)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.8792 -0.4104  0.1208  0.2854  1.4896
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.51042    0.04033  62.252   <2e-16 ***
## Surfacenorm -0.69583    0.04033 -17.255   <2e-16 ***
## Visiondome  -0.10000    0.04939  -2.025   0.0435 *
## Visionopen  -0.63125    0.04939 -12.781   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4418 on 476 degrees of freedom
## Multiple R-squared:  0.5055, Adjusted R-squared:  0.5023
## F-statistic: 162.2 on 3 and 476 DF,  p-value: < 2.2e-16
```

The reference category is Foam for Surface and Closed for Vision.

e) Perform the Tukey honest significant difference analysis of the two treatment factors, based on the additive model. Which Surface and Vision level differences are statistically significant, controlling the family-wise false postive rate at 0.05?

Answer:

```r
TukeyHSD(aov(fit_1c))
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = fit_1c)
##
## $Surface
##                 diff        lwr        upr p adj
## norm-foam -0.6958333 -0.775074 -0.6165927     0
##
## $Vision
##                 diff        lwr        upr      p adj
## dome-closed -0.10000 -0.2161194  0.01611942 0.1074035
## open-closed -0.63125 -0.7473694 -0.51513058 0.0000000
```

```
## open-dome    -0.53125 -0.6473694 -0.41513058 0.0000000
```

From the result we can see "norm-foam", "open-closed", "open-dome" are significantly different under 0.05 level.

Problem 2

The Problem 1 analysis of the `ctsib` data is technically incorrect, because we expect the 12 measurements from each subject to be more closely related (correlated) than observations between subjects. In other words, `Subject` is a blocking variable. The subject id is a number, but we should treat it as a factor (categorical label) variable. Therefore, in this experiment we have 40 blocks (the subjects), and 2 observations for each of the 6 treatment combinations within each block. Here are the numbers of observations per cell for the first 3 subjects (blocks), so you can see the design:

```
xtabs( ~ Surface+Vision+as.factor(Subject), data = ctsib)[,,1:3]
```

```
## , , as.factor(Subject) = 1
##
##         Vision
## Surface closed dome open
##    foam      2    2    2
##    norm      2    2    2
##
## , , as.factor(Subject) = 2
##
##         Vision
## Surface closed dome open
##    foam      2    2    2
##    norm      2    2    2
##
## , , as.factor(Subject) = 3
##
##         Vision
## Surface closed dome open
##    foam      2    2    2
##    norm      2    2    2
```

a) Here is the ANOVA table for the model that adds the blocking variable as a main effect in addition to the main effects and interactions between the two treatment factors:

```
modRCBD = lm(CTSIB~as.factor(Subject)+Surface*Vision, data=ctsib)
summary(aov(modRCBD))
```

```
##                     Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(Subject)  39  38.75    0.99   8.012 <2e-16 ***
## Surface              1  58.10   58.10 468.569 <2e-16 ***
```

```
## Vision                   2  36.84    18.42 148.539 <2e-16 ***
## Surface:Vision            2   0.20     0.10   0.823   0.44
## Residuals              435  53.94     0.12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Are there significant interactions? Explain.

Answer: The p value of interaction between "Surface" and "Vision" is 0.44, which is pretty large. Therefore we do not think there exists significant interaction here.

b) Comparing the ANOVA table part 2a) with the Anova table in Problem 1a), which sums of squares have changed and which ones remain the same? Same question for the different F values, how did each of them change (larger, smaller, unchanged)?

Answer: For sums of squares, "Vision", "Surface", and "Surface:Vision" stay the same and "Residuals" changed. For F values, "Surface", "Vision", and "Surface:Vision" all become larger.

c) Fit the additive model (main effects only for `as.factor(Subject)`, `Surface` and `Vision`), and show the corresponding analysis of variance table. Are the main effects significant? How have the F values of the main effects for `Vision` and `Surface` changed compared with the results in Problem 1c)?

