

Mesocosm Manuscript Analyses & Figures

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Importing and Organizing

Analyses and Graphs (Main)

Phragmites in Monoculture

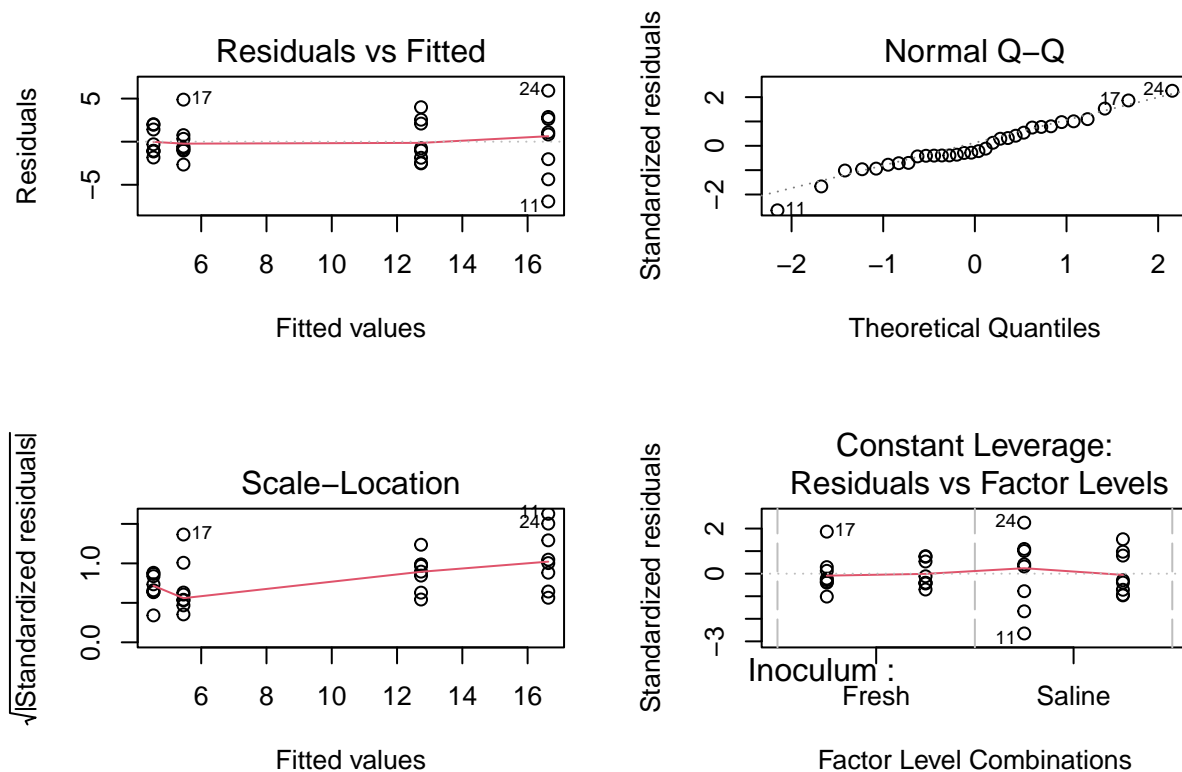
ANOVA

What are the effects of microbial inoculum, salinity, and their interaction on *Phragmites* biomass in monoculture pots?

```
#ANOVA
P.mono<-D%>%
  filter(Community.Type=="Phragmites")%>%
  filter(Inoculum!="Sterile")
p.mod1<-lm(Biomass~Inoculum*Salinity, dat=P.mono)
anova(p.mod1)

## Analysis of Variance Table
##
## Response: Biomass
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Inoculum      1 750.78   750.78 95.9591 1.514e-10 ***
## Salinity      1  46.40    46.40  5.9306  0.0215 *
## Inoculum:Salinity 1   17.75    17.75  2.2688  0.1432
## Residuals    28 219.07     7.82
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Examine residuals
par(mfrow=c(2,2))
plot(p.mod1)
```

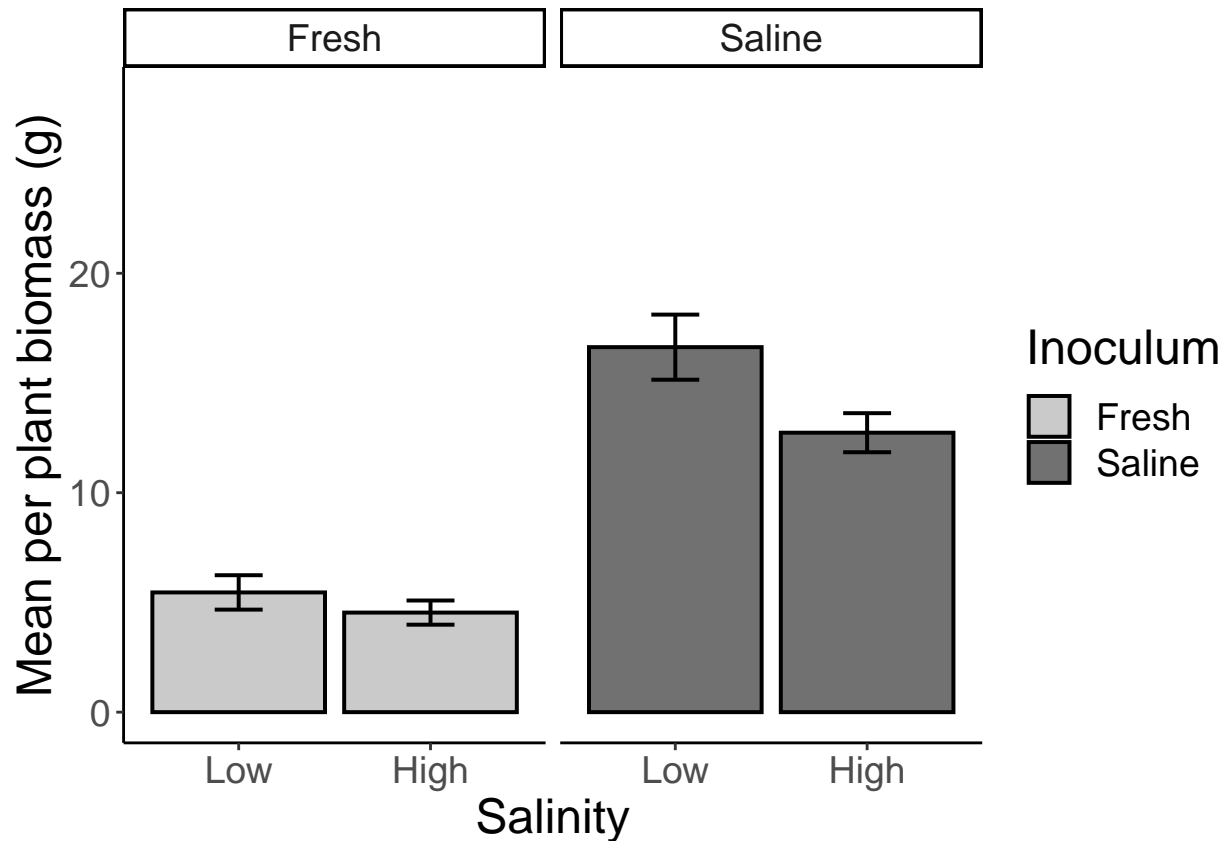


Bar Graph: Figure 1A

```
P.mono<-D%>%
  filter(Community.Type=="Phragmites")%>%
  filter(Inoculum!="Sterile")%>%
  group_by(Inoculum,Salinity)%>%
  summarise(mean=mean(Biomass),se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
P.mono$Salinity<-factor(P.mono$Salinity, levels=c("Low","High"))
ggplot(P.mono,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey70", "grey20"))+
  ylab("Mean per plant biomass (g)")+
  ylim(0,28)+
  facet_wrap(~Inoculum)
```



Phragmites in mixed community pots

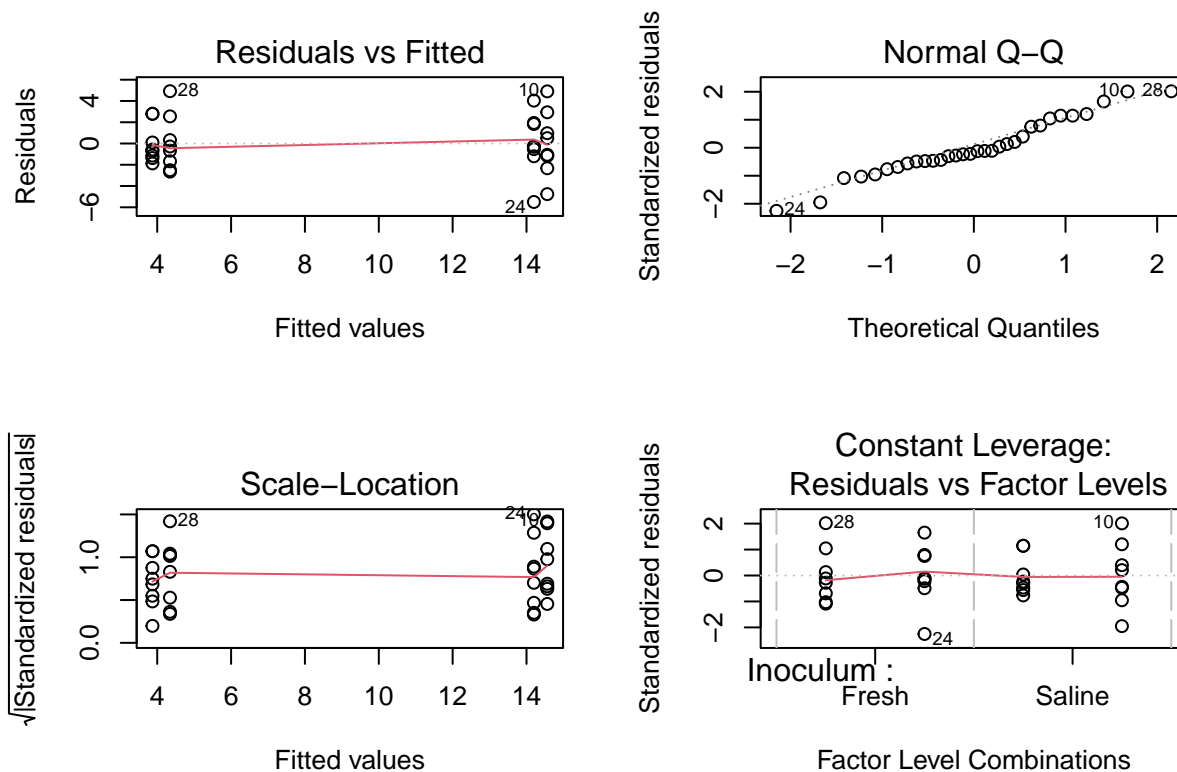
ANOVA

What are the effects of microbial inoculum, salinity, and their interaction on *Phragmites* biomass in mixed community (*Phragmites* + Native) pots?

```
P.mix<-D%>%
  filter(Community.Type=="Mixed")%>%
  filter(IN=="Invasive")%>%
  filter(Inoculum!="Sterile")
p.mod2<-lm(Biomass~Inoculum*Salinity, dat=P.mix)
anova(p.mod2)
```

```
## Analysis of Variance Table
##
## Response: Biomass
##          Df Sum Sq Mean Sq  F value    Pr(>F)
## Inoculum    1   0.03    0.03   0.0037   0.9518
## Salinity     1 844.26  844.26 123.9843 8.521e-12 ***
## Inoculum:Salinity 1   1.40    1.40   0.2060   0.6534
## Residuals   28 190.66    6.81
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Examine residuals
par(mfrow=c(2,2))
plot(p.mod2)
```

