Introduction to Linux

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http://barc.wi.mit.edu/hot_topics/

WHITEHEAD INSTITUTE

Outline

- Linux overview
  - Logging in to tak
  - Directory structure
  - Accessing Whitehead drives/finding your lab share
- Basic commands
- Exercises
- BaRC and Whitehead resources
- LSF

What is Linux?

- Linux is a family of open source Unix-like operating systems. The original Unix is proprietary.
- Our servers run a distribution of Linux, Ubuntu version 20.
- It is powerful, so large datasets can be analyzed.
- Many repetitive analyses or tasks can be easily automated.

How can we access our Linux server?

- Mac computers come with Unix: You can work on the Mac or use the shell to connect to a server.
- Windows computers need an ssh client like MobaXterm to connect to a Linux server.

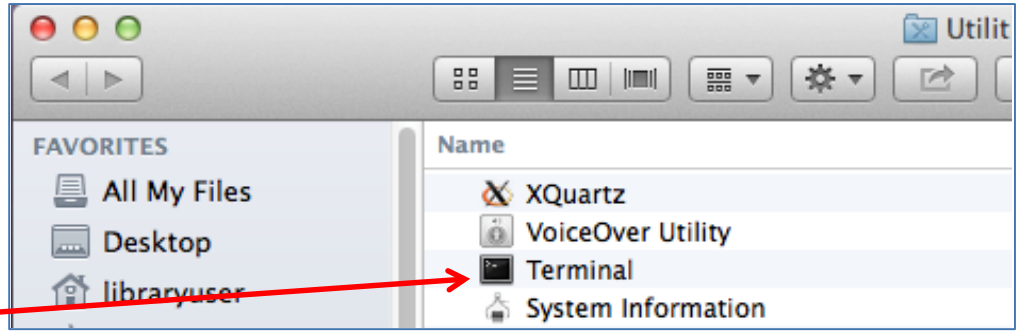
  https://mobaxterm.mobatek.net
- TAK is our Linux server. It has lots of software and databases already installed or downloaded.
- We have also access to 50 Linux serves that form our cluster.

Logging in to tak

- Requesting a tak account

  http://bioinfo.wi.mit.edu/bio/software/unix/bioinfoaccount.php
- Windows
  - MobaXterm
- Macs
  - Access through Terminal

Log in to tak for Mac



ssh –Y username@tak.wi.mit.edu

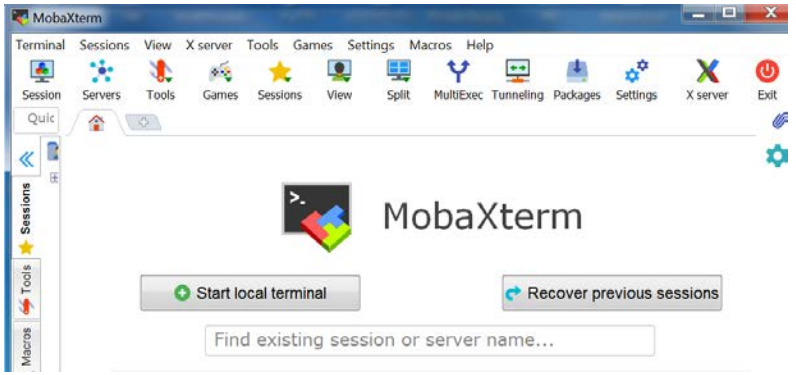
```
libraryuser — byuan@tak ~ — ssh — 79×24
Last login: Wed Oct  1 15:45:01 on ttys000
Library-Corei5-iMac-Epson:~ libraryuser$ ssh -Y byuan@tak.wi.mit.edu
  username@tak.wi.mit.edu's password:
```

```
Welcome to Ubuntu 18.04.3 LTS (GNU/Linux 4.15.0-58-generic x86_64)

 - System information as of Fri Sep 13 15:53:49 EDT 2019

  System load: 1.31              Memory usage: 7%   Processes:       597
  Usage of /:  8.0% of 438.14GB  Swap usage:   0%   Users logged in: 16

  * Find genomes at /nfs/genomes
  * Find bioinformatics datasets at /nfs/BaRC_datasets

byuan@tak ~$
```

