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Comparative metagenomic analysis using VIROME

 In 1 collection

DOI

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Keywords: comparing viral metagenome library, viral metagenome library, viral metagenome sequence, comparative metagenomic analysis, comparative analysis of viral community, using virome, use of virome, virome, virome pipeline, virome this tutorial, quantitative insights in microbial ecology package, metagenome, microbial ecology package, standards in genomic science, viral community, microbial ecology, genomic science

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/23088881/)]

[See site](#) for more information.

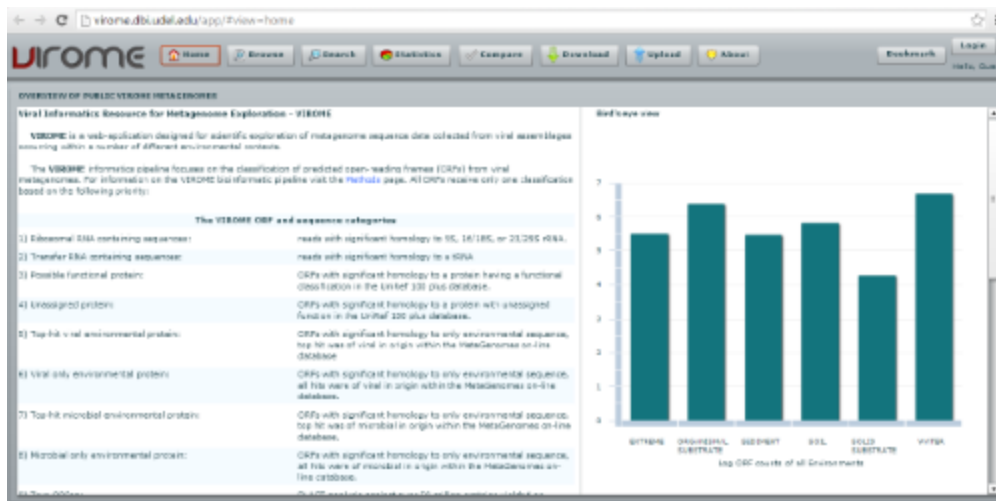
Guidelines

See full video below for more information.

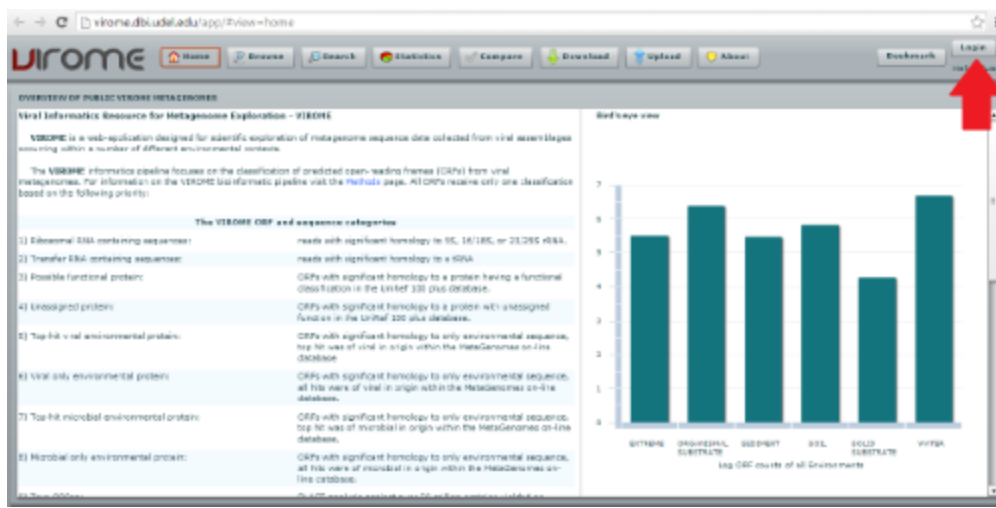
<https://www.youtube.com/embed/mL0qRR1uYUM>

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

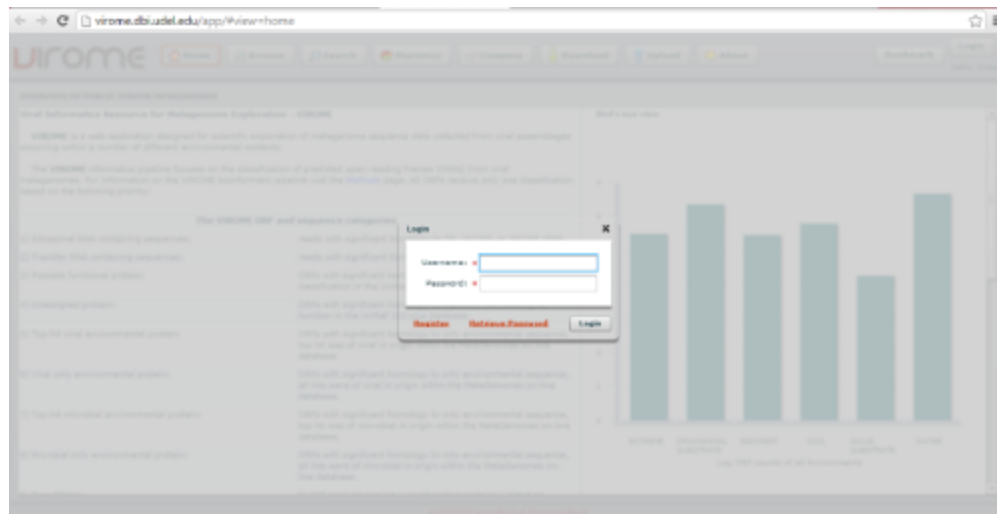
1 Go to VIROME web application.



2 Click the login button.



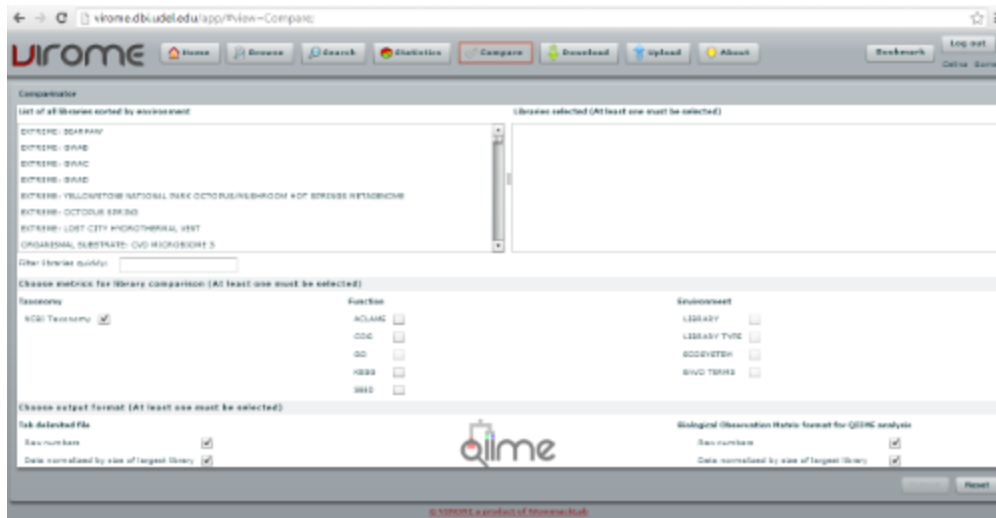
3 Enter username and password to authenticate into the application.



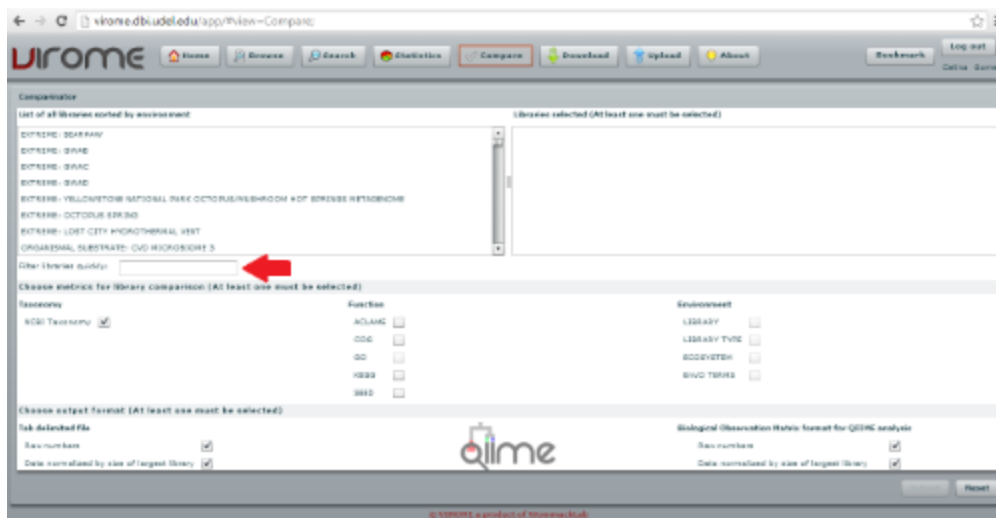
4 Click the compare button.



