

Galaxy Australia

Quick Start Guide for Bioplatforms Data Portal Users



If you're already an existing user of Galaxy Australia start at step
#7

otherwise start at step #1

1. The first time you submit data from the Bioplatforms Data Portal, an account will be made for you on Galaxy Australia

Click on the link shown in the red box to set your Galaxy password.

The screenshot shows the Galaxy Australia Data Portal interface. At the top, there are tabs for "Quick Start Guide - Go...", "Galaxy | Australia", and "BPA Development | T...". Below the tabs, there are input fields for "Genus" and "Species", both set to "is", and a "Clear" button. A "Search" button is also present. Below the search bar, there are links for "Show results on Map", "Export Data to Galaxy Australia for further analysis", "Export Search Results (CSV)", and "Export Search Results (BIOM)". A message box with a red border contains the text: "An account has been created for you on Galaxy Australia. Please reset your password, using the same email address you have registered with the Bioplatforms Data Portal." Below the message box, there is a table with two columns: "BPA Sample ID" and "BPA Project". The table contains data for samples 7827 through 7840, all of which are "Soil" projects.

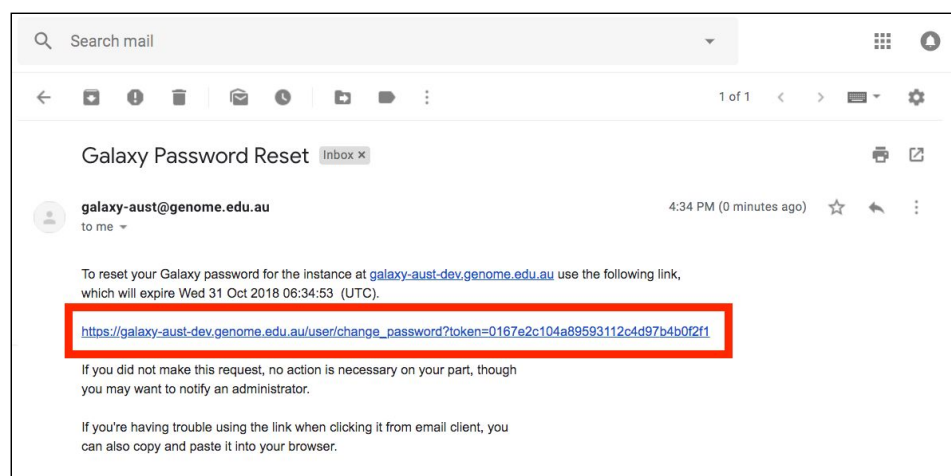
BPA Sample ID	BPA Project
7827	Soil
7828	Soil
7831	Soil
7832	Soil
7837	Soil
7838	Soil
7839	Soil
7840	Soil

