Wild Cards & Nano

A Beginner's Guide

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Contents

1 Learning Objectives

- Learn to use tab completion to simplify typing file and directory paths.

- Use of the asterisk * wildcard to match and select multiple files in a directory.
- View the contents of a file using commands such as `less`, `head`, or `cat`.
- Use Nano, a simple text editor, to create and edit files directly from terminal.

Class Exercise

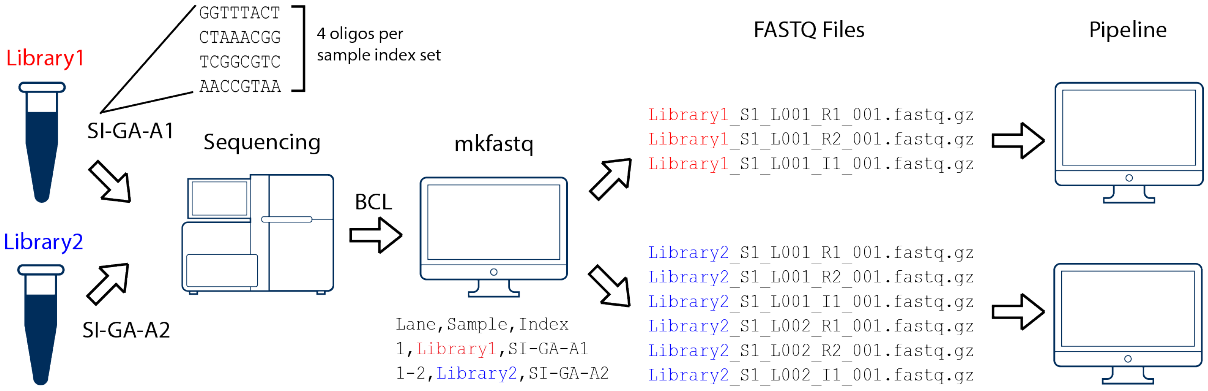
```
Please complete the following class activity below. You will have ~5 minutes to co

[Class-activity](https://forms.gle/6L5eDqiiLijc8i6H8)
```

---

2 Wild cards

The "*" wildcard:

Navigate to the `~/unit1_unix/raw_fastq` directory. This directory contains FASTQ files and these files contain the sequencing reads (nucleotide sequences) output from a high throughput sequencer.



```
Lane,Sample,Index
1,Library1,SI-GA-A1
1-2,Library2,SI-GA-A2
```

```
Library1_S1_L001_R1_001.fastq.gz
Library1_S1_L001_R2_001.fastq.gz
Library1_S1_L001_I1_001.fastq.gz

Library2_S1_L001_R1_001.fastq.gz
Library2_S1_L001_R2_001.fastq.gz
Library2_S1_L001_I1_001.fastq.gz
Library2_S1_L002_R1_001.fastq.gz
Library2_S1_L002_R2_001.fastq.gz
Library2_S1_L002_I1_001.fastq.gz
```

Figure 1: Typical NGS workflow

Let's see what is inside:

```
ls
```

```
## Irrel_kd_1.subset.fq  Irrel_kd_2.subset.fq  Irrel_kd_3.subset.fq  Mov10_oe_1.su
```

Let's take a moment to point a few things out:

- .fq vs .fastq
- .gz

> .gz is a file format used for compressed files. This is especially important when dealing with large data.

Class Exercise

```
Create a directory called ‘fastq‘ in ‘~/unit1_unix/raw_fastq‘ directory. Then chec
```

The * or wildcard character is a shortcut for "everything".

You can use the * by typing in shift + 8.

```
ls *.fq
```

> Notice, this lists every file that ends with a `fq` and our newly made directory **fastq** is missing.

```
Irrel_kd_1.subset.fq    Irrel_kd_3.subset.fq    Mov10_oe_2.subset.fq
Irrel_kd_2.subset.fq    Mov10_oe_1.subset.fq    Mov10_oe_3.subset.fq
```

2.1 Command History

You can easily access previous commands by hitting the up arrow key on your keyboard, this way you can step backwards through your command history. On the other hand, the down arrow key takes you forward in the command history.