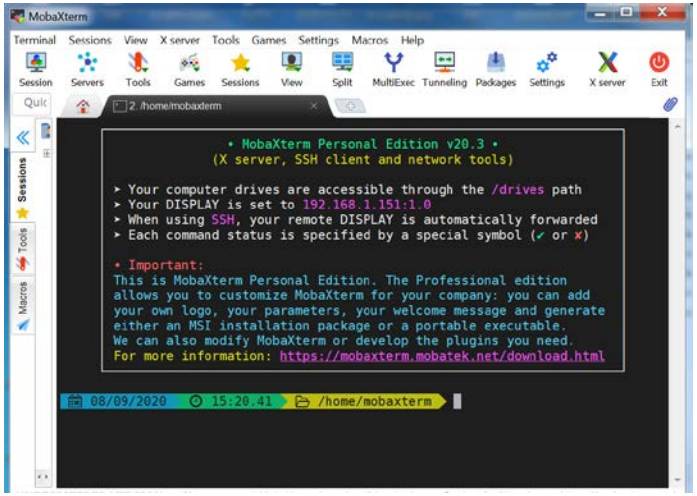
Connecting to tak from Windows

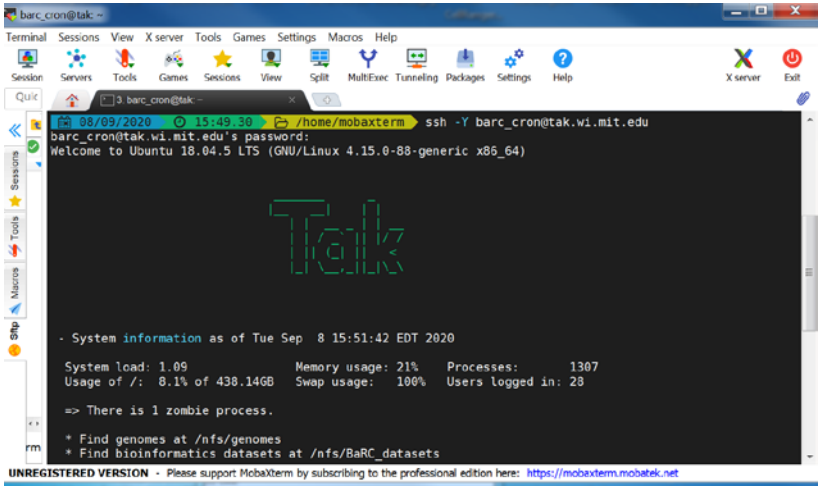
MobaXterm

1) Open MobaXterm



2) Click on the ”Start local terminal” button



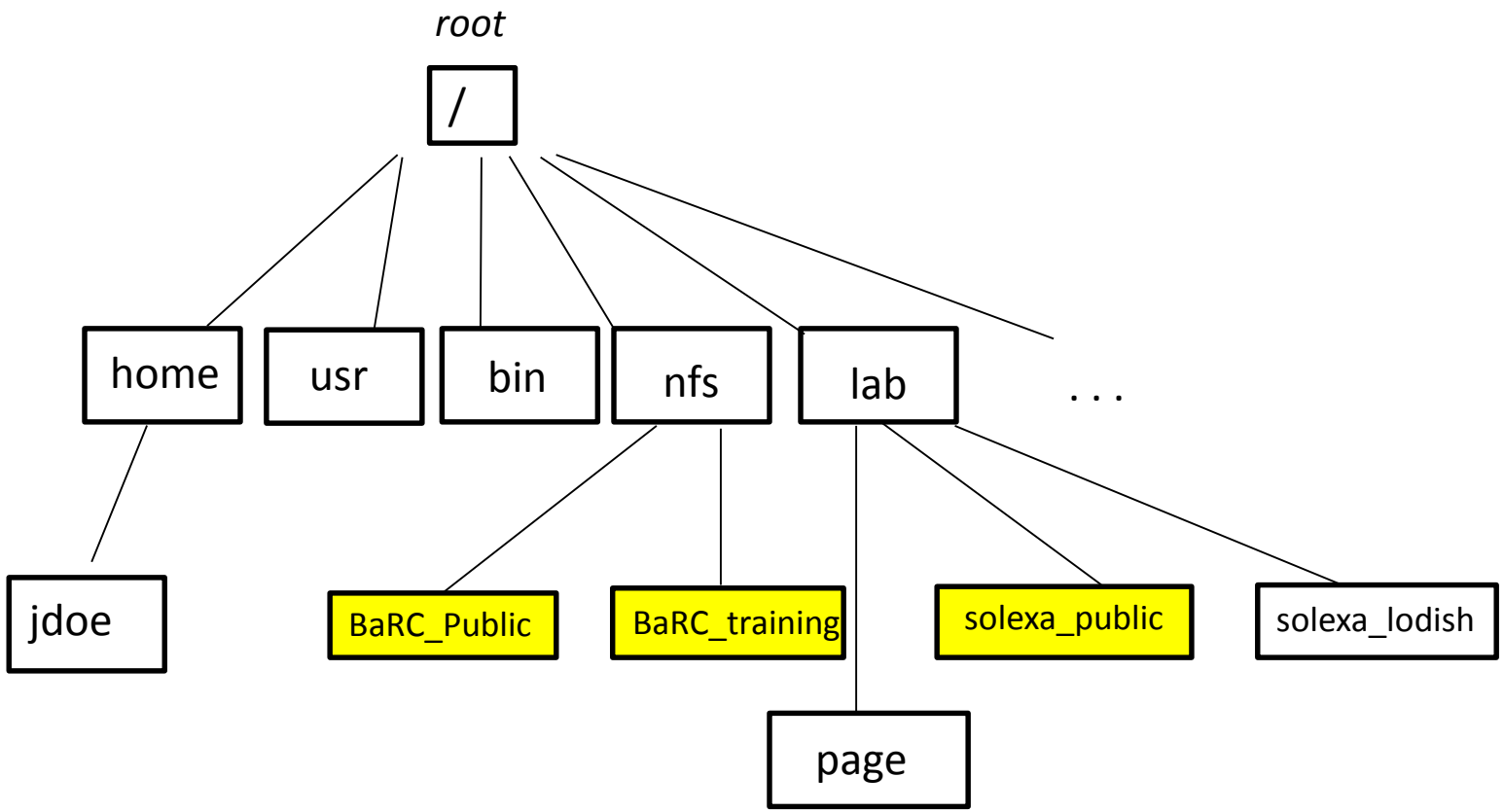


3) Type:

`ssh -Y username@tak.wi.mit.edu`

Note:
When you write the password you won’t see any characters being typed.