Answer:

```
modRCBDadd = lm(CTSIB~as.factor(Subject)+Surface+Vision, data=ctsib)
summary(aov(modRCBDadd))
```

```
##                     Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(Subject)  39  38.75    0.99   8.019 <2e-16 ***
## Surface              1  58.10   58.10 468.948 <2e-16 ***
## Vision               2  36.84   18.42 148.660 <2e-16 ***
## Residuals          437  54.14    0.12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

All of the main effects are significant and F values all become larger compared to 1(c).

d) Compute the ratio of the residual standard error $\hat{\sigma}$ for the model in Part 1c to the residual standard error for the model in Part 2c. What does this say about the relative efficiency of the completely randomized design compared with the randomized blocks design?

Answer:

```
rt = summary(fit_1c)$sig / summary(modRCBDadd)$sig
rt
```

```
## [1] 1.255022
```

```
rt^2
```

```
## [1] 1.575081
```

The ratio between two standard error is 1.2550 and the relative efficiency is 1.5751. This implies that CRD would need 57.51% more observations to obtain the same level precision as RCBD.

e) Using the additive model that included the subject as a blocking variable, redo the Tukey honest significant difference analysis of the two treatment factors, `Surface` and Vision. Which Surface and Vision level differences are statistically significant, controlling the family-wise false postive rate at 0.05? Hint: if using the TukeyHSD function, include the argument `which=c("Surface", "Vision")` to obtain results for those factors only and not show the $40 * 39/2 = 780$ blocking variable differences, which are not of interest.

Answer:

```r
TukeyHSD(aov(modRCBDadd), which = c("Surface", "Vision"))
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = modRCBDadd)
##
## $Surface
##                 diff        lwr        upr p adj
## norm-foam -0.6958333 -0.7589865 -0.6326801     0
##
## $Vision
##                 diff        lwr          upr       p adj
## dome-closed -0.10000 -0.1925497 -0.007450271 0.0305677
## open-closed -0.63125 -0.7237997 -0.538700271 0.0000000
## open-dome   -0.53125 -0.6237997 -0.438700271 0.0000000
```

From the result we can see "norm-foam", "dome-closed", "open-closed", and "open-dome" are significantly different under 0.05 level.

Problem 3

The `alfalfa` data in the `faraway` library are from an experiment to study yield from planted alfalfa seeds give different inoculum treatments. The experiment compared five treatments, A-E, where E was the control level. Two blocking variables were used: 1) `shade`, which is the distance of the location in the field from a tree line divided into 5 shade areas (1-5); and 2) `irrigation`, which is an irrigation measure divided into 5 levels. The experiment used an incomplete design such that each of the 5 treatments was given once for each level of shade and each level of irrigation, for a total of 25 observations.

a) To understand which combinations of variable levels were used in the experiment, display

the result of running the cross-tabulation command

$$\texttt{xtabs(yield} \sim \texttt{inoculum + shade + irrigation, data=alfalfa)}$$

as illustrated in the class notes on experimental design. Note that an entry in the cross-tab is 0 if that combination did not occur, and the entry is the response value if that combination did occur. Based on the information in the data write down the form of the 5×5 latin square used in this design. Rows should be levels of irrigation, columns should be levels of shade, and the entries in the table should be treatment labels.

Answer: First, let's see what **xtabs** gives us.

```
# load package
require('faraway')
# levels
xtabs(yield ~ inoculum + shade + irrigation, data = alfalfa)
```

```
## , , irrigation = 1
##
##         shade
## inoculum    1    2    3    4    5
##        A 33.8  0.0  0.0  0.0  0.0
##        B  0.0  0.0  0.0  0.0 34.8
##        C  0.0  0.0 35.8  0.0  0.0
##        D  0.0 37.0  0.0  0.0  0.0
##        E  0.0  0.0  0.0 33.2  0.0
##
## , , irrigation = 2
##
##         shade
## inoculum    1    2    3    4    5
##        A  0.0  0.0  0.0 37.1  0.0
##        B 33.7  0.0  0.0  0.0  0.0
##        C  0.0  0.0  0.0  0.0 39.1
##        D  0.0  0.0 35.6  0.0  0.0
##        E  0.0 28.8  0.0  0.0  0.0
##
## , , irrigation = 3
##
##         shade
## inoculum    1    2    3    4    5
##        A  0.0  0.0 36.9  0.0  0.0
##        B  0.0 33.5  0.0  0.0  0.0
##        C  0.0  0.0  0.0 37.4  0.0
##        D 30.4  0.0  0.0  0.0  0.0
##        E  0.0  0.0  0.0  0.0 32.7
##
```