Try it out! While on the command prompt hit the up arrow a few times, and then hit the down arrow a few times until you are back to where you started.

You can also review your recent commands with the `history` command. Just enter:

```
history
```

You should see a numbered list of commands, including the `history` command you just ran!

The wildcard `*` can be placed anywhere in your pattern. For example:

```
ls Mov10*fq
```

This lists only the files that begin with 'Mov10' and end with `fq`.

```
## Mov10_oe_1.subset.fq  Mov10_oe_2.subset.fq  Mov10_oe_3.subset.fq
```

So how does this actually work? The Shell (bash) considers an asterisk `*` to be a wildcard character that can match one or more occurrences of any character, including no character. In the example above the `*` took place of 13 characters!

> **Tip** - An asterisk/star is only one of the many wildcards in Unix, but this is the most powerful one and we will be using this one the most for our exercises.

2.2 The "?" wildcard

Another wildcard that is sometimes helpful is `?`

- `?` is similar to `*` except that it is a placeholder for exactly one position.
- Recall that `*` can represent any number of following positions, including no positions.
- To highlight this distinction lets look at a few examples. First, try this command:

```
ls /bin/d*
```

This will display all files in `/bin/` that start with "d" regardless of length. The `bin` directory is where some built-in programs are stored. However, if you only wanted the things in `/bin/` that start with "d" and are two characters long then you can use:

```
ls /bin/d?
```

Lastly, you can chain together multiple "?" marks to help specify a length. In the example below, you would be looking for all things in `/bin/` that start with a "d" and have a name length of three characters.

```
ls /bin/d??
```

!!! example "Class Exercise"

```
Perform each of the following tasks using a single ‘ls‘ command *without* navigati

1.  List all of the files in ‘/bin‘ that start with the letter ’c’

2.  List all of the files in ‘/bin‘ that contain the letter ’a’

3.  List all of the files in ‘/bin‘ that end with the letter ’o’

4. BONUS: List all of the files in ‘/bin‘ that start with ’ch’ and are only 5 lett
```

Answers

Click each question below to reveal the answer.

Question 1

ls /bin/c*

Question 2

ls /bin/*a*

Question 3

ls /bin/*o

BONUS

ls /bin/ch???

3 Examining Files

Now let’s explore a few more commands to examine files.

3.0.1 `cat` command

The easiest way to examine a file is to print out all of its contents using the command `cat`. We can test this out by printing the contents of `~/unit1_unix/other/sequences.fa`

```
cat sequences.fa
```

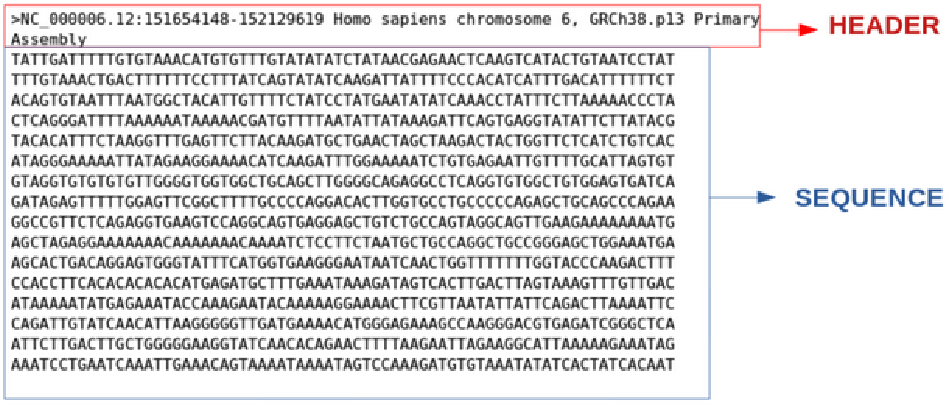
The `cat` command prints out the all the contents of `sequences.fa` to the screen.

