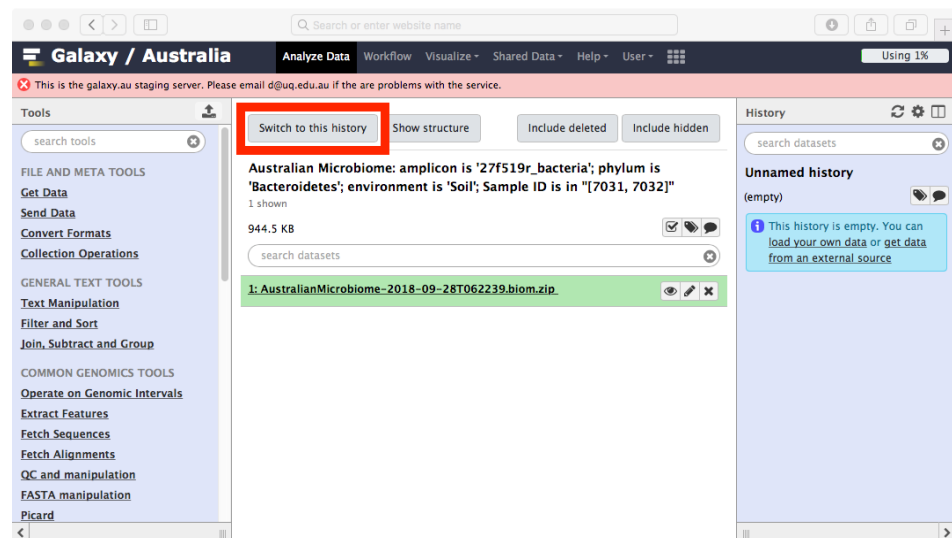


# Galaxy Australia

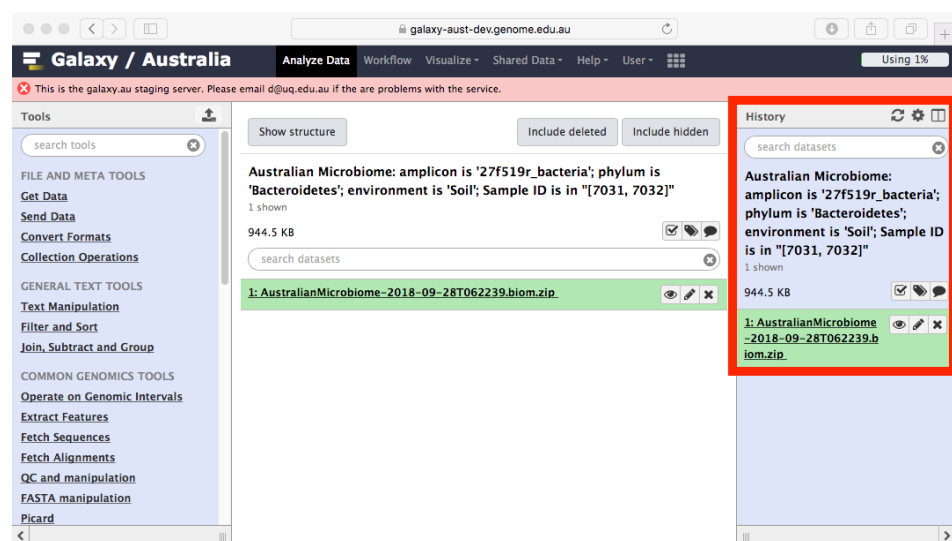
## Quick Start Guide for BPA Data Portal Users



