

Comparative metagenomic analysis using VIROME

Jaysheel Bhavsar, Shawn Polson, K. Eric Wommack

Abstract

This tutorial demonstrates the use of VIROME for comparing viral metagenome libraries analyzed with the VIROME pipeline as well as comparative analysis of viral communities using the Quantitative Insights in Microbial Ecology package (QIIME).

Wommack, K. E., J. Bhavsar, S. W. Polson, J. Chen, M. Dumas, S. Srinivasiah, M. Furman, S. Jamindar, and D. J. Nasko. 2012. VIROME: a standard operating procedure for analysis of viral metagenome sequences. *Standards in Genomic Sciences* 6:427-439 [[PMC3558967](https://pubmed.ncbi.nlm.nih.gov/22811111/)]

[See site](#) for more information.

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Guidelines

See full video below for more information.

Youtube link: <https://www.youtube.com/watch?v=mL0qRR1uYUM>

Protocol

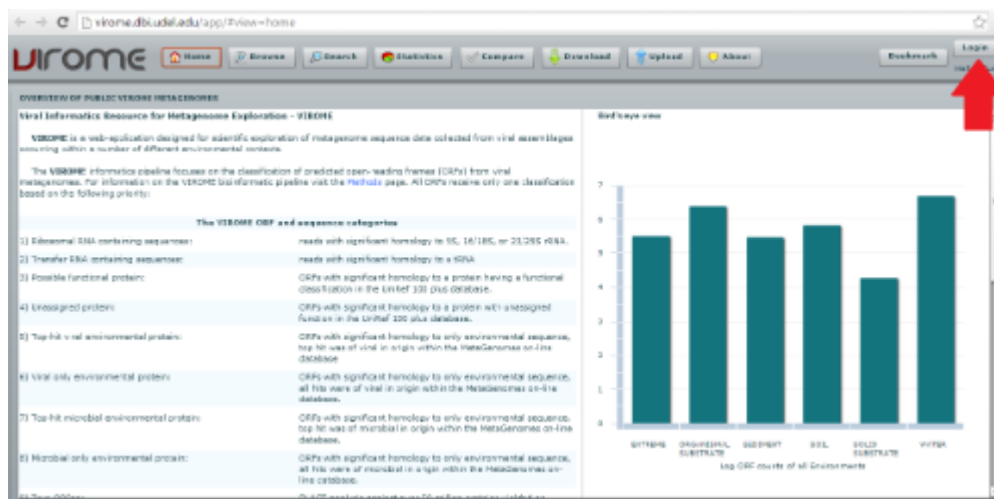
Step 1.

Go to [VIROME web application](#).



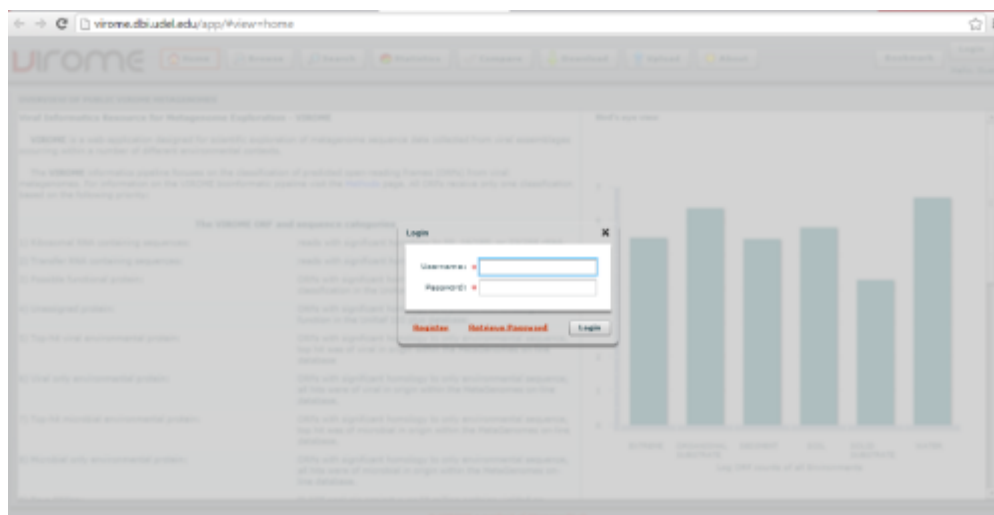
Step 2.

Click the login button.



Step 3.

Enter username and password to authenticate into the application.



Step 4.

Click the compare button.



Step 5.

The VIROME Comparinator will appear with a list of both private and public libraries.

Comparinator

List of all libraries sorted by environment:

- EXTREME: DEARFAY
- EXTREME: DVAH
- EXTREME: DVAH
- EXTREME: DVAH
- EXTREME: DVAH
- EXTREME: YELLOWTOWN NATIONAL PARK OCTOPUS/SHROOM K OF BRUSH METABOLISM
- EXTREME: OCTOPUS BRUSH
- EXTREME: LOFT CITY HYDROTHERMAL VENT
- ORGANISMAL SUBSTRATE: DVD MICROBIOME 5

Other library name(s):

Choose metrics for library comparison (At least one must be selected):

Taxonomy	Function	Environment
NCBI Taxonomy <input checked="" type="checkbox"/>	ADAMS <input type="checkbox"/>	LIBRARY <input type="checkbox"/>
	COG <input type="checkbox"/>	LIBRARY TYPE <input type="checkbox"/>
	GO <input type="checkbox"/>	GOEVESTER <input type="checkbox"/>
	KEGG <input type="checkbox"/>	BIOD THERM <input type="checkbox"/>
	SWISS <input type="checkbox"/>	

Choose output format (At least one must be selected):

Tab delimited file

San numbers ☒

Date normalized by size of target library ☒

Biological Observation Matrix format for QIIME analysis

San numbers ☒

Date normalized by size of target library ☒

Step 6.

Using the dialogue box below the list you can filter the libraries based on a search term.

Comparinator

List of all libraries sorted by environment:

- EXTREME: DEARFAY
- EXTREME: DVAH
- EXTREME: DVAH
- EXTREME: DVAH
- EXTREME: DVAH
- EXTREME: YELLOWTOWN NATIONAL PARK OCTOPUS/SHROOM K OF BRUSH METABOLISM
- EXTREME: OCTOPUS BRUSH
- EXTREME: LOFT CITY HYDROTHERMAL VENT
- ORGANISMAL SUBSTRATE: DVD MICROBIOME 5

Other library name(s):

Choose metrics for library comparison (At least one must be selected):

Taxonomy	Function	Environment
NCBI Taxonomy <input checked="" type="checkbox"/>	ADAMS <input type="checkbox"/>	LIBRARY <input type="checkbox"/>
	COG <input type="checkbox"/>	LIBRARY TYPE <input type="checkbox"/>
	GO <input type="checkbox"/>	GOEVESTER <input type="checkbox"/>
	KEGG <input type="checkbox"/>	BIOD THERM <input type="checkbox"/>
	SWISS <input type="checkbox"/>	

Choose output format (At least one must be selected):

Tab delimited file

San numbers ☒

Date normalized by size of target library ☒

Biological Observation Matrix format for QIIME analysis

San numbers ☒

Date normalized by size of target library ☒

Step 7.

Double click on library names to choose them for analysis.

📌 NOTES

Bonnie Hurwitz 16 Nov 2015

They will appear in the window panel to the right of the list.

Step 8.

Choose desired metric(s) for library comparison.

Virome Compare interface showing the 'Compare' tab. The 'Choose metrics for library comparison' section has a red arrow pointing to the 'Taxonomy' checkbox, which is checked. The 'Choose output format' section has a red arrow pointing to the 'Tab delimited file' checkbox, which is checked. The 'Submit' button is at the bottom right.

📌 NOTES

Bonnie Hurwitz 16 Nov 2015

Taxonomy, function, and environment options can be selected.

Step 9.

Choose the output format(s).

Virome Compare interface showing the 'Compare' tab. The 'Choose metrics for library comparison' section has a red arrow pointing to the 'Taxonomy' checkbox, which is checked. The 'Choose output format' section has a red arrow pointing to the 'Tab delimited file' checkbox, which is checked. The 'Submit' button is at the bottom right.

