

Biostat 561: Homework 8

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Homework 8 due May 29, 3:15pm

Link to Homework 8 submission: https://classroom.github.com/a/CamdT_zp

Question 1: Shell scripts

Write a shell script to

- Create 500 folders called `folder1`, `folder2`, ...
- In each of the folders, create a text file called `output_i.txt` containing the string “Output_of_simulation_i” where *i* is the number of the folder
- Edit the string in place (using `sed` or another command line regular expression parser) to replace all underscores with spaces
- Delete all of the folders. Make sure your script only deletes folders and files created by the script!

You should confirm that your script works as intended on your own computer. I strongly recommend using `vim` as a text editor to get used to writing scripts on the command line rather than with an interface.

Upload your shell script, but there is no need to upload the folders or their contents.

Question 2: Logging onto department clusters

Windows users

Download a secure shell (SSH) client (I recommend TeraTerm if you are not familiar with one already). Open up your SSH client and enter `bayes.biostat.washington.edu` in the `host` field and 22 in the `TCP port\#` field. Enter your UW NetID (e.g. mine is `adwillis`) and **Biostat password**.

What is the name of the directory that you are in when you login?

Mac/Linux users

Open terminal and type `ssh [myetid]@bayes.biostat.washington.edu`. Replace `[myetid]` with your UW NetID (e.g. mine is `adwillis`). Enter your **Biostat password** when prompted.

What is the name of the directory that you are in when you login?