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#Mesocosm Study Analysis
#Riley Morris

#Install packages
install.packages("ggplot2")
install.packages("devtools")
library(devtools)
install_github("easyGgplot2", "kassambara")
install.packages("EnvStats")
install.packages("dplyr")
install.packages("lme4")
install.packages("car")

#Package call
library(ggplot2)
library(readxl)
library(dplyr)
library(EnvStats)
library(easyGgplot2)
library(lme4)
library(car)

#Data import
BO_BMCount <- read_excel("C:/Users/Morris Clan/Dropbox/Academics/Education/03 - Master of Biology/BIOL 5909 -
Masters Thesis/Analysis/Fitness Analyses/MesocosmData2.xlsx")

BO_BMCount$Trial <- as.factor(BO_BMCount$Trial)
BO_BMCount$Treatment <- as.factor(BO_BMCount$Treatment)
BO_BMCount$Genotype <- as.factor(BO_BMCount$Genotype)
BO_BMCount$MBO <- as.factor(BO_BMCount$MBO)
BO_BMCount$TBO <- as.factor(BO_BMCount$TBO)

FitData <- split(BO_BMCount, BO_BMCount$Trial)
FitData3 <- subset(FitData$`2`, TBO == 3)
FitData3_3 <- subset(FitData3, MBO == 3)
FitData3_5 <- subset(FitData3, MBO == 5)
FitData3_7 <- subset(FitData3, MBO == 7)
FitData3_9 <- subset(FitData3, MBO == 9)
FitData5 <- subset(FitData$`2`, TBO == 5)
FitData5_3 <- subset(FitData5, MBO == 3)
FitData5_5 <- subset(FitData5, MBO == 5)
FitData5_7 <- subset(FitData5, MBO == 7)
FitData5_9 <- subset(FitData5, MBO == 9)
FitData7 <- subset(FitData$`2`, TBO == 7)
FitData7_3 <- subset(FitData7, MBO == 3)
FitData7_5 <- subset(FitData7, MBO == 5)
FitData7_7 <- subset(FitData7, MBO == 7)
FitData7_9 <- subset(FitData7, MBO == 9)
FitData9 <- subset(FitData$`2`, TBO == 9)
FitData9_3 <- subset(FitData9, MBO == 3)
FitData9_5 <- subset(FitData9, MBO == 5)
FitData9_7 <- subset(FitData9, MBO == 7)
FitData9_9 <- subset(FitData9, MBO == 9)
FitData35 <- rbind(FitData3_3, FitData3_5, FitData3_7, FitData3_9,
FitData5_3, FitData5_5, FitData5_7, FitData5_9,
FitData7_3, FitData7_5, FitData7_7, FitData7_9,
FitData9_3, FitData9_5, FitData9_7, FitData9_9)

n.TBO3 <- length(FitData35$TBO[FitData35$TBO == 3])
n.TBO5 <- length(FitData35$TBO[FitData35$TBO == 5])
n.TBO7 <- length(FitData35$TBO[FitData35$TBO == 7])
n.TBO9 <- length(FitData35$TBO[FitData35$TBO == 9])
n.MBO3 <- length(FitData35$MBO[FitData35$MBO == 3])
n.MBO5 <- length(FitData35$MBO[FitData35$MBO == 5])
n.MBO7 <- length(FitData35$MBO[FitData35$MBO == 7])
n.MBO9 <- length(FitData35$MBO[FitData35$MBO == 9])

#Turion Production
levels(BO_Fitness$MBO) <- c("MBO3", "MBO5", "MBO7", "MBO9")
ggplot(BO_Fitness, aes(as.numeric(TBO), colour = I("black"))) +
  geom_histogram(binwidth = 1, show.legend = F, alpha = 0.2) +
  facet_grid(~ BO_Fitness$MBO) +
  theme_bw() +
  theme(panel.grid = element_blank()) +
  xlab("Turion Birth Order") +
  xlim("3", "5", "7", "9") +
  ylab("Turion Yield")
levels(BO_Fitness$MBO) <- c("3", "5", "7", "9")

levels(BO_BMCount$MBO) <- c("MBO3", "MBO5", "MBO7", "MBO9")
ggplot(BO_BMCount, aes(as.numeric(TBO), colour = I("black"))) +
  geom_histogram(binwidth = 1, show.legend = F, alpha = 0.2) +
  facet_grid(~ BO_BMCount$MBO) +
  theme_bw() +
  theme(panel.grid = element_blank()) +
  xlab("Turion Birth Order") +
  xlim("3", "5", "7", "9") +
  ylab("Turion Yield")

