00-Basic-Linux-Commands

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1 Basic Linux Commands

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1.1 What Is Linux?

An operating system (OS), in its most general sense, is software that allows a user to run other applications on a computing device. An Operating is made of many components, but its two prime components are:

- Kernel
- Shell

Linux is an operating system's kernel. You might have heard of UNIX. Well, Linux is a UNIX clone. But it was actually created by Linus Torvalds from Scratch. Linux is free and open-source, that means that you can simply change anything in Linux and redistribute it in your own name! There are several Linux Distributions, commonly called "distros".

- Ubuntu Linux
- Red Hat Enterprise Linux
- Linux Mint
- Debian
- Fedora

Linux Shell or "Terminal"

Basically, a shell is a program that receives commands from the user and gives it to the OS to process, and it shows the output. Linux's shell is its main part. Its distros come in GUI (graphical user interface), but basically, Linux has a CLI (command line interface).

A *shell* in a Linux operating system takes input from you in the form of commands, processes it, and then gives an output. It is the interface through which a user works on the programs, commands, and scripts. A shell is accessed by a terminal which runs it. A *terminal* is a program you run that gives you access to the shell. There are many different terminal programs that vary across operating systems.

There are many reasons to learn about the shell. The most important reasons are that:

1. It is very common to encounter the shell and command-line-interfaces in scientific computing, so you will probably have to learn it eventually

2. The shell is a really powerful way of interacting with your computer. GUIs and the shell are complementary - by knowing both you will greatly expand the range of tasks you can accomplish with your computer. You will also be able to perform many tasks more efficiently.

The shell is just a program and there are many different shell programs that have been developed. The most common shell (and the one we will use) is called the Bourne-Again SHell (bash). Even if bash is not the default shell, it is usually installed on most systems and can be started by typing bash in the terminal. Many commands, especially a lot of the basic ones, work across the various shells but many things are different. I recommend sticking with bash and learning it well. (Here is a link for more information)

In this tutorial, we are going to cover the basic commands that we use in the shell of Linux.

1.2 Let's get started-Basic Commands

To open the terminal, press Ctrl+Alt+T

1.3 The Example: Manipulating Experimental Data Files

We will spend most of our time learning about the basics of the shell by manipulating some experimental data from a hearing test. To get the data for this test, you will need internet access. Just enter the command:

```
git clone https://github.com/gabayae/the-shell.git InPy
```

Followed by:

cd InPy

These 2 commands will grab all of the data needed we'll need.

One very basic command is echo. This command just prints text to the terminal. Try the command:

```
echo "Hello, World"
```

Then press enter. You should see the text "Hello, World" printed back to you. The echo command is useful for printing from a shell script, for displaying variables, and for generating known values to pass to other programs.

1.3.1 Moving around the file system

Let's learn how to move around the file system using command line programs. This is really easy to do using a GUI (just click on things). Once you learn the basic commands, you'll see that it is really easy to do in the shell too.

- 1. pwd First we have to know where we are. The program pwd (print working directory) tells you where you are sitting in the directory tree.
- 2. ls The command 1s will list the files in files in the current directory (pwd). Directories are often called "folders" because of how they are represented in GUIs. Directories are just listings of files. They can contain other files or directories.

Note:

- Directories are denoted in blue color.
- Files are denoted in white.
- You will find similar color schemes in different flavors of Linux.

Some terminals will not color the directory entries in this very convenient way. In those terminals, use ls -F instead of ls. The -F argument modifies the results so that a slash is placed at the end of directories. If the file is *executable* meaning that it can be run like a program, then a star will be placed at the end of the file name.

- 3. whoami Whenever you start up a terminal, you will start in a special directory called the home directory. Every user has their own home directory where they have full access to do whatever they want. For example, if our user ID is me, the pwd command tells us that we are in the /home/me directory. This is the home directory for the me user. That is our user name. You can always find out your user name by entering the command whoami.
- 4. cd Use the cd command to go to a directory. For example, if you are in the home folder, and you want to go to the Downloads folder, then you can type in cd Downloads. Remember, this command is case sensitive, and you have to type in the name of the folder exactly as it is.
- 5. mkdir & rmdir Use the mkdir command when you need to create a folder or a directory. For example, if you want to make a directory called MyFirstDirectory, then you can type mkdir MyFirstDirectory. Use rmdir to delete a directory. But rmdir can only be used to delete an empty directory. To delete a directory containing files, use rm.
- **6.** touch Lets create an empty file using the touch command. Enter the command:

touch testfile

Then list the contents of the directory again. You should see that a new entry, called testfile, exists. It is colored white meaning that it is a file, as opposed to a directory. The touch command just creates an empty file.