> `cat` stands for catenate; it has many uses and printing the contents of a files onto the terminal is one of them.

What does this file contain?

```
>SRR014849.1 EIXKN4201CFU84 length=93
GGGGGGGGGGGGGGGGCTTTTTTTGTTTGGAACCGAAAGGGTTTTGAATTTCAAACCCTTTTCGGTTTCCAACCTTCCAAAG

>gi|340780744|ref|NC_015850.1| Acidithiobacillus caldus SM-1 chromosome, complete
ATGAGTAGTCATTCAGCGCCGACAGCGTTGCAAGATGGAGCCGCGCTGTGGTCCGCCCTATGCGTCCAACTGGAGCTCGTCA
TCCGCAGCAGTTCAATACCTGGCTGCGGCCCCTGCGTGGCGAATTGCAGGGTCATGAGCTGCGCCTGCTCGCCCCCAATCCC
TCCGCGACTGGGTGCGTGAACGCATGGCCGAACTCGTCAAGGAACAGCTGCAGCGGATCGCTCCGGGTTTTGAGCTGGTCTT
CTGGACGAAGAGGCAGCAGCGGCGACATCGGCACCGACCGCGAGCATTGCGCCCGAGCGCAGCAGCGCACCCGGTGGTCACC
CAACCCAGCCTTCAACTTCCAGTCCTACGTCGAAGGGAAGTCCAATCAGCTCGCCCTGGCGGCAGCCCGCCAGGTTGCCCAG
CAGGCAAATCCTACAACCCACTGTACATTTATGGTGGTGTGGGCCTCGGCAAGACGCACCTCATGCAGGCCGTGGGCAACGA
CTGCAGCGGCAACCCGAGGCCAAGGTGCTCTATATCAGCTCCGAAGGCTTCATCATGGATATGGTGCGCTCGCTGCAACACA
CATCAACGACTTCAAACAGCGTTATCGCAAGCTGGACGCCCTGCTCATCGACGACATCCAGTTCTTTGCGGGCAAGGACCGC

>gi|129295|sp|P01013|OVAX_CHICK GENE X PROTEIN (OVALBUMIN-RELATED)
QIKDLLVSSSTDLDTTLVLVNAIYFKGMWKTAFNAEDTREMPFHVTKQESKPVQMMCMNNSFNVATLPAE
```