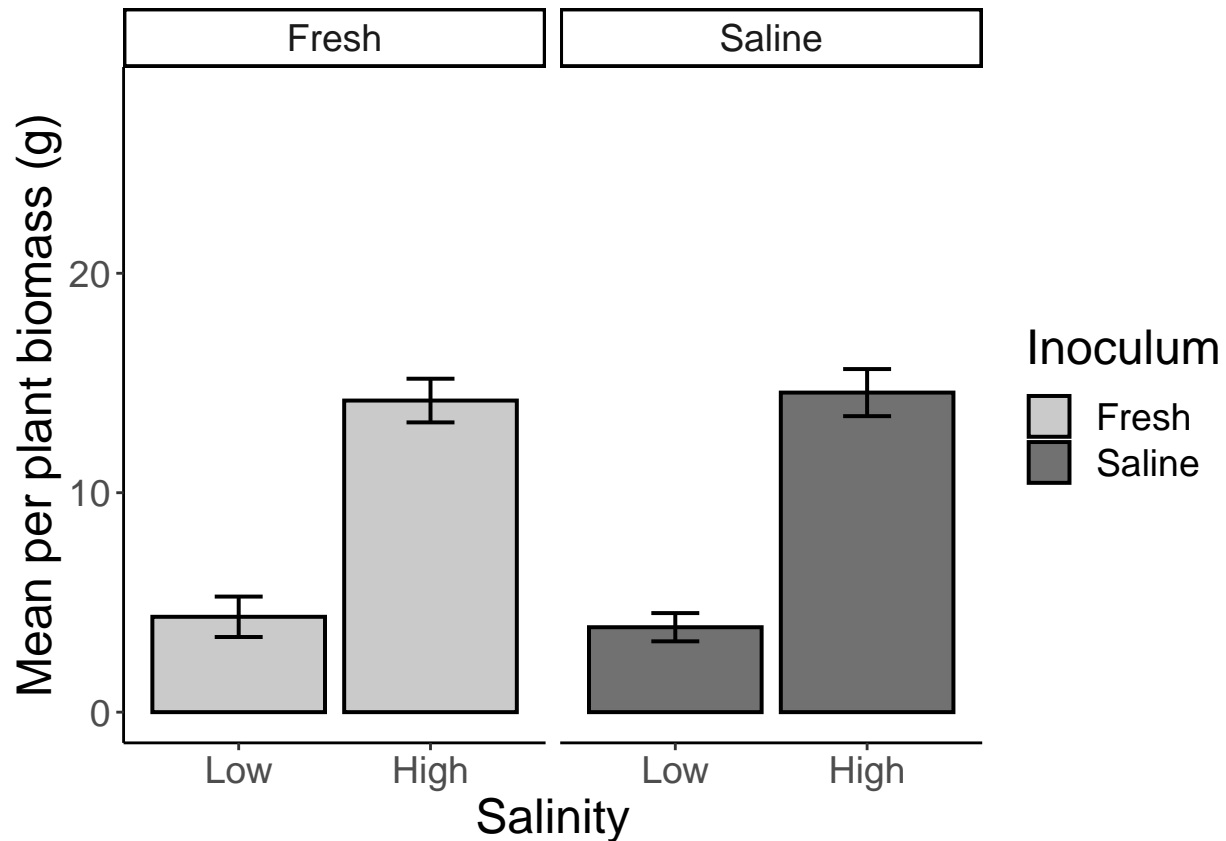


Bar Graph: Figure 1B.

```
P.mix<-D%>%
  filter(Community.Type=="Mixed")%>%
  filter(IN=="Invasive")%>%
  filter(Inoculum!="Sterile")%>%
  group_by(Inoculum,Salinity)%>%
  summarise(mean=mean(Biomass),se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
P.mix$Salinity<-factor(P.mix$Salinity, levels=c("Low","High"))
ggplot(P.mix,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey70", "grey20"))+
  ylab("Mean per plant biomass (g)")+
  ylim(0,28)+
  facet_wrap(~Inoculum)
```



Native in Native Community

ANOVA

What are the effects of microbial inoculum, salinity, and their interaction on native biomass in native community pots? The biomass from all three native species is combined.

```
N.nat<-D%>%
  filter(Community.Type=="Native")%>%
  filter(Inoculum!="Sterile")
Nmod1<-lm(Biomass~Inoculum*Salinity, dat=N.nat)
anova(Nmod1)

## Analysis of Variance Table
##
## Response: Biomass
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Inoculum      1  586.45   586.45  23.4661 4.247e-05 ***
## Salinity      1   31.32    31.32   1.2531  0.2725
## Inoculum:Salinity 1    3.27     3.27   0.1307  0.7204
## Residuals    28 699.75    24.99
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

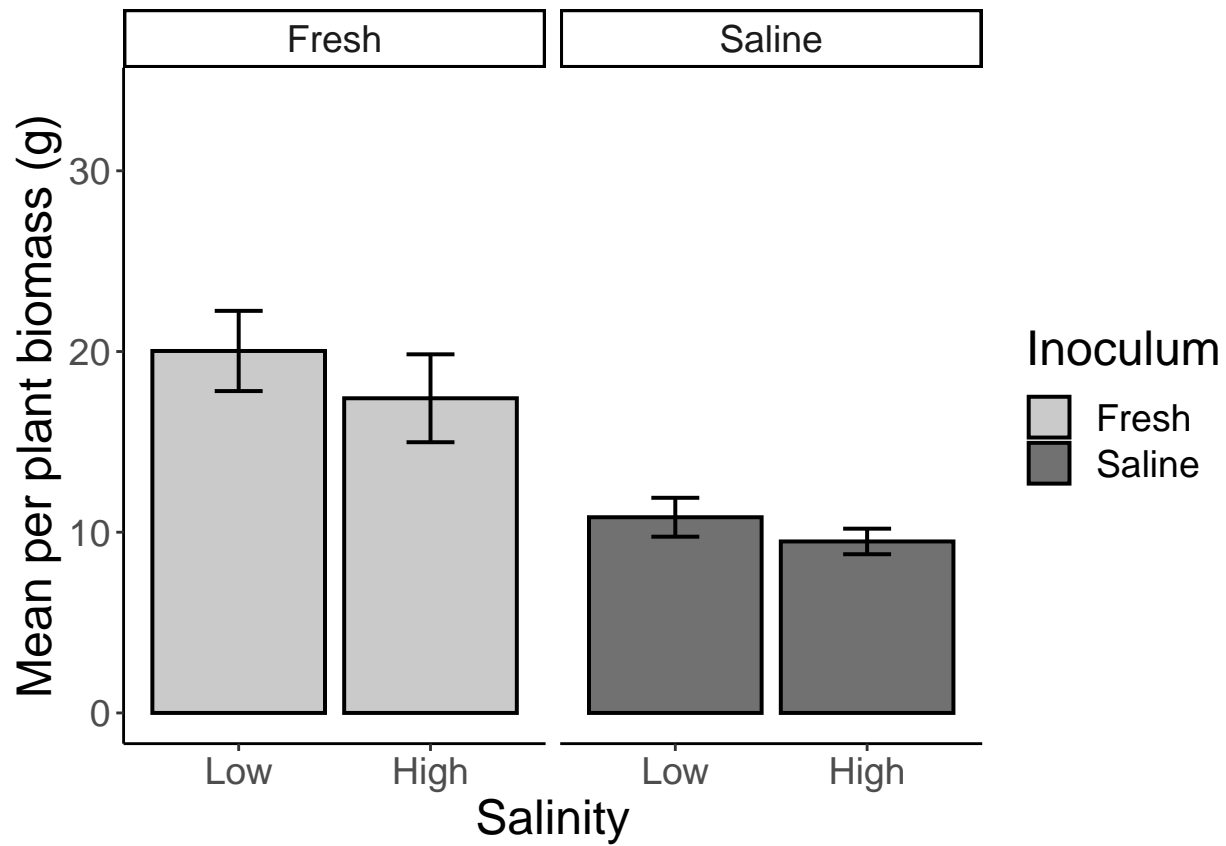
```
#Examine residuals
#par(mfrow=c(2,2))
#plot(Nmod1)
```

Bar Graph: Figure 1C

```
N.nat<-D%>%
  filter(Community.Type=="Native")%>%
  filter(Inoculum!="Sterile")%>%
  group_by(Inoculum,Salinity)%>%
  summarise(mean=mean(Biomass),se=std.error(Biomass))

