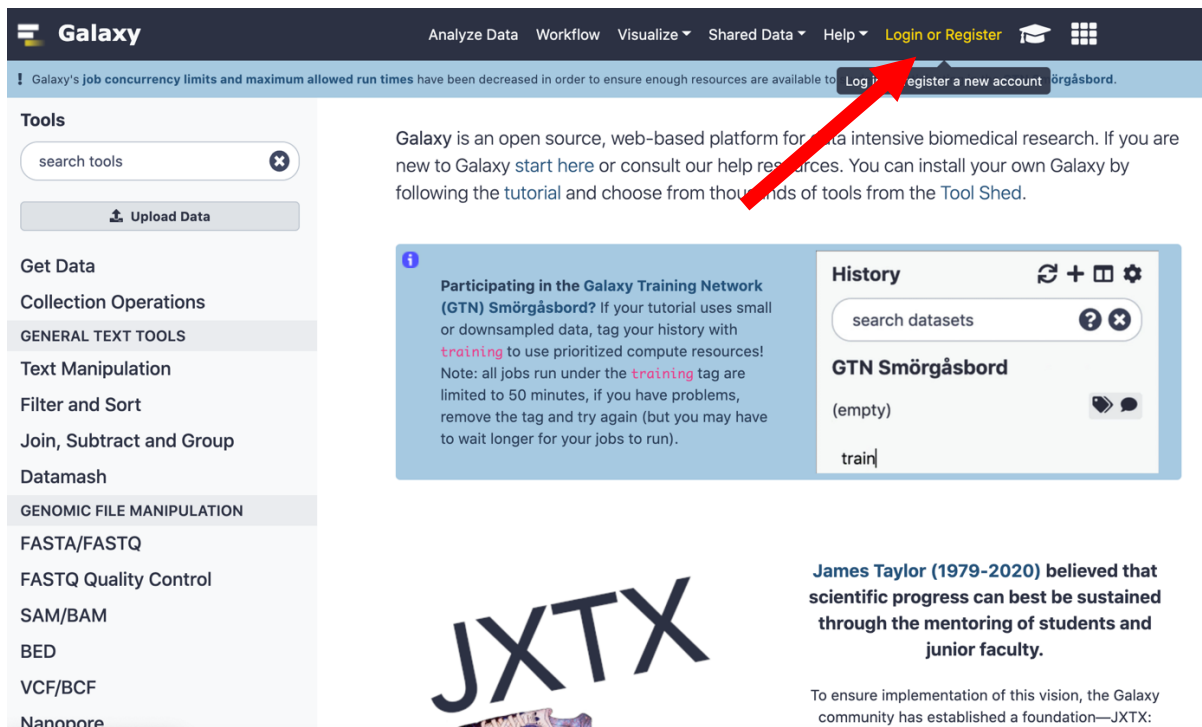**Great Basin College – Elko**
**Bioinformatics Workshop**
**UNR – Bioinformatics Core**
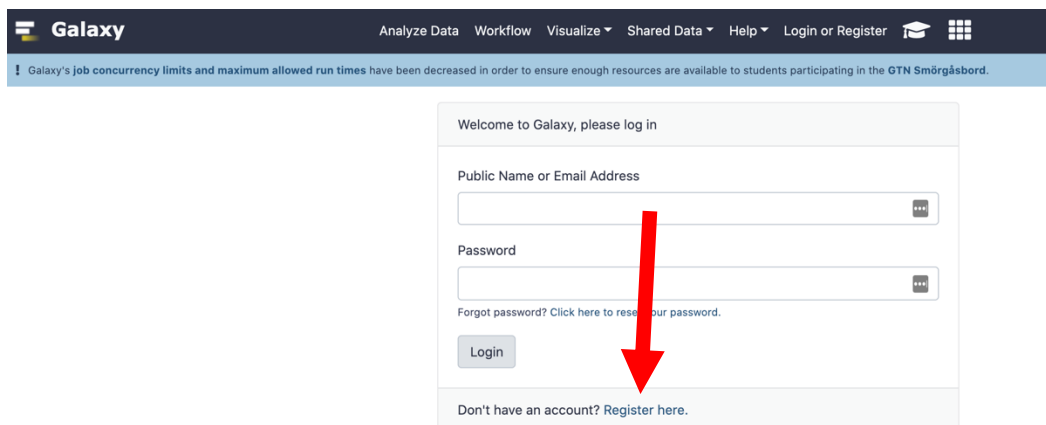**by: Dr. Hans Vasquez-Gross**

**Galaxy Tutorial and Walkthrough**

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



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

3. Fill out the registration from and click '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).