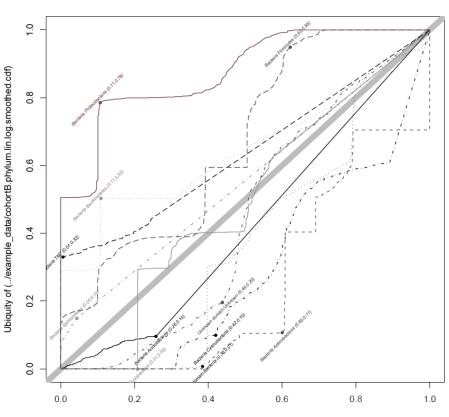
# **How to Generate Ubiquity-Ubiquity Plots (Two Cohort Analysis)**

In this example, we will generate ubiquity-ubiquity plots to compare two cohorts. Here we will need two different sets of summary files. The UU Plot compares two cohorts similar to a Quantile-Quantile (QQ) plot. At matching abundances the ubiquity of each taxa is draw.

### Comparison of Ubiquities



## $Ubiquity\ of\ (.../example\_data/cohortA.phylum.lin.log.smoothed.cdf)$

#### **Direct command line invocation**

### First, generate the CDF values for both cohorts

Generate CDF for cohort A

lib/Compute\_CDFs.r -i example\_data/cohortA.phylum.summary\_table.tsv

**OUTPUT**: example\_data/cohortA.phylum.lin.log.cdf

Generate CDF for cohort B

 $lib/Compute\_CDFs.r$  -i example\\_data/cohortB.phylum.summary\_table.tsv

**OUTPUT:** example\_data/cohortB.phylum.lin.log.cdf

Then, plot the CDF values

Here are 4 examples of how to generate the U-U Plots:

A) Generate the default grey scale U-U plot comparing all taxa:

lib/Compare\_CDFs.r -A example\_data/cohortA.phylum.lin.log.cdf \

-B example\_data/cohortB.phylum.lin.log.cdf \

-o example\_data/cohortA.phylum.lin.log.cdf\_cohortB.phylum.lin.log.cdf

**OUTPUT:** example\_data/cohortA.phylum.lin.log.cdf\_cohortB.phylum.lin.log.cdf.pdf

B) Generate a U-U plot for taxa with exceeding the ubiquity difference cutoff (-d) and exceeding the average abundance cutoff (-a):

lib/Compare\_CDFs.r -A example\_data/cohortB.phylum.lin.log.cdf \

-B example\_data/cohortA.phylum.lin.log.cdf -d 0.5 -a 0.001 \

-o cohortB\_cohortA.phylum.compare.cdf

**OUTPUT:** cohortB\_cohortA.phylum.compare.cdf

C) Assign color to each taxon

lib/Assign Colors.r -i example data/taxa.list

**OUTPUT :** example\_data/taxa.list.colormap.pdf example\_data/taxa.list.colormap

D) Same as that generated in option B, but using a color map:

lib/Compare\_CDFs.r -A example\_data/cohortA.phylum.lin.log.cdf \

-B example\_data/cohortB.phylum.lin.log.cdf -d 0.5 -a 0.001 \

-o cohortA\_cohortB.phylum.compare.cdf -c example\_data/taxa.list.colormap

**OUTPUT:** cohortA\_cohortB.phylum.compare.cdf

E) Plot all taxa in grey scale, but label the top 4 taxa with greater difference in ubiquity lib/Compare\_CDFs.r -A example\_data/cohortA.phylum.lin.log.cdf \

-B example\_data/cohortB.phylum.lin.log.cdf -t 4 \

-o example\_data/cohortA\_cohortB.phylum.compare.top4.cdf

**OUTPUT**: example\_data/cohortA\_cohortB.phylum.compare.top4.cdf.pdf

Note: Note all variations have been provided in these examples, but these should get you started.