## 'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

N.nat$Salinity<-factor(N.nat$Salinity, levels=c("Low","High"))
ggplot(N.nat,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey70", "grey20"))+
  ylab("Mean per plant biomass (g)")+
  ylim(0,34)+
  facet_wrap(~Inoculum)
```



Native in Mixed Community

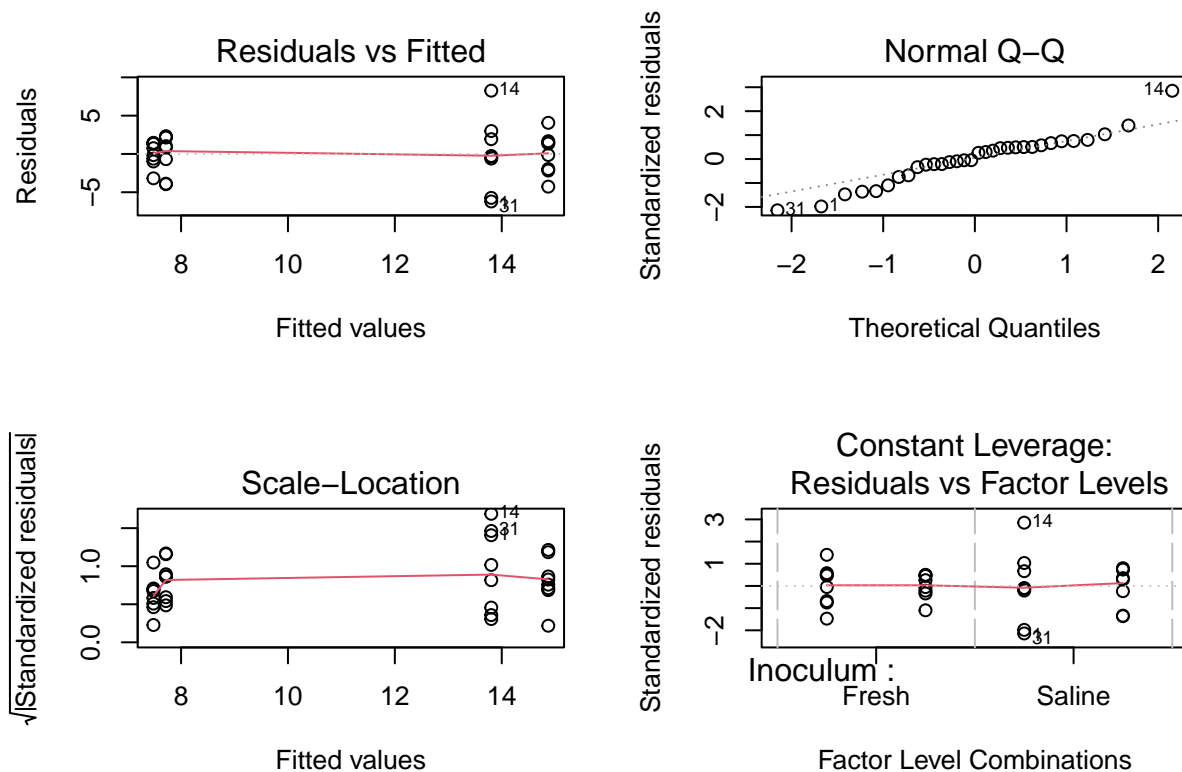
ANOVA

What are the effects of microbial inoculum, salinity, and their interaction on native biomass in mixed community (half native species + half *Phragmites*) pots? The biomass from all three native species is combined.

```
N.mix<-D%>%
  filter(Community.Type=="Mixed")%>%
  filter(IN=="Native")%>%
  filter(Inoculum!="Sterile")
Nmod2<-lm(Biomass~Inoculum*Salinity, dat=N.mix)
anova(Nmod2)

## Analysis of Variance Table
##
## Response: Biomass
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Inoculum       1   1.39    1.39  0.1448    0.7065
## Salinity       1 363.15   363.15 37.8505 1.216e-06 ***
## Inoculum:Salinity 1   3.38    3.38  0.3523    0.5576
## Residuals     28 268.64    9.59
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#Examine residuals
par(mfrow=c(2,2))
plot(Nmod2)
```

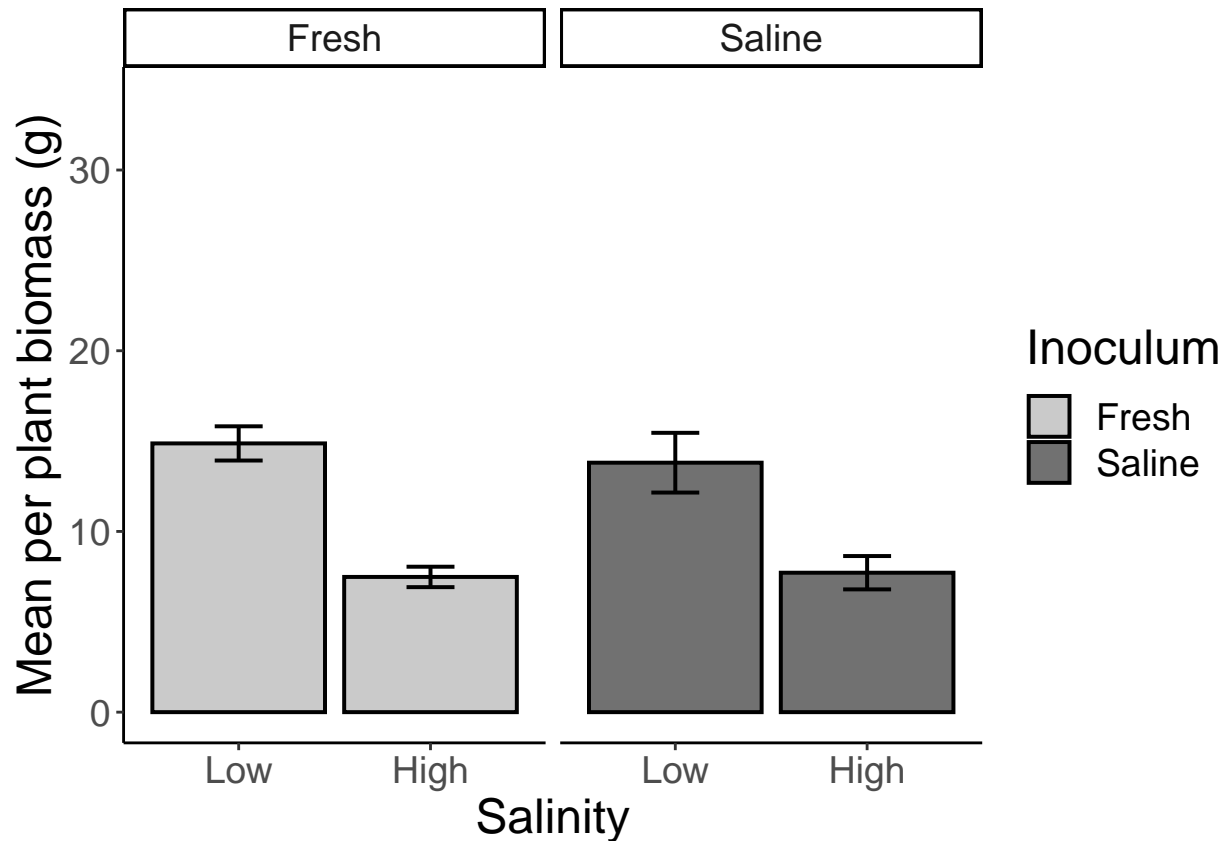


Bar Plot: Figure 1D

```
N.mix<-D%>%
  filter(Community.Type=="Mixed")%>%
  filter(IN=="Native")%>%
  filter(Inoculum!="Sterile")%>%
  group_by(Inoculum,Salinity)%>%
  summarise(mean=mean(Biomass),se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
N.mix$Salinity<-factor(N.mix$Salinity, levels=c("Low","High"))
ggplot(N.mix,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey70", "grey20"))+
  ylab("Mean per plant biomass (g)")+
  ylim(0,34)+
  facet_wrap(~Inoculum)
```

Supplemental Analyses and Graphs

Biomass analyses and Graphs Including Sterile Treatments

Phragmites in Monoculture

Post hoc Tukey Tests

What are the effects of microbial inoculum, salinity, and their interaction on *Phragmites* biomass in mono-culture pots?

#ANOVA

```
P.mono.dat<-D%>%
  filter(Community.Type=="Phragmites")
pt.mod<-lm(Biomass~Type, P.mono.dat)
pt.av<-aov(pt.mod)
summary(pt.av)
```

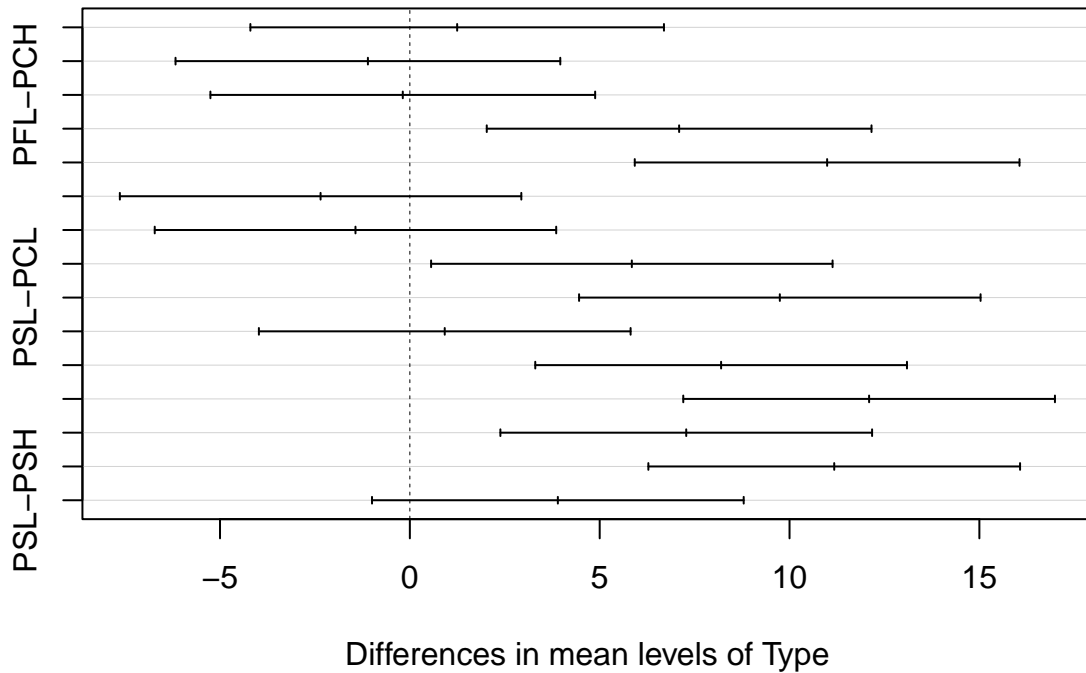
```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Type          5   941.3   188.25    17.63 4.16e-09 ***
## Residuals    39   416.4    10.68
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
tukey.test <- TukeyHSD(pt.av)
tukey.test
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = pt.mod)
##
## $Type
##      diff      lwr      upr      p adj
## PCL-PCH 1.2460317 -4.2006617 6.692725 0.9825558
## PFH-PCH -1.1053571 -6.1722009 3.961487 0.9858899
## PFL-PCH -0.1866071 -5.2534509 4.880237 0.9999975
## PSH-PCH 7.0925595 2.0257157 12.159403 0.0019817
## PSL-PCH 10.9904762 5.9236324 16.057320 0.0000015
## PFH-PCL -2.3513889 -7.6386322 2.935854 0.7654531
## PFL-PCL -1.4326389 -6.7198822 3.854604 0.9636275
## PSH-PCL 5.8465278 0.5592844 11.133771 0.0227785
## PSL-PCL 9.7444444 4.4572011 15.031688 0.0000336
## PFL-PFH 0.9187500 -3.9762862 5.813786 0.9928893
## PSH-PFH 8.1979167 3.3028805 13.092953 0.0001632
## PSL-PFH 12.0958333 7.2007972 16.990870 0.0000001
## PSH-PFL 7.2791667 2.3841305 12.174203 0.0009117
## PSL-PFL 11.1770833 6.2820472 16.072120 0.0000005
## PSL-PSH 3.8979167 -0.9971195 8.792953 0.1863147
```

