# **Module 9**: Integrating QIIME2 outputs with other analyses

# Learning Outcomes

- Be able to export QIIME2 files (qza) into human-readable formats (txt, tsv, or csv)

- Use bash to view text files

- Download R and RStudio

# Converting to a "human-readable" file

**.qza file**

**.txt, .tsv, .csv**



```
Feature ID      Taxon    Consensus
0006edaf32a13056b89b015df9cb42dd
0013c1743927ee19a962b903b8990896
0046b287d169234ab74c178db99c8941
ium     0.9
004c52d8f4a01bba8c7997309bb415e6
006f74c3dfc395131b9c87f36649ad35
0095c7897ff979012e8a189f89237d17
00bdcfc2a244073e026fe070ba80f81c
ured_bacterium  0.7
013585c3016ad6ecb49fff813d12a080
02625bdda0d8187ee701dbd333a7b850
028529ef374b2291211d5cac14f7c0a0
029f38558c12daad433d88f336cb26b5
02c5cdc2e870bb3f79ee8c5eaf2b4d09
0315e6f7a3f7c331bc0cec65134f53c8
04a75f1199d1bc6b58d19dd8aeb24520
04b5f628945c80ce624d2926e0582c98
```

```
d__Bacteria; p__Actinobacteriota; c__Actino
d__Bacteria; p__Verrucomicrobiota; c__Verru
d__Bacteria; p__Entotheonellaeota; c__Entot

d__Bacteria; p__Armatimonadota; c__uncultur
d__Bacteria; p__Bacteroidota; c__Bacteroidi
d__Bacteria; p__Actinobacteriota; c__MB-A2-
d__Bacteria; p__Verrucomicrobiota; c__Verru

d__Bacteria; p__Actinobacteriota; c__Thermo
d__Bacteria; p__Actinobacteriota; c__Thermo
d__Bacteria; p__Bacteroidota; c__Bacteroidi
d__Bacteria; p__Actinobacteriota; c__MB-A2-
d__Bacteria; p__Actinobacteriota; c__Acidim
d__Bacteria; p__Chloroflexi; c__KD4-96; o__
d__Bacteria; p__Proteobacteria; c__Gammapro
d__Bacteria; p__Actinobacteriota; c__Actino
```

