Linux for Biologists – Part 1

Robert Bukowski
Institute of Biotechnology
Bioinformatics Facility
(aka Computational Biology Service Unit - **CBSU**)

http://cbsu.tc.cornell.edu/lab/doc/Linux_workshop_Part1.pdf

Topics (color-coded by session)

- Why Linux?
- Logging in to (and out of) a Linux workstation
- Terminal window tricks
- Linux directory structure
- Working with files and directories
- Working with text files
- Graphics on Linux, running persistent multiple shells
- File transfer between Linux computer and the world
- Running applications
  - Note: this will only cover the Linux aspect of running applications; the functionality and the biological aspect are covered in other workshops (past and future) –see http://cbsu.tc.cornell.edu/workshops.aspx
- Harnessing the power of multiple processors
- Basics of (shell) scripting

Why Linux?

- Majority of bioinformatics/computational biology software developed only for Linux
- Most programs are command-line (i.e., launched by entering a command in a terminal window rather than through GUI)
- While various graphical and/or web user interfaces exist (e.g., Galaxy, CyVerse Discovery Environment, ~~BioHPC Web~~), but often struggle to provide level of flexibility needed in cutting-edge research
- Versatile scripting and system tools readily available on Linux allow customization of any analysis
- Learning Linux is a good investment

Logging in to a Linux machine

You need:

- **network name** of the Linux machine (e.g., **cbsumm15.tc.cornell.edu**)
- an account, i.e., **user ID** and **password** valid on the Linux machine

- on your laptop: remote access software (typically: **ssh client, VNC client**)

ssh: Secure Shell – provides access to alphanumeric terminal
VNC: Virtual Network Connection - provides access to graphical features (Desktop, GUIs, File Manager, Firefox, …)

- Linux is a **multi-access, multi-tasking** system: multiple users may be logged in and run multiple tasks on one machine at the same time, sharing resources (CPUs, memory, disk space)
  - This is what is happening during this workshop
  - After workshop: when using our machines for real work, you reserve it all for yourself. You can chose to allow a few other users (collaborators) or not
  - Our reservation system is not a part of Linux – it is an add-on we created to better manage access of multiple users to multiple machines

Logging in from Windows PC

- Install remote access software (**PuTTy**). For details, consult http://cbsu.tc.cornell.edu/lab/doc/Remote_access.pdf

- Use **PuTTy** to open a terminal window on the reserved workstation using **ssh** protocol, configure **X11 forwarding** (if you intend to run graphical software)
  - When connecting for the first time, a window will pop out about "caching server hostkey" – answer "Yes". The window will not appear next time around
  - Adjust colors, if desired
  - Save the configuration (e.g., under the machine's name)
  - while you are typing your password, the terminal will appear frozen – this is on purpose!

- You may open several terminal windows, if needed (in PuTTy – can use "Duplicate Session" function).

Logging in from Mac (or other Linux box)

Use native **ssh client** (already there - no need to install anything)

- Launch the Mac's terminal window and type

```
ssh -Y bukowski@cbsuwrkstX.tc.cornell.edu
```

(replace the "**cbsuwrkstX"** with your reserved workstation, and "bukowski" with your own user ID). Enter the password when prompted.

  - When connecting for the first time, a message will appear about "caching server hostkey" – answer "Yes". The message will not appear next time around
  - while you are typing your password, the terminal will appear frozen – this is on purpose!

- You may open several terminal windows, if needed, and log in to the workstation from each of them.

Logging out of a Linux machine

- While in terminal window, type **exit** or **Ctrl-d** - this will close the current terminal window

How to access BioHPC machines in the future (after workshop)

BioHPC User's Guide

http://cbsu.tc.cornell.edu/lab/userguide.aspx

Slides from workshop "Introduction to BioHPC Lab"

http://cbsu.tc.cornell.edu/lab/doc/Introduction_to_BioHPC_Lab_v5.pdf

Logging in to a BioHPC Linux machine from outside of campus

Users with Cornell NetID:

1. Install VPN client from CIT site (http://www.it.cornell.edu/services/vpn/howto/index.cfm)
2. Establish a VPN connection (see the CIT site for details)
3. ssh from your laptop to your reserved BioHPC machine as if connecting from campus

All users (those with NetID can use this procedure as well):

1. ssh from your laptop to **cbsulogin.tc.cornell.edu** or **cbsulogin2.tc.cornell.edu**
2. While on **cbsulogin** (or **cbsulogin2**), ssh to your reserved BioHPC machine using the Linux/Mac procedure from previous slides

Interacting with Linux in terminal window

- User communicates with Linux machine via **commands** typed in the **terminal window**
  - Commands are interpreted by a program referred to as **shell** – an interface between Linux and the user. We will be using the shell called **bash** (another popular shell is **tcsh**).
  - Typically, each command is typed in one line and "**entered**" by hitting the **Enter** key on the keyboard.
  - Commands deal with **files** and **processes**, e.g.,
    - request information (e.g., list user's files)
    - launch a simple task (e.g., rename a file)
    - start an application (e.g., Firefox web browser, BWA aligner, IGV viewer, …)
    - stop an application
  - In this part of the workshop we'll learn mostly about file management commands

Try a few simple commands:

List files and directories (more about it in a minute):

```
ls
ls -al
```

What kind of machine am I on (name, operating system, kernel version, etc.)?

```
uname -a
```

Where on disk am I now (i.e., Print Working Directory)?

```
pwd
```

Who else is logged in? For how long?

```
w
who
```

Use **Manual Pages** to learn more about each command – see all possible **command options**

```
man ls
```

```
man uname
```

Screen output from a command may be saved to disk

Each command produces two output streams: **standard output** (STDOUT) and **standard error** (STDERR). Normally, they both are displayed on the screen.

But they can be saved on disk ("redirected")

Save to separate files (file names are arbitrary) …

```
who  > OUT.log  2> ERR.log
```

… or save to a single file

```
who >& OUTERR.log
```

These files are text files and can be looked at with any text processing tool (more about it later)

```
less OUTERR.log
cat OUTERR.log
nano OUTERR.log
```

page through the file (use **more** to page forward)
print the file on screen
open file in text editor

Useful tricks

(may not work on all ssh or VNC clients…)

- Helpful tricks to avoid excessive command typing
  - Use **copy/paste**. Any text "mouse-selected" while holding the left mouse button is copied to clipboard. It may then be pasted, e.g., into a command, by clicking the **right** mouse button (PuTTy) or the **middle** button (when working through the console in 625 Rhodes).
  - Use **Up/Down arrow keys** – this will cycle through recently executed commands.
  - Use the **TAB key** – this will often present you with a list of choices after typing a part of a command – no need to remember everything.