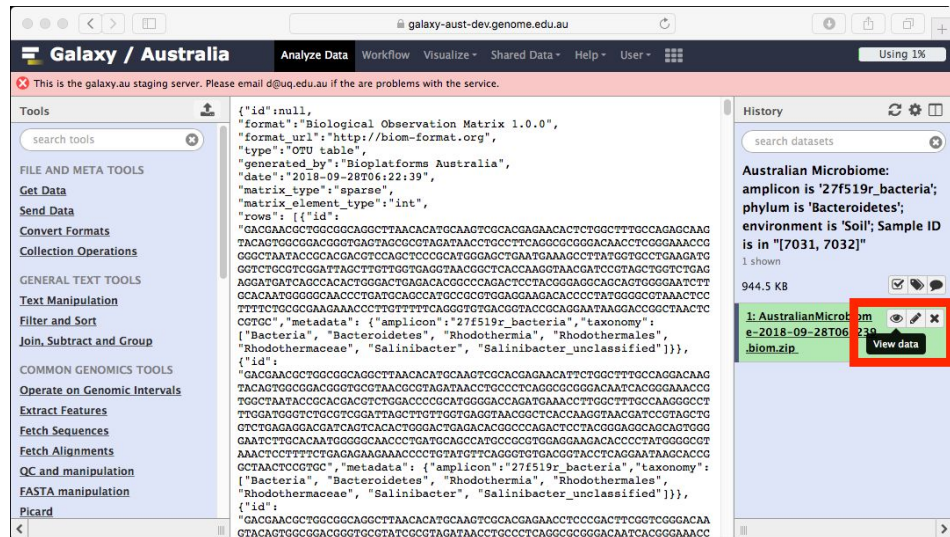
1. Click on **'Switch to this history'** to load your data from the BPA Data Portal



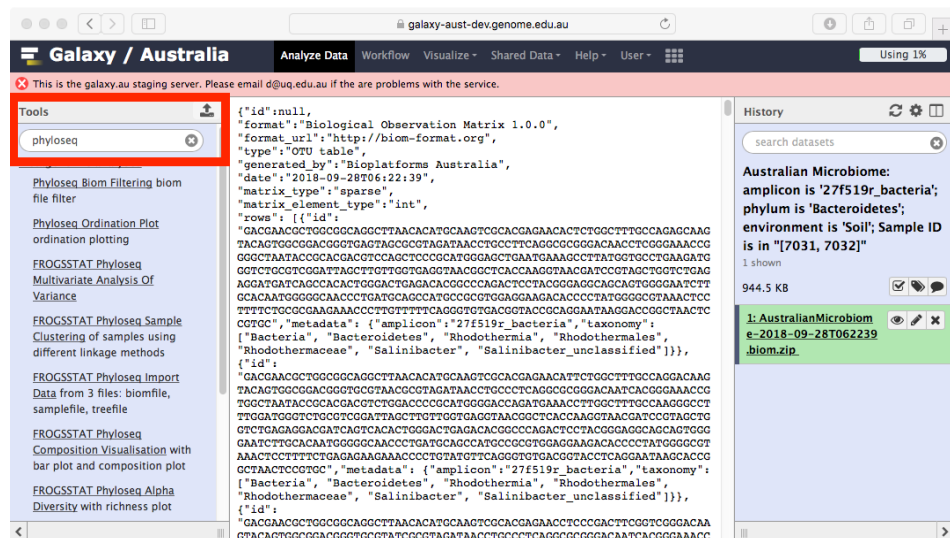
2. Your BIOM file from BPA Data Portal will be loaded into the **'History'** pane on the right



3. You can view the file by clicking on the **eye icon**. The file is loaded into the central pane



4. Search for a tool by **typing into the search box** at the top of the tools pane on the left



5. Select an input data file, change parameters and then click the 'Execute' button

Galaxy / Australia

Analyze Data Workflow Visualize Shared Data Help User Using 1%

This is the galaxy.au staging server. Please email d@uq.edu.au if there are problems with the service.

