Analyses_and_Plots

Austin Hammer

11/5/2019

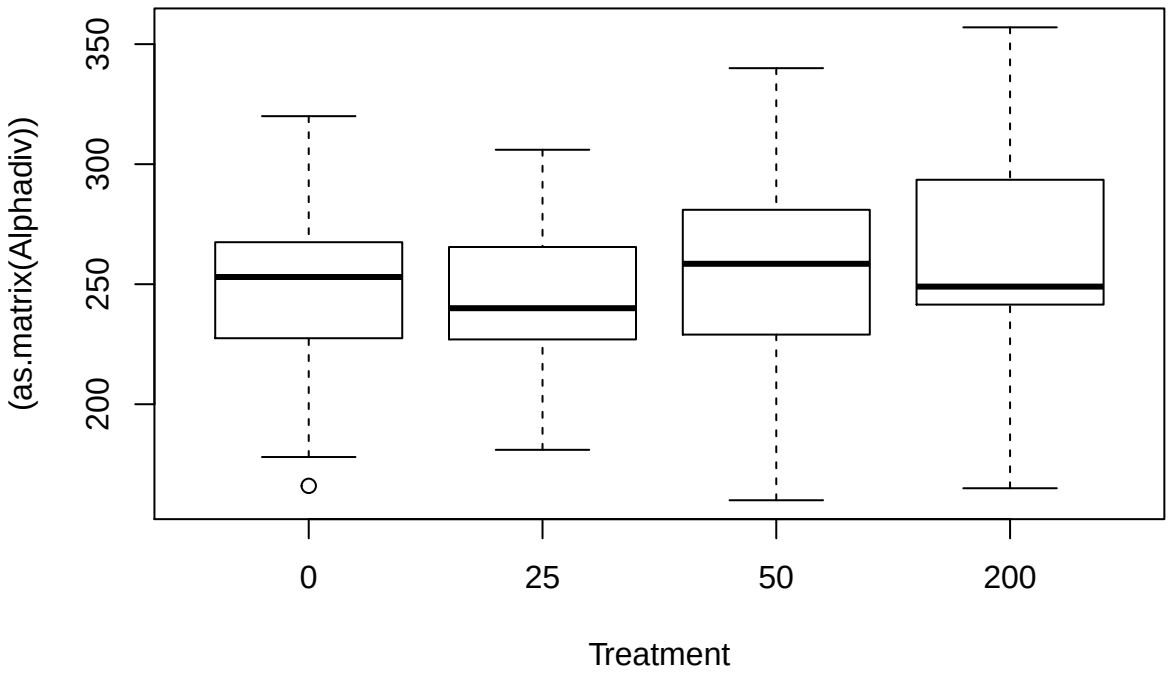
library("ggplot2")

library("dplyr") library("vegan") library("DESeq2") library("knitr")

```
## While the p-value for ANOVA of alphadiv~Treatment isn't extremely low (Pr(>F)~0.13), Shannon~Treatme
## Should maybe look at mean #ofgenera observed as a function of radiation level. Considering the low c
library("phyloseq")
sample_data(physeq1)$Alphadiv <- estimate_richness(physeq1, split=TRUE, measures=c("Observed"))
```

```
## Warning in estimate_richness(physeq1, split = TRUE, measures = c("Observed")): The data you have pro
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```

```
anova_df <- data.frame(sample_data(physeq1))
aov_results <- aov(as.matrix(Alphadiv) ~ Treatment*Sex, data=anova_df)
anova_results <- anova(aov_results)
some_plot <- boxplot((as.matrix(Alphadiv))~Treatment, data=anova_df)
```