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levels(BO_BMCount$MBO) <- c("3","5","7","9")

#Compare GRateC and GRateM
Fit_GRate1 <- lm(GRateM ~ GRateC, data = BO_BMCount)
Fit_GRate2 <- lm(GRateC ~ GRateM, data = BO_BMCount)
summary(Fit_GRate1)
summary(Fit_GRate2)

Fit_GRate3 <- lm(GRateM ~ GRateC, data = FitData$`1`)
Fit_GRate4 <- lm(GRateC ~ GRateM, data = FitData$`1`)
summary(Fit_GRate3)
summary(Fit_GRate4)
Fit_GRate5 <- lm(GRateM ~ GRateC, data = FitData$`2`)
Fit_GRate6 <- lm(GRateC ~ GRateM, data = FitData$`2`)
summary(Fit_GRate5)
summary(Fit_GRate6)
FitData2_Amb <- subset(FitData$`2`, Treatment == 1)
Fit_GRateAmb <- lm(GRateM ~ GRateC, data = FitData2_Amb)
summary(Fit_GRateAmb)
FitData2_Amb2 <- subset(FitData$`2`, Treatment == 2)
Fit_GRateAmb2 <- lm(GRateM ~ GRateC, data = FitData2_Amb2)
summary(Fit_GRateAmb2)
FitData2_Amb5 <- subset(FitData$`2`, Treatment == 3)
Fit_GRateAmb5 <- lm(GRateM ~ GRateC, data = FitData2_Amb5)
summary(Fit_GRateAmb5)

#Plot
#GRateCout vs GRateMass
levels(BO_BMCount$Trial) <- c("Trial 1","Trial 2")
levels(BO_BMCount$Treatment) <- c("Ambient","Amb+2°C","Amb+5°C")
ggplot(BO_BMCount, aes(GRateC, GRateM)) +
  geom_point(colour = 4, alpha = 0.5) +
  geom_smooth(method = loess, fullrange = T) +
  facet_grid(BO_BMCount$Treatment ~ BO_BMCount$Trial) +
  xlab("Growth Rate Based on Count") +
  ylab("Growth Rate Based on Dry Biomass") +
  theme_bw()
ggplot(BO_BMCount, aes(FinalCount, FinalMass)) +
  geom_point(aes(colour = BO_BMCount$Treatment), alpha = 0.5) +
  geom_smooth(method = loess, fullrange = T) +
  facet_grid( ~ BO_BMCount$Trial) +
  xlab("Growth Rate Based on Count") +
  ylab("Growth Rate Based on Dry Biomass") +
  theme_bw()
levels(BO_BMCount$Trial) <- c("1","2")
levels(BO_BMCount$Treatment) <- c("1","2","3")
#Count vs Mass
ggplot(BO_BMCount, aes(FinalCount,FinalMass)) +
  geom_point() +
  geom_smooth(method = lm) +
  xlab("Number of Fronds per Raft (#)") +
  ylab("Dry Biomass (g)") +
  theme_bw()
ggplot(BO_BMCount, aes(GRateC,GRateM)) +
  geom_point() +
  geom_smooth(method = lm) +
  xlab("Number of Fronds per Raft (#)") +
  ylab("Dry Biomass (g)") +
  theme_bw()

#1. Are there differences in growth rate among ponds?
#2. Are there differences in growth rate among treatments within the pond array?
#   (pond nested within treatment)
#3. Are the differences due to birth order? (mother and/or daughter)
#4. ALTERNATIVE ANALYSIS: BO as a single value
#5. ALTERNATIVE ANALYSIS: Non-parametric test
#Additional effects analyses

#Item #1: Differences in growth rate among ponds?
Fit_Pond <- lm(GRateC ~ Pond, data = BO_BMCount)
AOV_Pond <- aov(Fit_Pond)
summary(Fit_Pond)
summary(AOV_Pond)
anova(AOV_Pond)