Unix Directory Structure



See http://www.thegeekstuff.com/2010/09/linux-file-system-structure/ for more detailed info.
nfs and lab are directories specific to Whitehead

Accessing Shared Resources at Whitehead

- Unix
  - **/nfs/BaRC_Public**
  - **/nfs/BaRC_training**
  - **/lab/solexa_public**
- Windows (access using *Start Menu → Search*)
  - **\\wi-files1\BaRC_Public**
  - **\\wi-files1\BaRC_training**
  - **\\wi-bigdata\solexa_public**
- Macs (access using *Go → Connect to Server…*)
  - **smb://wi-files1/BaRC_Public**
  - **smb://wi-files1/BaRC_training**
  - **smb://wi-bigdata/solexa_public**

Where's my lab's share?

- http://it.wi.mit.edu/systems/file-storage/lab-share-paths

Get ready for the exercises

- Use this link to copy paste the commands for the exercises

http://barc.wi.mit.edu/education/hot_topics/IntroToLinux_2021/IntroToLinux_HandsOn.txt

- These folders contain today's slides and the material for the exercises

\\wi-files1\BaRC_Public\Hot_Topics\IntroToLinux_2021

cifs://wi-files1/BaRC_Public/Hot_Topics/IntroToLinux_2021

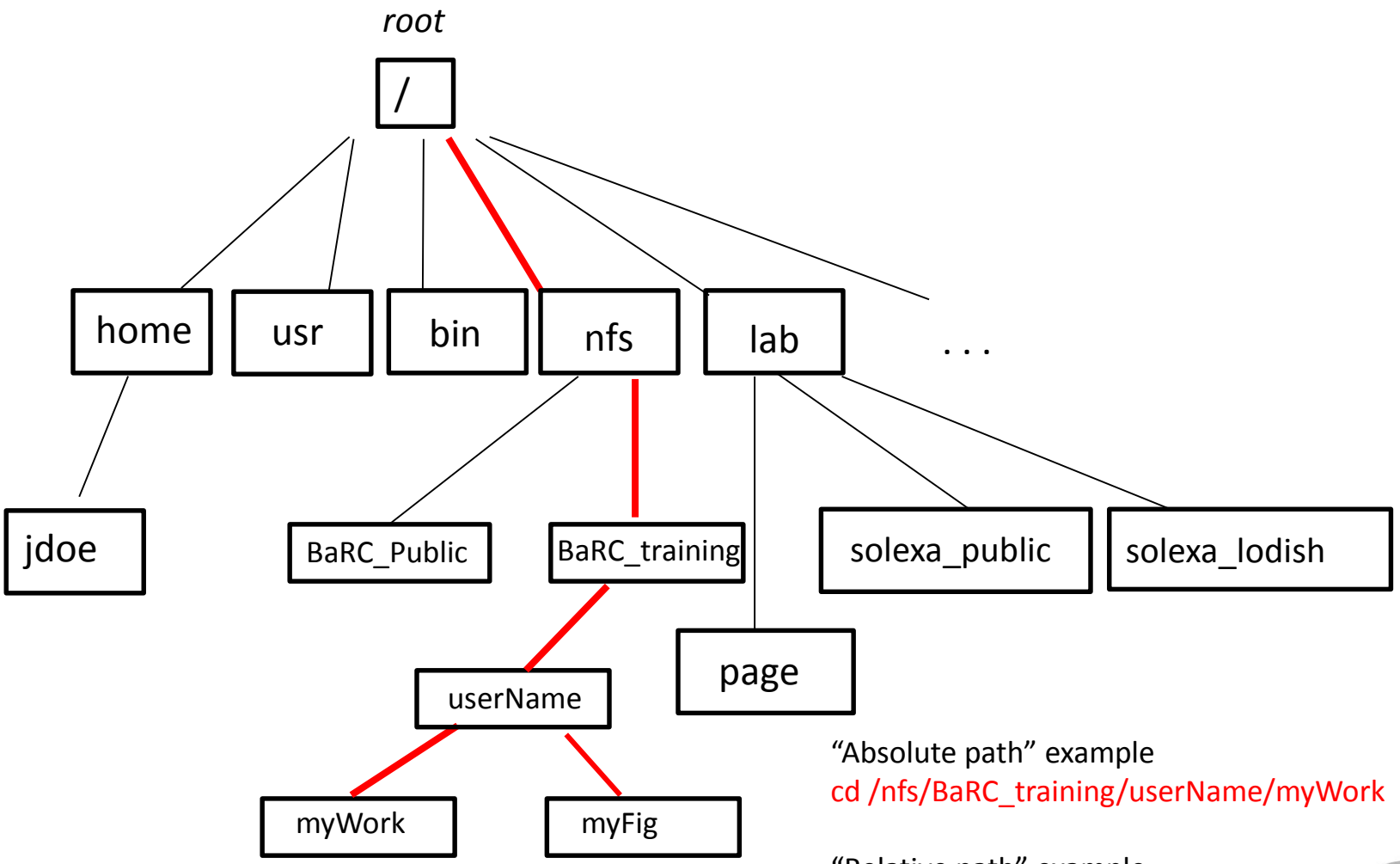
Unix/Linux Tips

- Use ↑ ↓ to reuse previous commands
- Ctrl-c: stop a process that is running
- Tab-completion:
  - Complete commands/file names
- Unix is case-sensitive

Basic commands
listing and organizing files/folders

- list the contents of a directory:
  `ls` [only show names]
  `ls -l` [long listing: show other information too]
  `ls -h` [human readable]
- make a directory: **`mkdir dirname`**
- change directory: **`cd dirname`**
- The directories . and ..
  The current directory (.) **`ls ./subfolder`**
  The parent directory (..)
  `cd ..` (go to the parent directory) **`ls ..`** (list to the parent directory)
- print working directory: **`pwd`**
- Go to your home directory: **`cd or cd ~`**
- Go to the previous directory: **`cd -`**

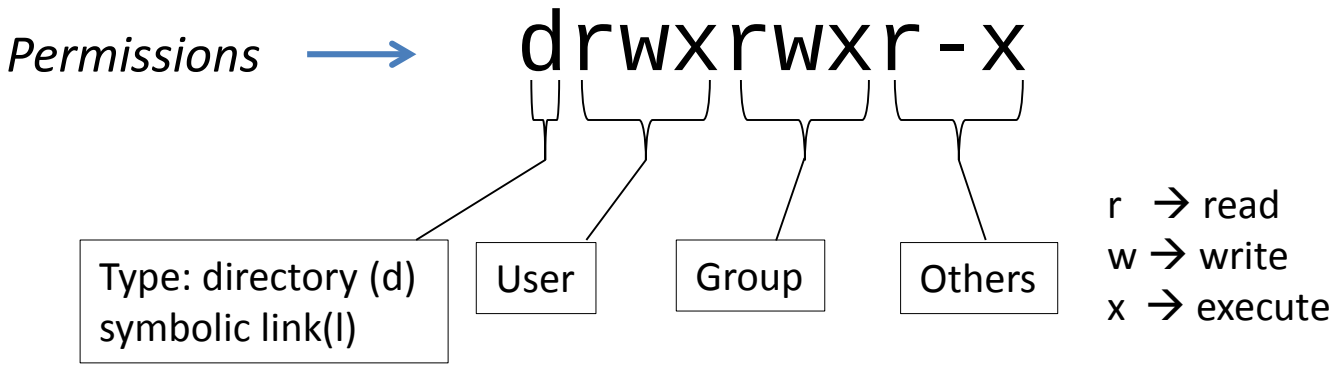
Relative and absolute paths



