# The Unix Shell

Content from Introducing the Shell

Last updated on 2023-06-09 | Edit this page

## OVERVIEW

### Questions

- What is a command shell and why would I use one?

### Objectives

- Explain how the shell relates to the keyboard, the screen, the operating system, and users' programs.
- Explain when and why command-line interfaces should be used instead of graphical interfaces.

## Background

Humans and computers commonly interact in many different ways, such as through a keyboard and mouse, touch screen interfaces, or using speech recognition systems. The most widely used way to interact with personal computers is called a **graphical user interface** (GUI). With a GUI, we give instructions by clicking a mouse and using menu-driven interactions.

While the visual aid of a GUI makes it intuitive to learn, this way of delivering instructions to a computer scales very poorly. Imagine the following task: for a literature search, you have to copy the third line of one thousand text files in one thousand different directories and paste it into a single file. Using a GUI, you would not only be clicking at your desk for several hours, but you could potentially also commit an error in the process of completing this repetitive task. This is where we take advantage of the Unix shell. The Unix shell is both a **command-line interface** (CLI) and a scripting language, allowing such repetitive tasks to be done automatically and fast. With the proper commands, the shell can repeat tasks with or without some modification as many times as we want. Using the shell, the task in the literature example can be accomplished in seconds.

## The Shell

The shell is a program where users can type commands. With the shell, it's possible to invoke complicated programs like climate modeling software or simple commands that create an empty directory with only one line of code. The most popular Unix shell is Bash (the Bourne Again SHell — so-called because it's derived from a shell written by Stephen Bourne). Bash is the default shell on most modern implementations of Unix and in most packages that provide Unix-like tools for Windows. Note that 'Git Bash' is a piece of software that enables Windows users to use a Bash like interface when interacting with Git.

Using the shell will take some effort and some time to learn. While a GUI presents you with choices to select, CLI choices are not automatically presented to you, so you must learn a few commands like new vocabulary in a language you're studying. However, unlike a spoken language, a small number of "words" (i.e. commands) gets you a long way, and we'll cover those essential few today.

The grammar of a shell allows you to combine existing tools into powerful pipelines and handle large volumes of data automatically. Sequences of commands can be written into a *script*, improving the reproducibility of workflows.

In addition, the command line is often the easiest way to interact with remote machines and supercomputers. Familiarity with the shell is near essential to run a variety of specialized tools and resources including high-performance computing systems. As clusters and cloud computing systems become more popular for scientific data crunching, being able to interact with the shell is becoming a necessary skill. We can build on the command-line skills covered here to tackle a wide range of scientific questions and computational challenges.

Let's get started.

When the shell is first opened, you are presented with a **prompt**, indicating that the shell is waiting for input.

BASH

```
$
```

The shell typically uses `$` as the prompt, but may use a different symbol. In the examples for this lesson, we'll show the prompt as `$`. Most importantly, *do not type the prompt* when typing commands. Only type the command that follows the prompt. This rule applies both in these lessons and in lessons from other sources. Also note that after you type a command, you have to press the `Enter` key to execute it.

The prompt is followed by a **text cursor**, a character that indicates the position where your typing will appear. The cursor is usually a flashing or solid block, but it can also be an underscore or a pipe. You may have seen it in a text editor program, for example.

Note that your prompt might look a little different. In particular, most popular shell environments by default put your user name and the host name before the `$`. Such a prompt might look like, e.g.:

BASH

```
nelle@localhost $
```

The prompt might even include more than this. Do not worry if your prompt is not just a short `$`. This lesson does not depend on this additional information and it should also not get in your way. The only important item to focus on is the `$` character itself and we will see later why.

So let's try our first command, `ls`, which is short for listing. This command will list the contents of the current directory:

BASH

```
$ ls
```

OUTPUT

```
Desktop     Downloads   Movies      Pictures
Documents   Library     Music       Public
```

CALLOUT

## COMMAND NOT FOUND

If the shell can't find a program whose name is the command you typed, it will print an error message such as:

BASH

```
$ ks
```

OUTPUT

```
ks: command not found
```

This might happen if the command was mis-typed or if the program corresponding to that command is not installed.

