Using ANOVA, Plotting the Data, and Multiple Comparison Tests in R: an Example from a Coastal Management Research Project

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February 11, 2015

Abstract

In this tutorial, I will demonstrate the use of the ANOVA commands in R, displaying the results of analysis of the data from a dredging study done in North Carolina. The student will learn to read data from a Systat file, then create factors and manipulate the data to complete a randomized block design ANOVA, with two factors and an interaction term. Box plots, plots of means with error bars, and an interaction plot will be produced to show how the means of each treatment group differ. Finally, I will demonstrate the use of multiple comparison procedures, which can be used to determine which of the treatment group means are statistically different.

1 Introduction

The use of ANOVA is widespread in ecology, social sciences, and geology. It is one of the most basic of all statistical tests. In ANOVA, a series of nominal categories or treatments are used as predictors (independent variables) of a given continuous response variable (dependent variable). In this chapter, I will explain in some detail the methods of an experimental dredging study, the experimental design used, the analysis of the data using the **aov()** command in R, interpreting the output, and make some basic plots of means, box plots, and an interaction plot. Finally, I will explain how to make some common multiple comparison procedures for treatment group means, finding the ones that differ significantly from the rest.

1.1 Dredge Spoil Disposal Experimental Methods

Disposal of dredged materials in the past has had considerable environmental impacts on wetlands and coastal habitats; however, the need to dredge canals, channels, and inlets in support of navigation in the coastal zone will continue in the future. One method of intertidal dredge disposal that is cost-effective

but has not been extensively studied for environmental impacts is the method of thin-layer dredge disposal (a patented process of the Aztec Development Co., Inc. P.O. Box 3348, Orlando FL 32802), in which a slurry of the dredged materials and water from the dredge site are sprayed in a jet-stream through the air onto an adjoining intertidal salt marsh. Thin-layer dredge material disposal has been suggested to have fewer environmental impacts when compared with other disposal methods, but the level of thickness of deposition that is without environmental impact has not been determined. In the analysis we will do here, a dredge spoil disposal experiment was done in Wysocking Bay, NC. The dredge spoils (or sediments) from a nearby canal were dispersed over a *Juncus roemerianus* marsh in a series of sixteen plots, each one $4.0\,\mathrm{m}^2$. Our objectives in this study were to simulate experimentally the effects of four levels of thin-layer dredge disposal (0 cm, 2 cm, 4 cm, and 10 cm thickness of dredged material) in a *Juncus roemerianus* dominated marsh near Wysocking Bay, NC that had not previously been used for disposal of dredged materials and to determine at what level there would be a significant impact on the vegetation biomass. We sampled vegetation biomass in September (at the end of the growing season in North Carolina) before the dredge spoil was applied to 16 replicate 4m x 4m plots in a randomized block design and again annually at 1, 2, 3, and 4 years after disposal of dredge material treatment. We measured the above-ground dry biomass of *Juncus roemerianus* at each time period by cutting and weighing the grass within four 20 cm x 20 cm quadrats selected at random within each of the plots.

