Exercise 6: using “screen” to create a persistent session

If not already done so, connect to your assigned workstation via ssh (using PuTTy or other ssh client)

In the terminal window, type **`screen`** and hit Enter. You just opened the first window in your screen session.

Type **`Ctrl-a c`** (i.e, press **`Ctrl`** key and while holding it press **`a`**, then let go of both keys and press **`c`**). Then do it one more time. You just opened two more screen windows within your session.

Execute the **`ls –al`** command in the current window. Then switch to the next window pressing **`Ctrl-a n`**. run the pwd command there, and switch to the next window hitting **`Ctrl-a n`** again. Switch to previous window using **`Ctrl-a p`**. As you cycle through the windows, you will see them as you last left them.

Simulate a network or power problem by closing the PuTTy terminal window (it “X” in the upper right corner).

Using PuTTy, connect to your assigned machine again. In the terminal window, type **`screen –list`**. You should see the screen session you left behind.

Type **`screen –d –r`**. This will re-connect you to your screen session. Cycle through the windows using **`Ctrl-a p, Ctrl-a n`**, or **`Ctrl-a “`**. Do you see your windows as you left them?

Gracefully detach your screen session using **`Ctrl-a d`** (all your windows will keep running). Then re-attach again using **`screen –d –r`**.

Terminate your screen session by hitting **`Ctrl-d`** in each window (this will terminate the current window). Doing it in the last window will terminate the screen session (a message will be displayed). Your main PuTTy terminal will keep running.

Exercise 7: connect to your assigned workstation using VNC

- Go to “My Reservations” page
  http://biohpc.cornell.edu/lab/lab.aspx , log in, click on “My Reservations” menu link
- Choose resolution (depends on your monitor)
- Click on “Connect VNC”
- Follow prompts to connect your VNC client to your VNC session
- Open terminal window in the VNC desktop by right-click on the desktop background and choosing “Open Terminal”.
- Disconnect (close VNC window) and then reconnect. Is the session still alive?

Exercise 8: using `scp` to transfer files between Linux machines

a) On server **`cbsufsrv7.biohpc.cornell.edu`** there is a directory **`/data1/Workshop/dir2transfer`** with some test files in it – all readable to you.

Copy this directory (with its content) to your scratch directory on your workshop machine.

```
cd /workdir/myid
scp –r myid@cbsufsrv7.biohpc.cornell.edu:/data1/Workshop/dir2transfer .
```

When done, verify the transfer and examine the directory you copied.

b) In your scratch directory **`(/workdir/myid`**) on your workshop machine, create a text file called **`myid_file`** (replace **`myid`** with your actual userid) containing string "**`This is my test file`**". Use your favorite text editor to create this file.

Copy the newly created file onto **`cbsufsrv7.biohpc.cornell.edu`** into the directory **`/data1/Workshop`**

```
cd /workdir/myid
scp myid_file myid@cbsufsrv7.biohpc.cornell.edu:/data1/Workshop
```

Exercise 8: batch download of files from sequencing facility

Open your e-mail, find a message “Test Illumina distribution e-mail” with an attachment **`download.sh`**

Transfer the attachment file onto your Linux machine. You can do one of the following:

Option 1:

- open the attachment in a text editor on your laptop and copy its contents to clipboard (using the mouse)
- in Linux machine terminal, open a new file (in a directory where you want your files downloaded to) using a text editor of your choice (e.g., nano or vi)
- Paste the contents of the clipboard to the new file on Linux machine and save that file.

Option 2:

- Save the attachment file on disk on your laptop
- Use a file transfer technique of your choice (interactive sftp client, command-line scp or sftp) to transfer the saved file from laptop to your Linux machine, to the directory where you want the fastq files to be downloaded to.

Once the file **`download.sh`** is ready on the Linux machine:

- Log in to the Linux machine (if not yet done so)
- cd to the directory where the download.sh file has been deposited
- Execute the file:

```
sh ./download.sh
```

Exercise 8: batch download of files from sequencing facility

(continued)

Once the download completes (should take about 1 second):

- Verify that the files have ben downloaded and that they have correct sizes (the same as in the notification e-ail)
  - Hint: use `ls -al` command
- Verify that MD5 sums of both files are the same as in the notification e-mail
  - Hint: run
```
md5sum file_1.fastq.gz file_2.fastq.gz
```
- Uncompress the files
  - Hint: use
```
gzip -d file_1.fastq.gz file_2.fastq.gz
```
- Count the sequences in each file
  - Hint: use
```
wc -l file_1.fastq file_2.fastq
```
- Open each file in a text editor on Linux machine (nano, vi)