## Nelle's Pipeline: A Typical Problem

Nelle Nemo, a marine biologist, has just returned from a six-month survey of the North Pacific Gyre, where she has been sampling gelatinous marine life in the Great Pacific Garbage Patch. She has 1520 samples that she's run through an assay machine to measure the relative abundance of 300 proteins. She needs to run these 1520 files through an imaginary program called `goostats.sh`. In addition to this huge task, she has to write up results by the end of the month, so her paper can appear in a special issue of *Aquatic Goo Letters*.

If Nelle chooses to run `goostats.sh` by hand using a GUI, she'll have to select and open a file 1520 times. If `goostats.sh` takes 30 seconds to run each file, the whole process will take more than 12 hours of Nelle's attention. With the shell, Nelle can instead assign her computer this mundane task while she focuses her attention on writing her paper.

The next few lessons will explore the ways Nelle can achieve this. More specifically, the lessons explain how she can use a command shell to run the `goostats.sh` program, using loops to automate the repetitive steps of entering file names, so that her computer can work while she writes her paper.

As a bonus, once she has put a processing pipeline together, she will be able to use it again whenever she collects more data.

In order to achieve her task, Nelle needs to know how to:

- navigate to a file/directory
- create a file/directory
- check the length of a file
- chain commands together
- retrieve a set of files
- iterate over files
- run a shell script containing her pipeline

### KEY POINTS

- A shell is a program whose primary purpose is to read commands and run other programs.
- This lesson uses Bash, the default shell in many implementations of Unix.
- Programs can be run in Bash by entering commands at the command-line prompt.
- The shell's main advantages are its high action-to-keystroke ratio, its support for automating repetitive tasks, and its capacity to access networked machines.
- A significant challenge when using the shell can be knowing what commands need to be run and how to run them.

Content from Navigating Files and Directories

Last updated on 2024-07-24 | Edit this page

### OVERVIEW

#### Questions

- How can I move around on my computer?
- How can I see what files and directories I have?
- How can I specify the location of a file or directory on my computer?

#### Objectives

- Explain the similarities and differences between a file and a directory.

- Translate an absolute path into a relative path and vice versa.
- Construct absolute and relative paths that identify specific files and directories.
- Use options and arguments to change the behaviour of a shell command.
- Demonstrate the use of tab completion and explain its advantages.

The part of the operating system responsible for managing files and directories is called the **file system**. It organizes our data into files, which hold information, and directories (also called 'folders'), which hold files or other directories.

Several commands are frequently used to create, inspect, rename, and delete files and directories. To start exploring them, we'll go to our open shell window.

First, let's find out where we are by running a command called `pwd` (which stands for 'print working directory'). Directories are like *places* — at any time while we are using the shell, we are in exactly one place called our **current working directory**. Commands mostly read and write files in the current working directory, i.e. 'here', so knowing where you are before running a command is important. `pwd` shows you where you are:

BASH

```
$ pwd
```

OUTPUT

```
/Users/nelle
```

Here, the computer's response is `/Users/nelle`, which is Nelle's **home directory**:

CALLOUT

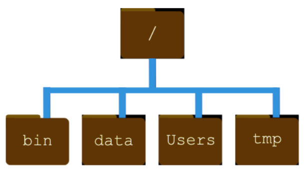
### HOME DIRECTORY VARIATION

The home directory path will look different on different operating systems. On Linux, it may look like `/home/nelle`, and on Windows, it will be similar to `C:\Documents and Settings\nelle` or `C:\Users\nelle`. (Note that it may look slightly different for different versions of Windows.) In future examples, we've used Mac output as the default - Linux and Windows output may differ slightly but should be generally similar.

We will also assume that your `pwd` command returns your user's home directory. If `pwd` returns something different, you may need to navigate there using `cd` or some commands in this lesson will not work as written. See Exploring Other Directories for more details on the `cd` command.

To understand what a 'home directory' is, let's have a look at how the file system as a whole is organized. For the sake of this example, we'll be illustrating the filesystem on our scientist Nelle's computer. After this illustration, you'll be learning commands to explore your own filesystem, which will be constructed in a similar way, but not be exactly identical.

On Nelle's computer, the filesystem looks like this:



The filesystem looks like an upside down tree. The topmost directory is the **root directory** that holds everything else. We refer to it using a slash character, `/`, on its own; this character is the leading slash in `/Users/nelle`.

Inside that directory are several other directories: `bin` (which is where some built-in programs are stored), `data` (for miscellaneous data files), `Users` (where users' personal directories are located), `tmp` (for temporary files that don't need to be stored long-term), and so on.