```
plot(tukey.test)
```

95% family-wise confidence level

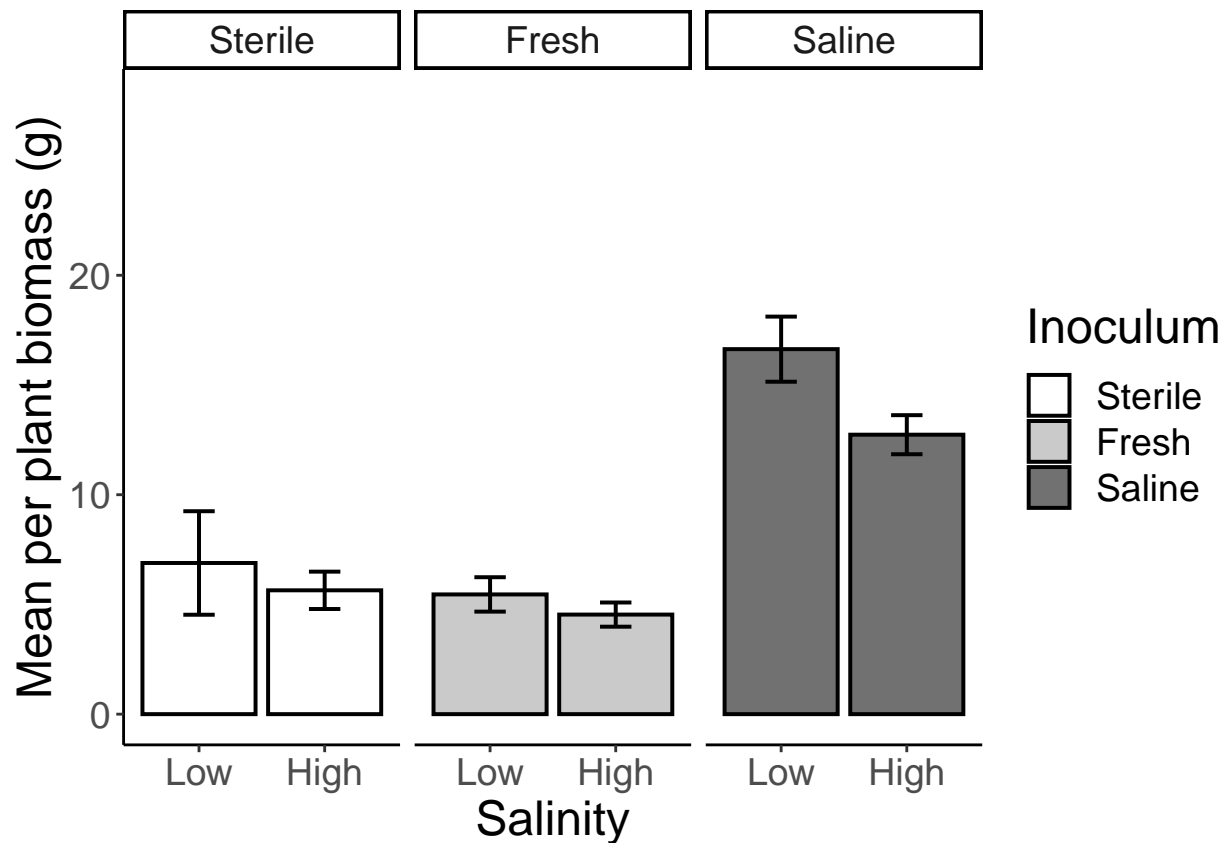


Bar Graph: Supplemental Figure 1A

```
P.mono<-D%>%
  filter(Community.Type=="Phragmites")%>%
  group_by(Inoculum,Salinity)%>%
  summarise(mean=mean(Biomass),se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
P.mono$Salinity<-factor(P.mono$Salinity, levels=c("Low","High"))
ggplot(P.mono,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("white","grey70", "grey20"))+
  ylab("Mean per plant biomass (g)")+
  ylim(0,28)+
  facet_wrap(~Inoculum)
```



Phragmites in mixed community pots

Post hoc Tukey test

```
P.mix.dat<-D%>%
  filter(Community.Type=="Mixed")%>%
  filter(IN=="Invasive")
pt.mod1<-lm(Biomass~Type, P.mix.dat)
pt.av1<-aov(pt.mod1)
summary(pt.av1)
```

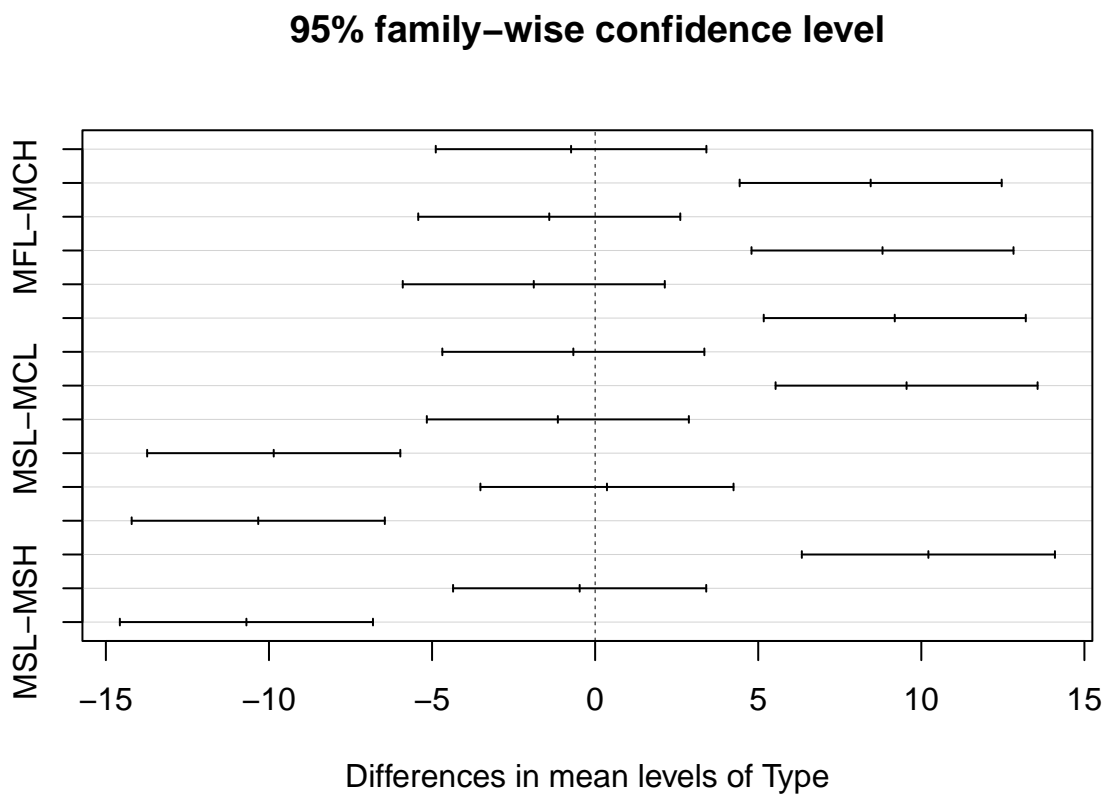
```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Type         5   992.8   198.56    29.52 1.98e-12 ***
## Residuals   40   269.1     6.73
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
tukey.test1 <- TukeyHSD(pt.av1)
tukey.test1
```

```
## Tukey multiple comparisons of means
```

```
##      95% family-wise confidence level
##
## Fit: aov(formula = pt.mod1)
##
## $Type
##           diff           lwr           upr      p adj
## MCL-MCH -0.7380952 -4.886376  3.410186 0.9944913
## MFH-MCH  8.4476190  4.431063 12.464175 0.0000026
## MFL-MCH -1.4065476 -5.423103  2.610008 0.8985868
## MSH-MCH  8.8101190  4.793563 12.826675 0.0000011
## MSL-MCH -1.8815476 -5.898103  2.135008 0.7257512
## MFH-MCL  9.1857143  5.169159 13.202270 0.0000005
## MFL-MCL -0.6684524 -4.685008  3.348103 0.9959704
## MSH-MCL  9.5482143  5.531659 13.564770 0.0000002
## MSL-MCL -1.1434524 -5.160008  2.873103 0.9555358
## MFL-MFH -9.8541667 -13.734528 -5.973805 0.0000000
## MSH-MFH  0.3625000 -3.517861  4.242861 0.9997507
## MSL-MFH -10.3291667 -14.209528 -6.448805 0.0000000
## MSH-MFL 10.2166667  6.336305 14.097028 0.0000000
## MSL-MFL -0.4750000 -4.355361  3.405361 0.9990699
## MSL-MSH -10.6916667 -14.572028 -6.811305 0.0000000
```

