

Plankton response to salinity (aka 2015 CSI Dispersal Experiment)

Jo Werba, Alex Stucy, Mike McCoy, Ariane Peralta with contributions from Mario Muscarella (phylogenetic analyses, data manipulation, mothur tools)

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Project Description: Analysis of salinity and dispersal of saline aquatic communities on bacterial community structure and function. Manuscript preparation for zooplankton/bacterioplankton community composition-function study.

Setting up working directory, packages

Loading data file

manipulate data files for statistical analyses and graphing

zooplankton community - bacterial community matrix comparisons

```
#matrix comparison - Is there a relationship between zooplankton and bacterial community? = YES Mantel  
dim(otu_final.ns)
```

```
## [1] 91 13435
```

```
zoop.ns <- read.csv("../data/zoop_CSI_NoSource.csv", row.names=1)  
#str(zoop.ns)  
dim(zoop.ns)
```

```
## [1] 93 31
```

```
#odd sites for bacteria CSI033 is ShortID ECU_CSI_034  
#odd sites for bacteria CSI101 is Short ID ECU_CSI_103  
#deleted IUbarcode CSI041 = CSI 42 - double check  
#CSI 27 has zero individuals after source tanks removed  
odd.sites <- c("27", "42", "103")
```

```
zoop.ns2 <- zoop.ns[setdiff(rownames(zoop.ns), odd.sites), ]  
dim(zoop.ns2)
```

```
## [1] 90 31
```

```
# Make Relative Abundance Matrices  
zoop.ns3 <- zoop.ns2[, -c(1:4)]  
zoopREL <- zoop.ns3  
for(i in 1:dim(zoop.ns3)[1]){  
  zoopREL[i,] <- zoop.ns3[i,]/sum(zoop.ns3[i,])  
}
```

```

# use csi_relabun.ns but drop CSI 27 sample/ IBarcode ID CSI026 is CSI-027
#csi_relabun.ns
odd.sites <- c("CSI026")
dim(csi_relabun.ns)

## [1] 91 13435
csi_relabun.ns2 <- csi_relabun.ns[setdiff(rownames(csi_relabun.ns), odd.sites), ]
dim(csi_relabun.ns2)

## [1] 90 13435
dim(zoop.ns3)

## [1] 90 27
dist.zoop <- vegdist(zoopREL, method = "bray")
dist.bact <- vegdist(csi_relabun.ns2, method = "bray")

require(ade4)
mantel.rtest(dist.zoop, dist.bact, nrepet = 999)

## Warning in is.euclid(m1): Zero distance(s)

## Monte-Carlo test
## Call: mantelnoneuclid(m1 = m1, m2 = m2, nrepet = nrepet)
##
## Observation: 0.4087414
##
## Based on 999 replicates
## Simulated p-value: 0.001
## Alternative hypothesis: greater
##
##      Std.Obs   Expectation   Variance
## 16.1636383905 -0.0004271101  0.0006408055

```

Calculating Diversity Metrics

```

# Rarefy Abundances (min abundance is 13,240. We are sampling to 13,000)
min(rowSums(otu_final.ns))

## [1] 13240
otu.rarefy <- rrarefy(otu_final.ns, 13000)

# Calculate Shannon H' (called shannon) using full data set (WITH source tanks)
shannon <- diversity(otu.rarefy, "shannon")

# Species Richness
richness <- rowSums((otu.rarefy >= 1))

# Pielou's evenness
J <- shannon/log(specnumber(otu.rarefy[, -c(1:1)]))

```

```

# Dombined design,shannon,richness,evenness - no source tanks
csi_otu.div <- cbind(design.ns.final,shannon,richness,J)

# Rarefy Abundances with SOURCES (min abundance is 13,240. We are sampling to 13,000)
min(rowSums(otu_final))

## [1] 13240

otu.rarefy <- rrarefy(otu_final, 13000)

# Calculate Shannon H' (called shannon) using full data set (WITH source tanks)
shannon.source <- diversity(otu.rarefy, "shannon")

# Species Richness
richness.source <- rowSums((otu.rarefy >= 1))

# Pielou's evenness
J.source <- shannon.source/log(specnumber(otu.rarefy[, -c(1:1)]))

# Dombined design,shannon,richness,evenness - no source tanks
csi_otu.div.source <- cbind(design_final, shannon.source,
                           richness.source,J.source)

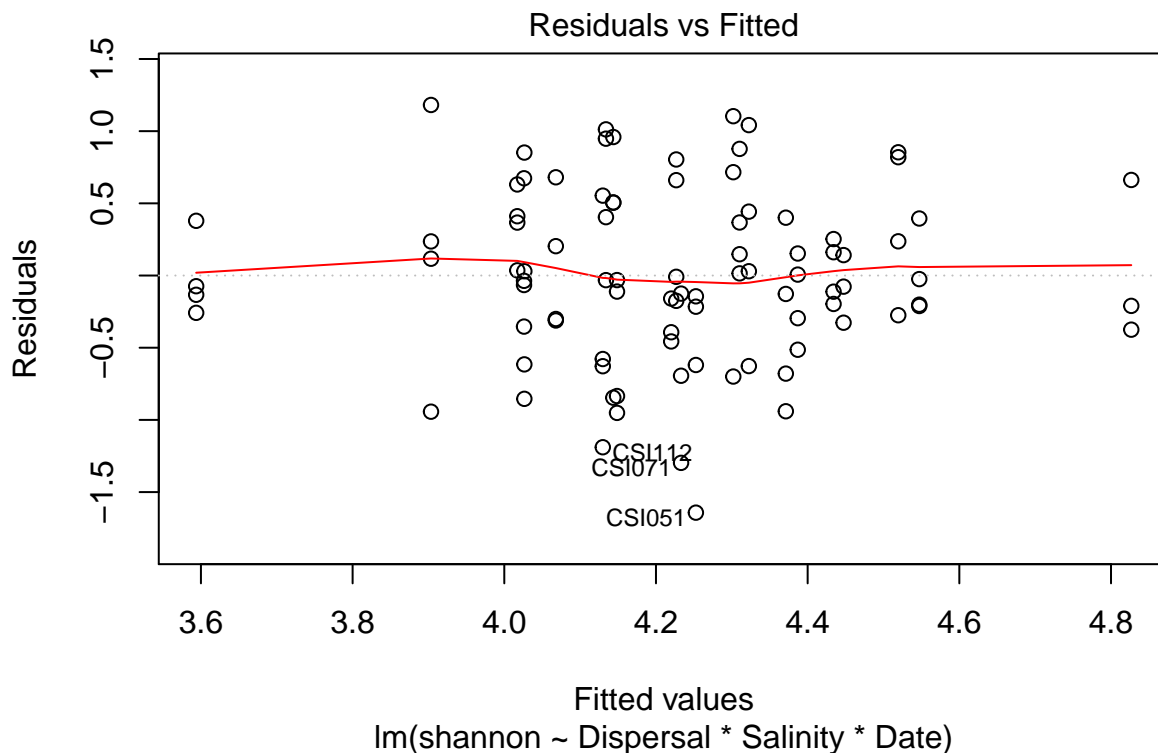
```

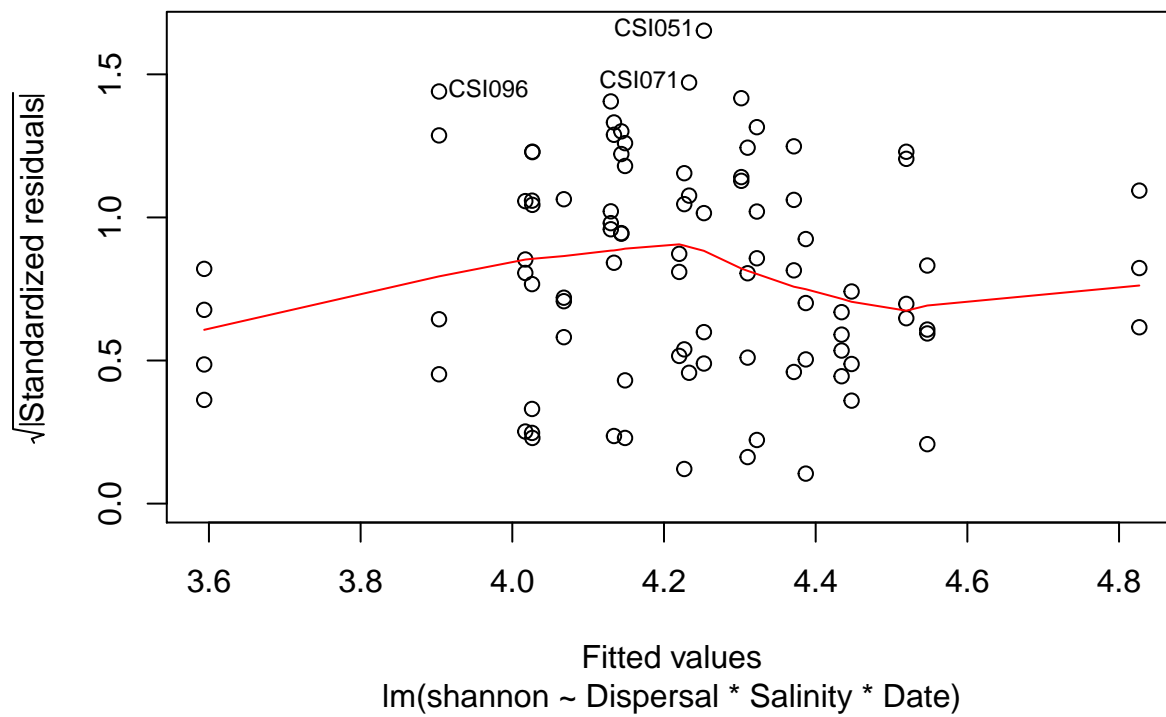
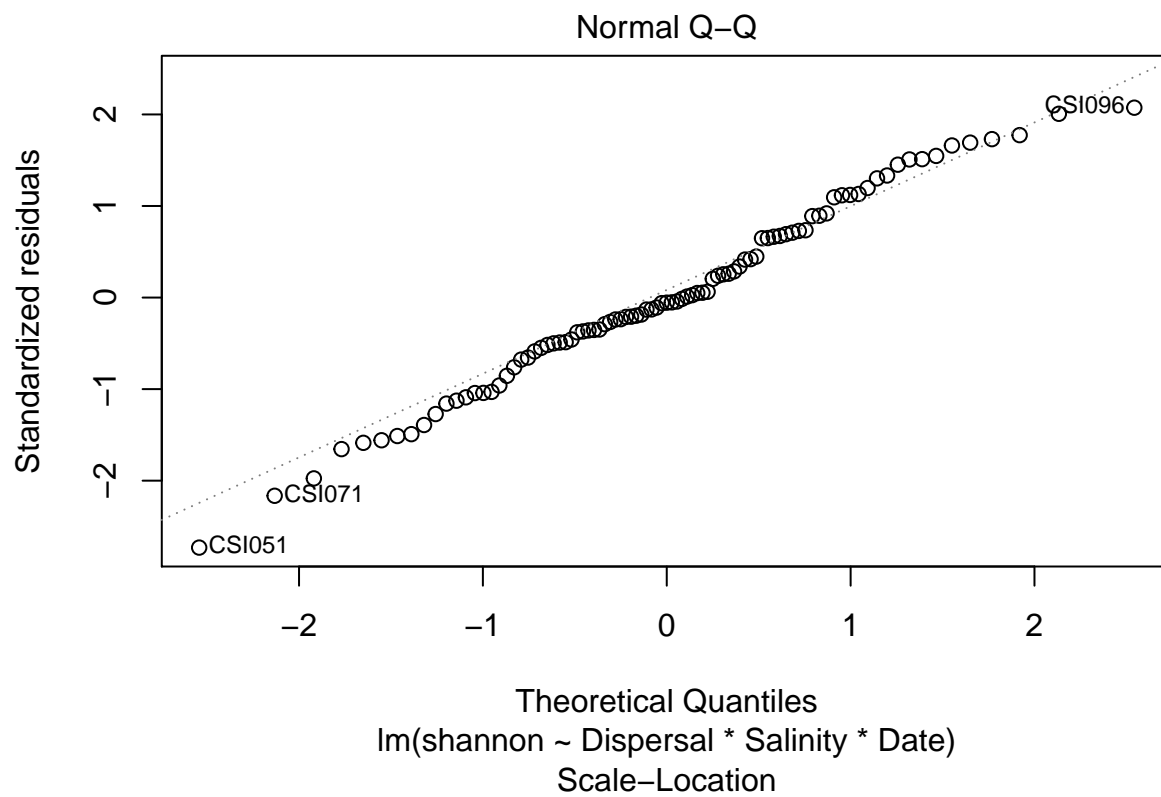
Testing salinity x dispersal influence on BACTERIAL DIVERSITY

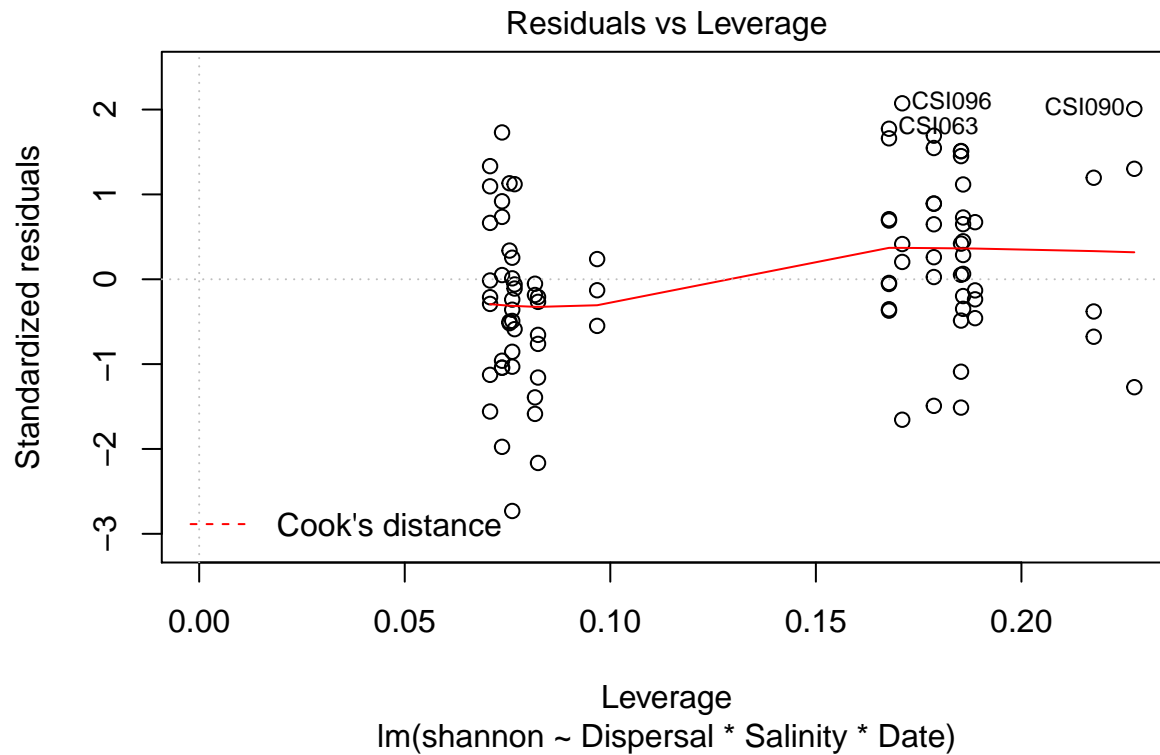
```

# run full parametric statistical model
shannon.lm <- lm(shannon ~ Dispersal*Salinity*Date, data = csi_otu.div)
plot(shannon.lm)

```







```
shannon.lm
```

```
##
## Call:
## lm(formula = shannon ~ Dispersal * Salinity * Date, data = csi_otu.div)
##
## Coefficients:
##              (Intercept)              Dispersal
##              2.72830              0.43271
##              Salinity              Date6/29/15
##              0.20443              0.71920
##              Date7/26/15              Dispersal:Salinity
##              1.53528              -0.05479
##              Dispersal:Date6/29/15              Dispersal:Date7/26/15
##              -0.14790              -0.34740
##              Salinity:Date6/29/15              Salinity:Date7/26/15
##              -0.07546              -0.21216
##              Dispersal:Salinity:Date6/29/15              Dispersal:Salinity:Date7/26/15
##              0.00158              0.04748
```

```
anova(shannon.lm)
```

```
## Analysis of Variance Table
##
## Response: shannon
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## Dispersal      1   0.0145  0.01448   0.0370  0.84800
## Salinity       1   0.2657  0.26573   0.6788  0.41247
## Date          2   0.5228  0.26140   0.6678  0.51573
## Dispersal:Salinity  1   0.6611  0.66114   1.6889  0.19752
## Dispersal:Date    2   0.1361  0.06807   0.1739  0.84071
```

```
## Salinity:Date          2  3.3027 1.65137  4.2185 0.01817 *
## Dispersal:Salinity:Date 2  0.2616 0.13081  0.3342 0.71695
## Residuals              79 30.9252 0.39146
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# run linear regression measured salinity used instead of 'factor' salinity
shannon.reg <- lm(shannon~Salinity_real, data = csi_otu.div)
summary(shannon.reg)
```

```
##
## Call:
## lm(formula = shannon ~ Salinity_real, data = csi_otu.div)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.63616 -0.44559  0.02797  0.45164  1.26216
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   4.13840    0.11819   35.01  <2e-16 ***
## Salinity_real  0.01265    0.01454    0.87   0.386
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6341 on 89 degrees of freedom
## Multiple R-squared:  0.008441, Adjusted R-squared:  -0.0027
## F-statistic: 0.7577 on 1 and 89 DF, p-value: 0.3864
```

```
# run for source tanks only
csi.div.source1 <- subset(csi_otu.div.source, Number == "1")
csi.div.source2 <- subset(csi_otu.div.source, Number == "2")
csi.div.source1 #salt source
```

```
##          CSI_ID      Date Date2 Replicate Number      Tank_Name
## CSI001 ECU_CSI_001 11-Jun-15      0         A      1 A1_2015-June11
## CSI012 ECU_CSI_012 11-Jun-15      0         B      1 B1_2015-June11
## CSI022 ECU_CSI_023 11-Jun-15      0         C      1 C1_2015-June11
## CSI044 ECU_CSI_221 26-Jul-15     45         A      1 A1_2015-July25
## CSI055 ECU_CSI_232 26-Jul-15     45         B      1 B1_2015-July25
## CSI065 ECU_CSI_243 26-Jul-15     45         C      1 C1_2015-July25
## CSI076 ECU_CSI_254 26-Jul-15     45         D      1 D1_2015-July25
## CSI087 ECU_CSI_089 29-Jun-15     18         A      1 A1_2015-June29
## CSI098 ECU_CSI_100 29-Jun-15     18         B      1 B1_2015-June29
## CSI108 ECU_CSI_111 29-Jun-15     18         C      1 C1_2015-June29
## CSI119 ECU_CSI_122 29-Jun-15     18         D      1 D1_2015-June29
##
##      Salinity Dispersal shannon.source richness.source J.source
## CSI001      13 Source13      4.875230      766 0.7342351
## CSI012      13 Source13      4.749902      767 0.7152193
## CSI022      13 Source13      4.668216      628 0.7247717
## CSI044      13 Source13      2.319490      206 0.4357479
## CSI055      13 Source13      4.329005      740 0.6553837
## CSI065      13 Source13      4.145018      461 0.6760503
## CSI076      13 Source13      4.805812      738 0.7278679
## CSI087      13 Source13      4.881676      770 0.7346289
## CSI098      13 Source13      4.944194      958 0.7203286
```

```
## CSI108      13 Source13      4.082716      507 0.6556961
## CSI119      13 Source13      4.374463      774 0.6577864
```

```
csi.div.source2 #fresh source
```