Let's load the data from the experiment for the treatments, plot numbers, block numbers and *Juncus* biomass data at each time period sampled. First, I will load the packages **foreign** and **gplots**, then load the data from my local drive into a data frame called JB. Then, I will print the data and list the names of each column in the data frame:

```
library("foreign", lib.loc = "C:/Program Files/R/R-3.0.2/library")
library("gplots", lib.loc = "C:/Program Files/R/R-3.0.2/library")

## KernSmooth 2.23 loaded
## Copyright M. P. Wand 1997-2009
##
## Attaching package:  'gplots'
##
## The following object is masked from 'package:stats':
##
##     lowess

setwd("~/CRM7008/HW3")
JB <- read.systat(file = "bijrSEP92SEP96.SYD")
print(JB)

##    PLOT TREAT BLOCK REP SEP92 SEP93 SEP94 SEP95 SEP96
```

```
## 1     1    10     1     1   47.9    7.2    6.7   18.5   19.1
## 2     1    10     1     2   25.1   27.6   17.1   15.6   30.3
## 3     1    10     1     3   25.4   51.2   31.9    4.2    0.0
## 4     1    10     1     4   36.2    8.2   14.5   22.6   26.9
## 5     2     4     1     1   32.1   31.6   12.8   25.9   18.9
## 6     2     4     1     2   19.6   13.3   25.8   27.7   34.1
## 7     2     4     1     3   40.9   28.7   12.4   10.0   40.2
## 8     2     4     1     4    4.6   33.3   15.2   27.9   15.8
## 9     3     2     1     1   55.0   22.3   24.1   43.7   28.7
## 10    3     2     1     2   48.7   52.2   31.2   15.5    8.0
## 11    3     2     1     3   22.9   15.8   60.5   26.3   33.9
## 12    3     2     1     4   34.3    4.2   41.5   23.0   22.8
## 13    4     0     1     1   17.9   60.3   49.2   46.8   90.3
## 14    4     0     1     2   39.2   57.6   72.7   41.1   52.8
## 15    4     0     1     3   58.5   83.8   50.4   32.9   36.7
## 16    4     0     1     4   58.0   79.8   24.4   36.4    0.0
## 17    5     2     2     1   37.1   36.7    7.7   29.5   21.3
## 18    5     2     2     2   42.2   19.1   37.0   50.9   61.8
## 19    5     2     2     3   12.8   58.3   92.8   40.0    0.0
## 20    5     2     2     4   53.8   39.2   33.6    5.8    0.0
## 21    6    10     2     1   26.4   13.2   12.5    9.0   40.5
## 22    6    10     2     2   20.7    0.0    0.0    8.2   12.2
## 23    6    10     2     3   24.1   17.6    8.1    0.0    0.0
## 24    6    10     2     4   41.9    0.0   22.1    0.0    0.0
## 25    7     4     2     1   21.9   11.0   40.9   26.8   13.5
## 26    7     4     2     2   42.9   16.8   76.8   31.4   25.5
## 27    7     4     2     3   35.9   65.3   21.8   84.9   20.5
## 28    7     4     2     4   23.8   49.8   21.3   29.8    0.0
## 29    8     0     2     1    4.9    9.3   35.5   29.4    8.2
## 30    8     0     2     2   27.0   15.1   42.1   31.5   13.2
## 31    8     0     2     3    9.3   22.6   33.5   16.1   32.6
## 32    8     0     2     4   15.0   42.8   20.9   29.7   18.0
## 33    9     0     3     1    0.4   19.5    8.9   16.9   43.3
## 34    9     0     3     2   15.1   46.0   31.1   17.5   22.3
## 35    9     0     3     3    0.0   13.0   21.0   30.8   28.9
## 36    9     0     3     4    0.2   31.8   28.1   28.1   38.5
## 37   10     4     3     1   69.4   38.5   37.6   32.1   26.4
## 38   10     4     3     2   32.5   63.2   19.2   13.5   36.4
## 39   10     4     3     3   28.5   55.3   16.5   32.8   36.8
## 40   10     4     3     4   48.7   19.5   47.1   29.4   54.8
## 41   11    10     3     1   27.0    2.7    0.0    2.0    8.3
## 42   11    10     3     2   48.6    0.0    3.6    0.0    0.0
## 43   11    10     3     3   29.2    0.0    0.0    0.3    0.0
## 44   11    10     3     4   12.2    0.0    0.0    5.9    0.0
## 45   12     2     3     1   46.8   22.0   44.9   55.8   54.9
```

```
## 46    12    2    3    2    39.8    18.8    42.6    49.2    58.7
## 47    12    2    3    3    35.9    15.8    31.5    41.2    23.8
## 48    12    2    3    4    44.9    31.6    76.4    24.8    42.1
## 49    13    0    4    1    85.8    45.3    20.8    44.7    42.8
## 50    13    0    4    2    25.8    40.3    46.5    33.0    48.4
## 51    13    0    4    3    43.7    40.7    23.2    62.5    46.9
## 52    13    0    4    4    45.8    81.0    28.4    72.3    25.4
## 53    14    2    4    1    58.2    18.8    19.0    58.2    47.5
## 54    14    2    4    2    52.6     7.0    42.2    24.3    45.4
## 55    14    2    4    3    54.5    24.8    63.4    54.3    36.0
## 56    14    2    4    4    23.5     6.6    26.8     7.5     0.0
## 57    15   10    4    1    46.1     8.7     0.0     0.2    10.4
## 58    15   10    4    2    47.6     0.0     0.0     1.6     6.4
## 59    15   10    4    3    29.8     7.6     0.1     2.6    10.2
## 60    15   10    4    4    22.1     0.0     0.0     0.0     0.0
## 61    16    4    4    1    17.0    17.8    28.3     4.2    27.2
## 62    16    4    4    2    70.5    43.1     9.6    38.5    32.6
## 63    16    4    4    3    40.3     1.9    85.9     4.2     0.0
## 64    16    4    4    4    38.1     0.0     0.0    14.7     0.0

names(JB)

## [1] "PLOT"   "TREAT" "BLOCK" "REP"    "SEP92" "SEP93" "SEP94" "SEP95" "SEP96"
```

Next, I will create a factor called Treat from the original column TREAT in the data frame using the **factor()** command. The output will now become a factor with four levels and will be stored as a vector. It is now a nominal data set, i.e., the data are no longer treated by R as numbers, but as names of categories, in this case, representing the four categories of dredge spoil depth, or the four levels (0,2,4,and 10 cm) of the treatment. This step is very important for ANOVA, as the ANOVA command **aov()** in R requires that the treatments are a factor prior to any analysis. I will do the same thing for the effect Block. In this study, a series of four blocks (with four plots per block) was established by the experimental design, arranged along an environmental gradient of marsh elevation. The experimental design established that four adjacent plots should taken together as a group with similar elevations, with Block 1 comprising the four plots farthest from Wysocking Bay, and Block 4 closest to Wysocking Bay. Within each block, each of the four dredge spoil treatments was assigned to plots at random. This way, the treatments would be dispersed along the marsh elevation gradient. Once again, Block is considered a nominal or categorical variable.

Finally, I will create response variables, making two vectors (numeric in this case) for the *Juncus* biomass prior to the experimental dredge study (Sep 1992) and after 1 year (Sep 93). For now, I will ignore the later years data, although this can be done in a similar way using these commands.