This is a FASTA file. FASTA format is a text-based format for representing either nucleotide or peptide sequences. The structure of a FASTA file is represented below where the header row always begins with the ">" symbol.



```
>NC_000006.12:151654148-152129619 Homo sapiens chromosome 6, GRCh38.p13 Primary
Assembly
TATTGATTTTTGTGTAAACATGTGTTTGTATATATCTATAACGAGAACTCAAGTCATACTGTAATCCTAT
TTTGTAAACTGACTTTTTTCCTTTATCAGTATATCAAGATTATTTTCCCACATCATTTGACATTTTTTCT
ACAGTGTAATTTAATGGCTACATTGTTTTCTATCCTATGAATATATCAAACCTATTTCTTAAAAACCCTA
CTCAGGGATTTTAAAAAATAAAAACGATGTTTTAATATTATAAAGATTCAGTGAGGTATATTCTTATACG
TACACATTTCTAAGGTTTGAGTTCTTACAAGATGCTGAACTAGCTAAGACTACTGGTTCTCATCTGTCAC
ATAGGGAAAAATTATAGAAGGAAAACATCAAGATTTGGAAAAATCTGTGAGAATTGTTTTGCATTAGTGT
GTAGGTGTGTGTGTTGGGGTGGTGGCTGCAGCTTGGGGCAGAGGCCTCAGGTGTGGCTGTGGAGTGATCA
GATAGAGTTTTTGGAGTTCGGCTTTTGCCCCAGGACACTTGGTGCCTGCCCCCAGAGCTGCAGCCCAGAA
GGCCGTTCTCAGAGGTGAAGTCCAGGCAGTGAGGAGCTGTCTGCCAGTAGGCAGTTGAAGAAAAAAAATG
AGCTAGAGGAAAAAAACAAAAAAACAAAATCTCCTTCTAATGCTGCCAGGCTGCCGGGAGCTGGAAATGA
AGCACTGACAGGAGTGGGTATTTCATGGTGAAGGGAATAATCAACTGGTTTTTTTGGTACCCAAGACTTT
CCACCTTCACACACACACATGAGATGCTTTGAAATAAAGATAGTCACTTGACTTAGTAAAGTTTGTTGAC
ATAAAAATATGAGAAATACCAAAGAATACAAAAAGGAAAACTTCGTTAATATTATTCAGACTTAAAATTC
CAGATTGTATCAACATTAAGGGGGTTGATGAAAACATGGGAGAAAGCCAAGGGACGTGAGATCGGGCTCA
ATTCTTGACTTGCTGGGGGAAGGTATCAACACAGAACTTTTAAGAATTAGAAGGCATTAAAAAGAAATAG
AAATCCTGAATCAAATTGAAACAGTAAAATAAAATAGTCCAAAGATGTGTAAATATATCACTATCACAAT
```

Figure 2: Fasta Example

Question: What command would I use to clear my terminal screen?

Answer

Ctrl + L

3.1 `less` command

`cat` is a terrific command, but notice what it is doing. It is **PRINTING** the file contents on the screen.

When the file is really big and has a ton of lines, this can be cumbersome to use. In practice, when you are running your analyses on the command-line you will most likely be dealing with large files so you need to learn how to view them.

Instead, we will use the `less` command

```
less Mov10_oe_1.subset.fq
```

Rather than printing to screen, the `less` command opens the file in a new buffer allowing you to navigate through it. Does this look familiar? You might remember encountering a similar interface when you used the `man` command. This is because `man` is using the `less` command to open up the documentation files! The keys used to move around the file are identical to the `man` command. Below we have listed some additional shortcut keys for navigating through your file when using `less`.

Shortcuts for `less`

key	action
SPACE	to go forward
b	to go backwards
g	to go to the beginning of the file
G	to go to the end of a file
q	to quit or exit `less`

Use the shortcut keys to move through your FASTQ file, we will explore these files in more detail later in the workshop.

3.1.1 Searching files with `less`

`less` also gives you a way of searching through files.

Just type in / to begin a search, you will see that the `/` will show up at the bottom of the `less` buffer. Let's say you are interested in searching for the following 8-letter adapter sequence:

```
/GGGATAA
```

Enter the name of the string of characters you would like to search for and hit the enter key. The interface will move to show you the location where that string is found, and highlight the string.

If you hit / then ENTER, `less` will just repeat the previous search.

`less` searches from the current location and works its way forward. For instance, the sequence `GGCGAATT` was found in our file, but if we started the search at the end of the file, `less` will not find it. You need to go to the beginning of the file and search.

To exit hit q.

3.2 `head` and `tail` commands

There is another way that we can peek inside files. In particular, if we just want to see the beginning or end of the file to see how it's formatted.

The commands are `head` and `tail` and they just let you look at the beginning and end of a file respectively.

```
head Mov10_oe_1.subset.fq
```

```
tail Mov10_oe_1.subset.fq
```

By default, the first or last 10 lines will be printed to screen. The `-n` option can be used with either of these commands to specify the number `n` lines of a file to display. For example, let's print the first/last line of the file:

```
head -n 20 Mov10_oe_1.subset.fq

tail -n 20 Mov10_oe_1.subset.fq
```

4 Good names for files and directories

Complicated names of files and directories can make your life painful when working on the command line. Here we provide a few useful tips for the names of your files and directories.

