

How to Estimate Number of Core (Single Cohort Analysis)

In this example, we will estimate the total number of core taxa found across all the samples in the input cohort file. The output file also gives the observed, median, lower bound, and upper bound of the number of core members within a specified confidence interval (interpreted from alpha).

Direct command line invocation

```
lib/Compute_Number_of_Core.r -i example_data/cohortB.phylum.summary_table.xls -u 0.8 -a 0.01
```

OUTPUT : *example_data/cohortB.phylum.core_statistics*