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



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



7 Double click on library names to choose them for analysis.

Note

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

8 Choose desired metric(s) for library comparison.

Note

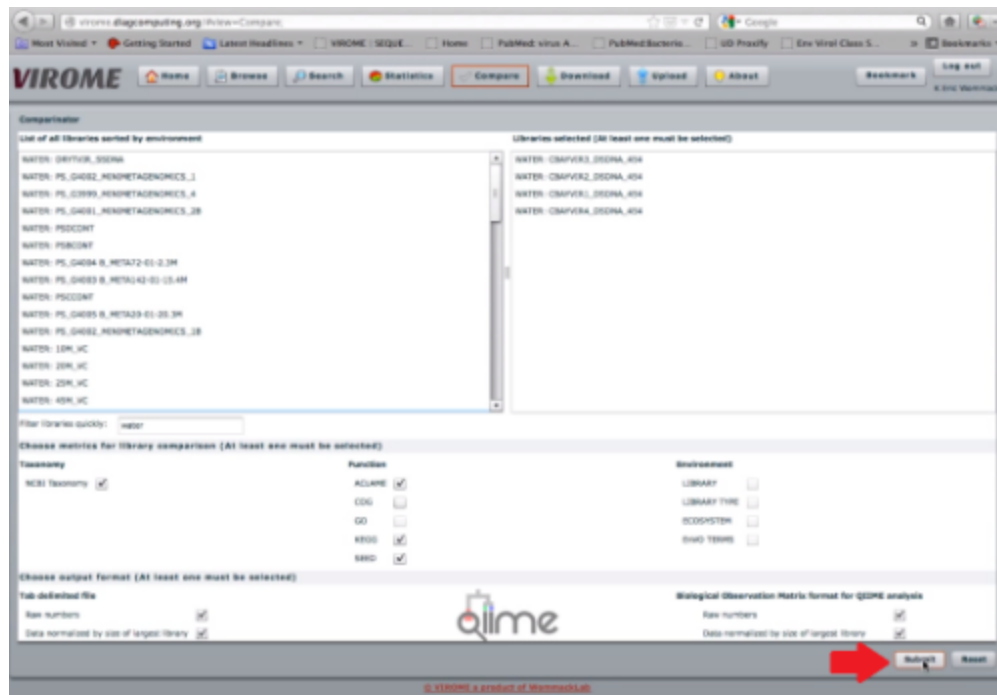
Taxonomy, function, and environment options can be selected.

9 Choose the output format(s).

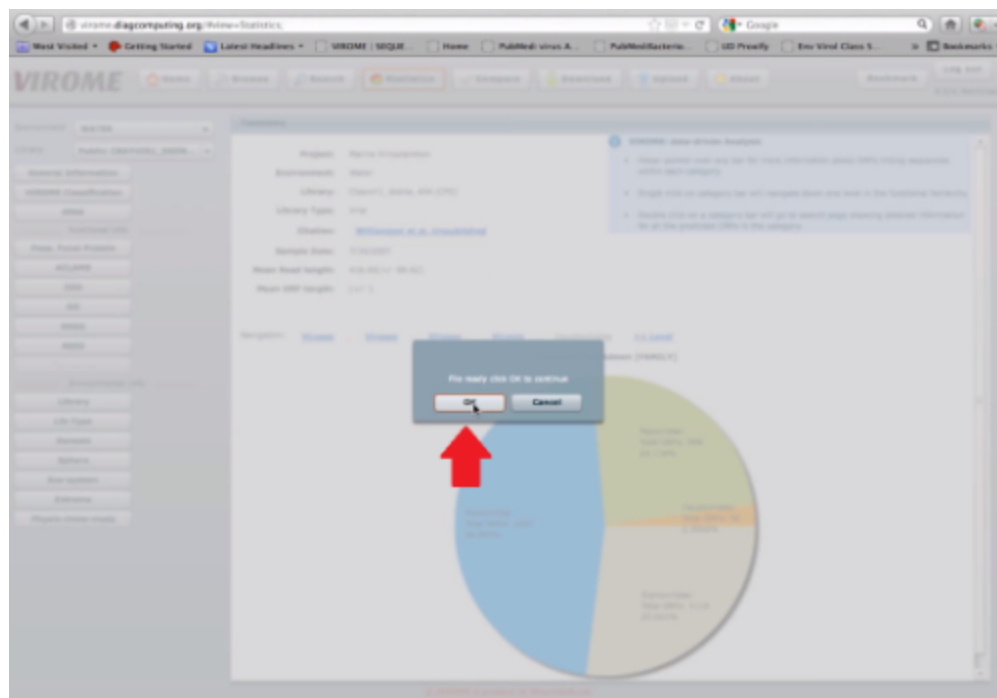
Note

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

10 Click "Submit".



11 Click "OK" to download data.



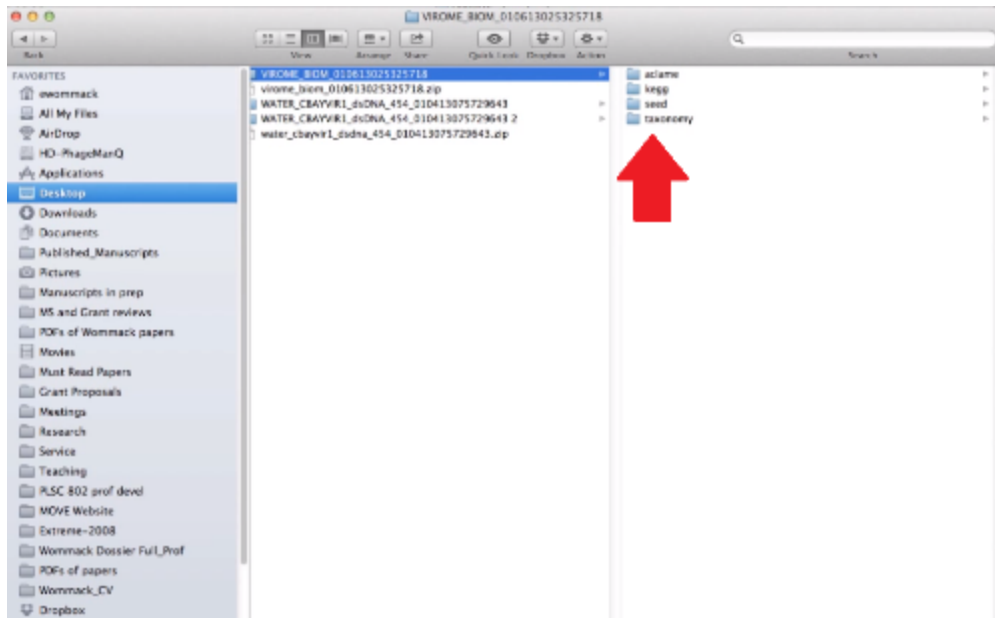
12 Once prompted to save the file, do not change the file name!

13 Navigate to the Finder.



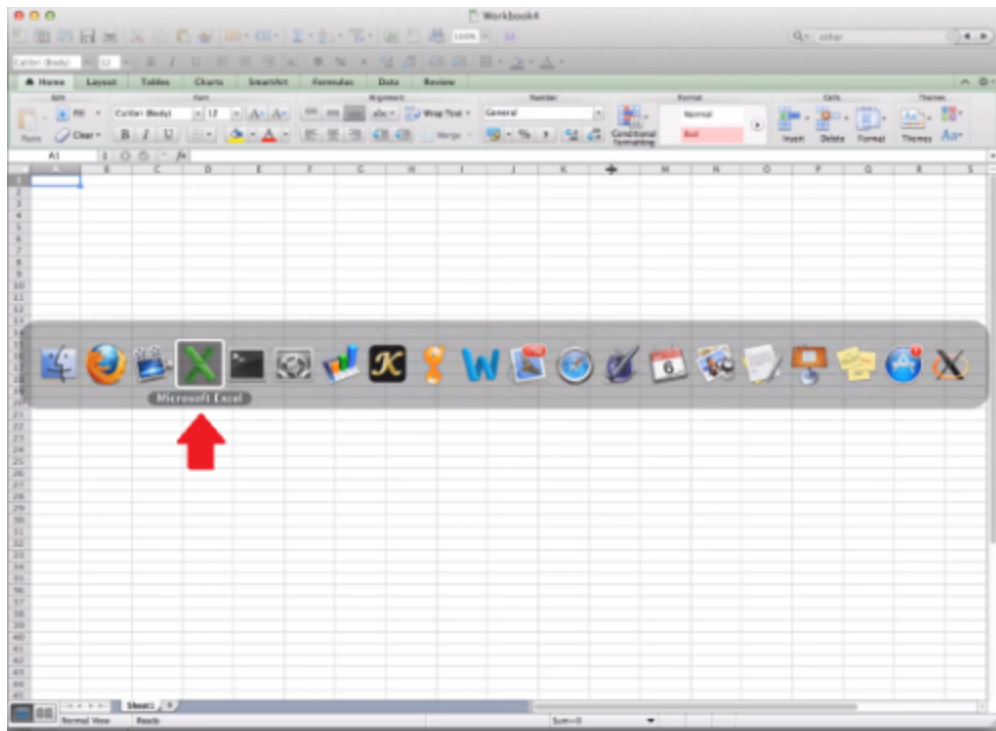
14 Double click to unzip the file.

