PERMANOVA

1. Read in data

- Week = 13
- Tow groups: 32 in PAT group and 36 in Control group

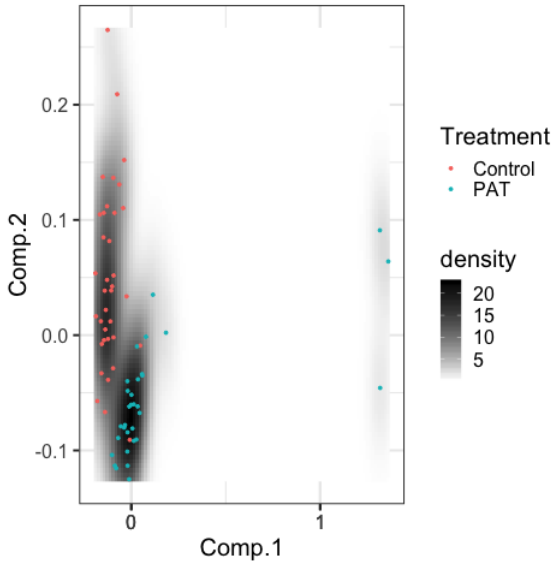
```
ind = (sample_data(phy.genus)$Week==13 &
         (sample_data(phy.genus)$Treatment != 'STAT'))
pseq = subset_samples(phy.genus,ind)
pseq.rel = microbiome::transform(pseq, "compositional")
otu = abundances(pseq.rel)
meta = meta(pseq.rel)
dim(otu) # 37 68; 37 kinds of microbiome, 68 subjects