#Plot
ggplot(BO_BMCount, aes(Pond, GRateC)) +
  geom_boxplot(aes(fill = BO_BMCount$Trial), alpha = 0.2) +
  theme_bw() +
  ggtitle("Growth Rate among Mesocosms") +
  xlab("Mesocosm") +
  ylab("Growth Rate") +
  stat_n_text(size = 3) +
  scale_fill_discrete(" ", labels = c("Trial 1","Trial 2"))

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#Item #2: Differences in growth rate among ponds due to treatment?
Lme_TreatFullC <- lmer(GRateC ~ Treatment + (1|Pond/Treatment), data = BO_BMCount)
summary(Lme_TreatFullC)
anova(Lme_TreatFullC)

Lme_TreatFullM <- lmer(GRateM ~ Treatment + (1|Pond/Treatment), data = BO_BMCount)
summary(Lme_TreatFullM)
anova(Lme_TreatFullM)

#Reduced Dataset
Lme_TreatRedC <- lmer(GRateC ~ Treatment + (1|Pond/Treatment), data = FitData35)
summary(Lme_TreatRedC)
anova(Lme_TreatRedC)

Lme_TreatRedM <- lmer(GRateM ~ Treatment + (1|Pond/Treatment), data = FitData35)
summary(Lme_TreatRedM)
anova(Lme_TreatRedM)

#Plots
ggplot(BO_BMCount, aes(MeanTemp, GRateC)) +
  geom_jitter(colour = "grey", position = position_jitter(0.02)) +
  geom_smooth(aes(colour = 4), method = lm, show.legend = F) +
  facet_grid(~ BO_BMCount$Trial) +
  theme_bw() +
  xlab("Mean Mesocosm Temperature") +
  ylab("Growth Rate")

#Categorical: boxplots
ggplot(FitData35, aes(Treatment, GRateM)) +
  geom_boxplot(colour = 4, alpha = 0.5) +
  theme_bw() +
  xlab("Treatment") +
  xlim(labels = c("Ambient", "Amb+2°C", "Amb+5°C")) +
  ylab("Growth Rate (biomass)")
ggplot(FitData35, aes(as.factor(TreatB), GRateM)) +
  geom_boxplot() +
  theme_bw() +
  xlab("Treatment") +
  ylab("Growth Rate (biomass)")

#Continuous: scatter
ggplot(FitData35, aes(as.numeric(Treatment), GRateM)) +
  geom_jitter(colour = 4, alpha = 0.5, position = position_jitter(0.05)) +
  stat_summary(fun.y = mean, geom = "line", colour = 4) +
  theme_bw() +
  xlab("Treatment") +
  ylab("Growth Rate (biomass)")
ggplot(FitData35, aes(Treatment, GRateM)) +
  geom_jitter(colour = 4, alpha = 0.5, position = position_jitter(0.05)) +
  geom_smooth(colour = 4, method = loess, se = F) +
  theme_bw() +
  xlab("Treatment") +
  ylab("Growth Rate (biomass)")
ggplot(FitData35, aes(Width, GRateM)) +
  geom_point(colour = 4, alpha = 0.5) +
  geom_smooth(colour = 4, method = lm, se = F) +
  theme_bw() +
  facet_grid(. ~ Treatment) +
  xlab("Turion Size") +
  ylab("Growth Rate (biomass)")

#Item #3: Are growth rate differences due to BO?
Lme_BOFullC <- lmer(GRateC ~ Treatment*MBO*TBO + (1|Pond/Treatment), data = BO_BMCount)
summary(Lme_BOFullC)
anova(Lme_BOFullC)

Lme_BOFullM <- lmer(GRateM ~ Treatment*MBO*TBO + (1|Pond/Treatment), data = BO_BMCount)
summary(Lme_BOFullC)
anova(Lme_BOFullC)

#Reduced Dataset
#Trial 1
Lme_BO1C <- lmer(GRateC ~ Treatment*MBO*TBO + (1|Pond/Treatment), data = FitData$`1`)
summary(Lme_BO2a)
anova(Lme_BO2a)

Lme_BO1M <- lmer(GRateM ~ Treatment*MBO*TBO + (1|Pond/Treatment), data = FitData$`1`)
summary(Lme_BO2b)
anova(Lme_BO2b)