15 One file for each metric selected should appear.



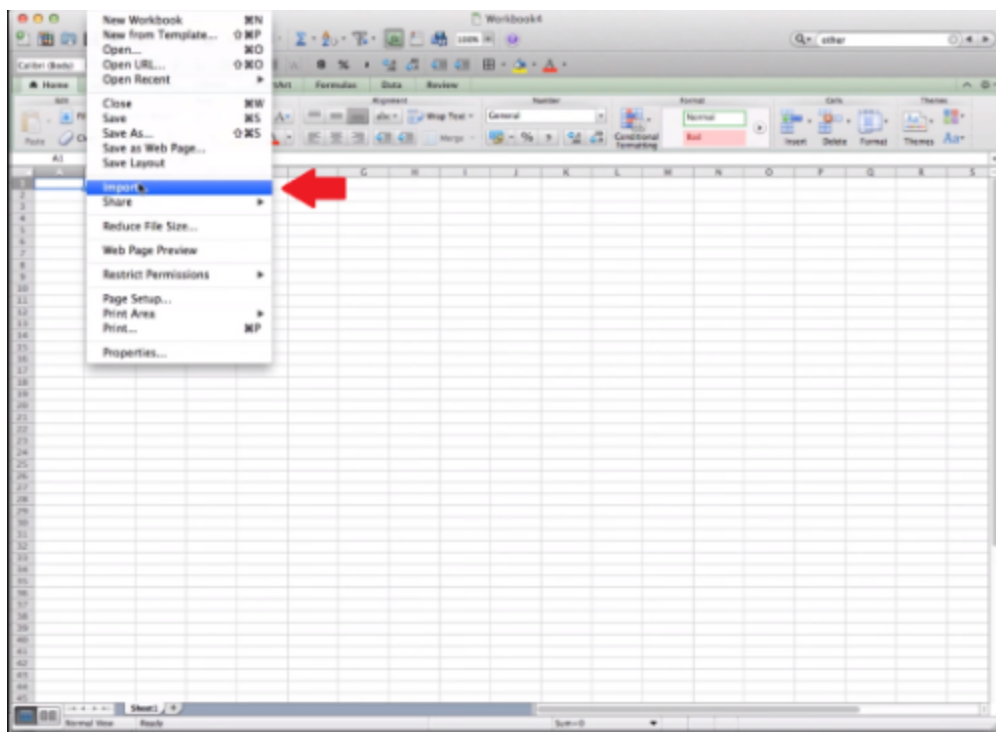
Excel example

16 Tab delimited files can be opened in Excel spreadsheet.

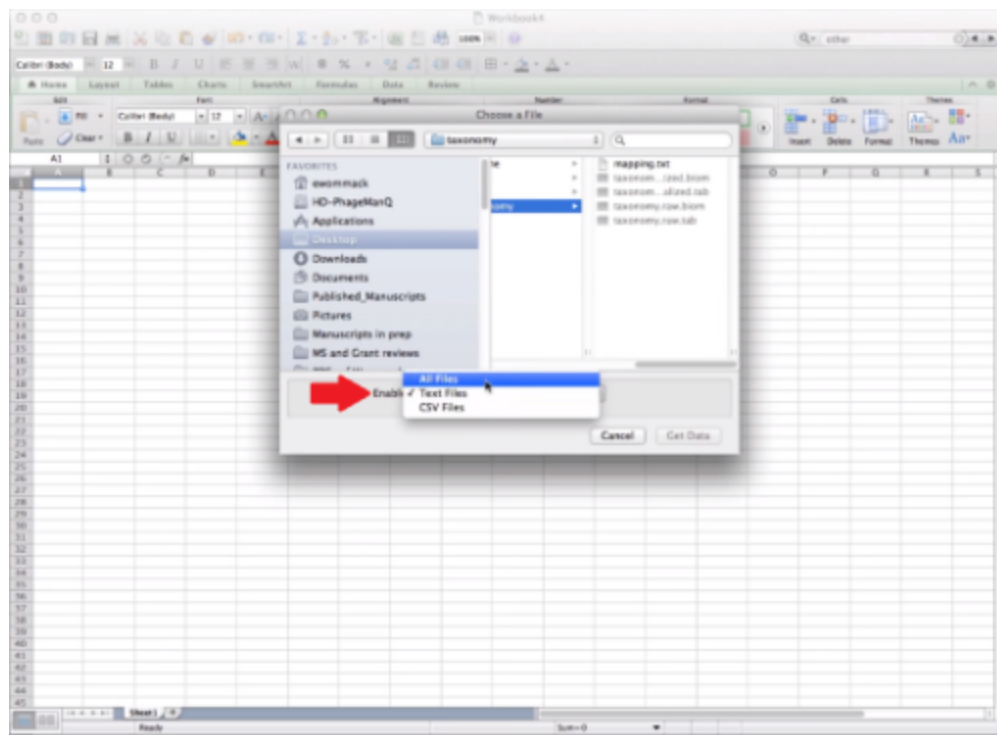


17 Navigate to the folder with the file.

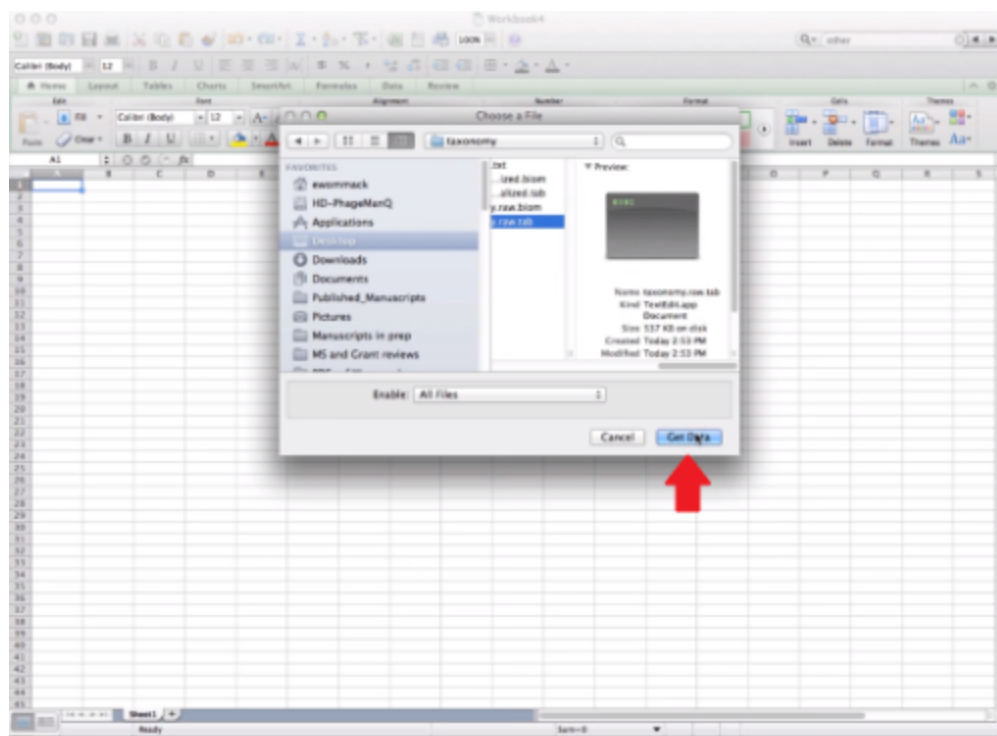
18 Import as text file.



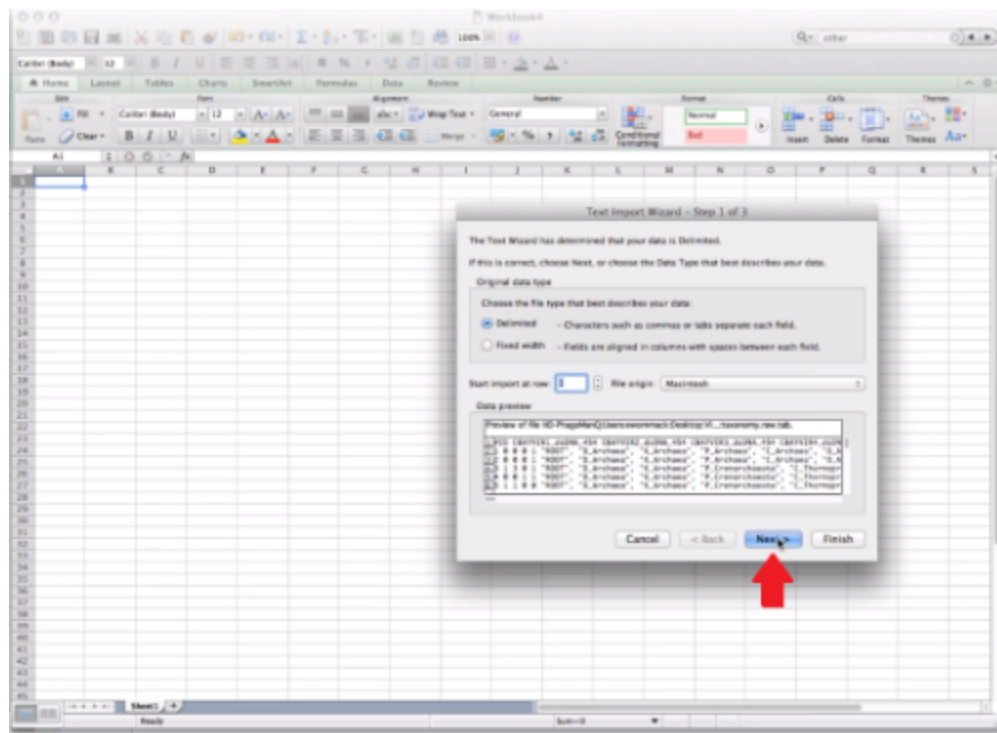
19 Enable "All file" types.



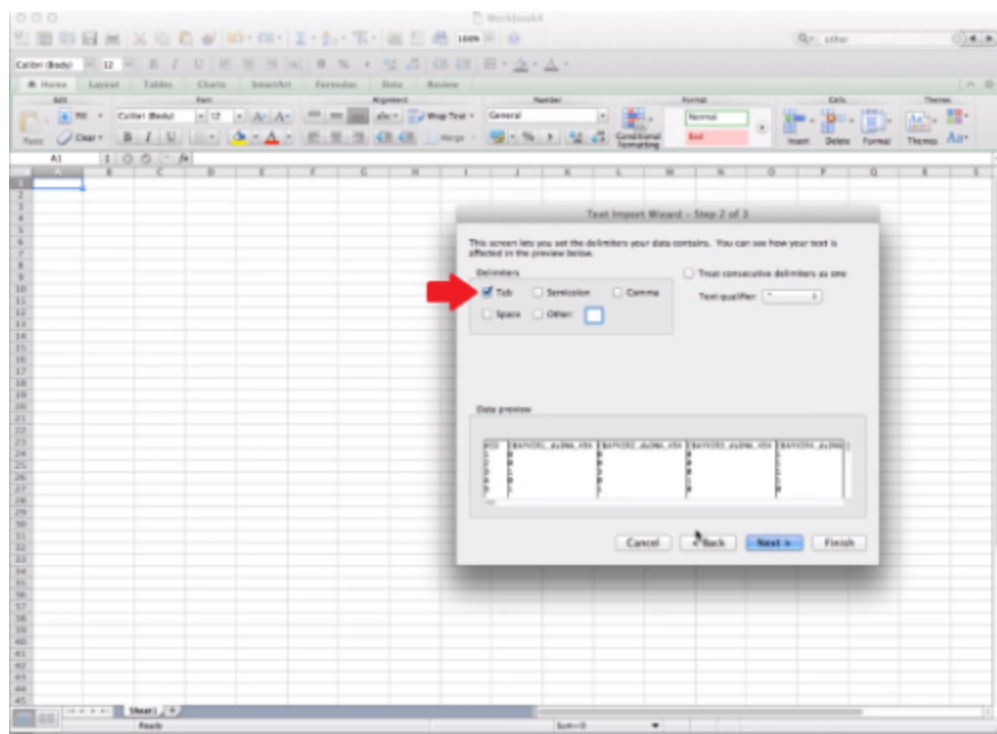
20 Click "Get Data".