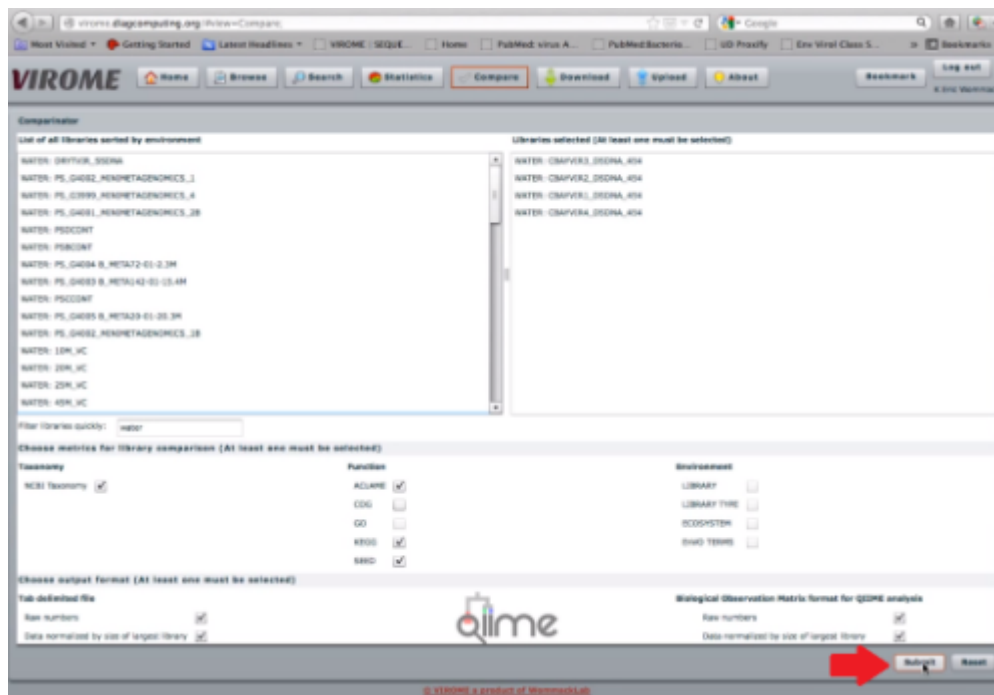
📌 NOTES

Bonnie Hurwitz 16 Nov 2015

Tab delimited file and Biological Observation Matrix format for QIIME analysis options can be selected.

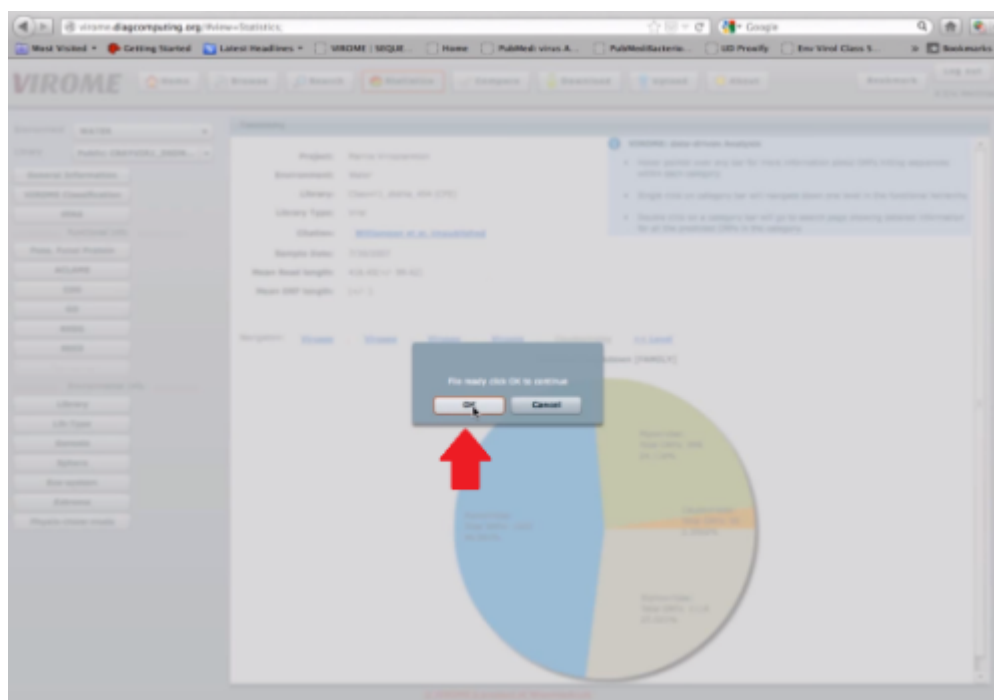
Step 10.

Click "Submit".



Step 11.

Click "OK" to download data.



Step 12.

Once prompted to save the file, do not change the file name!

Step 13.

Navigate to the Finder.

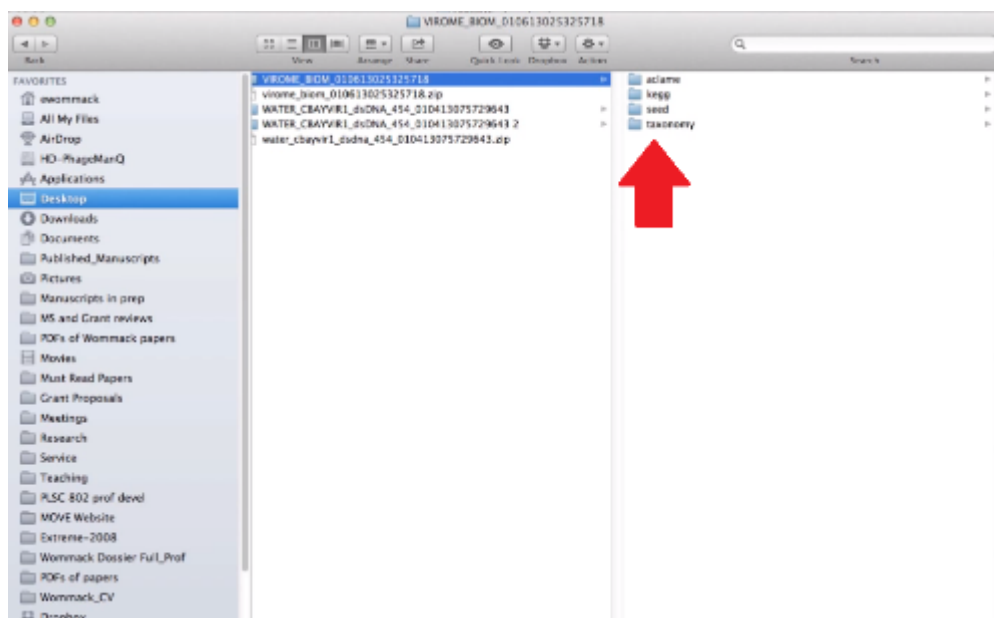


Step 14.

Double click to unzip the file.

Step 15.

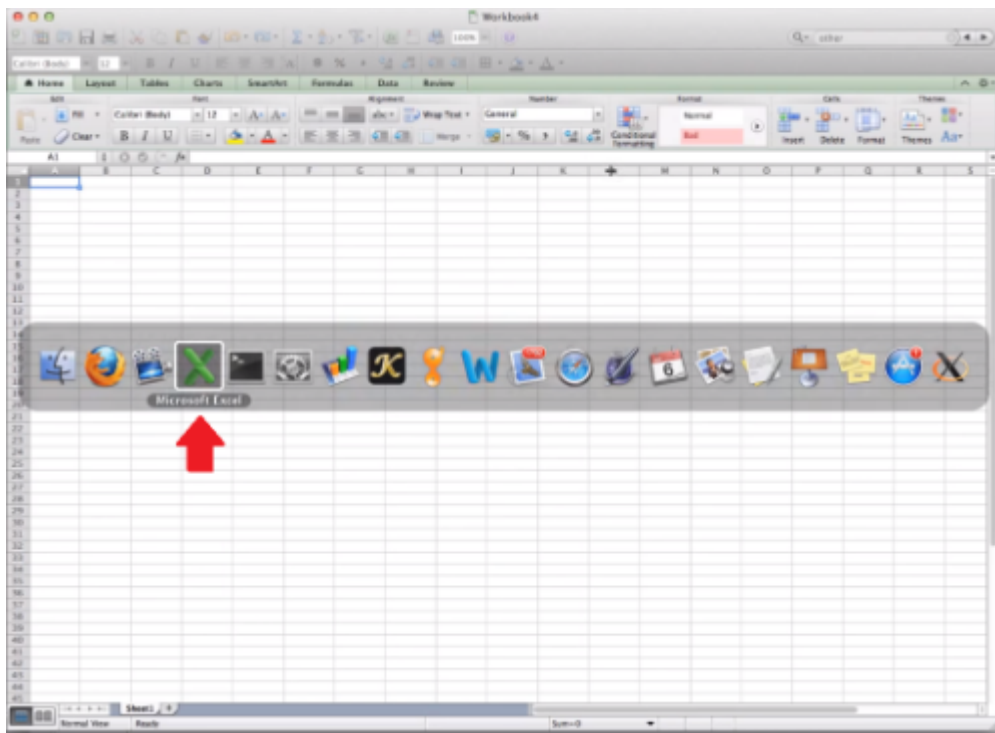
One file for each metric selected should appear.



Excel example

Step 16.

Tab delimited files can be opened in Excel spreadsheet.