**Text file organized as a data table where information is separated using a delimiter (ie. tab, comma, /)**

# Qiime2 Pipeline
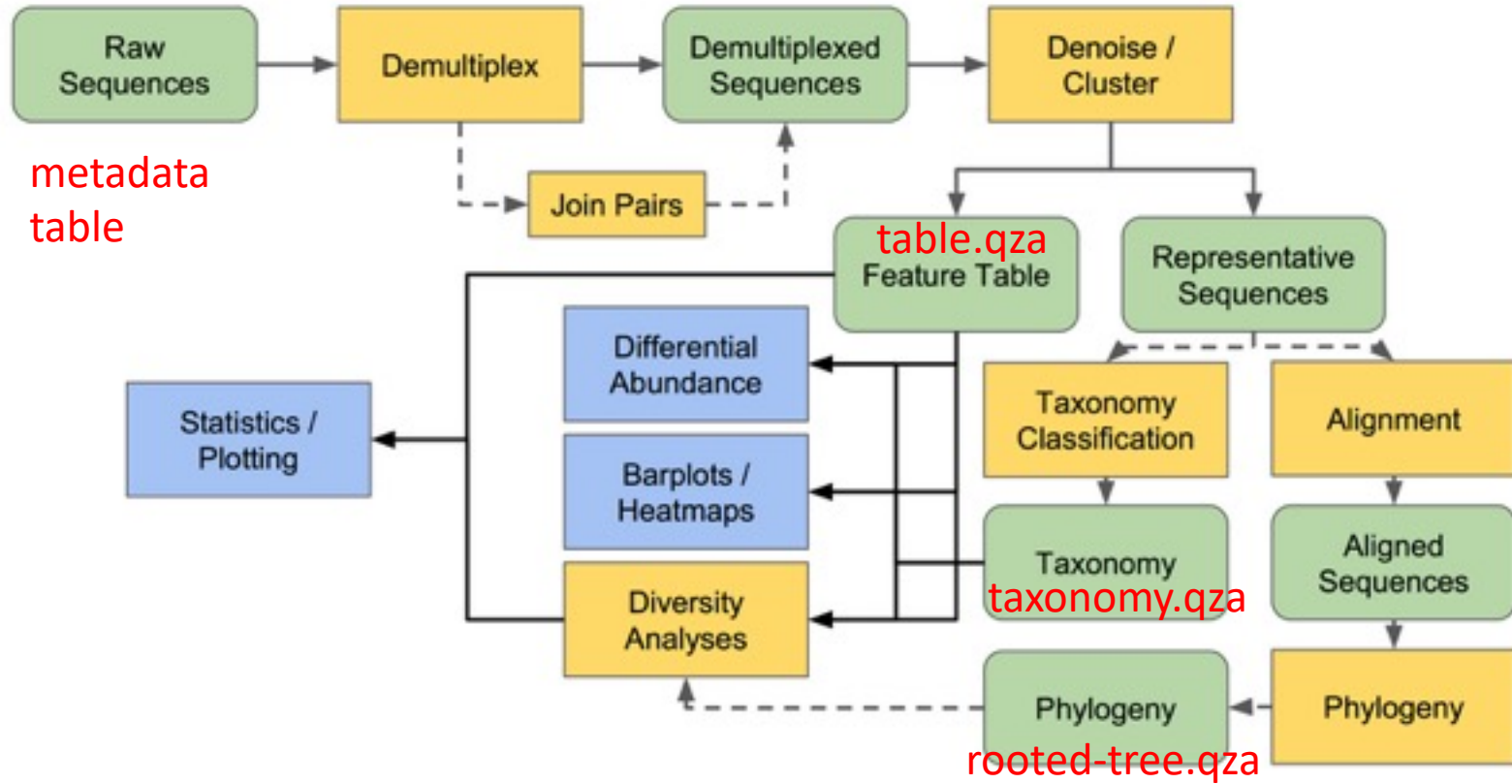
# QIIME Export Function

qiime tools export

--input-path FILE.qza

--output-path FILE_EXPORT_DIR
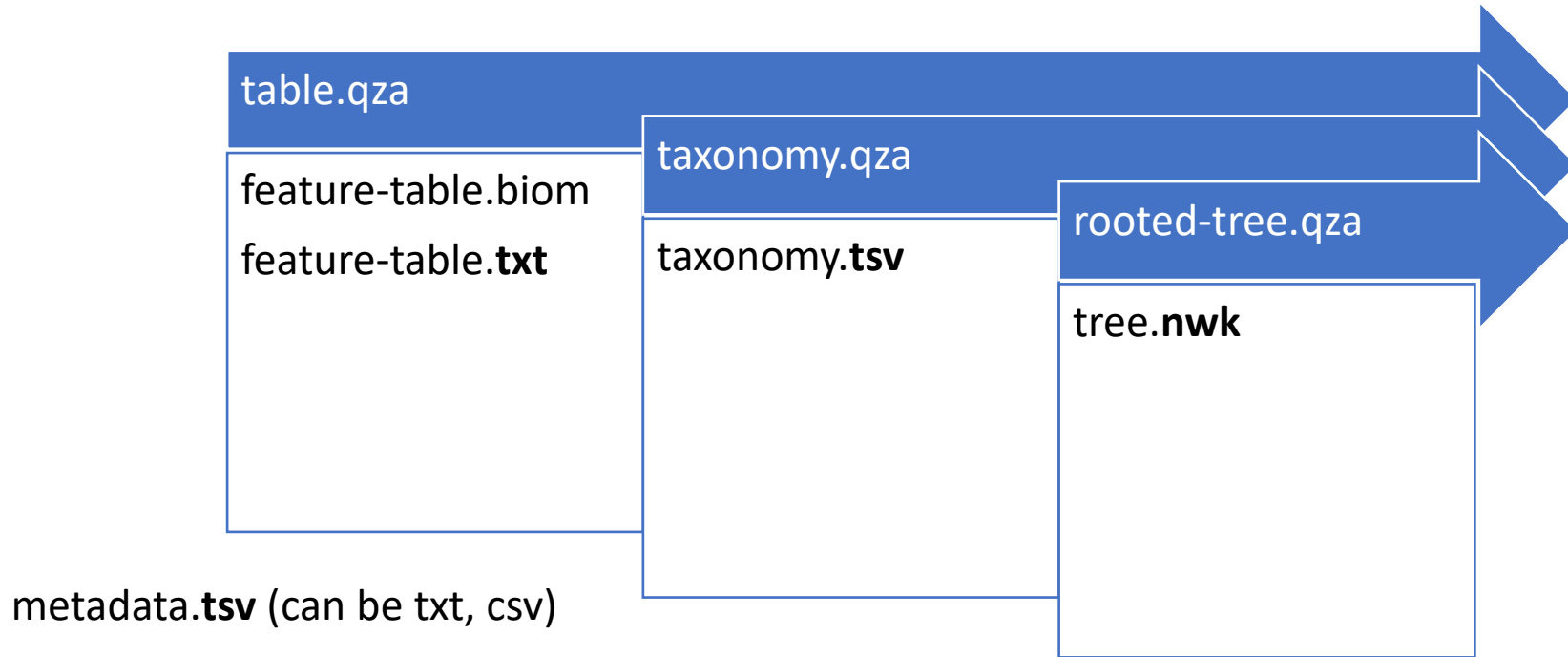

biom convert

-i feature-table.biom

--to-tsv -o feature-table.txt


More about biom files: https://biom-format.org/documentation/table_objects.html

# Converting all qza files

**table.qza**

feature-table.biom

feature-table.**txt**

**taxonomy.qza**

taxonomy.**tsv**

**rooted-tree.qza**

tree.**nwk**

metadata.**tsv** (can be txt, csv)

# Download R and RStudio

- [https://teacherscollege.screenstepslive.com/a/1135059-install-r-and-r-studio-for-mac](https://teacherscollege.screenstepslive.com/a/1135059-install-r-and-r-studio-for-mac)

- [https://teacherscollege.screenstepslive.com/a/1108074-install-r-and-r-studio-for-windows](https://teacherscollege.screenstepslive.com/a/1108074-install-r-and-r-studio-for-windows)