```
plot(tukey.test1)
```

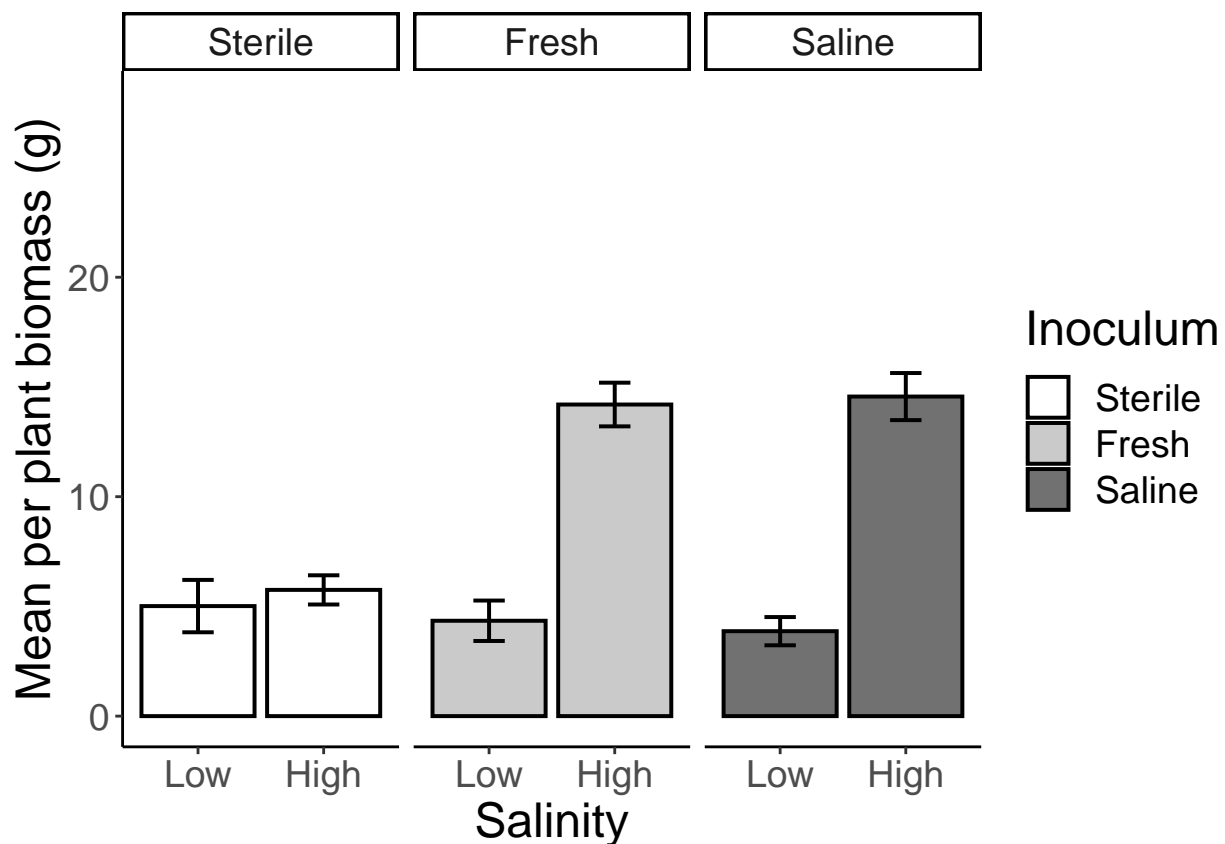


Bar Graph: Supplemental Figure 1B.

```
P.mix<-D%>%
  filter(Community.Type=="Mixed")%>%
  filter(IN=="Invasive")%>%
  group_by(Inoculum,Salinity)%>%
  summarise(mean=mean(Biomass),se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
P.mix$Salinity<-factor(P.mix$Salinity, levels=c("Low","High"))
ggplot(P.mix,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("white","grey70", "grey20"))+
  ylab("Mean per plant biomass (g)")+
  ylim(0,28)+
  facet_wrap(~Inoculum)
```



Native in Native Community

Post hoc Tukey Test

```
N.nat.dat<-D%>%
  filter(Community.Type=="Native")
pt.mod2<-lm(Biomass~Type, N.nat.dat)
pt.av2<-aov(pt.mod2)
summary(pt.av2)
```

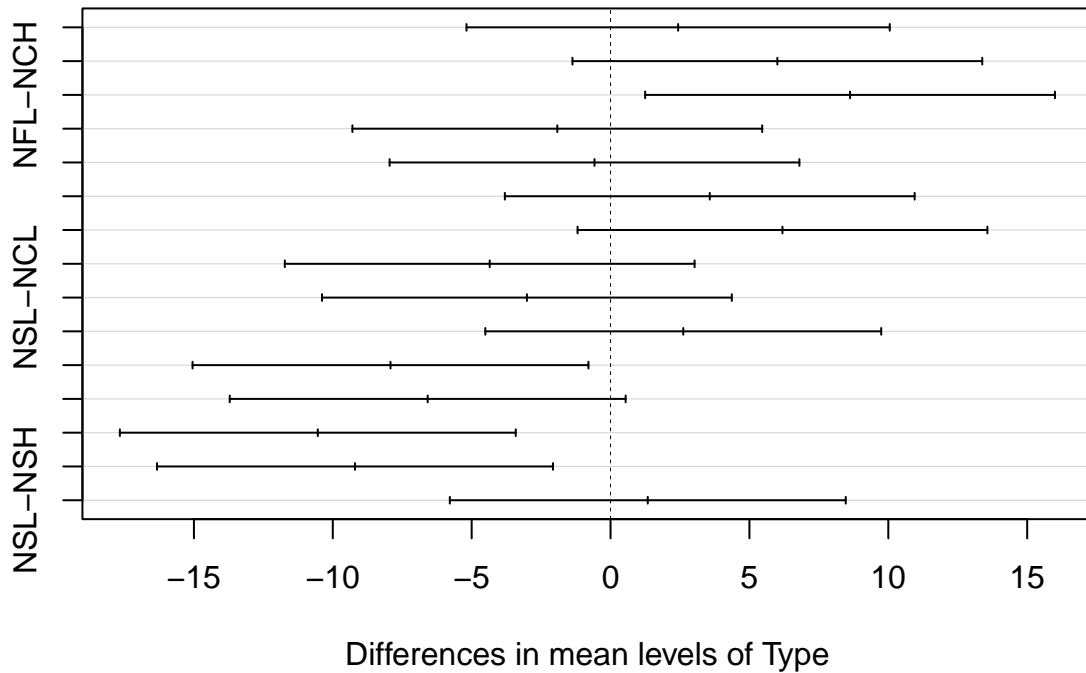
```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Type         5   673.9   134.78     5.94 0.000338 ***
## Residuals    40   907.6    22.69
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
tukey.test2 <- TukeyHSD(pt.av2)
tukey.test2
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = pt.mod2)
##
## $Type
##           diff           lwr           upr           p adj
## NCL-NCH    2.4333333   -5.185269  10.0519355  0.9290122
## NFH-NCH    6.0053571   -1.371323  13.3820370  0.1685301
## NFL-NCH    8.6228571    1.246177  15.9995370  0.0138033
## NSH-NCH   -1.9175595   -9.294239   5.4591203  0.9697244
## NSL-NCH   -0.5779762   -7.954656   6.7987037  0.9998951
## NFH-NCL    3.5720238   -3.804656  10.9487037  0.6975339
## NFL-NCL    6.1895238   -1.187156  13.5662037  0.1452692
## NSH-NCL   -4.3508929  -11.727573   3.0257870  0.4990302
## NSL-NCL   -3.0113095  -10.387989   4.3653703  0.8238071
## NFL-NFH    2.6175000   -4.509050   9.7440498  0.8788595
## NSH-NFH   -7.9229167  -15.049466  -0.7963669  0.0216913
## NSL-NFH   -6.5833333  -13.709883   0.5432165  0.0847236
## NSH-NFL  -10.5404167  -17.666966  -3.4138669  0.0009603
## NSL-NFL   -9.2008333  -16.327383  -2.0742835  0.0050188
## NSL-NSH    1.3395833   -5.786966   8.4661331  0.9928938
```