Excel example

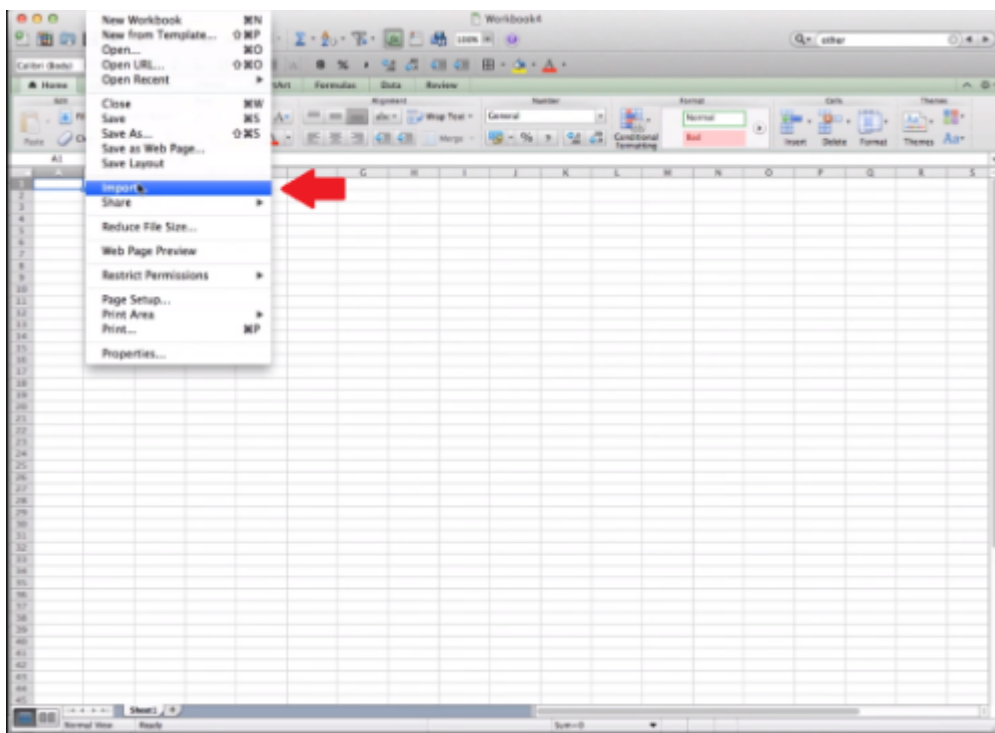
Step 17.

Navigate to the folder with the file.

Excel example

Step 18.

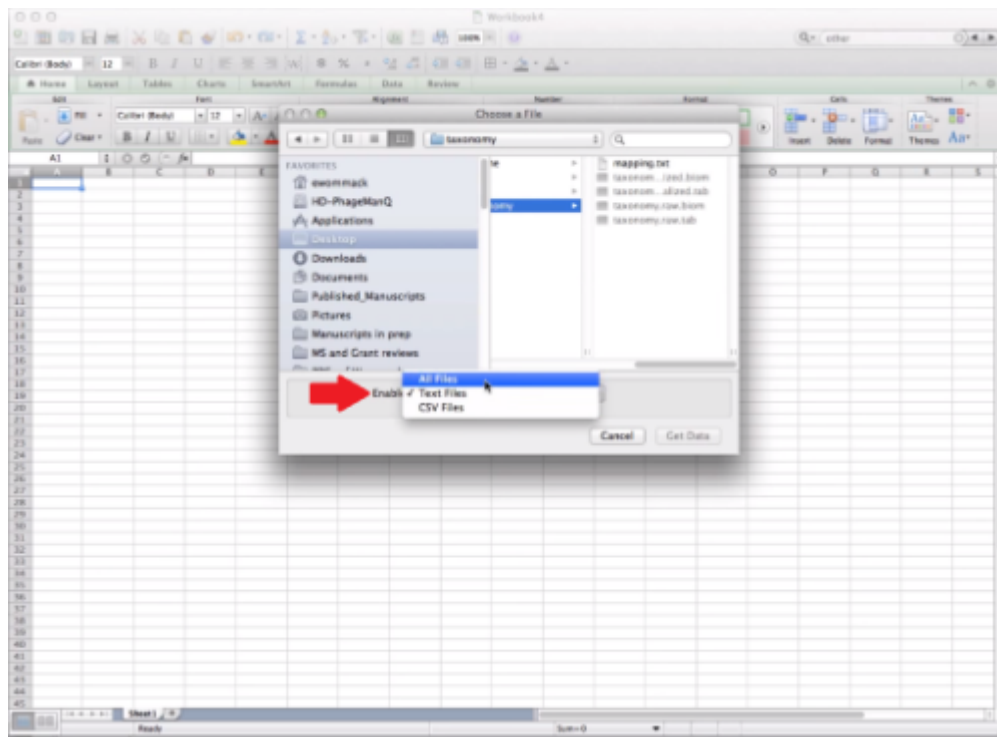
Import as text file.



Excel example

Step 19.

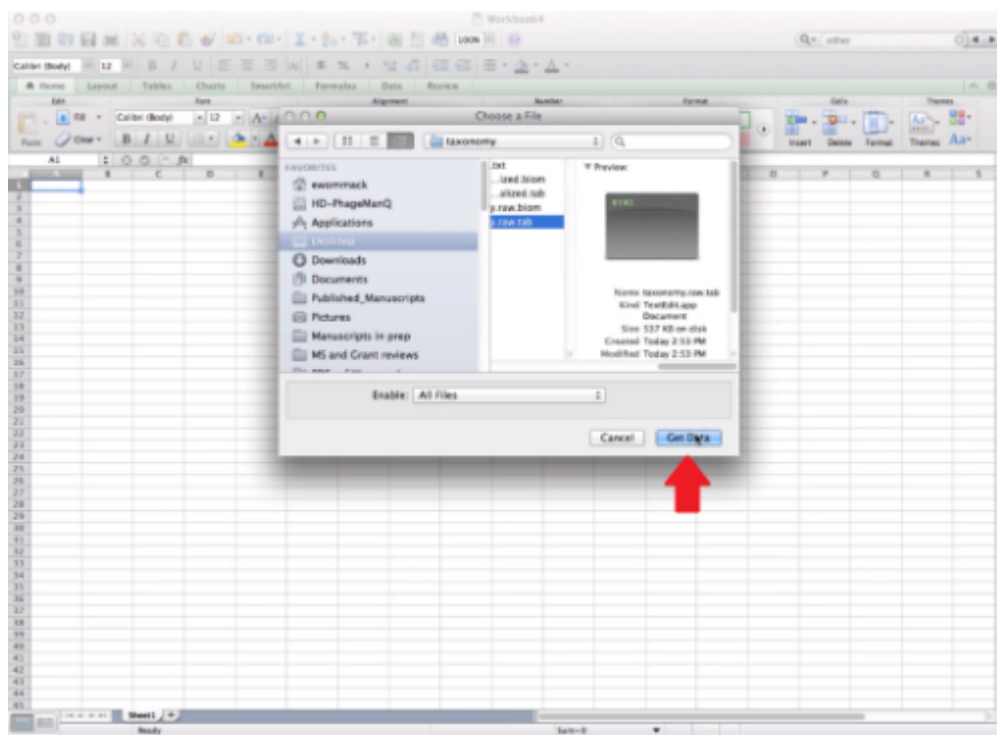
Enable "All file" types.



Excel example

Step 20.

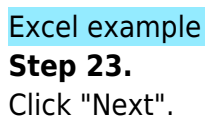
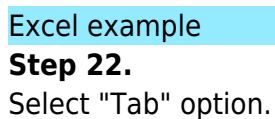
Click "Get Data".

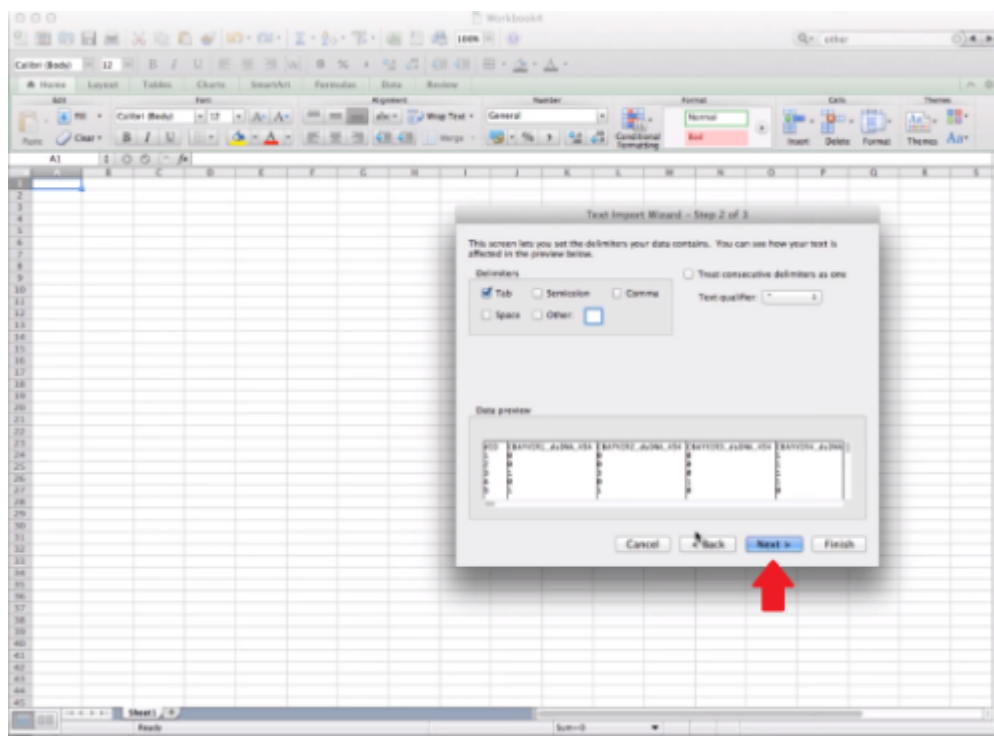


Excel example

Step 21.

Click "Next".