Tools

phyloseq

Metagenomic analyses

Phyloseq Biom Filtering biom file filter

Phyloseq Ordination Plot ordination plotting

FROGSSTAT Phyloseq Multivariate Analysis Of Variance

FROGSSTAT Phyloseq Sample Clustering of samples using different linkage methods

FROGSSTAT Phyloseq Import Data from 3 files: biomfile, samplefile, treefile

FROGSSTAT Phyloseq Composition Visualisation with bar plot and composition plot

FROGSSTAT Phyloseq Alpha Diversity with richness plot

FROGSSTAT Phyloseq Beta Diversity distance matrix

FROGSSTAT Phyloseq Structure Visualisation with heatmap plot and ordination plot

Workflows

Phyloseq Biom Filtering biom file filter (Galaxy Version 1.22.3.2) Options

Choose an input file type

BIOM File

Input File

1: AustralianMicrobiome-2018-09-28T062239.biom.zip

Select a taxonomic rank for the analysis

☐ Kingdom

☒ Phylum

☐ Class

☐ Order

☐ Family

☐ Genus

☐ Species

Number of the most abundant taxonomic rank units to keep in the filtered BIOM file

5

e.g. Phyla, Class and etc. as specified above. Select a value > 1.

Filter out OTUs. Remove OTUs from the analysis that do not appear more than X times in more than Y% of the samples. Specify value of X

5

Remove OTUs that do not appear more than X times (e.g., 5 times)

Specify value of Y (where 1.0 = 100%)

0.5

Execute

History

search datasets

Australian Microbiome: amplicon is '27F519r\_bacteria'; phylum is 'Bacteroidetes'; environment is 'Soil'; Sample ID is in "[7031, 7032]"

1 shown

944.5 KB

1: AustralianMicrobiome-2018-09-28T062239.biom.zip

6. When a job is submitted to the queue outputs files will appear in yellow

Galaxy / Australia

Analyze Data Workflow Visualize Shared Data Help User Using 1%

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FROGSSTAT Phyloseq Structure Visualisation with heatmap plot and ordination plot

Workflows

1 Job has been successfully added to the queue - resulting in the following datasets:

2: Phyloseq Biom Filtering on data 1.biom

3: Phyloseq Biom Filtering on data 1 Sample Abundance plot.html

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History

search datasets

Australian Microbiome: amplicon is '27F519r\_bacteria'; phylum is 'Bacteroidetes'; environment is 'Soil'; Sample ID is in "[7031, 7032]"

3 shown

944.5 KB

3: Phyloseq Biom Filtering on data 1 Sample Abundance plot.html

2: Phyloseq Biom Filtering on data 1.biom

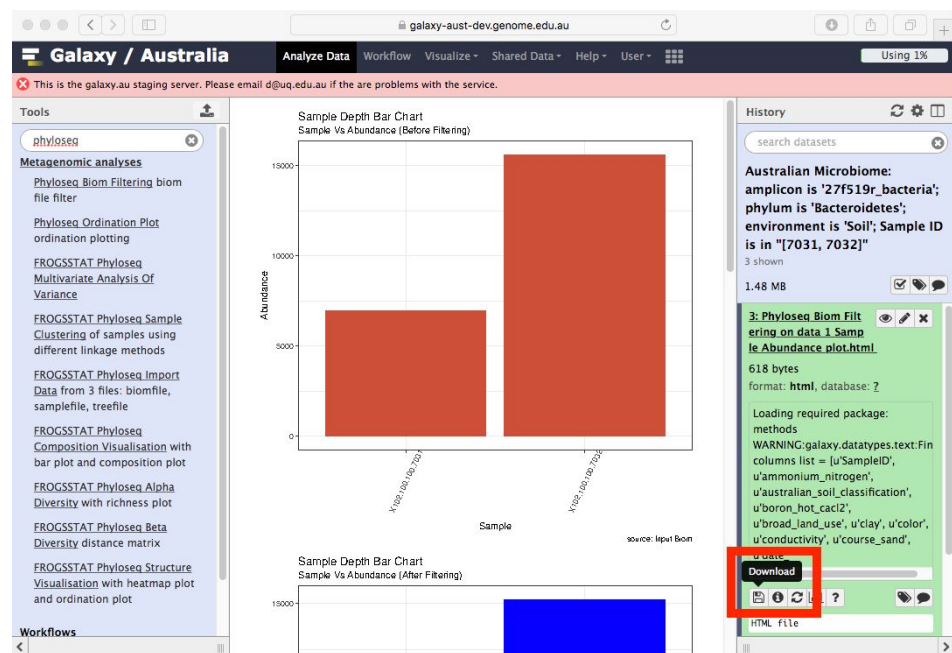
1: AustralianMicrobiome-2018-09-28T062239.biom.zip

