

PERMANOVA

Loading packages **vegan** multivariate analysis of ecological communities, and loading data.

Advantage for using this method: Non-parametric, no assumed distribution, based on dissimilarities.

```
library(vegan)
werra_sp <- read.csv(file = "/Users/chengqiwang/Downloads/werra_sp.csv",
                     header = T, sep = ",", stringsAsFactors = FALSE, row.names =
1)

werra_env <- read.csv(file = "/Users/chengqiwang/Downloads/werra_env.csv",
                      header = T, sep = ",", stringsAsFactors = FALSE)
```

1. Transform or standardize data

Sequencing reads is a large number and significant different vary groups. We'd better reduce the range/scale of it to about $10X^{(a)}$, $a \in (0,1)$

```
range(werra_sp^0.25)

## [1] 0.00000 10.98475
```

2. Calculate ecological resemblance

- Bray-Curtis dissimilarity (abundance weighted)
- Jaccard (presence/absence)
- Gower's non-continuous variables) (*Dissimilarity: 0 = sites are identical, 1 = sites do not share any species*)

```
dist_werra <- vegdist(werra_sp^0.25, method = "bray")
##nmds <- metaMDS(dist_werra)##global Multidimensional Scaling using
monoMDS
```

3. PERMANOVA

"adonis" is a function for the analysis and partitioning sums of squares using semimetric and metric distance matrices.

Null hypotheie : There is no different between these two or more comparable groups.

R-square is the important statistic for interpreting Adonis as it gives you the effect size. *(For example: an R-squared of 0.44 means that 44% of the variation in distances is explained by the grouping being tested. The p-value tells you whether or not this result was likely a result of chance. A p-value of 0.05 means that there is a 5% chance that you detected a difference between groups.)*

Small p-value with small R-square : this situation normally because of large sample size. Actually only small part can be explained, however large sample size make the p-value small.

```
pmv      <- adonis(werra_sp^0.25~position,data = werra_env,
                  permutations = 999,
                  method = "bray")

pmv

##
## Call:
## adonis(formula = werra_sp^0.25 ~ position, data = werra_env,
## permutations = 999, method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##          Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## position   1   0.72127 0.72127  3.9937 0.30736 0.014 *
## Residuals   9   1.62540 0.18060          0.69264
## Total      10   2.34666          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.Modify the effective size number

Omega-squared (ω^2) provides a less biased measure of effect size for ANOVA-type analyses by accounting for the mean-squared error of the observed samples.

$$R^2 = 1 - \frac{SS_A}{SS_T}$$

$$\omega^2 = \frac{SS_A - (a - 1) \frac{SS_W}{N - a}}{SS_T + \frac{SS_W}{N - a}}$$

```
df.rsd      <- pmv$aov.tab$Df[2]##degree of freedom of residual
df.dfd      <- pmv$aov.tab$Df[1]##degrees of freedom defined by the grouping
factor
SS.A        <- pmv$aov.tab$SumsOfSqs[1]##between-group sum of squares
SS.W        <- pmv$aov.tab$SumsOfSqs[2]##sum of the squares of distances
within groups
SS.T        <- pmv$aov.tab$SumsOfSqs[3]##total sum of squares

omega.sq     <- (SS.A-(df.dfd-1)*(SS.W/df.rsd))/(SS.T+SS.W/df.rsd);omega.sq
## [1] 0.2853952
```

Display the density plot of all F-test.

```
densityplot(permustats(pmv))
```