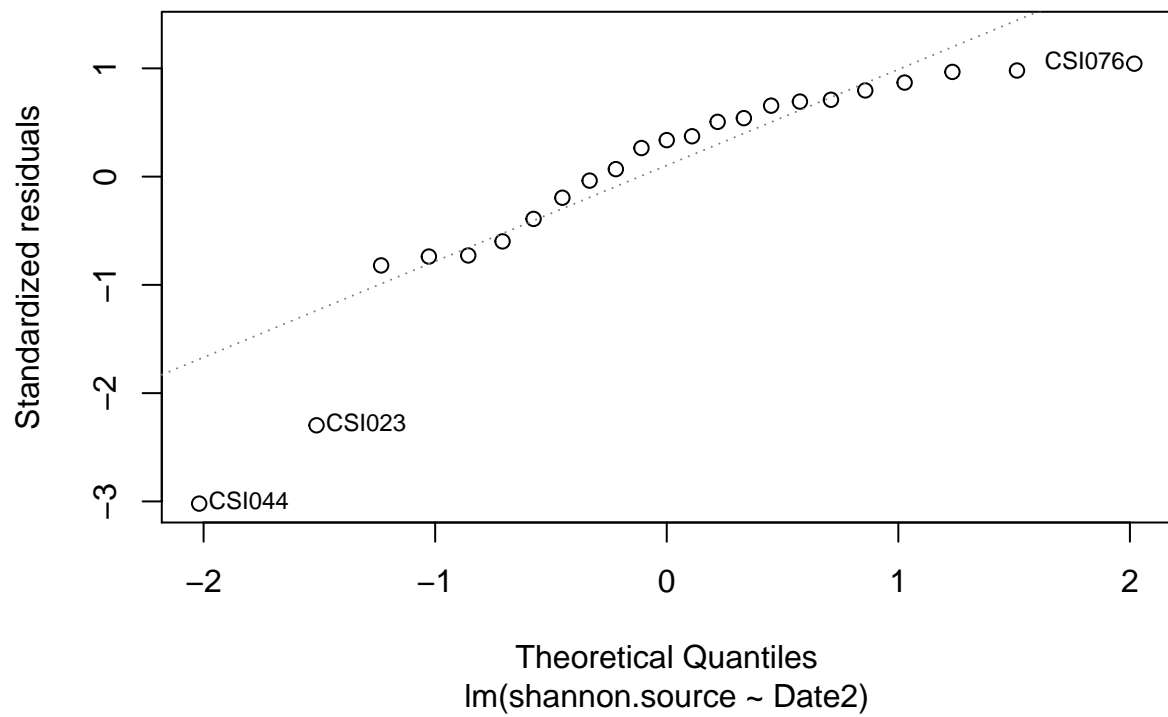
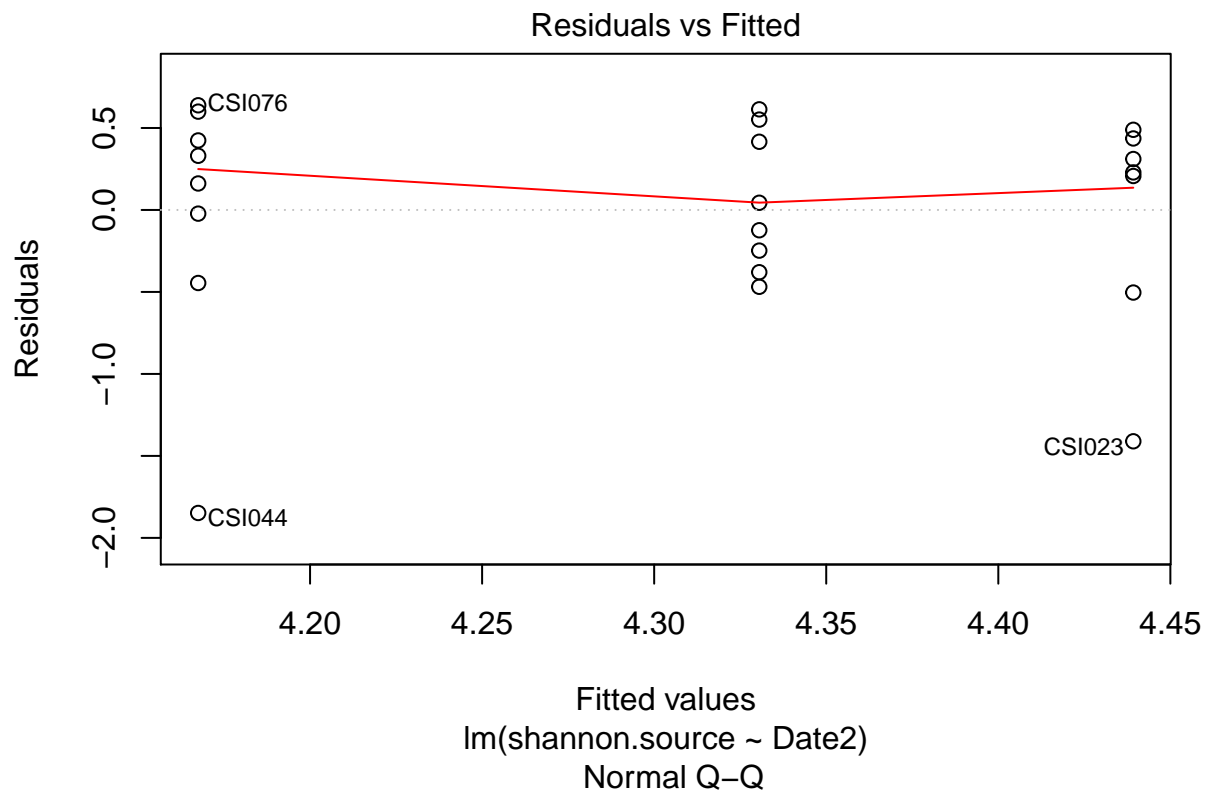
```
##          CSI_ID      Date Date2 Replicate Number      Tank_Name
## CSI002 ECU_CSI_002 11-Jun-15      0          A      2 A2_2015-June11
## CSI013 ECU_CSI_013 11-Jun-15      0          B      2 B2_2015-June11
## CSI023 ECU_CSI_024 11-Jun-15      0          C      2 C2_2015-June11
## CSI034 ECU_CSI_035 11-Jun-15      0          D      2 D2_2015-June11
## CSI045 ECU_CSI_222 26-Jul-15     45          A      2 A2_2015-July25
## CSI056 ECU_CSI_233 26-Jul-15     45          B      2 B2_2015-July25
## CSI066 ECU_CSI_244 26-Jul-15     45          C      2 C2_2015-July25
## CSI077 ECU_CSI_255 26-Jul-15     45          D      2 D2_2015-July25
## CSI088 ECU_CSI_090 29-Jun-15     18          A      2 A2_2015-June29
## CSI099 ECU_CSI_101 29-Jun-15     18          B      2 B2_2015-June29
## CSI109 ECU_CSI_112 29-Jun-15     18          C      2 C2_2015-June29
## CSI120 ECU_CSI_123 29-Jun-15     18          D      2 D2_2015-June29
##          Salinity Dispersal shannon.source richness.source J.source
## CSI002          0 Source0      3.935560      629 0.6108708
## CSI013          0 Source0      4.646364      766 0.6997666
## CSI023          0 Source0      3.028280      305 0.5296948
## CSI034          0 Source0      4.928134      934 0.7206554
## CSI045          0 Source0      3.721967      526 0.5942408
## CSI056          0 Source0      4.591572      658 0.7075708
## CSI066          0 Source0      4.497962      622 0.6993828
## CSI077          0 Source0      4.767109      689 0.7294465
## CSI088          0 Source0      3.862036      523 0.6169799
## CSI099          0 Source0      4.746454      716 0.7221926
## CSI109          0 Source0      4.206826      620 0.6544426
## CSI120          0 Source0      3.950825      464 0.6434690
```

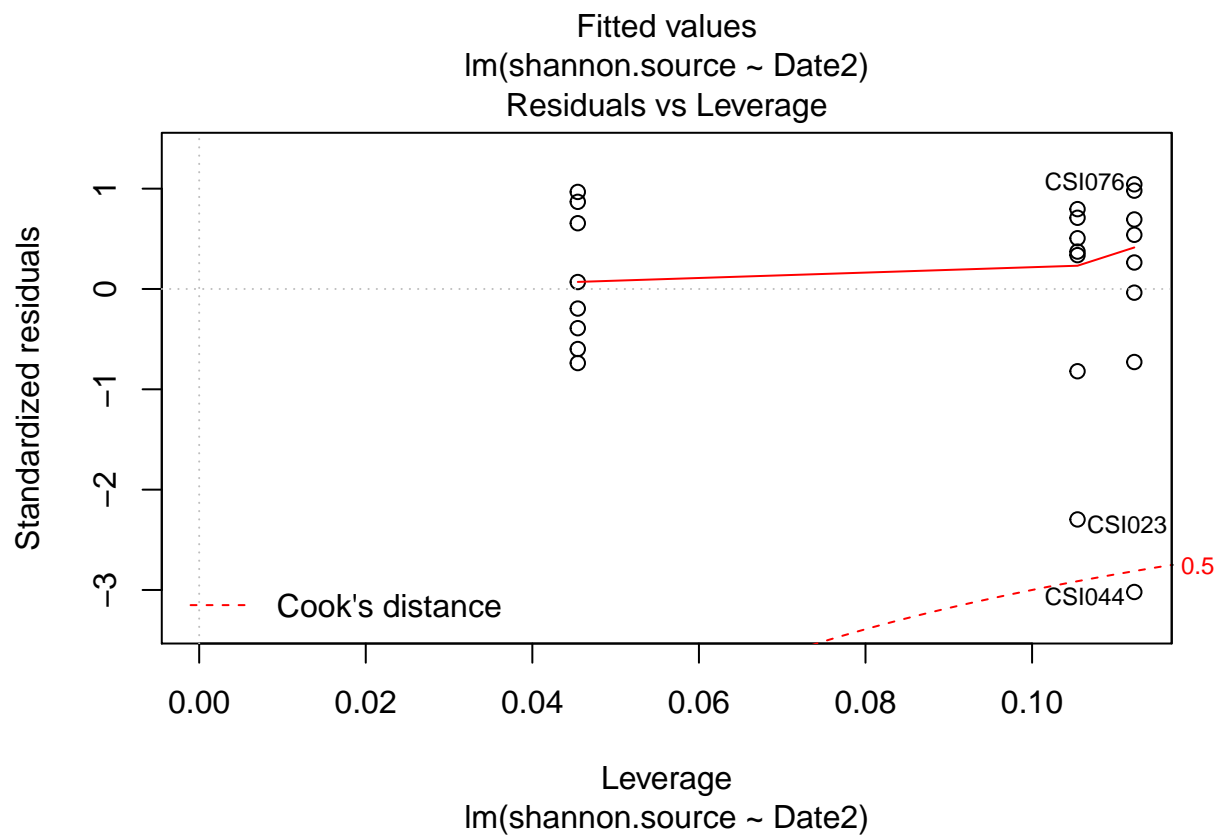
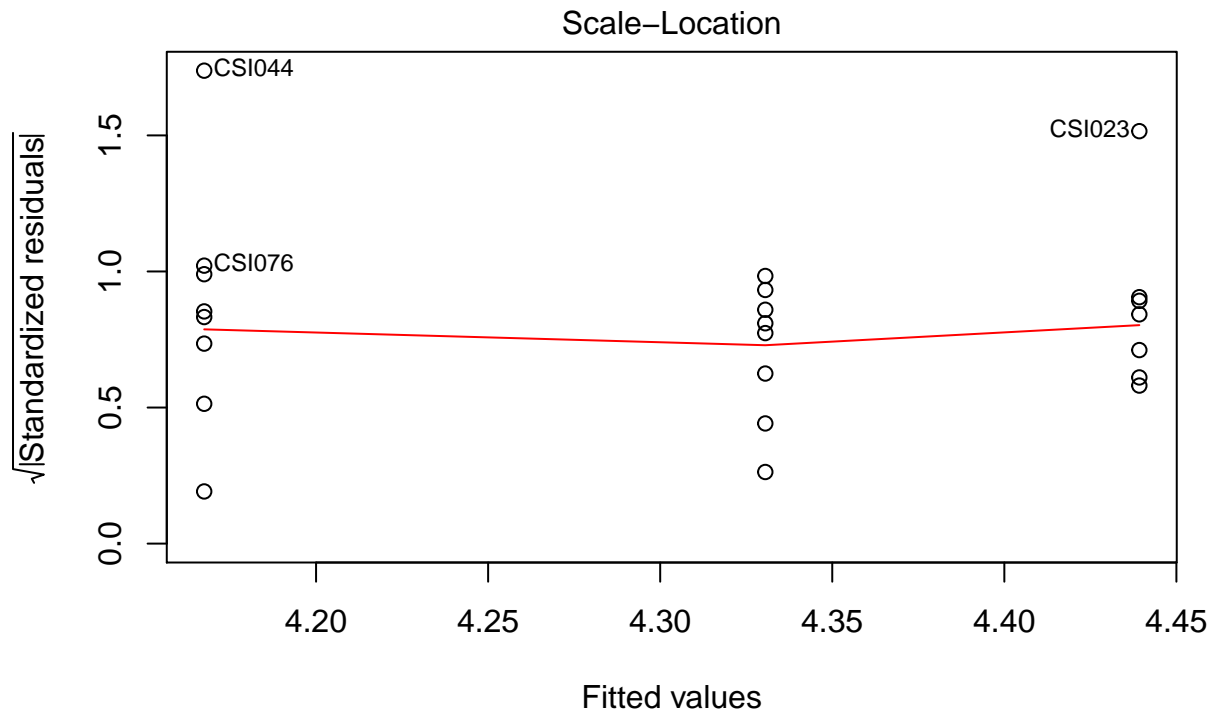
```
csi.div.source <- rbind(csi.div.source1,csi.div.source2)
dim(csi.div.source)
```

```
## [1] 23 11
```

```
Number1 <- as.factor(csi.div.source$Number)
```

```
shannon.lm.source <- lm(shannon.source ~ Date2, data = csi.div.source)
plot(shannon.lm.source)
```





```
summary(shannon.lm.source)
```

```
##
## Call:
## lm(formula = shannon.source ~ Date2, data = csi.div.source)
##
```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8480 -0.3138  0.2071  0.4300  0.6383
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.439233   0.210899  21.049 1.35e-15 ***
## Date2        -0.006039   0.007378  -0.818   0.422
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6494 on 21 degrees of freedom
## Multiple R-squared:  0.03091,    Adjusted R-squared:  -0.01523
## F-statistic: 0.6699 on 1 and 21 DF,  p-value: 0.4223
```

```
shannon.lm.source
```

```
##
## Call:
## lm(formula = shannon.source ~ Date2, data = csi.div.source)
##
## Coefficients:
## (Intercept)      Date2
##    4.439233    -0.006039
```

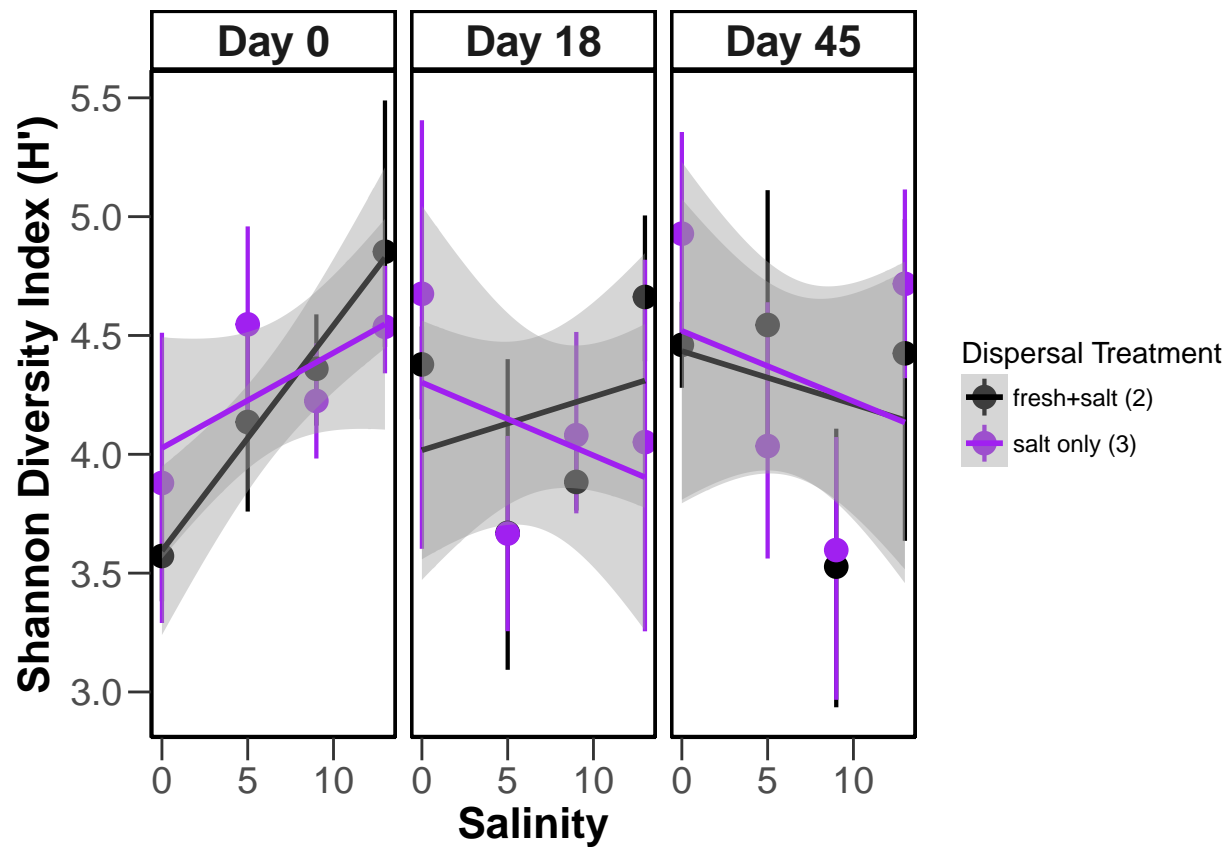
```
anova(shannon.lm.source)
```

