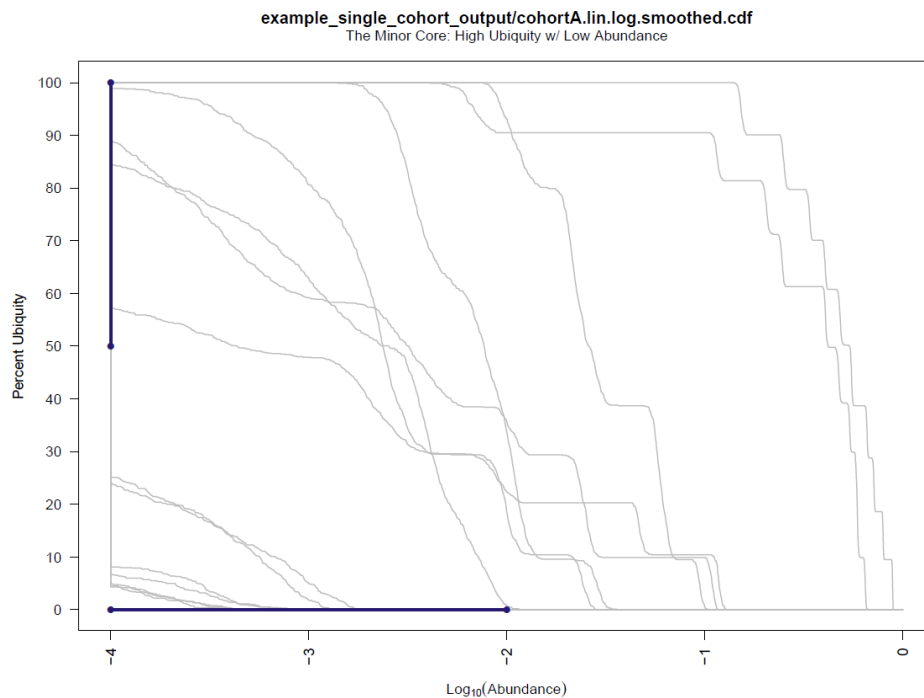


How to compute Other Core (Minor Core) Ub-Ab Plots (Single Cohort Analysis)

In this example, we will perform a minor core analysis using the Ub-Ab plot. The minor core is defined as taxa with “Low Abundance but High Ubiquity”.



Direct command line invocation

The default ubiquity cut off is 0.5 and abundance cut off is 0.01.

- 1.) Generate the intermediate CDF file on the input summary file:

```
lib/Compute_CDFs.r -i example_data/cohortB.phylum.summary_table.tsv
```

OUTPUT : example_data/cohortB.phylum.lin.log.cdf

- 2.) Plot the intermediate CDF file with the Ub-Ab plotting script modified for minor core analysis

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

OUTPUT: example_data/cohortB.phylum.lin.log.otherCore.u0.50.a0.01000.pdf

example_data/cohortB.phylum.lin.log.otherCore.u0.50.a0.01000.HiUb_LoAb.csv

example_data/cohortB.phylum.lin.log.otherCore.u0.50.a0.01000.LoUb_HiAb.csv