```
anova_lm <- lm(as.matrix(Alphadiv) ~Treatment, data=anova_df)
print(anova_results)
```

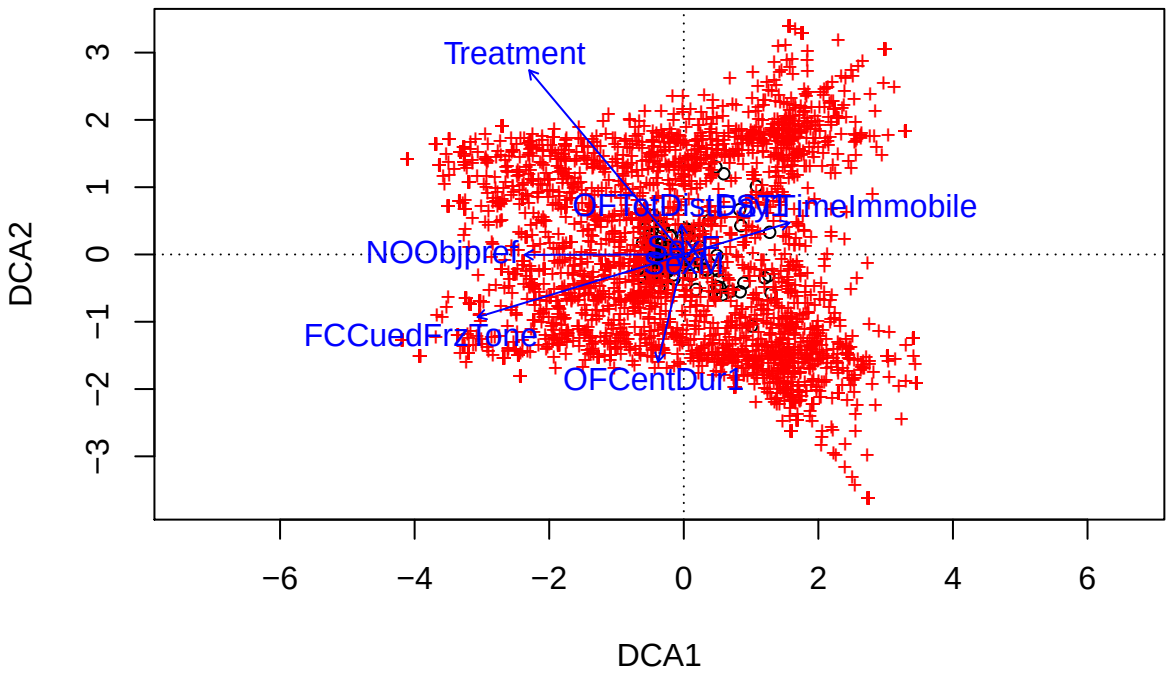
```
## Analysis of Variance Table
##
## Response: as.matrix(Alphadiv)
##               Df Sum Sq Mean Sq F value  Pr(>F)
## Treatment      1   5587  5587.4  3.5091 0.06417 .