```
## Analysis of Variance Table
##
## Response: shannon.source
##           Df Sum Sq Mean Sq F value Pr(>F)
## Date2      1  0.2825  0.28254   0.6699 0.4223
## Residuals 21  8.8573  0.42178
```

```
date_1 <- as.factor(design.ns.final$Date2)
labels <- c("0"="Day 0", "18"="Day 18", "45"="Day 45")
```

```
# Graphing Shannon Diversity - Treatment Salinity NO SOURCE
```

```
p <- ggplot(csi_otu.div, aes(x=Salinity, y=shannon, color=as.factor(Dispersal)))+ scale_color_manual(nam
p1=p+geom_smooth(method="lm")+facet_wrap(~Date2)+facet_grid(. ~ Date2, labeller=labeller(Date2 = labels
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.lin
```



```
ggsave("../figures/ms/shannon.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)
```

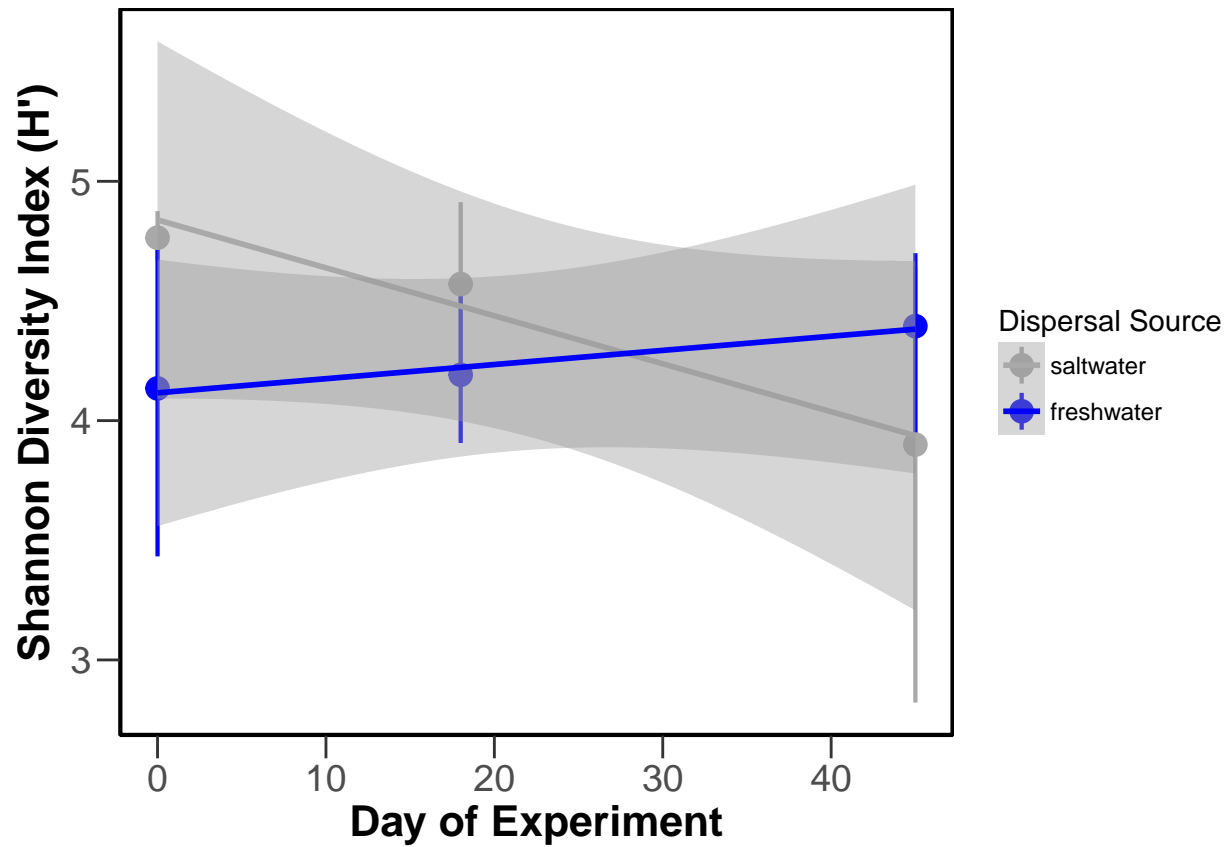
```
## Saving 6.5 x 4.5 in image
```

```
# Graphing Shannon Diversity - Treatment Salinity SOURCE ONLY
```

```
p <- ggplot(csi.div.source, aes(x=Date2, y=shannon.source, color=as.factor(Number1)))+ scale_color_manual(values=c("black", "purple"))
```

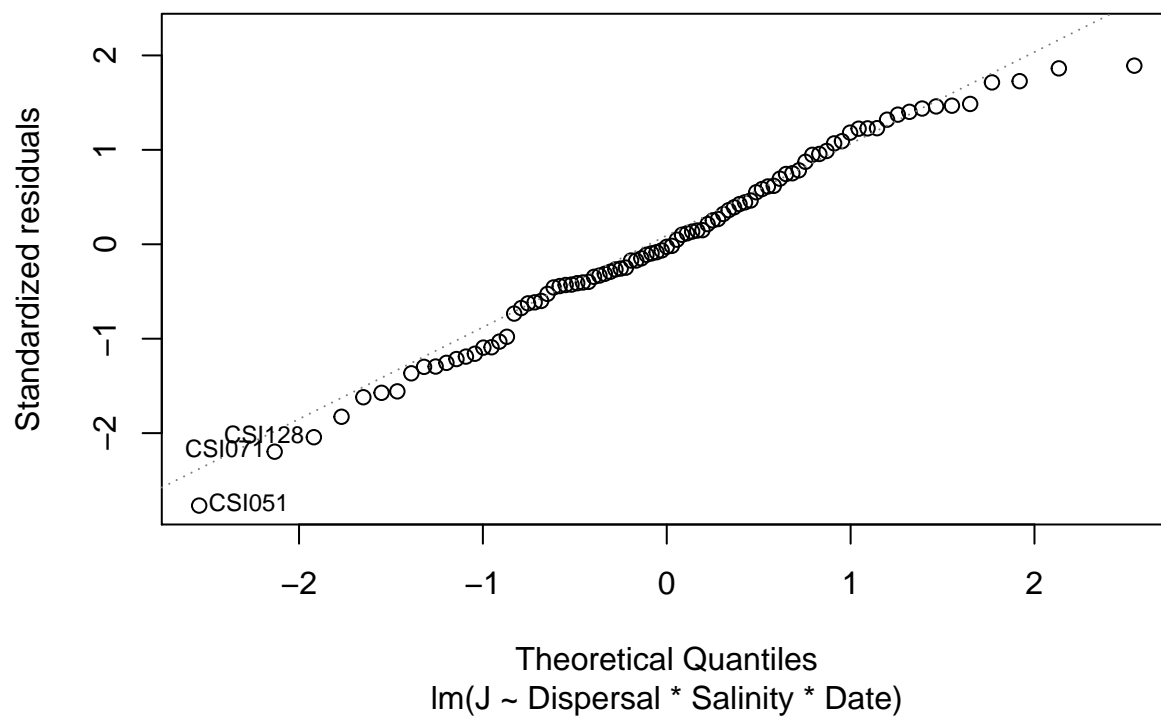
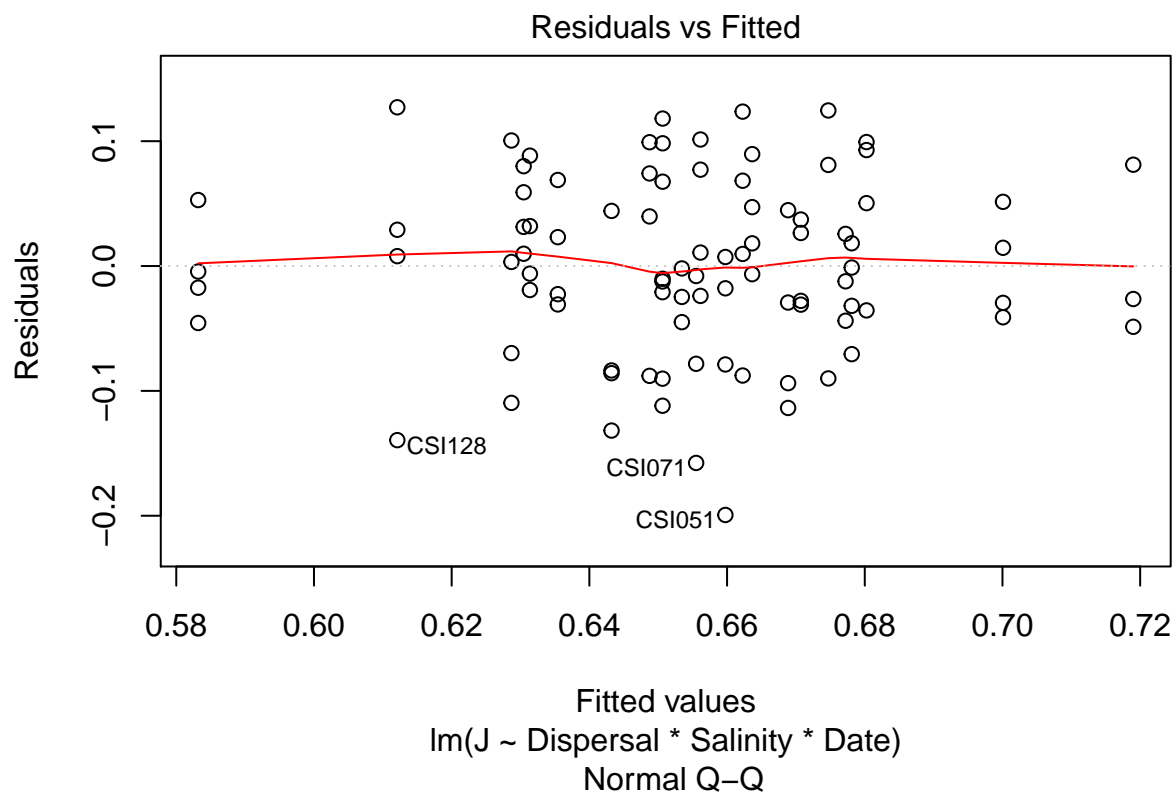
```
p1=p+geom_smooth(method="lm")
```

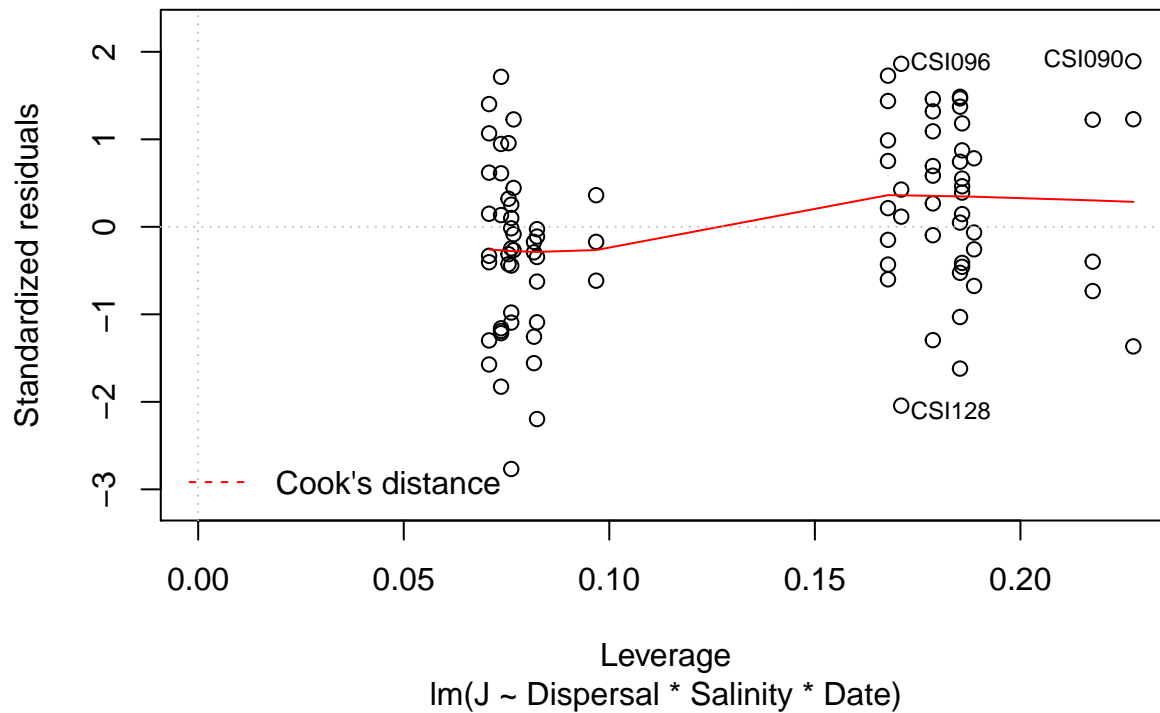
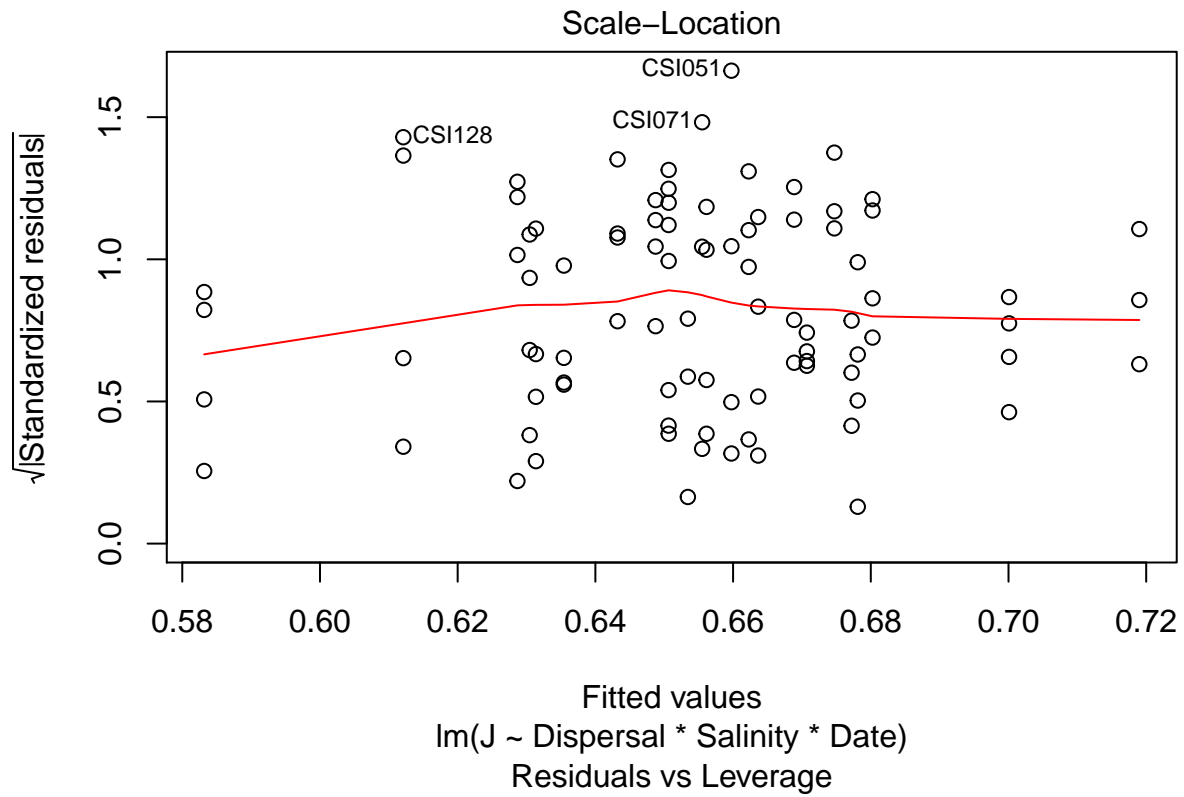
```
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.linetype = "solid")
```



```
ggsave("../figures/ms/shannon.source.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA,

## Saving 6.5 x 4.5 in image
# run full parametric statistical model
J.lm <- lm(J ~ Dispersal*Salinity*Date, data = csi_otu.div)
plot(J.lm)
```