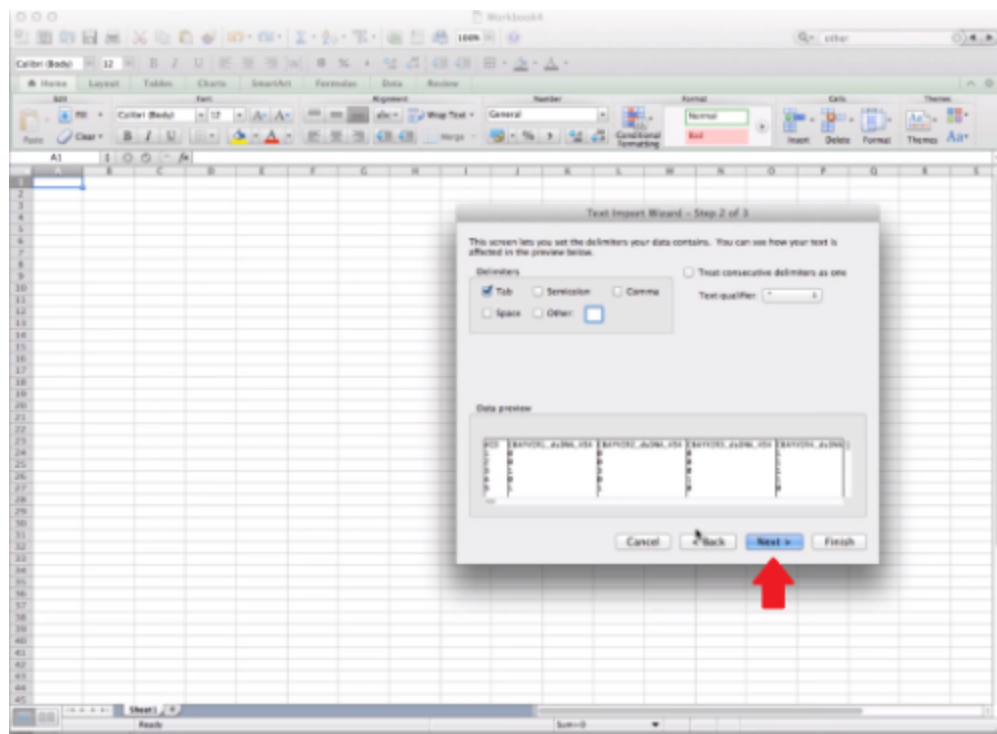
21 Click "Next".



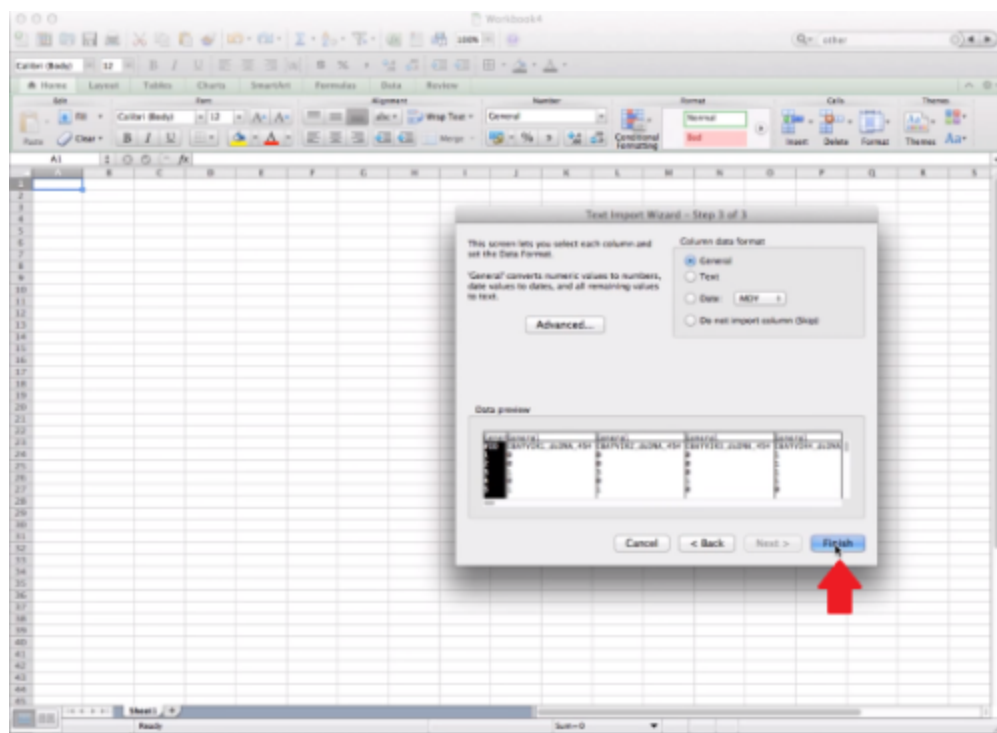
22 Select "Tab" option.



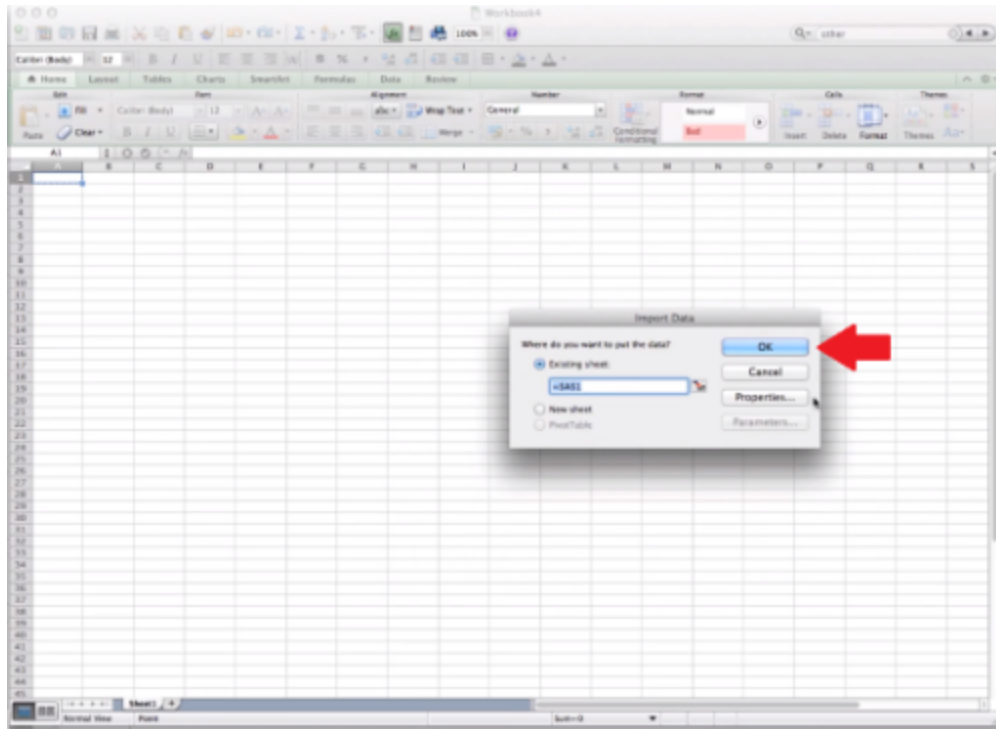
23 Click "Next".



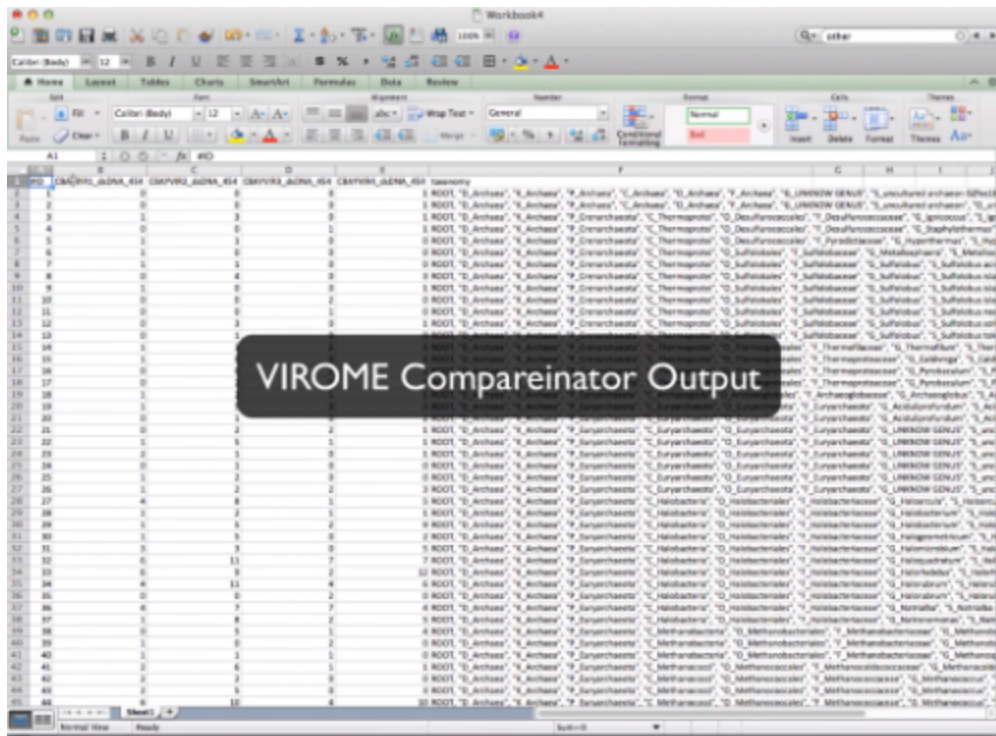
24 Click "Finish".