## Sex            1    314   313.6  0.1969 0.65824
## Treatment:Sex  1   5553  5552.7  3.4873 0.06499 .
## Residuals     93 148081  1592.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Loading required package: permute
```

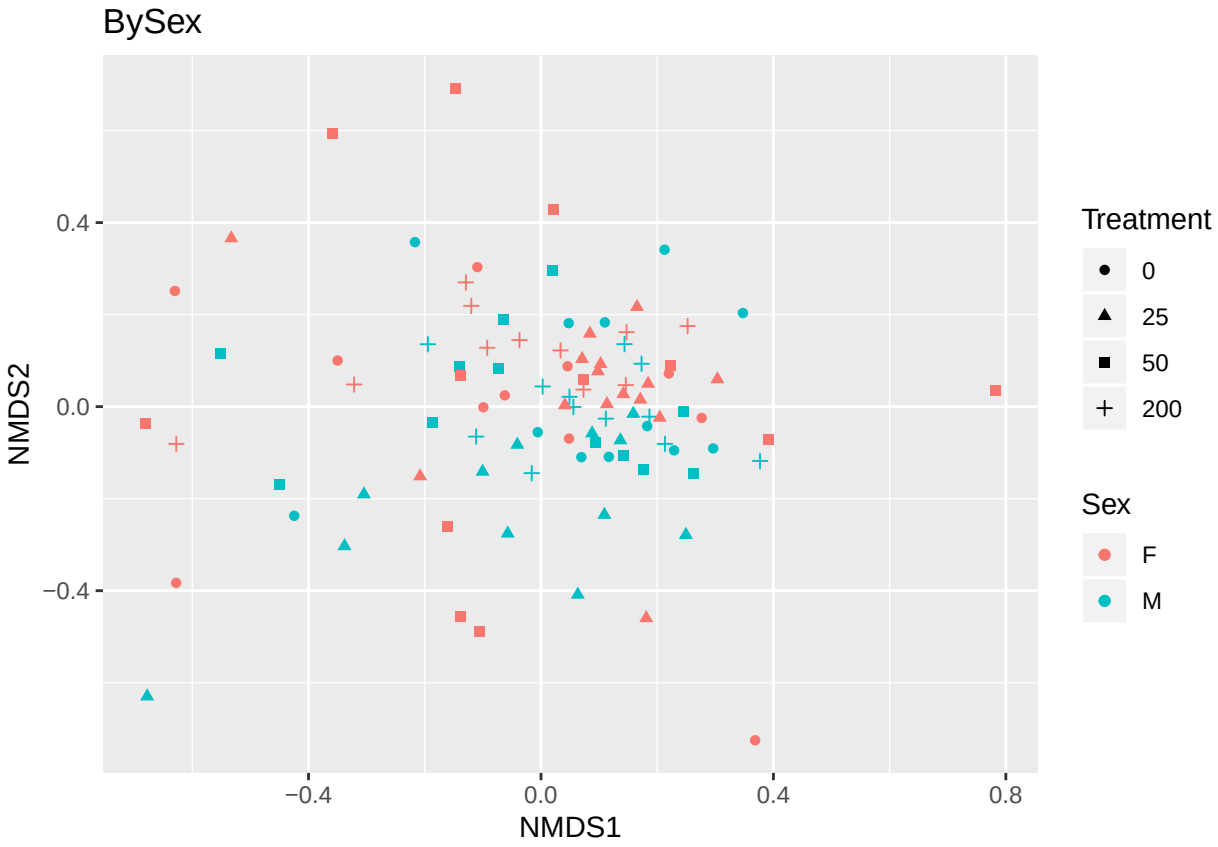
```
## Loading required package: lattice
```

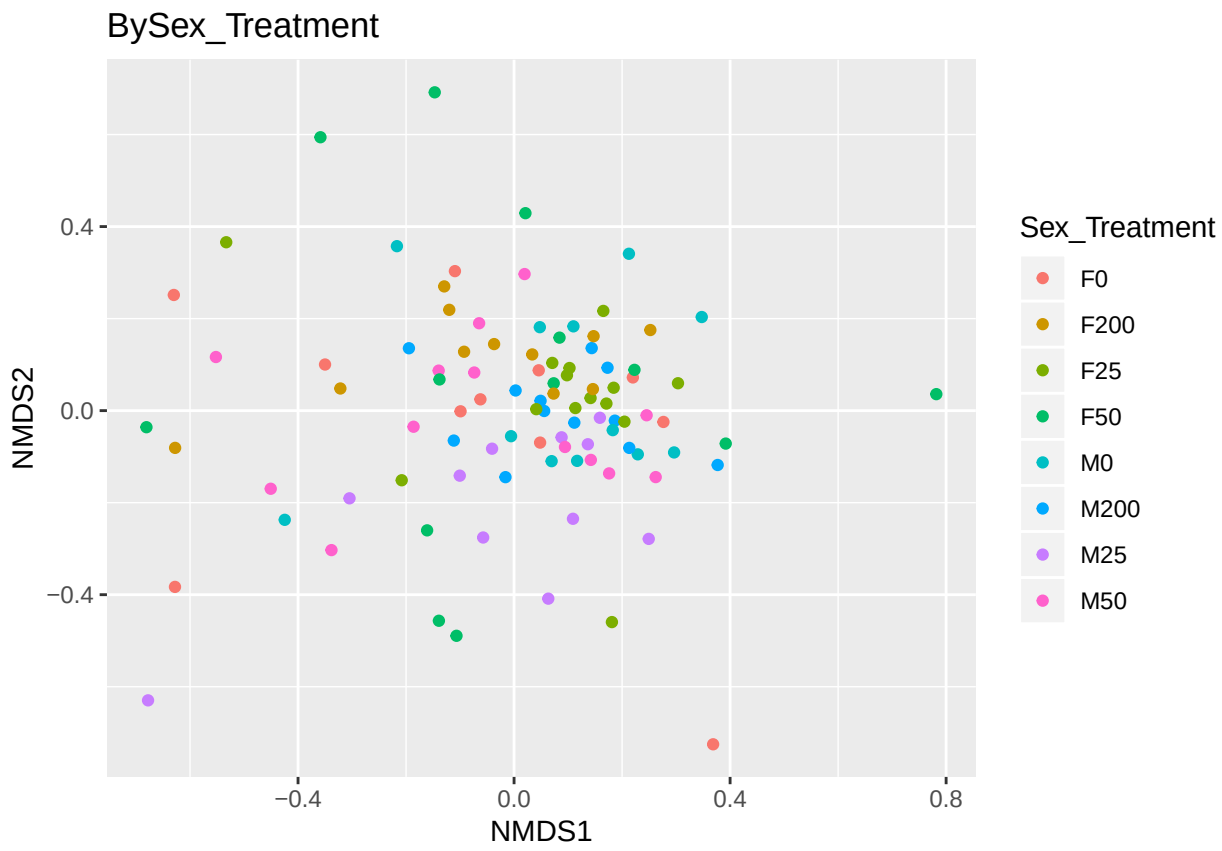
```
## This is vegan 2.5-5
```