2. You are taken to Galaxy Australia. Enter your email address and press 'Submit'

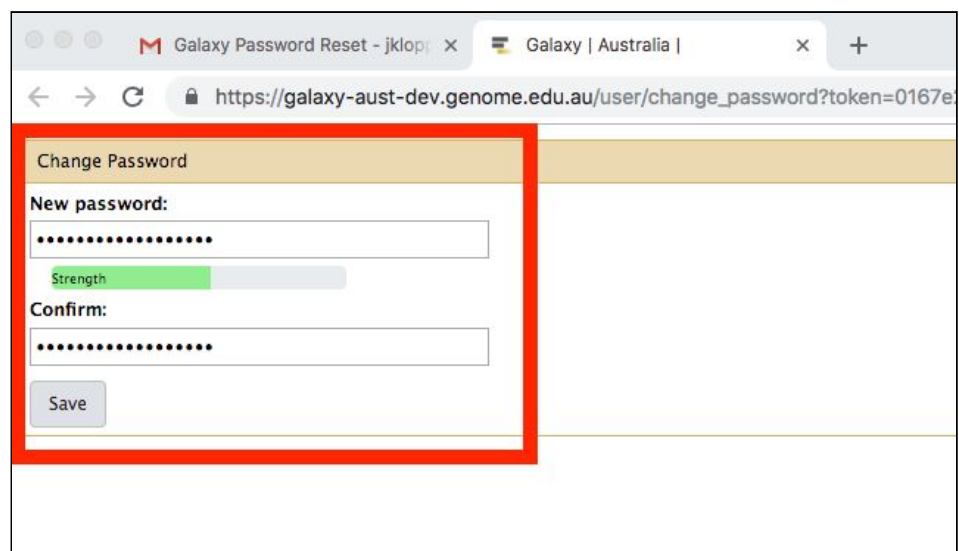


The screenshot shows a web browser window with the URL `galaxy-aust-dev.genome.edu.au`. The page has a navigation bar with links: "Quick Start Guide...", "Quick Start Guide...", "Galaxy | Australia", "* RDC Developmen...", "About - The Austra...", and "Bioplatforms OTU...". Below the navigation bar is a form titled "Reset Password". The form contains a label "Email:" followed by a text input field and a "Submit" button. A red rectangular box highlights the "Email:" label, the input field, and the "Submit" button.

3. In the email you receive, click on the link to set your password



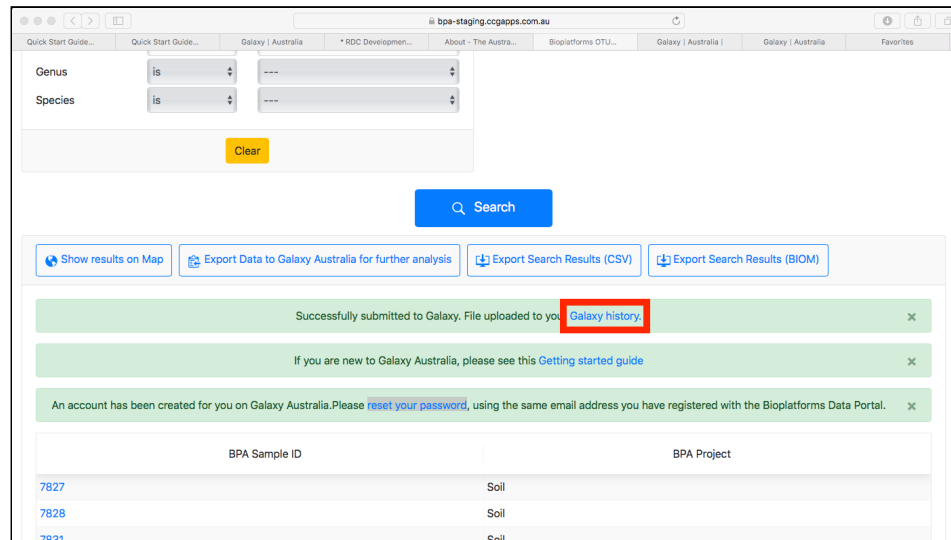
4. Choose your own password and click on save



The screenshot shows a web browser window with the URL `https://galaxy-aust-dev.genome.edu.au/user/change_password?token=0167e2c104a89593112c4d97b4b0f2f1`. The page has a navigation bar with links: "Galaxy Password Reset - jklop...", "Galaxy | Australia |", and a "+" button. Below the navigation bar is a form titled "Change Password". The form contains a label "New password:" followed by a text input field. Below the input field is a "Strength" indicator, which is a green bar. Below the "Strength" indicator is a label "Confirm:" followed by a text input field. Below the input field is a "Save" button. A red rectangular box highlights the "New password:" label, the input field, the "Strength" indicator, the "Confirm:" label, the input field, and the "Save" button.