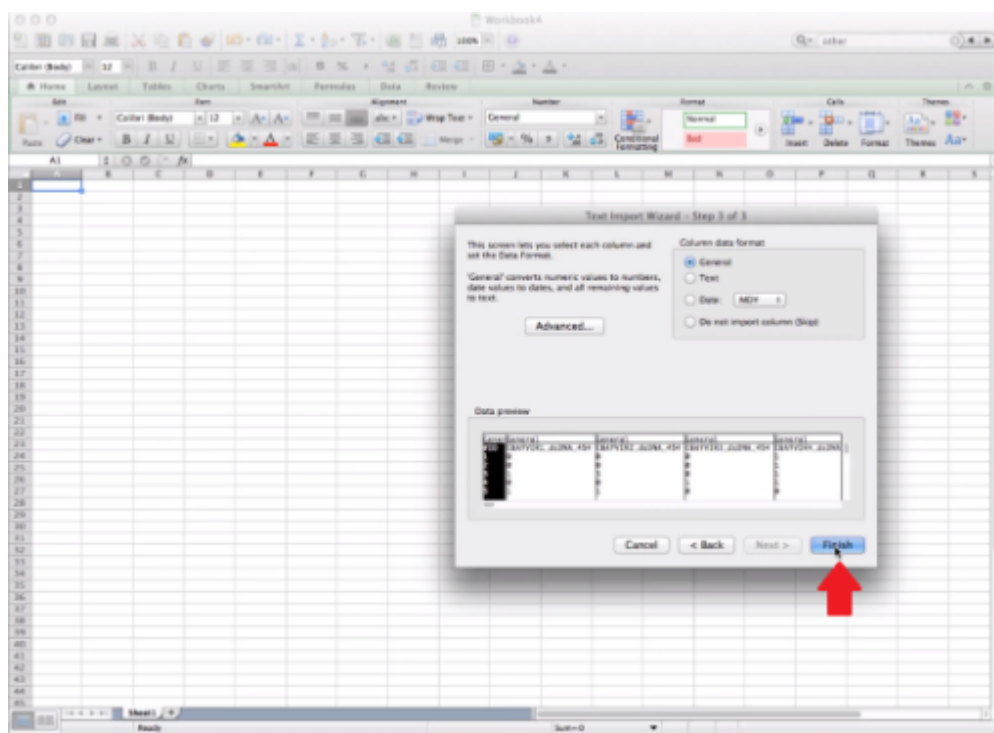




Excel example

Step 24.

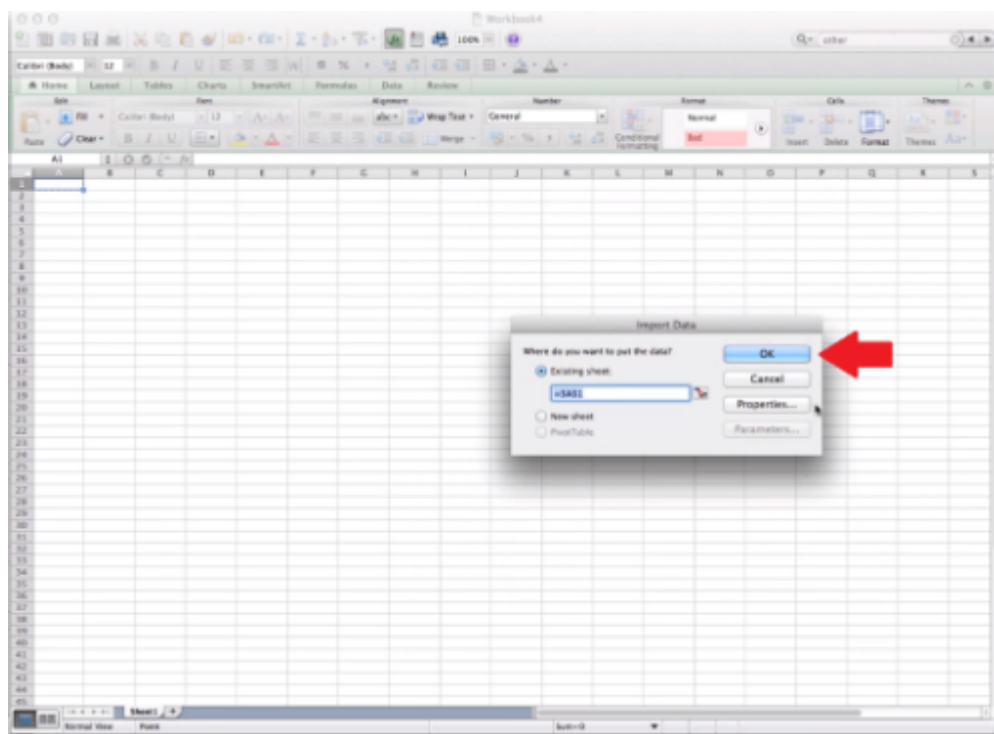
Click "Finish".



Excel example

Step 25.

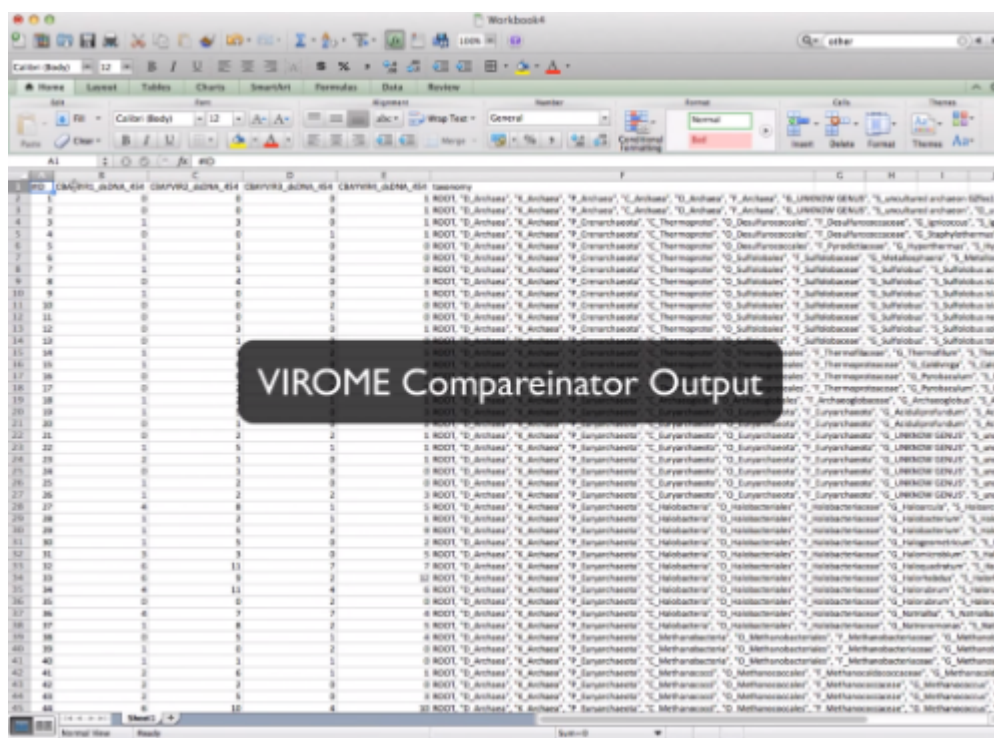
Click "OK".



Excel example

Step 26.

VIROME Comparinator output will appear.



Excel example

Step 27.

For more detailed description [see video](#).

LINK:

<https://www.youtube.com/watch?v=mL0qRR1uYUM&feature=youtu.be&t=2m48s>

QIIME example

Step 28.