25 Click "OK".



26 VIROME Comparinator output will appear.



27 For more detailed description [see video. https://www.youtube.com/watch?v=mL0qRR1uYUM&feature=youtu.be&t=2m48s](https://www.youtube.com/watch?v=mL0qRR1uYUM&feature=youtu.be&t=2m48s)

QIIME example

28 Open QIIME terminal window.

```
MacQIIME_1.6.0-20121220_OS10.6 — user14@ip-10-46-137-178: /mnt/user14/assembly — bash — 149x59
MacQIIME: shage-man-q:acLane $ pwd
/Applications/bioinfo/MacQIIME_1.6.0-20121220_OS10.6/Chey-Sanger-454/acLane
MacQIIME: shage-man-q:acLane $ cd ..
MacQIIME: shage-man-q:Chey-Sanger-454 $ ls -l
total 1152
drwxr-xr-x  5 evomach  evomach    179 Jan  2 18:22 V10000_B10013895534975
drwxr-xr-x  10 evomach  evomach    442 Jan  2 18:05 acLane
drwxr-xr-x  16 evomach  evomach    546 Jan  2 18:15 seed
drwxr-xr-x  12 evomach  evomach    488 Jan  2 21:54 taxonomy
-rw-r--r--  1 evomach  admin      507115 Jan  2 09:57 v10000_b10013895534975.zip
MacQIIME: shage-man-q:Chey-Sanger-454 $ cd taxonomy/
MacQIIME: shage-man-q:taxonomy $ ls -l
total 18744
-rw-r--r--  1 evomach  evomach    48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r--  1 evomach  evomach    48 Dec 27 17:10 beta_metrics.txt
-rw-r--r--  1 evomach  evomach   1040318 Jan  2 21:54 gtest.txt
-rw-r--r--  1 evomach  evomach    405 Jan  2 21:54 mapping.txt
-rw-r--r--  1 evomach  evomach   2232722 Jan  2 09:56 taxonomy.normalized.biom
-rw-r--r--  1 evomach  evomach   1001789 Jan  2 09:55 taxonomy.normalized.tab
-rw-r--r--  1 evomach  evomach   1207879 Jan  2 09:56 taxonomy.row.biom
-rw-r--r--  1 evomach  evomach   957935 Jan  2 09:55 taxonomy.row.tab
drwxr-xr-x  16 evomach  evomach    544 Jan  2 10:20 taxonomy_beta_sang_454
MacQIIME: shage-man-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_Chey_sang_454 -m mapping.txt
MacQIIME: shage-man-q:taxonomy $ pwd
/Applications/bioinfo/MacQIIME_1.6.0-20121220_OS10.6/Chey-Sanger-454/taxonomy
MacQIIME: shage-man-q:taxonomy $ ls -l
total 18744
-rw-r--r--  1 evomach  evomach    48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r--  1 evomach  evomach    48 Dec 27 17:10 beta_metrics.txt
-rw-r--r--  1 evomach  evomach   1040318 Jan  2 21:54 gtest.txt
-rw-r--r--  1 evomach  evomach    405 Jan  2 21:54 mapping.txt
drwxr-xr-x  9 evomach  evomach    386 Jan  3 10:14 tax_Chey_sang_454
-rw-r--r--  1 evomach  evomach   1253733 Jan  2 09:56 taxonomy.normalized.biom
-rw-r--r--  1 evomach  evomach   1001789 Jan  2 09:55 taxonomy.normalized.tab
-rw-r--r--  1 evomach  evomach   1207879 Jan  2 09:56 taxonomy.row.biom
-rw-r--r--  1 evomach  evomach   957935 Jan  2 09:55 taxonomy.row.tab
drwxr-xr-x  16 evomach  evomach    544 Jan  2 10:20 taxonomy_beta_sang_454
MacQIIME: shage-man-q:taxonomy $ cd ..
MacQIIME: shage-man-q:Chey-Sanger-454 $ ls
V10000_B10013895534975  seed                                v10000_b10013895534975.zip
acLane                  taxonomy                            v10000_b10013895534975.zip
MacQIIME: shage-man-q:Chey-Sanger-454 $ cd ..
MacQIIME: shage-man-q:MacQIIME_1.6.0-20121220_OS10.6 $ ls
Chey-Sanger-454  Chey454-Only  README.txt  MacQIIME
Chey-induced-vs-Free-16M-ORF-CHEP  install.s  scripts
MacQIIME: shage-man-q:MacQIIME_1.6.0-20121220_OS10.6 $ cd Chey454-Only/
MacQIIME: shage-man-q:Chey454-Only $ ls -l
total 8
drwxr-xr-x  2 evomach  evomach    220 Jan  3 14:55 acLane
drwxr-xr-x  2 evomach  evomach    220 Jan  3 14:55 bugs
drwxr-xr-x  2 evomach  evomach    220 Jan  3 14:55 seed
drwxr-xr-x  2 evomach  evomach    220 Jan  3 14:55 taxonomy
MacQIIME: shage-man-q:Chey454-Only $ cd taxonomy/
MacQIIME: shage-man-q:taxonomy $ ls
mapping.txt  taxonomy.normalized.biom  taxonomy.normalized.tab  taxonomy.row.biom  taxonomy.row.tab
MacQIIME: shage-man-q:taxonomy $
```

Note

MacQIIME used for this example.

29 Run summarize taxa through plots script.

```
MacQIIME 1.6.0-20121220_0510.6 -- user14@ip-10-46-137-178: /mnt/user14/assembly -- bash -- 149x59
MacQIIME phage-run-q:sclean $ pwd
/Applications/BioInfo/MacQIIME 1.6.0-20121220_0510.6/Chay-Sanger-454/sclean
MacQIIME phage-run-q:sclean $ cd ..
MacQIIME phage-run-q:Chay-Sanger-454 $ ls -l
total 1152
drwxr-xr-x 5 evomack evomack 178 Jan 2 10:22 VIRUSE_BIOM_816013095534075
drwxr-xr-x 13 evomack evomack 542 Jan 2 10:05 sclean
drwxr-xr-x 10 evomack evomack 348 Jan 2 10:18 seed
drwxr-xr-x 12 evomack evomack 408 Jan 2 21:54 taxonomy
-rw-r--r-- 1 evomack admin 107115 Jan 2 09:57 vtrose_biom_816013095534075.rlp
MacQIIME phage-run-q:Chay-Sanger-454 $ cd taxonomy/
MacQIIME phage-run-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 evomack evomack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 evomack evomack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 evomack evomack 1040310 Jan 2 21:54 gist.txt
-rw-r--r-- 1 evomack evomack 405 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 evomack evomack 1251723 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 evomack evomack 1001789 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 evomack evomack 1207079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 evomack evomack 957925 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x 16 evomack evomack 544 Jan 2 10:25 taxonomy_beta_sung_454
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py taxonomy.normalized.biom -o tax_Obay_sung_454 -m mapping.txt
MacQIIME phage-run-q:taxonomy $ pwd
/Applications/BioInfo/MacQIIME 1.6.0-20121220_0510.6/Chay-Sanger-454/taxonomy
MacQIIME phage-run-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 evomack evomack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 evomack evomack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 evomack evomack 1040310 Jan 2 21:54 gist.txt
-rw-r--r-- 1 evomack evomack 405 Jan 2 21:54 mapping.txt
drwxr-xr-x 9 evomack evomack 306 Jan 3 10:14 tax_Obay_sung_454
-rw-r--r-- 1 evomack evomack 1251723 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 evomack evomack 1001789 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 evomack evomack 1207079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 evomack evomack 957925 Jan 2 09:55 taxonomy.raw.tab
drwxr-xr-x 16 evomack evomack 544 Jan 2 10:25 taxonomy_beta_sung_454
MacQIIME phage-run-q:taxonomy $ cd ..
MacQIIME phage-run-q:Chay-Sanger-454 $ ls
VIRUSE_BIOM_816013095534075 seed vtrose_biom_816013095534075.rlp
sclean taxonomy
MacQIIME phage-run-q:Chay-Sanger-454 $ cd ..
MacQIIME phage-run-q:MacQIIME 1.6.0-20121220_0510.6 $ ls
Chay-Sanger-454 Chay454-Only P2402.txt scripts
MacQIIME phage-run-q:MacQIIME 1.6.0-20121220_0510.6 $ cd Chay454-Only/
MacQIIME phage-run-q:Chay454-Only $ ls -l
total 0
drwxr-xr-x 7 evomack evomack 258 Jan 3 10:55 sclean
drwxr-xr-x 7 evomack evomack 258 Jan 3 10:55 seed
drwxr-xr-x 7 evomack evomack 258 Jan 3 10:55 taxonomy
MacQIIME phage-run-q:Chay454-Only $ cd tax
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py
mapping.txt taxonomy.normalized.biom taxonomy.raw.biom taxonomy.raw.tab
MacQIIME phage-run-q:taxonomy $ summarize_taxa_through_plots.py
```