```
anova(J.lm)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: J
```

```
##
```

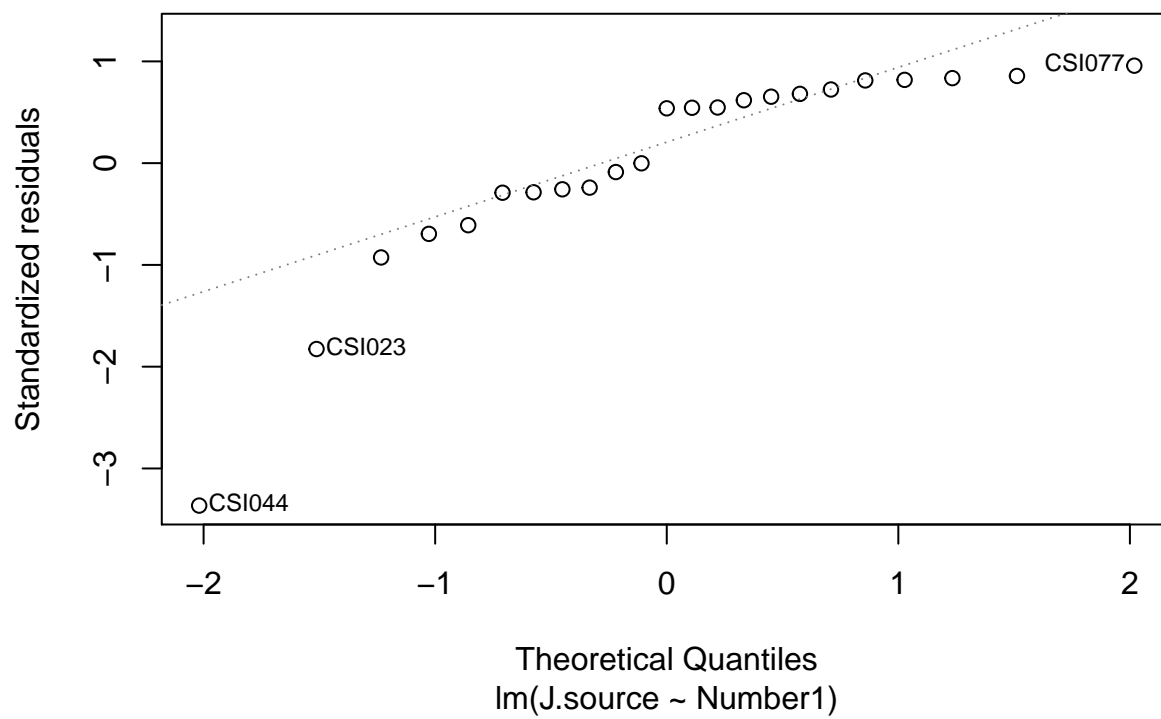
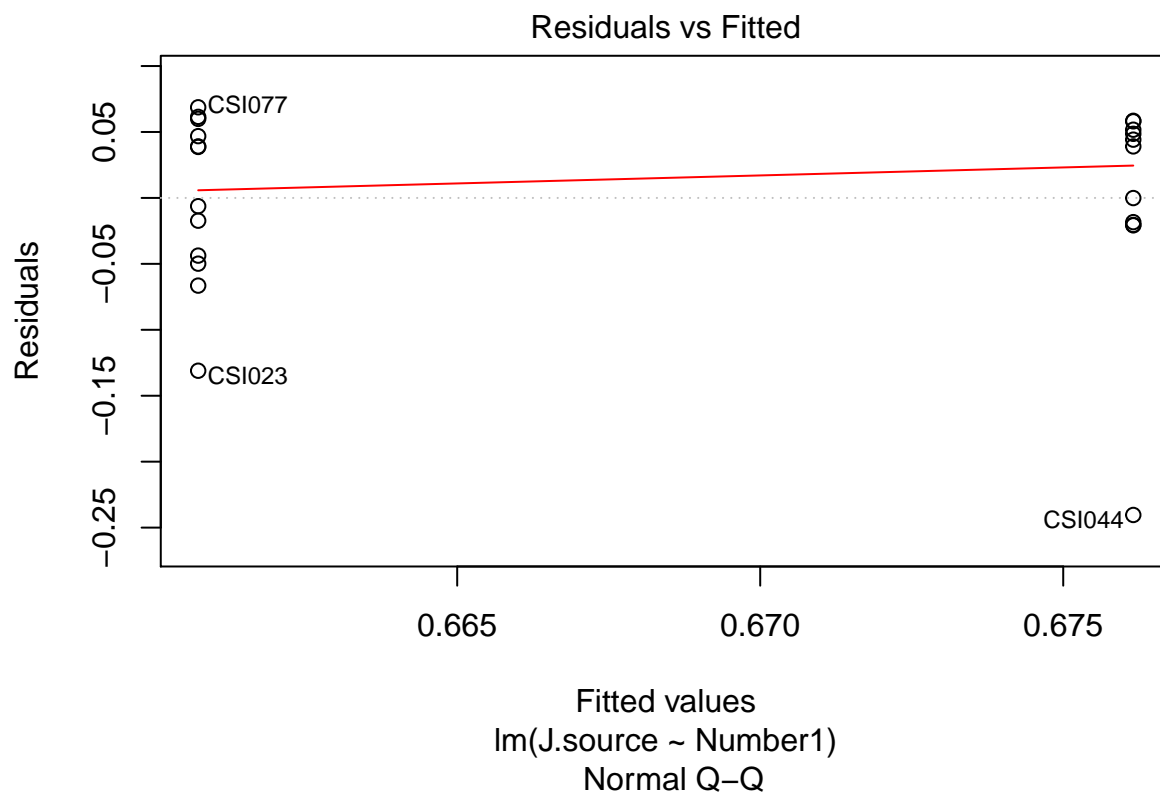
```
      Df Sum Sq Mean Sq F value Pr(>F)
```

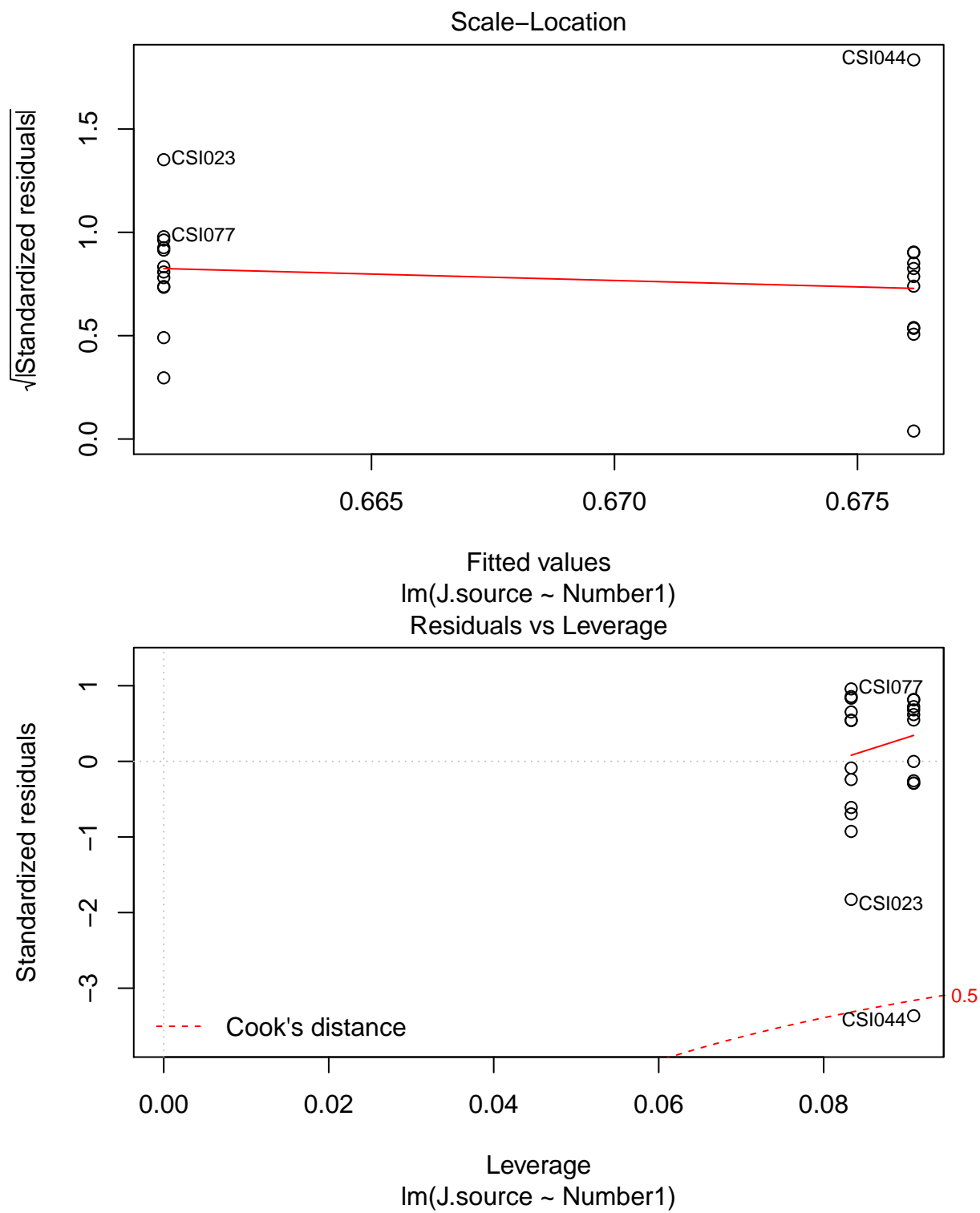
```
## Dispersal          1 0.00075 0.0007501 0.1335 0.71581
## Salinity           1 0.00491 0.0049090 0.8737 0.35279
## Date              2 0.00584 0.0029182 0.5194 0.59692
## Dispersal:Salinity 1 0.00809 0.0080888 1.4396 0.23379
## Dispersal:Date     2 0.00214 0.0010692 0.1903 0.82710
## Salinity:Date      2 0.04195 0.0209768 3.7333 0.02823 *
## Dispersal:Salinity:Date 2 0.00422 0.0021109 0.3757 0.68804
## Residuals         79 0.44389 0.0056189
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# run linear regression measured salinity used instead of 'factor' salinity
J.reg <- lm(J~Salinity_real, data = csi_otu.div)
summary(J.reg)

##
## Call:
## lm(formula = J ~ Salinity_real, data = csi_otu.div)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.197102 -0.047584 -0.001222  0.055425  0.155337
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.643325   0.014062  45.748  <2e-16 ***
## Salinity_real 0.001658   0.001729   0.958    0.34
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07544 on 89 degrees of freedom
## Multiple R-squared:  0.01022,    Adjusted R-squared:  -0.0009044
## F-statistic: 0.9187 on 1 and 89 DF,  p-value: 0.3404

# run for source tanks only
J.lm.source <- lm(J.source ~ Number1, data = csi.div.source)
plot(J.lm.source)
```





```
summary(J.lm.source)
```

```
##
## Call:
## lm(formula = J.source ~ Number1, data = csi.div.source)
##
```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.24041 -0.02062  0.03866  0.05016  0.06872
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.67616    0.02259  29.926  <2e-16 ***
## Number12     -0.01543    0.03128  -0.493    0.627
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07494 on 21 degrees of freedom
## Multiple R-squared:  0.01145,    Adjusted R-squared:  -0.03562
## F-statistic: 0.2433 on 1 and 21 DF,  p-value: 0.6269
```

```
anova(J.lm.source)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: J.source
```

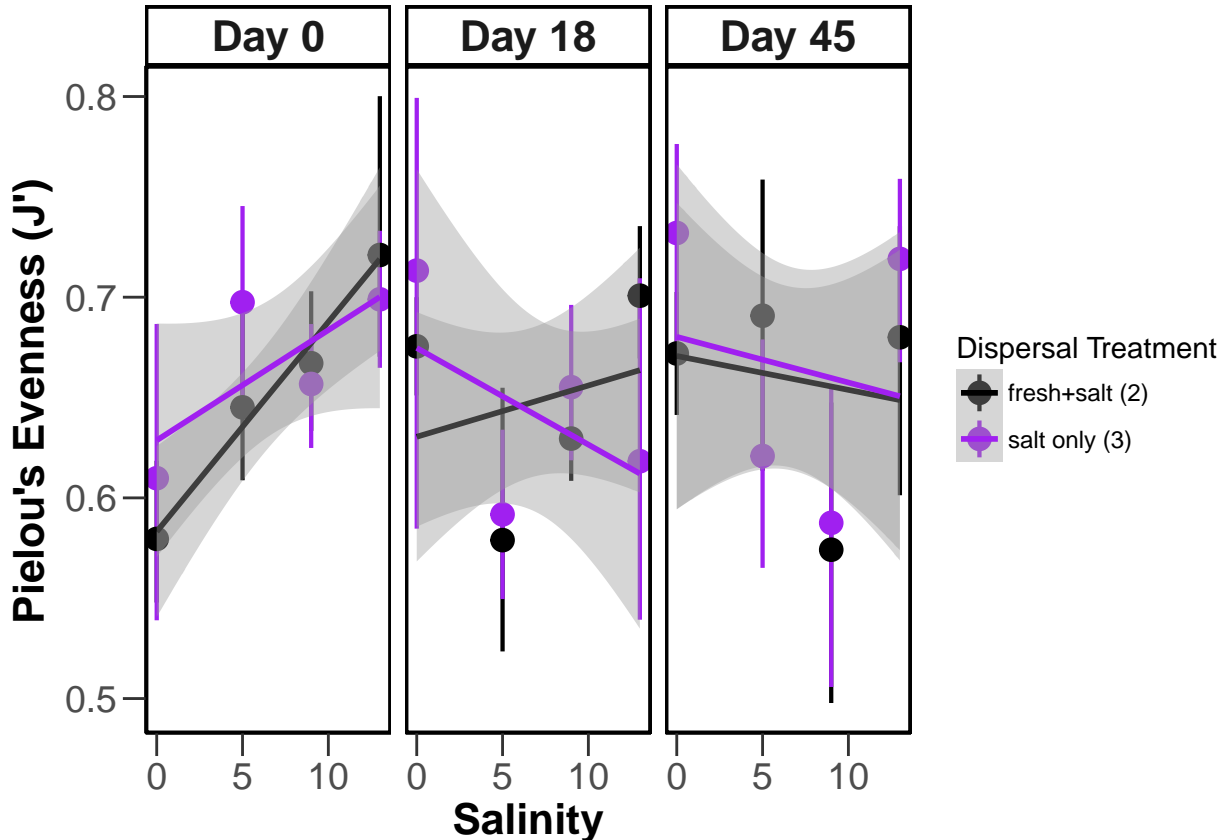
```
##           Df    Sum Sq   Mean Sq F value Pr(>F)
```

```
## Number1     1  0.001366  0.0013664   0.2433  0.6269
```

```
## Residuals  21  0.117922  0.0056153
```

```
# Graphing Pielous J - Treatment Salinity
```

```
p <- ggplot(csi_otu.div, aes(x=Salinity, y=J, color=as.factor(Dispersal))) + scale_color_manual(name="Dispersal Treatment", values=c("black", "purple"))
p1=p+geom_smooth(method="lm")+facet_wrap(~Date2)+facet_grid(. ~ Date2, labeller=labeler(Date2 = labels.Date2))
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.lin
```



```
ggsave("../figures/ms/pielousj.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)
```

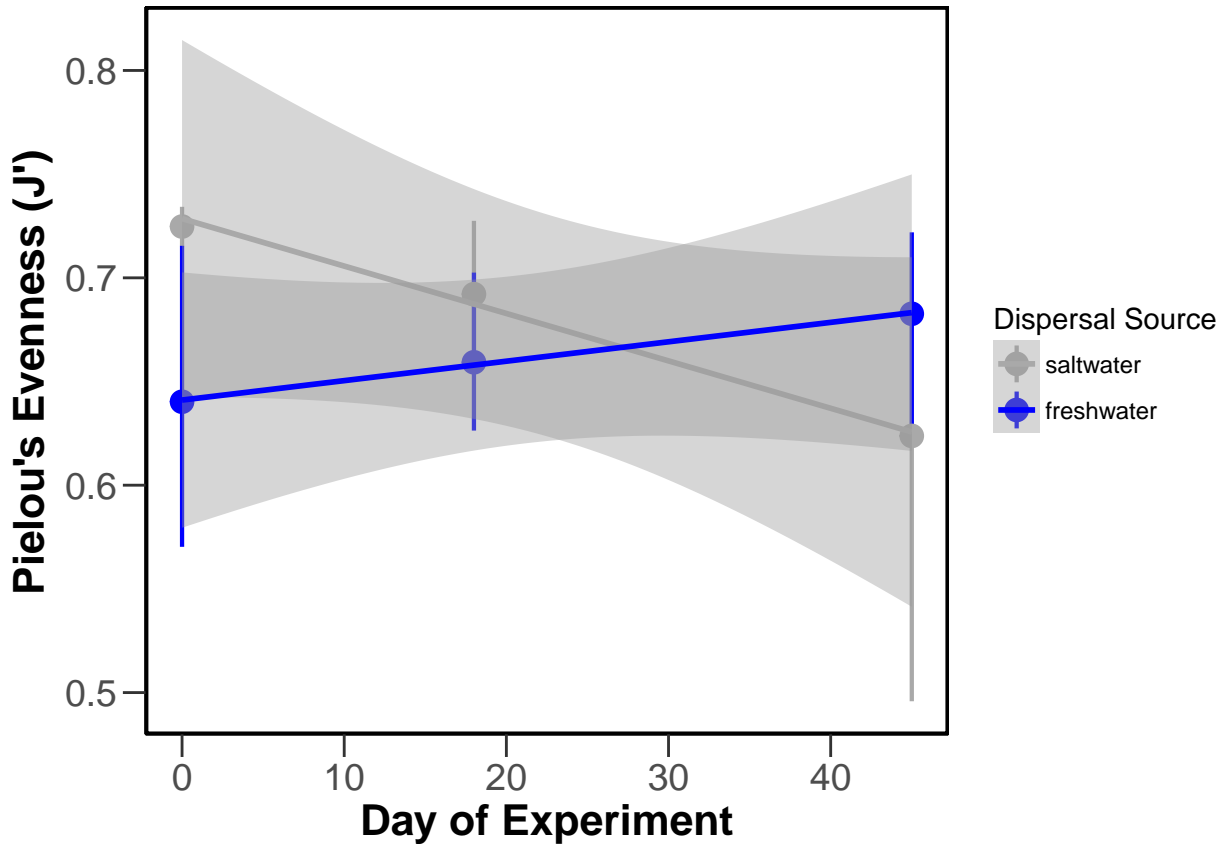
```
## Saving 6.5 x 4.5 in image
```

```
# Graphing Pielous J - Treatment Salinity SOURCE ONLY
```

```
p <- ggplot(csi.div.source, aes(x=Date2, y=J.source, color=as.factor(Number1)))+ scale_color_manual(name="Dispersal Source", values=c("saltwater", "freshwater"))
```

```
p1=p+geom_smooth(method="lm")
```

```
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.limits = c(0, 45))
```