Useful tricks

- Helpful tricks to avoid excessive command typing

  `history` command: list all recently used commands – can copy a desired command and paste it to execute again, or refer to a command by its index

Examples:

```
history
```

(*list all remembered commands)*

```
history | less
```

(list all remembered commands page by page)

```
history | grep workdir
```

(list all remembered commands containing string "workdir")

Files and directory tree

Data and **programs** are stored in **files** on **disk storage**

Each **file** has a **name** and **directory** (a.k.a. **folder**)

directory – a logical location on disk

(directory, name) pair uniquely specifies the file

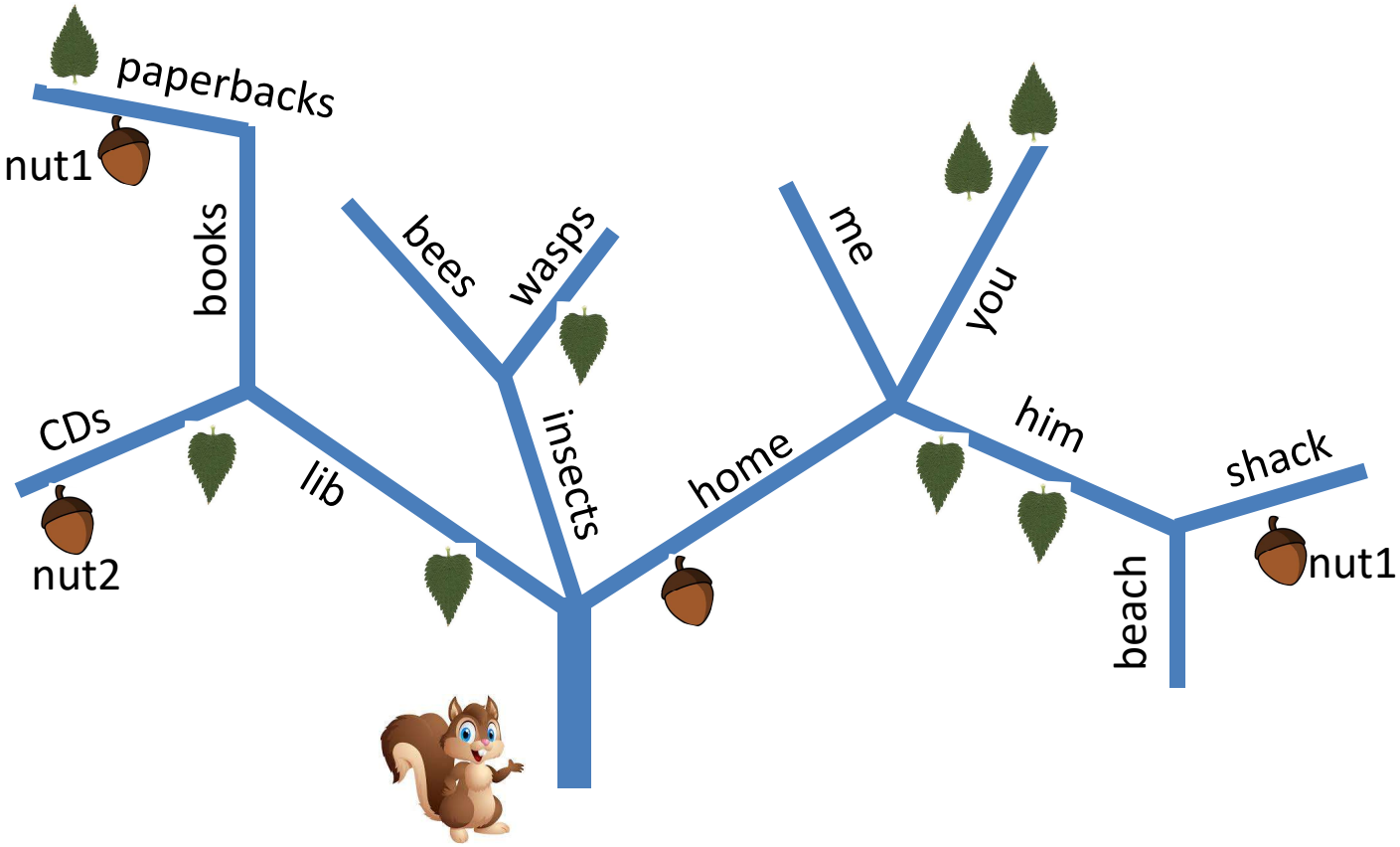
a **directory** may hold **files** and/or **other directories**

directories form tree structure

Linux directory tree

Branches = **directories**

leaves, nuts = **files**



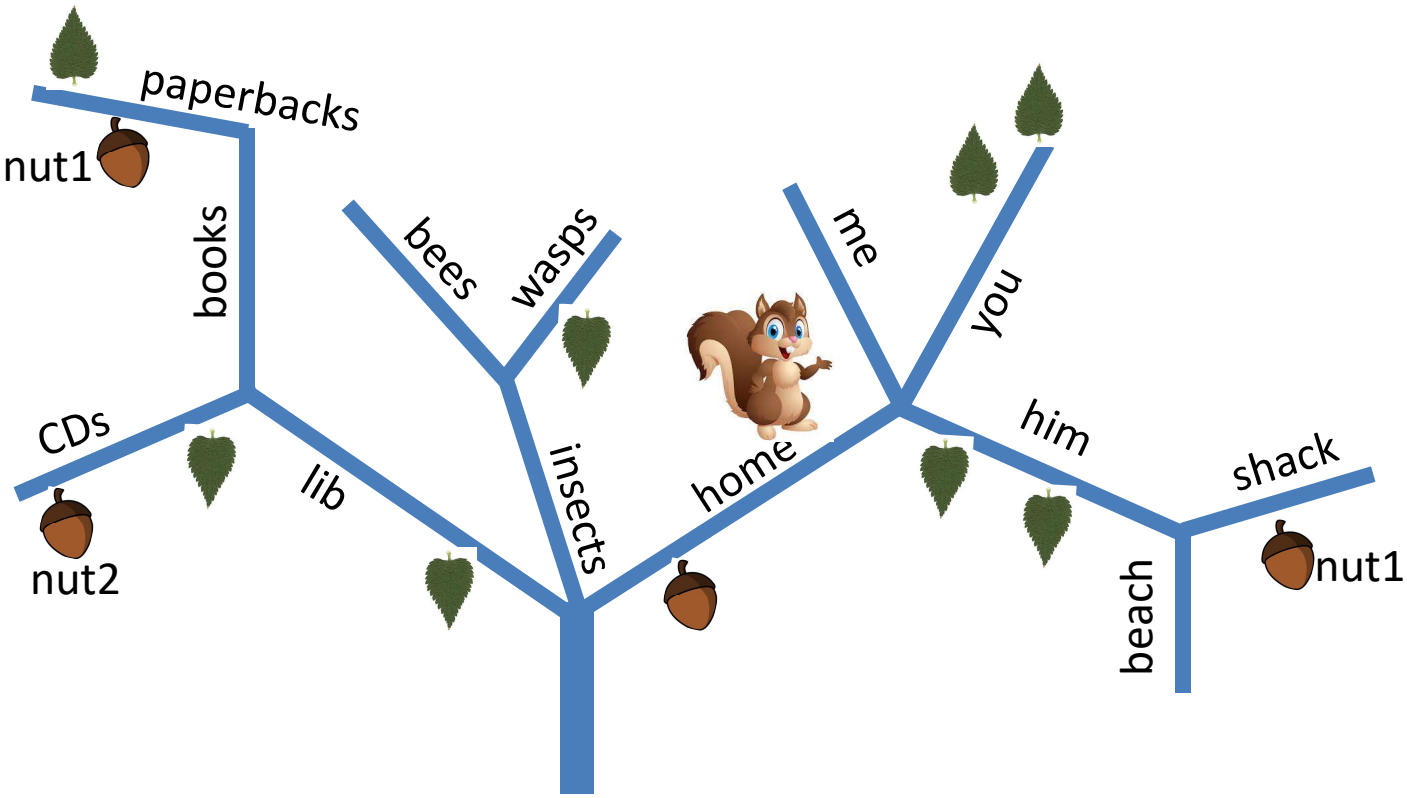
Direct squirrel to **nut1** (on the right) using commands:

