To filter the out\_table\_no\_singletons\_no\_chimeras.biom file to remove the C1 to C10 and blank samples.

filter\_samples\_from\_otu\_table.py -i otus/otu\_table\_no\_singletons\_no\_chimeras.biom -o qiime\_reannalysis\_0220/filter\_samples\_from\_otu\_table/filtered\_otu\_table\_no\_singletons\_no\_chimeras.biom --sample\_id\_fp qiime\_reannalysis\_0220/filter\_samples\_from\_otu\_table/ids.txt --negate\_sample\_id\_fp

Plot taxa graphs using disease as category with above filtered biom file

summarize\_taxa\_through\_plots.py -o qiime\_reannalysis\_0220/filter\_samples\_from\_otu\_table/ -i qiime\_reannalysis\_0220/filter\_samples\_from\_otu\_table/filtered\_otu\_table\_no\_singletons\_no\_chimeras.biom -m qiime\_reannalysis\_0220/filter\_samples\_from\_otu\_table/170703\_UNC22\_0361\_B86T3.mapping\_1\_corrected.txt -c Disease -f

Plot taxa graphs using Disease Race as category with above filtered biom file

summarize\_taxa\_through\_plots.py -o qiime\_reannalysis\_0220/filter\_samples\_from\_otu\_table/ -i qiime\_reannalysis\_0220/filter\_samples\_from\_otu\_table/filtered\_otu\_table\_no\_singletons\_no\_chimeras.biom -m qiime\_reannalysis\_0220/filter\_samples\_from\_otu\_table/170703\_UNC22\_0361\_B86T3.mapping\_1\_corrected.txt -c RaceDis -f -s

For all these scrips use the mentioned mapping file.

04/23/2018

**Summarize taxa through species level including C1 to C10 samples**

summarize\_taxa.py -i ./../otus/otu\_table\_no\_singletons\_no\_chimeras.biom -L2,3,4,5,6,7 -o ./summarize\_taxa\_including\_C1\_C10/

Hello,

My GOAL is to get the following output using qiime scripts:

1. species level taxonomic summary of my data
2. at the same time summarize OTU by category and plot different charts.

There are two SCRIPTS I have tried so far to do this.

1. Summarize\_taxa\_through\_plots.py: a mapping category argument (-c) along with mapping file (-m) can be passed to this script to get part (II) of my goal. This script won’t give species level information though, something that can be done using following script #2.
2. A combination of summarize\_taxa.py and plot\_taxa\_summary.py: These scripts can give the desired taxonomic level information of my goal, but I didn’t find anything if these scripts can be used to summarize OTU by category.

06/05/2018

Summarize taxa through plots including C1 to C10 samples.

Filter samples to take out blank sample.

filter\_samples\_from\_otu\_table.py -i otus/otu\_table\_no\_singletons\_no\_chimeras.biom -o qiime\_reannalysis\_0220/summarize\_taxa\_C1\_C10\_disR/blank\_filtered\_otu\_table\_no\_singletons\_no\_chimeras.biom --sample\_id\_fp qiime\_reannalysis\_0220/summarize\_taxa\_C1\_C10\_disR/ids.txt --negate\_sample\_id\_fp

Race Disease grouping

summarize\_taxa\_through\_plots.py -o qiime\_reannalysis\_0220/summarize\_taxa\_C1\_C10\_disR/RaceDis -i qiime\_reannalysis\_0220/summarize\_taxa\_C1\_C10\_disR/blank\_filtered\_otu\_table\_no\_singletons\_no\_chimeras.biom -m qiime\_reannalysis\_0220/summarize\_taxa\_C1\_C10\_disR/170703\_UNC22\_0361\_B86T3.mapping\_1\_corrected.txt -c RaceDis

Disease grouping

summarize\_taxa\_through\_plots.py -o qiime\_reannalysis\_0220/summarize\_taxa\_C1\_C10\_disR/Disease -i qiime\_reannalysis\_0220/summarize\_taxa\_C1\_C10\_disR/blank\_filtered\_otu\_table\_no\_singletons\_no\_chimeras.biom -m qiime\_reannalysis\_0220/summarize\_taxa\_C1\_C10\_disR/170703\_UNC22\_0361\_B86T3.mapping\_1\_corrected.txt -c Disease