

Photographic_Bleaching

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Loading in required libraries.

Reading in quality controlled color data.

Protocol for ImageJ Bleaching Score Analysis found here.

```
Data <- read.csv("RAnalysis/data/color_score/color_score_colonies.csv", header=T, sep="," , na.string="N")
Data <- na.omit(Data) # removing all rows with NA values
Data$SP.Time.ID <- paste0(Data$ColonyID, "_", Data$Photo_date, "_", Data$treatment) # generating a groupi

#make photo.date a factor
Data$Photo_date = as.factor(Data$Photo_date)
```

Normalize coral color to color standards.

```
Data$Red.Norm.Coral <- Data$Red_coral/Data$Red_standard #normalize to standard
Data$Green.Norm.Coral <- Data$Green_coral/Data$Green_standard #normalize to standard
Data$Blue.Norm.Coral <- Data$Blue_coral/Data$Blue_standard #normalize to standard
```

Principal components analysis to reduce color score to single value representing the majority of the variance

```
score <- Data %>% select("ColonyID", "treatment", "genotype", "tank.num", "Photo_date", "Period", "SP.Time.ID")
blch.scor <- score %>% select("Red.Norm.Coral", "Green.Norm.Coral", "Blue.Norm.Coral") #subset dataframe
blch.scor <- as.matrix(blch.scor) #create matrix
rownames(blch.scor) <- score$SP.Time.ID #name columns in matrix

dist <- vegdist(blch.scor, method="euclidean") #calculate distance matrix of color scores

PCA.color <- princomp(dist) #run principal components analysis
PCA.color # view variance explained by PCs
```

```
## Call:
## princomp(x = dist)
##
## Standard deviations:
##      Comp.1      Comp.2      Comp.3      Comp.4      Comp.5      Comp.6
## 5.040370e+00 3.306822e+00 6.296869e-01 5.337312e-01 3.758244e-01 2.117522e-01
##      Comp.7      Comp.8      Comp.9      Comp.10      Comp.11      Comp.12
```

##	1.812661e-01	1.544898e-01	1.362027e-01	1.070146e-01	9.772188e-02	8.181071e-02
##	Comp.13	Comp.14	Comp.15	Comp.16	Comp.17	Comp.18
##	6.827680e-02	6.508467e-02	5.400698e-02	5.220087e-02	4.725283e-02	4.153029e-02
##	Comp.19	Comp.20	Comp.21	Comp.22	Comp.23	Comp.24
##	3.932913e-02	3.553545e-02	3.306034e-02	3.219140e-02	3.067941e-02	2.818712e-02
##	Comp.25	Comp.26	Comp.27	Comp.28	Comp.29	Comp.30
##	2.698527e-02	2.634908e-02	2.330911e-02	2.203884e-02	2.137489e-02	2.000187e-02
##	Comp.31	Comp.32	Comp.33	Comp.34	Comp.35	Comp.36
##	1.883881e-02	1.852883e-02	1.703958e-02	1.699736e-02	1.642819e-02	1.575175e-02
##	Comp.37	Comp.38	Comp.39	Comp.40	Comp.41	Comp.42
##	1.537211e-02	1.488427e-02	1.454332e-02	1.396422e-02	1.306331e-02	1.302957e-02
##	Comp.43	Comp.44	Comp.45	Comp.46	Comp.47	Comp.48
##	1.228816e-02	1.220449e-02	1.198772e-02	1.139009e-02	1.099507e-02	1.057572e-02
##	Comp.49	Comp.50	Comp.51	Comp.52	Comp.53	Comp.54
##	1.049092e-02	1.008653e-02	9.945285e-03	9.297230e-03	9.081710e-03	8.973942e-03
##	Comp.55	Comp.56	Comp.57	Comp.58	Comp.59	Comp.60
##	8.768489e-03	8.591405e-03	8.531593e-03	8.458304e-03	8.166522e-03	8.037005e-03
##	Comp.61	Comp.62	Comp.63	Comp.64	Comp.65	Comp.66
##	7.979337e-03	7.599793e-03	7.446989e-03	7.361667e-03	7.280099e-03	6.939759e-03
##	Comp.67	Comp.68	Comp.69	Comp.70	Comp.71	Comp.72
##	6.800597e-03	6.745095e-03	6.720598e-03	6.506867e-03	6.367152e-03	6.292722e-03
##	Comp.73	Comp.74	Comp.75	Comp.76	Comp.77	Comp.78
##	6.129784e-03	5.991344e-03	5.855249e-03	5.724118e-03	5.613223e-03	5.475701e-03
##	Comp.79	Comp.80	Comp.81	Comp.82	Comp.83	Comp.84
##	5.444411e-03	5.388912e-03	5.247951e-03	5.126000e-03	5.075080e-03	4.998606e-03
##	Comp.85	Comp.86	Comp.87	Comp.88	Comp.89	Comp.90
##	4.967835e-03	4.925400e-03	4.852873e-03	4.727579e-03	4.661009e-03	4.600950e-03
##	Comp.91	Comp.92	Comp.93	Comp.94	Comp.95	Comp.96
##	4.532901e-03	4.474108e-03	4.396819e-03	4.370409e-03	4.319429e-03	4.269467e-03
##	Comp.97	Comp.98	Comp.99	Comp.100	Comp.101	Comp.102
##	4.193292e-03	4.121796e-03	4.042199e-03	3.998163e-03	3.983063e-03	3.921581e-03
##	Comp.103	Comp.104	Comp.105	Comp.106	Comp.107	Comp.108
##	3.764474e-03	3.725028e-03	3.703014e-03	3.643476e-03	3.630929e-03	3.599729e-03
##	Comp.109	Comp.110	Comp.111	Comp.112	Comp.113	Comp.114
##	3.566891e-03	3.542023e-03	3.499211e-03	3.459244e-03	3.430081e-03	3.406180e-03
##	Comp.115	Comp.116	Comp.117	Comp.118	Comp.119	Comp.120
##	3.361524e-03	3.311071e-03	3.267090e-03	3.217164e-03	3.182113e-03	3.153394e-03
##	Comp.121	Comp.122	Comp.123	Comp.124	Comp.125	Comp.126
##	3.146543e-03	3.112188e-03	3.089537e-03	3.080890e-03	3.040322e-03	3.030106e-03
##	Comp.127	Comp.128	Comp.129	Comp.130	Comp.131	Comp.132
##	2.997647e-03	2.942041e-03	2.936099e-03	2.921836e-03	2.889546e-03	2.880024e-03
##	Comp.133	Comp.134	Comp.135	Comp.136	Comp.137	Comp.138
##	2.850648e-03	2.840361e-03	2.820965e-03	2.796074e-03	2.781437e-03	2.767353e-03
##	Comp.139	Comp.140	Comp.141	Comp.142	Comp.143	Comp.144
##	2.735785e-03	2.727107e-03	2.687316e-03	2.667828e-03	2.613706e-03	2.610851e-03
##	Comp.145	Comp.146	Comp.147	Comp.148	Comp.149	Comp.150
##	2.577644e-03	2.572855e-03	2.563944e-03	2.529950e-03	2.522256e-03	2.466497e-03
##	Comp.151	Comp.152	Comp.153	Comp.154	Comp.155	Comp.156
##	2.458810e-03	2.446376e-03	2.438397e-03	2.432264e-03	2.379843e-03	2.355003e-03
##	Comp.157	Comp.158	Comp.159	Comp.160	Comp.161	Comp.162
##	2.351984e-03	2.321596e-03	2.313964e-03	2.267328e-03	2.248315e-03	2.236039e-03
##	Comp.163	Comp.164	Comp.165	Comp.166	Comp.167	Comp.168
##	2.232273e-03	2.218878e-03	2.210994e-03	2.192774e-03	2.188296e-03	2.170932e-03
##	Comp.169	Comp.170	Comp.171	Comp.172	Comp.173	Comp.174