```
plot(tukey.test2)
```

95% family-wise confidence level

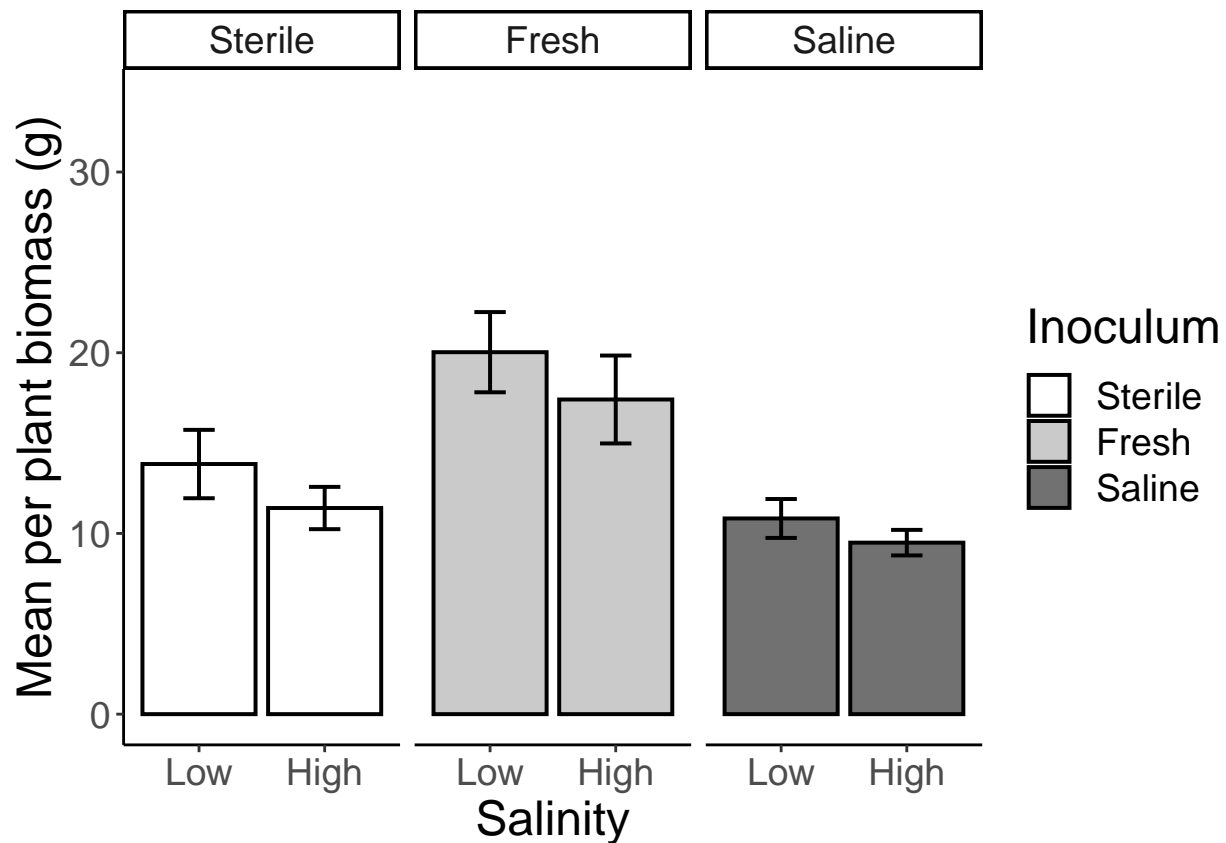


Bar Graph: Supplemental Figure 1C

```
N.nat<-D%>%
  filter(Community.Type=="Native")%>%
  group_by(Inoculum,Salinity)%>%
  summarise(mean=mean(Biomass),se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
N.nat$Salinity<-factor(N.nat$Salinity, levels=c("Low","High"))
ggplot(N.nat,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("white","grey70", "grey20"))+
  ylab("Mean per plant biomass (g)")+
  ylim(0,34)+
  facet_wrap(~Inoculum)
```

Native in Mixed Community

Tukey Post hoc Test

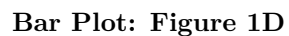
```
N.mix.dat<-D%>%
  filter(Community.Type=="Mixed")%>%
  filter(IN=="Native")
pt.mod3<-lm(Biomass~Type, N.mix.dat)
pt.av3<-aov(pt.mod3)
summary(pt.av3)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Type         5   786.1   157.21    10.31 2.11e-06 ***
## Residuals   40   609.9    15.25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
tukey.test3 <- TukeyHSD(pt.av3)
tukey.test3
```

```
## Tukey multiple comparisons of means
```

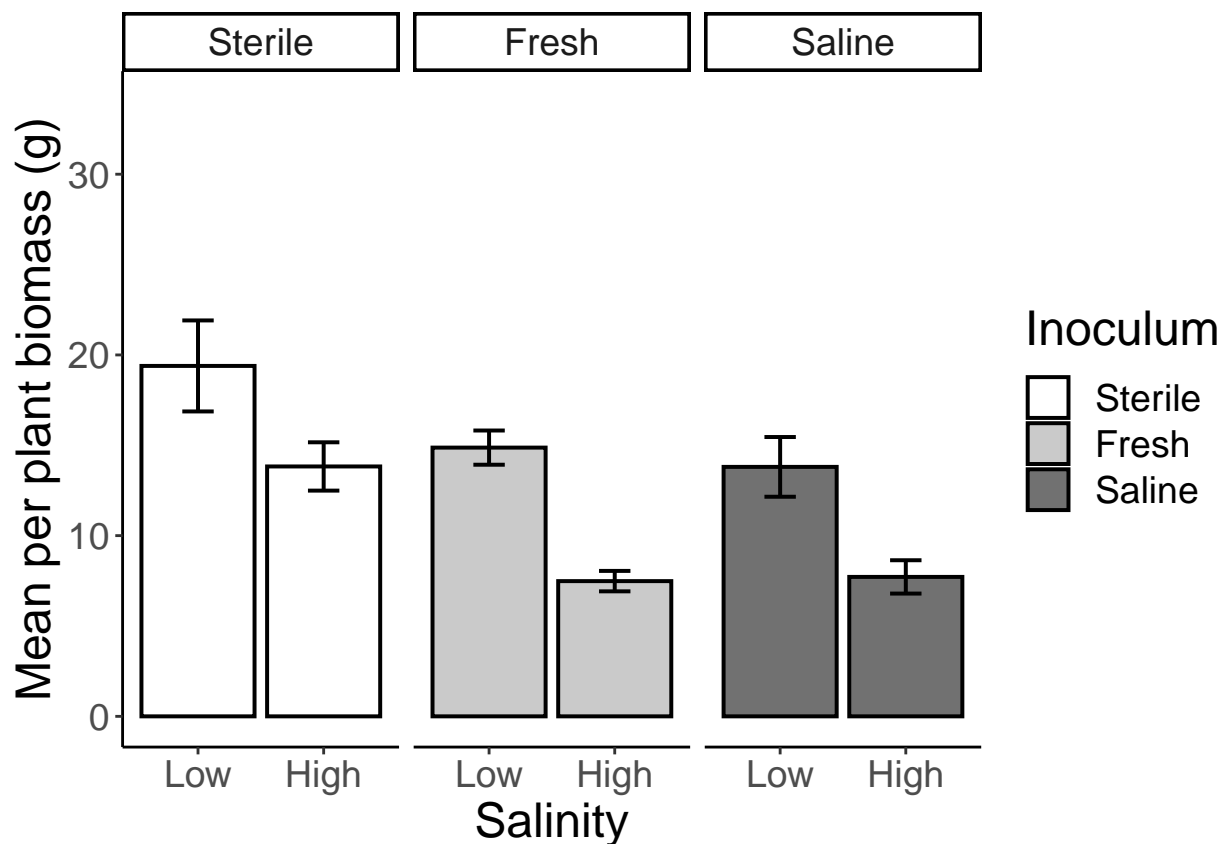
```
plot(tukey.test3)
```



```
N.mix<-D%>%
  filter(Community.Type=="Mixed")%>%
  filter(IN=="Native")%>%
  group_by(Inoculum,Salinity)%>%
  summarise(mean=mean(Biomass),se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
N.mix$Salinity<-factor(N.mix$Salinity, levels=c("Low","High"))
ggplot(N.mix,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("white","grey70", "grey20"))+
  ylab("Mean per plant biomass (g)")+
  ylim(0,34)+
  facet_wrap(~Inoculum)
```



Native Biomass Analyses- Separated by native species

Native Community-

something weird is going on here

```
NatSp1<-BM%>%
  filter(Inoculum!="Sterile")%>%
  filter(Community.Type=="Native")%>%
  select(c(1,2,3,4,5,16,17,18))%>%
  gather(key="Species", value="Biomass", c(SL.tot, SP.tot, SC.tot))
NatSp1b<-NatSp1%>%
  mutate(Salinity=factor(NatSp1$Salinity, levels=c("Low","High")))
```

Sagittaria lancifolia ANOVA

```
x<-NatSp1%>%
  filter(Species=="SL.tot")
modx<-lm(Biomass~Salinity*Inoculum, dat=x)
anova(modx)
```

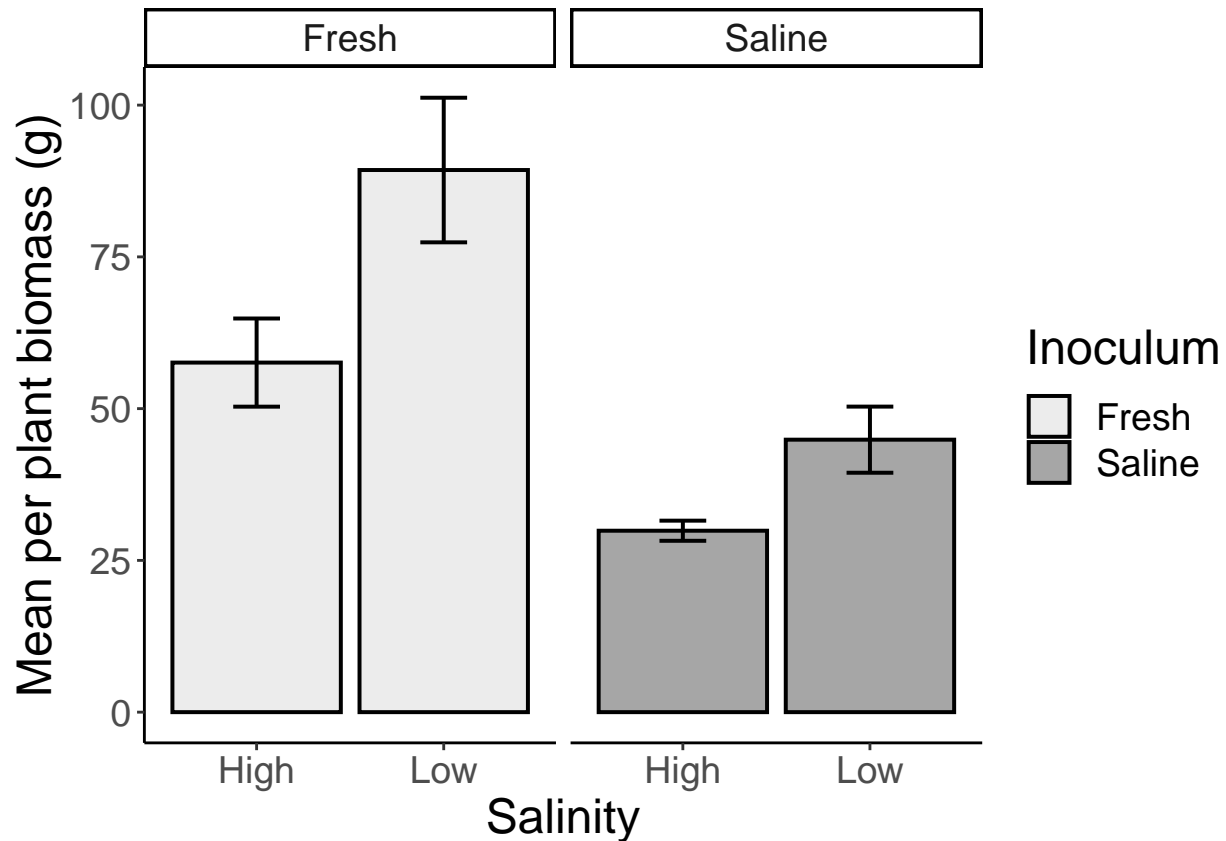
```
## Analysis of Variance Table
##
## Response: Biomass
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Salinity      1  4365.0   4365.0   9.6147 0.004372 **
## Inoculum      1 10401.9  10401.9  22.9116 4.97e-05 ***
## Salinity:Inoculum 1    558.9    558.9   1.2312 0.276619
## Residuals    28 12712.0    454.0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Bar Graph

```
NatSp2<-NatSp1%>%
  filter(Species=="SL.tot")%>%
  group_by(Inoculum, Salinity)%>%
  summarise(mean=mean(Biomass), se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
ggplot(NatSp2,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey90","grey50"))+
  ylab("Mean per plant biomass (g)")+
  facet_wrap(~Inoculum)
```