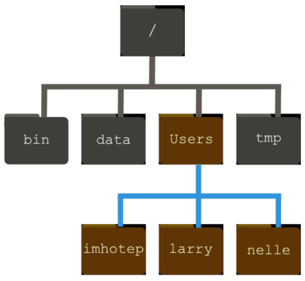
We know that our current working directory `/Users/nelle` is stored inside `/Users` because `/Users` is the first part of its name. Similarly, we know that `/Users` is stored inside the root directory `/` because its name begins with `/`.

CALLOUT

### SLASHES

Notice that there are two meanings for the `/` character. When it appears at the front of a file or directory name, it refers to the root directory. When it appears *inside* a path, it's just a separator.

Underneath `/Users`, we find one directory for each user with an account on Nelle's machine, her colleagues *imhotep* and *larry*.



The user *imhotep*'s files are stored in `/Users/imhotep`, user *larry*'s in `/Users/larry`, and Nelle's in `/Users/nelle`. Nelle is the user in our examples here; therefore, we get `/Users/nelle` as our home directory. Typically, when you open a new command prompt, you will be in your home directory to start.

Now let's learn the command that will let us see the contents of our own filesystem. We can see what's in our home directory by running `ls`:

BASH

```
$ ls
```

OUTPUT

```
Applications Documents    Library      Music        Public
Desktop      Downloads    Movies       Pictures
```

(Again, your results may be slightly different depending on your operating system and how you have customized your filesystem.)

`ls` prints the names of the files and directories in the current directory. We can make its output more comprehensible by using the `-F` **option** which tells `ls` to classify the output by adding a marker to file and directory names to indicate what they are:

- a trailing `/` indicates that this is a directory
- `@` indicates a link
- `*` indicates an executable

Depending on your shell's default settings, the shell might also use colors to indicate whether each entry is a file or directory.

BASH

```
$ ls -F
```

OUTPUT

```
Applications/ Documents/    Library/      Music/        Public/
Desktop/      Downloads/    Movies/       Pictures/
```

Here, we can see that the home directory contains only **sub-directories**. Any names in the output that don't have a classification symbol are **files** in the current working directory.

CALLOUT

### CLEARING YOUR TERMINAL

If your screen gets too cluttered, you can clear your terminal using the `clear` command. You can still access previous commands using ↑ and ↓ to move line-by-line, or by scrolling in your terminal.

## Getting help

`ls` has lots of other **options**. There are two common ways to find out how to use a command and what options it accepts — **depending on your environment, you might find that only one of these ways works:**

1. We can pass a `--help` option to any command (available on Linux and Git Bash), for example:

BASH

```
$ ls --help
```

2. We can read its manual with `man` (available on Linux and macOS):

BASH

```
$ man ls
```

We'll describe both ways next.

CALLOUT

### HELP FOR BUILT-IN COMMANDS

Some commands are built in to the Bash shell, rather than existing as separate programs on the filesystem. One example is the `cd` (change directory) command. If you get a message like `No manual entry for cd`, try `help cd` instead. The `help` command is how you get usage information for Bash built-ins.

### The `--help` option

Most bash commands and programs that people have written to be run from within bash, support a `--help` option that displays more information on how to use the command or program.

BASH

```
$ ls --help
```

OUTPUT

```
Usage: ls [OPTION]... [FILE]...
List information about the FILEs (the current directory by default).
Sort entries alphabetically if neither -cftuvSUX nor --sort is specified.

Mandatory arguments to long options are mandatory for short options, too.
  -a, --all                  do not ignore entries starting with .
  -A, --almost-all           do not list implied . and ..
      --author               with -l, print the author of each file
  -b, --escape               print C-style escapes for nongraphic characters
      --block-size=SIZE      scale sizes by SIZE before printing them; e.g.,
                               '--block-size=M' prints sizes in units of
                               1,048,576 bytes; see SIZE format below
  -B, --ignore-backups       do not list implied entries ending with ~
  -c                         with -lt: sort by, and show, ctime (time of last
                               modification of file status information);
                               with -l: show ctime and sort by name;
                               otherwise: sort by ctime, newest first
  -C                         list entries by columns
      --color[=WHEN]         colorize the output; WHEN can be 'always' (default
                               if omitted), 'auto', or 'never'; more info below
  -d, --directory            list directories themselves, not their contents
  -D, --dired                generate output designed for Emacs' dired mode
  -f                         do not sort, enable -aU, disable -ls --color
  -F, --classify             append indicator (one of */=>@|) to entries
...        ...        ...
```

CALLOUT

### WHEN TO USE SHORT OR LONG OPTIONS

When options exist as both short and long options:

- Use the short option when typing commands directly into the shell to minimize keystrokes and get your task done faster.
- Use the long option in scripts to provide clarity. It will be read many times and typed once.

