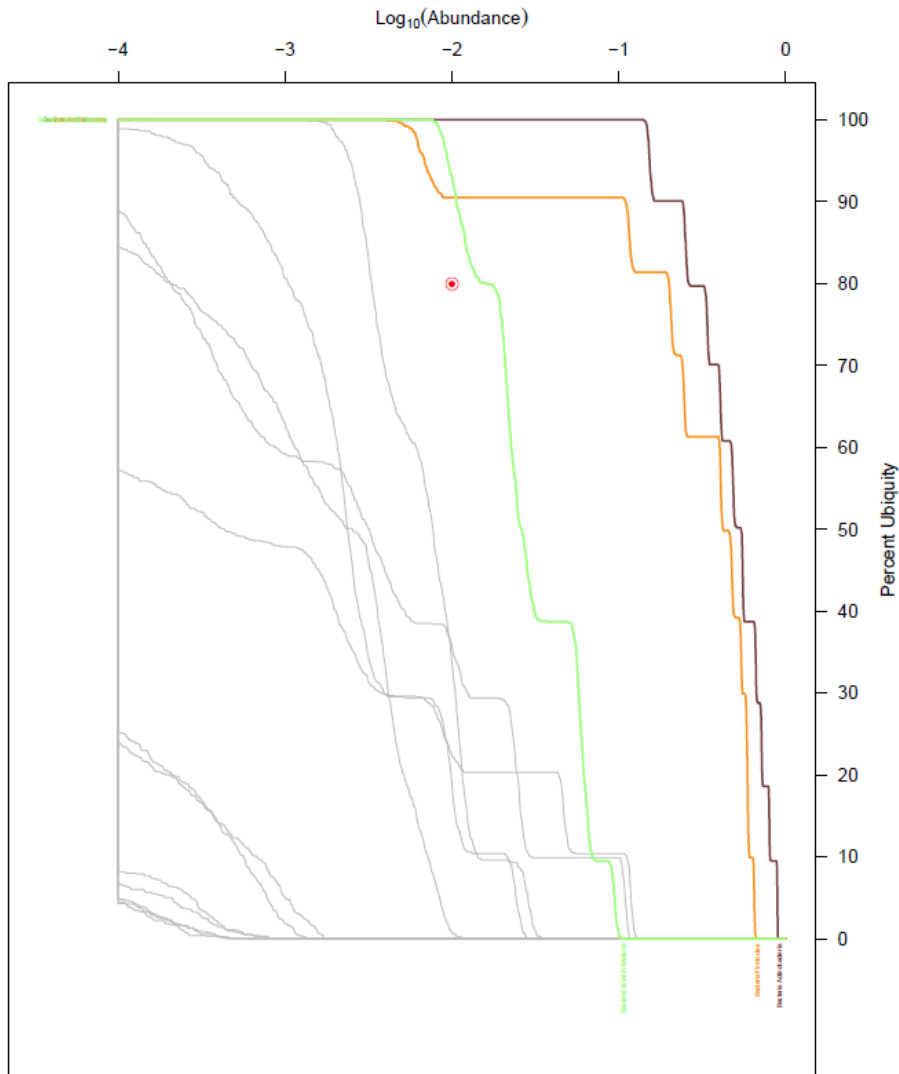


## How to generate the Ubiquity-Abundance Plot (Single Cohort Analysis)

The Ub-Ab plot describes the relationship between abundance and ubiquity. The core taxonomic members are defined by the taxa that exceed a specified abundance and ubiquity. This is demarked by the red bull's eye. The taxa that are considered in the core by this definition are colored and the remaining are greyed out for clarity. There are 3 core in this analysis.



## Direct command line invocation

### First, generate the CDF values

Compute the CDF estimates for each taxon in the summary file.

- A) Go (cd) into “*example\_data*” directory.
- B) Run script “*Compute\_CDFs.r*” on the summary file.

```
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

A few options are provided as examples:

- A) Generate plot without cutoffs, plotting all taxa in grey:

```
lib/Plot_CDFs.r -i example_data/cohortB.phylum.lin.log.cdf
```

**OUTPUT :** *example\_data/cohortB.phylum.lin.log.u0.00.a0.00000.pdf*

- B) Generate plot by only drawing core members in grey:

```
lib/Plot_CDFs.r -i example_data/cohortB.phylum.lin.log.cdf -u 0.80 -a 0.01
```

**OUTPUT :** *example\_data/cohortB.phylum.lin.log.u0.80.a0.01000.pdf*  
*example\_data/cohortB.phylum.lin.log.u0.80.a0.01000.csv*

- C) Generate plots, with colors:

In this example, first get the list of taxa you want to assign colors to in file “*taxa.list*”

- 1.) Assign colors to each of the taxa:

```
lib/Assign_Colors.r -i example_data/taxa.list
```

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

- 2.) Use color map file to annotate the Ub-Ab plot:

```
lib/Plot_CDFs.r -i example_data/cohortB.phylum.lin.log.cdf \  
-u 0.8 -a 0.01 -c example_data/taxa.list.colormap \  
-o example_data/testPositive.phylum.lin.log.colorMap
```

**OUTPUT :** *example\_data/testPositive.phylum.lin.log.colorMap.u0.80.a0.01000.pdf*  
*example\_data/testPositive.phylum.lin.log.colorMap.u0.80.a0.01000.csv*

Note: The -r option is available to set non-core taxa to grey. Otherwise, non-core taxa will not be drawn if the -u and -a options are greater than 0.