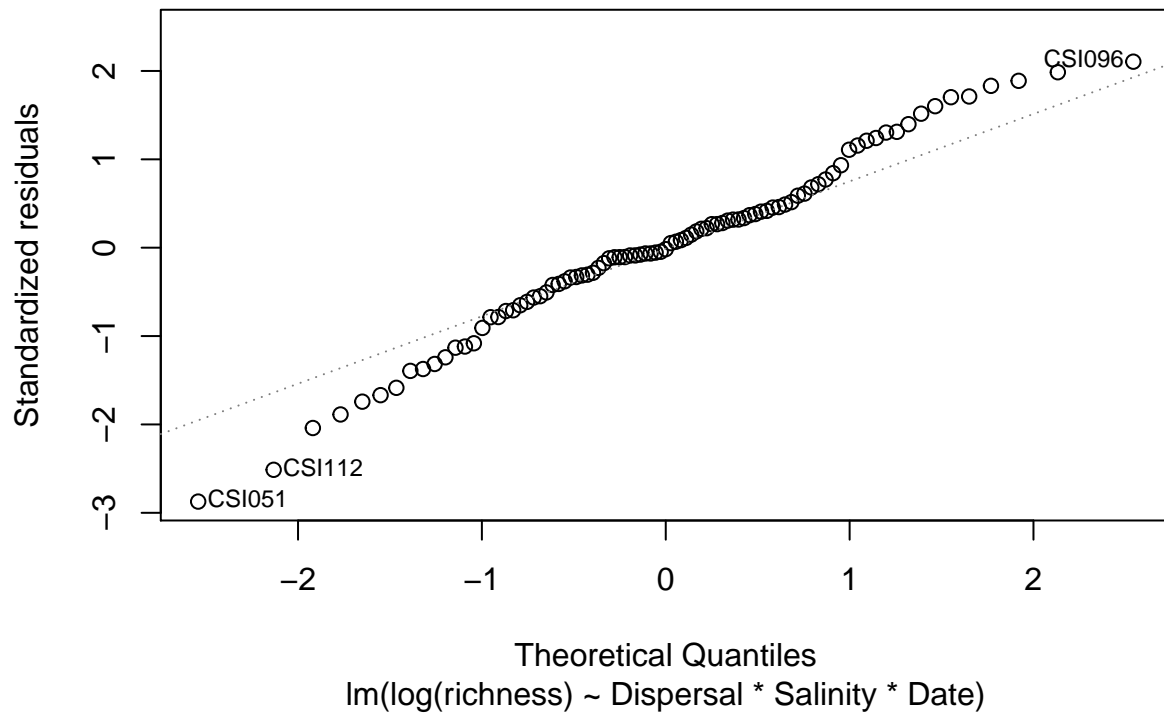
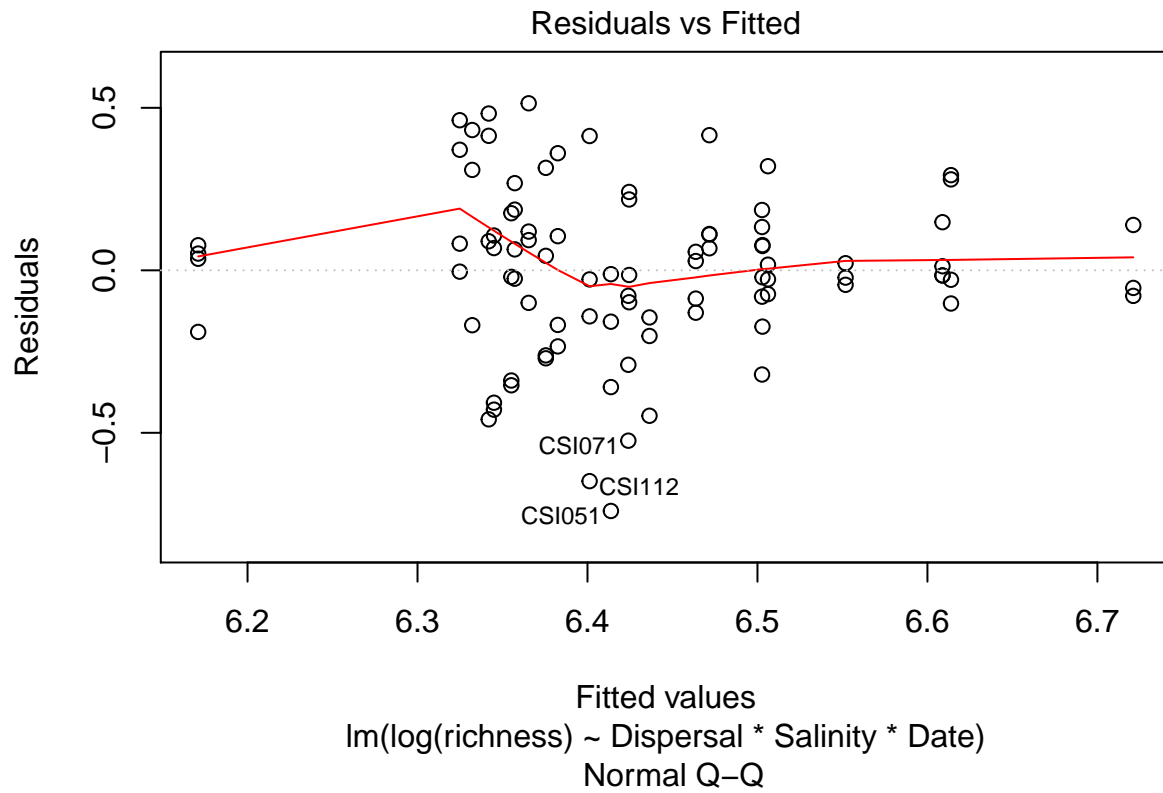
```
ggsave("../figures/ms/pielousj.source.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)
```

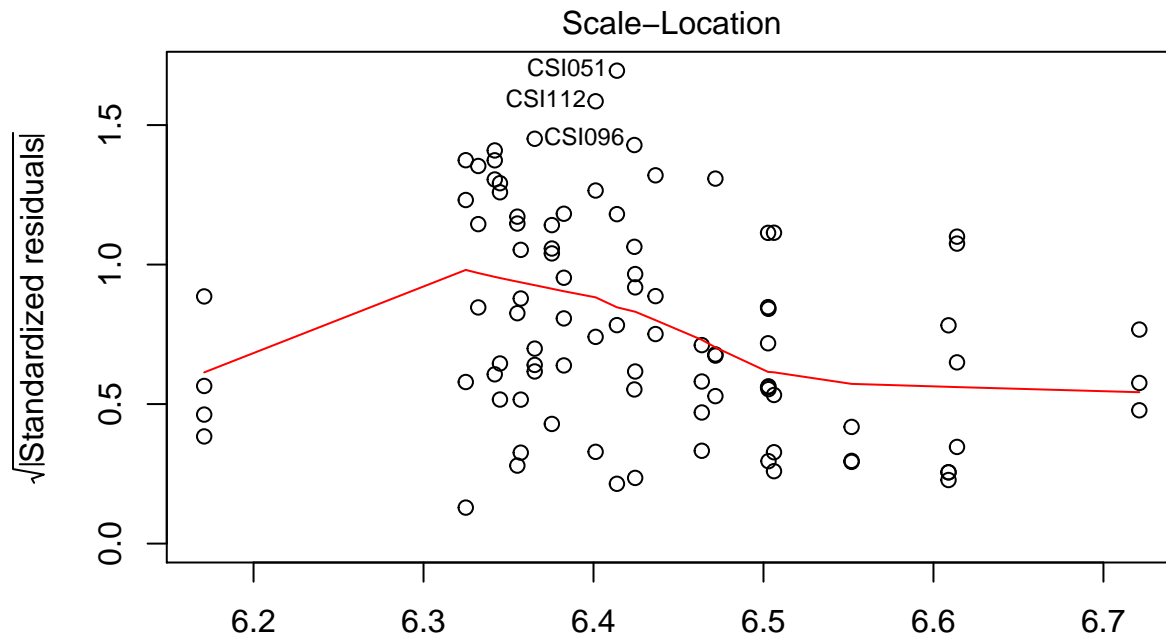
```
## Saving 6.5 x 4.5 in image
```

```
# run full parametric statistical model
```

```
richness.lm <- lm(log(richness) ~ Dispersal*Salinity*Date, data = csi_otu.div)
```

```
plot(richness.lm)
```





```
richness.lm
```

```
##
## Call:
## lm(formula = log(richness) ~ Dispersal * Salinity * Date, data = csi_otu.div)
##
## Coefficients:
```

```
##              (Intercept)                Dispersal
##              5.76188                0.20454
##              Salinity                Date6/29/15
##              0.10735                0.64534
##              Date7/26/15            Dispersal:Salinity
##              0.83697                -0.03252
##              Dispersal:Date6/29/15    Dispersal:Date7/26/15
##              -0.22955                -0.19954
##              Salinity:Date6/29/15      Salinity:Date7/26/15
##              -0.08604                -0.12450
## Dispersal:Salinity:Date6/29/15    Dispersal:Salinity:Date7/26/15
##              0.02626                0.03082
```

```
anova(richness.lm)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: log(richness)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Dispersal      1  0.0090  0.00903    0.1256  0.724026
## Salinity       1  0.0124  0.01240    0.1725  0.679010
## Date          2  0.1164  0.05819    0.8093  0.448842
## Dispersal:Salinity  1  0.0847  0.08469    1.1778  0.281109
## Dispersal:Date    2  0.0200  0.01001    0.1392  0.870242
## Salinity:Date     2  0.7868  0.39339    5.4712  0.005952 **
## Dispersal:Salinity:Date  2  0.0969  0.04846    0.6740  0.512565
## Residuals      79  5.6803  0.07190
```

```
## ---
```

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

```
# run linear regression measured salinity used instead of 'factor' salinity
```

```
richness.reg <- lm(richness~Salinity_real, data = csi_otu.div)
```

```
summary(richness.reg)
```

```
##
```

```
## Call:
```

```
## lm(formula = richness ~ Salinity_real, data = csi_otu.div)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -355.61 -120.45   -6.45   113.91   370.19
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   627.679     31.285   20.063  <2e-16 ***
## Salinity_real    2.217       3.848    0.576    0.566
```

```
## ---
```

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

```
##
```

```
## Residual standard error: 167.8 on 89 degrees of freedom
```

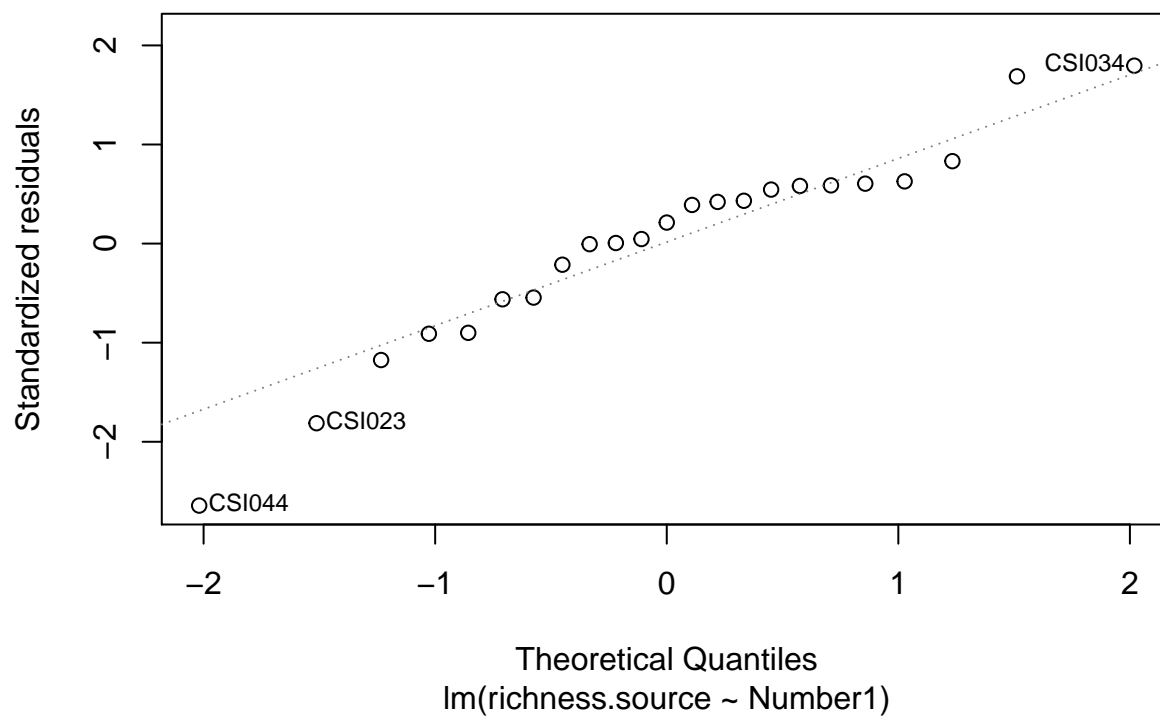
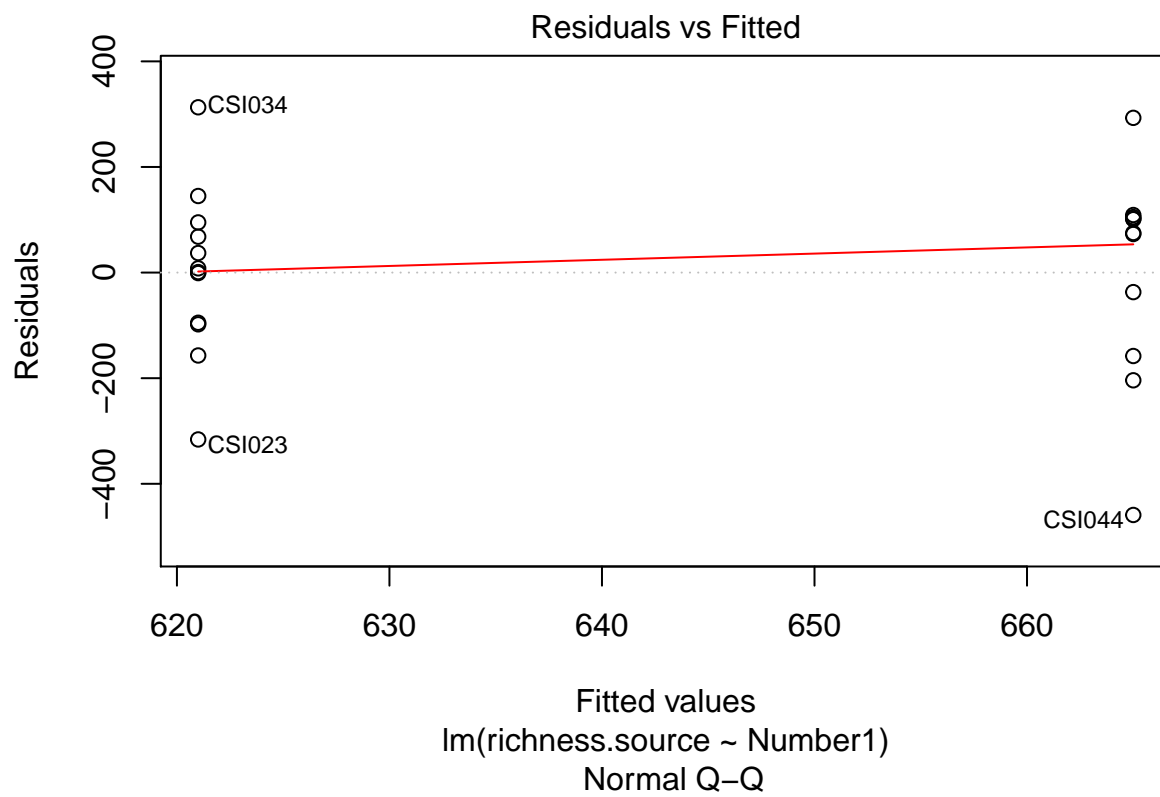
```
## Multiple R-squared:  0.003715,    Adjusted R-squared:  -0.007479
```