##	2.164422e-03	2.153464e-03	2.147608e-03	2.138137e-03	2.119747e-03	2.086855e-03
##	Comp.175	Comp.176	Comp.177	Comp.178	Comp.179	Comp.180
##	2.078267e-03	2.055368e-03	2.052496e-03	2.037647e-03	2.027434e-03	2.016227e-03
##	Comp.181	Comp.182	Comp.183	Comp.184	Comp.185	Comp.186
##	2.004572e-03	1.996323e-03	1.987405e-03	1.975862e-03	1.968571e-03	1.942219e-03
##	Comp.187	Comp.188	Comp.189	Comp.190	Comp.191	Comp.192
##	1.934869e-03	1.928502e-03	1.903305e-03	1.892318e-03	1.890959e-03	1.867471e-03
##	Comp.193	Comp.194	Comp.195	Comp.196	Comp.197	Comp.198
##	1.861338e-03	1.843773e-03	1.831365e-03	1.805497e-03	1.802637e-03	1.796445e-03
##	Comp.199	Comp.200	Comp.201	Comp.202	Comp.203	Comp.204
##	1.795585e-03	1.790345e-03	1.780135e-03	1.778613e-03	1.769049e-03	1.745935e-03
##	Comp.205	Comp.206	Comp.207	Comp.208	Comp.209	Comp.210
##	1.739519e-03	1.738177e-03	1.733474e-03	1.696171e-03	1.692757e-03	1.689824e-03
##	Comp.211	Comp.212	Comp.213	Comp.214	Comp.215	Comp.216
##	1.679662e-03	1.647476e-03	1.645162e-03	1.638211e-03	1.634599e-03	1.632511e-03
##	Comp.217	Comp.218	Comp.219	Comp.220	Comp.221	Comp.222
##	1.605194e-03	1.590512e-03	1.587403e-03	1.579092e-03	1.561203e-03	1.560652e-03
##	Comp.223	Comp.224	Comp.225	Comp.226	Comp.227	Comp.228
##	1.552243e-03	1.548076e-03	1.534876e-03	1.511510e-03	1.510421e-03	1.504090e-03
##	Comp.229	Comp.230	Comp.231	Comp.232	Comp.233	Comp.234
##	1.497023e-03	1.471733e-03	1.460790e-03	1.459040e-03	1.438332e-03	1.434750e-03
##	Comp.235	Comp.236	Comp.237	Comp.238	Comp.239	Comp.240
##	1.431662e-03	1.426657e-03	1.416576e-03	1.400149e-03	1.385721e-03	1.379393e-03
##	Comp.241	Comp.242	Comp.243	Comp.244	Comp.245	Comp.246
##	1.378433e-03	1.364944e-03	1.356076e-03	1.350963e-03	1.348725e-03	1.346166e-03
##	Comp.247	Comp.248	Comp.249	Comp.250	Comp.251	Comp.252
##	1.335511e-03	1.325887e-03	1.322489e-03	1.306292e-03	1.299885e-03	1.285714e-03
##	Comp.253	Comp.254	Comp.255	Comp.256	Comp.257	Comp.258
##	1.274988e-03	1.274121e-03	1.268601e-03	1.260367e-03	1.258837e-03	1.240127e-03
##	Comp.259	Comp.260	Comp.261	Comp.262	Comp.263	Comp.264
##	1.229763e-03	1.219684e-03	1.216119e-03	1.207773e-03	1.206569e-03	1.200264e-03
##	Comp.265	Comp.266	Comp.267	Comp.268	Comp.269	Comp.270
##	1.199622e-03	1.181125e-03	1.180401e-03	1.177765e-03	1.165386e-03	1.159399e-03
##	Comp.271	Comp.272	Comp.273	Comp.274	Comp.275	Comp.276
##	1.147381e-03	1.142688e-03	1.138843e-03	1.129466e-03	1.121793e-03	1.111056e-03
##	Comp.277	Comp.278	Comp.279	Comp.280	Comp.281	Comp.282
##	1.101618e-03	1.095006e-03	1.094192e-03	1.090142e-03	1.085116e-03	1.083873e-03
##	Comp.283	