#Trial 2
Lme_BO2C <- lmer(GRateC ~ Treatment*MBO*TBO + (1|Pond/Treatment), data = FitData$`2`)
summary(Lme_BO2C)
anova(Lme_BO2C)

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Lme_BO2M <- lmer(GRateM ~ Treatment*MBO*TBO + (1|Pond/Treatment), data = FitData$`2`)
summary(Lme_BO2M)
anova(Lme_BO2M)

#T2(3|5)
Lme_BO35C <- lmer(GRateC ~ Treatment*MBO*TBO + (1|Pond/Treatment), data = FitData35)
summary(Lme_BO35C)
anova(Lme_BO35C)

#NOTE: THIS IS THE MAIN ANALYSIS
Lme_BO35M <- lmer(GRateM ~ Treatment*MBO*TBO + (1|Pond/Treatment), data = FitData35)
summary(Lme_BO35M)
anova(Lme_BO35M)
ranova(Lme_Main)

#Plot
levels(FitData$`2`$Trial) <- c("Trial 1", "Trial 2")
levels(FitData35$MBO) <- c("MBO3, n = 61", "MBO5, n = 67", "MBO7, n = 0", "MBO9, n = 0")
ggplot(BO_BMCount, aes(MeanTemp, GRateC)) +
  geom_text(aes(label = Pond, colour = Pond)) +
  theme_bw() +
  theme(legend.position = "bottom")
ggplot(FitData35, aes(Treatment, GRateC, colour = TBO)) +
  geom_jitter(position = position_jitter(0.02), alpha = 0.5) +
  geom_smooth(data = FitData35,
              aes(group = TBO, colour = TBO),
              method = lm,
              se = F,
              fullrange = T) +
  theme_bw() +
  facet_grid( ~ FitData35$MBO) +
  xlab("Temperature Treatment") +
  ylab("Growth Rate (dry biomass)") +
  scale_colour_discrete("Turion Birth Order",
                        labels = c("TBO3, n = 66", "TBO5, n = 62", "TBO7, n = 0", "TBO9, n = 0")) +
  theme(legend.position = "bottom") +
  scale_x_discrete(labels = c("Ambient", "Amb+2°C", "Amb+5°C"))

levels(FitData$`2`$Trial) <- c("Trial 1", "Trial 2")
levels(FitData35$MBO) <- c("MBO3, n = 61", "MBO5, n = 67", "MBO7, n = 0", "MBO9, n = 0")
ggplot(FitData35, aes(Treatment, GRateC, colour = as.factor(TBO))) +
  geom_jitter(position = position_jitter(0.02), alpha = 0.5) +
  geom_smooth(data = FitData35,
              aes(group = as.factor(TBO), colour = as.factor(TBO)),
              method = lm,
              se = F,
              fullrange = T) +
  theme_bw() +
  facet_grid( ~ as.factor(FitData35$MBO)) +
  xlab("Temperature Treatment") +
  # xlim(labels = c("Ambient", "Amb+2°C", "Amb+5°C")) +
  ylab("Growth Rate (dry biomass)") +
  scale_colour_discrete("Turion Birth Order",
                        labels = c("TBO3, n = 66", "TBO5, n = 62", "TBO7, n = 0", "TBO9, n = 0")) +
  theme(legend.position = "bottom") +
  scale_x_continuous(labels = c("Ambient", " ", "Amb+2°C", " ", " ", "Amb+5°C"))

levels(FitData$`2`$Trial) <- c("Trial 1", "Trial 2")
levels(FitData$`2`$MBO) <- c("MBO3", "MBO5", "MBO7", "MBO9")
ggplot(FitData$`2`, aes(Treatment, GRateC, colour = as.factor(TBO))) +
  geom_jitter(position = position_jitter(0.02), alpha = 0.5) +
  geom_smooth(data = FitData$`2`,
              aes(group = as.factor(TBO), colour = as.factor(TBO)),
              method = lm,
              se = F,
              fullrange = T) +
  theme_bw() +
  facet_grid( ~ as.factor(FitData$`2`$MBO)) +
  xlab("Temperature Treatment") +
  ylab("Growth Rate (dry biomass)") +
  scale_colour_manual("Turion Birth Order",
                      labels = c("TBO3", "TBO5", "TBO7", "TBO9")) +
  scale_color_manual(name = "Turion Birth Order",
                     values = c("#E69F00", "#0072B2", "#009E73", "#CC79A7")) +
  theme(legend.position = "bottom") +
  scale_x_continuous(labels = c("Amb.", " ", "Amb+2°C", " ", " ", "Amb+5°C")) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