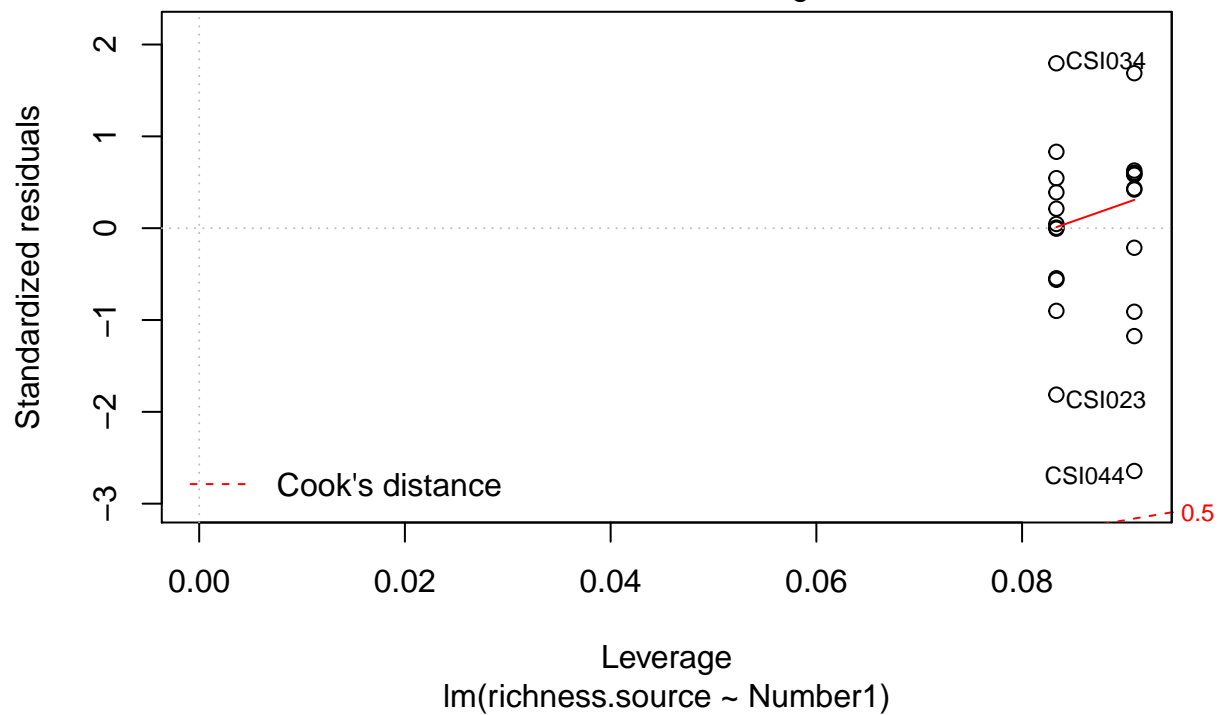
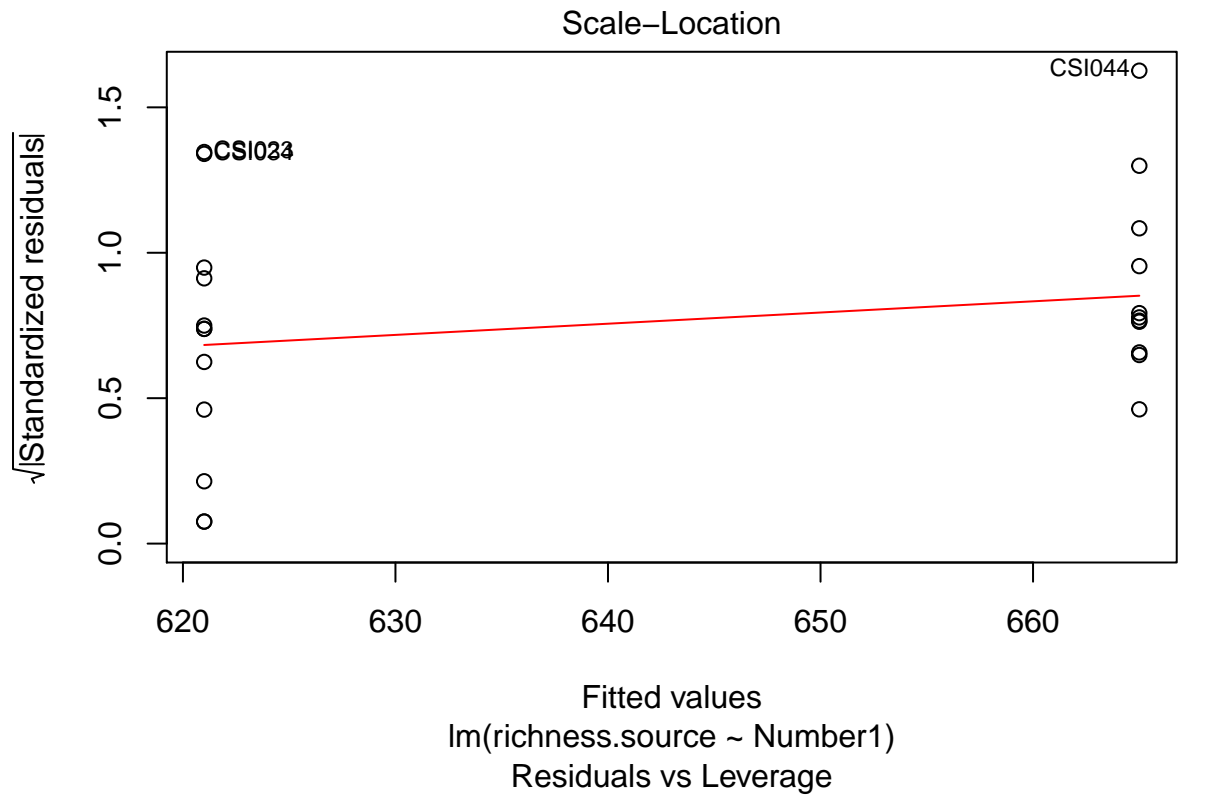
```
## F-statistic: 0.3319 on 1 and 89 DF,  p-value: 0.566
```

```
# run for source tanks only
```

```
richness.lm.source <- lm(richness.source ~ Number1, data = csi.div.source)
```

```
plot(richness.lm.source)
```





```
summary(richness.lm.source)
```

```
##
## Call:
## lm(formula = richness.source ~ Number1, data = csi.div.source)
##
```



```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -459.0  -96.5   37.0  101.5  313.0
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    665.0       54.9  12.114 6.12e-11 ***
## Number12      -44.0       76.0  -0.579   0.569
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 182.1 on 21 degrees of freedom
## Multiple R-squared:  0.01571,    Adjusted R-squared:  -0.03116
## F-statistic: 0.3352 on 1 and 21 DF,  p-value: 0.5688
```

```
richness.lm.source
```

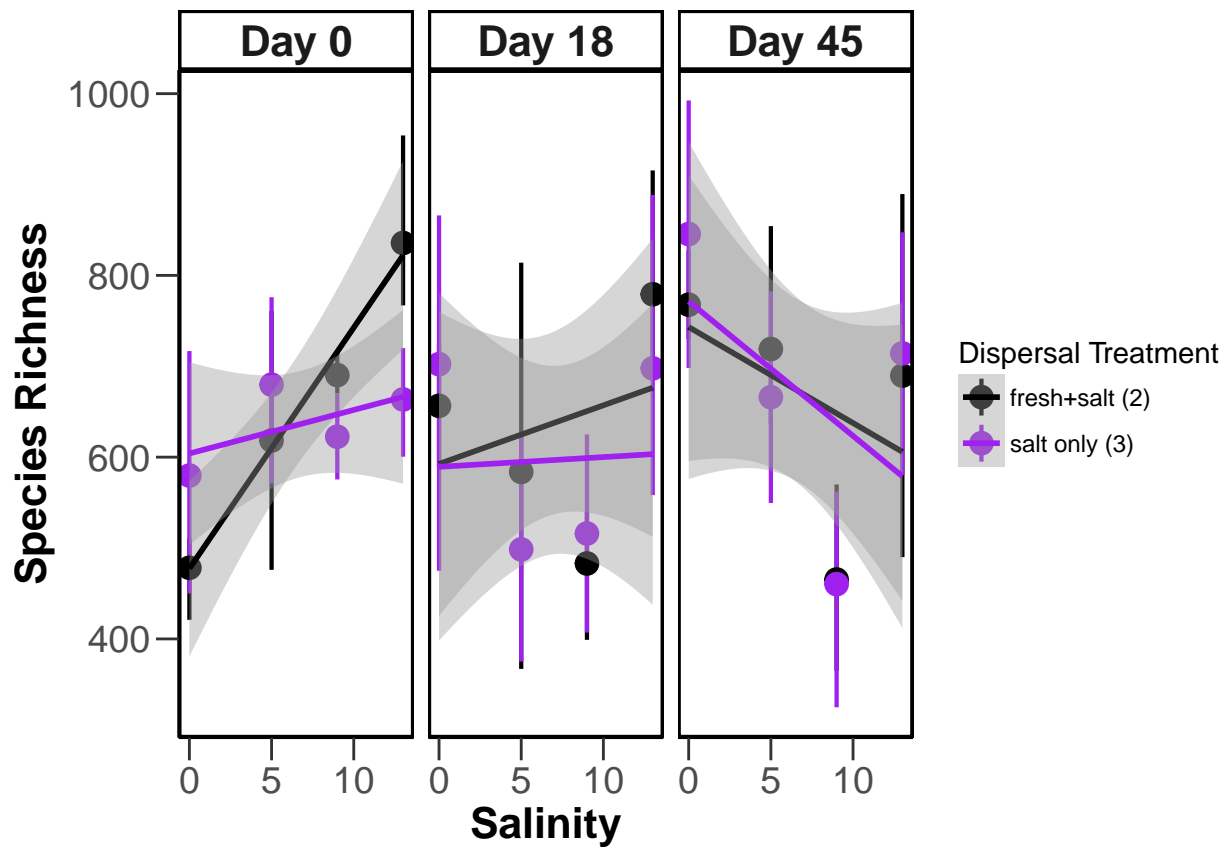
```
##
## Call:
## lm(formula = richness.source ~ Number1, data = csi.div.source)
##
## Coefficients:
## (Intercept)      Number12
##           665           -44
```

```
anova(richness.lm.source)
```

```
## Analysis of Variance Table
##
## Response: richness.source
##           Df Sum Sq Mean Sq F value Pr(>F)
## Number1    1 11111   11111   0.3352 0.5688
## Residuals 21 696156   33150
```

```
# Graphing richness - Treatment Salinity
```

```
p <- ggplot(csi_otu.div, aes(x=Salinity, y=richness, color=as.factor(Dispersal)))+ scale_color_manual(n
p1=p+geom_smooth(method="lm")+facet_wrap(~Date2)+facet_grid(. ~ Date2, labeller=labeller(Date2 = labels
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.lin
```



```
ggsave("../figures/ms/richness.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)
```

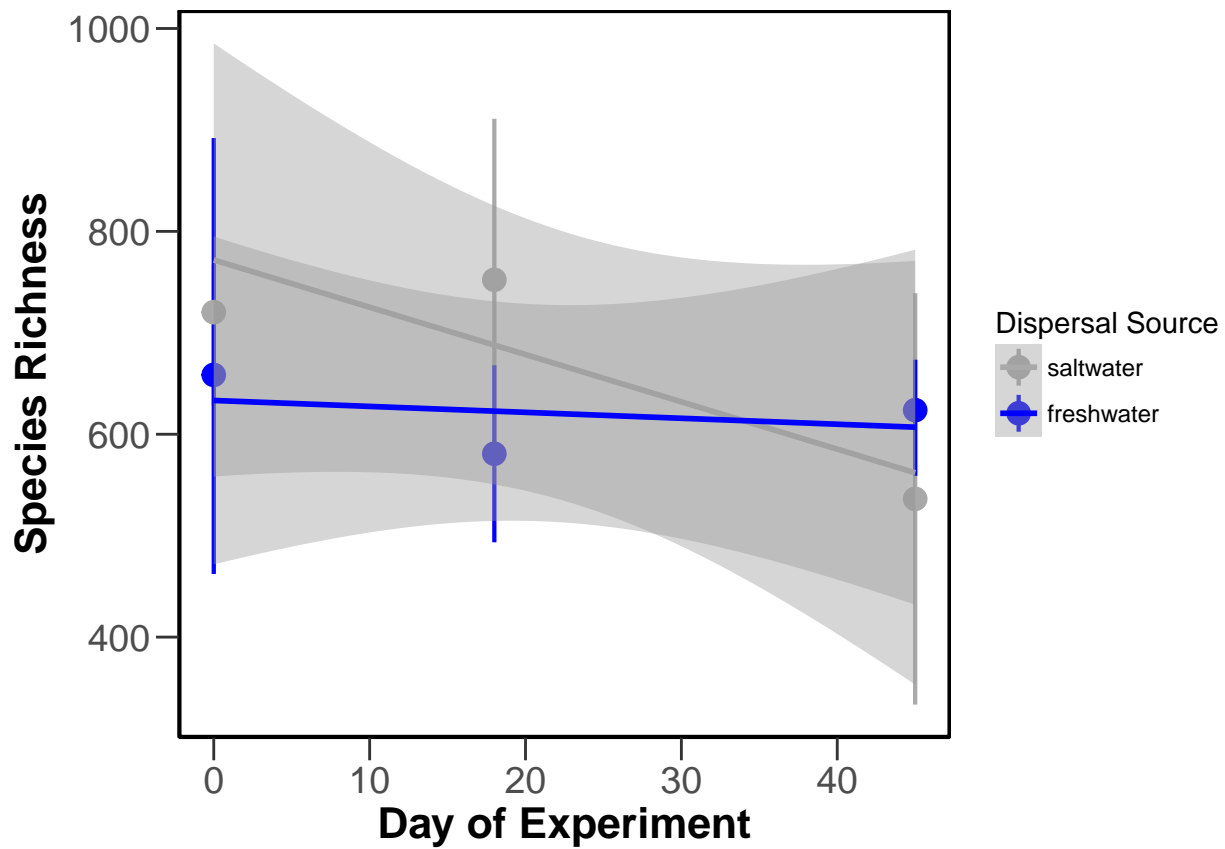
```
## Saving 6.5 x 4.5 in image
```

```
# Graphing richness - Treatment Salinity SOURCE ONLY
```

```
p <- ggplot(csi.div.source, aes(x=Date2, y=richness.source, color=as.factor(Number1)))+ scale_color_manual(values=c("black", "purple"))
```

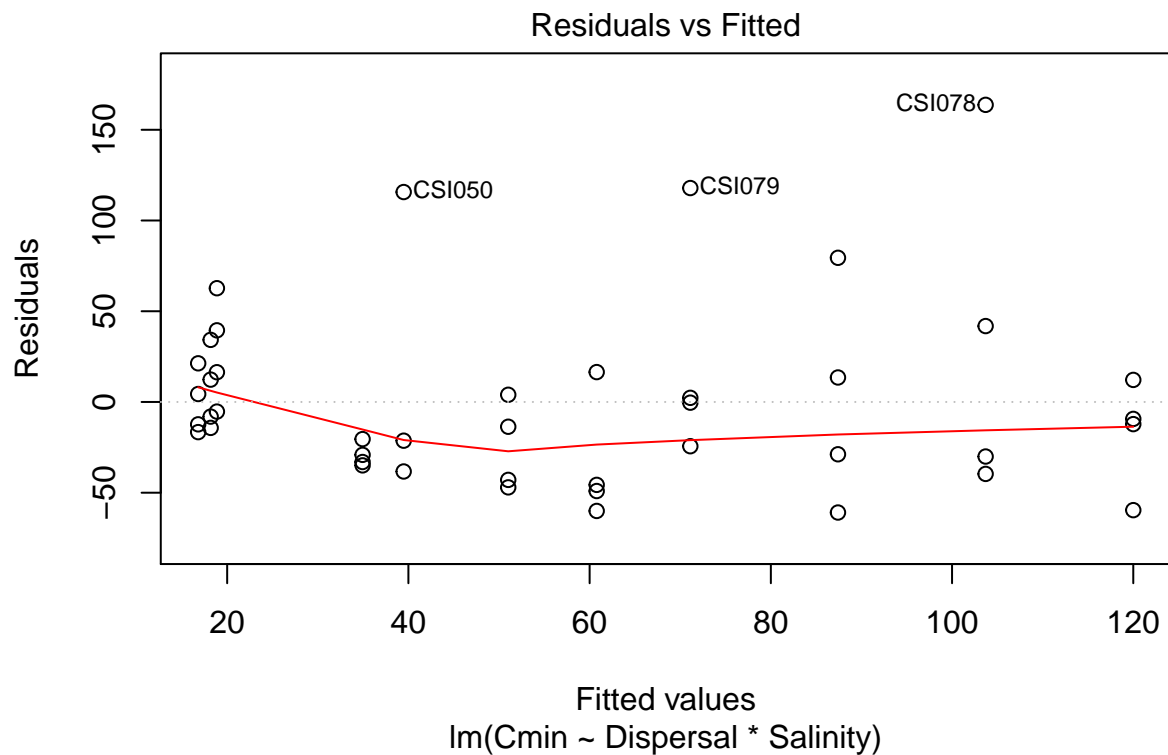
```
p1=p+geom_smooth(method="lm")
```

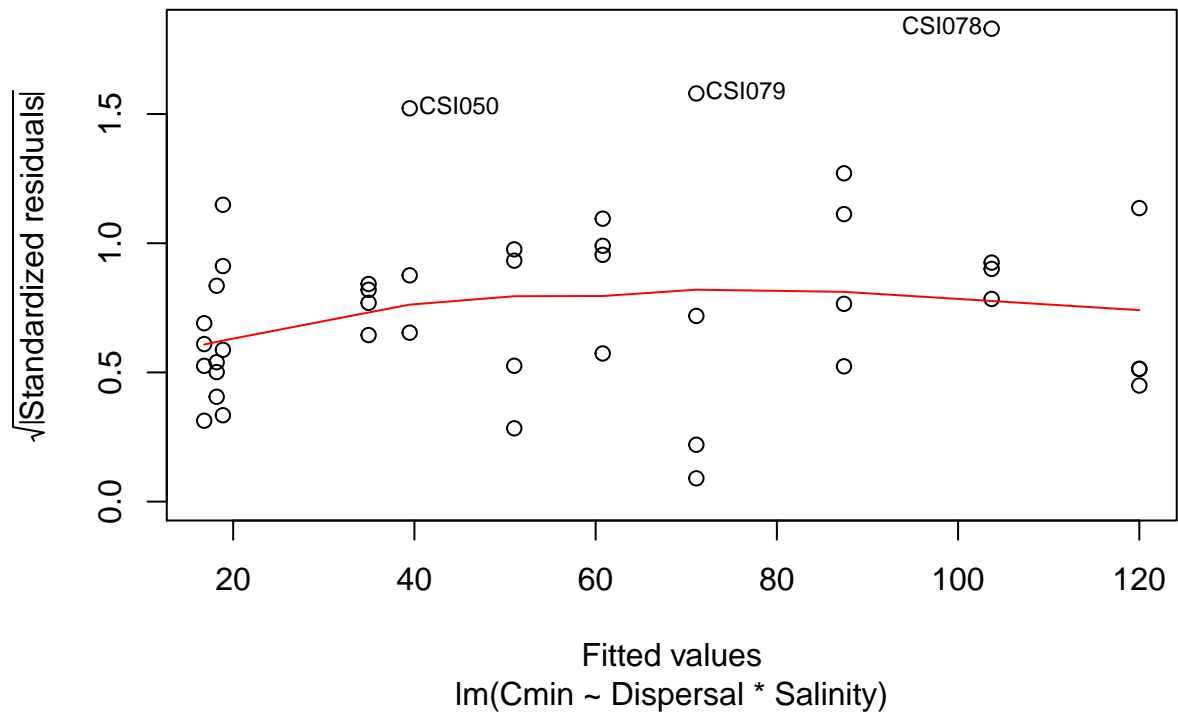
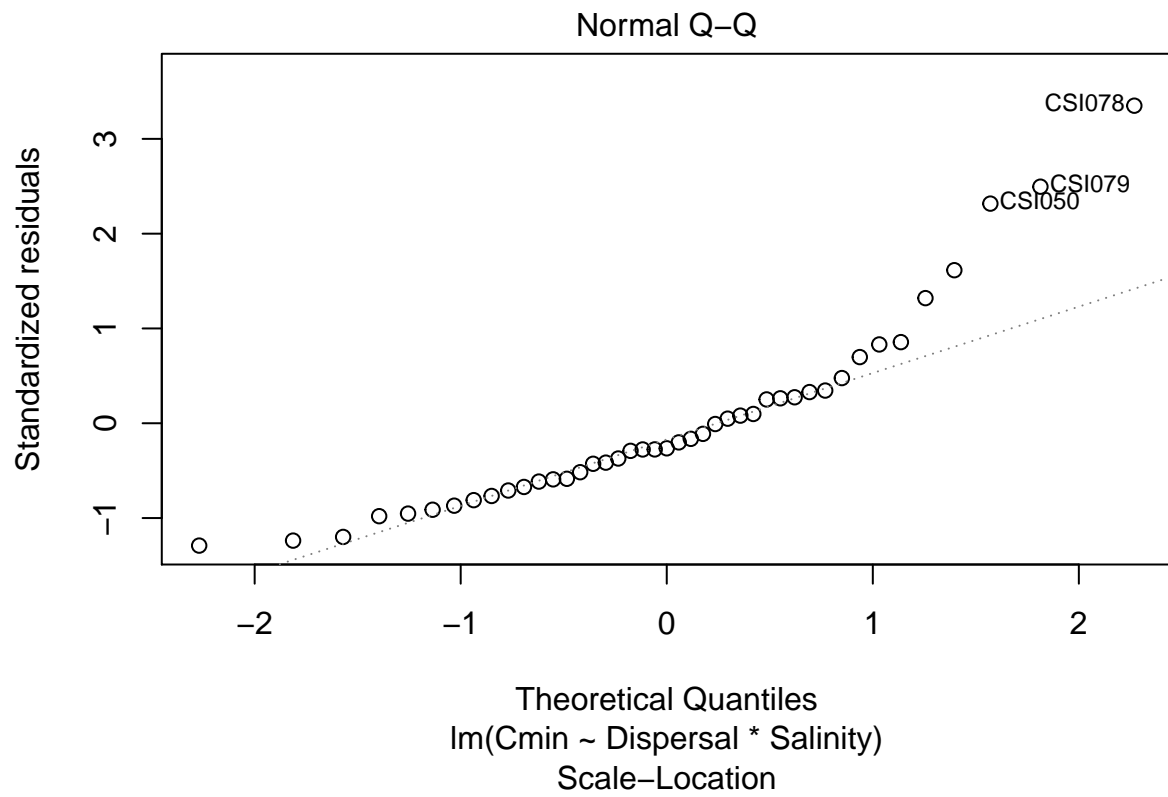
```
p1 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.limits=c(0, 10))
```