Command

summarize_taxa_through_plots.py

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 stage-man-q:aclean $ pwd
/Applications/Bratislava/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/aclean
MacQIIME stage-man-q:aclean $ cd ..
MacQIIME stage-man-q:CBay-Sanger-454 $ ls -l
total 1152
-rw-r--r-- 1 evoanack evoanack 178 Jan 2 18:22 virome_biom_818213895534975
-rw-r--r-- 1 evoanack evoanack 442 Jan 2 18:05 aclean
-rw-r--r-- 1 evoanack evoanack 548 Jan 2 18:18 seed
-rw-r--r-- 1 evoanack evoanack 480 Jan 2 21:54 taxonomy
-rw-r--r-- 1 evoanack admin 107115 Jan 2 09:27 virome_biom_818213895534975.zip
MacQIIME stage-man-q:CBay-Sanger-454 $ cd taxonomy/
MacQIIME stage-man-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 evoanack evoanack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 evoanack evoanack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 evoanack evoanack 1045310 Jan 2 21:54 gtest.txt
-rw-r--r-- 1 evoanack evoanack 495 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 evoanack evoanack 1231732 Jan 2 09:14 taxonomy.normalized.biom
-rw-r--r-- 1 evoanack evoanack 1001709 Jan 2 09:15 taxonomy.normalized.tab
-rw-r--r-- 1 evoanack evoanack 1207079 Jan 2 09:14 taxonomy.raw.biom
-rw-r--r-- 1 evoanack evoanack 957015 Jan 2 09:15 taxonomy.raw.tab
-rw-r--r-- 1 evoanack evoanack 957025 Jan 2 09:10 taxonomy_beta_sung_454
-rw-r--r-- 1 evoanack evoanack 544 Jan 2 10:20 taxonomy_beta_sung_454
MacQIIME stage-man-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sung_454 -s mapping.txt
MacQIIME stage-man-q:taxonomy $ pwd
/Applications/Bratislava/MacQIIME_1.6.0-20121220_OS10.6/CBay-Sanger-454/taxonomy
MacQIIME stage-man-q:taxonomy $ ls -l
total 10764
-rw-r--r-- 1 evoanack evoanack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 evoanack evoanack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 evoanack evoanack 1045310 Jan 2 21:54 gtest.txt
-rw-r--r-- 1 evoanack evoanack 495 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 evoanack evoanack 388 Jan 3 10:14 tax_CBay_sung_454
-rw-r--r-- 1 evoanack evoanack 1231732 Jan 2 09:14 taxonomy.normalized.biom
-rw-r--r-- 1 evoanack evoanack 1001709 Jan 2 09:15 taxonomy.normalized.tab
-rw-r--r-- 1 evoanack evoanack 1207079 Jan 2 09:14 taxonomy.raw.biom
-rw-r--r-- 1 evoanack evoanack 957015 Jan 2 09:15 taxonomy.raw.tab
-rw-r--r-- 1 evoanack evoanack 544 Jan 2 10:20 taxonomy_beta_sung_454
MacQIIME stage-man-q:taxonomy $ cd ..
MacQIIME stage-man-q:CBay-Sanger-454 $ ls
virome_biom_818213895534975 seed virome_biom_818213895534975.zip
aclean 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-Duty 6240C.txt macqime
CBay-induced vs free SAM-DRETT-CBAY hotball.s scripts
MacQIIME stage-man-q:MacQIIME_1.6.0-20121220_OS10.6 $ cd CBay454-Duty/
MacQIIME stage-man-q:CBay454-Duty $ ls -l
total 0
-rw-r--r-- 1 evoanack evoanack 220 Jan 3 14:55 aclean
-rw-r--r-- 1 evoanack evoanack 220 Jan 3 14:55 bugs
-rw-r--r-- 1 evoanack evoanack 220 Jan 3 14:55 seed
-rw-r--r-- 1 evoanack evoanack 220 Jan 3 14:55 taxonomy
MacQIIME stage-man-q:CBay454-Duty $ 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 $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom
```

Command

-i taxonomy.normalized.biom

31 Choose output file. (Example command below)


```
MacOSME 1.6.0-20121220_OS10.6 — user14@ip-10-46-137-178: /mnt/user14/assembly — bash — 140x50
MacOSME: shage-man-q:ac1ane $ pwd
/Applications/Bratis/MacOSME 1.6.0-20121220_OS10.6/CBay-Sanger-454/ac1ane
MacOSME: shage-man-q:ac1ane $ cd ..
MacOSME: shage-man-q:CBay-Sanger-454 $ ls -l
total 3152
drwxr-xr-x  5 evenback evenback   178 Jan  2 13:22 VIROME_BIOM_R18213095534975
drwxr-xr-x  2 evenback evenback    42 Jan  2 13:25 ac1ane
drwxr-xr-x 10 evenback evenback   548 Jan  2 13:15 seed
drwxr-xr-x 12 evenback evenback   408 Jan  2 21:54 taxonomy
-rw-r--r--  1 evenback admin  507115 Jan  2 09:57 virome_biom_R18213095534975.zip
MacOSME: shage-man-q:CBay-Sanger-454 $ cd taxonomy/
MacOSME: shage-man-q:taxonomy $ ls -l
total 10764
-rw-r--r--  1 evenback evenback    48 Dec 27 17:16 alpha_metrics.txt
-rw-r--r--  1 evenback evenback    48 Dec 27 17:02 beta_metrics.txt
-rw-r--r--  1 evenback evenback 1040318 Jan  2 21:54 gtest.txt
-rw-r--r--  1 evenback evenback   405 Jan  2 21:54 mapping.txt
-rw-r--r--  1 evenback evenback 1251733 Jan  2 00:16 taxonomy.normalized.biom
-rw-r--r--  1 evenback evenback 1001795 Jan  2 00:15 taxonomy.normalized.tab
-rw-r--r--  1 evenback evenback 1207079 Jan  2 00:16 taxonomy.raw.biom
-rw-r--r--  1 evenback evenback  957935 Jan  2 00:15 taxonomy.raw.tab
drwxr-xr-x 16 evenback evenback   544 Jan  2 10:25 taxonomy_beta_sang_454
MacOSME: shage-man-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sang_454 -w mapping.txt
MacOSME: shage-man-q:taxonomy $ pwd
/Applications/Bratis/MacOSME 1.6.0-20121220_OS10.6/CBay-Sanger-454/taxonomy
MacOSME: shage-man-q:taxonomy $ ls -l
total 10764
-rw-r--r--  1 evenback evenback    48 Dec 27 17:16 alpha_metrics.txt
-rw-r--r--  1 evenback evenback    48 Dec 27 17:02 beta_metrics.txt
-rw-r--r--  1 evenback evenback 1040318 Jan  2 21:54 gtest.txt
-rw-r--r--  1 evenback evenback   405 Jan  2 21:54 mapping.txt
drwxr-xr-x  9 evenback evenback   384 Jan  2 10:14 tax_CBay_sang_454
-rw-r--r--  1 evenback evenback 1251733 Jan  2 00:16 taxonomy.normalized.biom
-rw-r--r--  1 evenback evenback 1001795 Jan  2 00:15 taxonomy.normalized.tab
-rw-r--r--  1 evenback evenback 1207079 Jan  2 00:16 taxonomy.raw.biom
-rw-r--r--  1 evenback evenback  957935 Jan  2 00:15 taxonomy.raw.tab
drwxr-xr-x 16 evenback evenback   544 Jan  2 10:25 taxonomy_beta_sang_454
MacOSME: shage-man-q:taxonomy $ cd ..
MacOSME: shage-man-q:CBay-Sanger-454 $ ls
VIROME_BIOM_R18213095534975  seed                               virome_biom_R18213095534975.zip
ac1ane                      taxonomy
MacOSME: shage-man-q:CBay-Sanger-454 $ ls
VIROME_BIOM_R18213095534975  seed                               virome_biom_R18213095534975.zip
ac1ane                      taxonomy
MacOSME: shage-man-q:CBay-Sanger-454 $ cd ..
MacOSME: shage-man-q:MacOSME 1.6.0-20121220_OS10.6 $ ls
CBay-Sanger-454  CBay454-Only  MacOSME 1.6.0-20121220_OS10.6  scripts
MacOSME: shage-man-q:MacOSME 1.6.0-20121220_OS10.6 $ cd CBay454-Only/
MacOSME: shage-man-q:CBay454-Only $ ls -l
total 0
drwxr-xr-x  7 evenback evenback   258 Jan  5 14:55 ac1ane
drwxr-xr-x  7 evenback evenback   258 Jan  5 14:55 kops
drwxr-xr-x  7 evenback evenback   258 Jan  5 14:25 seed
drwxr-xr-x  7 evenback evenback   258 Jan  5 14:55 taxonomy
MacOSME: shage-man-q:CBay454-Only $ cd taxonomy/
MacOSME: shage-man-q:taxonomy $ ls
mapping.txt                      taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacOSME: shage-man-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o CB454tax_summ
```

Command

```
-o CB454tax_summ
```

32 Designate the mapping file.