Spartina patens ANOVA

```
x<-NatSp1%>%
  filter(Species=="SP.tot")
modx<-lm(Biomass~Salinity*Inoculum, dat=x)
anova(modx)
```

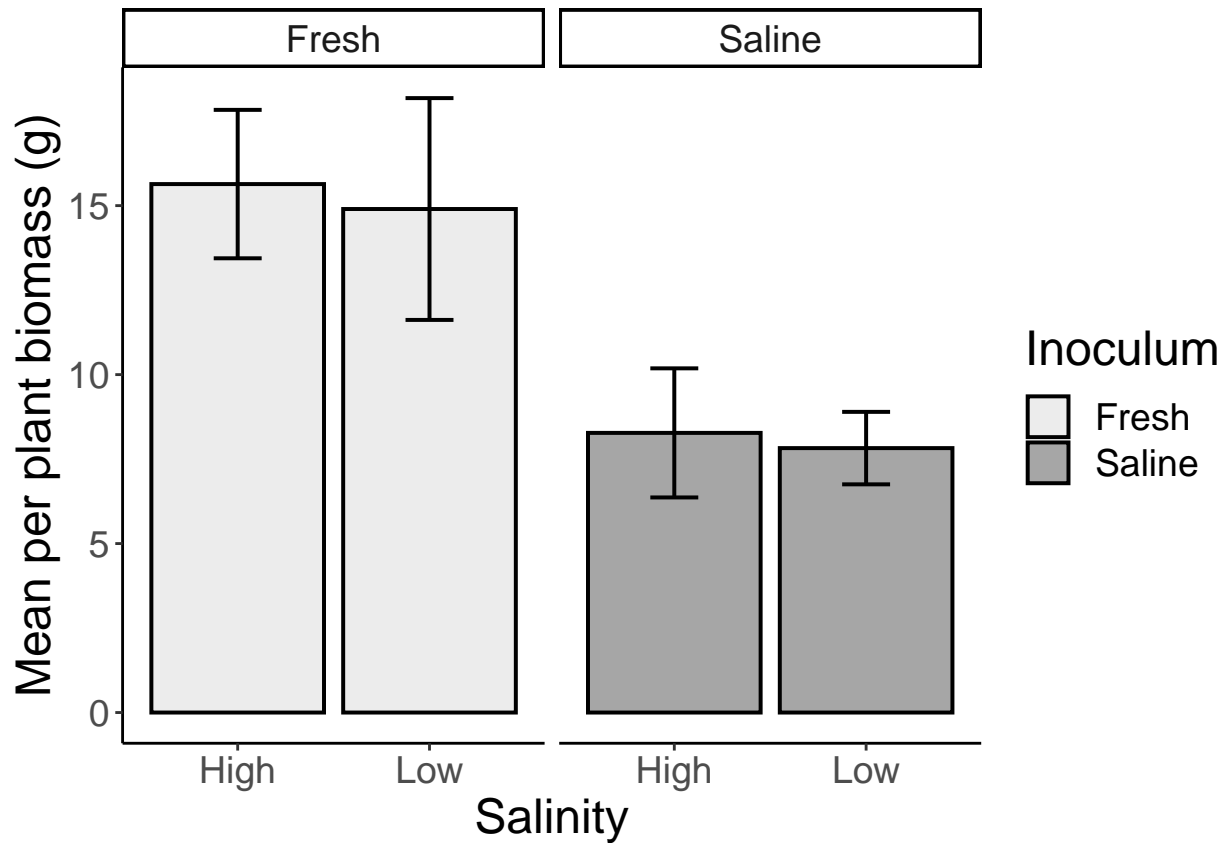
```
## Analysis of Variance Table
##
## Response: Biomass
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Salinity    1    2.82    2.82  0.0692 0.794495
## Inoculum     1  416.88  416.88 10.2223 0.003429 **
## Salinity:Inoculum 1    0.17    0.17  0.0041 0.949687
## Residuals   28 1141.89   40.78
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Bar Graph

```
NatSp2<-NatSp1%>%
  filter(Species=="SP.tot")%>%
  group_by(Inoculum, Salinity)%>%
  summarise(mean=mean(Biomass), se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
ggplot(NatSp2,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey90","grey50"))+
  ylab("Mean per plant biomass (g)")+
  facet_wrap(~Inoculum)
```



Schoenoplectus californicus ANOVA

```
x<-NatSp1%>%
  filter(Species=="SC.tot")
modx<-lm(Biomass~Salinity*Inoculum, dat=x)
anova(modx)
```

Analysis of Variance Table

##

Response: Biomass

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Salinity    1  949.4   949.39   3.7017 0.06458 .
## Inoculum    1  524.1   524.07   2.0433 0.16394
```

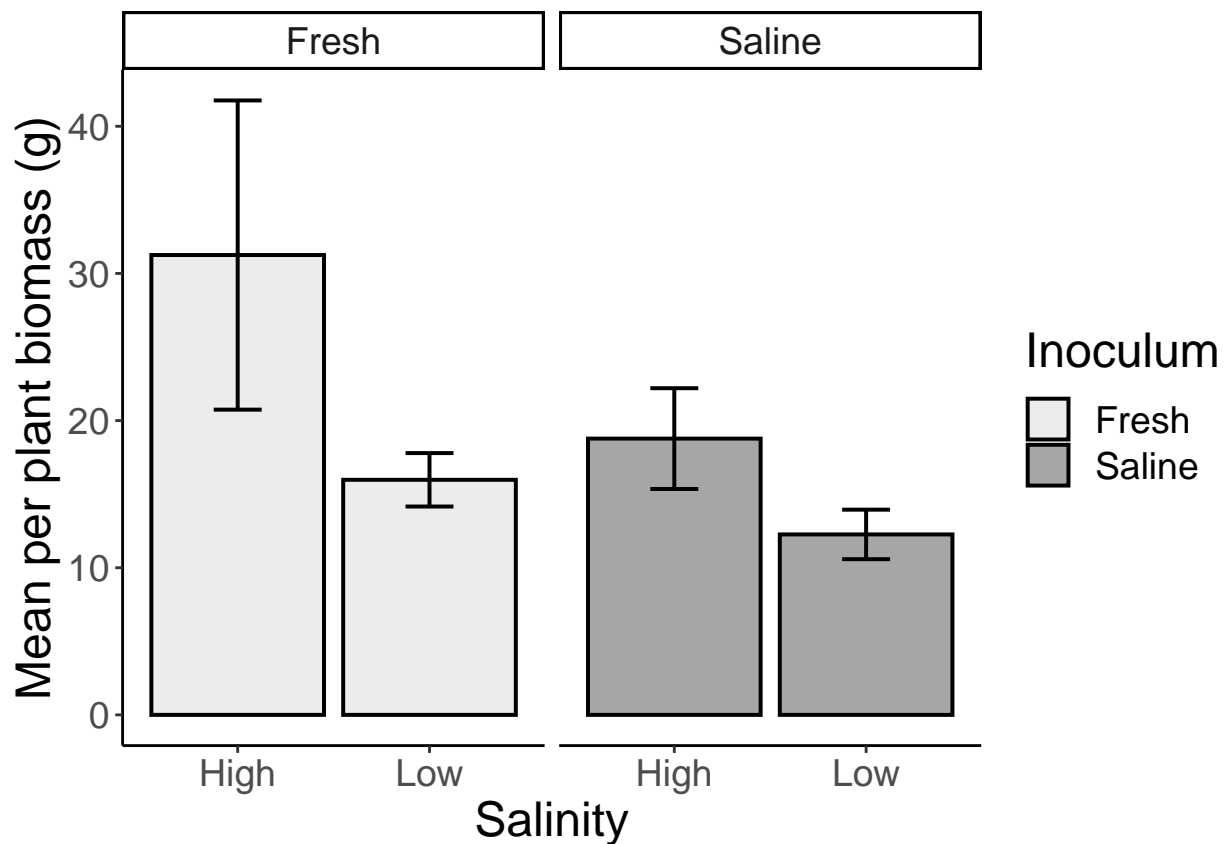
```
## Salinity:Inoculum 1 153.6 153.56 0.5987 0.44554
## Residuals      28 7181.3 256.48
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Bar Graph

```
NatSp2<-NatSp1%>%
  filter(Species=="SC.tot")%>%
  group_by(Inoculum, Salinity)%>%
  summarise(mean=mean(Biomass), se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
ggplot(NatSp2,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey90","grey50"))+
  ylab("Mean per plant biomass (g)")+
  facet_wrap(~Inoculum)
```



Mixed Community

Native Community