✓ protocols.io

11

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Open QIIME terminal window.

```
MacQIIME 1.6.0-20121220.OS10.6 -- user14@ip-10-46-137-178: /mnt/user14/assembly -- bash -- 149x59
MacQIIME stage-man-q:ac1ane $ pwd
Applications/Utilities/MacQIIME 1.6.0-20121220.OS10.6/CBay-Sanger-454/ac1ane
MacQIIME stage-man-q:ac1ane $ cd ..
MacQIIME stage-man-q:CBay-Sanger-454 $ ls -l
total 1152
drwxr-xr-x@ 5 swinsack swinsack 179 Jan 2 10:22 VIROME_BIOM_R18213895534875
drwxr-xr-x@ 12 swinsack swinsack 442 Jan 2 10:05 ac1ane
drwxr-xr-x@ 10 swinsack swinsack 544 Jan 2 10:18 seed
drwxr-xr-x@ 12 swinsack swinsack 408 Jan 2 21:54 taxonomy
drwxr-xr-x@ 1 swinsack admin 587115 Jan 2 09:57 virome_biom_R18213895534875.zip
MacQIIME stage-man-q:CBay-Sanger-454 $ cd taxonomy/
MacQIIME stage-man-q:taxonomy $ ls -l
total 10744
drwxr-xr-x@ 1 swinsack swinsack 48 Dec 27 17:10 alpha_metrics.txt
drwxr-xr-x@ 1 swinsack swinsack 48 Dec 27 17:02 beta_metrics.txt
drwxr-xr-x@ 1 swinsack swinsack 1040310 Jan 2 21:54 gtest.txt
drwxr-xr-x@ 1 swinsack swinsack 485 Jan 2 21:54 mapping.txt
drwxr-xr-x@ 1 swinsack swinsack 1251732 Jan 2 09:56 taxonomy.normalized.biom
drwxr-xr-x@ 1 swinsack swinsack 1081789 Jan 2 09:55 taxonomy.normalized.tab
drwxr-xr-x@ 1 swinsack swinsack 1287079 Jan 2 09:56 taxonomy.raw.biom
drwxr-xr-x@ 1 swinsack swinsack 957935 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x@ 16 swinsack swinsack 544 Jan 2 10:25 taxonomy_beta_sang_454
MacQIIME stage-man-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sang_454 -m mapping.txt
MacQIIME stage-man-q:taxonomy $ pwd
Applications/Utilities/MacQIIME 1.6.0-20121220.OS10.6/CBay-Sanger-454/taxonomy
MacQIIME stage-man-q:taxonomy $ ls -l
total 10744
drwxr-xr-x@ 1 swinsack swinsack 48 Dec 27 17:10 alpha_metrics.txt
drwxr-xr-x@ 1 swinsack swinsack 48 Dec 27 17:02 beta_metrics.txt
drwxr-xr-x@ 1 swinsack swinsack 1040310 Jan 2 21:54 gtest.txt
drwxr-xr-x@ 1 swinsack swinsack 485 Jan 2 21:54 mapping.txt
drwxr-xr-x@ 1 swinsack swinsack 544 Jan 2 10:25 tax_CBay_sang_454
drwxr-xr-x@ 1 swinsack swinsack 1251732 Jan 2 09:56 taxonomy.normalized.biom
drwxr-xr-x@ 1 swinsack swinsack 1081789 Jan 2 09:55 taxonomy.normalized.tab
drwxr-xr-x@ 1 swinsack swinsack 1287079 Jan 2 09:56 taxonomy.raw.biom
drwxr-xr-x@ 1 swinsack swinsack 957935 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x@ 16 swinsack swinsack 544 Jan 2 10:25 taxonomy_beta_sang_454
MacQIIME stage-man-q:taxonomy $ cd ..
MacQIIME stage-man-q:CBay-Sanger-454 $ ls
VIROME_BIOM_R18213895534875 seed virome_biom_R18213895534875.zip
ac1ane taxonomy
MacQIIME stage-man-q:CBay-Sanger-454 $ ls
VIROME_BIOM_R18213895534875 seed virome_biom_R18213895534875.zip
ac1ane taxonomy
MacQIIME stage-man-q:CBay-Sanger-454 $ cd ..
MacQIIME stage-man-q:MacQIIME 1.6.0-20121220.OS10.6 $ ls
CBay-Sanger-454 CBay454-Only P2IOME.txt macotime
CBay-induced-vs-free-GSM-D87T-CBAT testfail.s scripts
MacQIIME stage-man-q:MacQIIME 1.6.0-20121220.OS10.6 $ cd CBay454-Only/
MacQIIME stage-man-q:CBay454-Only $ ls -l
total 0
drwxr-xr-x@ 7 swinsack swinsack 220 Jan 6 14:55 ac1ane
drwxr-xr-x@ 7 swinsack swinsack 220 Jan 6 14:55 hugg
drwxr-xr-x@ 7 swinsack swinsack 220 Jan 6 14:55 seed
drwxr-xr-x@ 7 swinsack swinsack 220 Jan 6 14:55 taxonomy
MacQIIME stage-man-q:CBay454-Only $ cd taxonomy/
MacQIIME stage-man-q:taxonomy $ ls
mapping.txt taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacQIIME stage-man-q:taxonomy $
```

NOTES

Bonnie Hurwitz 19 Nov 2015

MacQIIME used for this example.

QIIME example

Step 29.

Run summarize taxa through plots script.


```

MacQIIME_1.6.0-20121220_OS10.6 -- user14@ip-10-46-137-178: /mnt/user14/assembly -- bash -- 149x59
MacQIIME phage-run-q:acilme $ pwd
/Applications/Bratnfo/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/acilme
MacQIIME phage-run-q:acilme $ cd ..
MacQIIME phage-run-q:CBay-Sanger-454 $ ls -l
total 3152
drwxr-xr-x 5 swanack swanack 178 Jan 2 10:22 VIROME_BIOM_R10213095534975
drwxr-xr-x 13 swanack swanack 442 Jan 3 10:05 acilme
drwxr-xr-x 10 swanack swanack 548 Jan 2 10:10 seed
drwxr-xr-x 12 swanack swanack 980 Jan 2 21:54 taxonomy
-rw-r--r-- 1 swanack swanack 587115 Jan 2 09:57 virome_biom_R10213095534975.rlp
MacQIIME phage-run-q:CBay-Sanger-454 $ cd taxonomy/
MacQIIME phage-run-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 swanack swanack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 swanack swanack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 swanack swanack 1040310 Jan 2 21:54 gtest.txt
-rw-r--r-- 1 swanack swanack 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 swanack swanack 1251729 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 swanack swanack 1881789 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 swanack swanack 1287079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 swanack swanack 957935 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x 16 swanack swanack 544 Jan 2 10:25 taxonomy_beta_sang_454
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sang_454 -w mapping.txt
MacQIIME phage-run-q:taxonomy $ pwd
/Applications/Bratnfo/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/taxonomy
MacQIIME phage-run-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 swanack swanack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 swanack swanack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 swanack swanack 1040310 Jan 2 21:54 gtest.txt
-rw-r--r-- 1 swanack swanack 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 swanack swanack 1251729 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 swanack swanack 1881789 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 swanack swanack 1287079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 swanack swanack 957935 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x 16 swanack swanack 544 Jan 2 10:25 taxonomy_beta_sang_454
MacQIIME phage-run-q:CBay-Sanger-454 $ ls
VIROME_BIOM_R10213095534975 seed taxonomy
MacQIIME phage-run-q:CBay-Sanger-454 $ ls
VIROME_BIOM_R10213095534975 seed taxonomy
MacQIIME phage-run-q:CBay-Sanger-454 $ cd ..
MacQIIME phage-run-q:MacQIIME_1.6.0-20121220_OS10.6 $ ls
CBay-Sanger-454 CBay454-Only README.txt MacQIIME
CBay-induced-vs-free GEM-DIFF-CBAT install.s scripts
MacQIIME phage-run-q:MacQIIME_1.6.0-20121220_OS10.6 $ cd CBay454-Only/
MacQIIME phage-run-q:CBay454-Only $ ls -l
total 0
drwxr-xr-x 7 swanack swanack 220 Jan 3 14:55 acilme
drwxr-xr-x 7 swanack swanack 220 Jan 3 14:55 kegg
drwxr-xr-x 7 swanack swanack 220 Jan 3 14:55 seed
drwxr-xr-x 7 swanack swanack 220 Jan 3 14:55 taxonomy
MacQIIME phage-run-q:CBay454-Only $ cd taxonomy/
MacQIIME phage-run-q:taxonomy $ ls
mapping.txt taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom

```

cmd **COMMAND**

summarize_taxa_through_plots.py

QIIME example

Step 30.

Choose input file. (Example command below)

```

MacQIIME_1.6.0-20121220_OS10.6 -- user14@ip-10-46-137-178: /mnt/user14/assembly -- bash -- 149x59
MacQIIME phage-run-q:acilme $ pwd
/Applications/Bratnfo/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/acilme
MacQIIME phage-run-q:acilme $ cd ..
MacQIIME phage-run-q:CBay-Sanger-454 $ ls -l
total 3152
drwxr-xr-x 5 swanack swanack 178 Jan 2 10:22 VIROME_BIOM_R10213095534975
drwxr-xr-x 13 swanack swanack 442 Jan 3 10:05 acilme
drwxr-xr-x 10 swanack swanack 548 Jan 2 10:10 seed
drwxr-xr-x 12 swanack swanack 980 Jan 2 21:54 taxonomy
-rw-r--r-- 1 swanack swanack 587115 Jan 2 09:57 virome_biom_R10213095534975.rlp
MacQIIME phage-run-q:CBay-Sanger-454 $ cd taxonomy/
MacQIIME phage-run-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 swanack swanack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 swanack swanack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 swanack swanack 1040310 Jan 2 21:54 gtest.txt
-rw-r--r-- 1 swanack swanack 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 swanack swanack 1251729 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 swanack swanack 1881789 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 swanack swanack 1287079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 swanack swanack 957935 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x 16 swanack swanack 544 Jan 2 10:25 taxonomy_beta_sang_454
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sang_454 -w mapping.txt
MacQIIME phage-run-q:taxonomy $ pwd
/Applications/Bratnfo/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/taxonomy
MacQIIME phage-run-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 swanack swanack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 swanack swanack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 swanack swanack 1040310 Jan 2 21:54 gtest.txt
-rw-r--r-- 1 swanack swanack 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 swanack swanack 1251729 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 swanack swanack 1881789 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 swanack swanack 1287079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 swanack swanack 957935 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x 16 swanack swanack 544 Jan 2 10:25 taxonomy_beta_sang_454
MacQIIME phage-run-q:CBay-Sanger-454 $ ls
VIROME_BIOM_R10213095534975 seed taxonomy
MacQIIME phage-run-q:CBay-Sanger-454 $ ls
VIROME_BIOM_R10213095534975 seed taxonomy
MacQIIME phage-run-q:CBay-Sanger-454 $ cd ..
MacQIIME phage-run-q:MacQIIME_1.6.0-20121220_OS10.6 $ ls
CBay-Sanger-454 CBay454-Only README.txt MacQIIME
CBay-induced-vs-free GEM-DIFF-CBAT install.s scripts
MacQIIME phage-run-q:MacQIIME_1.6.0-20121220_OS10.6 $ cd CBay454-Only/
MacQIIME phage-run-q:CBay454-Only $ ls -l
total 0
drwxr-xr-x 7 swanack swanack 220 Jan 3 14:55 acilme
drwxr-xr-x 7 swanack swanack 220 Jan 3 14:55 kegg
drwxr-xr-x 7 swanack swanack 220 Jan 3 14:55 seed
drwxr-xr-x 7 swanack swanack 220 Jan 3 14:55 taxonomy
MacQIIME phage-run-q:CBay454-Only $ cd taxonomy/
MacQIIME phage-run-q:taxonomy $ ls
mapping.txt taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom

```

cmd **COMMAND**

-i taxonomy.normalized.biom

QIIME example

Step 31.