```
MacDIME 1.6.0-20121220_OS10.6 -- user14@ip-10-46-137-178: /mnt/user14/assembly -- bash -- 149x59
MacQ11ME phage-wan-q:aclean $ pwd
/Applications/bratnfo/MacQ11ME 1.6.0-20121220_OS10.6/CBay-Sanger-454/aclean
MacQ11ME phage-wan-q:aclean $ cd ..
MacQ11ME phage-wan-q:CBay-Sanger-454 $ ls -l
total 1152
-rw-r--r-- 1 ecsmack ecsmack 178 Jan 2 18:22 VIR086_B108_01021309554075
-rw-r--r-- 1 ecsmack ecsmack 442 Jan 2 18:05 aclean
-rw-r--r-- 1 ecsmack ecsmack 348 Jan 2 18:19 seed
-rw-r--r-- 1 ecsmack ecsmack 408 Jan 2 21:54 taxonomy
-rw-r--r-- 1 ecsmack ecsmack 107115 Jan 2 09:57 virusse_biom_01021309554075.zip
MacQ11ME phage-wan-q:CBay-Sanger-454 $ cd taxonomy/
MacQ11ME phage-wan-q:taxonomy $ ls -l
total 10784
-rw-r--r-- 1 ecsmack ecsmack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 ecsmack ecsmack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 ecsmack ecsmack 1040310 Jan 2 21:54 glst.txt
-rw-r--r-- 1 ecsmack ecsmack 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 ecsmack ecsmack 1251722 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 ecsmack ecsmack 1001709 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 ecsmack ecsmack 1287079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 ecsmack ecsmack 957935 Jan 2 09:55 taxonomy.raw.tab
-rw-r--r-- 1 ecsmack ecsmack 544 Jan 2 10:25 taxonomy_beta_sang_454
MacQ11ME phage-wan-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sang_454 -m mapping.txt
MacQ11ME phage-wan-q:taxonomy $ pwd
/Applications/bratnfo/MacQ11ME 1.6.0-20121220_OS10.6/CBay-Sanger-454/taxonomy
MacQ11ME phage-wan-q:taxonomy $ ls -l
total 10784
-rw-r--r-- 1 ecsmack ecsmack 48 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 ecsmack ecsmack 48 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 ecsmack ecsmack 1040310 Jan 2 21:54 glst.txt
-rw-r--r-- 1 ecsmack ecsmack 485 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 ecsmack ecsmack 396 Jan 3 10:14 tax_CBay_sang_454
-rw-r--r-- 1 ecsmack ecsmack 1251722 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 ecsmack ecsmack 1001709 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 ecsmack ecsmack 1287079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 ecsmack ecsmack 957935 Jan 2 09:55 taxonomy.raw.tab
-rw-r--r-- 1 ecsmack ecsmack 544 Jan 2 10:25 taxonomy_beta_sang_454
MacQ11ME phage-wan-q:taxonomy $ cd ..
MacQ11ME phage-wan-q:CBay-Sanger-454 $ ls
VIR086_B108_01021309554075 seed virusse_biom_01021309554075.zip
aclean taxonomy
MacQ11ME phage-wan-q:CBay-Sanger-454 $ ls
VIR086_B108_01021309554075 seed virusse_biom_01021309554075.zip
aclean taxonomy
MacQ11ME phage-wan-q:CBay-Sanger-454 $ cd ..
MacQ11ME phage-wan-q:MacQ11ME 1.6.0-20121220_OS10.6 $ ls
CBay-Sanger-454 CBay454-Div1 README.txt scripts
CBay-induced-via-freq GEM-SMRT-CBay hostall.s
MacQ11ME phage-wan-q:MacQ11ME 1.6.0-20121220_OS10.6 $ cd CBay454-Div1/
MacQ11ME phage-wan-q:CBay454-Div1 $ ls -l
total 8
-rw-r--r-- 7 ecsmack ecsmack 256 Jan 5 14:55 aclean
-rw-r--r-- 7 ecsmack ecsmack 220 Jan 5 14:55 ksgp
-rw-r--r-- 7 ecsmack ecsmack 220 Jan 5 14:55 seed
-rw-r--r-- 7 ecsmack ecsmack 220 Jan 5 14:55 taxonomy
MacQ11ME phage-wan-q:CBay454-Div1 $ cd taxonomy/
MacQ11ME phage-wan-q:taxonomy $ ls
mapping.txt taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacQ11ME phage-wan-q:taxonomy $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_CBay_sang_454 -m mapping.txt
```

Command

-m mapping.txt

33 Run full script. (Example command below)