CALLOUT

### UNSUPPORTED COMMAND-LINE OPTIONS

If you try to use an option that is not supported, `ls` and other commands will usually print an error message similar to:

BASH

```
$ ls -j
```

ERROR

```
ls: invalid option -- 'j'
Try 'ls --help' for more information.
```

## The `man` command

The other way to learn about `ls` is to type

BASH

```
$ man ls
```

This command will turn your terminal into a page with a description of the `ls` command and its options.

To navigate through the `man` pages, you may use `↑` and `↓` to move line-by-line, or try `b` and `Spacebar` to skip up and down by a full page. To search for a character or word in the `man` pages, use `/` followed by the character or word you are searching for. Sometimes a search will result in multiple hits. If so, you can move between hits using `N` (for moving forward) and `Shift` + `N` (for moving backward).

To **quit** the `man` pages, press `q` .

CALLOUT

### MANUAL PAGES ON THE WEB

Of course, there is a third way to access help for commands: searching the internet via your web browser. When using internet search, including the phrase `unix man page` in your search query will help to find relevant results.

GNU provides links to its manuals including the core GNU utilities, which covers many commands introduced within this lesson.

CHALLENGE

### EXPLORING MORE `ls` OPTIONS

You can also use two options at the same time. What does the command `ls` do when used with the `-l` option? What about if you use both the `-l` and the `-h` option?

Some of its output is about properties that we do not cover in this lesson (such as file permissions and ownership), but the rest should be useful nevertheless.

Solution

The `-l` option makes `ls` use a **l**ong listing format, showing not only the file/directory names but also additional information, such as the file size and the time of its last modification. If you use both the `-h` option and the `-l` option, this makes the file size '**h**uman readable', i.e. displaying something like `5.3K` instead of `5369` .

CHALLENGE

### LISTING IN REVERSE CHRONOLOGICAL ORDER

By default, `ls` lists the contents of a directory in alphabetical order by name. The command `ls -t` lists items by time of last change instead of alphabetically. The command `ls -r` lists the contents of a directory in reverse order. Which file is displayed last when you combine the `-t` and `-r` options? Hint: You may need to use the `-l` option to see the last changed dates.

Solution

The most recently changed file is listed last when using `-rt` . This can be very useful for finding your most recent edits or checking to see if a new output file was written.

## Exploring Other Directories

Not only can we use `ls` on the current working directory, but we can use it to list the contents of a different directory. Let's take a look at our `Desktop` directory by running `ls -F Desktop` , i.e., the command `ls` with the `-F` **option** and the **argument** `Desktop` . The argument `Desktop` tells `ls` that we want a listing of something other than our current working directory:

BASH

```
$ ls -F Desktop
```

OUTPUT

```
shell-lesson-data/
```

Note that if a directory named `Desktop` does not exist in your current working directory, this command will return an error. Typically, a `Desktop` directory exists in your home directory, which we assume is the current working directory of your bash shell.

Your output should be a list of all the files and sub-directories in your Desktop directory, including the `shell-lesson-data` directory you downloaded at the setup for this lesson. (On most systems, the contents of the `Desktop` directory in the shell will show up as icons in a graphical user interface behind all the open windows. See if this is the case for you.)

Organizing things hierarchically helps us keep track of our work. While it's possible to put hundreds of files in our home directory just as it's possible to pile hundreds of printed papers on our desk, it's much easier to find things when they've been organized into sensibly-named subdirectories.

Now that we know the `shell-lesson-data` directory is located in our Desktop directory, we can do two things.

First, using the same strategy as before, we can look at its contents by passing a directory name to `ls` :

BASH

```
$ ls -F Desktop/shell-lesson-data
```

OUTPUT

```
exercise-data/  north-pacific-gyre/
```

Second, we can actually change our location to a different directory, so we are no longer located in our home directory.