"Absolute path" example
cd /nfs/BaRC_training/userName/myWork

"Relative path" example
cd ../myFig

Who do you want to be able to read and/or modify your files?



- Use **chmod** to change permissions
  - user(u), group(g), others(o), all(a)
  - `chmod u+x foo.pl` (user can execute)
  - `chmod g-w foo.pl` (group can't write)

```
ls -l myFile.txt
-rw-r--r-- 1 thiruvil barc 0 2012-10-10 13:32 myFile.txt

chmod g+w myFile.txt
ls myFile.txt
-rw-rw-r-- 1 thiruvil barc 0 2012-10-10 13:32 myFile.txt
```

Basic commands
copying, moving files, getting help

- copy: cp
- move: mv
- remove: rm
- remove directory: rmdir
- get help on a command: man {command}
- Run a program in the background: &

Do Exercises 1, 2 and 3

Displaying the contents of a file on the screen

- cat filename: Dump a file to the screen
- more filename: Progressively dump a file to the screen: ENTER = one line down SPACEBAR = page down q=quit
- less filename: like more but with extended capabilities
- head filename: Show the first few lines of a file
- head -n filename: Show the first n lines of a file
- tail filename: Show the last few lines of a file
- tail -n filename: Show the last n lines of a file
- clear: clear screen

Editing a File

- Command-line editors
  - pico
  - nano
  - emacs (`emacs –nw`)
  - vi
- Graphical editors (Windows users need an X-windows emulator)

  Note: may not be part of standard installation
  - nedit
  - gedit
  - xemacs
- Put an & at the end of command line to run it in the background when using a graphical editor so that you can continue to use the terminal window

  e.g. `gedit myFile.txt&`

Output Redirection and Piping

- Write output of a command to file
  - Write to output file
    - `sort myFile.txt > myFile_sorted.txt`
  - Over-write output file (if it exists)
    - `sort myFile.txt >| myFile_sorted.txt`
  - Append to output file
    - `sort myFile.txt >> myFile_sorted.txt`