`/`	get on the main trunk (referred to as **root**)
`some_name/`	from where you are, turn into branch "**`some_name`**"
`../`	return to the previous branch (closer to root)
`./`	stay where you are

Using these, direction from the ground to **`nut1`** will be:

`/home/him/shack/nut1`

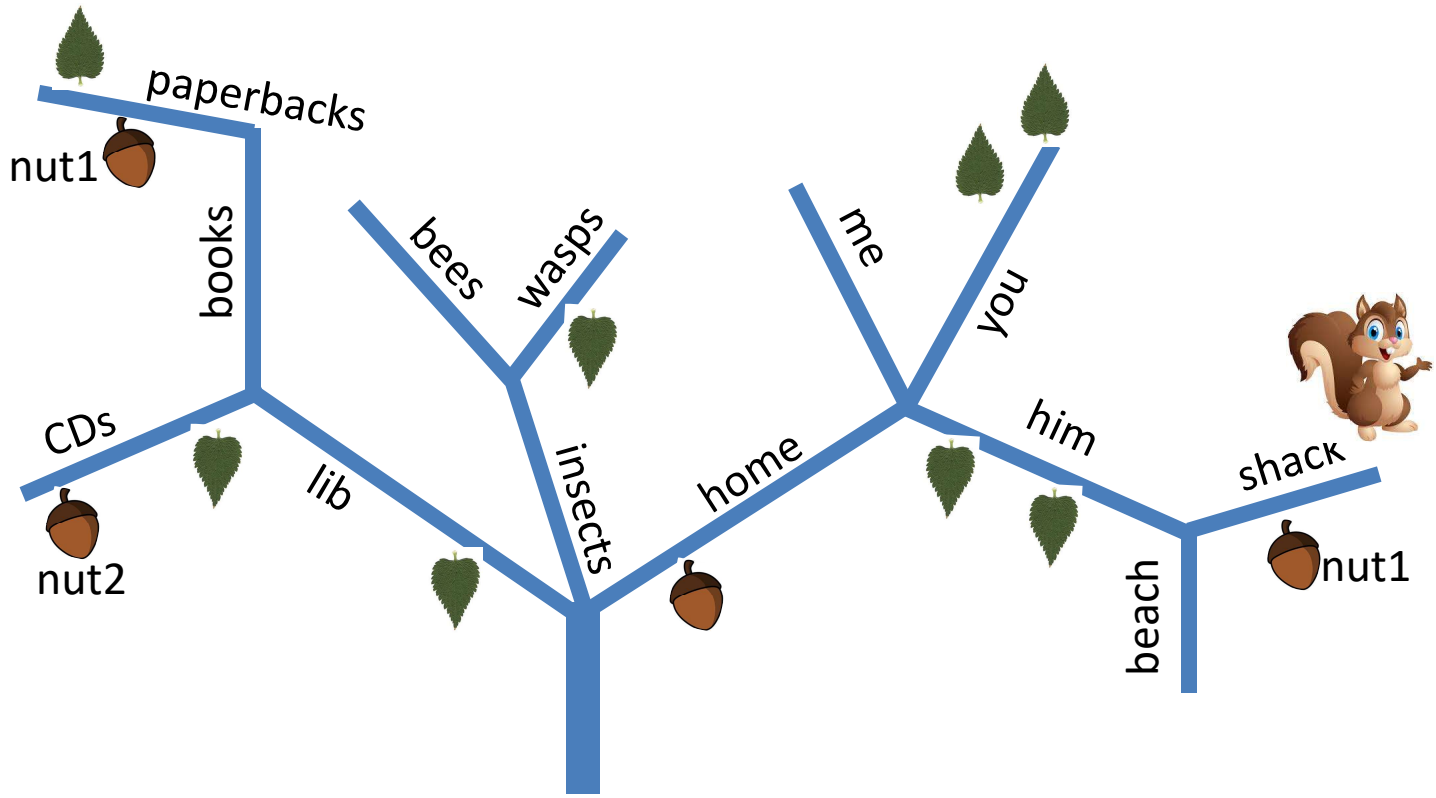
This is called **absolute path** (starting from the trunk)



Assume squirrel sitting on **`home`** rather than on the ground. We could make him jump to the ground and use the absolute path. Instead, we can simplify:

```
him/shack/nut1
```

