

1 Describe the data and analyses

```
<?xml version="1.0"?>
<axiome>
  <def name="" type=""/>
  <panda forward="" reverse="" version="">
    <sample tag=""/>
  </panda>
  <alpha/>
  <beta/>
  <mrpp/>
  <duleg/>
</axiome>
```

2 Run AXIOME on the file

```
$ axiome exp.ax
```

3 Invoke make to run analyses

```
$ make
```

AXIOME

Plugins (version 1.6)



PANDAsseq

PAired-eND Assembly of Illumina sequences

<panda/>



Non-negative Matrix Factorization

Alternative higher-dimensional decomposition

<nmf/>



SSUnique

Unique lineage finder

<ssunique/>



MRPP Analysis

Multiple Response Permutation Procedure

<mrpp/>



Indicator Species

Dufrene-Legendre Indicator Species

<duleg/>



User-Defined Analyses



Quantitative Insights Into Microbial Ecology



Clustering

uclust or CD-HIT sequence clustering

<otu-method="">



BIOM OTU Table



Tree Building

Building phylogenetic trees

<phylogeny-method="">



alpha-diversity

Chao1, phylogenetic diversity/richness

<alpha/>



beta-diversity

Rarified/summarized by taxonomic level

<beta/>



Taxonomic Composition

<taxaplot/>



Rank-Abundance

<rankabundance/>