sudo mount -t vboxsf Shared /home/qiime/Desktop/Shared\_Folder/Shared\_linux/

Analysis using RDP taxonomy biom file: input file- RDP taxa added biom file. Output - blank sample removed rdp biom file. This file then stored in new folder named RDpbiom\_plots\_diversity. This output file will further be used to run diversity analysis and biom summary. Here you can use the original biom file or output of pick\_open\_ref\_otu.py output biom file as well.

The steps here use core\_diversity.py pipeline to get taxa plots, taxonomy summaries etc.

filter\_samples\_from\_otu\_table.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDP095\_otu\_table\_taxa\_metadata\_mc2biom.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_samplesremoved.biom

-m /home/qiime/Desktop/Shared\_Folder/Shared\_linux/pandu\_mapping\_file\_copy\_corrected.txt

-s 'Health\_status:\*,!NA'

Summarize the output file:

biom summarize-table

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_summary.txt

Run add metadata on this blank removed rdp file

biom add-metadata

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata.biom

--sample-metadata-fp /home/qiime/Desktop/Shared\_Folder/Shared\_linux/pandu\_mapping\_file\_copy\_blank\_removed.txt #### this just added sample metadata, so now running again after summary for observation metadata

Summarize the output file:

biom summarize-table

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata\_summary.txt

Run add observation metadata on this sample metadata added rdp file

biom add-metadata

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata\_obs.biom

--observation-metadata-fp /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/rdp\_results\_095/rep\_set\_tax\_assignments.txt

--observation-header OTUID,taxonomy,confidence

--sc-separated taxonomy --float-fields confidence

Get summary of the above file

biom summarize-table

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata\_obs.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata\_summary\_obs.txt

Run core diversity on this file

core\_diversity\_analyses.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata\_obs.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/Core\_diversity\_RDP/

-m /home/qiime/Desktop/Shared\_Folder/Shared\_linux/pandu\_mapping\_file\_copy\_blank\_removed.txt

-c Health\_status

-t /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/pynast/filtered\_alignment/rep\_phylo.tre -e 3071

Run core diversity on this file for absolute abundance+counts

core\_diversity\_analyses.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/RDPbiom\_samplesremoved\_metadata\_obs.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/Core\_diversity\_RDP\_absolute\_abundance/

-m /home/qiime/Desktop/Shared\_Folder/Shared\_linux/pandu\_mapping\_file\_copy\_blank\_removed.txt

-c Health\_status

-t /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/pynast/filtered\_alignment/rep\_phylo.tre -e 3071

-p /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/parameters.txt --suppress\_alpha\_diversity --suppress\_beta\_diversity

The core\_diversity.py pipeline gives taxonomy summary till genus level. To get the species level classification summarize\_taxonomy.py was run with level set to 7.

Requested: 4/19/2016

summarize\_taxa.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/Core\_diversity\_RDP/taxa\_plots\_Health\_Status\_Species\_level/Health\_status\_otu\_table\_sorted.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/RDPbiom\_plots\_corediversity/Core\_diversity\_RDP/taxa\_plots\_Health\_Status\_Species\_level/

-L 7

Analysis using BLAST taxonomy biom file: input file-original biom file. output- blank sample removed rdp biom file. This file then stored in new folder named BLAST biom\_plots\_diversity. This output file will further be used to run diversity analysis and biom summary. Here you can use the original biom file or output of pick\_open\_ref\_otu.py output biom file as well.

filter\_samples\_from\_otu\_table.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/otu\_table\_mc2.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_samplesremoved.biom

-m /home/qiime/Desktop/Shared\_Folder/Shared\_linux/pandu\_mapping\_file\_copy\_corrected.txt

-s 'Health\_status:\*,!NA'

Summarize the output file:

biom summarize-table

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_summary.txt

Run add metadata on this blank removed rdp file

biom add-metadata

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata.biom

--sample-metadata-fp /home/qiime/Desktop/Shared\_Folder/Shared\_linux/pandu\_mapping\_file\_copy\_blank\_removed.txt #### this just added sample metadata, so now running again after summary for observation metadata

Summarize the output file:

biom summarize-table

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata\_summary.txt

Run add observation metadata on this sample metadata added rdp file

biom add-metadata

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata\_obs.biom

--observation-metadata-fp /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/blast\_results/rep\_set\_tax\_assignments.txt --observation-header OTUID,taxonomy,evalue

--sc-separated taxonomy

--float-fields evalue

Get summary of the above file

biom summarize-table

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata\_obs.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata\_summary\_obs.txt

Run core diversity on this file

core\_diversity\_analyses.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata\_obs.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/Core\_diversity\_BLAST/

-m

/home/qiime/Desktop/Shared\_Folder/Shared\_linux/pandu\_mapping\_file\_copy\_blank\_removed.txt

-c Health\_status

-t /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/pynast/filtered\_alignment/rep\_phylo.tre -e 3071

--suppress\_beta\_diversity

Run core diversity on this file for absolute abundance+counts

core\_diversity\_analyses.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/BLASTbiom\_samplesremoved\_metadata\_obs.biom

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/BLASTbiom\_plots\_corediversity/Core\_diversity\_BLAST\_absolute\_abundance/

-m /home/qiime/Desktop/Shared\_Folder/Shared\_linux/pandu\_mapping\_file\_copy\_blank\_removed.txt

-c Health\_status

-t /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/pynast/filtered\_alignment/rep\_phylo.tre

-e 3071

-p /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/sammed\_Results\_still\_in\_progress/parameters.txt

--suppress\_alpha\_diversity

--suppress\_beta\_diversity

Pick otu uclust Methodology (This method failed! No results are available for this method)

pick\_otus.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/Galaxy\_new\_seqs.fasta

-m uclust\_ref

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/uclust\_pickotu\_supressed/

-z

Pick rep set

pick\_rep\_set.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/uclust\_pickotu\_supressed/Galaxy\_new\_seqs\_otus.txt

-f /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/Galaxy\_new\_seqs.fasta

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/uclust\_pickotu\_supressed/rep\_set.fna

Assign taxonomy

assign\_taxonomy.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/uclust\_pickotu\_supressed/rep\_set.fna

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/uclust\_pickotu\_supressed/rdp\_results\_095/

-m rdp

-c 0.95

Align Sequences

align\_seqs.py

-i /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/uclust\_pickotu\_supressed/rep\_set.fna

-o /home/qiime/Desktop/Shared\_Folder/Shared\_linux/uclust\_galaxy\_new\_seq\_fna/uclust\_pickotu\_supressed/pynast/ -p 0.50 -d /home/qiime/Desktop/Shared\_Folder/Shared\_linux/gold.fa