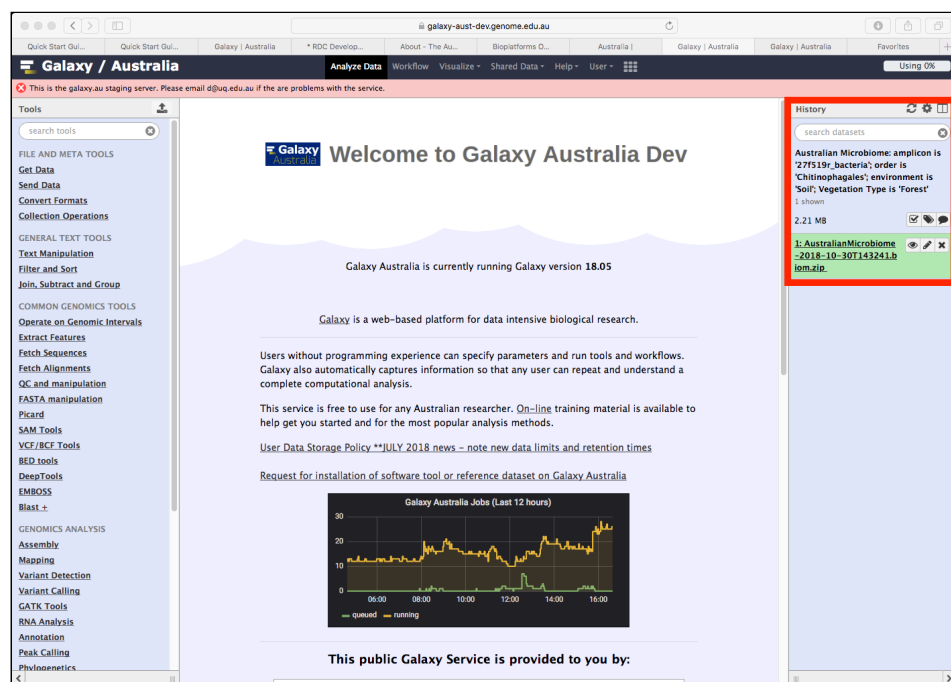
5. Go back to the Bioplatforms Data Portal.

When your data transfer to Galaxy is finished, click on the 'Galaxy History' link