Comp.284	Comp.285	Comp.286	Comp.287	Comp.288
##	1.080091e-03	1.069979e-03	1.063533e-03	1.055453e-03	1.051244e-03	1.045130e-03
##	Comp.289	Comp.290	Comp.291	Comp.292	Comp.293	Comp.294
##	1.037905e-03	1.019941e-03	1.009762e-03	1.008179e-03	1.006411e-03	9.872284e-04
##	Comp.295	Comp.296	Comp.297	Comp.298	Comp.299	Comp.300
##	9.831612e-04	9.816839e-04	9.792276e-04	9.720337e-04	9.578819e-04	9.517944e-04
##	Comp.301	Comp.302	Comp.303	Comp.304	Comp.305	Comp.306
##	9.484399e-04	9.445668e-04	9.389836e-04	9.273165e-04	9.268288e-04	9.264108e-04
##	Comp.307	Comp.308	Comp.309	Comp.310	Comp.311	Comp.312
##	8.940274e-04	8.926646e-04	8.893836e-04	8.713891e-04	8.672677e-04	8.527217e-04
##	Comp.313	Comp.314	Comp.315	Comp.316	Comp.317	Comp.318
##	8.467582e-04	8.326001e-04	8.182166e-04	8.068463e-04	7.886184e-04	7.827531e-04
##	Comp.319	Comp.320	Comp.321	Comp.322	Comp.323	Comp.324
##	7.785282e-04	7.619267e-04	7.569728e-04	7.478286e-04	7.431940e-04	7.342221e-04
##	Comp.325	Comp.326	Comp.327	Comp.328	Comp.329	Comp.330
##	7.030908e-04	6.963579e-04	6.761963e-04	6.754651e-04	6.693085e-04	6.644328e-04
##	Comp.331	Comp.332	Comp.333	Comp.334	Comp.335	Comp.336

```
## 6.606586e-04 6.578559e-04 6.304369e-04 6.232563e-04 6.058417e-04 5.855124e-04
## Comp.337 Comp.338 Comp.339 Comp.340 Comp.341 Comp.342
## 5.768542e-04 5.700406e-04 5.510442e-04 5.172550e-04 4.893665e-04 4.883332e-04
## Comp.343 Comp.344 Comp.345 Comp.346 Comp.347 Comp.348
## 4.864131e-04 4.811739e-04 3.905283e-04 3.267504e-04 3.186541e-04 5.277737e-08
## Comp.349 Comp.350 Comp.351 Comp.352 Comp.353 Comp.354
## 2.861649e-08 2.100271e-08 1.005172e-08 7.346569e-09 3.453043e-09 0.000000e+00
## Comp.355 Comp.356 Comp.357 Comp.358 Comp.359 Comp.360
## 0.000000e+00 0.000000e+00 0.000000e+00 0.000000e+00 0.000000e+00 0.000000e+00
##
## 360 variables and 360 observations.

Blch <- as.data.frame(-PCA.color$scores[,1]) #extract PC1
Blch$SP.Time.ID <- rownames(blch.scor) # add the sample names to the bleaching score

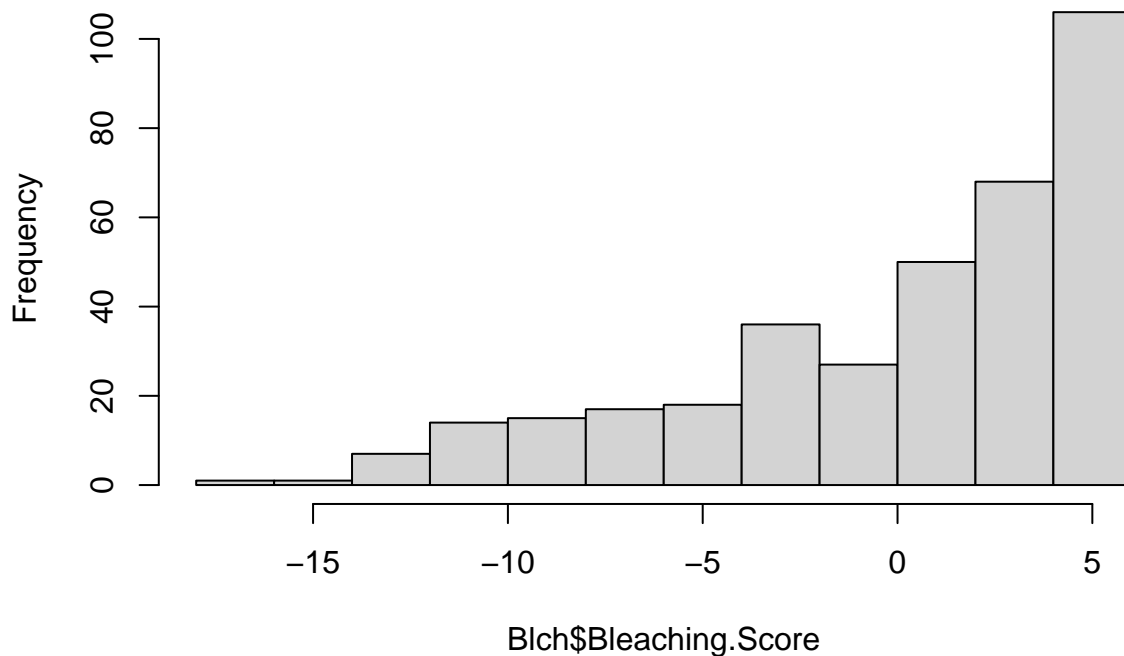
Blch <- left_join(Blch, Data, by="SP.Time.ID") #make a dataframe of PC1 and experiment factors
colnames(Blch) #view column names

## [1] "-PCA.color$scores[, 1]" "SP.Time.ID" "ColonyID"
## [4] "treatment" "genotype" "tank.num"
## [7] "ExperimentalDay" "Period" "Photo_date"
## [10] "Photo_ID" "Red_standard" "Green_standard"
## [13] "Blue_standard" "Red_coral" "Green_coral"
## [16] "Blue_coral" "Tech" "Notes"
## [19] "Red.Norm.Coral" "Green.Norm.Coral" "Blue.Norm.Coral"

names(Blch)[1] <- "Bleaching.Score" #name column

hist(Blch$Bleaching.Score)
```

