

UNIX practice

On the UNIX command line. Go into your bigdata folder. If you have not used the cluster before then you will be in the **gen220** project. Or you may have your own lab bigdata folder.

See [Text Editors in UNIX](#) While it takes a few steps to install and setup, [Visual-Studio](#) is a great resource you can edit on your local machine but saves changes on HPCC. See https://hpcc.ucr.edu/manuals/hpc_cluster/selected_software/vscode/

This should work

```
cd ~/bigdata
```

but if it doesn't

```
cd /bigdata/gen220/$USER # will go into your bigdata folder for the class
```

But if you already had an account on the cluster then # if the above doesn't work you are likely already in a lab group on HPCC

```
cd /bigdata/$GROUP/$USER # should work since $USER is your login and $GROUP is your primary
# you can see what groups you are in by typing
groups
```

For your homework: 1. Accept the homework 1 problem - (see link in Canvas).

2. Create a folder to work in on HPCC (or your own computer): `mkdir -p ~/bigdata/gen220/homework` and then `cd ~/bigdata/gen220/homework` 3.

Checkout the GEN220 data folder `git clone https://github.com/biodataprogram/GEN220_data.git`

Now you want to make a folder for your work for this class

The steps look like this:

```
# you can make a folder for GEN220
mkdir gen220
go into that folder
cd gen220
# now use git to checkout the class data folder
git clone https://github.com/biodataprogram/GEN220_data.git
# now go into this folder
cd GEN220_data
```

Look around in the folder. Go into the **tabular** folder where I've stored some tab or comma delimited data. You will later need to copy a file from this folder into your homework folder.

4. Checkout the homework 1 github repository created in step 2. (if you [setup SSH keys](#) in github

```
git clone git@github.com:biodataprogram/2025-hw1-YOURGITHUBID
```

OR for the https will need to [create a token as your password](#))

```
git clone https://github.com/biodataprogram/2025-hw1-YOURGITHUBID.git
```

6. Go into your folder (`cd 2025-hw1-YOURGITHUBID`).
7. Edit a script in there called `filesize.sh`; you can do this in jupyter on web, you can edit on the command line with `nano`, `vi`, or `emacs`, or you can [use visual studio tunnel](#)
8. Add some code to this script which achieve the directions at the bottom of this
9. Test it out (run the `./filecount.sh`).
10. To submit your homework (and you can do this more than once), this requires doing `git commit` and then `git push`

```
# this step saves a version of the code
git commit -m "This is a homework 1 solution" filesize.sh
# this step will push the data from HPCC or your computer UP to the github site
# this step will request your username (YOURGITHUBID) and your password (that TOKEN I mentioned)
# if you have setup github account with SSH keys then it will ask you for your SSH key password
git push
```

9. you can repeat doing edits to the file, commit, and push to github.

Tasks for Homework 1

1. copy the `threatened-species.csv.gz` file - see info here [HW1](#) or you can just run the included `./setup.sh` script to download. but also encourage you to practice with `cp` command.
2. Write a script called `answer1.sh`:
 - print out the size of the `threatened-species.csv.gz` using `du` or `ls -l`
 - Count the number of lines in file
 - Print out the number of unique phyla, `order_name` in the table using `cut`, `sort`, `uniq`
 - count how many kingdom FUNGI are present in the file?
3. Check in your changes with `git commit -m 'a message'` and `git push` to save the changes to github.