The command to change locations is `cd` followed by a directory name to change our working directory. `cd` stands for 'change directory', which is a bit misleading. The command doesn't change the directory; it changes the shell's current working directory. In other words it changes the shell's settings for what directory we are in. The `cd` command is akin to double-clicking a folder in a graphical interface to get into that folder.

Let's say we want to move into the `exercise-data` directory we saw above. We can use the following series of commands to get there:

BASH

```
$ cd Desktop
$ cd shell-lesson-data
$ cd exercise-data
```

These commands will move us from our home directory into our Desktop directory, then into the `shell-lesson-data` directory, then into the `exercise-data` directory. You will notice that `cd` doesn't print anything. This is normal. Many shell commands will not output anything to the screen when successfully executed. But if we run `pwd` after it, we can see that we are now in `/Users/nelle/Desktop/shell-lesson-data/exercise-data` .

If we run `ls -F` without arguments now, it lists the contents of `/Users/nelle/Desktop/shell-lesson-data/exercise-data` , because that's where we now are:

BASH

```
$ pwd
```

OUTPUT

```
/Users/nelle/Desktop/shell-lesson-data/exercise-data
```

BASH

```
$ ls -F
```

OUTPUT

```
alkanes/  animal-counts/  creatures/  numbers.txt  writing/
```

We now know how to go down the directory tree (i.e. how to go into a subdirectory), but how do we go up (i.e. how do we leave a directory and go into its parent directory)? We might try the following:

BASH

```
$ cd shell-lesson-data
```

ERROR

```
-bash: cd: shell-lesson-data: No such file or directory
```

But we get an error! Why is this?

With our methods so far, `cd` can only see sub-directories inside your current directory. There are different ways to see directories above your current location; we'll start with the simplest.

There is a shortcut in the shell to move up one directory level. It works as follows:

BASH

```
$ cd ..
```

`..` is a special directory name meaning "the directory containing this one", or more succinctly, the **parent** of the current directory. Sure enough, if we run `pwd` after running `cd ..`, we're back in `/Users/nelle/Desktop/shell-lesson-data`:

BASH

```
$ pwd
```

OUTPUT

```
/Users/nelle/Desktop/shell-lesson-data
```

The special directory `..` doesn't usually show up when we run `ls`. If we want to display it, we can add the `-a` option to `ls -F`:

BASH

```
$ ls -F -a
```

OUTPUT

```
./  ../  exercise-data/  north-pacific-gyre/
```

`-a` stands for 'show all' (including hidden files); it forces `ls` to show us file and directory names that begin with `.`, such as `..` (which, if we're in `/Users/nelle`, refers to the `/Users` directory). As you can see, it also displays another special directory that's just called `.`, which means 'the current working directory'. It may seem redundant to have a name for it, but we'll see some uses for it soon.

Note that in most command line tools, multiple options can be combined with a single `-` and no spaces between the options; `ls -F -a` is equivalent to `ls -Fa`.

CALLOUT

### OTHER HIDDEN FILES

In addition to the hidden directories `..` and `.`, you may also see a file called `.bash_profile`. This file usually contains shell configuration settings. You may also see other files and directories beginning with `.`. These are usually files and directories that are used to configure different programs on your computer. The prefix `.` is used to prevent these configuration files from cluttering the terminal when a standard `ls` command is used.

These three commands are the basic commands for navigating the filesystem on your computer: `pwd`, `ls`, and `cd`. Let's explore some variations on those commands. What happens if you type `cd` on its own, without giving a directory?

BASH

```
$ cd
```

How can you check what happened? `pwd` gives us the answer!

BASH

```
$ pwd
```

OUTPUT

```
/Users/nelle
```

It turns out that `cd` without an argument will return you to your home directory, which is great if you've got lost in your own filesystem.

Let's try returning to the `exercise-data` directory from before. Last time, we used three commands, but we can actually string together the list of directories to move to `exercise-data` in one step:

BASH

```
$ cd Desktop/shell-lesson-data/exercise-data
```

Check that we've moved to the right place by running `pwd` and `ls -F`.

If we want to move up one level from the data directory, we could use `cd ..`. But there is another way to move to any directory, regardless of your current location.

So far, when specifying directory names, or even a directory path (as above), we have been using **relative paths**. When you use a relative path with a command like `ls` or `cd`, it tries to find that location from where we are, rather than from the root of the file system.

However, it is possible to specify the **absolute path** to a directory by including its entire path from the root directory, which is indicated by a leading slash. The leading `/` tells the computer to follow the path from the root of the file system, so it always refers to exactly one directory, no matter where we are when we run the command.