- Piping "|": use output of one command as input for another command
  - `sort myFile.txt | more`

Parsing a File: cut
Word count: wc

- Select columns of interest

```
cut –f 9,12-15 myGeneValues.txt > col_9.12to15.txt
```

Options:

-f output only these fields

-d field delimiter, default is “\t”

- Count number of lines/words/characters in file

```
wc myFile
```

wc -w (count words only)

wc -l (count lines only)

Do Exercises 4, 5, 6 and 7

Sorting and removing redundancy sort and uniq

- Sort on column(s)

```
sort -k 3,3 myGeneExpression.txt | more
```

Options:

-n, --numeric-sort compare according to string numerical value
-g, --general-numeric-sort compare according to general numerical value
-r reverse
-k pos1,pos2 start sorting at pos1, end it at pos2
-t, --field-separator=SEP use SEP instead of non-blank to blank transition

- Get only unique entries

```
uniq mySortedGenes.txt > myUniqGenes.txt
```

Options:

-c count entries
-d duplicate counts

make sure that the file is sorted before running uniq

Do Exercises 8 and 9

Searching the contents of a file

- **grep** (global regular expression print)

  Find words, or patterns, occurring in lines of a file

```
grep TMEM geneList.txt
TMEM131
TMEM9B
TMEM14C
TMEM66
TMEM49
```

Options:

-v select non-matching lines

-i ignore case

-n print line number

Example: get TMEM but exclude TMEM14C

```
grep TMEM geneList.txt | grep -v "TMEM14C" | more
```

Do Exercise 10

Getting Files

- Getting files or directories
  - Files

```
wget http://data.broadinstitute.org/igv/projects/downloads/2.4/IGVSource_2.4.2.zip
```

  - Directories from (outside) servers

```
scp –r origin destination
scp -r userName@serverToCopyFrom:/pathToFolderTocopyFrom  .
scp -r jdoe@copper.broadinstitute.org:/broad/lab/works  .
```

(Un)Compressing Files

- .gz file

  Compress: **gzip** file.txt (file.txt.gz will be created)

  Uncompress: **gunzip** file.txt.gz (file.txt will be created)

- .tar.gz file

  Compress: **tar –czvf** myFiles.tar.gz myFiles

  Uncompress: **tar –xzvf** myFiles.tar.gz

  Options
  -c create an archive
  -x extract an archive
  -f FILE name of archive
  -v be verbose, list all files being archived/extracted
  -z create/extract archive with gzip/gunzip

- View compressed files using:

  zmore, **zgrep**

Other useful commands

- Remove the end of line character introduced by programs like Excel

```
fromdos file.txt
(works for files modified on a Mac or PC)
```