Histogram of Blch\$Bleaching.Score



Plot data for outliers and Write out Color Score dataframe

```
Blch.meanse <- Blch %>% group_by(treatment, Photo_date) %>% #group data by factors
  summarise(mean = mean(Bleaching.Score), #calculate mean by group
            sem = std.error(Bleaching.Score)) #calculate sem by group

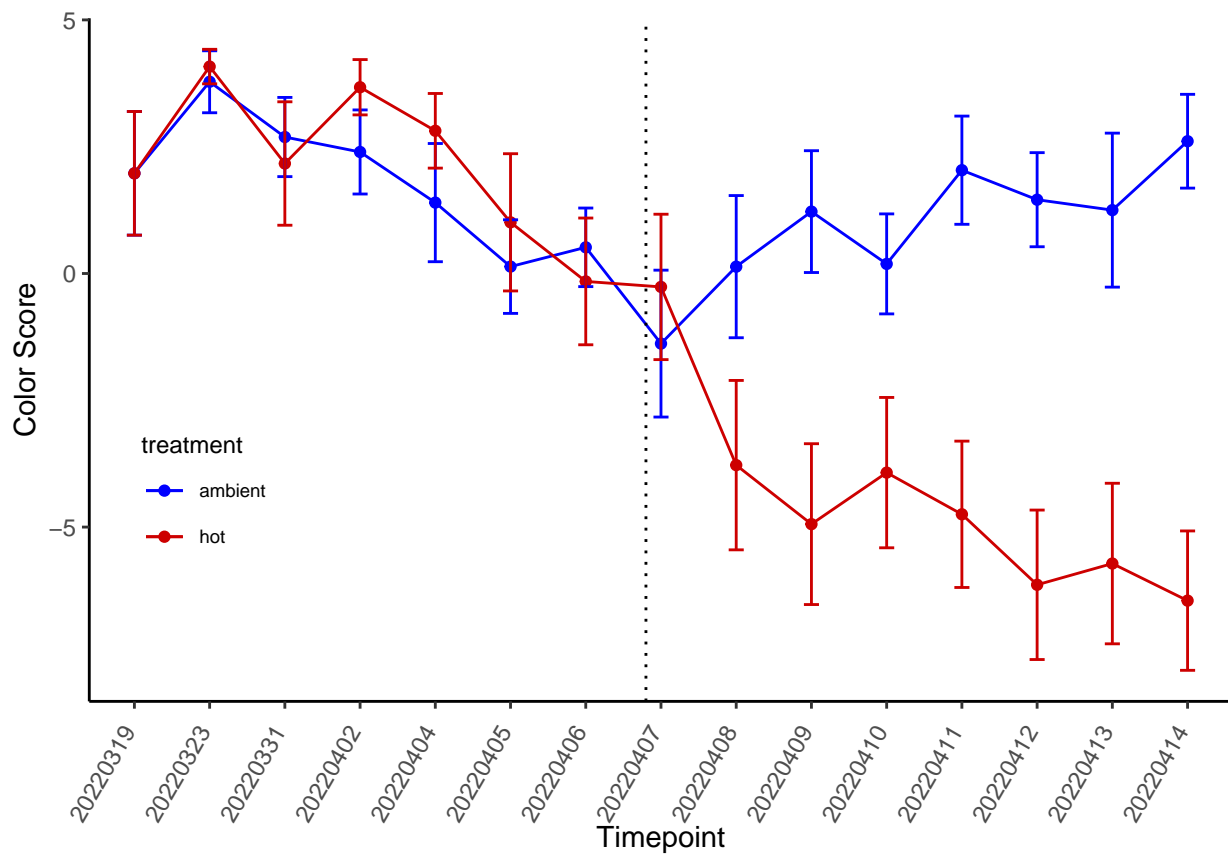
## `summarise()` has grouped output by 'treatment'. You can override using the `.groups` argument.

# Assign labels to use for figure
#species.names <- list(
#  'Mcapitata'="Montipora capitata",
#  'Pacuta'="Pocillopora acuta")
#species_labeller <- function(variable,value){
#  return(species.names[value])}

cols <- c("blue", "red3") #set colors

pdf("RAnalysis/output/color_score/colorscore_with_outliers_colonies.pdf")
Blch_plot1 <- ggplot(Blch.meanse, aes(x=Photo_date, y = mean, group = treatment, color = treatment)) +
  geom_line() + geom_point() + #plot points and lines
  #facet_grid(~Species, scales = "free", labeller = species_labeller) + #facet by Species
  geom_errorbar(aes(ymin=mean-sem, ymax=mean+sem), width=.2) + #plot sem error bars
  scale_color_manual(values = cols) + #color points
  xlab("Timepoint") + #label x axis
  ylab("Color Score") + # label y axis
  theme_classic() + #set theme
  theme(legend.position = c(0.1,0.3)) + #set legend position
  theme(legend.text = element_text(size = 7)) + #set legend text size
  theme(legend.title = element_text(size = 9)) + #set legend text title size
  geom_vline(xintercept = c(7.8), colour="black", linetype="dotted") + #add vertical line
  theme(plot.title = element_text(face = 'bold.italic', size = 12, hjust = 0)) + #set font
  #scale_x_discrete(breaks = c("Week1", "Week2", "Week4", "Week6", "Week8", "Week12", "Week16"), labels
  theme(axis.text.x = element_text(angle = 60, vjust = 1.2, hjust = 1.3)) + #Set the text angle
  theme(panel.border = element_blank(), #set theme
        panel.grid.major = element_blank(), #set theme
        panel.grid.minor = element_blank(), #set theme
        # Change axis line
        axis.line = element_line(colour = "black"))
Blch_plot1 #view plot
dev.off()

## pdf
## 2
Blch_plot1
```