7. When the job is done, output files will change to green. Click on the **eye icon** to view a output file



8. Clicking on the output file name will show more options.

Select the **disk icon** to download to your computer





9. Click on the **info** button to see the record of the tool, input files and parameters you used

The screenshot shows the Galaxy Australia web interface. On the left is a sidebar with 'Tools' and 'Workflows' sections. The main panel displays the 'Phyloseq Biom Filtering' tool's 'Dataset Information' and 'Job Information'. The 'History' panel on the right shows a list of jobs, with the selected job '3: Phyloseq Biom Filtering on data 1 Sample Abundance plot.html' highlighted. A red box highlights the 'View details' button in the history panel.

**Phyloseq Biom Filtering**

**Dataset Information**

Number: 3  
 Name: Phyloseq Biom Filtering on data 1 Sample Abundance plot.html  
 Created: Thu 27 Sep 2018 22:26:51 (UTC)  
 Filesize: 618 bytes  
 Dbkey: ?  
 Format: html

**Job Information**

Galaxy Tool ID: testtoolshed.g2.bx.psu.edu/repos/simon-gladman/phyloseq\_filter/biom\_filter/1.22.3.2  
 Galaxy Tool Version: 1.22.3.2  
 Tool Version: R version 3.4.1 (2017-06-30) -- "Single Candle", phyloseq version 1.22.3  
 Tool Standard Output: stdout  
 Tool Standard Error: stderr  
 Tool Exit Code: 0  
 History Content API ID: Odb6188ade7b40a8  
 Job API ID: 7144c79a666b0567  
 History API ID: 008e41993e80641a  
 UUID: 86bc16bc-f41b-4bfb-b010-3a39f2a8fdea  
 Full Path: /mnt/galaxy/files/000/288/dataset\_288661.dat

**Tool Parameters**

Input Parameter	Value	Note for rerun
Choose an input file type	set_biom	

10. You can quickly re-run a tool by clicking on the **recycle** button to load it, then easily change parameters for example.

The screenshot shows the Galaxy Australia web interface with the 'Phyloseq Biom Filtering' tool configuration panel. The 'Input File' is set to '1: AustralianMicrobiome-2018-09-28T062239.biom.zip'. The 'Select a taxonomic rank for the analysis' section has 'Phylum' selected. The 'Number of the most abundant taxonomic rank units to keep in the filtered BIOM file' is set to 5. The 'Filter out OTUs. Remove OTUs from the analysis that do not appear more than X times in more than Y% of the samples. Specify value of X' is set to 5. The 'Specify value of Y (where 1.0 = 100%)' is set to 0.5. A red box highlights the 'Run this job again' button in the bottom right corner.

**Phyloseq Biom Filtering biom file filter (Galaxy Version 1.22.3.2)**

Choose an input file type  
 BIOM File

Input File  
 1: AustralianMicrobiome-2018-09-28T062239.biom.zip

Select a taxonomic rank for the analysis

☐ Kingdom  
☒ Phylum  
☐ Class  
☐ Order  
☐ Family  
☐ Genus  
☐ Species

Number of the most abundant taxonomic rank units to keep in the filtered BIOM file  
 5  
 e.g. Phyla, Class and etc. as specified above. Select a value > 1.

Filter out OTUs. Remove OTUs from the analysis that do not appear more than X times in more than Y% of the samples. Specify value of X  
 5  
 Remove OTUs that do not appear more than X times (e.g., 5 times)

Specify value of Y (where 1.0 = 100%)  
 0.5

**Run this job again**