```

```
## [1] 37 68
```

```
dim(meta) # 68, 53; 68 subjects and 53 features
```

```
## [1] 68 53
```

2. Visualize the population density and highlight sample groups



3. PERMANOVA significance test for group-level differences

```
permanova <- adonis(t(otu) ~ Treatment,
                    data = meta, permutations=99, method = "bray")
permanova
```

```
##
## Call:
## adonis(formula = t(otu) ~ Treatment, data = meta, permutations = 99,      method = "bray")
##
## Permutation: free
```

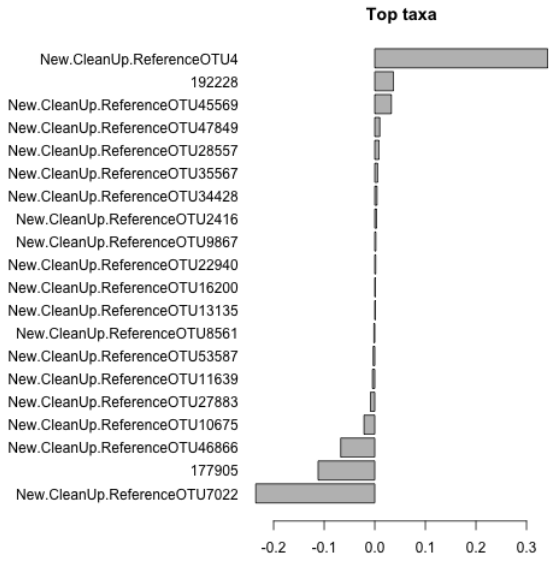
```
## Number of permutations: 99
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Treatment  1    1.2610 1.26102  29.573 0.30943   0.01 **
## Residuals 66    2.8143 0.04264         0.69057
## Total     67    4.0753                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

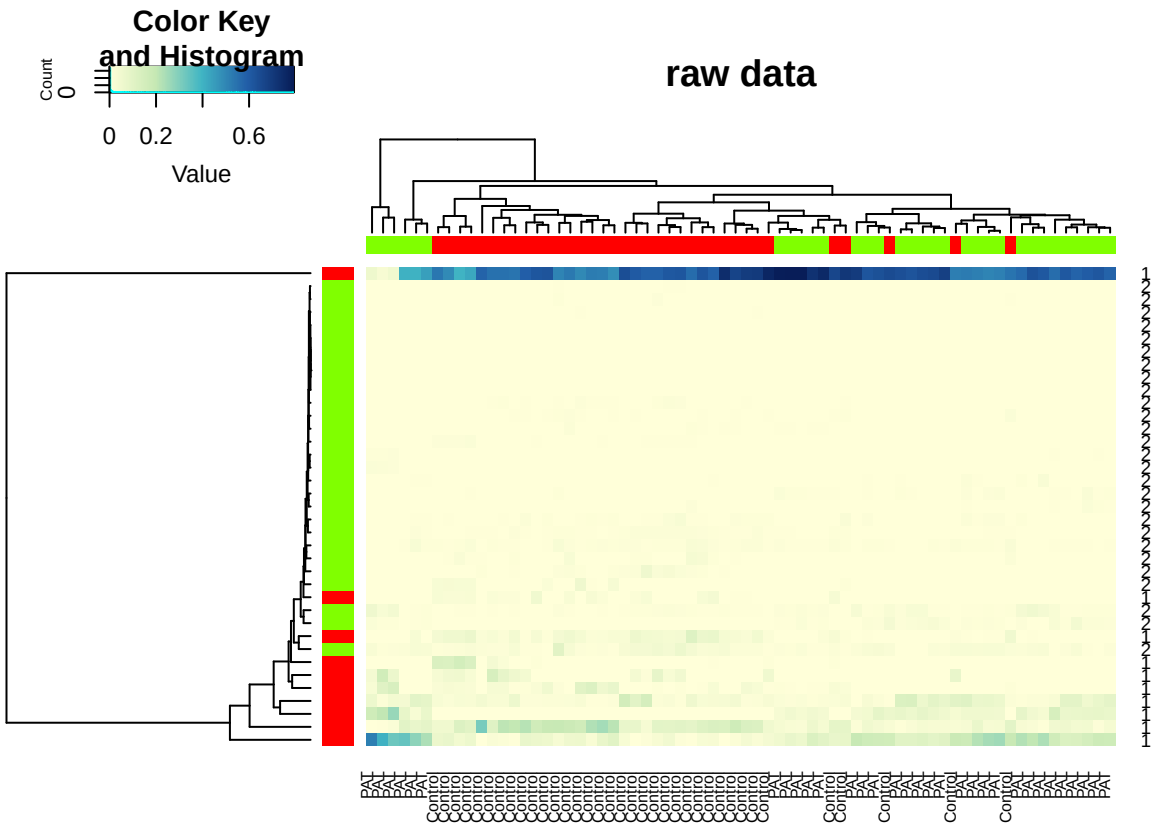