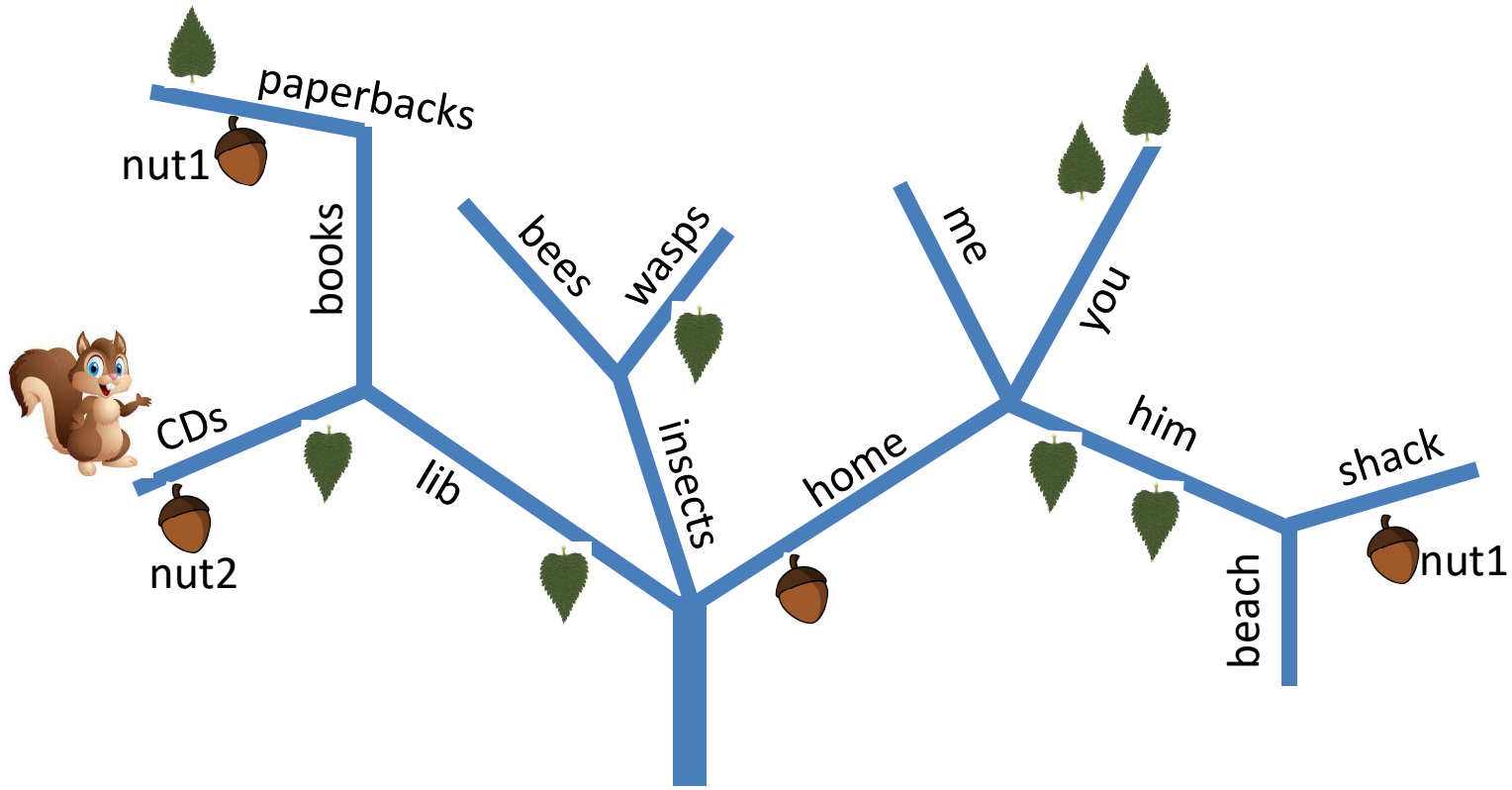
This is called **relative path** (starting from where “we are”)



Assume squirrel sitting on **`shack`**. We could make him jump to the ground and use the absolute path. Instead, we can simplify:

`nut1` or `./nut1`

This is called **relative path** (starting from where “we are”)



Assume squirrel sitting on **CDs**. We could make him jump to the ground and use the absolute path. Instead, we can simplify:

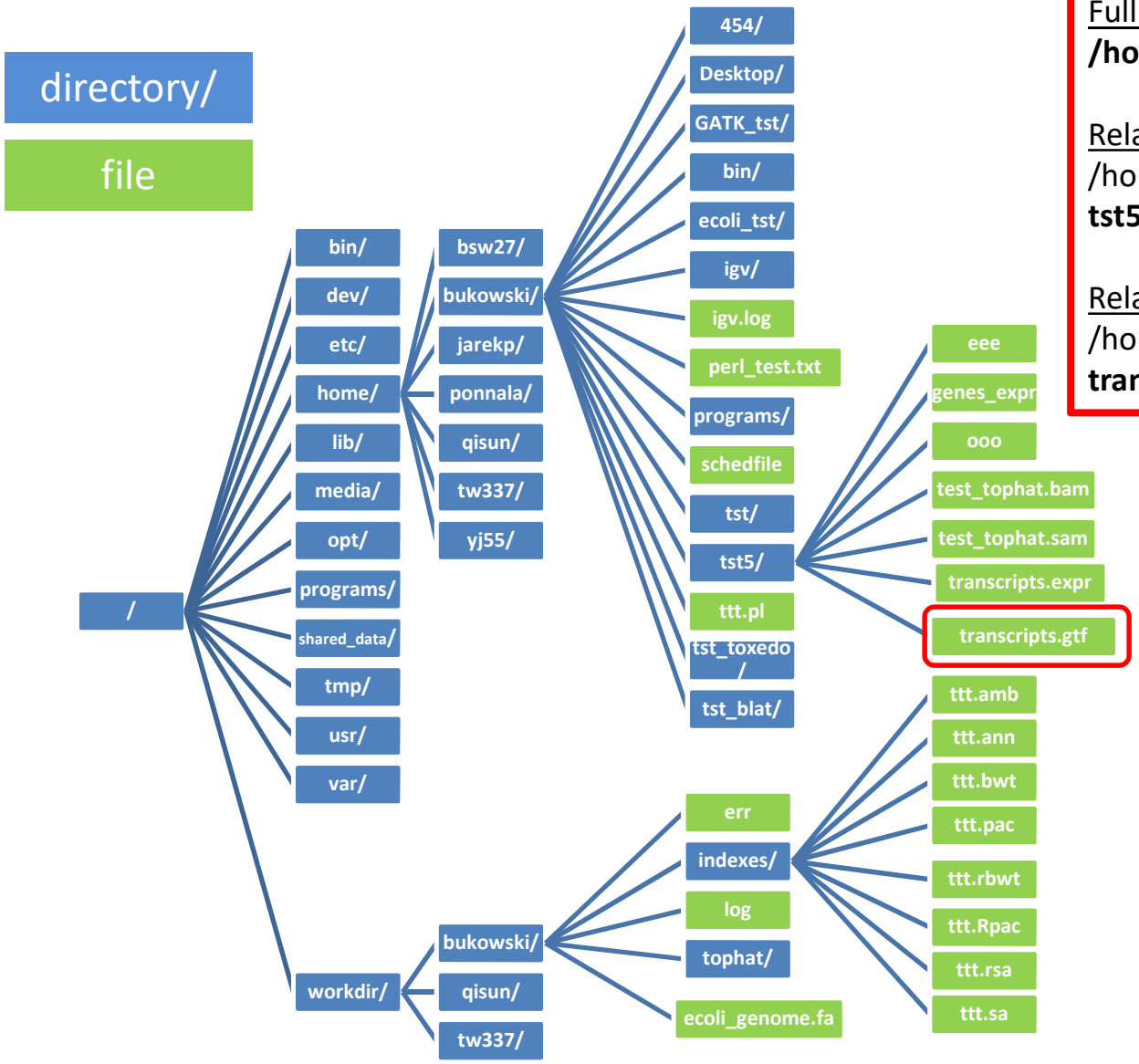
```
../../home/him/shack/nut1
```

Another example of **relative path**. Could also use, for example,

```
../../insects/bees/../wasps/../../home/me/../him/shack/nut1
```

Sounds unnecessarily long, but sometimes useful

Example of directory tree (more real)



Referring to files:

Full path:
/home/bukowski/tst5/transcripts.gtf

Relative path (i.e., relative to /home/bukowski)
tst5/transcripts.gtf

Relative path (i.e., relative to /home/bukowski/tst5)
transcripts.gtf

Storage organization at BioHPC

1 – 12 TB

/workdir
/SSD
...