Choose output file. (Example command below)

```
MacQIIME 1.6.0-20121220.OS10.6 — user14@ip-10-46-137-178: /mnt/user14/assembly — bash — 149x59
MacQIIME phage-run-q:ac1ane $ pwd
/Applications/BratBio/MacQIIME.1.6.0-20121220.OS10.6/CBay-Sanger-454/ac1ane
MacQIIME phage-run-q:ac1ane $ cd ..
MacQIIME phage-run-q:CBay-Sanger-454 $ ls -l
total 3152
drwxr-xr-x 5 swannack swannack 170 Jan 2 19:22 VIR001_0100_010213095534075
drwxr-xr-x 12 swannack swannack 440 Jan 2 19:05 ac1ane
drwxr-xr-x 10 swannack swannack 340 Jan 2 19:13 seed
drwxr-xr-x 12 swannack swannack 400 Jan 2 21:54 taxonomy
-rw-r--r-- 1 swannack admin 587115 Jan 2 09:57 virome_brow_010213095534075.zip
MacQIIME phage-run-q:CBay-Sanger-454 $ cd taxonomy/
MacQIIME phage-run-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 swannack swannack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 swannack swannack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 swannack swannack 1040310 Jan 2 21:54 gtest.txt
-rw-r--r-- 1 swannack swannack 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 swannack swannack 2251722 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 swannack swannack 1001700 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 swannack swannack 1207079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 swannack swannack 957935 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x 16 swannack swannack 544 Jan 2 10:20 taxonomy_beta_sang_454
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sang_454 -w mapping.txt
MacQIIME phage-run-q:taxonomy $ pwd
/Applications/BratBio/MacQIIME.1.6.0-20121220.OS10.6/CBay-Sanger-454/taxonomy
MacQIIME phage-run-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 swannack swannack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 swannack swannack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 swannack swannack 1040310 Jan 2 21:54 gtest.txt
drwxr-xr-x 9 swannack swannack 300 Jan 2 10:54 tax_CBay_sang_454
-rw-r--r-- 1 swannack swannack 2251722 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 swannack swannack 1001700 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 swannack swannack 1207079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 swannack swannack 957935 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x 16 swannack swannack 544 Jan 2 10:20 taxonomy_beta_sang_454
MacQIIME phage-run-q:taxonomy $ cd ..
MacQIIME phage-run-q:CBay-Sanger-454 $ ls
VIR001_0100_010213095534075 seed virome_brow_010213095534075.zip
ac1ane taxonomy
MacQIIME phage-run-q:CBay-Sanger-454 $ ls
VIR001_0100_010213095534075 seed virome_brow_010213095534075.zip
ac1ane taxonomy
MacQIIME phage-run-q:CBay-Sanger-454 $ cd ..
MacQIIME phage-run-q:MacQIIME 1.6.0-20121220.OS10.6 $ ls
CBay-Sanger-454 CBay454-Only README.txt MacQIIME
CBay-induced-se-from-GM-BERT-CBay install.scripts
MacQIIME phage-run-q:CBay454-Only $ cd CBay454-Only/
MacQIIME phage-run-q:CBay454-Only $ ls -l
total 0
drwxr-xr-x 7 swannack swannack 256 Jan 4 14:55 ac1ane
drwxr-xr-x 7 swannack swannack 220 Jan 4 14:55 kmgp
drwxr-xr-x 7 swannack swannack 220 Jan 4 14:55 seed
drwxr-xr-x 7 swannack swannack 220 Jan 4 14:55 taxonomy
MacQIIME phage-run-q:CBay454-Only $ cd taxonomy/
MacQIIME phage-run-q:taxonomy $ ls
mapping.txt taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o CB454tax_summ
```

cmd **COMMAND**

-o CB454tax_summ

QIIME example

Step 32.

Designate the mapping file.

```

MacQIIME_1.6.0-20121220_OS10.6 -- user14@ip-10-46-137-178 /mnt/user14/assembly -- bash -- 149x59
MacQIIME phage-wan-q:acclase $ pwd
/Applications/brainforge/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/acclase
MacQIIME phage-wan-q:acclase $ cd ..
MacQIIME phage-wan-q:CBay-Sanger-454 $ ls -l
total 1152
-rw-r--r-- 1 evenmach evenmach 178 Jan 2 10:22 VIROME_BIOM_010213095534075
-rw-r--r-- 13 evenmach evenmach 442 Jan 2 10:45 acclase
-rw-r--r-- 12 evenmach evenmach 348 Jan 2 10:10 seed
-rw-r--r-- 1 evenmach evenmach 488 Jan 2 21:54 taxonomy
-rw-r--r-- 1 evenmach admin 507115 Jan 2 09:57 virome_biom_010213095534075.zip
MacQIIME phage-wan-q:CBay-Sanger-454 $ cd taxonomy/
MacQIIME phage-wan-q:taxonomy $ ls -l
total 10704
-rw-r--r-- 1 evenmach evenmach 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 evenmach evenmach 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 evenmach evenmach 1043210 Jan 2 21:54 gtax.txt
-rw-r--r-- 1 evenmach evenmach 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 evenmach evenmach 1251733 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 evenmach evenmach 1001709 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 evenmach evenmach 1207879 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 evenmach evenmach 957935 Jan 2 09:55 taxonomy.raw.tab
-rw-r--r-- 1 evenmach evenmach 544 Jan 2 10:23 taxonomy_beta_sung_454
MacQIIME phage-wan-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sung_454 -w mapping.txt
MacQIIME phage-wan-q:taxonomy $ pwd
/Applications/brainforge/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/taxonomy
MacQIIME phage-wan-q:taxonomy $ ls -l
total 10704
-rw-r--r-- 1 evenmach evenmach 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 evenmach evenmach 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 evenmach evenmach 1043210 Jan 2 21:54 gtax.txt
-rw-r--r-- 1 evenmach evenmach 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 evenmach evenmach 1251733 Jan 2 09:56 tax_CBay_sung_454
-rw-r--r-- 1 evenmach evenmach 1207879 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 evenmach evenmach 1001709 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 evenmach evenmach 1207879 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 evenmach evenmach 957935 Jan 2 09:55 taxonomy.raw.tab
-rw-r--r-- 1 evenmach evenmach 544 Jan 2 10:23 taxonomy_beta_sung_454
MacQIIME phage-wan-q:taxonomy $ cd ..
MacQIIME phage-wan-q:CBay-Sanger-454 $ ls
VIROME_BIOM_010213095534075 seed virome_biom_010213095534075.zip
acclase taxonomy
MacQIIME phage-wan-q:CBay-Sanger-454 $ ls
VIROME_BIOM_010213095534075 seed virome_biom_010213095534075.zip
acclase taxonomy
MacQIIME phage-wan-q:CBay-Sanger-454 $ cd ..
MacQIIME phage-wan-q:MacQIIME_1.6.0-20121220_OS10.6 $ ls
CBay-Sanger-454 CBay454-Only README.txt MacQIIME
CBay-induced-vs-free GEM-DEXT-CBAT install.scripts
MacQIIME phage-wan-q:MacQIIME_1.6.0-20121220_OS10.6 $ cd CBay454-Only/
MacQIIME phage-wan-q:CBay454-Only $ ls -l
total 0
-rw-r--r-- 7 evenmach evenmach 235 Jan 6 14:55 acclase
-rw-r--r-- 7 evenmach evenmach 230 Jan 6 14:55 kagg
-rw-r--r-- 7 evenmach evenmach 230 Jan 6 14:55 seed
-rw-r--r-- 7 evenmach evenmach 230 Jan 6 14:55 taxonomy
MacQIIME phage-wan-q:CBay454-Only $ cd taxonomy/
MacQIIME phage-wan-q:taxonomy $ ls
mapping.txt taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacQIIME phage-wan-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o CBay454tax_sums -w mapping.txt

```



cmd **COMMAND**
-m mapping.txt

QIIME example

Step 33.