This allows us to move to our `shell-lesson-data` directory from anywhere on the filesystem (including from inside `exercise-data`). To find the absolute path we're looking for, we can use `pwd` and then extract the piece we need to move to `shell-lesson-data`.

BASH

```
$ pwd
```

OUTPUT

```
/Users/nelle/Desktop/shell-lesson-data/exercise-data
```

BASH

```
$ cd /Users/nelle/Desktop/shell-lesson-data
```

Run `pwd` and `ls -F` to ensure that we're in the directory we expect.

CALLOUT

### TWO MORE SHORTCUTS

The shell interprets a tilde ( `~` ) character at the start of a path to mean "the current user's home directory". For example, if Nelle's home directory is `/Users/nelle` , then `~/data` is equivalent to `/Users/nelle/data` . This only works if it is the first character in the path; `here/there/~/elsewhere` is *not* `here/there/Users/nelle/elsewhere` .

Another shortcut is the `-` (dash) character. `cd` will translate `-` into *the previous directory I was in*, which is faster than having to remember, then type, the full path. This is a *very* efficient way of moving *back and forth between two directories* – i.e. if you execute `cd -` twice, you end up back in the starting directory.

The difference between `cd ..` and `cd -` is that the former brings you *up*, while the latter brings you *back*.

---

Try it! First navigate to `~/Desktop/shell-lesson-data` (you should already be there).

BASH

```
$ cd ~/Desktop/shell-lesson-data
```

Then `cd` into the `exercise-data/creatures` directory

BASH

```
$ cd exercise-data/creatures
```

Now if you run

BASH

```
$ cd -
```

you'll see you're back in `~/Desktop/shell-lesson-data` . Run `cd -` again and you're back in `~/Desktop/shell-lesson-data/exercise-data/creatures`

CHALLENGE

## ABSOLUTE VS RELATIVE PATHS

Starting from `/Users/nelle/data`, which of the following commands could Nelle use to navigate to her home directory, which is `/Users/nelle`?

1. `cd .`
2. `cd /`
3. `cd /home/nelle`
4. `cd ../..`
5. `cd ~`
6. `cd home`
7. `cd ~/data/..`
8. `cd`
9. `cd ..`

Solution

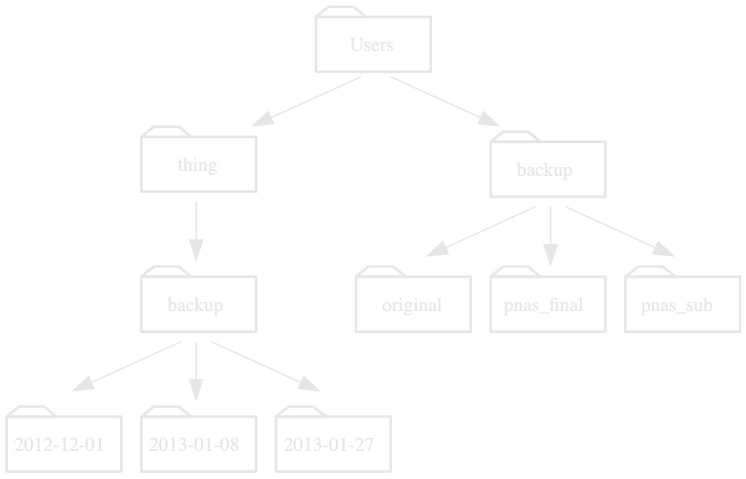
1. No: `.` stands for the current directory.
2. No: `/` stands for the root directory.
3. No: Nelle's home directory is `/Users/nelle`.
4. No: this command goes up two levels, i.e. ends in `/Users`.
5. Yes: `~` stands for the user's home directory, in this case `/Users/nelle`.
6. No: this command would navigate into a directory `home` in the current directory if it exists.
7. Yes: unnecessarily complicated, but correct.
8. Yes: shortcut to go back to the user's home directory.
9. Yes: goes up one level.

CHALLENGE

## RELATIVE PATH RESOLUTION

Using the filesystem diagram below, if `pwd` displays `/Users/thing`, what will `ls -F ../backup` display?