```
## , , irrigation = 4
##
##          shade
## inoculum    1    2    3    4    5
##        A  0.0 34.6  0.0  0.0  0.0
##        B  0.0  0.0  0.0 38.1  0.0
##        C 32.7  0.0  0.0  0.0  0.0
##        D  0.0  0.0  0.0  0.0 37.4
##        E  0.0  0.0 26.7  0.0  0.0
##
## , , irrigation = 5
##
##          shade
## inoculum    1    2    3    4    5
##        A  0.0  0.0  0.0  0.0 36.4
##        B  0.0  0.0 35.1  0.0  0.0
##        C  0.0 33.4  0.0  0.0  0.0
##        D  0.0  0.0  0.0 34.1  0.0
##        E 24.4  0.0  0.0  0.0  0.0
```

From the R result, we can present the form of Latin square design as below.

Block	Shade1	Shade2	Shade3	Shade4	Shade5
Irrig1	A	D	C	E	B
Irrig2	B	E	D	A	C
Irrig3	D	B	A	C	E
Irrig4	C	A	E	B	D
Irrig5	E	C	B	D	A

b) Fit the additive linear model and display the model summary. Informally, which of the treatments appear to increase the yield the most compared to the control, E?

Answer: We can fit the additive linear model as below.

```
lmod <- lm(yield ~ inoculum + shade + irrigation, data = alfalfa)
summary(lmod)
```

```
##
## Call:
## lm(formula = yield ~ inoculum + shade + irrigation, data = alfalfa)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.024  -0.604   0.036   1.016   1.936
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
```

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```
## (Intercept)    33.464         1.263  26.500 5.11e-12 ***
## inoculumB       -0.720         1.108  -0.650 0.527883
## inoculumC       -0.080         1.108  -0.072 0.943607
## inoculumD       -0.860         1.108  -0.776 0.452490
## inoculumE       -6.600         1.108  -5.959 6.62e-05 ***
## shade2            2.460        1.108   2.221 0.046343 *
## shade3            3.020        1.108   2.727 0.018376 *
## shade4            4.980        1.108   4.496 0.000731 ***
## shade5            5.080        1.108   4.587 0.000625 ***
## irrigation2      -0.060        1.108  -0.054 0.957688
## irrigation3      -0.740        1.108  -0.668 0.516684
## irrigation4      -1.020        1.108  -0.921 0.375214
## irrigation5      -2.240        1.108  -2.023 0.065993 .
## ---
## Signif. codes:   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.751 on 12 degrees of freedom
## Multiple R-squared:  0.876,  Adjusted R-squared:  0.7519
## F-statistic: 7.062 on 12 and 12 DF,  p-value: 0.0009624
```

As the coefficients of treatment are all negative and $\hat{\beta}_{\text{inoculumE}}$ represents the difference between treatment A and treatment E, we may conclude that treatment A increase the yield the most compare to the control E.

c) Display diagnostic plots for the fitted model. Are there any concerning patterns in the residuals versus fitted values, quantile-quantile plot of studentized residuals, or scale plot of absolute residuals versus fitted values?

