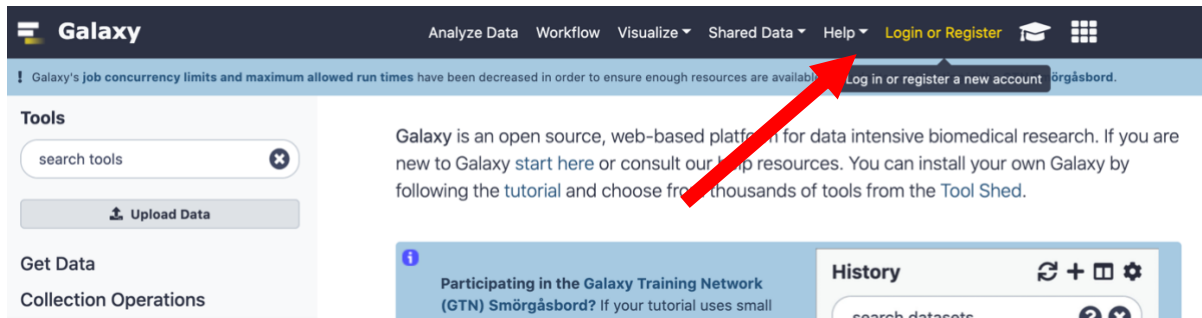**N** Research & Innovation – Nevada Bioinformatics Center
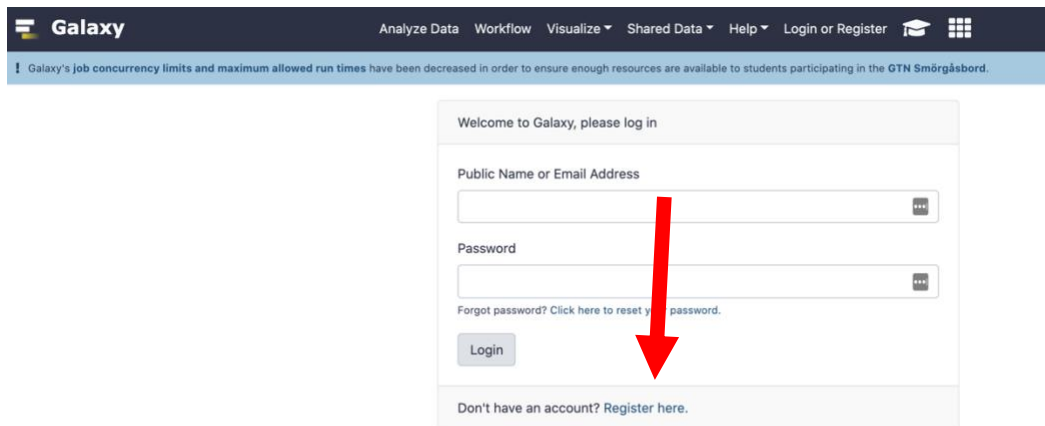**This section is presented by Dr. Hans Vasquez-Gross**

Getting Stated with Galaxy

1. Prior to workshop, please create 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 form and click 'Create'. Afterwards, verify you can login to Galaxy.

BONUS: View the PowerPoint presentation "A short introduction to Galaxy" to familiarize yourself with Galaxy – no worries we will cover this material in the workshop as well.

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

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

Hands-on Session: SRA to Galaxy: SARS-CoV-2 Variant Analysis

Main Learning Objectives:
- how to find and retrieve data from NCBI/Entrez
- bring data into the Galaxy platform
- downstream analysis
  - map Illumina sequenced reads to the Sars-cov-2 Wuhan genome reference.
  - use mapping results for variant calling (variant analysis): both SNPs and structural variants
- create a human-readable report in HTML format which can be opened on your local browser
- interpret, summarize, and present results

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