1. `../backup: No such file or directory`
2. `2012-12-01 2013-01-08 2013-01-27`
3. `2012-12-01/ 2013-01-08/ 2013-01-27/`
4. `original/ pnas_final/ pnas_sub/`



Solution

1. No: there *is* a directory `backup` in `/Users`.
2. No: this is the content of `Users/thing/backup`, but with `..`, we asked for one level further up.
3. No: see previous explanation.
4. Yes: `../backup/` refers to `/Users/backup/`.

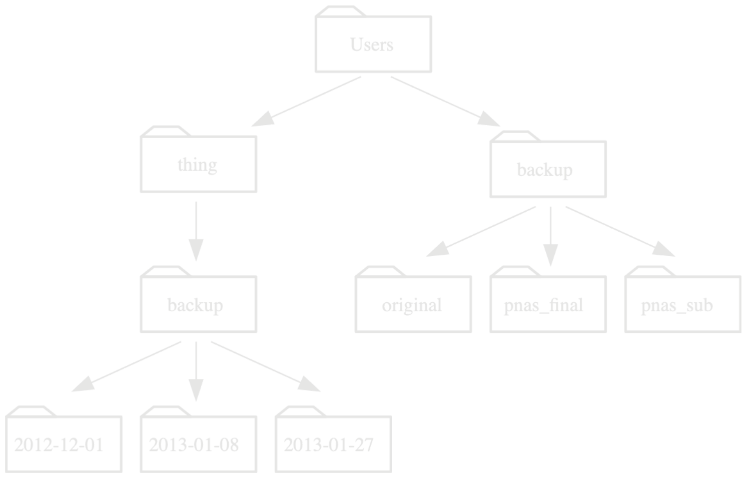
CHALLENGE

### `ls` READING COMPREHENSION

Using the filesystem diagram below, if `pwd` displays `/Users/backup`, and `-r` tells `ls` to display things in reverse order, what command(s) will result in the following output:

OUTPUT

```
pnas_sub/ pnas_final/ original/
```



1. `ls pwd`
2. `ls -r -F`
3. `ls -r -F /Users/backup`

Solution

1. No: `pwd` is not the name of a directory.
2. Yes: `ls` without directory argument lists files and directories in the current directory.
3. Yes: uses the absolute path explicitly.

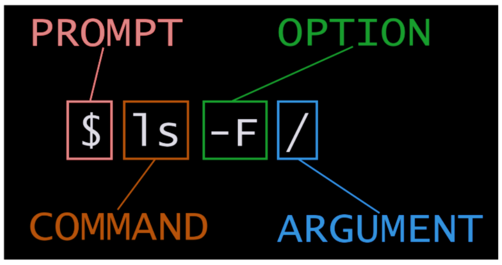
## General Syntax of a Shell Command

We have now encountered commands, options, and arguments, but it is perhaps useful to formalise some terminology.

Consider the command below as a general example of a command, which we will dissect into its component parts:

BASH

```
$ ls -F /
```



`ls` is the **command**, with an **option** `-F` and an **argument** `/`. We've already encountered options which either start with a single dash ( `-` ), known as **short options**, or two dashes ( `--` ), known as **long options**. [Options] change the behavior of a command and Arguments tell the command what to operate on (e.g. files and directories). Sometimes options and arguments are referred to as **parameters**. A command can be called with more than one option and more than one argument, but a command doesn't always require an argument or an option.

You might sometimes see options being referred to as **switches** or **flags**, especially for options that take no argument. In this lesson we will stick with using the term *option*.

Each part is separated by spaces. If you omit the space between `ls` and `-F` the shell will look for a command called `ls-F`, which doesn't exist. Also, capitalization can be important. For example, `ls -s` will display the size of files and directories alongside the names, while `ls -S` will sort the files and directories by size, as shown below:

BASH

```bash
$ cd ~/Desktop/shell-lesson-data
$ ls -s exercise-data
```

OUTPUT

```
total 28
 4 animal-counts   4 creatures  12 numbers.txt   4 alkanes   4 writing
```

Note that the sizes returned by `ls -s` are in *blocks*. As these are defined differently for different operating systems, you may not obtain the same figures as in the example.

BASH

```bash
$ ls -S exercise-data
```

OUTPUT

```
animal-counts  creatures  alkanes  writing  numbers.txt
```

Putting all that together, our command `ls -F /` above gives us a listing of files and directories in the root directory `/`. An example of the output you might get from the above command is given below:

BASH

```bash
$ ls -F /
```

OUTPUT

```
Applications/         System/
Library/              Users/
Network/              Volumes/
```

## Nelle’s Pipeline: Organizing Files

Knowing this much about files and directories, Nelle is ready to organize the files that the protein assay machine will create.