/home
/programs
/shared_data

/workdir
/SSD
...

/home
/programs
/shared_data

/workdir
/SSD
...

/home
/programs
/shared_data

Network

File server
700 + 300 TB

/disk/home

/disk/programs

/disk/shared_data

Local file systems (fast, few users, temporary)

Network file systems (slow, many users, permanent)

Never process files located in network directories!

Instead:

Copy files to `/workdir` or `/SSD` and process them there. When finished, copy results back to `/home/yourID`

Storage

Linux directory structure is *continuous*, i.e. regardless of the physical location of storage it all seems to be part of one directory tree starting from root (/).

Not easy to tell which storage is local and which global just by a name. Remember the setup at BioHPC machines:

- **Networked storage**
  /home
  /shared_data
  /programs
- **Local storage**
  /workdir
  /SSD
  /local_data

Will look different on other machines or centers – always check description!

`df` command provides some insight…

… and also tells how much disk space is available on various file systems:

```
df -h
```

```
[bukowski@cbsumm05 ~]$ df -h
Filesystem                                Size  Used Avail Use% Mounted on
/dev/mapper/rhel_cbsumm05-root            200G   22G  179G  11% /
devtmpfs                                   63G     0   63G   0% /dev
tmpfs                                      63G   80K   63G   1% /dev/shm
tmpfs                                      63G   26M   63G   1% /run
tmpfs                                      63G     0   63G   0% /sys/fs/cgroup
/dev/md126p1                              871G   72M  827G   1% /SSD
/dev/mapper/rhel_cbsumm05-home            3.5T  662G  2.8T  19% /local
/dev/sda2                                 497M  124M  373M  25% /boot
cbsugfs1:/home                            553T  526T   19T  97% /glusterfs/home
128.84.3.177@tcp1:128.84.3.176@tcp1:/lustre1  141T   28T  114T  20% /home
[bukowski@cbsumm05 ~]$
```

local

local
/workdir, /local_data

networked
/home
/programs
/shared_data

These are network devices – starting with "computername:/"

Checking my disk space

How much disk space is taken by my files?

```
du -hs .
```

(displays combined size of all files in the current directory (“ . ”) and recursively in all its subdirectories)

```
du -h --max-depth=1 .
```

(as above, but sizes of each subdirectory are also displayed)

May take some time if you have a lot of small files

Traversing directory tree

Right after logging in or opening a terminal window, "you are" in your **home directory** (e.g., **`/home/bukowski`**).

Where am I?

```
pwd
```

*(**p**rint **w**orking **d**irectory) – show the **current directory**; any **relative path** you specify will be relative to this place*

Navigating through directories

```
cd
```

C**hange (current) **d**irectory; without additional arguments, this command will take you to your **home directory

```
cd /workdir/bukowski/indexes
```

***C**hange (current) **d**irectory from wherever to /workdir/bukowski/indexes.*

```
cd indexes
```

***C**hange (current) **d**irectory to indexes (will work if the current directory contains "indexes")*

```
cd ../
```

***C**hange (current) **d**irectory one level back (closer to the root)*

```
cd ../../../
```

***C**hange (current) **d**irectory three levels back (closer to the root)*

```
cd ./
```

***C**hange (current) **d**irectory to the **same one** (i.e., do nothing). Note: **./** or just **.** refers to the current directory.*

Working with Directories

Creating directories

```
mkdir /home/bukowski/my_new_dir
```

Make a new directory called "my_new_dir" in /home/bukowski

```
mkdir my_new_dir
```

Make a new directory called "my_new_dir" in the current directory

Removing directories

```
rmdir  /home/bukowski/my_new_dir
```

Remove directory called "my_new_dir" in /home/bukowski – will fail if the directory is not empty

```
rm –Rf  /home/bukowski/my_new_dir
```

Remove directory called "my_new_dir" in /home/bukowski with all its content (i.e. all files and subdirectories will be gone)

```
rm –Rf  my_new_dir
```

Remove directory called "my_new_dir" in current directory with all its content (i.e. all files and subdirectories will be gone)

Listing content (files and subdirectories) of a directory

ls

(list)

```
ls
```

List files and directories in current directory (in short) format

```
ls -al
```

List all files and directories in current directory in long format

```
ls -al /home/bukowski/tst
```

List content of /home/bukowski/tst (which does not have to be the current directory)

```
ls -alt *.txt
```

Lists all files and directories with names ending with ".txt" in the current directory, sorted according to modification time (use **ls –altr** *to sort in reverse)*

```
ls -alS
```

Lists content of the current directory sorted according to size (use **ls –alSr** *to sort in reverse)*

```
ls -al | less
```

Lists content of the current directory using pagination – useful if the file list is long (SPACE bar will take you to the next page, "q" will exit)

pipe

Output from first command is "piped" as input to the second

LOTS more options for ls – try `man ls` to see them all (may be intimidating).

Listing content of a directory

`ls -al`

```
bukowski@cbsuwrkst2:~
total 80
drwxr-xr--  5 bukowski bukowski 4096 Dec  3 11:58 454
drwxr-xr--  5 bukowski bukowski 4096 Jan  6 11:30 454_2.5.3
drwxrwxr-x  3 bukowski bukowski 4096 Jan  6 11:30 bin
drwxr-xr-x  2 bukowski bukowski 4096 Nov 22 15:55 Desktop
drwxrwxr-x  4 bukowski bukowski 4096 Jan 26 13:49 ecoli_tst
drwxrwxr-x  2 bukowski bukowski 4096 Feb 18 17:25 GATK_tst
drwxrwxr-x  3 bukowski bukowski 4096 Dec 15 11:35 igv
-rw-rw-r--  1 bukowski bukowski 3595 Jan 21 13:47 igv.log
-rw-rw-r--  1 bukowski bukowski  401 Nov 24 11:07 perl_test.txt
drwxrwxr-x 19 bukowski bukowski 4096 Feb 18 17:23 programs
-rw-rw-r--  1 bukowski bukowski  231 Dec  1 10:16 schedfile
drwxrwxr-x  2 bukowski bukowski 4096 Feb  1 11:26 stacks_tst
drwxrwxr-x  2 bukowski bukowski 4096 Dec  1 11:27 tst
drwxrwxr-x  6 bukowski bukowski 4096 Nov 29 14:22 tst2
drwxrwxr-x  8 bukowski bukowski 4096 Nov 29 15:52 tst3
drwxrwxr-x  6 bukowski bukowski 4096 Nov 29 15:41 tst4
drwxrwxr-x  2 bukowski bukowski 4096 Dec 21 15:17 tst5
drwxrwxr-x  2 bukowski bukowski 4096 Jan 17 17:14 tst_blat
drwxrwxr-x  3 bukowski bukowski 4096 Dec 22 10:56 tst_toxedo
-rwxr--r--  1 bukowski bukowski  106 Feb  2 10:08 ttt.pl
```