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```
Treat <- factor(JB$TREAT)
Block <- factor(JB$BLOCK)
Sep92 <- JB$SEP92
Sep93 <- JB$SEP93
```

Let's examine the data for normality and heterogeneity of variances. We used a **qqnorm() shapiro.test()** commands earlier to examine distributions for normality. So, we will do that again. We will also use Bartlett's test to examine the treatment groups' variances to see any one group has a variance that is very different from the other groups. This is done with the command **bartlett.test(y x)**, where y is the vector with the response variable and x is the treatment group vector. One assumption in ANOVA is that the treatment groups all share a similar variance, i.e., that there is homegeneity of variances among the groups. If one group has a very high variance, with points widely dispersed around the mean, and the others have low variance, the ANOVA may not reveal siginficant differences among the means, rather a significant difference in the variances. Bartlett's test is to verify that the assumption of homogeneity of variances amoung groups being compared in ANOVA are met.

```
par(mfrow = c(2, 1))
qqnorm(Sep92)   #normal probability plot for pre-dredge data
qqnorm(Sep93)   #normal probability plot for post-dredge data
```

Normal Q–Q Plot
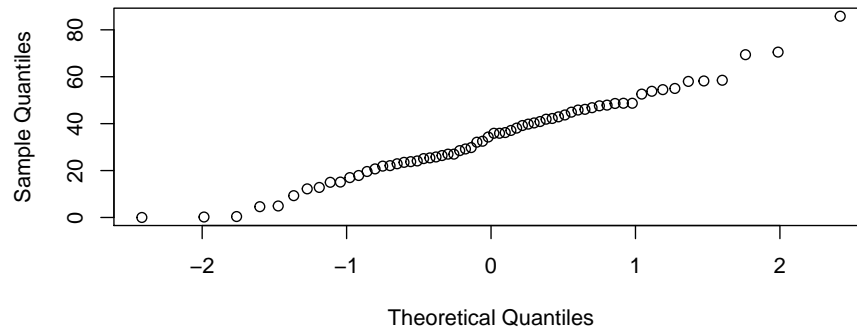
Normal Q–Q Plot
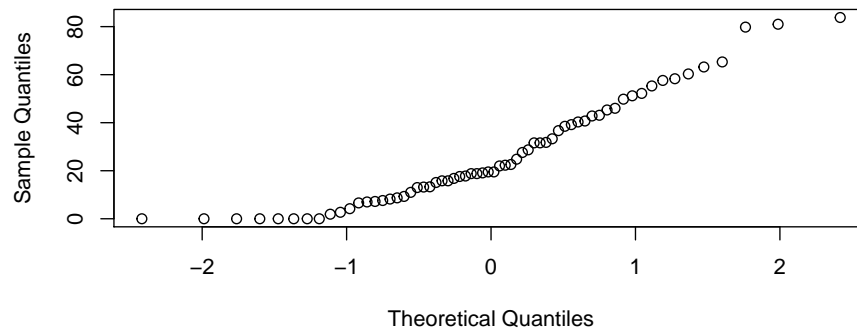

```r
shapiro.test(Sep92)  #normality test using Shaprio-Wilk test

##
##  Shapiro-Wilk normality test
##
## data:  Sep92
## W = 0.9858, p-value = 0.675

shapiro.test(Sep93)

##
##  Shapiro-Wilk normality test
##
## data:  Sep93
## W = 0.9213, p-value = 0.0005637

bartlett.test(Sep92 ~ Treat)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Sep92 by Treat
## Bartlett's K-squared = 11.18, df = 3, p-value = 0.0108

bartlett.test(Sep93 ~ Treat)

##
##  Bartlett test of homogeneity of variances
##
## data:  Sep93 by Treat
## Bartlett's K-squared = 5.905, df = 3, p-value = 0.1163
```

As the tests above show, the data from Sep 1992 were not significantly different from normal, but the variances were heterogeneous. In contrast, the data from Sep 1993 were significantly different from normal, but the variances were homogeneous among the treatments. These two results suggest that a log transformation of the original data would be beneficial, both to conform to the assumption of normality and homogeneity of variance. I then ran two ANOVA analyses, using a log-10 transformation, one for the comparison of mean biomass in each treatment before dredge disposal and one after, storing the resulting ANOVA fit and using the **summary()** command to see the ANOVA Tables.

```
fitSep92 <- aov(Sep92 ~ Treat * Block)
fitSep93 <- aov(Sep93 ~ Treat * Block)
fitlogSep92 <- aov(log(Sep92 + 1) ~ Treat * Block)
fitlogSep93 <- aov(log(Sep93 + 1) ~ Treat * Block)
summary(fitSep92)

##             Df Sum Sq Mean Sq F value Pr(>F)
## Treat        3   1579     526    2.27  0.092 .
## Block        3   2520     840    3.62  0.019 *
## Treat:Block  9   4987     554    2.39  0.025 *
## Residuals   48  11123     232
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(fitSep93)

##             Df Sum Sq Mean Sq F value Pr(>F)
## Treat        3   9604    3201   13.26  2e-06 ***
## Block        3   2000     667    2.76 0.0521 .
## Treat:Block  9   8170     908    3.76 0.0012 **
## Residuals   48  11588     241
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(fitlogSep92)

##              Df Sum Sq Mean Sq F value  Pr(>F)
## Treat        3   8.20   2.734    8.15 0.00017 ***
## Block        3   5.77   1.925    5.74 0.00193 **
## Treat:Block  9  19.42   2.158    6.44 6.1e-06 ***
## Residuals   48  16.09   0.335
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(fitlogSep93)

##              Df Sum Sq Mean Sq F value  Pr(>F)
## Treat        3   42.6   14.19   19.01 2.9e-08 ***
## Block        3    7.9    2.62    3.52  0.0220 *
## Treat:Block  9   19.6    2.18    2.92  0.0077 **
## Residuals   48   35.8    0.75
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

As we can see from the summaries of the untransformed data, there were no significant differences among means of the *Juncus* biomass in the plots in each of the 4 treatments prior to the dredge disposal in Sep 1992, but there were significant differences after 1 year in Sep 1993. This means at least one of the treatment group means differed significantly than the others. The Block effect was significant in Sep 92 but barely significant in Sep 93. Finally, the interaction effect(Treat x Block) was significant in both years.

