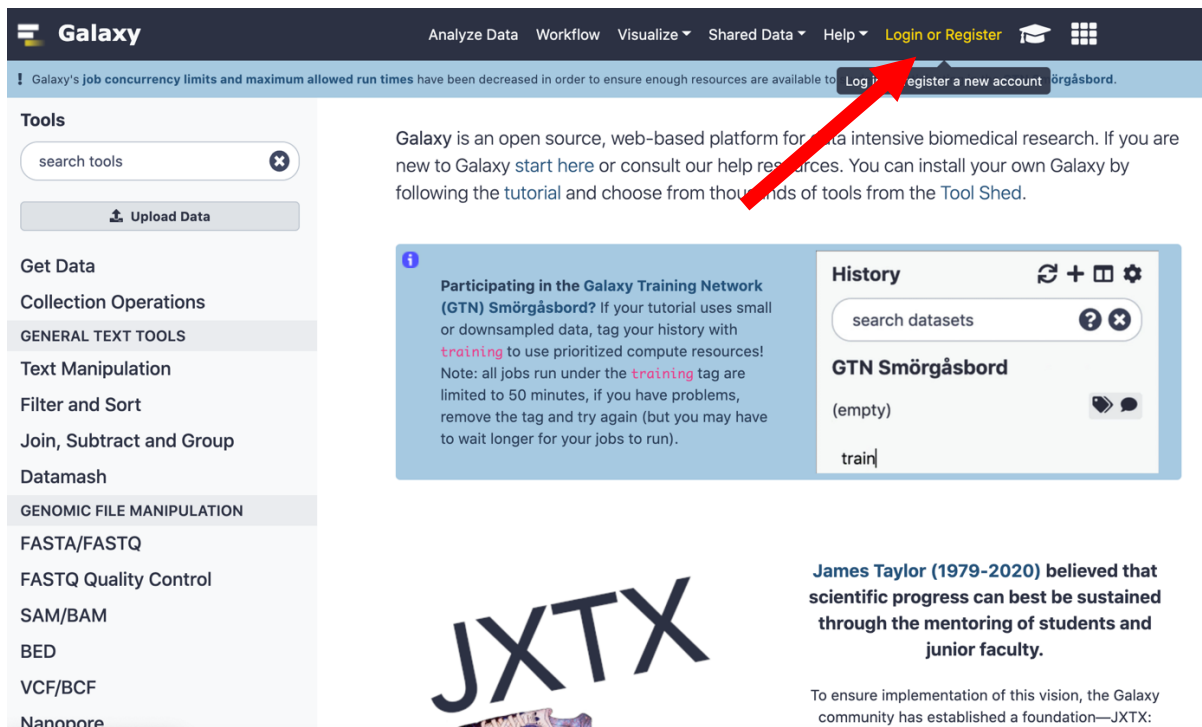


Great Basin College – Elko
Bioinformatics Workshop
UNR – Bioinformatics Core
by: Dr. Hans Vasquez-Gross