File permissions (“d” means this is a directory)

Owner and group

Size (in bytes) – meaningful for files, but not directories

Last modification time

File name (directories in blue, executable files in green)

Exercise 1

1. Create your temporary directory in the scratch file system **`/workdir`**
2. create a subdirectory (of that new directory), called **`mytmp`**.
3. Verify the subdirectory **`mytmp`** has been created
4. list contents of **`mytmp`**
5. remove **`mytmp`**

Working with files

There are many types of files. Here are the most important:

- **Text files** (human-readable; can be viewed and modified using a text editor)
  - Text documents (e.g., README files)
  - Data in text format (e.g., FASTA, FASTQ, VCF, …)
  - Scripts:
    - Shell scripts (usually `*.sh` or `*.csh`)
    - Perl scripts (usually `*.pl`)
    - Python scripts (usually `*.py`)
    - …

Working with files

- **Binary files** (not human-readable; cannot be viewed using a text editor)
  - Executables (e.g., samtools, bwa, bowtie, firefox)
  - Data in binary format (e.g, BAM files, index files for BWA or Bowtie, formatted BLAST databases)
  - Compressed files (usually `*.gz`, `*.zip`, `*.bz2`,…, but extensions not necessary) – often text files re-formatted to save space on disk or packaged directory trees

Working with files

There are many types of files. Here are the most important:

- **Symbolic links**: pointers to other files or directories.

```
cd /programs/bin/samtools
ls -al samtools
```

```
lrwxrwxrwx 1 root root 30 Apr 16  2013 samtools -> ../../samtools-1.2/samtools
```

In the example above, file **`/programs/bin/samtools/samtools`** is a symbolic link to **`/programs/samtools-1.2/samtools`**.

Note the "l" character in the first column of output from "**`ls -al`**".

Working with files

Where do files come from?

They are created by various programs, e.g.,

- Text editors
- File compression tools
- Aligners
- Assemblers
- …
- System commands (copy, move, rename, etc.)
- Screen output redirection (>, >&)
- Remote copy tools (scp, sftp, wget, Firefox)

Creating an empty file (zero size):

```
touch my_file
```

`my_file` is empty (so one can't say if it is a text file or binary file…)

Working with files

File and directory names – best practices

- Names are case-sensitive (**`MyFile`**, **`myfile`**, **`myFile`** are all different!)
- Use only **letters** (upper- and lower-case), **numbers** from 0 to 9, a **dot** (.), and an **underscore** (_) [good example: **`This_is_myFile99.abc`**]
- Avoid other characters, as they may have special meaning to either Linux, or to the application you are trying to run. **Do not use "space"** or other special characters [bad example: **`This is my&File#^99.abc`**]
- Use of special characters in file names is possible if absolutely necessary, but will lead to problems if done incorrectly.
- "Extensions" (like **`.zip`**, **`.gz`**, **`.ps`**,…) are commonly used to denote the type of file, but are typically not necessary to "open" a file. While working in command line terminal you always explicitly specify a program which is supposed to work with (open) this file.

Basic operations on files - summary

Listing

```
ls
ls -al
```

Copying

```
cp  <path_to_source>  <path_to_destination>
```

Moving and/or renaming

```
mv <path_to_source> <path_to_destination>
```

Deleting

```
rm <path_to_file>
```

Deleting whole directory with all its content

```
rm -Rf <path_to_directory>
```

Working with files

Copying a file

```
cp    <source file>    <destination file>
```

Examples:

```
cp sample_data.fa /workdir/bukowski/sample.fa
```

(copy file sample_data.fa from the current directory to /workdir/bukowski and give the copy a name sample.fa; destination directory must exist)

```
cp /workdir/bukowski/my_script.sh .
```

(copy file myscript.sh from /workdir/bukowski to the current directory under the same file name)

```
cp /home/bukowski/*.fastq  /workdir/bukowski
```

(copy all files with file names ending with ".fastq" from /home/bukowski to /workdir/bukowski; destination directory must exist)

```
cp -R /workdir/bukowski/tst5 /home/bukowski
```

(if tst5 is a directory, it will be copied with all its files and subdirectories to directory /home/bukowski/tst5; if /home/bukowski/tst5 did not exist, it will be created).

Try `man cp` for all options to the **cp** command.

Working with files

Moving and renaming files

```
mv <source_file>    <destination_file>
```

Examples:

```
mv my_file_one my_file_two
```

(change the name of the file my_file_one in the current directory)

```
mv my_file_one /workdir/bukowski
```

(move the file my_file_one from the current directory to /workdir/bukowski without changing file name; the file will be removed from the current directory)

```
mv /workdir/bukowski/my_file_two ./my_file_three
```

(move the file my_file_two from /workdir/bukowski to the current directory changing the name to my_file_three; the file will be removed from /workdir/bukowski)

Try `man mv` for all options to the **`mv`** command….

Working with files

Removing (deleting) files

```
rm    <file_name>
```

Examples:

```
rm my_file_one
```
(delete file my_file_one from the current directory)

```
rm /workdir/bukowski/my_file_two
```
(delete file my_file_two from directory /workdir/bukowski)

```
rm -Rf ./tst5
```
(if tst5 is a subdirectory in the current directory, it will be removed with all its files and directories)

Try `man rm` for all options to the **`rm`** command….

Working with files

What kind of file is this?

Since there are no strict naming conventions for various file types, it is not always clear what kind of file we deal with. When in doubt, try the `file` command:

```
cd  /programs/samtools-0.1.11
file samtools
```

this is an executable program….

```
samtools: ELF 64-bit LSB executable, AMD x86-64, version 1
(SYSV), for GNU/Linux 2.6.9, dynamically linked (uses shared
libs), for GNU/Linux 2.6.9, not stripped
```

… which uses "shared" libraries", i.e., may not work if moved to other machine where these libraries are absent

Working with files

Looking for a file

```
find . -name  PHG47_sorted.bam -print
```

(look for all files called **`PHG47_sorted.bam`** *in the current directory and recursively in all its subdirectories)*

```
find /data1 -name "*PHG47*" -print
```

*(look for all files having "***`PHG47`***" in the name, located in /data1 or recursively in its subdirectories)*

Try `man find` for many more options

Working with files: archiving and compression

To save disk space, we can **compress** large files if we do not intend to use them for a while. Files downloaded from the web are typically compressed and sometimes need to be uncompressed before processing can take place.