Now, let's get rid of testfile. To remove a file, just enter the command:

rm testfile

The rm command can be used to remove files. If you enter ls again, you will see that testfile is gone.

7. man & -help To know more about a command and how to use it, use the man command. It shows the manual pages of the command. For example, man cd shows the manual pages of the cd command. Typing in the command name and the argument helps it show which ways the command can be used (e.g., cd --help).

1.3.2 Examining the contents of other directories**

By default, the 1s commands lists the contents of the working directory (i.e. the directory you are in). You can always find the directory you are in using the pwd command. However, you can also give 1s the names of other directories to view. Navigate to the home directory if you are not already there. Then enter the command:

ls InPy

This will list the contents of the Inpy directory without you having to navigate there. Now enter:

ls InPy/shell-lesson

This prints the contents of shell-lesson. The cd command works in a similar way. Try entering:

cd InPy/shell-lesson

and you will jump directly to shell-lesson without having to go through the intermediate directory.

1.3.3 Full vs. Relative Paths

The cd command takes an argument which is the directory name. Directories can be specified using either a *relative* path a full *path*. The directories on the computer are arranged into a hierarchy. The absolute path tells you where a directory is in that hierarchy. Navigate to the home directory. Now, enter the pwd command and you should see something like:

/home/me

which is the full name of your home directory. This tells you that you are in a directory called me, which sits inside a directory called home which sits inside the very top directory in the hierarchy. The very top of the hierarchy is a directory called / which is usually referred to as the *root directory*. So, to summarize: me is a directory in home which is a directory in /.

Now enter the following command:

cd /home/me/InPy/shell-lesson

This jumps to shell. Now go back to the home directory. We saw earlier that the command:

cd InPy/shell-lesson

had the same effect - it took us to the shell-lesson directory. But, instead of specifying the absolute path (/home/me/InPy/shell-lesson), we specified a relative path. In other words, we specified the path relative to our current directory. A absolute path always starts with a /. A relative path does not. You can usually use either a absolute path or a relative path depending on what is most convenient. If we are in the home directory, it is more convenient to just enter the relative path since it involves less typing.

1.3.4 Exercise:

Now, list the contents of the /bin directory. Do you see anything familiar in there?

1.3.5 Saving time with shortcuts

There are some shortcuts which you should know about. Dealing with the home directory is very common. So, in the shell the tilde character, ~, is a shortcut for your home directory. Navigate to the shell directory, then enter the command:

ls ~

This prints the contents of your home directory, without you having to type the absolute path. The shortcut . . always refers to the directory above your current directory. Thus:

ls ..

prints the contents of the /home/me/InPy. You can chain these together, so:

prints the contents of /home/me which is your home directory. Finally, the special directory always refers to your current directory. So, ls, ls ., and ls ./././. all do the same thing, they print the contents of the current directory. This may seem like a useless shortcut right now, but we'll see when it is needed in a little while.

To summarize, the commands ls ~, ls ~/., ls ../../, and ls /home/me all do exactly the same thing. These shortcuts are not necessary, they are provided for your convenience.

Our data set: Cochlear Implants

A cochlear implant is a small electronic device that is surgically implanted in the inner ear to give deaf people a sense of hearing. More than a quarter of a million people have them, but there is still no widely-accepted benchmark to measure their effectiveness. In order to establish a baseline for such a benchmark, our supervisor got teenagers with CIs to listen to audio files on their computer and report:

- 1. the quietest sound they could hear
- 2. the lowest and highest tones they could hear
- 3. the narrowest range of frequencies they could discriminate

To participate, subjects attended our laboratory and one of our lab techs played an audio sample, and recorded their data - when they first heard the sound, or first heard a difference in the sound. Each set of test results were written out to a text file, one set per file. Each participant has a unique subject ID, and a made-up subject name. Each experiment has a unique experiment ID. The experiment has collected 351 files so far.