4. Checking the homogeneity condition

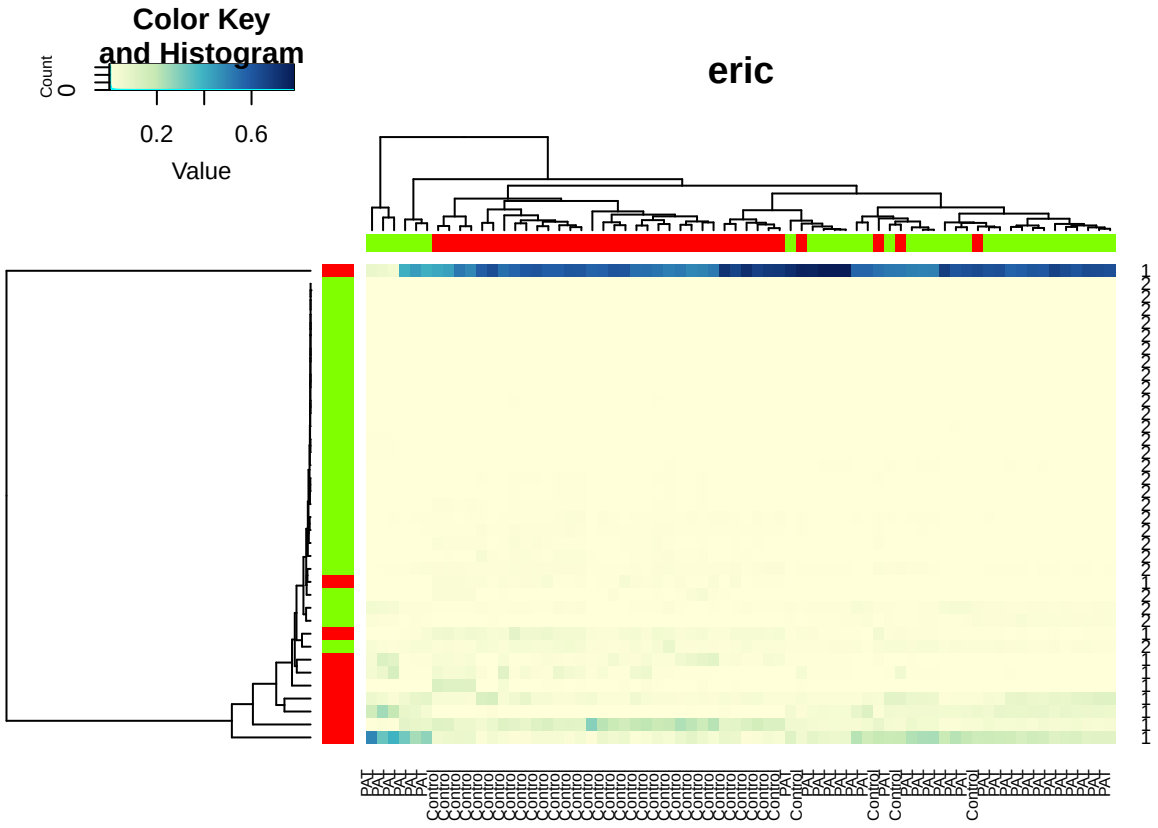
```
dist = vegdist(t(otu))
anova(betadisper(dist, meta$Treatment))
```

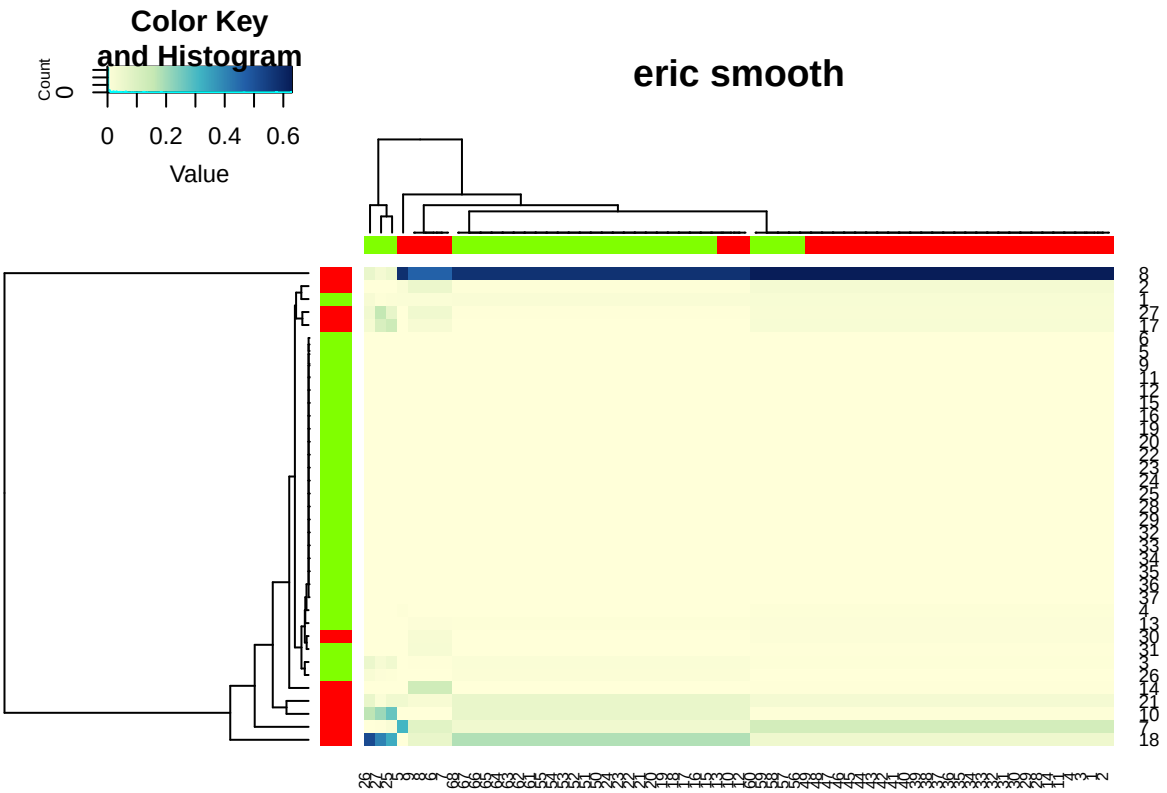
```
## Analysis of Variance Table
##
## Response: Distances
##           Df  Sum Sq   Mean Sq F value Pr(>F)
## Groups     1 0.00043 0.0004343  0.0319 0.8588
## Residuals 66 0.89910 0.0136228
```