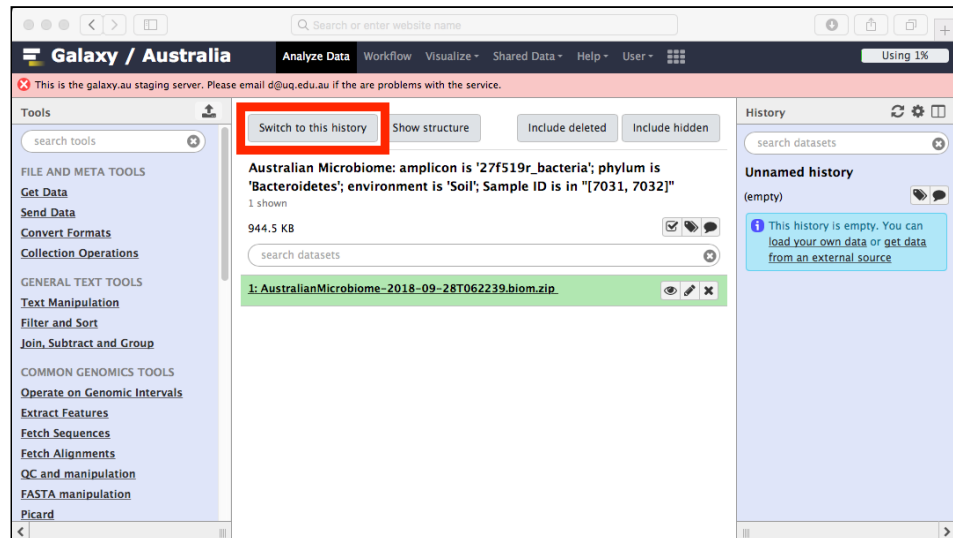


6. Your BIOM file from Bioplatforms Data Portal will be loaded into the 'History' pane on the right

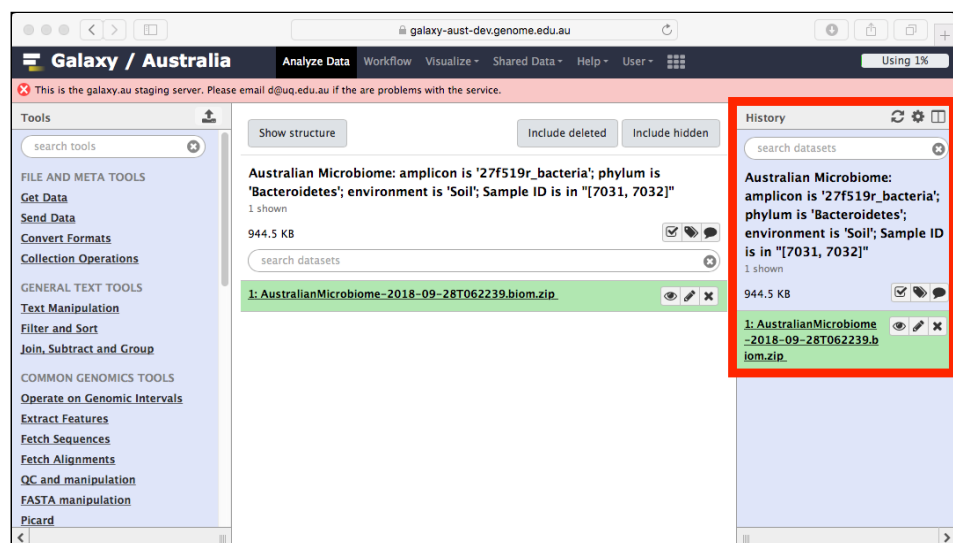
Go to Step 9.



7. If you are an existing user of Galaxy Australia. Click on **'Switch to this history'** to load your data from the BPA Data Portal



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



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 the are problems with the service.

Tools

search tools

FILE AND META TOOLS

[Get Data](#)

[Send Data](#)

[Convert Formats](#)

[Collection Operations](#)

GENERAL TEXT TOOLS

[Text Manipulation](#)

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COMMON GENOMICS TOOLS

[Operate on Genomic Intervals](#)

[Extract Features](#)

[Fetch Sequences](#)

[Fetch Alignments](#)

[QC and manipulation](#)

[FASTA manipulation](#)

[Picard](#)

```
{'id':null,
  "format":"Biological Observation Matrix 1.0.0",
  "format_url":"http://biom-format.org",
  "type":"OTU table",
  "generated_by":"Bioplatforms Australia",
  "date":"2018-09-28T06:22:39",
  "matrix_type":"sparse",
  "matrix_element_type":"int",
  "rows":[{"id":
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    GGGCTTAATACCGCCAGCATCTCCAGCTCCCGATCGGAGCGAGTGAATGAACGCTTATCGCTTCGAGAGAG
    GCTCGCTCGCGATGATCTCTCGCGAGATACGCGTCCAGGAGCAATGATCGCTACGCTCGCTCGAG
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    CGTGC","metadata":{"amplicon":"27F519r_bacteria","taxonomy":
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    "Rhodothermaceae","Salinibacter","Salinibacter_unclassified"]}},
    {'id':
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    TGGCTAATACCGACGACGCTCTGACGCCGCTAGCGGAGCAGATGAACCTTGCTTTCGCTCGCAAGGCGCT
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    GCTCGAGAGAGCGACGAGCCGACCTGCGAGCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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    "Rhodothermaceae","Salinibacter","Salinibacter_unclassified"]}},
    {'id':
    "GACGAACCTCGGGCGAGGCTTAACACATCGCAAGTCGCACGAGAACTCTCGCTTTCGCGGGAGCA
    GTACATGCGCGAGCGGTGCGCTCTGCGTATGAAATCTGCCCTTCAGCGCGGAGCAATCGACGGAGAAC
```