The data is a bit of a mess! There are inconsistent file names, there are extraneous "NOTES" files that we'd like to get rid of, and the data is spread across many directories. We are going to use shell commands to get this data into shape. By the end we would like to:

- 1. Put all of the data into one directory called "alldata"
- 2. Have all of the data files in there, and ensure that every file has a ".txt" extension
- 3. Get rid of the extraneous "NOTES" files

If we can get through this example in the available time, we will move onto more advanced shell topics...

1.3.6 Saving time with wild cards

Navigate to the shell-lesson/data/thomas directory. This directory contains our hearing test data for Thomas. If we type ls, we will see that there are a bunch of files which are just four digit numbers. By default, ls lists all of the files in a given directory. The * character is a shortcut for "everything". Thus, if you enter ls *, you will see all of the contents of a given directory. Now try this command:

ls *1

This lists every file that ends with a 1. This command:

ls /usr/bin/*.sh

lists every file in /usr/bin that ends in the characters .sh. And this command:

ls *4*1

lists every file in the current directory which contains the number 4, and ends with the number 1. There are four such files: 0241, 0341, 0431, and 0481.

So how does this actually work? Well...when the shell (bash) sees a word that contains the * character, it automatically looks for files that match the given pattern. In this case, it identified four such files. Then, it replaced the *4*1 with the list of files, separated by spaces. In other the two commands:

ls *4*1

ls 0241 0341 0431 0481

are exactly identical. The 1s command cannot tell the difference between these two things.

1.3.7 Exercise:

Do each of the following using a single ls command without navigating to a different directory. 1. List all of the files in /bin that contain the letter a 2. List all of the files in /bin that contain the letter a or the letter b 3. List all of the files in /bin that contain the letter a AND the letter b

1.3.8 nano, vi, vim

nano and vi or vim are already installed text editors in the Linux command line. The nano command is a good text editor that denotes keywords with color and can recognize most languages. And vi or vim are simpler than *nano*. You can create a new file or modify a file using this editor. For example, if you need to make a new file named *check.txt*, you can create it by using the command nano check.txt. You can save your files after editing by using the sequence Ctrl+X, then Y (or N for no).

1.3.9 Exercise:

Using text editor of your choice, i.e. nano or vi, create a file that you will name username.txt and fill it with some information about you. For instance, your full names, your country of origin, your scentific background and where you see yourself in the next ten years or anything you feel like adding.

1.3.10 Saving time with tab completion

Navigate to the home directory. Typing out directory names can waste a lot of time. When you start typing out the name of a directory, then hit the tab key, the shell will try to fill in the rest of the directory name. For example, enter:

cd I<tab>

The shell will fill in the rest of the directory name for InPy. Now enter:

ls 3<tab><tab>

When you hit the first tab, nothing happens. The reason is that there are multiple directories in the home directory which start with 3. Thus, the shell does not know which one to fill in. When you hit tab again, the shell will list the possible choices.

Tab completion can also fill in the names of programs. For example, enter e<tab><tab>. You will see the name of every program that starts with an e. One of those is echo. If you enter ec<tab> you will see that tab completion works.

1.3.11 Command History

You can easily access previous commands. Hit the up arrow.

Hit it again. You can step backwards through your command history. The down arrow takes your forwards in the command history.

~C will cancel the command you are writing, and give you a fresh prompt.

1.3.12 Examining Files

The easiest way to examine a file is to just print out all of the contents using the program cat. Enter the following command:

cat appaloosa.txt

This prints out the contents of the appaloosa.txt file. If you enter:

cat appaloosa.txt appaloosa.txt

It will print out the contents of appaloosa.txt twice. cat just takes a list of file names and writes them out one after another (this is where the name comes from, cat is short for concatenate).

cat is a terrific program, but when the file is really big, it can be annoying to use. The program, less, is useful for this case. Enter the following command:

less shell-lesson/dictionary.txt

`less` opens the file, and lets you navigate through it. The commands

are identical to the man program. Use "space" to go forward and hit the "b" key to go backwards. The "g" key goes to the beginning of the file and "G" goes to the end. Finally, hit "q" to quit.

less also gives you a way of searching through files. Just hit the "/" key to begin a search. Enter the name of the word you would like to search for and hit enter. It will jump to the next location where that word is found. Try searching the dictionary.txt file for the word "cat". If you hit "/" then "enter", less will just repeat the previous search. less searches from the current location and works its way forward. If you are at the end of the file and search for the word "cat", less will not find it. You need to go to the beginning of the file and search.