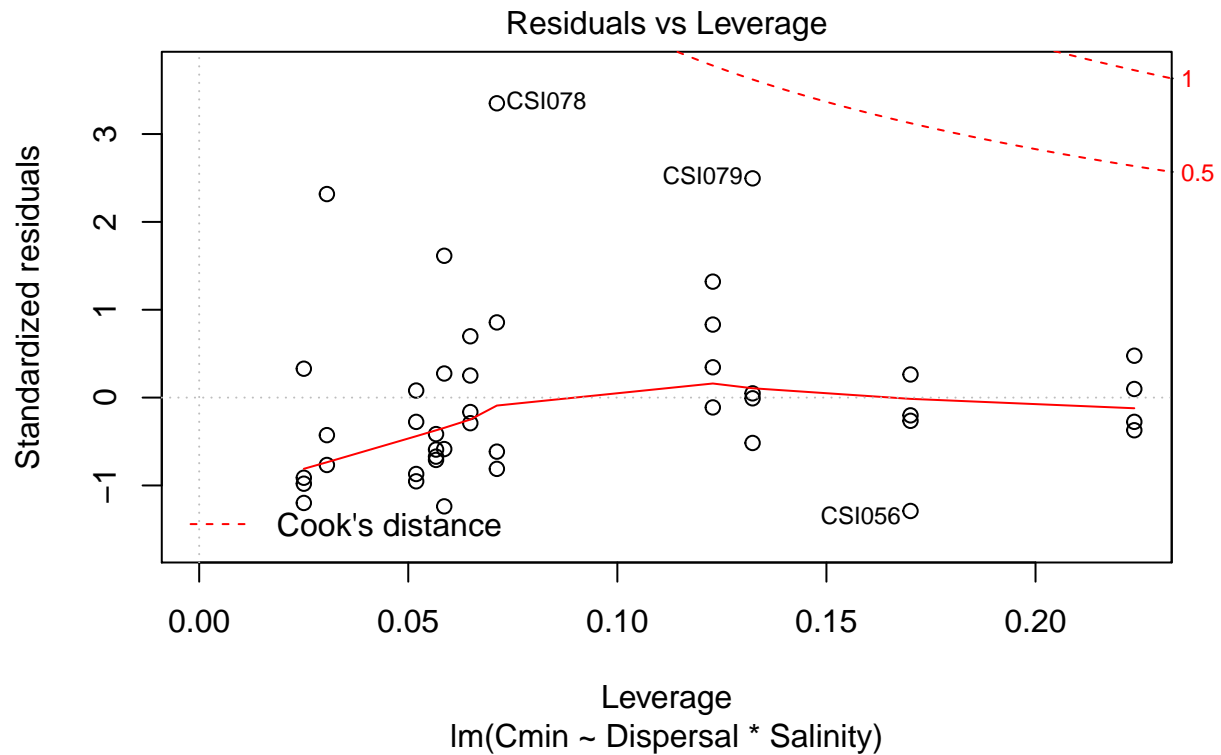


```
ggsave("../figures/ms/richness.source.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA)
```

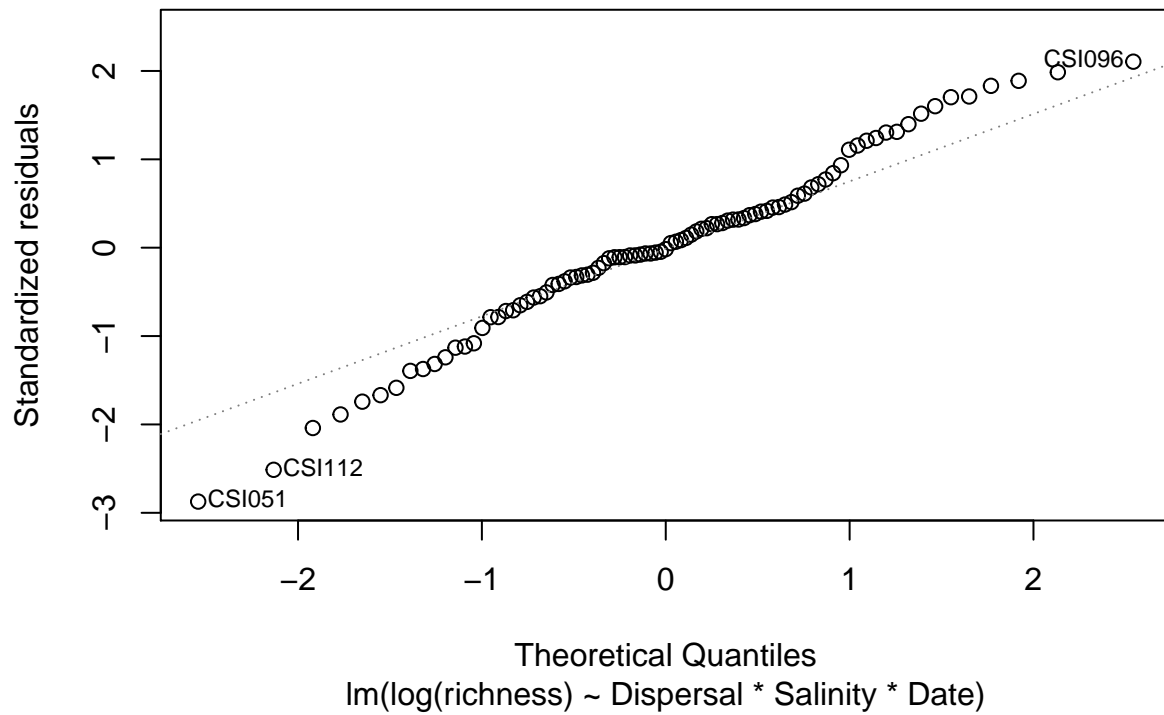
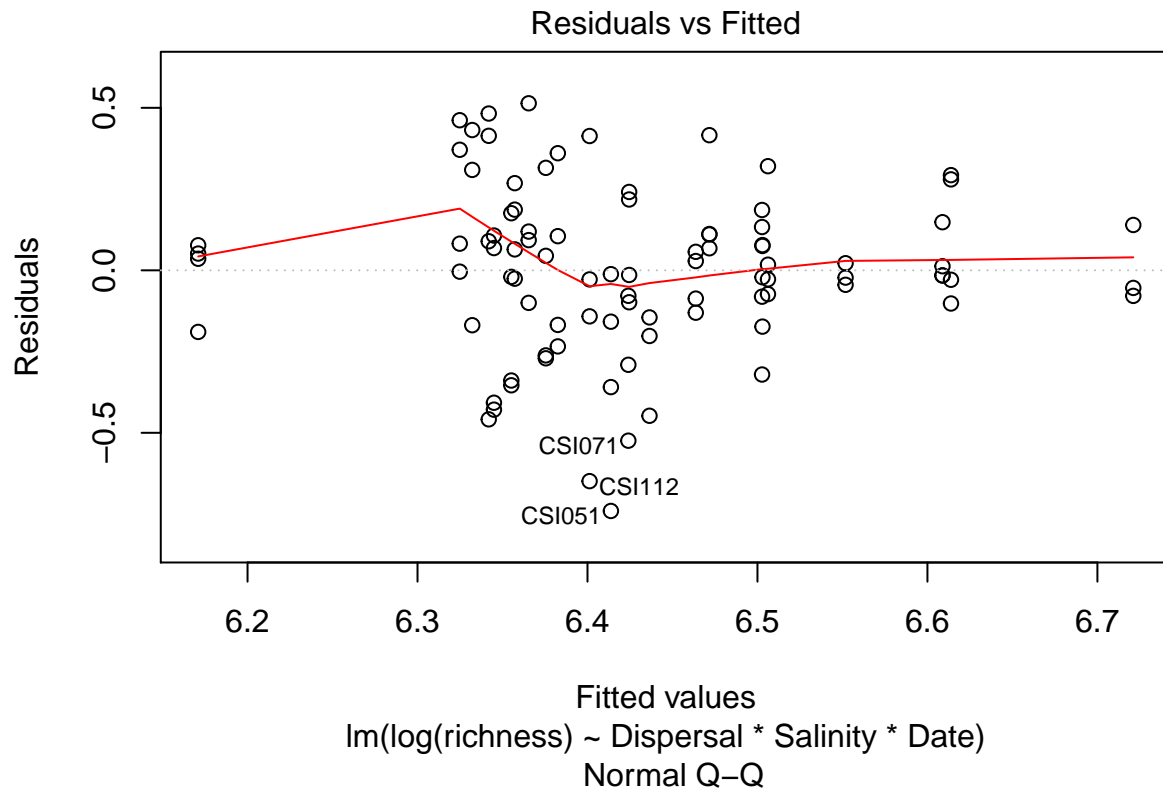
```
## Saving 6.5 x 4.5 in image
```

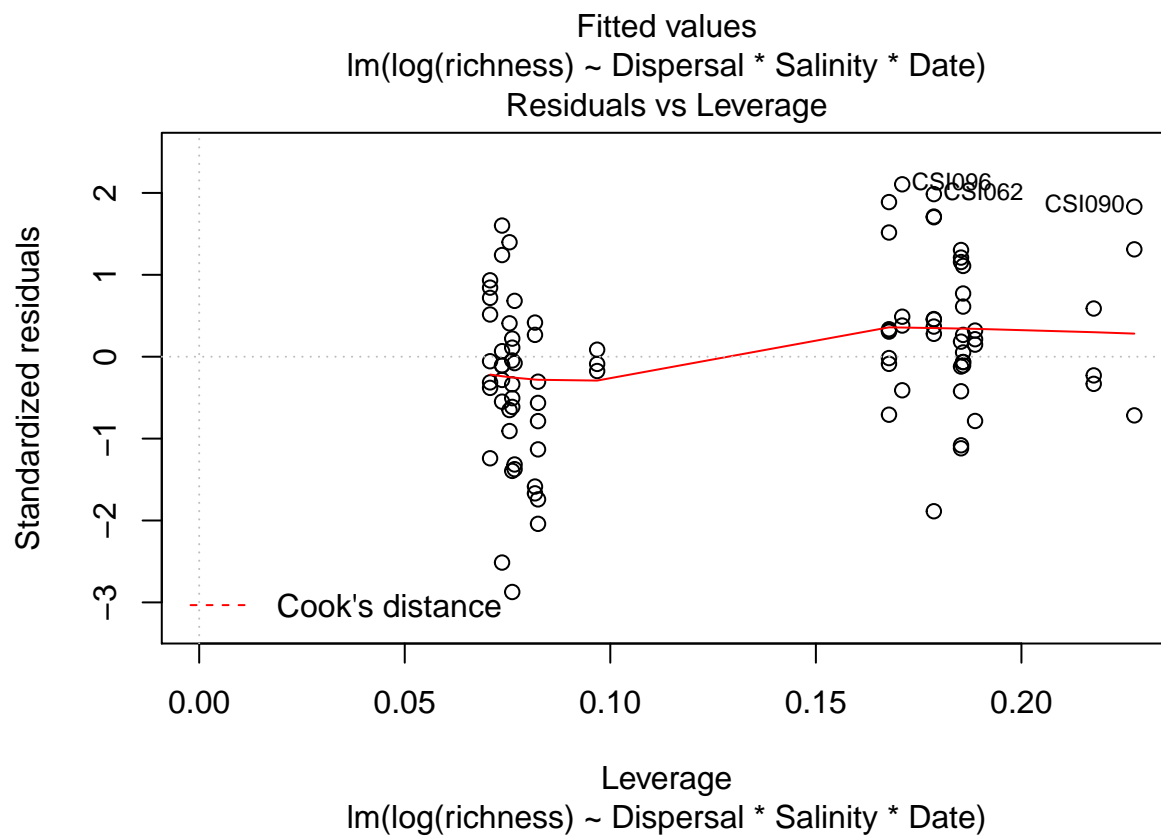
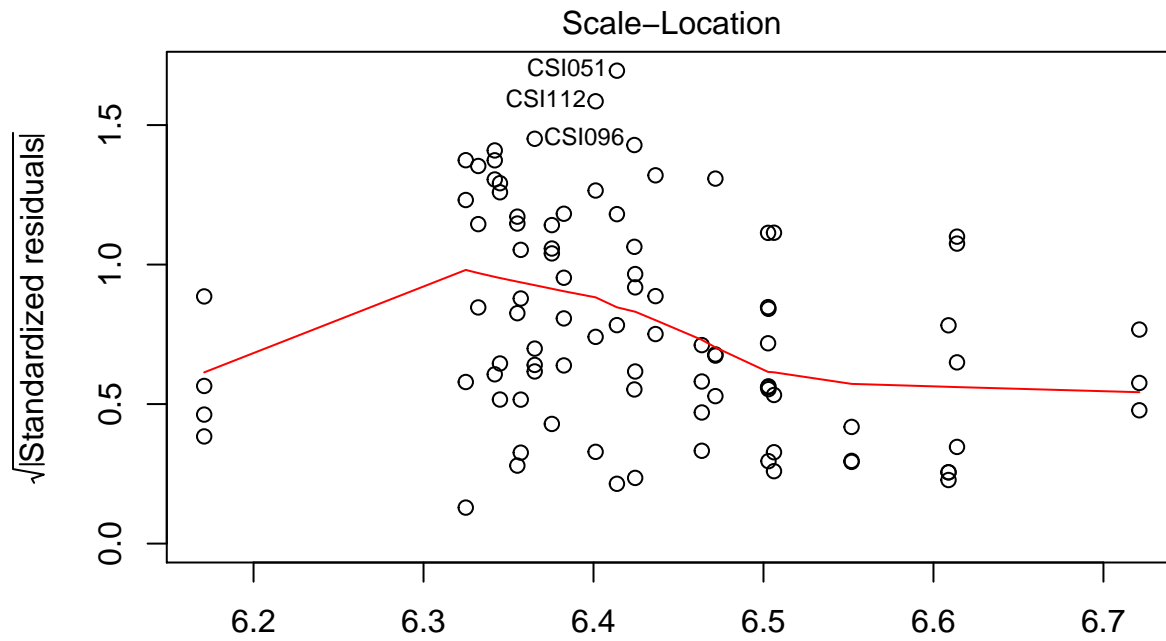






```
##
## Call:
## lm(formula = Cmin ~ Dispersal * Salinity, data = design.env.full)
##
## Coefficients:
##      (Intercept)      Dispersal      Salinity
##          120.000         -16.295          -7.938
## Dispersal:Salinity
##           1.306
##
## Analysis of Variance Table
##
## Response: Cmin
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Dispersal   1   6461    6461   2.5121 0.1210545
## Salinity    1  41108   41108  15.9828 0.0002756 ***
## Dispersal:Salinity 1   2902    2902   1.1283 0.2946673
## Residuals  39 100309    2572
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] 91 13451
## [1] 31 13451
```





```
##
## Call:
## lm(formula = log(richness) ~ Dispersal * Salinity * Date, data = csi_otu.div)
##
## Coefficients:
##              (Intercept)              Dispersal
```

```

##              5.76188              0.20454
##              Salinity              Date6/29/15
##              0.10735              0.64534
##              Date7/26/15              Dispersal:Salinity
##              0.83697              -0.03252
##              Dispersal:Date6/29/15              Dispersal:Date7/26/15
##              -0.22955              -0.19954
##              Salinity:Date6/29/15              Salinity:Date7/26/15
##              -0.08604              -0.12450
## Dispersal:Salinity:Date6/29/15 Dispersal:Salinity:Date7/26/15
##              0.02626              0.03082

## Analysis of Variance Table
##
## Response: log(richness)
##              Df Sum Sq Mean Sq F value Pr(>F)
## Dispersal      1 0.0090 0.00903  0.1256 0.724026
## Salinity       1 0.0124 0.01240  0.1725 0.679010
## Date          2 0.1164 0.05819  0.8093 0.448842
## Dispersal:Salinity 1 0.0847 0.08469  1.1778 0.281109
## Dispersal:Date  2 0.0200 0.01001  0.1392 0.870242
## Salinity:Date   2 0.7868 0.39339  5.4712 0.005952 **
## Dispersal:Salinity:Date 2 0.0969 0.04846  0.6740 0.512565
## Residuals      79 5.6803 0.07190
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Call:
## lm(formula = Cmin ~ Dispersal * Salinity, data = csi.full.ns.Cmin)
##
## Coefficients:
##              (Intercept)              Dispersal              Salinity
##              82.6185              -3.8559              -3.7776
## Dispersal:Salinity
##              -0.1041

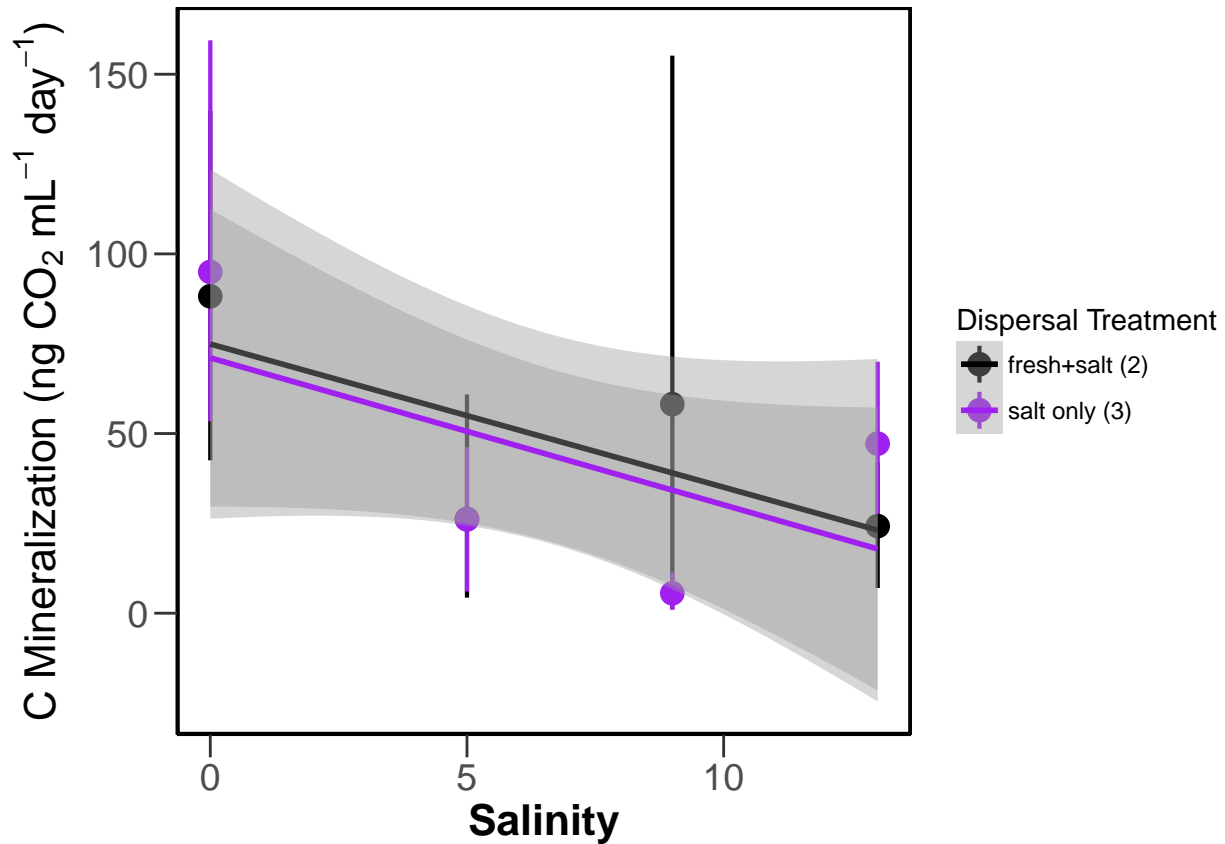
## Analysis of Variance Table
##
## Response: Cmin
##              Df Sum Sq Mean Sq F value Pr(>F)
## Dispersal      1    206    205.8  0.0874 0.76974
## Salinity       1 12012 12011.7  5.1015 0.03219 *
## Dispersal:Salinity 1      2      2.0  0.0008 0.97699
## Residuals     27 63572  2354.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Call:
## lm(formula = Cmin ~ Salinity_real, data = csi.full.ns.Cmin)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -51.84  -31.68  -15.30   20.82  118.96
##