History

search datasets

Australian Microbiome:
amplicon is '27F519r_bacteria';
phylum is 'Bacteroidetes';
environment is 'Soil'; Sample ID
is in '7031, 7032'

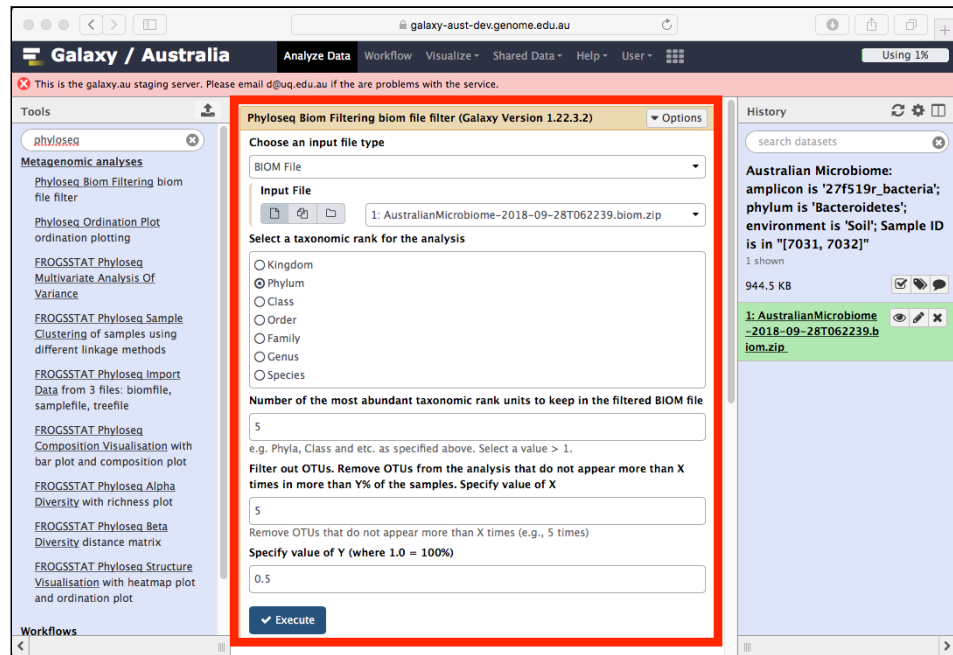
1 shown

944.5 KB

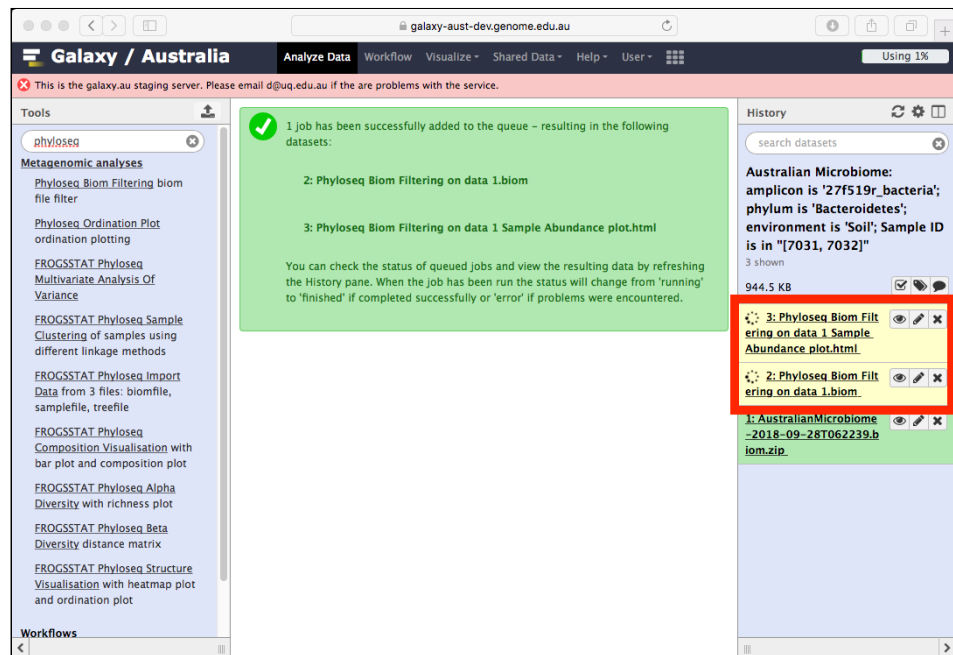
1: Australian Microbiome
e-2018-09-28T06:22:39
biom.zip