From the summaries of the log_10-transformed data, once again we see there were significant differences ($p = 0.00017$) among group means of the *Juncus* biomass prior to the dredge disposal on the plots in Sep 1992. However in Sep 1993, there were highly significant ($p = 2.9x10^{-8}$) differences in the dredge disposal treatments after 1 year. This implies that at least one of the treatment group means differed significantly than the others. Just as in teh untransformed data, the Block effect was significant in Sep 92 ($p = 0.00193$) and in Sep 93 ($p = 0.0220$). Finally, the interaction effect(Treat x Block) was significant in both years.

These results are difficult to interpret, in part because there is so much variability in the plots in Sep 92. This variation will be apparent when we visualize the treatments and block means and error bars in plots below. Dredge spoils were not yet applied at this time, yet there were significant treatment and blocking effects. It is not clear why the *Juncus* biomass means would vary by treatment prior to the application of dredge spoil deposition (it is a natural marsh environment with many animal and storm-caused disturbances), although blocking effects may be due to natural elevation changes across blocks. We can only attribute to random chance that differences would occur among the plot means, and these were associated by chance with the treatment levels,

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especially the controls, even though the probability is very small that such differences would happend by chance alone (rejecting the null with p = 0.09 with untransformed data or p = 0.00017 chance in the log-transformed data set). It is somewhat comforting to see the probabilities of rejecting the null hypothesis of equality of means decline significantly for the dredge spoil treatments in Sep 1993 (p = 2 x 10^6 for the raw data and $p = 2.9x10^{\hat{}}8$ for the log_10-transformed data). Clearly there was some natural variablity in *Juncus* biomass present at the site prior to conducting the experiments. A different approach to analyzing these data would be to use a repeated measures approach, using each plot as its own baseline control, and which we will attempt in a later chapter.
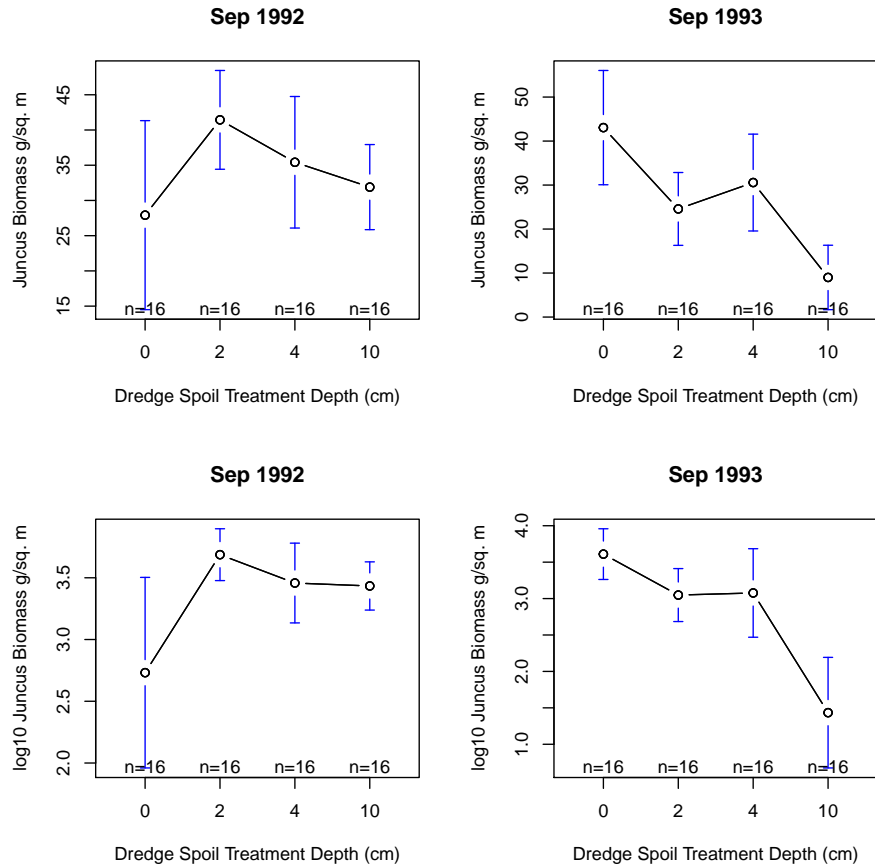