`Don’t use spaces.`

Spaces can make a name more meaningful, but since spaces are used to separate arguments on the command line it is better to avoid them in names of files and directories. You can use - or _ instead (e.g. fastq-data-files/ rather than fastq data files/). To test this out, try typing mkdir fastq data files and see what directory (or directories!) are made when you check with ls -F.

1. Don’t begin the name with - (dash).
2. Don’t begin the name with numbers.
3. Stick with letters in the beginning and then use numbers, . (period), - (dash), or an _ (underscore) in the middle of the file or directory name.

You may have noticed by now that all the files we are using are named ‘something dot something’.

- This is just a convention; we can call a file mythesis or almost anything else we want. However, most people use two-part names most of the time to help them (and their programs) tell different kinds of files apart.

Figure 3: File Extension

- The second part of such a name is called the filename extension and indicates what type of data the file holds: **.txt** signals a plain text file, **.pdf** indicates a PDF document, **.png** is a PNG image, and so on.
- This is just a convention, albeit an important one. Files merely contain bytes; it’s up to us and our programs to interpret those bytes according to the rules for plain text files, PDF documents, configuration files, images, and so on.

- However, naming a PNG image of a whale as whale.mp3 doesn't somehow magically turn it into a recording of whale song, though it might cause the operating system to associate the file with a music player program. In this case, if someone double-clicked whale.mp3 in a file explorer program,the music player will automatically (and erroneously) attempt to open the whale.mp3 file.

Figure 4: Whale.mp3

---

5 Writing files

We've been able to do a lot of work with files that already exist, but what if we want to create our own files?

In order to create or edit files we will need to use a **text editor**. When we say, "text editor," we really do mean "text". These editors can only work with plain character data, not tables, images, or any other media. Text editors can generally be grouped into two categories: **command-line editors** and **graphical user interface editors**.

5.1 Command-line editors

Some popular editors include:

- Emacs
- Vim
- Gedit

These are editors which are generally available for use on high-performance compute clusters. There are also simpler editors available for use on the cluster (e.g. Nano), but tend to have limited functionality. We will use Nano in this lesson.

5.2 Nano

Nano is a simple text editor for UNIX/Linux operating systems. Nano is easy-to-use but has its' limitations.

5.2.1 Creating or editing a file with Nano

To create a new file or edit an existing one type:

```
nano filename
```

Type the following in your terminal:

```
nano colors.txt
```

After pressing the Enter key, the nano editor appears. Notice the following elements:

- the top line displays the version of nano in the left corner and the name of the file being edited
- the 3rd line from the bottom indicates the status of the file you're editing; it shows that color.txt is a "New File"
- the last two lines of the screen present a menu of useful shortcuts for nano. They all will require you to use the control button on your laptop.

```
  GNU nano 2.3.1              File: colors.txt




                                  [ New File ]
^G Get Help    ^O WriteOut    ^R Read File   ^Y Prev Page   ^K Cut Text    ^C Cur Pos
^X Exit        ^J Justify     ^W Where Is    ^V Next Page   ^U UnCut Text  ^T To Spell
```