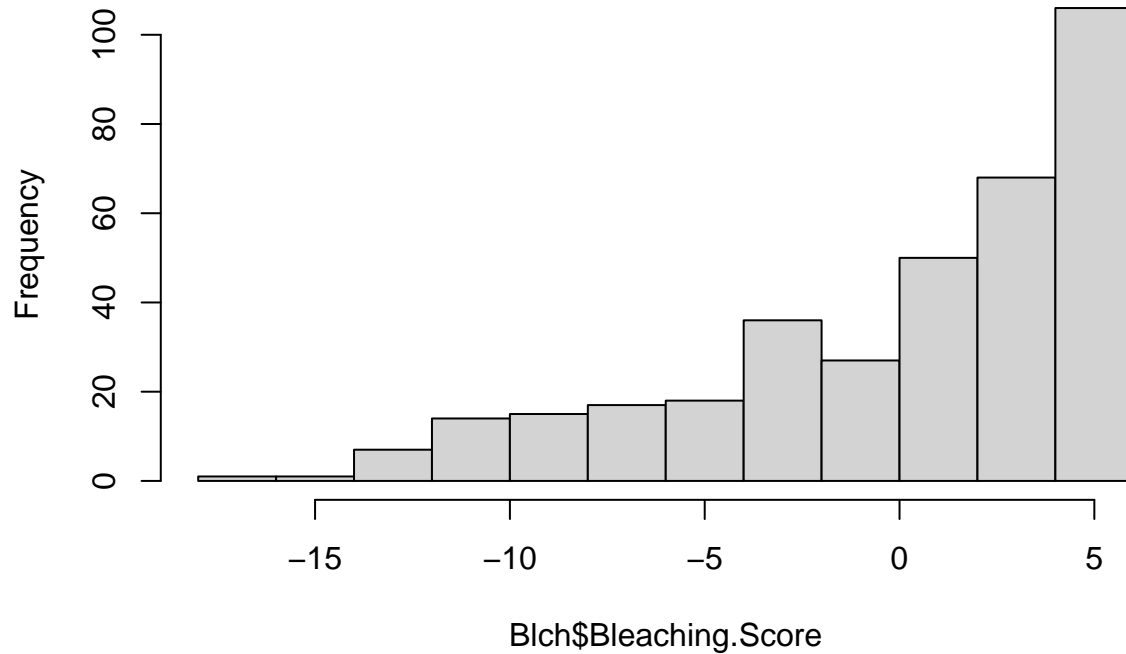


```
write.table(Blch, file = "RAnalysis/output/color_score/color_score_colony_output.csv", append = FALSE, col.names = TRUE, row.names = FALSE)
```

Detect and Remove Outliers

```
hist(Blch$Bleaching.Score) #view data distribution
```

Histogram of Blch\$Bleaching.Score

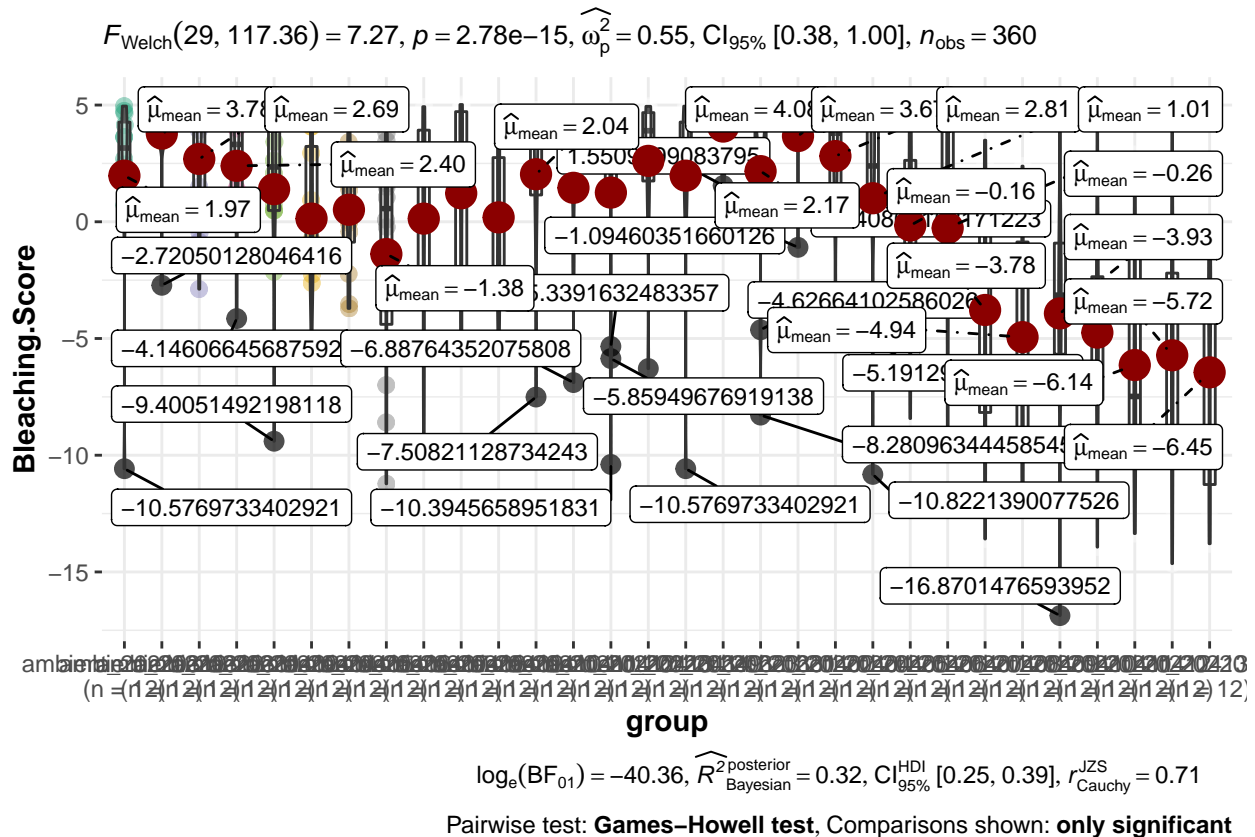


```
Blch$group <- paste0(Blch$treatment, "_", Blch$Photo_date)

#identify outliers
outlier.plot <- ggbetweenstats(Blch,group, Bleaching.Score, outlier.tagging = TRUE)

## Warning: Number of labels is greater than default palette color count.
## Try using another color `palette` (and/or `package`).
##
outlier.plot

## Warning: ggrepel: 1 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
## Warning: ggrepel: 11 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```



```
#set quantile values
q <- c(0.25, 0.75)