Next, I made some plots, in this case making multiple plots in a grid on the same page. I first changed the way the plots will appear in the graphical display window using the **par(mfrow=c(number of rows, number of columns))** to create multiple plots on the same output graphic. The par(mfrow=c(2,2)) will make a 2 x 2 grid for the plots and par(mfrow=c(3,2)) will make a grid with 3 rows and 2 columns, a separate plot in cell of the grid. The **boxplot()** command is in base R. This plots the medians and the boxes:

```
par(mfrow = c(2, 2))
boxplot(Sep92 ~ Treat, xlab = "Dredge Spoil Treatment Depth (cm)", ylab = "Juncus Biomass g/
    main = "Sep 1992")
boxplot(Sep93 ~ Treat, xlab = "Dredge Spoil Treatment Depth (cm)", ylab = "Juncus Biomass g/
    main = "Sep 1993")
boxplot(Sep92 ~ Block, xlab = " Experimental Block", ylab = "Juncus Biomass g/sq. m",
    main = "Sep 1992")
boxplot(Sep93 ~ Block, xlab = "Experimental Block", ylab = "Juncus Biomass g/sq. m",
    main = "Sep 1993")
```
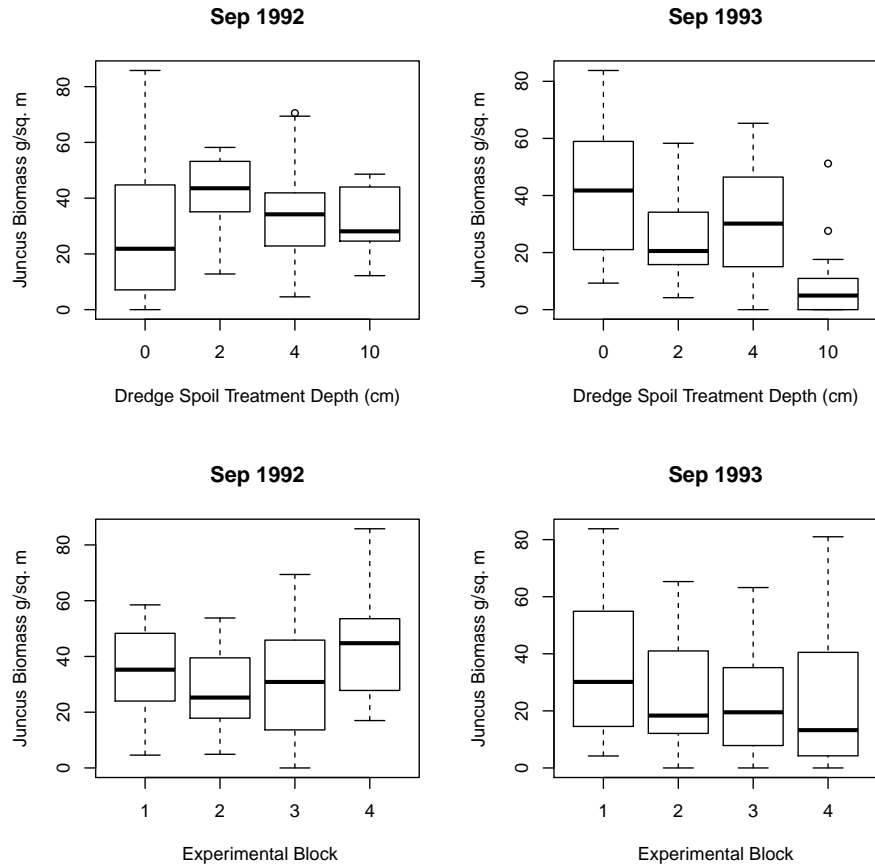
The **plotmeans()** command is from the gplot package; it plots the means and error bars.

```
par(mfrow = c(2, 2))
plotmeans(Sep92 ~ Treat, type = "b", xlab = "Dredge Spoil Treatment Depth (cm)",
    ylab = "Juncus Biomass g/sq. m", main = "Sep 1992")
plotmeans(Sep93 ~ Treat, type = "b", xlab = "Dredge Spoil Treatment Depth (cm)",
    ylab = "Juncus Biomass g/sq. m", main = "Sep 1993")
plotmeans(log(Sep92 + 1) ~ Treat, type = "b", xlab = "Dredge Spoil Treatment Depth (cm)",
    ylab = "log10 Juncus Biomass g/sq. m", main = "Sep 1992")
plotmeans(log(Sep93 + 1) ~ Treat, type = "b", xlab = "Dredge Spoil Treatment Depth (cm)",
    ylab = "log10 Juncus Biomass g/sq. m", main = "Sep 1993")
```

Sep 1992

Juncus Biomass g/sq. m

n=16   n=16   n=16   n=16

0   2   4   10

Dredge Spoil Treatment Depth (cm)

Sep 1993

Juncus Biomass g/sq. m

n=16   n=16   n=16   n=16

0   2   4   10

Dredge Spoil Treatment Depth (cm)

Sep 1992

log10 Juncus Biomass g/sq. m

n=16   n=16   n=16   n=16

0   2   4   10

Dredge Spoil Treatment Depth (cm)

Sep 1993

log10 Juncus Biomass g/sq. m

n=16   n=16   n=16   n=16

0   2   4   10

Dredge Spoil Treatment Depth (cm)

Next, I will plot the interaction plots, first for the untransformed data and then the log_10-transformed data.

```
par(mfrow = c(2, 2))
interaction.plot(Treat, Block, Sep92, type = "b", main = "raw data Sep 92")
interaction.plot(Treat, Block, Sep93, type = "b", main = "raw data Sep 93")
interaction.plot(Treat, Block, log(Sep92 + 1), type = "b", main = "Log transformed data Sep
interaction.plot(Treat, Block, log(Sep93 + 1), type = "b", main = "Log transformed data Sep
```