1.3.13 Redirection

Let's turn to the experimental data from the hearing tests that we began with. This data is located in the shell-lesson/data directory. Each subdirectory corresponds to a particular participant in

the study. Navigate to the **bert** subdirectory in **data**. There are a bunch of text files which contain experimental data results. Lets print them all:

cat au*

Now enter the following command:

cat au* > ../all_data

This tells the shell to take the output from the cat au* command and dump it into a new file called ../all_data. To verify that this worked, examine the all_data file. If all_data had already existed, we would overwritten it. So the > character tells the shell to take the output from what ever is on the left and dump it into the file on the right. The >> characters do almost the same thing, except that they will append the output to the file if it already exists.

1.3.14 Exercise:

Use >>, to append the contents of all of the files which contain the number 4 in the directory:

/home/me/InPy/shell-lesson/data/gerdal

to the existing all_data file. Thus, when you are done all_data should contain all of the experiment data from Bert and any experimental data file from gerdal that contains the number 4.

1.3.15 Creating, moving, copying, and removing

We've created a file called all_data using the redirection operator >. This file is critical - it's our analysis results - so we want to make copies so that the data is backed up. Lets copy the file using the cp command. The cp command backs up the file. Navigate to the data directory and enter:

```
cp all_data all_data_backup
```

Now all_data_backup has been created as a copy of all_data. We can move files around using the command my. Enter this command:

```
mv all_data_backup /tmp/
```

This moves all_data_backup into the directory /tmp. The directory /tmp is a special directory that all users can write to. It is a temporary place for storing files. Data stored in /tmp is automatically deleted when the computer shuts down.

The mv command is also how you rename files. Since this file is so important, let's rename it:

```
mv all_data all_data_IMPORTANT
```

Now the file name has been changed to all data IMPORTANT. Let's delete the backup file now:

rm /tmp/all_data_backup

1.3.16 Exercise:

Do the following: 1. Rename the all_data_IMPORTANT file to all_data. 2. Create a directory in the data directory called foo 3. Then, copy the all_data file into foo

1.3.17 Count the words

The wc program (word count) counts the number of lines, words, and characters in one or more files. Make sure you are in the data directory, then enter the following command:

```
wc bert/* gerdal/*4*
```

For each of the files indicated, wc has printed a line with three numbers. The first is the number of lines in that file. The second is the number of words. Finally, the total number of characters is indicated. The final line contains this information summed over all of the files. Thus, there were 10445 characters in total.

Remember that the bert/* and gerdal/*4* files were merged into the all_data file. So, we should see that all_data contains the same number of characters:

```
wc all_data
```

Every character in the file takes up one byte of disk space. Thus, the size of the file in bytes should also be 10445. Let's confirm this:

```
ls -l all_data
```

Remember that ls -l prints out detailed information about a file and that the fifth column is the size of the file in bytes.

1.3.18 Exercise:

Figure out how to get wc to print the length of the longest line in all_data.

1.3.19 The awesome power of the Pipe

Suppose I wanted to only see the total number of character, words, and lines across the files bert/* and gerdal/*4*. I don't want to see the individual counts, just the total. Of course, I could just do:

```
wc all_data
```

Since this file is a concatenation of the smaller files. Sure, this works, but I had to create the all_data file to do this. Thus, I have wasted a precious 7062 bytes of hard disk space. We can do this without creating a temporary file, but first I have to show you two more commands: head and tail. These commands print the first few, or last few, lines of a file, respectively. Try them out on all_data:

```
head all_data tail all_data
```

The -n option to either of these commands can be used to print the first or last n lines of a file. To print the first/last line of the file use:

```
head -n 1 all_data
tail -n 1 all_data
```

Let's turn back to the problem of printing only the total number of lines in a set of files without creating any temporary files. To do this, we want to tell the shell to take the output of the wc

bert/* gerdal/*4* and send it into the tail -n 1 command. The | character (called pipe) is used for this purpose. Enter the following command:

```
wc bert/* gerdal/Data0559 | tail -n 1
```

This will print only the total number of lines, characters, and words across all of these files. What is happening here? Well, tail, like many command line programs will read from the *standard input* when it is not given any files to operate on. In this case, it will just sit there waiting for input. That input can come from the user's keyboard *or from another program*. Try this:

```
tail -n 2
```

Notice that your cursor just sits there blinking. Tail is waiting for data to come in. Now type:

French fries

are

good

then ^d. You should see the lines:

are good

printed back at you. The ^d keyboard shortcut inserts an *end-of-file* character. It is sort of the standard way of telling the program "I'm done entering data". The | character is replaces the data from the keyboard with data from another command. You can string all sorts of commands together using the pipe.