#Item #4: Effects of using a single composite BO value
#BO3 = MBO3,TBO3
#BO4a = MBO3,TBO5
#BO4b = MBO5,TBO3
#BO5 = MBO5,TBO5

#T2(3|5) - 3 BO categories

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Lme_3BO1 <- lmer(GRateM ~ Treatment*ThreeBO + (1|Pond/Treatment), data = FitData35)
summary(Lme_3BO)
anova(Lme_3BO)

#T2{3|5} - 4 BO categories
Lme_4BO <- lmer(GRateM ~ Treatment*FourBO + (1|Pond/Treatment), data = FitData35)
summary(Lme_4BO)
anova(Lme_4BO)

#Plot
#BOXPLOTS
levels(FitData35$Treatment) <- c("Ambient", "Amb+2°C", "Amb+5°C")
ggplot(FitData35, aes(ThreeBO, GRateM)) +
  geom_boxplot() +
  facet_grid( ~ Treatment) +
  theme_bw() +
  xlab("Birth Order") +
  ylab("Growth Rate (dry biomass)")
ggplot(FitData35, aes(FourBO, GRateM)) +
  geom_boxplot() +
  facet_grid( ~ Treatment) +
  theme_bw() +
  xlab("Birth Order") +
  ylab("Growth Rate (dry biomass)")
#SCATTER PLOTS
ggplot(FitData35, aes(as.numeric(ThreeBO), GRateM)) +
  geom_jitter(colour = alpha(4,0.5), position = position_jitter(0.02)) +
  geom_smooth(method = loess, se = F) +
  theme_bw() +
  xlab("Birth Order") +
  stat_n_text(size = 3) +
  ylab("Growth Rate (dry biomass)")
levels(FitData35$Treatment) <- c("1", "2", "3")

#Other Analyses
#1. Genotype
Fit_Gen <- lm(GRateC ~ Genotype, data = BO_BMCount)
AOV_Gen <- aov(Fit_Gen)
summary(Fit_Gen)
summary(AOV_Gen)
TukeyHSD(AOV_Gen)

Lme_Gen <- lmer(GRateC ~ Treatment + Genotype + (1|Pond/Treatment), data = FitData35)
summary(Lme_Gen)
anova(Lme_Gen)
glht(Lme_Gen, linfct = mcp(MeanTemp = "Tukey"))
glht(Lme_Gen, linfct = mcp(Genotype = "Tukey"))

#Plot
levels(BO_BMCount$Genotype) = c("Genotype 1", "Genotype 2")
gg1 <- ggplot(BO_BMCount, aes(MeanTemp, GRateC)) +
  geom_jitter(aes(colour = BO_BMCount$Genotype), alpha = 0.3, position = position_jitter(0.04)) +
  geom_smooth(method = lm, aes(group = BO_BMCount$Genotype, colour = BO_BMCount$Genotype), se = F) +
  theme_bw() +
  #facet_grid( ~ ReactTime$Genotype) +
  ggtitle("All Mesocosm Data") +
  xlab("Mean Mesocosm Temperature (deg C)") +
  #xlim(labels = c("10", "18", "26")) +
  ylab("Growth Rate (hrs)") +
  scale_colour_discrete("Genotype", labels = c("Genotype 1", "Genotype 2")) +
  theme(legend.position = "bottom")
gg2 <- ggplot(FitData35, aes(MeanTemp, GRateC)) +
  geom_jitter(aes(colour = FitData35$Genotype), alpha = 0.3, position = position_jitter(0.04)) +
  geom_smooth(method = lm, aes(group = FitData35$Genotype, colour = FitData35$Genotype), se = F) +
  theme_bw() +
  #facet_grid( ~ ReactTime$Genotype) +
  ggtitle("Only BO3 & BO5 Data") +
  xlab("Mean Mesocosm Temperature (deg C)") +
  #xlim(labels = c("10", "18", "26")) +
  ylab("Growth Rate (hrs)") +
  scale_colour_discrete("Genotype", labels = c("Genotype 1", "Genotype 2")) +
  theme(legend.position = "bottom")
ggplot2::multiplot(gg1, gg2, col = 1)
levels(ReactTime$Genotype) = c("1", "2")