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raw data Sep 92

raw data Sep 93

Log transformed data Sep 92

Log transformed data Sep 93
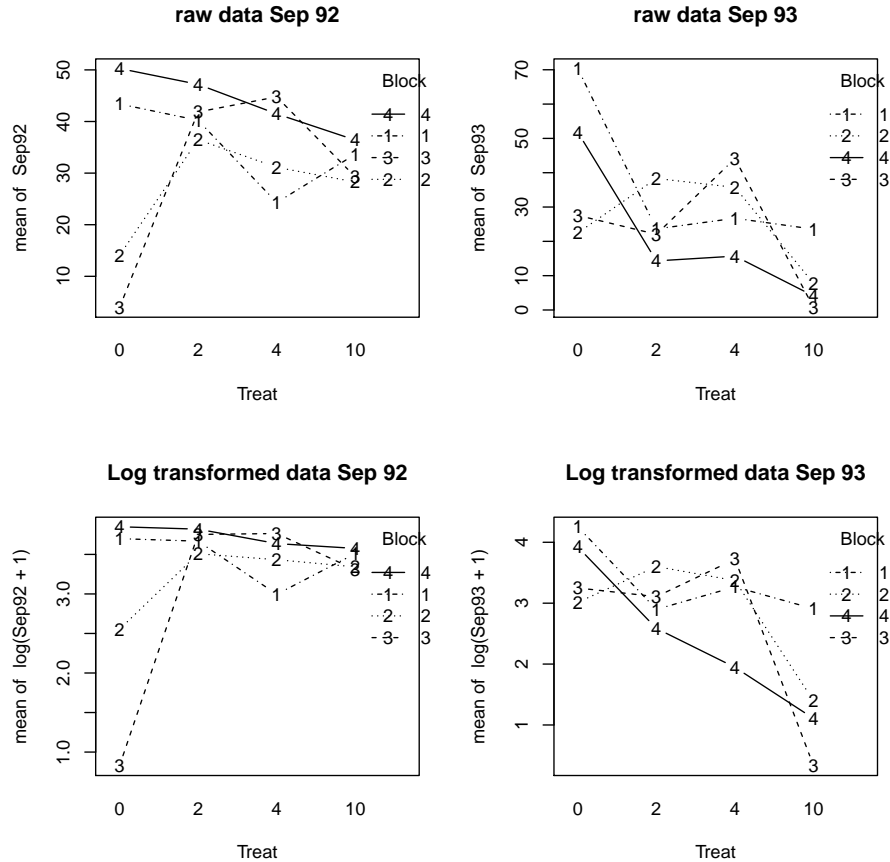
Interaction plots are extremely useful when comparing two-way ANOVA interaction terms, here with our dredge spoil treatment by block effects. The plots are showing the mean *Juncus* biomass for each combination of Treat and Block in this experiment.

2 Multiple Comparison Tests

When the treatment factor is significant, at least one of the means differed significantly from the others. But, which mean was the different one? Were more than one of the means different? To find out, we use a multiple comparison test. Here are several tests commonly used:

- Pairwise t-test computes all pairwise t-tests in base R

- LSD - Fisher's Least Significant Difference in package agricolae

- Tukey's HSD Honestly Significant Difference in base R

- Student-Neuman-Keuls (SNK) multiple range test in package agricolae. Similar to Tukey's HSD test, but only controls for comparisons of interest specified a prior by user. Less conservative than Tukey's.

- Bonferroni correction - a correction to the Type I error probability is often used to avoid concluding there is a significant difference between group means, when it is due by chance alone. The Type I error increases with the number of comparison tests done. In 100 such tests, with an $\alpha = 0.05$ there would be 5 significant tests due to chance alone from the multiple tests, even when there is no difference among the groups. To obtain the bonferroni adjusted Type I error, the unadjusted values of p are multiplied by the number of tests (6 in the case here). Bonferroni corrections are very conservative, and there are others available in R (Holm is the default) I will do it both ways (unadjusted and bonferroni-adjusted) below so you can see how they relate.

To implement the pairwise.t.test() command with a Bonferroni adjustment in R, run the following commands:

```
pairwise.t.test(Sep93, Treat, p.adj = "none")

##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  Sep93 and Treat
##
##    0       2      4
## 2  0.0080  -      -
## 4  0.0686  0.3769 -
## 10 4.3e-06 0.0242 0.0022
##
## P value adjustment method: none

pairwise.t.test(Sep93, Treat, p.adj = "bonferroni")

##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  Sep93 and Treat
##
##    0       2      4
## 2  0.048   -      -
## 4  0.411   1.000  -
## 10 2.6e-05 0.145  0.013
##
## P value adjustment method: bonferroni
```