```
MacOS10.15.0-20212229_0510.6 — user14@ip-10-46-137-178: /mnt/user14/assembly — python2.7 — 149x59
Applications/BIOM/BIOM_1.6.0-20212229_0510.6/Day-Sanger-454/assembly
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ ls -l
total 1152
-rw-r--r-- 1 root root 170 Jan 2 10:22 virome_biom_010213095534075
-rw-r--r-- 1 root root 442 Jan 2 10:22 a1a1a1
-rw-r--r-- 1 root root 340 Jan 2 10:22 seed
-rw-r--r-- 1 root root 480 Jan 2 21:54 taxonomy
-rw-r--r-- 1 root root 56715 Jan 2 09:57 virome_biom_010213095534075.zip
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ cd taxonomy/
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ ls -l
total 10704
-rw-r--r-- 1 root root 40 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 root root 40 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 root root 1043210 Jan 2 21:54 g1a1a1
-rw-r--r-- 1 root root 403 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 root root 1251733 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 root root 1207079 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 root root 1207079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 root root 557551 Jan 2 09:55 taxonomy.raw.tab
-rw-r--r-- 1 root root 144 Jan 2 10:22 taxonomy_beta_summ_454
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o tax_C454tax_summ -m mapping.txt
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ pwd
Applications/BIOM/BIOM_1.6.0-20212229_0510.6/Day-Sanger-454/assembly
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ ls -l
total 10704
-rw-r--r-- 1 root root 40 Dec 27 17:10 alpha_metrics.txt
-rw-r--r-- 1 root root 40 Dec 27 17:02 beta_metrics.txt
-rw-r--r-- 1 root root 1043210 Jan 2 21:54 g1a1a1
-rw-r--r-- 1 root root 403 Jan 2 21:54 mapping.txt
-rw-r--r-- 1 root root 480 Jan 2 10:22 tax_C454tax_summ_454
-rw-r--r-- 1 root root 1251733 Jan 2 09:56 taxonomy.normalized.biom
-rw-r--r-- 1 root root 1207079 Jan 2 09:55 taxonomy.normalized.tab
-rw-r--r-- 1 root root 1207079 Jan 2 09:56 taxonomy.raw.biom
-rw-r--r-- 1 root root 557551 Jan 2 09:55 taxonomy.raw.tab
-rw-r--r-- 1 root root 144 Jan 2 10:22 taxonomy_beta_summ_454
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ cd ..
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ ls
virome_biom_010213095534075 seed virome_biom_010213095534075.zip
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ cd ..
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ ls
Day-Sanger-454 Day-Sanger-454-only README.txt assembly
Day-Sanger-454 Day-Sanger-454-only README.txt assembly
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ cd Day-Sanger-454/
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ ls -l
total 0
-rw-r--r-- 1 root root 230 Jan 6 14:55 a1a1a1
-rw-r--r-- 1 root root 230 Jan 6 14:55 a1a1a1
-rw-r--r-- 1 root root 230 Jan 6 14:55 a1a1a1
-rw-r--r-- 1 root root 230 Jan 6 14:55 a1a1a1
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ cd taxonomy/
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ ls
mapping.txt taxonomy.normalized.biom taxonomy.normalized.tab taxonomy.raw.biom taxonomy.raw.tab
MacOS10.15.0-20212229_0510.6/Day-Sanger-454/assembly $ summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o CB454tax_summ -m mapping.txt
```

Command

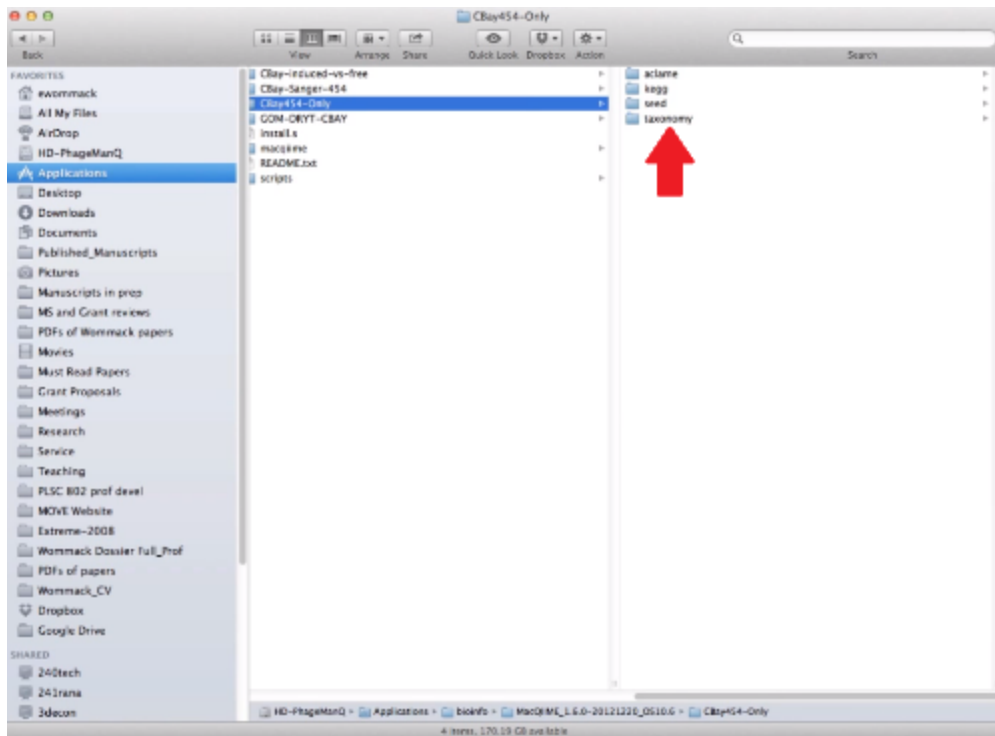
```
summarize_taxa_through_plots.py -i taxonomy.normalized.biom -o
CB454tax_summ -m mapping.txt
```

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

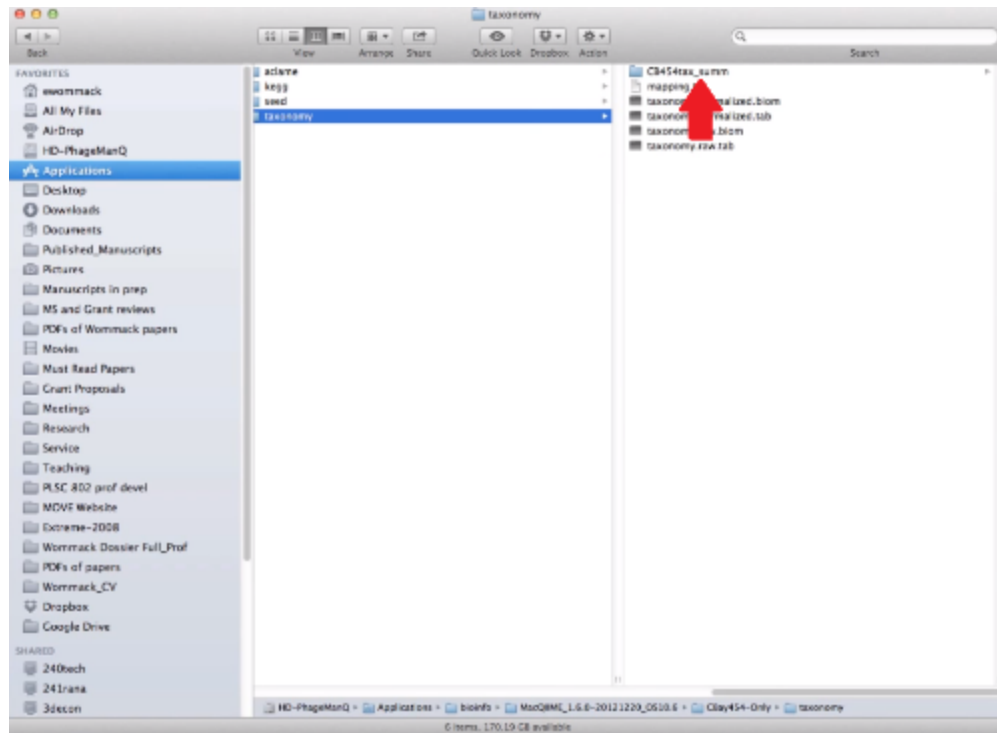
35 Navigate to the Finder.



36 Look in taxonomy folder.



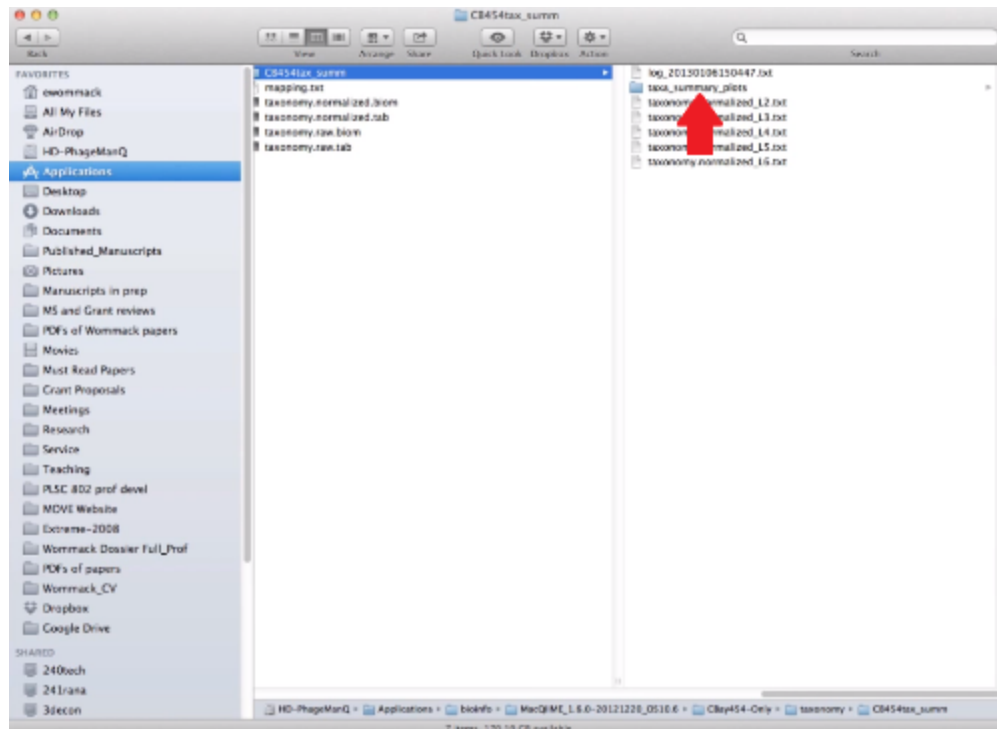
37 Open taxonomic summary folder.



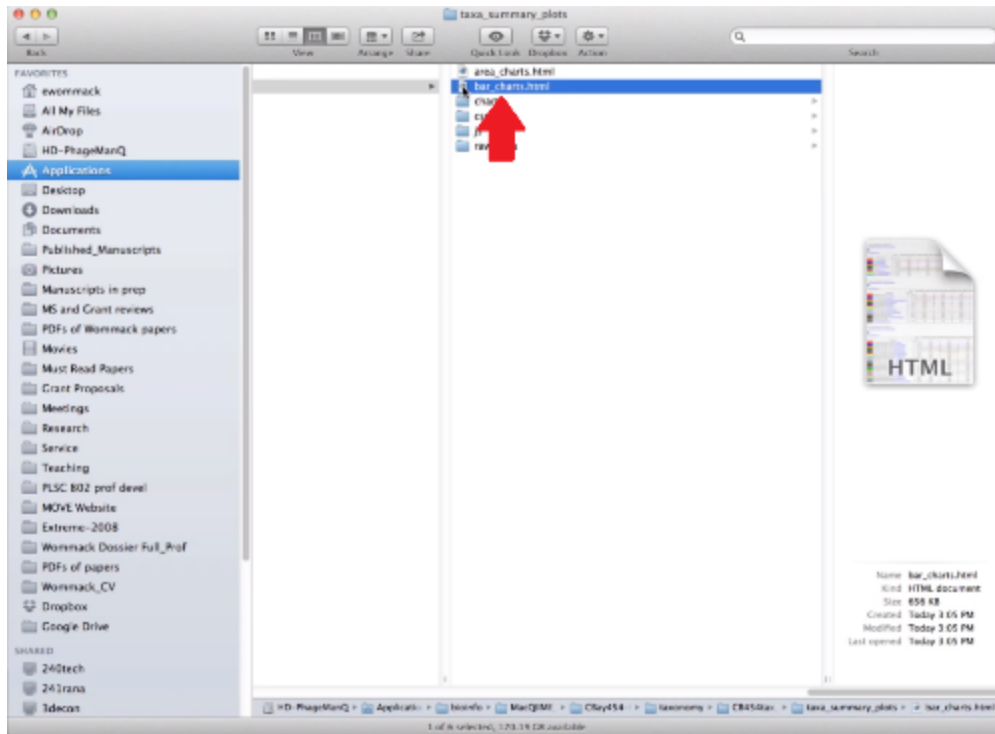
Note

The name should match the output file designated in QIIME.

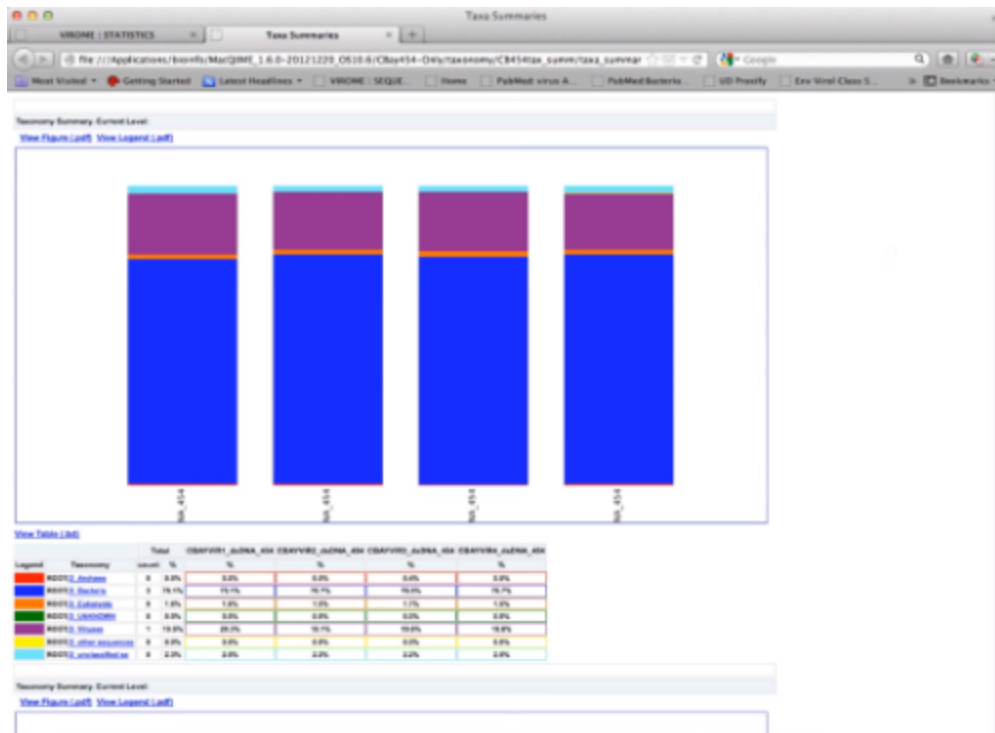
38 Open taxonomy summary plots folder.



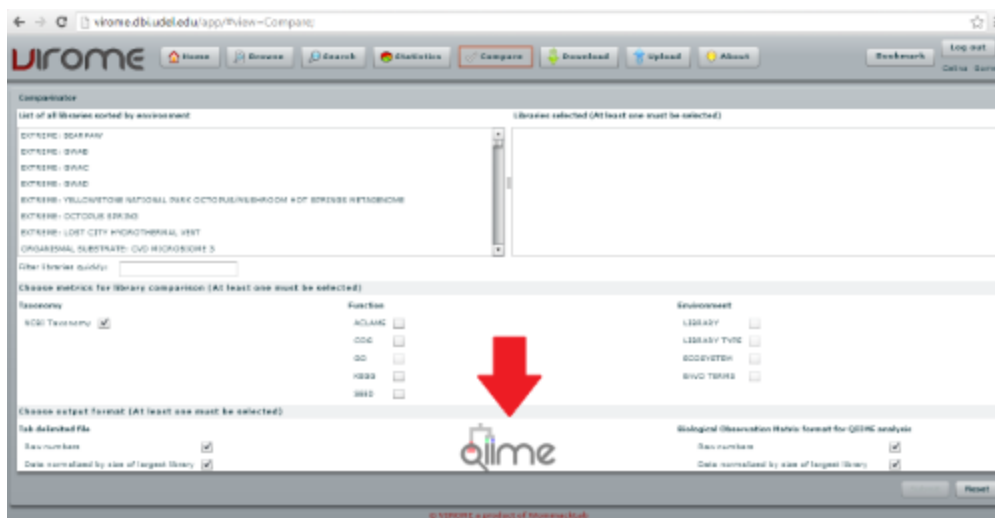
39 Open the bar charts with a web browser.



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



- 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)



<http://qiime.org/>

Note

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



Note

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

- 42 For more detailed example [see video](#).
- 43 For full video tutorial see guidelines. <https://www.youtube.com/watch?v=mL0qRR1uYUM>