#Mean Differences
FitData35_Low <- FitData35[FitData35$MeanTemp == 21.30275]
FitData35_High <- FitData35[FitData35$MeanTemp == 26.67126]
mean(FitData35_Low$GRateC[FitData35_Low$Genotype == 1], na.rm = T)
mean(FitData35_Low$GRateC[FitData35_Low$Genotype == 2], na.rm = T)
mean(FitData35_High$GRateC[FitData35_High$Genotype == 1], na.rm = T)
mean(FitData35_High$GRateC[FitData35_High$Genotype == 2], na.rm = T)

#size
Fit_Size1 <- lm(GRateM ~ Width, data = BO_BMCount)

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summary(Fit_Size1)
anova(Fit_Size1)
Fit_Size2a <- lm(GRateM ~ Width, data = FitData35)
summary(Fit_Size2a)
anova(Fit_Size2a)
Fit_Size2b <- lm(GRateM ~ Treatment + Width, data = FitData35)
summary(Fit_Size2b)
anova(Fit_Size2b)
Fit_Size2c <- lm(GRateM ~ Treatment + Width + TBO, data = FitData35)
summary(Fit_Size2c)
anova(Fit_Size2c)
Fit_Size2d <- lm(GRateM ~ Treatment + Width + TBO + MBO + Genotype, data = FitData35)
summary(Fit_Size2d)
anova(Fit_Size2d)
Lme_Size3a <- lmer(GRateM ~ Width + (1|Pond/Treatment), data = FitData35)
summary(Lme_Size3a)
anova(Lme_Size3a)
Lme_Size3b <- lmer(GRateM ~ Treatment + Width + (1|Pond/Treatment), data = FitData35)
summary(Lme_Size3b)
anova(Lme_Size3b)
ranova(Lme_Size3b)
Lme_Size3b <- lmer(GRateM ~ Treatment + Width + (1|Pond/Treatment), data = FitData$`2`)
summary(Lme_Size3b)
anova(Lme_Size3b)
ranova(Lme_Size3b)
Lme_Size3c <- lmer(GRateM ~ Treatment + Width + TBO + (1|Pond/Treatment), data = FitData35)
summary(Lme_Size3c)
anova(Lme_Size3c)
Lme_Size3d <- lmer(GRateM ~ Treatment + Width + TBO + MBO + (1|Pond/Treatment), data = FitData35)
summary(Lme_Size3d)
anova(Lme_Size3d)

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#Plot
ggplot(FitData35, aes(Width, GRateM)) +
  geom_point() +
  facet_grid( ~ Trial) +
  theme_bw()
ggplot(FitData35, aes(as.numeric(TBO), Width)) +
  geom_jitter(colour = 4, alpha = 0.5, position = position_jitter(0.02)) +
  geom_smooth(method = lm) +
  facet_grid( ~ MBO) +
  xlab("Turion Birth Order") +
  xlim(labels = c("TBO3", "TBO5")) +
  ylab("Turion Size (mm)") +
  theme_bw()
ggplot(FitData35, aes(Width, GRateM)) +
  geom_point(aes(colour = TBO), alpha = 0.5) +
  geom_smooth(aes(group = TBO, colour = TBO), method = lm) +
  facet_grid(MBO ~ Treatment) +
  ylab("Growth Rate") +
  xlab("Turion Size (mm)") +
  theme_bw()
ggplot(BO_BMCount, aes(Width, GRateM)) +
  geom_point(aes(colour = TBO), alpha = 0.5) +
  geom_smooth(aes(group = TBO, colour = TBO), method = lm) +
  facet_grid(MBO ~ Treatment) +
  ylab("Growth Rate") +
  xlab("Turion Size (mm)") +
  theme_bw()
ggplot(FitData35, aes(Width, GRateM)) +
  geom_point(aes(colour = TBO), alpha = 0.5) +
  geom_smooth(aes(colour = TBO, group = TBO), method = lm, se = F) +
  facet_grid(Treatment ~ Pond) +
  ylab("Growth Rate") +
  xlab("Turion Size (mm)") +
  theme_bw()