Answer: We can create the diagnostics plot as below.

```
par(mfrow = c(2, 2))
plot(lmod)
```
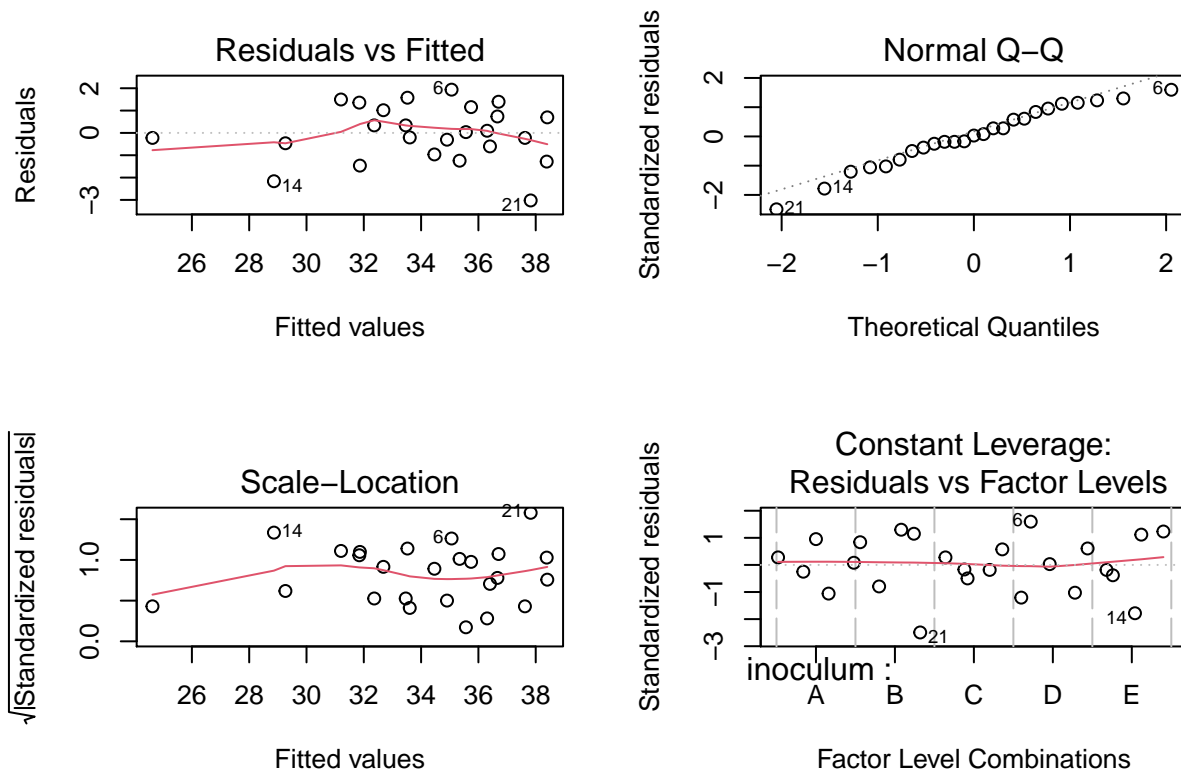
From residual versus fitted plot, we don't really see any issue with the linearity assumption given the sparseness of the data for low fitted values. Any deviation from a straight line could easily occur by change. From the QQ-plot, we see that the tails deviate slightly from the normal distribution, but again this could easily occur by chance in a small sample so no great concern. From the scale-location plot, we see some trend of the smoothing red line but it is reasonably flat, so it is unlikely to affect the efficiency of the least squares estimator. *Note: there is an art to interpreting these graphs, so any logical description of the results is acceptable.*

d) As illustrated in the notes, use the "drop1" method to test the perform F tests of the blocking and treatment factors. What do you conclude from the results?

Answer: We can perform it as below.

```
drop1(lmod, test = 'F')
```

```
## Single term deletions
##
## Model:
## yield ~ inoculum + shade + irrigation
##            Df Sum of Sq     RSS    AIC F value    Pr(>F)
## <none>                   36.799 35.665
## inoculum    4   155.894 192.694 69.056 12.7091 0.000284 ***
## shade       4    87.402 124.202 58.076  7.1254 0.003533 **
## irrigation  4    16.562  53.362 36.955  1.3502 0.307872
## ---
```

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

From the result, we see that the blocking factor `shade` is significant but the blocking factor `irrigation` is not significant; and the treatment factor `inoculum` is significant under a significance level of 5%.

e) Perform a Tukey honest significant differences analysis of the differences between treatment means. Because of the lack of orthoginality between treatment and blocking factors, we can't use the `aov` and `TukeyHSD` functions to do the job. Instead we have to compute directly as illustrated in the notes on latin squares and balanced incomplete block designs. To get started, observe that the margin of error (confidence interval half-width) for Tukey HSD paired differences has the form

$$\texttt{qtukey(0.95, nmeans, df)} * se_{\text{diff}}/\sqrt{2}$$

where `nmeans` is the number of different means being compared, `df` is the residual degrees of freedom for the model, and se_{diff} is the standard error treatment differences reported for the non-reference treatment coefficients in the model summary. Determine which pairs of treatments have significantly different mean yields.

Answer: We compute the margin as below.

```
cv <- qtukey(.95, length(alfalfa$inoculum), df.residual(lmod))
se <- coef(summary(lmod))[2, 2]
margin <- cv * se / sqrt(2)
betas <- c(0, coef(lmod)[2:5])
names(betas)[1] <- "inoculumA"
abs(outer(betas, betas, '-')) > margin
```

```
##           inoculumA inoculumB inoculumC inoculumD inoculumE
## inoculumA     FALSE     FALSE     FALSE     FALSE      TRUE
## inoculumB     FALSE     FALSE     FALSE     FALSE      TRUE
## inoculumC     FALSE     FALSE     FALSE     FALSE      TRUE
## inoculumD     FALSE     FALSE     FALSE     FALSE      TRUE
## inoculumE      TRUE      TRUE      TRUE      TRUE     FALSE
```

As we can see, using Tukey method, there are significant differences between each of the treatment mean of groups A, B, C, D and the control group mean of E. We did not detect any significant differences between the treatment groups A-D. In summary $\{A, B, C, D\} > E$.