```
NatSp<-BM%>%
  filter(Inoculum!="Sterile")%>%
  filter(Community.Type=="Mixed")%>%
  select(c(1,2,3,4,5,16,17,18))%>%
  gather(key="Species", value="Biomass", c(SL.tot, SP.tot, SC.tot))%>%
  #mutate(Biomass=Biomass/2)%>%
  mutate(Salinity=factor(NatSp1$Salinity, levels=c("Low","High")))
```

Sagittaria lancifolia ANOVA

```
x<-NatSp%>%
  filter(Species=="SL.tot")
modx<-lm(Biomass~Salinity*Inoculum, dat=x)
anova(modx)
```

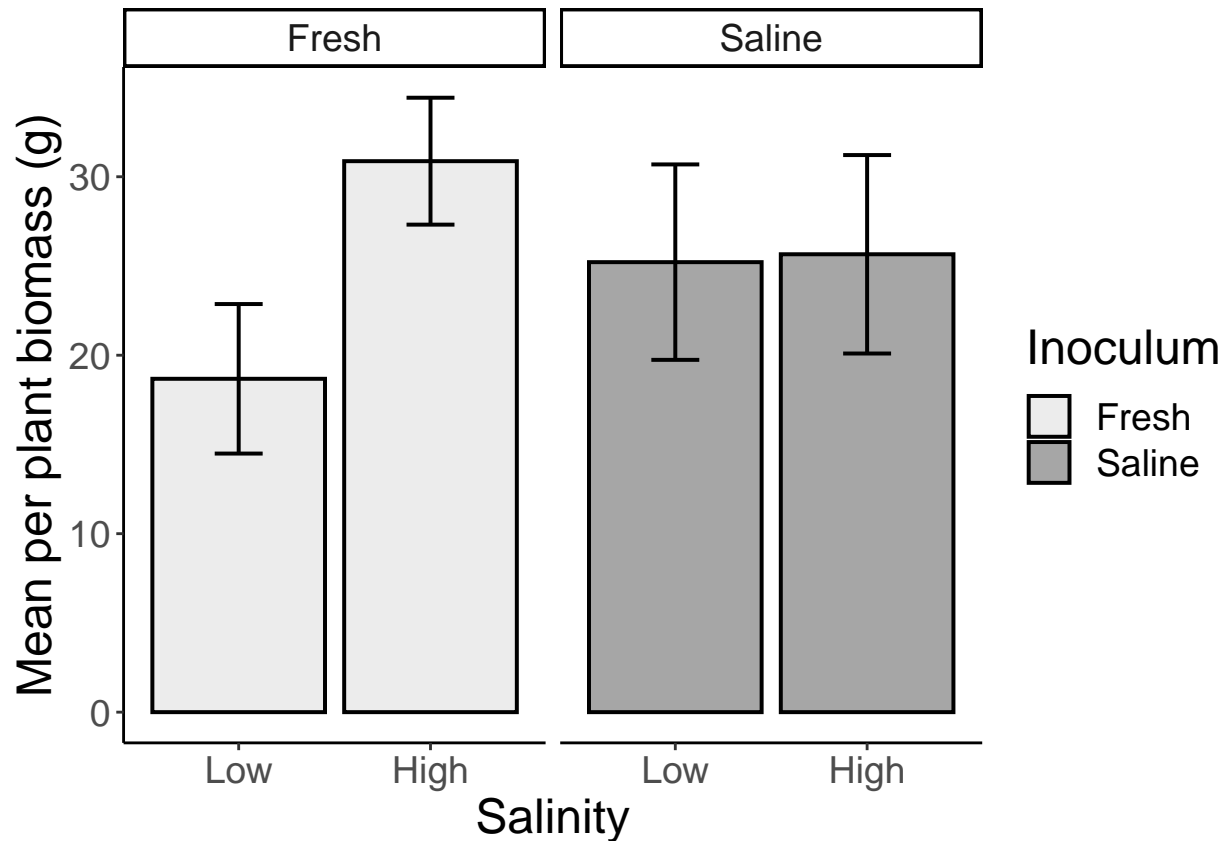
```
## Analysis of Variance Table
##
## Response: Biomass
##           Df Sum Sq Mean Sq F value Pr(>F)
## Salinity    1  327.7   327.68   1.7380 0.1981
## Inoculum     1    3.4     3.43   0.0182 0.8936
## Salinity:Inoculum 1  271.9   271.92   1.4422 0.2398
## Residuals   28 5279.1   188.54
```

Bar Graph

```
NatSp2<-NatSp%>%
  filter(Species=="SL.tot")%>%
  group_by(Inoculum, Salinity)%>%
  summarise(mean=mean(Biomass), se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
ggplot(NatSp2,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey90","grey50"))+
  ylab("Mean per plant biomass (g)")+
  facet_wrap(~Inoculum)
```

Spartina patens ANOVA

```
x<-NatSp%>%
  filter(Species=="SP.tot")
modx<-lm(Biomass~Salinity*Inoculum, dat=x)
anova(modx)
```

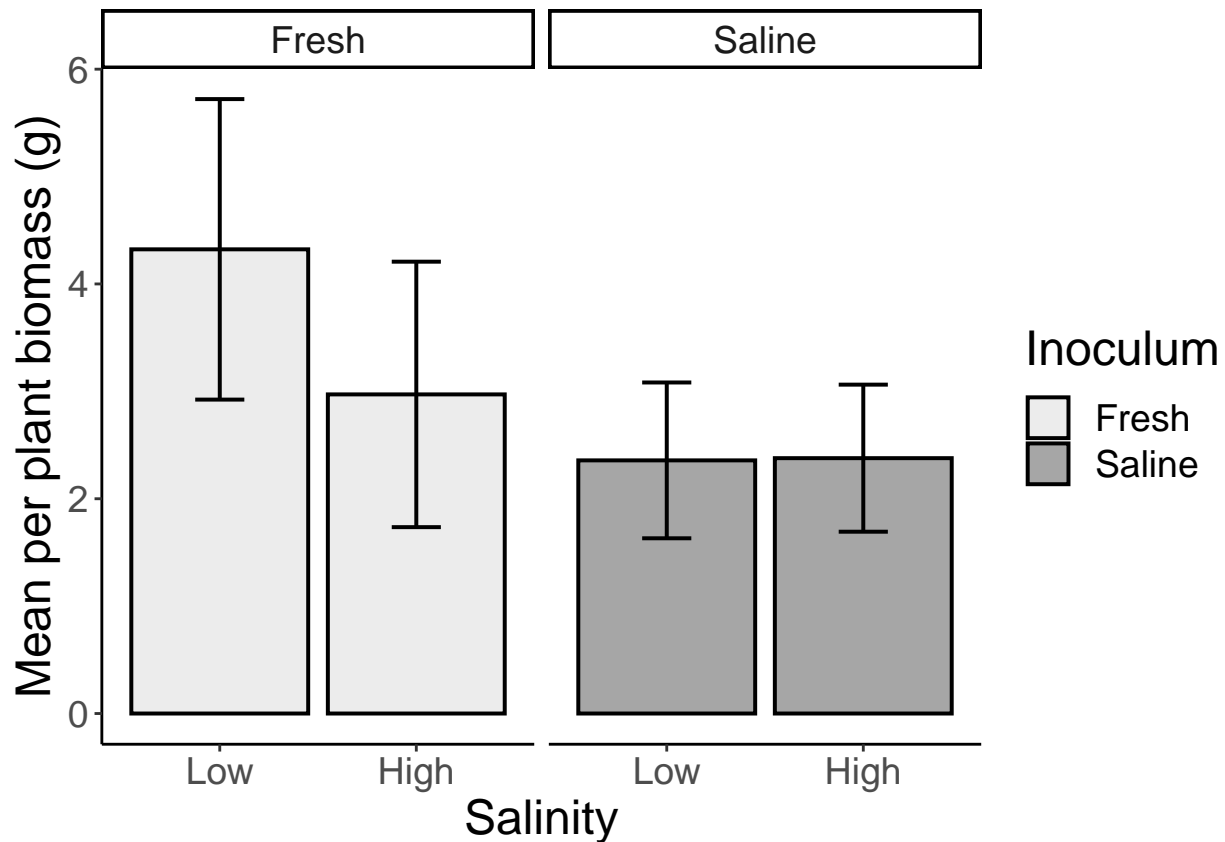
```
## Analysis of Variance Table
##
## Response: Biomass
##          Df Sum Sq Mean Sq F value Pr(>F)
## Salinity    1   5.445   5.4450   0.5843 0.4510
## Inoculum     1  12.890  12.8896   1.3831 0.2495
## Salinity:Inoculum 1   3.703   3.7029   0.3973 0.5336
## Residuals  28 260.943   9.3194
```

Bar Graph

```
NatSp2<-NatSp%>%
  filter(Species=="SP.tot")%>%
  group_by(Inoculum, Salinity)%>%
  summarise(mean=mean(Biomass), se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
ggplot(NatSp2,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey90","grey50"))+
  ylab("Mean per plant biomass (g)")+
  facet_wrap(~Inoculum)
```



Schoenoplectus californicus ANOVA

```
x<-NatSp%>%
  filter(Species=="SC.tot")
modx<-lm(Biomass~Salinity*Inoculum, dat=x)
anova(modx)
```

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

```
##
```

```
## Response: Biomass
```

```
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Salinity    1  18.30   18.301    1.2707 0.26920
## Inoculum     1  18.94   18.939    1.3150 0.26119
## Salinity:Inoculum 1  78.97   78.969    5.4831 0.02654 *
## Residuals   28 403.26   14.402
```

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

Bar Graph

```
NatSp2<-NatSp%>%
  filter(Species=="SC.tot")%>%
  group_by(Inoculum, Salinity)%>%
  summarise(mean=mean(Biomass), se=std.error(Biomass))
```

'summarise()' has grouped output by 'Inoculum'. You can override using the '.groups' argument.

```
ggplot(NatSp2,aes(x=Salinity,y=mean,fill=Inoculum)) +
  theme_classic()+
  theme(legend.position="right",text = element_text(size=18)) +
  geom_bar(stat="identity",size=0.7,alpha= 0.7, color="black" ) +
  geom_errorbar(aes(ymax=mean+se, ymin=mean-se),width=.25,size=0.70)+
  scale_fill_manual(values=c("grey90","grey50"))+
  ylab("Mean per plant biomass (g)")+
  facet_wrap(~Inoculum)
```