Run full script. (Example command below)

```

MacQIIME_1.6.0-20121220_OS10.6 -- user14@ip-10-46-137-178 /mnt/user14/assembly -- python2.7 -- 149x59
/Applications/brainforge/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/acclase
MacQIIME phage-wan-q:acclase $ cd ..
MacQIIME phage-wan-q:CBay-Sanger-454 $ ls -l
total 1152
-rw-r--r-- 1 evenmach evenmach 178 Jan 2 10:22 VIROME_BIOM_010213095534075
-rw-r--r-- 13 evenmach evenmach 442 Jan 2 10:45 acclase
-rw-r--r-- 12 evenmach evenmach 348 Jan 2 10:10 seed
-rw-r--r-- 1 evenmach evenmach 488 Jan 2 21:54 taxonomy
-rw-r--r-- 1 evenmach admin 507115 Jan 2 09:57 virome_biom_010213095534075.zip
MacQIIME phage-wan-q:CBay-Sanger-454 $ cd taxonomy/
MacQIIME phage-wan-q:taxonomy $ ls -l
total 10704
-rw-r--r-- 1 evenmach evenmach 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 evenmach evenmach 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 evenmach evenmach 1043210 Jan 2 21:54 gtax.txt
-rw-r--r-- 1 evenmach evenmach 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 evenmach evenmach 1251733 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 evenmach evenmach 1001709 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 evenmach evenmach 1207879 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 evenmach evenmach 957935 Jan 2 09:55 taxonomy.raw.tab
-rw-r--r-- 1 evenmach evenmach 544 Jan 2 10:23 taxonomy_beta_sung_454
MacQIIME phage-wan-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sung_454 -w mapping.txt
MacQIIME phage-wan-q:taxonomy $ pwd
/Applications/brainforge/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/taxonomy
MacQIIME phage-wan-q:taxonomy $ ls -l
total 10704
-rw-r--r-- 1 evenmach evenmach 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 evenmach evenmach 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 evenmach evenmach 1043210 Jan 2 21:54 gtax.txt
-rw-r--r-- 1 evenmach evenmach 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 evenmach evenmach 1251733 Jan 2 09:56 tax_CBay_sung_454
-rw-r--r-- 1 evenmach evenmach 1207879 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 evenmach evenmach 1001709 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 evenmach evenmach 1207879 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 evenmach evenmach 957935 Jan 2 09:55 taxonomy.raw.tab
-rw-r--r-- 1 evenmach evenmach 544 Jan 2 10:23 taxonomy_beta_sung_454
MacQIIME phage-wan-q:taxonomy $ cd
VIROME_BIOM_010213095534075 seed virome_biom_010213095534075.zip
acclase taxonomy
MacQIIME phage-wan-q:CBay-Sanger-454 $ ls
VIROME_BIOM_010213095534075 seed virome_biom_010213095534075.zip
acclase taxonomy
MacQIIME phage-wan-q:CBay-Sanger-454 $ cd ..
MacQIIME phage-wan-q:MacQIIME_1.6.0-20121220_OS10.6 $ ls
CBay-Sanger-454 CBay454-Only README.txt MacQIIME
CBay-induced-vs-free GEM-DEXT-CBAT install.scripts
MacQIIME phage-wan-q:MacQIIME_1.6.0-20121220_OS10.6 $ cd CBay454-Only/
MacQIIME phage-wan-q:CBay454-Only $ ls -l
total 0
-rw-r--r-- 7 evenmach evenmach 235 Jan 6 14:55 acclase
-rw-r--r-- 7 evenmach evenmach 230 Jan 6 14:55 kagg
-rw-r--r-- 7 evenmach evenmach 230 Jan 6 14:55 seed
-rw-r--r-- 7 evenmach evenmach 230 Jan 6 14:55 taxonomy
MacQIIME phage-wan-q:CBay454-Only $ cd taxonomy/
MacQIIME phage-wan-q:taxonomy $ ls
mapping.txt taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacQIIME phage-wan-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o CBay454tax_sums -w mapping.txt

```

cmd **COMMAND**


```
summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o CB454tax_summ -m mapping.txt
```

QIIME example

Step 34.

QIIME will generate stacked bar plots based on the taxonomic data created in VIROME.

QIIME example

Step 35.

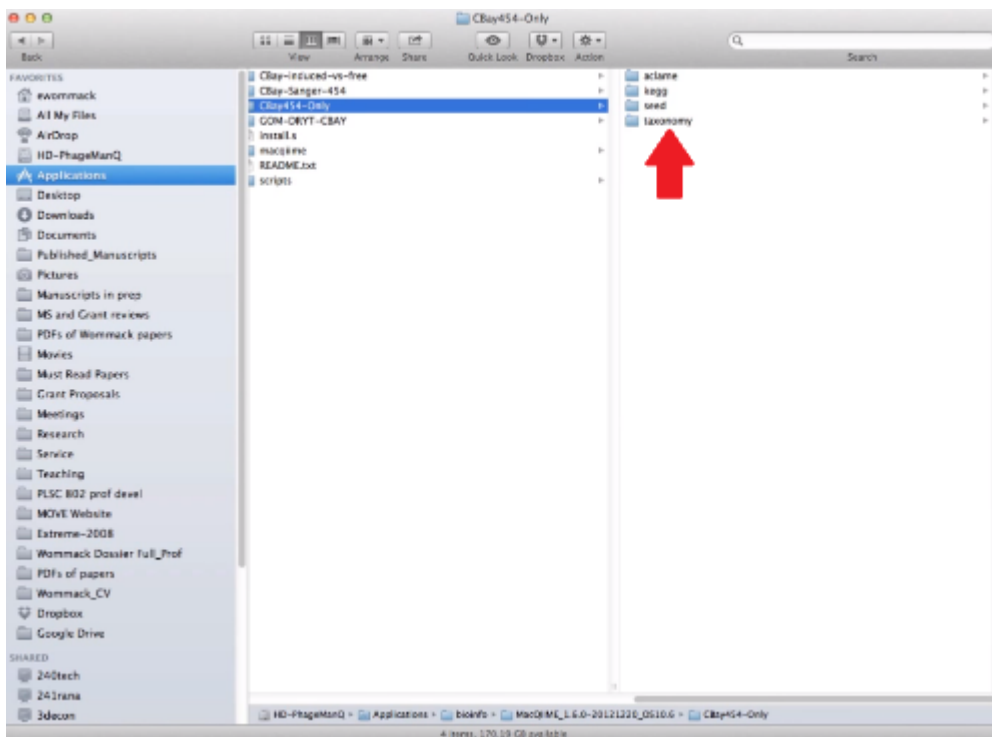
Navigate to the Finder.



QIIME example

Step 36.

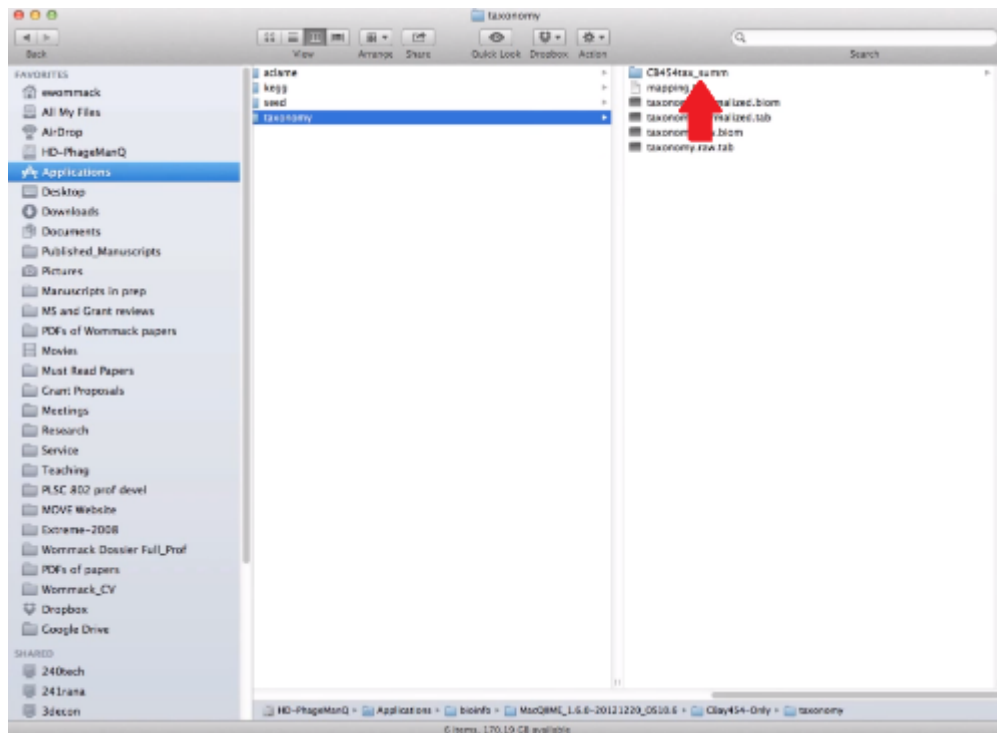
Look in taxonomy folder.



QIIME example

Step 37.

Open taxonomic summary folder.