Common compressed formats and compression/decompression tools:

Format (extension)	Tool	Function
gz	gzip	Compress a single file
bz2	bzip2	Compress a single file
zip	zip	Make compressed archive (single file) of a directory structure; same as on Windows
tar	tar	Make an archive (single file) of a directory structure
tgz (tar.gz)	tar	Make a compressed archive (single file) of a directory structure

Compression works best (i.e., saves most disk space) for text files (e.g., large FASTQ files).

Getting help about compression tools:

- `gzip -h, bzip2 --help, zip, tar --help`
- `man gzip, man bzip2, man zip, man tar` (may be intimidating…)

File compression: examples

- **gzip (gz)**

```
gzip my_file
```

(compresses file my_file*, producing its compressed version,* `my_file.gz`*)*

```
gzip -d my_file.gz
```

(decompress my_file.gz*, producing its original version* `my_file`*)*

- **bzip2**

```
bzip2 my_file
```

(compresses file my_file*, producing its compressed version,* `my_file.bz2`*)*

```
bunzip2 my_file.bz2
```

(decompress my_file.bz2*, producing its original version* `my_file`*)*

Archiving and compression: examples

- **zip**

```
zip  my_file.zip  my_file1  my_file2  my_file3
```

(create a compressed archive called my_files.zip*, containing three files:* my_file1, my_file2, my_file3*)*

```
zip -r my_file.zip  my_file1  my_dir
```

(if my_dir *is a directory, create an archive* my_file.zip *containing the file* my_file1 *and the directory* my_dir *with all its content)*

```
zip -l my_file.zip
```

(list contents of the zip archive my_file.zip*)*

```
unzip my_files.zip
```

(decompress the archive into the constituent files and directories

Archiving with tar: examples

- **tar**

```
tar -cvf  my_file.tar  my_file1  my_file2  my_dir
```

(create a compressed archive called my_files.tar*, containing files* my_file1, my_file2 *and the directory* my_dir *with all its content)*

```
tar -tvf   my_file.tar
```

(list contents of the tar archive my_file.tar*)*

```
tar -xvf  my_files.tar
```

(decompress the archive into the constituent files and directories)

Archiving and compression with tar: examples

- **tgz** (also, tar.gz – essentially a combo of “tar” and “gzip”)

```
tar -czvf my_file.tgz  my_file1  my_file2  my_dir
```

(create a compressed archive called my_files.tgz*, containing files* my_file1, my_file2 *and the directory* my_dir *with all its content)*

```
tar -tzvf my_file.tgz
```

(list contents of the tar archive my_file.tar*)*

```
tar -xzvf my_files.tgz
```

(decompress the archive into the constituent files and directories)

Exercise 2

1. If not yet present, create directory **`/workdir/your_id`** (replace **`your_id`** by your real userID).
2. Copy the file **`examples.tgz`** located in **`/shared_data/Linux_workshop`** to your temporary directory
3. Unpack the file **`examples.tgz`** and list the resulting files and directories
4. Check the type of each file (hint use the **`file`** command)
5. Create a new directory in **`/workdir/your_id`**, called **`sequences`**
6. Move the files **`flygenome.fa`** and **`short_reads.fastq`** to directory sequences
7. Create a new directory in **`/workdir/your_id`**, called **`shellscripts`**
8. Move all shell scripts (i.e., all files with names ending with "**`.sh`**") from directory **`scripts`** to the newly created directory **`shellscripts`**
9. Remove the directory **`scripts`**

Working with text files

Linux features standard tools for text file processing:

Function	tool
Text editing	**vi, nano, gedit, …**
Page through the file	**less, more**
Select lines from top, bottom, or middle of file	**head, tail**
Select lines containing a string	**grep**
Select columns	**cut**
Append rows to a file	**cat**
Append columns to a file	**paste**
Sort a file over column(s)	**sort**
Count lines, words, characters	**wc**
Advanced, text-focused scripting tools	**awk, sed**
General scripting tools (not only in Linux)	**perl, python**

Working with text files: editors

vim

- Available on all UNIX-like systems (Linux included), i.e., also on BioHPC workstations (type **vi** or **vi file_name**)
- Free Windows implementation available (once you learn vi, you can just use one editor everywhere)
- Runs locally on Linux machine (no network transfers)
- User interface rather peculiar (no nice buttons to click, need to remember quite a few keyboard commands instead)
- Some love it, some hate it

nano

- Available on most Linux machines (our workstations included; type **nano** or **nano file_name**)
- Intuitive user interface. Keyboard commands-driven, but help always displayed on bottom bar (unlike in vi).
- Runs locally on Linux machine (no network transfers during editing)

gedit (installed on BioHPC workstations; just type **gedit** or **gedit file_name** to invoke)

- X-windows application – need to have X-manager running on client PC.
- May be slow on slow networks…

edit+ (http://www.editplus.com/)

- Commercial product
- Runs on a local machine (laptop) and transfers data to/from Linux workstation as needed
- Can browse Linux directories in a Windows-like file explorer
- May be slow on slow networks
- Some people swear by it

vi basics

Opening a file:

vi my_reads.fastq (open the file my_reads.fastq in the current directory for editing; if the file does not exist, it will be created)

Command mode: typing will issue commands to the editor (rather than change text itself)
Edit mode: typing will enter/change text in the document

<Esc> exit edit mode and enter command mode (this is the most important key – use it whenever you are lost)

The following commands will **take you to edit mode**:

i enter insert mode
r single replace
R multiple replace
a move one character right and enter insert mode
o start a new line under current line
O start a new line above the current line

The following commands **operate in command mode (hit <Esc> before using them)**

x delete one character at cursor position
dd delete the current line
G go to end of file
1G go to beginning of file
154G go to line 154
$ go to end of line
1 go to beginning of line
:q! exit without saving
:w save (but not exit)
:wq! save and exit

Arrow keys: move cursor around (in both modes)

Working with text files

Viewing text files

```
less README.txt
```

(display the content of the file README.txt in the current directory dividing the file into pages; press SPACE bar to go to the next page or use up/down arrows)

```
head -100 my_reads.fastq
```

(display first 100 lines of the file my_reads.fastq in the current directory)

```
tail -100 my_reads.fastq
```

(display last 100 lines of the file my_reads.fastq in the current directory)

pipe
Output from first command is "piped" as input to the second

```
tail -1000 my_reads.fastq | less
```

(extract the last 1000 lines of the file my_reads.fastq and display them page by page)

```
head -1000 my_reads.fastq | tail -100
```

(display lines 901 through 1000 of the file my_reads.fastq). Note the **"|"** character: it pipes the output from one command as input to another

```
cat my_reads.fastq
```

(print the file on screen)

```
cat my_reads.fastq >> reads_all
```

(append a file to the end of another)

```
wc  my_reads.fastq
```

(display the number of lines, words, and characters in a file)

Working with text files

Looking for a string in a text file:

```
grep "Error: lane" calc.log
```

(display all lines of the file **`calc.log`** *in the current directory which contain the string "Error: lane")*