# calculate quantile values by time and Treatment groups
Quants <- Blch %>%
  group_by(treatment, Photo_date) %>%
  summarize(quant25 = quantile(Bleaching.Score, probs = q[1]),
            quant75 = quantile(Bleaching.Score, probs = q[2]),
            IQRbyGroup = IQR(Bleaching.Score))

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

# add a group name by pasting Time and Treatment
Quants$group <- paste0(Quants$treatment, "_", Quants$Photo_date)

#Calculate Quantile upper and lower ranges
Quants$upper <- Quants$quant75 + 1.5 * Quants$IQRbyGroup # Upper Range
Quants$lower <- Quants$quant25 - 1.5 * Quants$IQRbyGroup # Lower Range

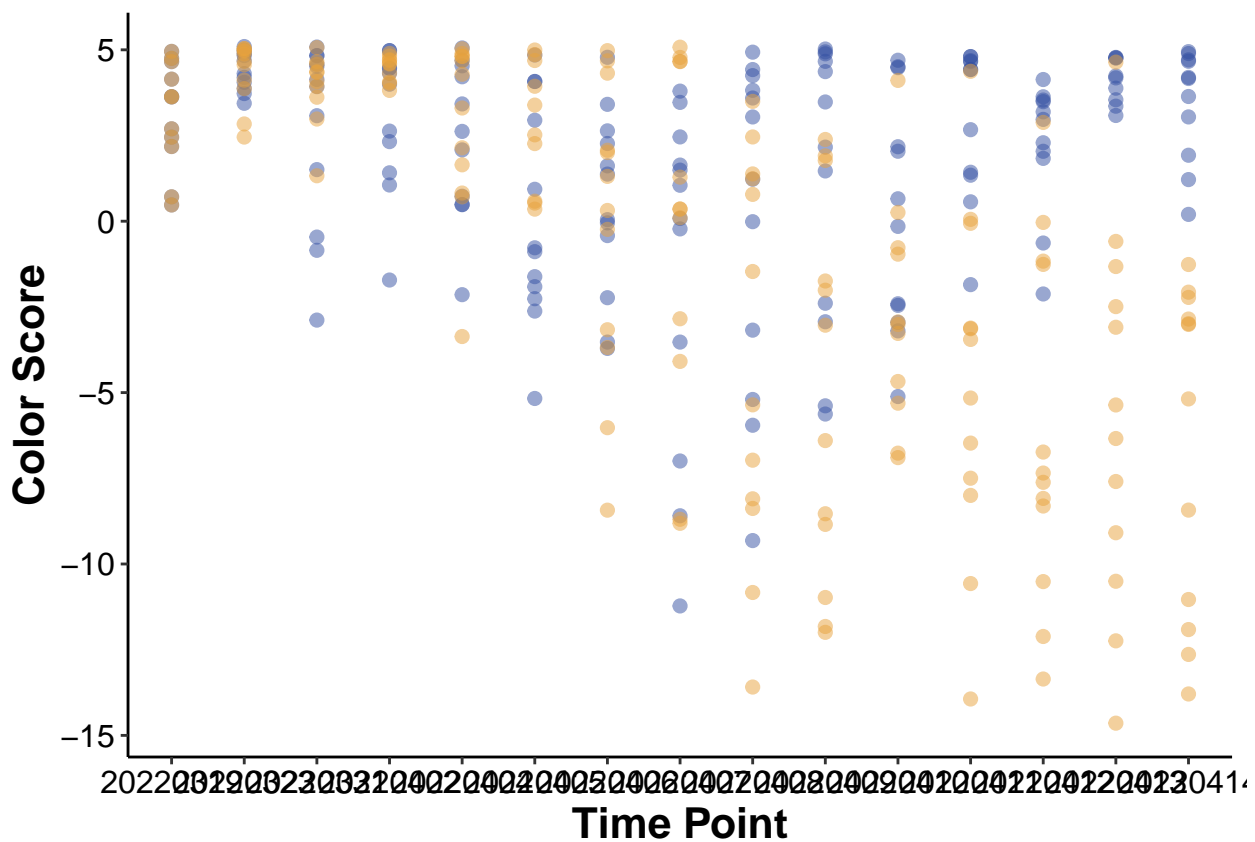
#join outlier cutoffs with rate data
data <- left_join(Blch, Quants)

## Joining, by = c("treatment", "Photo_date", "group")

#remove outliers from rates
data <- data %>%
  filter(Bleaching.Score < upper) %>%
  filter(Bleaching.Score > lower)
```



```
# Visualize data following outlier removal
r_plot<-data %>%
  ggplot(., aes(x = Photo_date, y = Bleaching.Score, colour=treatment)) +
  geom_point(aes(fill=treatment, group=interaction(treatment, Photo_date)), pch = 21, size=2, alpha=0.5) +
  xlab("Time Point") +
  scale_fill_manual(name="treatment", values=c("#3450A3", "#E9A33D"))+
  scale_color_manual(name="treatment", values=c("#3450A3", "#E9A33D"))+
  ylab("Color Score") +
  theme_classic() +
  theme(legend.position="none",
        axis.title=element_text(face="bold", size=16),
        axis.text=element_text(size=12, color="black"),
        legend.title=element_text(face="bold", size=14),
        legend.text=element_text(size=12)); r_plot
```



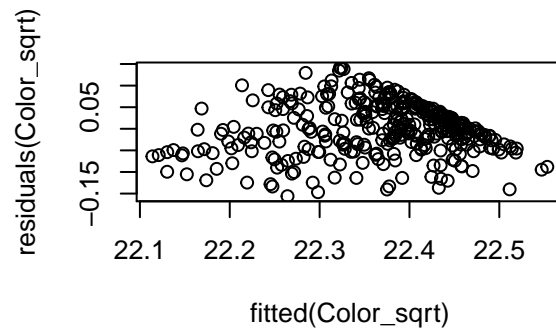
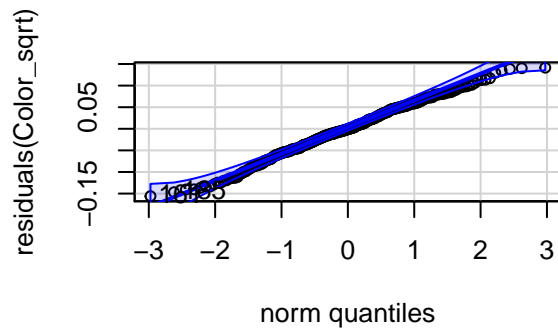
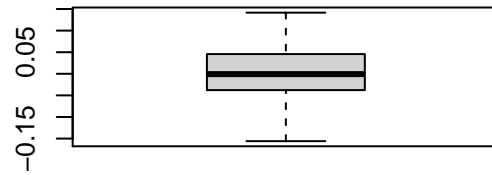
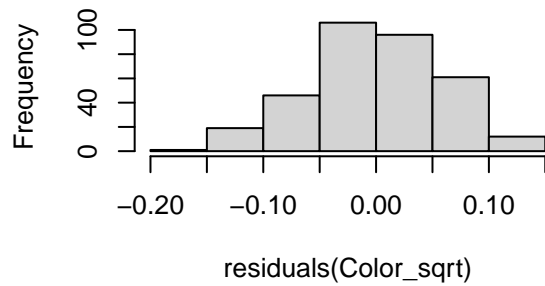
Testing Transformations