The philosophy behind these command line programs is that none of them really do anything all that impressive. BUT when you start chaining them together, you can do some really powerful things really efficiently. If you want to be proficient at using the shell, you must learn to become proficient with the pipe and redirection operators: |, >, >>.

A sorting example

Let's create a file with some words to sort for the next example. We want to create a file which contains the following names:

Bob

Alice

Diane

Charles

To do this, we need a program which allows us to create text files. There are many such programs, the easiest one which is installed on almost all systems is called nano. Navigate to /tmp and enter the following command:

```
nano to-be-sorted
```

Now enter the four names as shown above. When you are done, press ^O to write out the file. Press enter to use the file name to-be-sorted. Then press ^x to exit nano.

When you are back to the command line, enter the command:

```
sort to-be-sorted
```

Notice that the names are now printed in alphabetical order.

1.3.20 Exercise:

Use the echo command and the append operator, >>, to append your name to the file, then sort it and make a new file called Sorted.

Let's navigate back to thw-shell/data. Enter the following command:

```
wc bert/* | sort -k 3 -n
```

We are already familiar with what the first of these two commands does: it creates a list containing the number of characters, words, and lines in each file in the **bert** directory. This list is then piped into the **sort** command, so that it can be sorted. Notice there are two options given to sort:

- 1. -k 3: Sort based on the third column
- 2. -n: Sort in numerical order as opposed to alphabetical order

Notice that the files are sorted by the number of characters.

1.3.21 Exercise:

Combine the wc, sort, head and tail commands so that only the wc information for the largest file is listed

Hint: To print the smallest file, use: wc bert/* | sort -k 3 -n | head -n 1

1.4 Searching files

You can search the contents of a file using the command grep. The grep program is very powerful and useful especially when combined with other commands by using the pipe. Navigate to the bert directory. Every data file in this directory has a line which says "Range". The range represents the smallest frequency range that can be discriminated. Lets list all of the ranges from the tests that bert conducted:

grep	Range	*						

Short Exercise:

Create an executable script called smallestrange in the data directory, that is similar to the smallest script, but prints the file containing the file with the smallest Range. Use the commands grep, sort, and tail to do this.

1.5 Finding files

The find program can be used to find files based on arbitrary criteria. Navigate to the data directory and enter the following command:

find . -print

This prints the name of every file or directory, recursively, starting from the current directory. Let's exclude all of the directories:

```
find . -type f -print
```

This tells find to locate only files. Now try these commands:

```
find . -type f -name "*1*"
find . -type f -name "*1*" -or -name "*2*" -print
find . -type f -name "*1*" -and -name "*2*" -print
```

The find command can acquire a list of files and perform some operation on each file. Try this command out:

```
find . -type f -exec grep Volume {} \;
```

This command finds every file starting from .. Then it searches each file for a line which contains the word "Volume". The {} refers to the name of each file. The trailing \; is used to terminate the command. This command is slow, because it is calling a new instance of grep for each item the find returns.

A faster way to do this is to use the xargs command:

```
find . -type f -print | xargs grep Volume
```

find generates a list of all the files we are interested in, then we pipe them to xargs. xargs takes the items given to it and passes them as arguments to grep. xargs generally only creates a single instance of grep (or whatever program it is running).

Short Exercise:

Navigate to the data directory. Use one find command to perform each of the operations listed below (except number 2, which does not require a find command):

- 1. Find any file whose name is "NOTES" within data and delete it
- 2. Create a new directory called cleaneddata
- 3. Move all of the files within data to the cleaneddata directory
- 4. Rename all of the files to ensure that they end in .txt (note: it is ok for the file name to end in .txt.txt

Hint: If you make a mistake and need to start over just do the following:

- 1. Navigate to the shell directory
- 2. Delete the data directory
- 3. Enter the command: git checkout -- data You should see that the data directory has reappeared in its original state