Intro to Unix/Command Line

BIOL 435/535: Bioinformatics

March 10, 2022

Using the command line

Mac

Terminal

PC

Command Terminal (non-UNIX)

PuTTY

ChromeOS

Secure Shell

Unix basic commands

command -options standard_input > standard_output

standard_error will print to the screen

Unix basic commands (and Google is your friend)

```
cd – change directory (cd ~ = ET Go Home)
Is – lists files inside a directory (ls -l)
pwd - print working directory
cp – copies a file from one place to another
mv – moves a file from one place to another (including renaming)
rm – removes a file/directory (-r option required for removing a directory BE VERY CAREFUL!!)
mkdir – make a new directory (aka folder)
echo - print to the terminal
head – shows the top part of a file
tail - shows the bottom of a file
wc -l - List the number of lines in a file
cat – print the ENTIRE file's contents
wget - retrieve a file from a url
watch – watch a command in action, updates every 2 seconds
ssh – open a secure shell (encrypted connection between two computers)
screen – open a virtual ssh session – won't get disconnected!
scp - secure copy protocol (encrypted file transfer)
ftp – file transfer protocol (unencrypted file transfer)
more - read a file, little-by-little
```

```
chmod – modify file/folder permissions
unzip – unzip a compressed zip file
gzip – compress a file
gunzip – unzip a .gz file
tar – make/unpack a tarball
du -h – List your disk usage
diff – Compare two files, line by line
env – Print current environmental
variables to the screen
vi/vim - text editor BE VERY
CAREFUL!!
nano – text editor BE VERY CAREFUL!!
emacs – Text editor BE VERY
CAREFUL!!
```

SSH (secure shell)

ssh username@server

Need a VPN to logon to Discovery HPC

Some additional considerations

./bash_rc file controls your environment

Object-oriented programming, and variable assignment

- \$HOME
- \$USER
- \$PATH

Don't use spaces or weird characters in file names

• Escape character allows you to deal with them (e.g., dont\ name\ your\ files\ like\ this\ .txt)

Job Submission

Specifies the resources requested

Specifies the command to be run

Bash Language

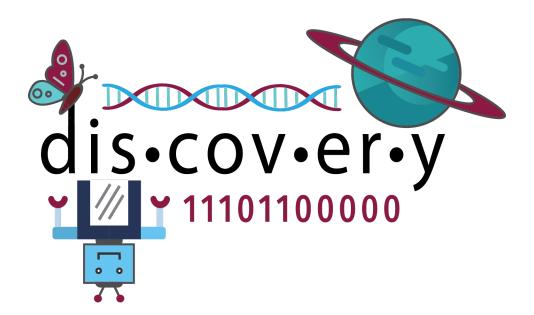
Job Submission

```
#!/bin/bash
#SBATCH --time=24:00:00
#SBATCH --mem=1G
#SBATCH --partition=class
#SBATCH -- job-name=blastn
#SBATCH --ntasks=24
#SBATCH --nodes=1
#SBATCH --cpus-per-task=1
#SBATCH --mail-user=joel.sharbrough@nmt.edu
#SBATCH --mail-type=ALL
#SBATCH --error=blastn.err
#SBATCH --output=blastn.out
module load blast
```

blastn -db mtDNA.fasta -query query.fasta -outfmt 6 -max_target_seqs 1 -out mtDNA.out -num_threads 24

Next up: <u>Discovery HPC On-Boarding</u>

HW #6 HPC VPN form (already done)



First writing assignment is due in two weeks (3/14)