We can see in the resulting table that the 0-cm and 10-cm treatment means are highly significantly different ($p = 2.6x10^{-5}$), but the 0-cm and 2-cm means are just barely different ($p = 0.048$). What other means differ and which means do not differ? Let's try Tukey's Honest Significant Difference. For this, we run the command on the list output from aov(Sep93 Treat*Block):

```
fitSep93 <- aov(Sep93 ~ Treat * Block)
TukeyHSD(fitSep93)

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Sep93 ~ Treat * Block)
##
## $Treat
##          diff      lwr      upr  p adj
## 2-0   -18.481 -33.101  -3.8611 0.0080
## 4-0   -12.487 -27.108   2.1327 0.1187
## 10-0  -34.056 -48.676 -19.4361 0.0000
## 4-2     5.994  -8.626  20.6139 0.6966
## 10-2  -15.575 -30.195  -0.9548 0.0327
## 10-4  -21.569 -36.189  -6.9486 0.0015
##
## $Block
##          diff     lwr      upr  p adj
## 2-1 -10.019 -24.64   4.6014 0.2750
## 3-1 -12.463 -27.08   2.1577 0.1199
## 4-1 -14.594 -29.21   0.0264 0.0506
## 3-2  -2.444 -17.06  12.1764 0.9703
## 4-2  -4.575 -19.20  10.0452 0.8386
## 4-3  -2.131 -16.75  12.4889 0.9799
##
## $`Treat:Block`
##                 diff      lwr      upr  p adj
## 2:1-0:1   -46.750  -86.442   -7.0576 0.0083
## 4:1-0:1   -43.650  -83.342   -3.9576 0.0188
## 10:1-0:1  -46.825  -86.517   -7.1326 0.0081
## 0:2-0:1   -47.925  -87.617   -8.2326 0.0060
## 2:2-0:1   -32.050  -71.742    7.6424 0.2443
## 4:2-0:1   -34.650  -74.342    5.0424 0.1502
## 10:2-0:1  -62.675 -102.367  -22.9826 0.0001
## 0:3-0:1   -42.800  -82.492   -3.1076 0.0233
## 2:3-0:1   -48.325  -88.017   -8.6326 0.0053
## 4:3-0:1   -26.250  -65.942   13.4424 0.5641
## 10:3-0:1  -69.700 -109.392  -30.0076 0.0000
## 0:4-0:1   -18.550  -58.242   21.1424 0.9399
```

