# Laboratory 6: Computing distance matrices; PCoA

Objectives:

- basic distance matrix manipulations;
- Principal Coordinate Analysis.

1. Study the phyloseq distance() tutorial: http://joey711.github.com/phyloseq/distance
2. Load the provided RData image of Nature 488, pp. 621-626 data.
3. Compute Jensen-Shannon Divergence distance of the fecal samples.
4. Use meandist() to calculate intra- and inter- group distance for the Treatment factor variable. Plot the barplot of intra-group distances.
5. Use dudi.pco() to perform PCoA of the JSD distances of fecal samples
   I. How many components do we want to keep? Why?
6. Calculate percent inertia explained by each component kept.
7. Use s.class() function to plot the projection of the data with Treatment variable.
8. Use s.value() function to plot additional phenotypes on the projection of the data.
9. Using cor function explore correlations of the additional phenotypes with the principal coordinates.
10. Plot correlations in #11.
11. Perform PCoA analysis on the entire dataset (not just fecal samples) and produce plots with respect to Location and Treatment variables and their interactions.
12. How do we remove the effect of the Location variable in PCoA analysis? TIP: `?wca`