Looking for a string in a group of text files:

```
grep "Error: lane"  *.out
```

(display all files **`*.out`** *in the current directory which contain the string "Error: lane"; also display the lines containing that string)*

Looking for lines which do **not** contain a string (ignore case)

```
grep -i -v "some STring" my_file
```

Look for lines containing "AAA" surrounded by TABs

```
grep -P  "\tAAA\t"  my_file
```

cut/paste examples

File1

```
a b c
g h i
d e f
j k l
```

File2

```
 1  2  3
 7  8  9
 4  5  6
10 11 12
```

TAB-delimited files

```
cut -f 1,3 File1
```

```
a c
g i
d f
j l
```

```
cut -f 1 --complement File1
```

```
b c
h i
e f
k l
```

```
paste File1 File2
```

```
a b c  1  2  3
g h i  7  8  9
d e f  4  5  6
j k l 10 11 12
```

"**-**" means that the second file is to be read from **STDIN** (passed on through **pipe** "**|**")

```
cut -f 1,3 File1 | paste File2 -
```

```
 1  2  3 a c
 7  8  9 g i
 4  5  6 d f
10 11 12 j l
```

`sort` command

Let **`File`** contain a TAB- or space-delimited table

```
sort File
```

(sort **`File`** *alphabetically over whole rows)*

```
sort -k 2,2 -k 3,3n  -k 5,5nr  File  > new_File
```

(sort **`File`** *alphabetically over column 2, then numerically from small to large over column 3, and then numerically from large to small over column 5; write result to file* **`new_File`***)*

```
sort -u File
```

(sort **`File`** *keeping only unique rows)*

See `man sort` for lot's more information

Working with text files

Files transferred **to Linux machine from a Windows or Mac machine** often have line endings incompatible with Linux (depends on transfer software used and its settings)

To fix line endings, use **`dos2unix`** command

```
dos2unix my_file
```

```
mac2unix my_file
```

(the file **`my_file`** *will have linux line endings)*

```
dos2unix -n my_file my_file_converted
```

```
mac2unix -n my_file  my_file_converted
```

(the file **`my_file_converted`** *will have linux line endings, the original file* **`my_file`** *will be kept)*

Working with text files

NOTE: Text files prepared using advanced text processors (e.g., MS Word) will cause problems when used as input to Linux applications.

If you have to use such files on Linux – always save as "**Plain Text**"

File permissions

```
drwxrwxr-x  16 root    ak735_0001 16384 Feb 18 11:38 .
drwxr-xr-x 549 root    root       73728 Feb 24 16:55 ..
drwx------  12 aab227  aab227     16384 Feb 26 09:35 aab227
drwx------   8 ajs592  ajs592     12382 Jan 13 10:00 ajs592
drwx------   7 ak735   ak735      12371 Oct  4 17:29 ak735
-rw-rw-r--   1 am2472  am2472        10 Feb  7 10:23 am2472
drwx------   8 as2847  as2847     16384 Nov  8 10:11 as2847
drwxrwxr-x   3 as2847  ak735_0001  8238 Dec  5 16:18 data
drwx------  16 dc584   dc584      36864 Feb 21 08:33 dc584
drwx------  25 fg237   fg237      16384 Feb 11 12:42 fg237
drwx------  20 lda42   lda42      16384 Feb 18 10:31 lda42
drwx------   5 lm529   lm529       8363 Oct  4 21:45 lm529
-rwx------   1 root    root          60 Jun 17  2013 mvd
drwx------   6 nrd44   nrd44       8400 Feb 17 11:39 nrd44
drwx------   6 rb565   rb565      12364 Oct  4 21:46 rb565
```

d r w x r w x r w x: User (owner), Group, Others

"d": directory (or "-" if file); "r": read permission; "w": write permission; "x": execute permission (or permission to "cd" if it is a directory); "-": no permission

Examples:

`data`:

- is a directory ("d" in the first column)
- everybody can read and "cd" to it, but not write ("`r-x`" in the last three columns)
- owner (**`as2847`**) and everybody in the group (**`ak735_0001`**) can also write to it

`am2472`:

- is a file readable by everybody and writable by owner and his group
- the file is not executable by anyone

`rb565`:

- is a directory accessible only by owner

Changing file permissions

chmod command – some examples

```
chmod  o-rwx /home/bukowski
```

make my home directory inaccessible to others ("o")

```
chmod  ug+x  my script.pl
```

make the file my_script.pl (in the current directory) executable by the owner ("u") and the members of the group ("g").

```
chmod  a-w /workdir/bukowski/my_file
```

deny all ("a"), including the owner, the right to write to the file my_file *(in* /workdir/bukowski*) – will prevent accidental deletion*

Try **man chmod** for more information (may be somewhat intimidating!)

Want to make your files accessible to some (but not all) other users? Contact us!

- we would need to make sure that you and those other users are in the same user groups

Exercise 3

Among the files used in Exercise 2, there is a file **`ZmB73_5b_FGS.gff`**, describing gene annotations in maize. The file is TAB-delimited (check this!) with following columns:

1. Chromosome
2. Source
3. Feature
4. Start position
5. End position
6. Score
7. Strand
8. Frame
9. Attribute

Tasks:

Look into the file to examine its structure (use **`more`**,**`cat`** or a text editor)

Create a new file, containing only **gene** features, with columns 9, 1, 4, and 5 (in this order)

Sort this new file over **Chromosome** and **End position**

Examine the sorted file in a text editor

Appendix

Exercise 1: solution

```
cd /workdir

pwd

mkdir my_id
```

(replace **my_id** with your own userID)

```
ls -al

mkdir my_id/mytmp

ls  -al

ls -al mytmp

rmdir mytmp
```

Exercise 2: solution

```
cd /workdir

mkdir bukowski

cd bukowski

cp /shared_data/Linux_workshop/examples.tgz .

tar -xzvf examples.tgz

ls -al

ls -al scripts

file * scripts/*

mkdir sequences

mv flygenome.fa short_reads.fastq sequences

mkdir shellscripts

mv scripts/*.sh shellscripts

ls -al shellscripts

rm -Rf scripts
```

Exercise 3: solution

Extract the genic lines to a temporary file

```
grep -P "\tgene\t"  ZmB73_5b_FGS.gff > tmp_gene
```

Extract the last column to another temporary file

```
cut –f 9 tmp_gene > tmp_gene_attr
```

Get columns 1,4,5 and paste them to the right or column 9

```
cut -f 1,4,5 tmp_gene | paste tmp_gene_attr - > final_file
```

Sort the file obtained above

```
sort –k 2,2 –k 4,4n final_file > final_file_sorted
```

Remove the temporary files

```
rm  tmp_gene  tmp_gene_attr  final_file
```

Examine the final sorted file

```
vi final_file_sorted
nano final_file_sorted
```

…