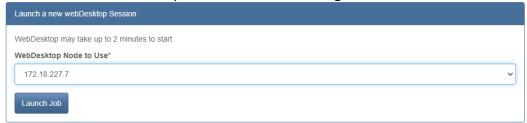
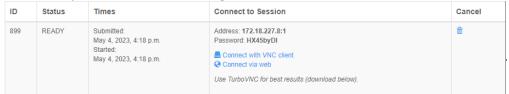
## SWE2023 Module 2 Setup:

- 1. In a web browser of your choice, go to biohpc WebDesktop: https://portal.biohpc.swmed.edu/intranet/terminal/webdesktop/
  - a. Login to your BioHPC account if you haven't already
- 2. Launch a new Web desktop session on the following Node: 172.18.227.7



3. Once launched you should see something like this:



- 4. If you haven't downloaded VNC, there is a link appropriate for your OS above the web desktop session box. Download this before proceeding.
- 5. Click connect with VNC client. A download should start automatically in your web browser. Once complete, click the download file.
- 6. Login to the Node with your biohpc username/password.
- 7. At this point you should see something like this:



8. Navigate to the terminal



- 9. Move to/create a directory where you would like to store your code for this module.
  - If you are unfamiliar with navigating the linux tutorial, see: Intro to linux slides
- 10. Clone the repo using the following command: git clone <a href="https://github.com/UTSW-Software-Engineering-Course-2023/module 2 materials.git">https://github.com/UTSW-Software-Engineering-Course-2023/module 2 materials.git</a>
- 11. Change directories into the cloned repo. The ls should look like this:

[s184945@NucleusC008 SWE2023]\$ ls
activateVAEGANEnv.sh activateWeekendEnv.sh installWeekendEnv.sh keys lecture materials README.md tasks

12. Install the conda environments you will be using throughout the week. Enter the following commands:

source installVAEGANEnv.sh source installWeekendEnv.sh source activateVAEGANEnv.sh conda deactivate source activateWeekendEnv.sh

- 13. Each time you create a new webdesktop session, you will need to reactivate the conda environments you will be using.
  - For the Weekend, you will be using: source activateWeekendEnv.sh
  - For the remainder of the module, you will be using: source activateVAEGANEnv.sh
- 14. Now you are ready to begin working with VSCode! This is already installed on the cluster, however you will need to load it into your session by entering the following command:

module load vscode

15. Last, to launch vscode in your current directory enter:

code.

## All together, your terminal should look something like this:

```
(base) [s184945@NucleusC007 SWE2023]$ ls activateWeekendEnv.sh installVAEGANEnv.sh installWeekendEnv.sh keys lecture_materials README.md tasks (base) [s184945@NucleusC007 SWE2023]$ source installVAEGANEnv.sh installWeekendEnv.sh keys lecture_materials README.md tasks (base) [s184945@NucleusC007 SWE2023]$ source installWeekendEnv.sh Installed kernelspec VAE_GAN_env_new in /home2/s184945/.local/share/jupyter/kernels/nanocourse2022Tf (/home2/s184945/anaconda3) [s184945@NucleusC007 SWE2023]$ source installWeekendEnv.sh Installed kernelspec Nanocourse2022Tf in /home2/s184945/.local/share/jupyter/kernels/nanocourse2022tf (/home2/s184945/anaconda3) [s184945@NucleusC007 SWE2023]$ source activateVAEGANEnv.sh (/archive/course/SWE22/shared/SWE2023_week2/CondaEnvs/VAE_GAN_env_new) [s184945@NucleusC007 SWE2023]$ conda deactivate (/home2/s184945/anaconda3) [s184945@NucleusC007 SWE2023]$ source activateWeekendEnv.sh (/archive/course/SWE22/shared/SWE2023_week2/CondaEnvs/Nanocourse2022TF) [s184945@NucleusC007 SWE2023]$ module load vscode (/archive/course/SWE22/shared/SWE2023_week2/CondaEnvs/Nanocourse2022TF) [s184945@NucleusC007 SWE2023]$ code . (/archive/course/SWE22/shared/SWE2023_week2/CondaEnvs/Nanocourse2022TF) [s184945@NucleusC007 SWE2023]$ [
```