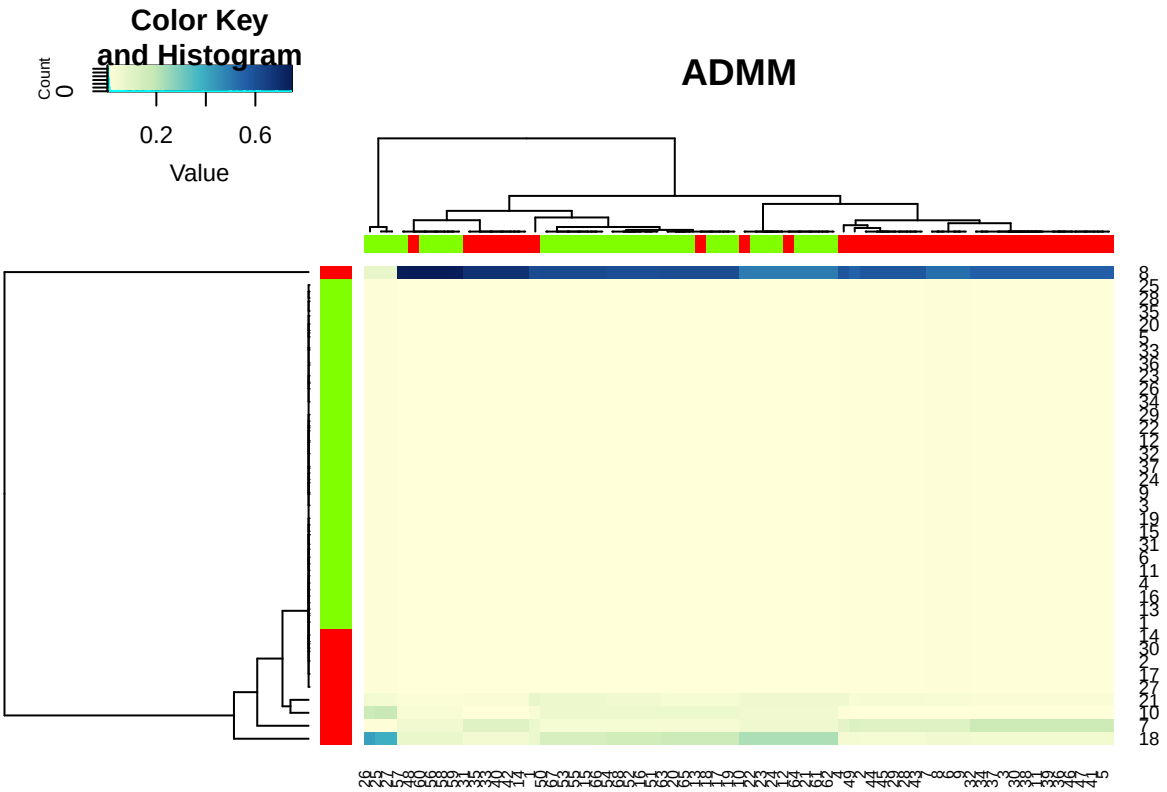
5. Show coefficients for the top taxa separating the groups

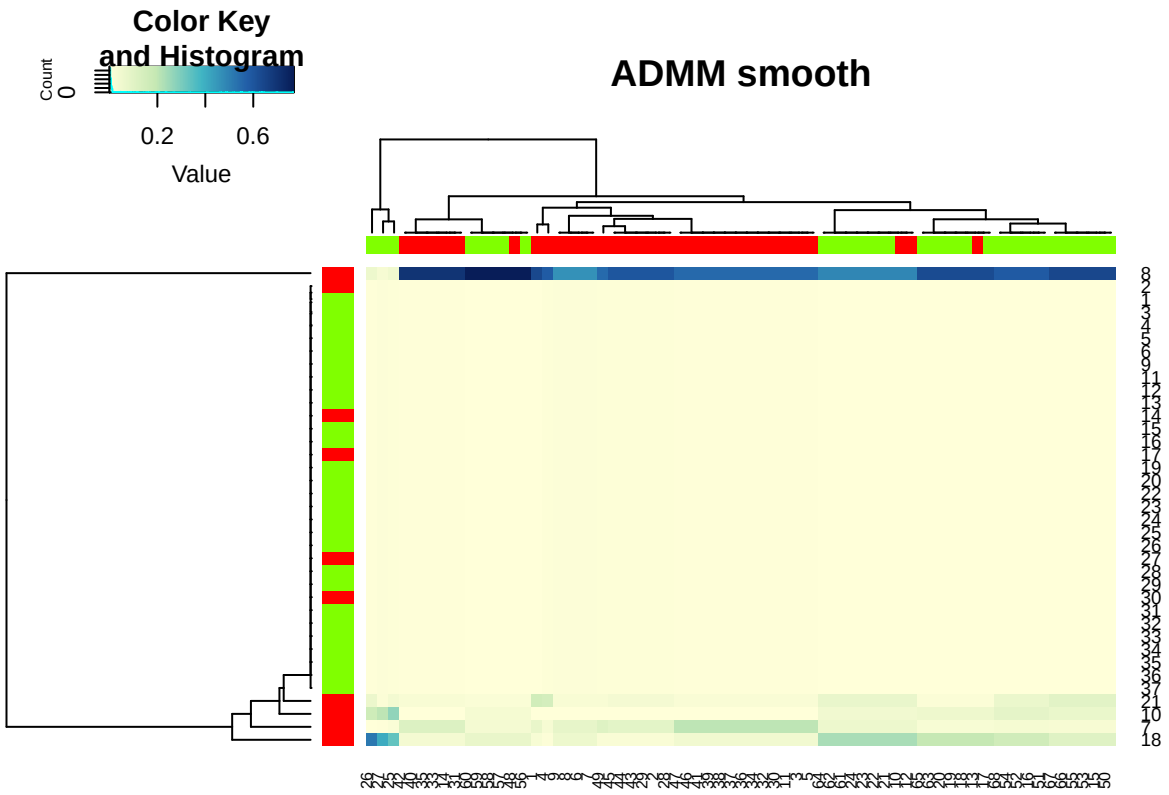



Color Key
and Histogram
Count
0
0
0.2
0.6
Value
raw data


Color Key
and Histogram
Count
0
0.2
0.6
Value
eric


Color Key
and Histogram
Count
0
0
0.2
0.4
0.6
Value
eric smooth


Color Key
and Histogram
Count
0
0.2
0.6
Value
ADMM


Color Key
and Histogram
Count
0
0.2
0.6
Value
ADMM smooth