```
#Our random factor is `(1|PLUG.ID)` because fragments were repeatedly measured
Color_sqrt <- lmer(((Bleaching.Score+500)^(1/2)) ~ treatment*Photo_date + (1|ColonyID), na.action=na.omit)
par(mfrow = c(2, 2))
hist(residuals(Color_sqrt)) #view distribution
boxplot(residuals(Color_sqrt)) #view distribution
qqPlot(residuals(Color_sqrt)) #view qq
```

```
## [1] 161 185
```

```
plot(fitted(Color_sqrt), residuals(Color_sqrt)) #view variance
```

Histogram of residuals(Color_sqrt)

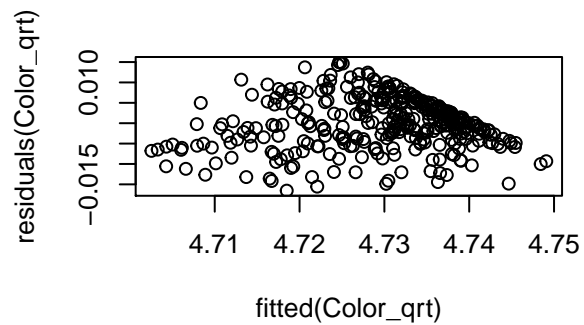
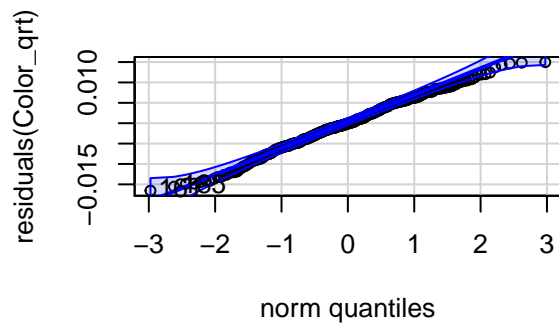
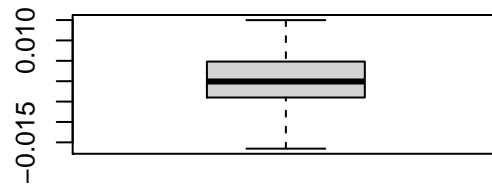
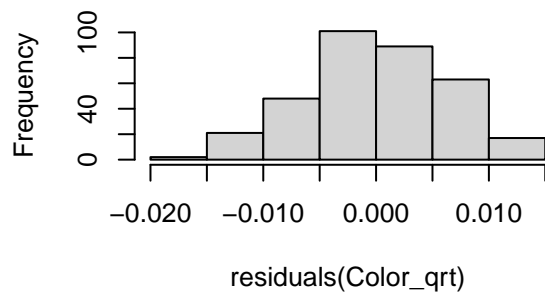


```
Color_qrt <- lmer(((Bleaching.Score+500)^(1/4)) ~ treatment*Photo_date + (1|ColonyID), na.action=na.omit)
par(mfrow = c(2, 2))
hist(residuals(Color_qrt))#view distribution
boxplot(residuals(Color_qrt))#view distribution
qqPlot(residuals(Color_qrt))#view qq
```

```
## [1] 161 185
```

```
plot(fitted(Color_qrt), residuals(Color_qrt))#view variance
```

Histogram of residuals(Color_qrt)

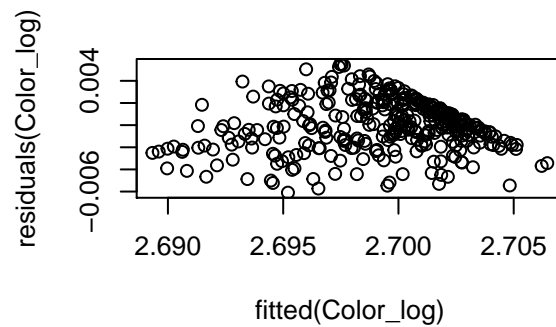
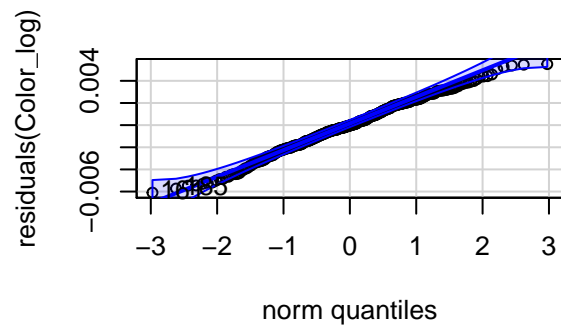
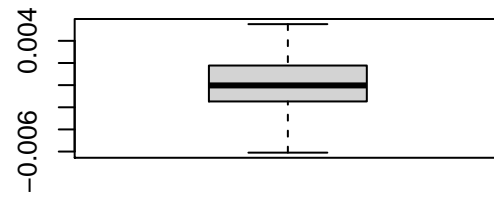
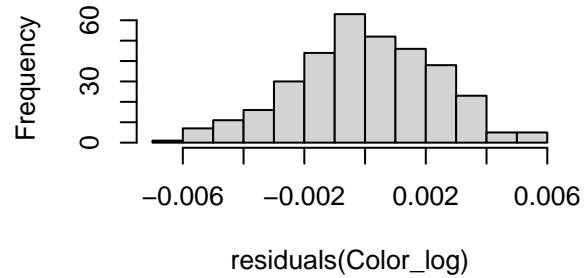