- See all your commands

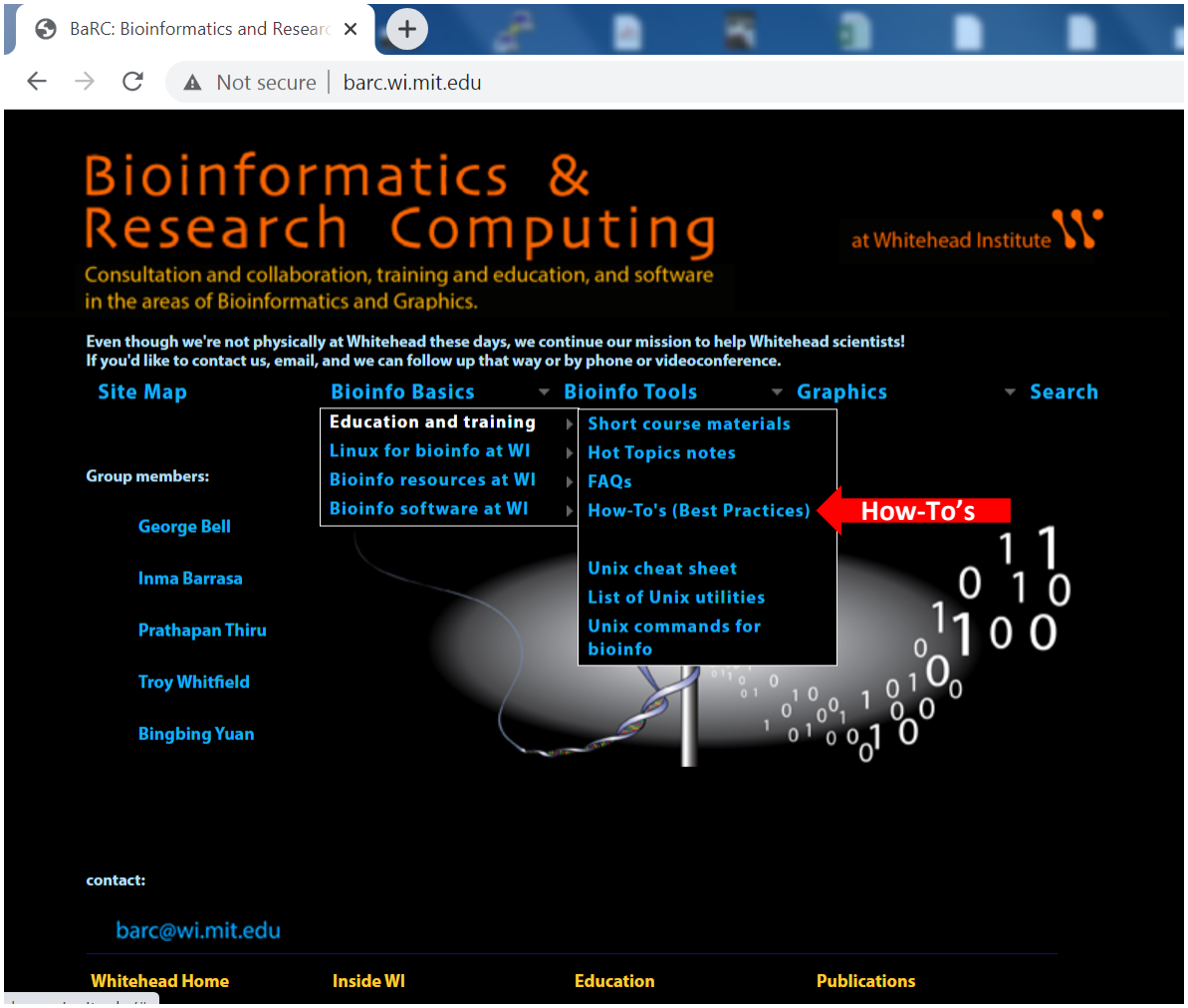
```
history
```

- See all the hidden characters on the file

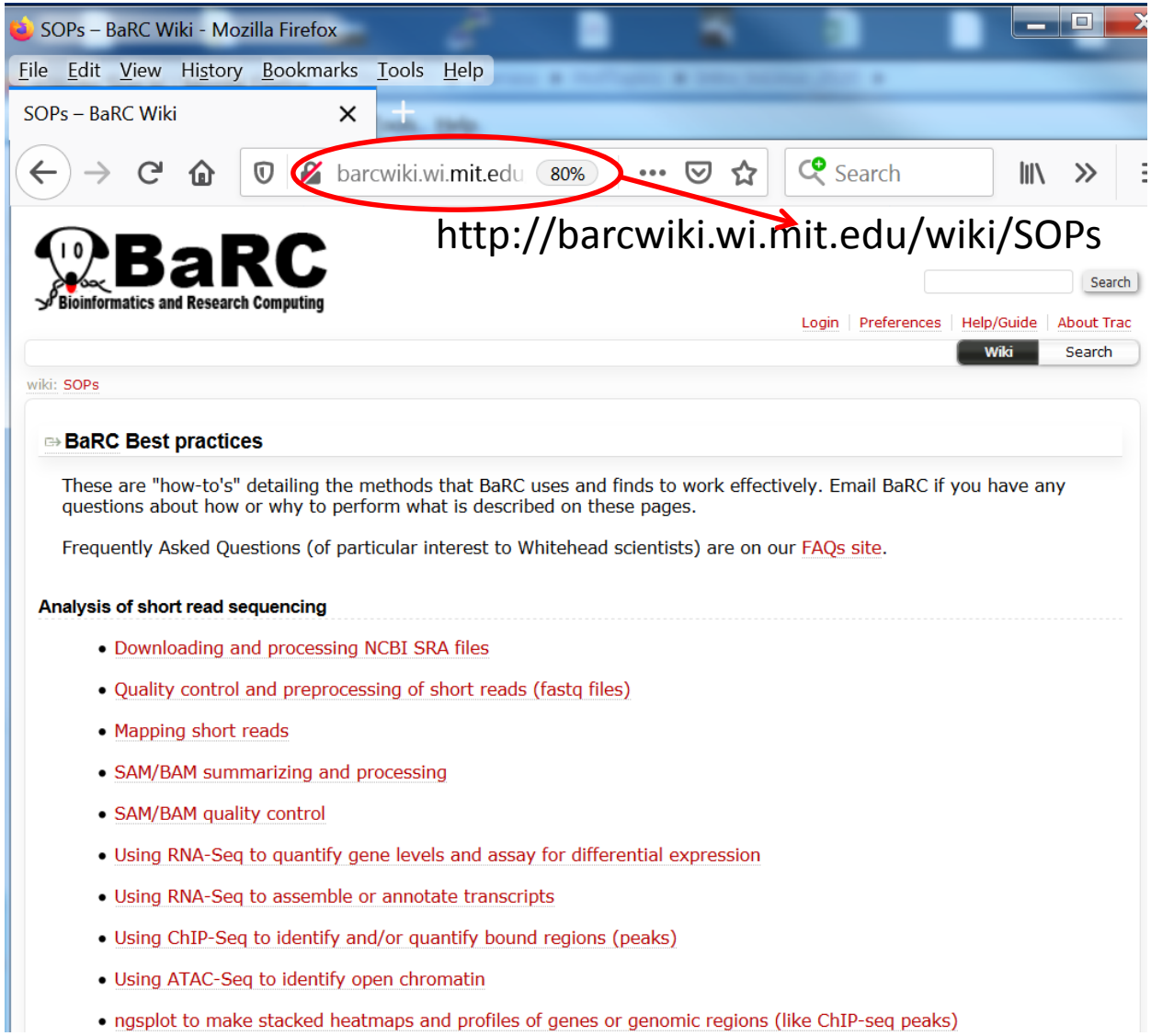
```
cat -A file.txt
```

BaRC Resources

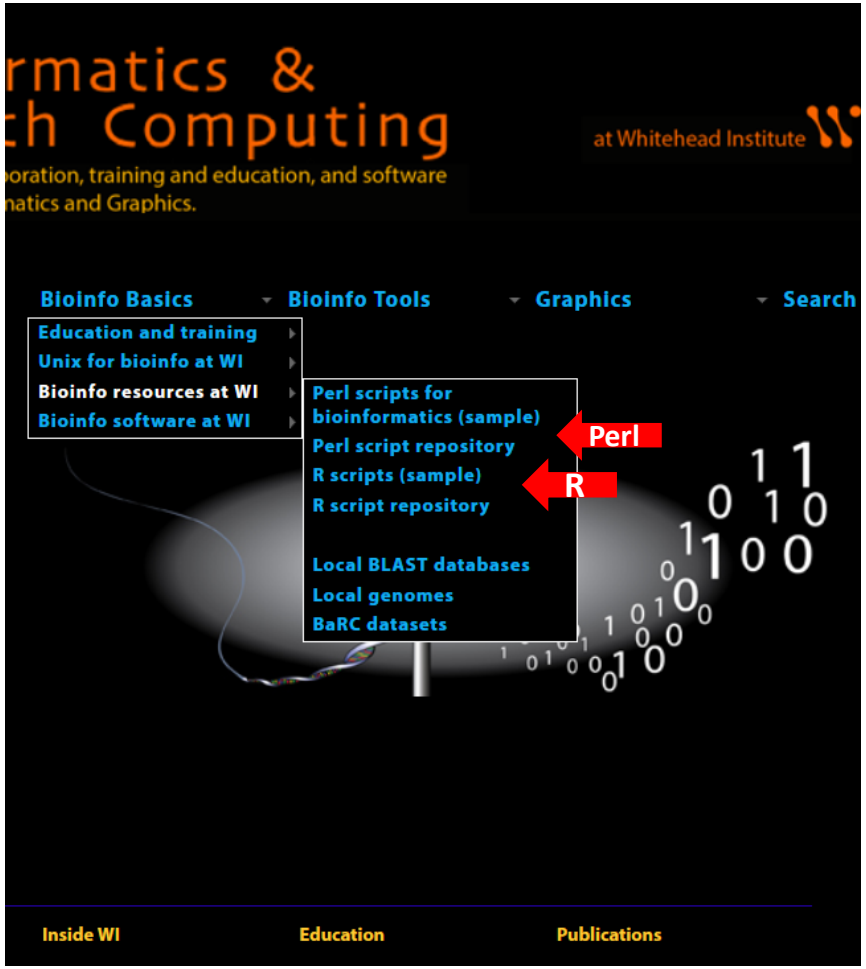
http://barc.wi.mit.edu/



BaRC Best practices



Unix Commands and BaRC Scripts



Running scripts on Unix

- Perl, R or Python scripts

  bed2gff.pl or **./bed2gff.pl** or **path/bed2gff.pl**
  run_rma_customCDF.R or **./run_rma_customCDF.R**
  myScript.py or **./myScript.py**

- Java Archive (JAR)

  java -Xmx1000m -jar /usr/local/share/IGVTools/igv.jar

- The script has to be executable to be run

  -rwxrwxr-x 1 byuan barc 2331 Mar 5 2013 bed2gff.pl

- The script that will be executed depends on the path written in front of the script name

  "bed2gff.pl": Unix looks for that script in your path
  "./bed2gff.pl": Unix looks for that script in the current folder path

BaRC code

Script type	Location
Perl	/nfs/BaRC_Public/BaRC_code/Perl
R	/nfs/BaRC_Public/BaRC_code/R
Python	/nfs/BaRC_Public/BaRC_code/Python

Commonly used data stored locally at Whitehead

Location	Description
/nfs/genomes \\wi-files1\genomes cifs://wi-files1/genomes	Genome data: gff, gtf, fasta, bowtie indexed files, blat indexed file, etc. for several organisms nfs_genomes_info.html has summary table
/nfs/seq/Data	Sequence data, including blast databases, for several organisms
/nfs/BaRC_datasets \\wi-files1\BaRC_datasets cifs://wi-files1/BaRC_datasets	BaRC_datasets.html in that folder has a summary table

Submitting jobs to the cluster
LSF Commands

- bsub to submit jobs

```
bsub wc –l reads.fq
bsub “sort foo.txt > sorted.txt”
```