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#### #Chemistry Data

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#pH
Fit_pH <- lm(GRateM ~ Treatment + pH, data = BO_BMCount)
AOV_pH <- aov(Fit_pH)
summary(Fit_pH)
summary(AOV_pH)
Fit_pH <- lm(GRateM ~ Treatment + pH + TBO, data = BO_BMCount)
AOV_pH <- aov(Fit_pH)
summary(Fit_pH)
summary(AOV_pH)
Fit_pH <- lm(GRateM ~ Treatment + pH, data = FitData35)
AOV_pH <- aov(Fit_pH)
summary(Fit_pH)
summary(AOV_pH)
Fit_pH <- lm(GRateM ~ Treatment + pH + TBO, data = FitData35)
AOV_pH <- aov(Fit_pH)
summary(Fit_pH)
summary(AOV_pH)

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#Plot
levels(FitData35$Treatment) <- c("Ambient", "Amb+2°C", "Amb+5°C")
ggplot(FitData35, aes(pH, GRateM)) +
  geom_point(colour = 4, alpha = 0.5) +
  geom_smooth(method = lm) +
  facet_grid( ~ Treatment) +
  theme_bw()
ggplot(BO_BMCount, aes(pH, GRateM)) +
  geom_point(colour = 4, alpha = 0.5) +
  geom_smooth(method = lm) +
  facet_grid(Treatment ~ Trial) +
  theme_bw()
levels(FitData35$Treatment) <- c("1", "2", "3")
#Dissolved Oxygen
Fit_DO <- lm(GRateM ~ Treatment + DO, data = BO_BMCount)
AOV_DO <- aov(Fit_DO)
summary(Fit_DO)
summary(AOV_DO)
Fit_DO <- lm(GRateM ~ Treatment + DO + TBO, data = BO_BMCount)
AOV_DO <- aov(Fit_DO)
summary(Fit_DO)
summary(AOV_DO)
Fit_DO <- lm(GRateM ~ Treatment + DO, data = FitData35)
AOV_DO <- aov(Fit_DO)
summary(Fit_DO)
summary(AOV_DO)
Fit_DO <- lm(GRateM ~ Treatment + DO + TBO, data = FitData35)
AOV_DO <- aov(Fit_DO)
summary(Fit_DO)
summary(AOV_DO)
#Total Dissolved Solids
Fit_TDS <- lm(GRateM ~ Treatment + TDS, data = BO_BMCount)
AOV_TDS <- aov(Fit_TDS)
summary(Fit_TDS)
summary(AOV_TDS)
Fit_TDS <- lm(GRateM ~ Treatment + TDS + TBO, data = BO_BMCount)
AOV_TDS <- aov(Fit_TDS)
summary(Fit_TDS)
summary(AOV_TDS)
Fit_TDS <- lm(GRateM ~ Treatment + TDS, data = FitData35)
AOV_TDS <- aov(Fit_TDS)
summary(Fit_TDS)
summary(AOV_TDS)
Fit_TDS <- lm(GRateM ~ Treatment + TDS + TBO, data = FitData35)
AOV_TDS <- aov(Fit_TDS)
summary(Fit_TDS)
summary(AOV_TDS)
#Electrical Conductivity
Fit_EC <- lm(GRateM ~ Treatment + EC, data = BO_BMCount)
AOV_EC <- aov(Fit_EC)
summary(Fit_EC)
summary(AOV_EC)
Fit_EC <- lm(GRateM ~ Treatment + EC + TBO, data = BO_BMCount)
AOV_EC <- aov(Fit_EC)
summary(Fit_EC)
summary(AOV_EC)
Fit_EC <- lm(GRateM ~ Treatment + EC, data = FitData35)
AOV_EC <- aov(Fit_EC)
summary(Fit_EC)
summary(AOV_EC)
Fit_EC <- lm(GRateM ~ Treatment + EC + TBO, data = FitData35)
AOV_EC <- aov(Fit_EC)
summary(Fit_EC)
summary(AOV_EC)
#Oxygen Reduction Potential
Fit_ORP <- lm(GRateM ~ Treatment + ORP, data = BO_BMCount)
AOV_ORP <- aov(Fit_ORP)
summary(Fit_ORP)
summary(AOV_ORP)
Fit_ORP <- lm(GRateM ~ Treatment + ORP + TBO, data = BO_BMCount)
AOV_ORP <- aov(Fit_ORP)
summary(Fit_ORP)
summary(AOV_ORP)
Fit_ORP <- lm(GRateM ~ Treatment + ORP, data = FitData35)
AOV_ORP <- aov(Fit_ORP)
summary(Fit_ORP)
summary(AOV_ORP)
Fit_ORP <- lm(GRateM ~ Treatment + ORP + TBO, data = FitData35)
AOV_ORP <- aov(Fit_ORP)
summary(Fit_ORP)
summary(AOV_ORP)
#Resistivity
Fit_Res <- lm(GRateM ~ Treatment + Res, data = BO_BMCount)
AOV_Res <- aov(Fit_Res)
summary(Fit_Res)

```