NOTES

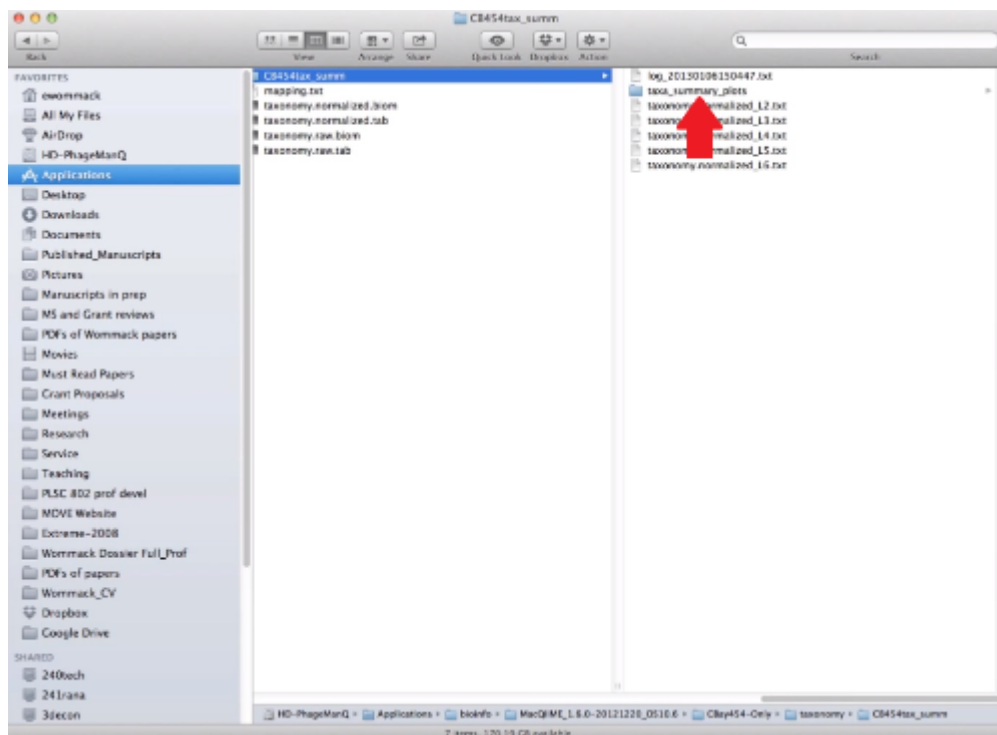
Bonnie Hurwitz 19 Nov 2015

The name should match the output file designated in QIIME.

QIIME example

Step 38.

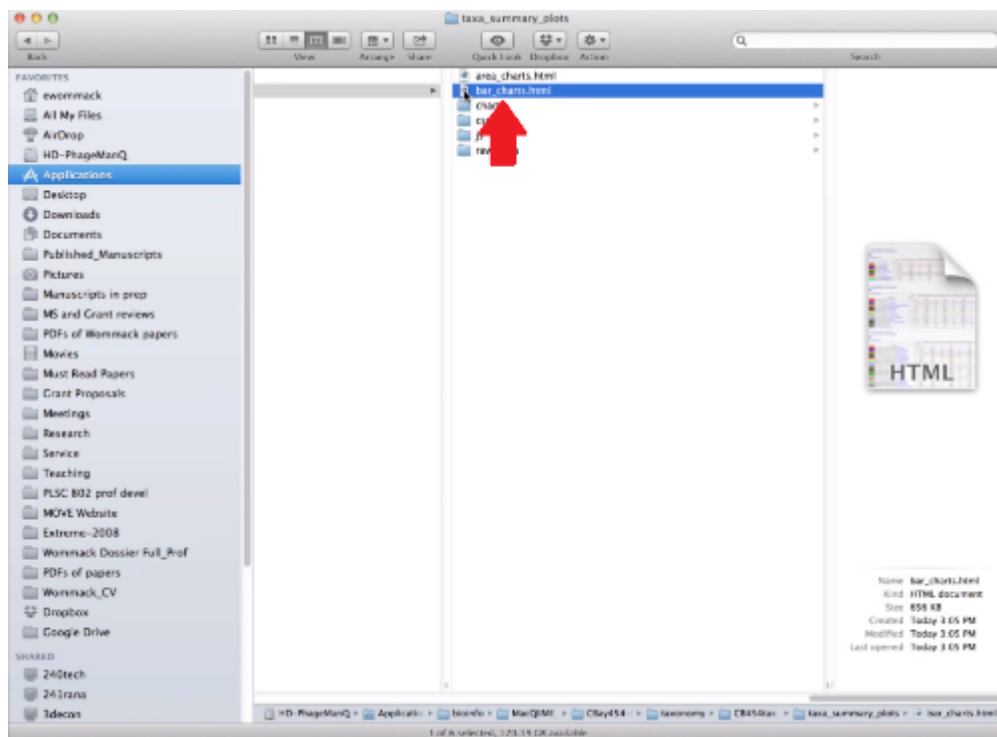
Open taxonomy summary plots folder.



QIIME example

Step 39.

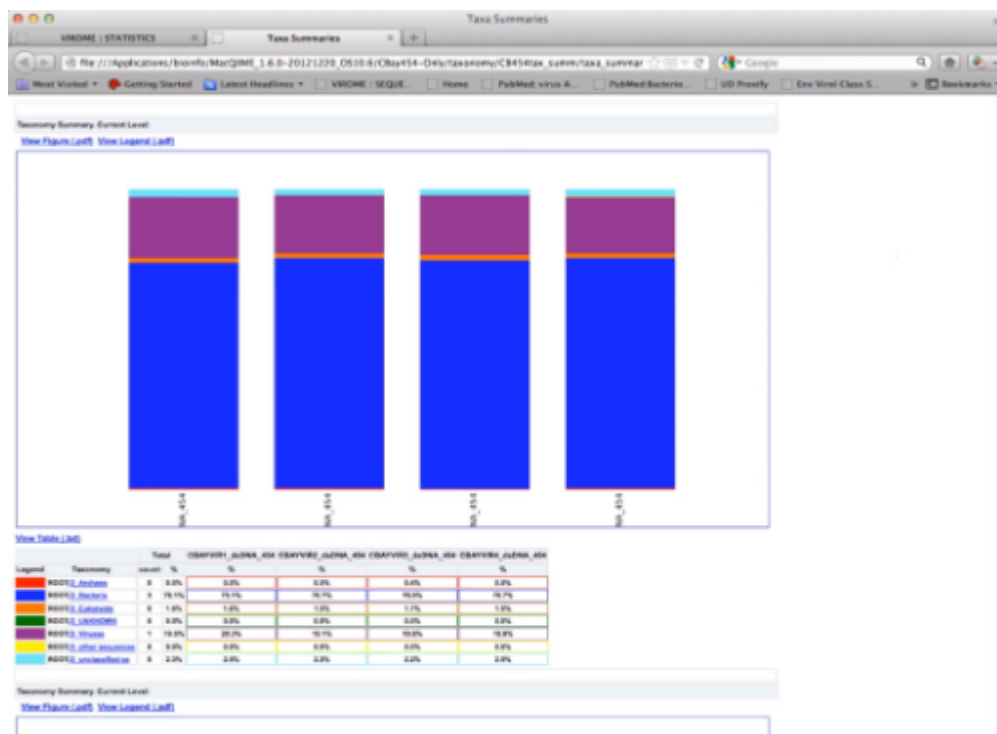
Open the bar charts with a web browser.



QIIME example

Step 40.

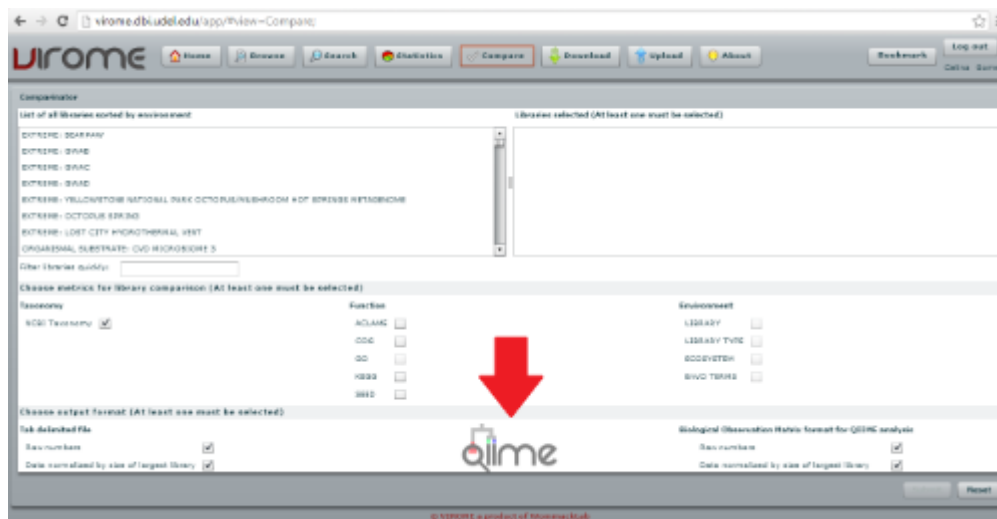
Output of libraries that were compared can be seen according to different taxonomic levels that occurred in the biom file.



QIIME example

Step 41.

In the VIROME Comparinator, click on the QIIME logo for a direct link to the QIIME homepage with information on the package. (Alternatively use link provided in this step)



🔗 **LINK:**
<http://qiime.org/>

📌 **NOTES**

Bonnie Hurwitz 17 Nov 2015

QIIME can produce many outputs including rarefaction curves to compare alpha diversity pipeline.

Bonnie Hurwitz 17 Nov 2015

Can also run beta diversity pipeline to compare libraries in principal component analysis in the King viewer.

Qiime example

Step 42.

For more detailed example [see video](#).

Step 43.

For full video tutorial see guidelines.

🔗 **LINK:**
<https://www.youtube.com/watch?v=mL0qRR1uYUM>