Options:

-e error_file
-o standard_out_file
-m machine (send the job to that machine)
-n number (use that many processors in the cluster)
bsub -n 4 -R "span[hosts=1]“(use 4 processors all in the same machine in the cluster)

- bjobs to view your jobs

```
bjobs
```

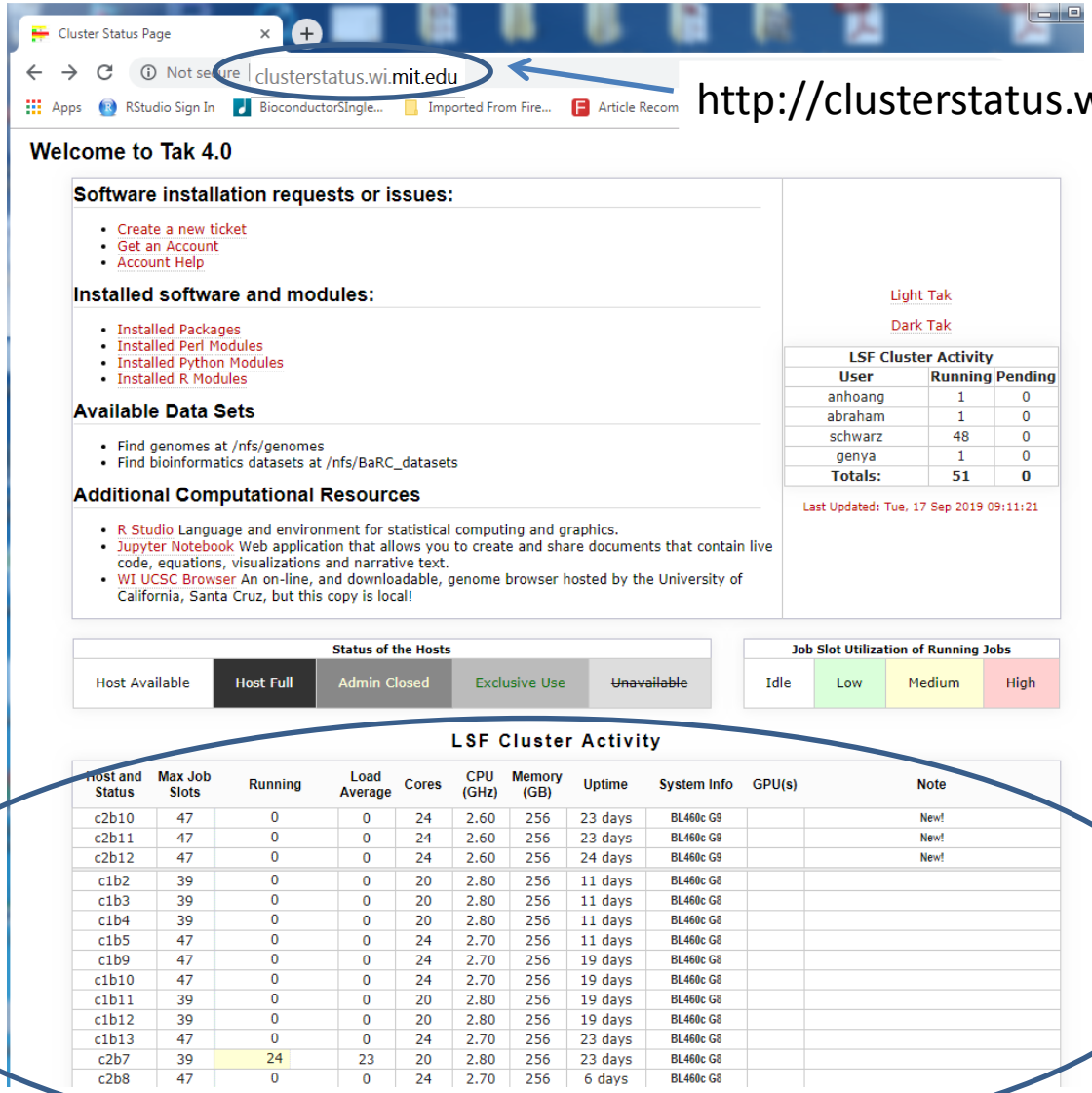
- bkill to kill a job

```
bkill 237878
```

“bkill 0” will kill all your jobs

By default the user will receive an email with the job status when the job finishes or stops

LSF Cluster Activity



Further Reading

- BaRC: Unix Info

http://bioinfo.wi.mit.edu/bio/education/unix_intro.php

http://bioinfo.wi.mit.edu/bio/bioinfo/scripts/#unix

- LSF Cluster (incl. examples)

http://bioinfo.wi.mit.edu/bio/bioinfo/docs/LSF_help.php

- Whitehead IT Computing Tutorials

http://it.wi.mit.edu/training-tutorials/computing-tutorials

Upcoming Hot Topics

- Unix: Beyond the Basics (Oct 19th)
- Python: An Introduction - November
- Python: Advanced Topics – November

http://barc.wi.mit.edu/education/hot_topics/upcoming/