```

summary(AOV_Res)
Fit_Res <- lm(GRateM ~ Treatment + Res + TBO, data = BO_BMCount)
AOV_Res <- aov(Fit_Res)
summary(Fit_Res)
summary(AOV_Res)
Fit_Res <- lm(GRateM ~ Treatment + Res, data = FitData35)
AOV_Res <- aov(Fit_Res)
summary(Fit_Res)
summary(AOV_Res)
Fit_Res <- lm(GRateM ~ Treatment + Res + TBO, data = FitData35)
AOV_Res <- aov(Fit_Res)
summary(Fit_Res)
summary(AOV_Res)
summary(AOV_ORP)
#Surface Temperature
Fit_STemp <- lm(GRateM ~ Treatment + Temp, data = BO_BMCount)
AOV_STemp <- aov(Fit_STemp)
summary(Fit_STemp)
summary(AOV_STemp)
Fit_STemp<- lm(GRateM ~ Treatment + Temp + TBO, data = BO_BMCount)
AOV_STemp <- aov(Fit_STemp)
summary(Fit_STemp)
summary(AOV_STemp)
Fit_STemp <- lm(GRateM ~ Treatment + Temp, data = FitData35)
AOV_STemp <- aov(Fit_STemp)
summary(Fit_STemp)
summary(AOV_STemp)
Fit_STemp <- lm(GRateM ~ Treatment + Temp + TBO, data = FitData35)
AOV_STemp <- aov(Fit_STemp)
summary(Fit_STemp)
summary(AOV_STemp)

#Plot
g1 <- data.frame(x=BO_BMCount$Pond,y=BO_BMCount$MeanTemp)
g2 <- data.frame(x=BO_BMCount$Pond,y=BO_BMCount$Temp)
ggplot(g1,aes(x,y)) +
  geom_point(aes(colour = "Bottom Temperature")) +
  geom_point(data = g2, aes(colour = "Surface Temperature")) +
  theme_bw()

#Mass of One Frond
levels(BO_BMCount$Trial) <- c("Trial 1","Trial 2")
ggplot(FitData$2`, aes(as.numeric(TreatB),FrondMass)) +
  geom_jitter(aes(colour = TBO), alpha = 0.5, position = position_jitter(0.02)) +
  geom_smooth(aes(group = TBO, colour = TBO), method = lm, se = F) +
  #facet_grid(TBO ~ .) +
  xlab("Temperature Treatment") +
  xlim(labels = c("Ambient","Amb+5°C")) +
  ylab("Mass of One Frond (g)") +
  theme_bw()
levels(BO_BMCount$Trial) <- c("1","2")

#Power Analysis
pwr.anova.test(k=48, f=0.28, sig.level = 0.05, power = 0.80)
#No. Groups: k = 48 (4xTBO * 4xMBO * 3xTreatments = 48 groups)
#No. Observations: n = x
#Effect Size: f = 0.25 (small = 0.1, med = 0.25, large = 0.4)
#sig. = 0.05 (Type I error probability)
#power = 0.80 (1 minus type II error probability)
#Effect Size
#Cohen's d = (mean1 - mean2)/SE1&2
#mean1 = mean GRateM for MBO3|TBO3
M1 <- mean(FitData3_3$GRateM)
#mean2 = mean GRateM for MBO9|TBO9
M2 <- mean(FitData5_3$GRateM)
#Standard Error = SD/sqr(n)
FitSD <- rbind(FitData3_3,FitData5_3)
SD <- sd(FitSD$GRateM)
EffSize <- (M2-M1)/SD
EffSize

```