```
Color_log <- lmer(log10((Bleaching.Score+500)) ~ treatment*Photo_date + (1|ColonyID), na.action=na.omit)
par(mfrow = c(2, 2))
hist(residuals(Color_log))#view distribution
boxplot(residuals(Color_log))#view distribution
qqPlot(residuals(Color_log))#view qq
```

```
## [1] 161 185
```

```
plot(fitted(Color_log), residuals(Color_log))#view variance
```

Histogram of residuals(Color_log)

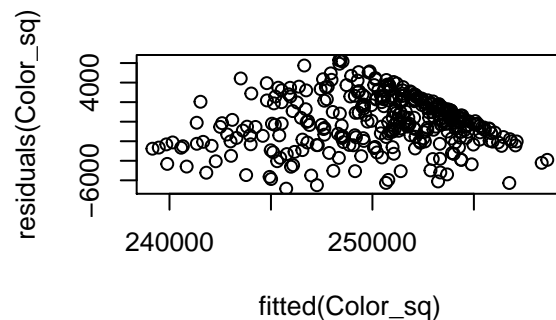
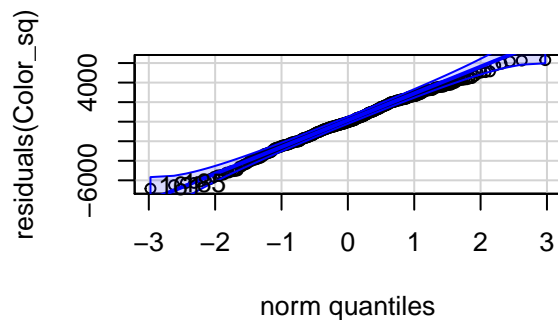
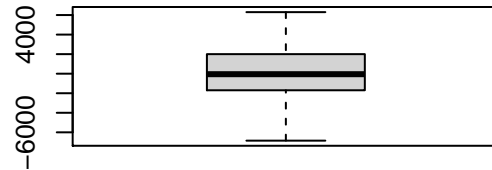
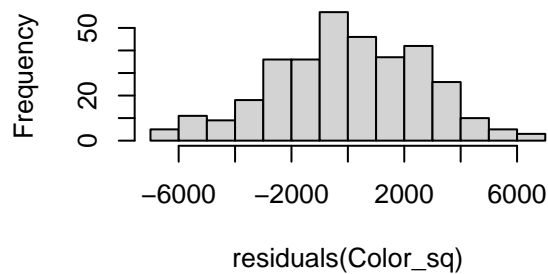


```
Color_sq <- lmer(((Bleaching.Score+500)^2) ~ treatment*Photo_date + (1|ColonyID), na.action=na.omit, data=Color_sq)
par(mfrow = c(2, 2))
hist(residuals(Color_sq))#view distribution
boxplot(residuals(Color_sq))#view distribution
qqPlot(residuals(Color_sq))#view qq
```

```
## [1] 161 185
```

```
plot(fitted(Color_sq), residuals(Color_sq))#view variance
```

Histogram of residuals(Color_sq)



#The data transformation chosen was

Analyze Color Score using Mixed effect modeling and Plot data

```
Color_sq <- lmer(((Bleaching.Score+500)^2) ~ treatment*Photo_date + (1|ColonyID), na.action=na.omit, da

## significance of model
Anova(Color_sq, df="lme4", type='III') # Type III Wald chisquare tests

## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: ((Bleaching.Score + 500)^2)
##               Chisq Df Pr(>Chisq)
## (Intercept)    57019.0892  1 < 2.2e-16 ***
## treatment        0.0555  1    0.8137
## Photo_date      52.9417 14  1.946e-06 ***
## treatment:Photo_date 172.3781 14 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Blch.meanse <- data %>% group_by(treatment, Photo_date) %>% #group data by factors
  summarise(mean = mean(Bleaching.Score), #calculate mean by group
            sem = std.error(Bleaching.Score)) #calculate sem by group

## `summarise()` has grouped output by 'treatment'. You can override using the `.groups` argument.
pdf("RAnalysis/output/color_score/colors_score_without_outliers_colonies.pdf")
Blch_plot2 <- ggplot(Blch.meanse, aes(x=Photo_date, y = mean, group = treatment, color = treatment)) +
```

```

geom_line() + geom_point() + #plot points and lines
#facet_grid(~Species, scales = "free", labeller = species_labeller) + #facet by Species
geom_errorbar(aes(ymin=mean-sem, ymax=mean+sem), width=.2) + #plot sem error bars
scale_color_manual(values = cols) + #color points
xlab("Timepoint") + #label x axis
ylab("Color Score") + # label y axis
theme_classic() + #set theme
theme(legend.position = c(0.1,0.3)) + #set legend position
theme(legend.text = element_text(size = 7)) + #set legend text size
theme(legend.title = element_text(size = 9)) + #set legend text title size
geom_vline(xintercept = c(7.8), colour="black", linetype="dotted") + #add vertical line
theme(plot.title = element_text(face = 'bold.italic', size = 12, hjust = 0)) + #set font
#scale_x_discrete(breaks = c("Week1", "Week2", "Week4", "Week6", "Week8", "Week12", "Week16"), labels
theme(axis.text.x = element_text(angle = 60, vjust = 1.2, hjust = 1.3)) + #Set the text angle
theme(panel.border = element_blank(), #set theme
panel.grid.major = element_blank(), #set theme
panel.grid.minor = element_blank(), #set theme
# Change axis line
axis.line = element_line(colour = "black"))
Blch_plot2 #view plot
dev.off()

```

```

## pdf
## 2

```

Blch_plot2