```

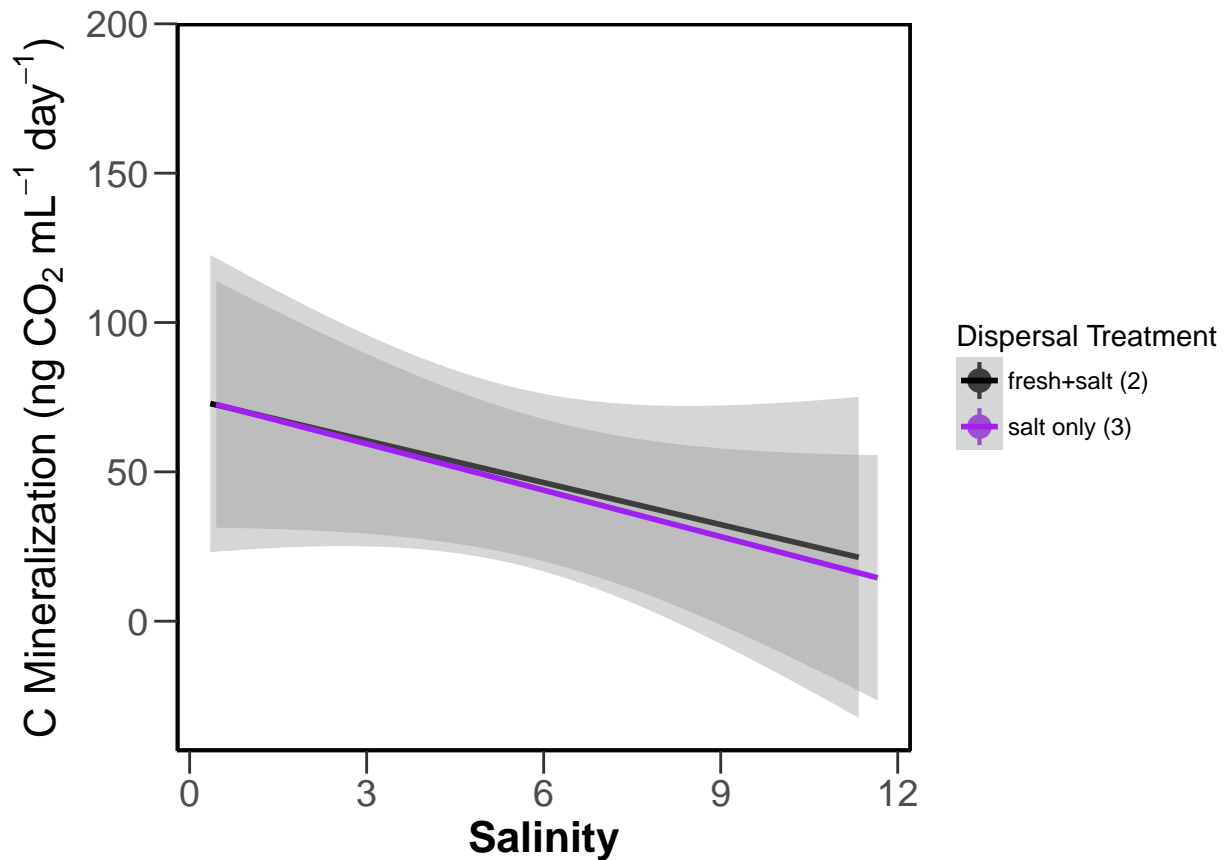


```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    74.849    15.137    4.945 2.96e-05 ***
## Salinity_real  -4.973     2.161   -2.301  0.0288 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 47.01 on 29 degrees of freedom
## Multiple R-squared:  0.1544, Adjusted R-squared:  0.1252
## F-statistic: 5.295 on 1 and 29 DF,  p-value: 0.02877
```



```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 31 rows containing missing values (geom_pointrange).
```



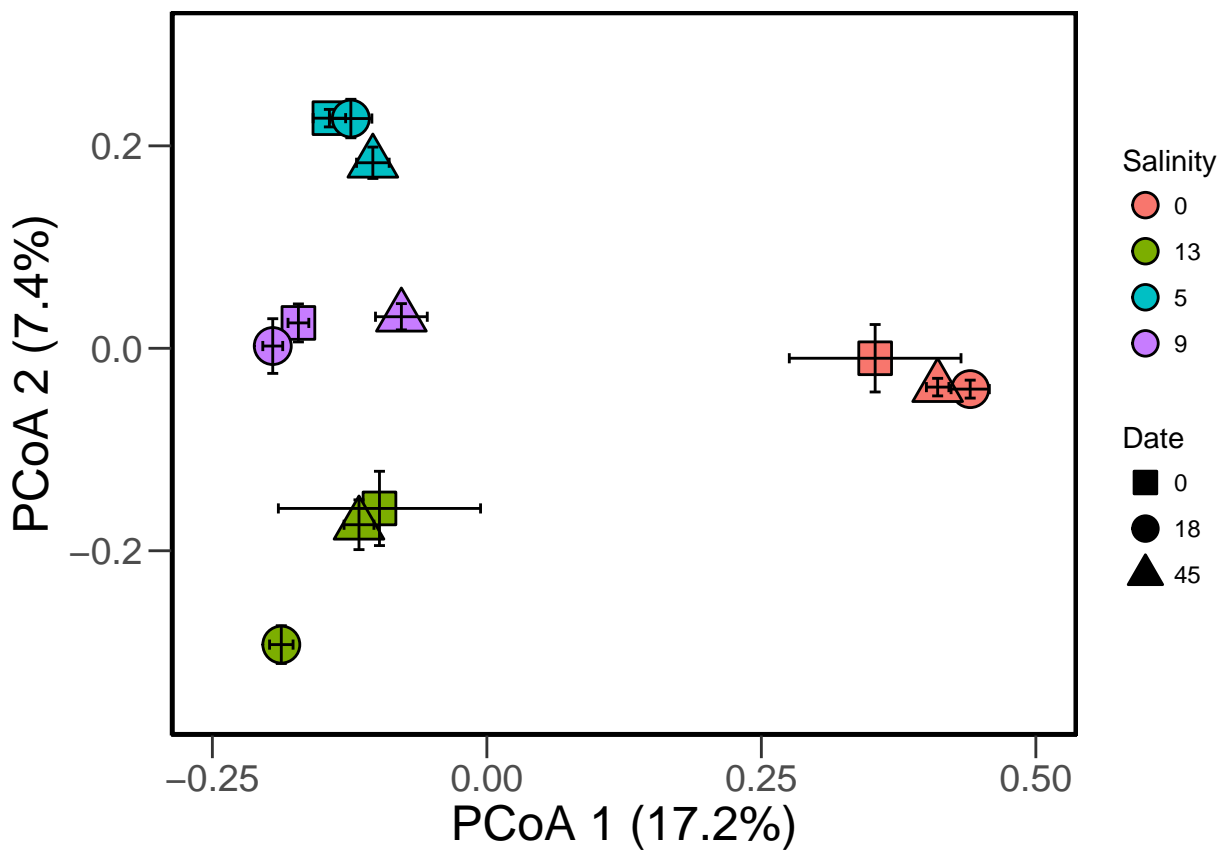
```
## Saving 6.5 x 4.5 in image
## Warning: Removed 31 rows containing missing values (geom_pointrange).
## Loading required package: labdsv
## Loading required package: mgcv
## This is mgcv 1.8-23. For overview type 'help("mgcv-package")'.
## Loading required package: cluster
##
## Attaching package: 'labdsv'
## The following object is masked from 'package:stats':
##
##   density
##
## Call:
## adonis(formula = csi.full.ns[, -c(1:16)] ~ Date2 * Dispersal * Salinity, data = csi.full.ns, per
##
## Permutation: free
## Number of permutations: 1000
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model    R2  Pr(>F)
## Date2         1      1.781  1.7812  5.5846 0.05232 0.000999 ***
```

```
## Dispersal          1      0.248  0.2482  0.7783  0.00729  0.808192
## Salinity           1      3.905  3.9045 12.2420  0.11469  0.000999 ***
## Date2:Dispersal    1      0.162  0.1617  0.5070  0.00475  1.000000
## Date2:Salinity     1      0.917  0.9172  2.8759  0.02694  0.000999 ***
## Dispersal:Salinity  1      0.297  0.2966  0.9298  0.00871  0.520480
## Date2:Dispersal:Salinity 1      0.263  0.2632  0.8251  0.00773  0.701299
## Residuals         83     26.472  0.3189                0.77757
## Total              90     34.045                1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] 17.2
## [1] 7.4
```

PCoA Plot Design without Source

Plot (ggplot)

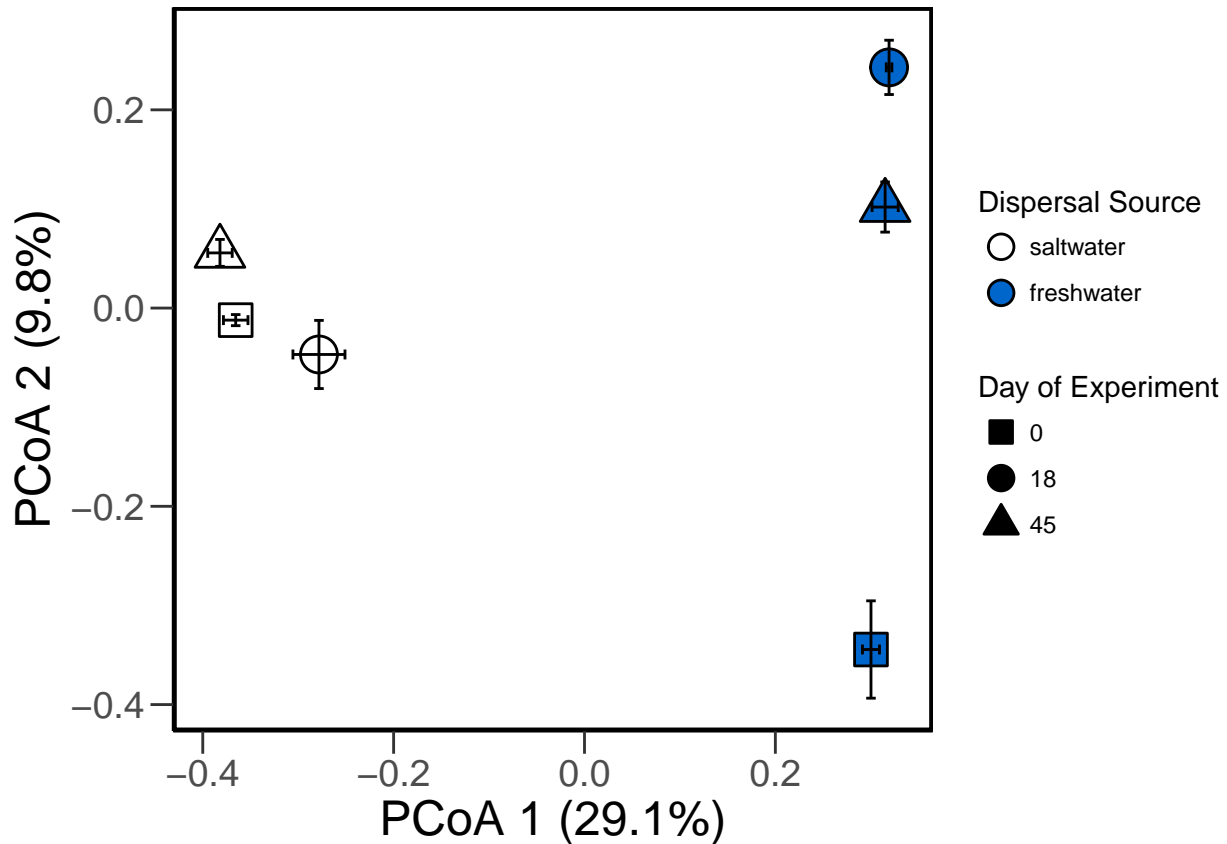


```
## Saving 6.5 x 4.5 in image
```

PCoA sources only

PCoA plot sources only

PLOT GGPLOT sources only



```
## Saving 6.5 x 4.5 in image
```

```
#Is there a relationship between bacterial community composition and decomposition rate? used matrix comparison
```

```
#str(csi.full.ns.Cmin)
```

```
df.bcc <- csi.full.ns.Cmin[,-c(1:16)] #bacteria
```

```
df.env.bcc <- csi.full.ns.Cmin[,c(1:16)] #env
```

```
df.decomp <- csi.full.ns.Cmin[,c(12:14)] #decomp
```

```
df.decompCmin <- csi.full.ns.Cmin[,c(12:15)] #decompCmin
```

```
#bray curtis for bact comm
```

```
dist.bcc <- vegdist(df.bcc, method = "bray")
```

```
#euclidean distance for leaf litter decomp
```

```
dist.decomp <- vegdist(df.decomp, method = "euclidean")
```

```
#euclidean distance for leaf litter decomp and Cmin
```

```
dist.decompCmin <- vegdist(df.decompCmin, method = "euclidean")
```

```
#matrix comparison
```

```
mantel.rtest(dist.bcc, dist.decomp, nrepet = 999) #bacteria compared to decomp correlation r = 0.231, P = 0.001
```

```
## Monte-Carlo test
```

```
## Call: mantel.rtest(m1 = dist.bcc, m2 = dist.decomp, nrepet = 999)
##
## Observation: 0.2309126
##
## Based on 999 replicates
## Simulated p-value: 0.003
## Alternative hypothesis: greater
##
##      Std.Obs   Expectation      Variance
## 2.9322487245 -0.0004736831  0.0062269236

mantel.rtest(dist.bcc, dist.decompCmin, nrepet = 999) #bacteria compared to decompCmin correlation r =

## Monte-Carlo test
## Call: mantel.rtest(m1 = dist.bcc, m2 = dist.decompCmin, nrepet = 999)
##
## Observation: 0.2116409
##
## Based on 999 replicates
## Simulated p-value: 0.006
## Alternative hypothesis: greater
##
##      Std.Obs   Expectation      Variance
## 3.005121143 -0.002729001  0.005088663

#Redundancy Analysis
f <- df.bcc ~ Maple_dmass + Spartina_dmass + Phrag_dmass + Cmin
df.rda <- dbrda(f, data=df.env.bcc, distance="bray")
anova(df.rda, by="terms", model="direct")

## Permutation test for dbrda under direct model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = df.bcc ~ Maple_dmass + Spartina_dmass + Phrag_dmass + Cmin, data = df.env.bcc)
##           Df SumOfSqs      F Pr(>F)
## Maple_dmass    1  0.8322 2.4026 0.003 **
## Spartina_dmass  1  0.6253 1.8054 0.026 *
## Phrag_dmass    1  0.3183 0.9189 0.539
## Cmin           1  0.5641 1.6286 0.036 *
## Residual      26  9.0056
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

RsquareAdj(df.rda)

## $r.squared
## [1] 0.2062415
##
## $adj.r.squared
## [1] 0.08412478
```

```
plot(df.rda)
```