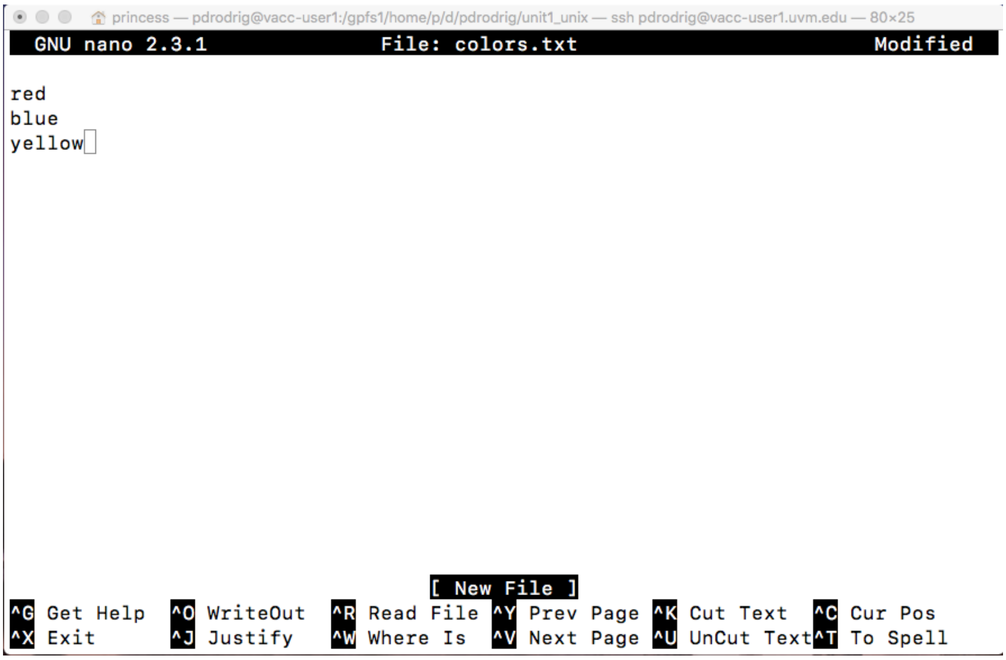
Figure 5: Nano Screen

At this point we can begin typing:

```
red
blue
yellow
```

Notice that after your first keystroke, the word “Modified appears in the upper-right corner. This shows that you have changed the contents of your file but it has not been saved yet.

- **Saving your work:** To save your edited file to disk, press Ctrl-o. Nano displays the current filename. (To save the file under a different name, delete the filename that Nano displays and type a new one.) Press Enter.
- **Exiting Nano:** To exit Nano, press control + x. If you made any changes since the last save, Nano will ask whether or not to save them. Type `y` for yes or `n` for no. Press Enter.



```
  GNU nano 2.3.1             File: colors.txt                        Modified

red
blue
yellow















                                 [ New File ]
^G Get Help  ^O WriteOut  ^R Read File ^Y Prev Page ^K Cut Text  ^C Cur Pos
^X Exit      ^J Justify   ^W Where Is  ^V Next Page ^U UnCut Text^T To Spell
```

Figure 6: Nano Screen - Modified

```
  GNU nano 2.3.1             File: colors.txt                        Modified

red
blue
yellow
















Save modified buffer (ANSWERING "No" WILL DESTROY CHANGES) ?
 Y Yes
 N No           ^C Cancel
```

Figure 7: Saving with Nano

5.2.2 Summary Basic nano commands

key	action
control + X	exit from the editor
control + A	Let’s you jump from the beginning of the line
control + E	Let’s you jump from the end of the line
control + V	Scroll page down
control + Y	Scroll page up
control + O	Save the file
control + K	It cuts the entire selected line

Class Exercise

```
**You will have ~5 minutes to complete**

1. Make a copy of ‘get-pip.py‘ from this location ‘/gpfs1/cl/mmg3320/course_materi
2. Open ‘get-pip.py‘
3. Copy and paste the 3rd line as the answer for the final participation grade que
4. Exit and return to terminal
```

---

6 Summary: Commands, options, and keystrokes covered

The wildcard *

- can represent zero or more other characters
- can be placed anywhere in your pattern

```
~           # home dir
.           # current dir
..          # parent dir
*           # wildcard
```

```
ctrl + c    # cancel current command
ctrl + a    # start of line
ctrl + e    # end of line
ctrl + l    # clear your terminal screen
history
cat         # prints out the all the contents of file
less        # allows you to view and move through file content
head        # allows you to view beginning of file
tail        # allows you to view end of file
```

---

7 Citation

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