```
## Warning in decorana(data.frame(otu_table(physeq1))): some species were
## removed because they were missing in the data
```



```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.2327549
## Run 1 stress 0.2324568
## ... New best solution
## ... Procrustes: rmse 0.02348782  max resid 0.1653986
## Run 2 stress 0.2322478
## ... New best solution
## ... Procrustes: rmse 0.02992067  max resid 0.2489023
## Run 3 stress 0.2446837
## Run 4 stress 0.2386528
## Run 5 stress 0.2368839
## Run 6 stress 0.2573674
## Run 7 stress 0.2362006
## Run 8 stress 0.2440469
## Run 9 stress 0.2411261
## Run 10 stress 0.2388389
## Run 11 stress 0.2344879
## Run 12 stress 0.2506096
## Run 13 stress 0.2429105
## Run 14 stress 0.2364733
## Run 15 stress 0.2452196
## Run 16 stress 0.2469909
## Run 17 stress 0.2439238
## Run 18 stress 0.2503994
## Run 19 stress 0.2423484
## Run 20 stress 0.2463975
## *** No convergence -- monoMDS stopping criteria:
##     20: stress ratio > sratmax
```


BySex
NMDS2
NMDS1
0.4
0.0
−0.4
−0.4
0.0
0.4
0.8
Treatment
0
25
50
200
Sex
F
M




```
## Using adonis to evaluate the importance of covariates in explaining variation in the ordination prod
set.seed(1)
physeq1 <- rarefy_even_depth(physeq1)
```

```
## You set `rngseed` to FALSE. Make sure you've set & recorded
##  the random seed of your session for reproducibility.
## See `?set.seed`

## ...

## 620TUs were removed because they are no longer
## present in any sample after random subsampling

## ...
```

```
physeq1.dist <- vegdist(otu_table(physeq1), method="bray")
sampledf <- data.frame(sample_data(physeq1))
set.seed(1)
perm.results.treatment <- adonis(physeq1.dist ~ Treatment*Sex, data=sampledf, permutations=5000)
perm.results.treatment
```

```
##
## Call:
```

```
## adonis(formula = physeq1.dist ~ Treatment * Sex, data = sampledf,      permutations = 5000)
##
## Permutation: free
## Number of permutations: 5000
##
## Terms added sequentially (first to last)
##
##               Df SumsOfSqs MeanSqs F.Model      R2    Pr(>F)
## Treatment      3    0.9693 0.32312  1.5485 0.04629 0.0002000 ***
## Sex            1    0.5456 0.54556  2.6145 0.02605 0.0002000 ***
## Treatment:Sex  3    0.8565 0.28551  1.3682 0.04090 0.0005999 ***
## Residuals     89   18.5712 0.20867         0.88677
## Total         96   20.9426                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```