[illegible]

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



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

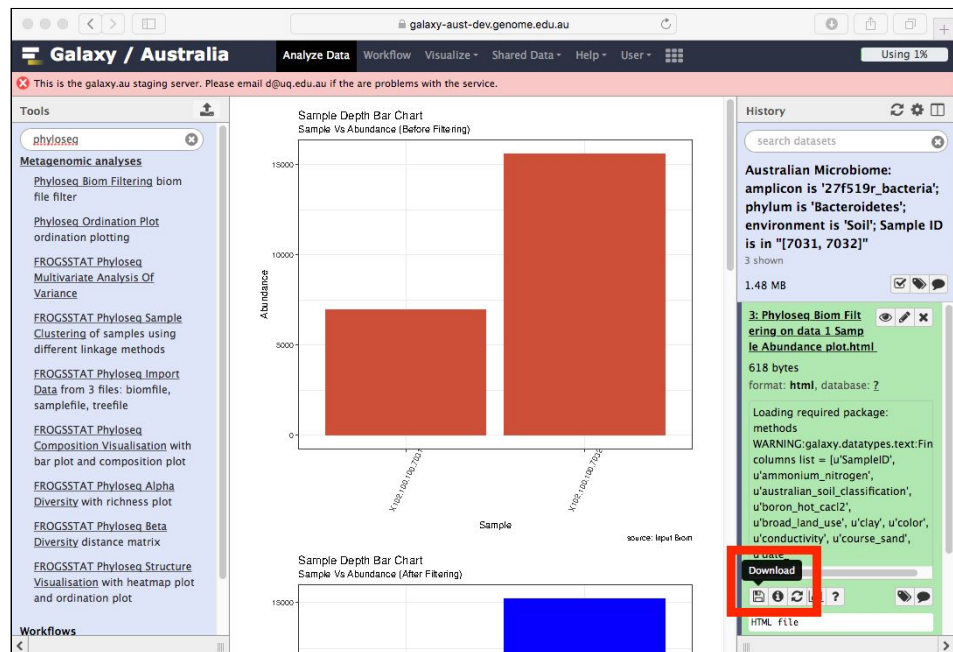


13. When the job is done, output files will change to green. Click on the **eye** icon to view a output file



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

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



15. 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 'Tools' sidebar with 'Metagenomic analyses' selected. The main panel displays the 'Phyloseq Biom Filtering' tool's 'Dataset Information' and 'Job Information'. On the right, the 'History' panel shows a list of jobs. The job '3: Phyloseq Biom Filtering on data 1 Sample Abundance plot.html' is selected, and its 'View details' button is highlighted with a red box. The details panel shows the tool's parameters and a warning about the required package 'methods'.

16. 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 biom file filter' tool's 'Options' 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' section has '5' entered. The 'Specify value of Y (where 1.0 = 100%)' is set to 0.5. The 'Run this job again' button is highlighted with a red box.

Note that Galaxy Australia is not intended for long term data storage, and according to the [Galaxy Australia Data Storage Policy](#), data and histories will be automatically deleted after a period of 3 months. To maintain a copy of your data outputs and/or histories, ensure that you [copy output data off the service](#) within 3 months of generation.