

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.



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.