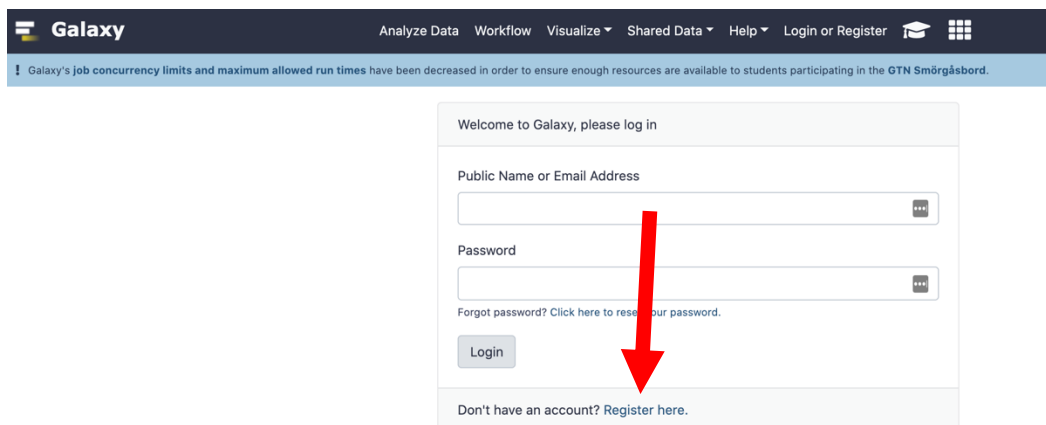
Galaxy Tutorial and Walkthrough

1. Before the first day of instruction, please register a Galaxy Account here:
<https://usegalaxy.org/>



The screenshot shows the Galaxy web interface. The top navigation bar includes links for 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'Login or Register'. A red arrow points to the 'Login or Register' link. Below the navigation bar, there is a message about job concurrency limits. The left sidebar contains a 'Tools' section with a search bar and an 'Upload Data' button. The main content area displays a welcome message and a 'History' section with a search bar. A red arrow points to the 'Login or Register' link in the top navigation bar.

2. Then, click the register link towards the bottom of the login dialog box



The screenshot shows the Galaxy login dialog box. It contains fields for 'Public Name or Email Address' and 'Password', a 'Forgot password?' link, a 'Login' button, and a 'Don't have an account? Register here.' link. A red arrow points to the 'Register here.' link.

3. Fill out the registration form and click 'Create'.

Galaxy's job concurrency limits and maximum allowed run times have been decreased in order to ensure enough resources are available to students participating in the GTN Smörgåsbord.

Please register only one account. The usegalaxy.org service is provided free of charge and has limited computational and data storage resources. Registration and usage of multiple accounts is tracked and such accounts are subject to termination and data deletion.

Galaxy Web Portal Service Agreement

1) Use of Service. The Galaxy Web Portal is a free, public, Internet accessible resource (the "Service"). Data transfer and data storage are not encrypted. If there are restrictions on the way your research data can be stored and used, please consult your local institutional review board or the project principal investigator before uploading it to any public site, including this Service. If you have protected data, large data storage requirements, or short deadlines you are encouraged to set up your own local Galaxy instance and not use this Service. Your access to the service may be revoked at any time for reasons deemed necessary by the operators of the Service.

2) Accounts and Service Limitations. You may choose to register an account with the Service. Your registration data is primarily used so you may persistently store data on the Service and use advanced Galaxy features such as sharing and workflows. The operators of the Service will not provide your registration data to any third party unless required to do so by law. Your access to the Service is provided under the condition that you abide by any published quotas on data storage, job submissions, or any other limitations placed on the public Service. Attempts to subvert these limits by creating multiple accounts or through any other method may result in termination of all associated accounts.

3) Disclaimer. The Service is provided to you on an "AS IS" BASIS and WITHOUT WARRANTY, either express or implied, including, without limitation, the warranties of non-infringement, merchantability or fitness for a particular purpose. THE ENTIRE RISK AS TO THE QUALITY OF THE SERVICE IS WITH YOU. This DISCLAIMER OF WARRANTY constitutes an essential part of this service

Create a Galaxy account

Email Address
youremailaddress@gmail.com

Password
.....

Confirm password
.....

Public name
Your PublicName

Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least three characters in length and contain only lower-case letters, numbers, dots, underscores, and dashes ('.', '_', '-').

Create

4. Afterwards, verify you can login to Galaxy.

BONUS: View the powerpoint presentation ["A short introduction to Galaxy"](#) to familiarize yourself with Galaxy. This link is one of the introduction presentations for Galaxy which we will also be going over during the beginning of the workshop so that students may ask questions.

After we familiarize ourselves with navigating in Galaxy, we will run through a real use-case example analyzing multiple Sars-cov-2 samples that have been sequenced and freely available through NCBI/Entrez.

Since Galaxy is a widely used platform for bioinformatic analysis, there have been many training modules developed that are freely available from their main website here: <https://training.galaxyproject.org/training-material/>

In the main workshop, we will go over on how to get data from NCBI/Entrez, bring it into the Galaxy platform, then continue with downstream analysis to eventually map ILLUMINA sequenced reads to the Sars-cov-2 Wuhan genome reference. These mapping results will then be used to call variants, both SNPs and structural variants. Lastly, we will create a human-readable report in HTML format which can be opened on your local browser which will summarize the results.

Main Workshop Tutorial: <https://training.galaxyproject.org/training-material/topics/variant-analysis/tutorials/sars-cov-2/tutorial.html>

You will also get this tutorial emailed as a PDF, which can easily be printed (14 pages).