

This document provides instructions on how to install and enter the environment to run the Genelytics pipeline.

Requirements:

- Must run on x86 architecture (i.e. Windows machines)
- Windows Subsystem for Linux, WSL (install instructions below)

Steps:

1. Download the project repository:
 - Download project repository from Dr. Almeyda or from the project github:
<https://github.com/brooks-hw/Bioinformatics-Capstone-CS-490>
2. Install WSL
 - Press the windows key (or enter search bar)
 - Type "powershell," right click and "run as administrator"
 - Type the command: "wsl --install"
 - Restart PC to properly ensure installation
3. Install Ubuntu:
 - A command shell labeled "Ubuntu" may pop up, if so skip next step
 - If not → Enter search bar again and type "Ubuntu"
 - It will then install and likely take a few minutes
 - Create a username and password when prompted (Simple password helps, doesn't need to be super secure, especially if using personal computer)
 - Once complete, you are now inside a Linux virtual environment while on windows.
4. Update Ubuntu Packages:
 - Type "sudo apt update && sudo apt upgrade -y" to pull the most recent versions of necessary packages. (this may require you to type in password)
 - This shell will be your work environment, all tools will be hosted and run here
5. Download Miniforge:
 - Run: "cd ~" to navigate to the root directory
 - Run the following command (inside of the Ubuntu window): 'wget https://github.com/conda-forge/miniforge/releases/latest/download/Miniforge3-Linux-x86_64.sh -O [miniforge.sh](https://github.com/conda-forge/miniforge/releases/latest/download/Miniforge3-Linux-x86_64.sh)'

Followed by: 'bash [miniforge.sh](#)'

- Type 'yes' when asked to accept the license
 - Press 'Enter' when prompted to install to
/home/username/miniforge3
(this makes Conda visible to your PC upon restarting the terminal)
 - Type 'yes' when asked to 'initialize conda?'
 - Close your Ubuntu terminal and reopen it to activate conda
6. Install Mamba (faster version of Conda for some parts):
- Run: 'conda install -n base mamba -c conda-forge -y'
 - If successfully installed, the project environment is ready to be built
7. Create the Genelytics Conda environment:
- Navigate to the project directory (wherever it's located on your computer), to do this type: **"cd /mnt/c/Users/<WINDOWS_USERNAME>/"**
 - After the last / type "Desktop" or "Downloads" or wherever you have the project folder. At each step of the way, you can type "ls" to see what files/folders are currently in that directory. From there you can "cd" into them as necessary
 - An example entire command may be:
"cd /mnt/c/Users/John/Desktop/Genelytics-Project"
**Note that your project folder may be called something different (feel free to rename it to something easy to type)*
 - Run: "mamba env create -f environment.yml" to create the mamba environment containing the necessary dependencies
**This will likely take a few minutes to install everything*
 - Activate the environment by running: "conda activate genelytics"
 - You should now see something like:
(genelytics) student\$DESKTOP:~\$
8. After entering the environment, you are ready to run the pipeline.
- Ensure you are currently inside the same directory (folder) that contains "ProcFast.py"
 - While still inside the genelytics environment, run:
"python ProcFast.py --port 500X" to initialize the program
 - Each user will need to use a different port, so change the command accordingly (example --port 5000, --port 5001, --port 5002)
 - It should now initialize and say something such as:
Running on http://127.0.0... along with other info.

- Open a browser and navigate to: `http://localhost:500X` (use the same port number as initialized with above) and the dashboard will appear.
 - Once here, use the tools as necessary via the upload boxes, the outputs will be located in the same folder as your main project
9. After you're finished:
- Run CTRL+C to stop the program from running
 - Close Ubuntu

Additional Info/Comments:

- The command line can be very specific, if you're getting errors at any step, copy them (with CTRL+C) and give them to ChatGPT or any other LLM and it will most likely help you find the root issue.
- Most steps listed here should be general knowledge to CS students so I recommend reaching out to someone in CS if you encounter any issues along the way.