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## 2:4-0:1     -56.075  -95.767 -16.3826 0.0006
## 4:4-0:1     -54.675  -94.367 -14.9826 0.0009
## 10:4-0:1    -66.300 -105.992 -26.6076 0.0000
## 4:1-2:1       3.100  -36.592  42.7924 1.0000
## 10:1-2:1     -0.075  -39.767  39.6174 1.0000
## 0:2-2:1      -1.175  -40.867  38.5174 1.0000
## 2:2-2:1      14.700  -24.992  54.3924 0.9921
## 4:2-2:1      12.100  -27.592  51.7924 0.9990
## 10:2-2:1    -15.925  -55.617  23.7674 0.9832
## 0:3-2:1       3.950  -35.742  43.6424 1.0000
## 2:3-2:1      -1.575  -41.267  38.1174 1.0000
## 4:3-2:1      20.500  -19.192  60.1924 0.8782
## 10:3-2:1    -22.950  -62.642  16.7424 0.7627
## 0:4-2:1      28.200  -11.492  67.8924 0.4439
## 2:4-2:1      -9.325  -49.017  30.3674 1.0000
## 4:4-2:1      -7.925  -47.617  31.7674 1.0000
## 10:4-2:1    -19.550  -59.242  20.1424 0.9117
## 10:1-4:1     -3.175  -42.867  36.5174 1.0000
## 0:2-4:1      -4.275  -43.967  35.4174 1.0000
## 2:2-4:1      11.600  -28.092  51.2924 0.9994
## 4:2-4:1       9.000  -30.692  48.6924 1.0000
## 10:2-4:1    -19.025  -58.717  20.6674 0.9274
## 0:3-4:1       0.850  -38.842  40.5424 1.0000
## 2:3-4:1      -4.675  -44.367  35.0174 1.0000
## 4:3-4:1      17.400  -22.292  57.0924 0.9638
## 10:3-4:1    -26.050  -65.742  13.6424 0.5766
## 0:4-4:1      25.100  -14.592  64.7924 0.6360
## 2:4-4:1     -12.425  -52.117  27.2674 0.9986
## 4:4-4:1     -11.025  -50.717  28.6674 0.9996
## 10:4-4:1    -22.650  -62.342  17.0424 0.7788
## 0:2-10:1     -1.100  -40.792  38.5924 1.0000
## 2:2-10:1     14.775  -24.917  54.4674 0.9917
## 4:2-10:1     12.175  -27.517  51.8674 0.9989
## 10:2-10:1   -15.850  -55.542  23.8424 0.9839
## 0:3-10:1      4.025  -35.667  43.7174 1.0000
## 2:3-10:1     -1.500  -41.192  38.1924 1.0000
## 4:3-10:1     20.575  -19.117  60.2674 0.8753
## 10:3-10:1   -22.875  -62.567  16.8174 0.7667
## 0:4-10:1     28.275  -11.417  67.9674 0.4394
## 2:4-10:1     -9.250  -48.942  30.4424 1.0000
## 4:4-10:1     -7.850  -47.542  31.8424 1.0000
## 10:4-10:1   -19.475  -59.167  20.2174 0.9141
## 2:2-0:2      15.875  -23.817  55.5674 0.9837
## 4:2-0:2      13.275  -26.417  52.9674 0.9972
## 10:2-0:2    -14.750  -54.442  24.9424 0.9918
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## 0:3-0:2      5.125  -34.567  44.8174 1.0000
## 2:3-0:2     -0.400  -40.092  39.2924 1.0000
## 4:3-0:2     21.675  -18.017  61.3674 0.8277
## 10:3-0:2   -21.775  -61.467  17.9174 0.8229
## 0:4-0:2     29.375  -10.317  69.0674 0.3762
## 2:4-0:2     -8.150  -47.842  31.5424 1.0000
## 4:4-0:2     -6.750  -46.442  32.9424 1.0000
## 10:4-0:2   -18.375  -58.067  21.3174 0.9441
## 4:2-2:2     -2.600  -42.292  37.0924 1.0000
## 10:2-2:2   -30.625  -70.317   9.0674 0.3103
## 0:3-2:2    -10.750  -50.442  28.9424 0.9997
## 2:3-2:2    -16.275  -55.967  23.4174 0.9796
## 4:3-2:2      5.800  -33.892  45.4924 1.0000
## 10:3-2:2   -37.650  -77.342   2.0424 0.0798
## 0:4-2:2     13.500  -26.192  53.1924 0.9967
## 2:4-2:2    -24.025  -63.717  15.6674 0.7013
## 4:4-2:2    -22.625  -62.317  17.0674 0.7801
## 10:4-2:2   -34.250  -73.942   5.4424 0.1625
## 10:2-4:2   -28.025  -67.717  11.6674 0.4544
## 0:3-4:2     -8.150  -47.842  31.5424 1.0000
## 2:3-4:2    -13.675  -53.367  26.0174 0.9962
## 4:3-4:2      8.400  -31.292  48.0924 1.0000
## 10:3-4:2   -35.050  -74.742   4.6424 0.1386
## 0:4-4:2     16.100  -23.592  55.7924 0.9814
## 2:4-4:2    -21.425  -61.117  18.2674 0.8392
## 4:4-4:2    -20.025  -59.717  19.6674 0.8958
## 10:4-4:2   -31.650  -71.342   8.0424 0.2618
## 0:3-10:2    19.875  -19.817  59.5674 0.9010
## 2:3-10:2    14.350  -25.342  54.0424 0.9938
## 4:3-10:2    36.425   -3.267  76.1174 0.1042
## 10:3-10:2   -7.025  -46.717  32.6674 1.0000
## 0:4-10:2    44.125    4.433  83.8174 0.0166
## 2:4-10:2     6.600  -33.092  46.2924 1.0000
## 4:4-10:2     8.000  -31.692  47.6924 1.0000
## 10:4-10:2   -3.625  -43.317  36.0674 1.0000
## 2:3-0:3     -5.525  -45.217  34.1674 1.0000
## 4:3-0:3     16.550  -23.142  56.2424 0.9763
## 10:3-0:3   -26.900  -66.592  12.7924 0.5234
## 0:4-0:3     24.250  -15.442  63.9424 0.6879
## 2:4-0:3    -13.275  -52.967  26.4174 0.9972
## 4:4-0:3    -11.875  -51.567  27.8174 0.9992
## 10:4-0:3   -23.500  -63.192  16.1924 0.7319
## 4:3-2:3     22.075  -17.617  61.7674 0.8083
## 10:3-2:3   -21.375  -61.067  18.3174 0.8415
## 0:4-2:3     29.775   -9.917  69.4674 0.3544
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## 2:4-2:3     -7.750  -47.442  31.9424 1.0000
## 4:4-2:3     -6.350  -46.042  33.3424 1.0000
## 10:4-2:3   -17.975  -57.667  21.7174 0.9529
## 10:3-4:3   -43.450  -83.142  -3.7576 0.0198
## 0:4-4:3      7.700  -31.992  47.3924 1.0000
## 2:4-4:3    -29.825  -69.517   9.8674 0.3517
## 4:4-4:3    -28.425  -68.117  11.2674 0.4306
## 10:4-4:3   -40.050  -79.742  -0.3576 0.0459
## 0:4-10:3    51.150   11.458  90.8424 0.0024
## 2:4-10:3    13.625  -26.067  53.3174 0.9963
## 4:4-10:3    15.025  -24.667  54.7174 0.9902
## 10:4-10:3    3.400  -36.292  43.0924 1.0000
## 2:4-0:4    -37.525  -77.217   2.1674 0.0821
## 4:4-0:4    -36.125  -75.817   3.5674 0.1110
## 10:4-0:4   -47.750  -87.442  -8.0576 0.0063
## 4:4-2:4      1.400  -38.292  41.0924 1.0000
## 10:4-2:4   -10.225  -49.917  29.4674 0.9999
## 10:4-4:4   -11.625  -51.317  28.0674 0.9993
```

The conclusions of each of these multiple comparisons tests are similar, with 0-cm and 2-cm, 0-cm and 10-cm, 10-cm and 2-cm, and 10-cm and 4-cm differing with the p-values listed. Also the Block effects are compared, and Blocks 1 and 4 are different, are the Blocks at each end of the elevation gradient. Finally, the numerous comparisons for each mean within a combination of treatment by block (interaction means) are compared, and some of these are significantly different. Look at the interaction plot while examining this table's output to see which differences that are significant ones make sense.

3   Conclusions

Although there were some significant differences in biomass in the pre-disposal plots, within 12 months of the experimental application of dredged material, areas that had received thick layers of dredge spoil (10 cm) had significantly less *Juncus roemerianus* biomass than control plots and areas that received thin layers of dredge disposal (2 cm and 4 cm) slightly less *Juncus roemerianus*. However, in later analysis not reported here, we found that five years and six months following treatment, that the *Juncus roemerianus* biomass appeared to have recovered to within its natural range of variation in the areas that had received 10 cm of dredge spoil. The results of this study indicate that *Juncus roemerianus* can recover significantly five years after receiving 10-cm thick layers of dredge disposal.

4   Acknowledgments