She creates a directory called `north-pacific-gyre` (to remind herself where the data came from), which will contain the data files from the assay machine and her data processing scripts.

Each of her physical samples is labelled according to her lab’s convention with a unique ten-character ID, such as ‘NENE01729A’. This ID is what she used in her collection log to record the location, time, depth, and other characteristics of the sample, so she decides to use it within the filename of each data file. Since the output of the assay machine is plain text, she will call her files `NENE01729A.txt`, `NENE01812A.txt`, and so on. All 1520 files will go into the same directory.

Now in her current directory `shell-lesson-data`, Nelle can see what files she has using the command:

BASH

```bash
$ ls north-pacific-gyre/
```

This command is a lot to type, but she can let the shell do most of the work through what is called **tab completion**. If she types:

BASH

```bash
$ ls nor
```

and then presses `Tab` (the tab key on her keyboard), the shell automatically completes the directory name for her:

BASH

```bash
$ ls north-pacific-gyre/
```

Pressing `Tab` again does nothing, since there are multiple possibilities; pressing `Tab` twice brings up a list of all the files.

If Nelle then presses `G` and then presses `Tab` again, the shell will append ‘goo’ since all files that start with ‘g’ share the first three characters ‘goo’.

BASH

```bash
$ ls north-pacific-gyre/goo
```

To see all of those files, she can press `Tab` twice more.

BASH

```bash
ls north-pacific-gyre/goo
goodiff.sh   goostats.sh
```

This is called **tab completion**, and we will see it in many other tools as we go on.

### KEY POINTS

- The file system is responsible for managing information on the disk.
- Information is stored in files, which are stored in directories (folders).
- Directories can also store other directories, which then form a directory tree.
- `pwd` prints the user's current working directory.
- `ls [path]` prints a listing of a specific file or directory; `ls` on its own lists the current working directory.
- `cd [path]` changes the current working directory.
- Most commands take options that begin with a single `-`.
- Directory names in a path are separated with `/` on Unix, but `\` on Windows.
- `/` on its own is the root directory of the whole file system.
- An absolute path specifies a location from the root of the file system.
- A relative path specifies a location starting from the current location.
- `.` on its own means 'the current directory'; `..` means 'the directory above the current one'.

Content from Working With Files and Directories

Last updated on 2025-09-15 | Edit this page

### OVERVIEW

#### Questions

- How can I create, copy, and delete files and directories?
- How can I edit files?

#### Objectives

- Delete, copy and move specified files and/or directories.
- Create files in that hierarchy using an editor or by copying and renaming existing files.
- Create a directory hierarchy that matches a given diagram.

# Creating directories

We now know how to explore files and directories, but how do we create them in the first place?

In this episode we will learn about creating and moving files and directories, using the `exercise-data/writing` directory as an example.

## Step one: see where we are and what we already have

We should still be in the `shell-lesson-data` directory on the Desktop, which we can check using:

BASH

```
$ pwd
```

OUTPUT

```
/Users/nelle/Desktop/shell-lesson-data
```

Next we'll move to the `exercise-data/writing` directory and see what it contains:

BASH

```
$ cd exercise-data/writing/
$ ls -F
```

OUTPUT

```
haiku.txt  LittleWomen.txt
```

### Create a directory

Let's create a new directory called `thesis` using the command `mkdir thesis` (which has no output):

BASH

```
$ mkdir thesis
```

As you might guess from its name, `mkdir` means 'make directory'. Since `thesis` is a relative path (i.e., does not have a leading slash, like `/what/ever/thesis`), the new directory is created in the current working directory:

BASH

```
$ ls -F
```

OUTPUT

```
haiku.txt  LittleWomen.txt  thesis/
```

Since we've just created the `thesis` directory, there's nothing in it yet:

BASH

```
$ ls -F thesis
```

Note that `mkdir` is not limited to creating single directories one at a time. The `-p` option allows `mkdir` to create a directory with nested subdirectories in a single operation:

BASH

```
$ mkdir -p ../project/data ../project/results
```

The `-R` option to the `ls` command will list all nested subdirectories within a directory. Let's use `ls -FR` to recursively list the new directory hierarchy we just created in the `project` directory:

BASH

```
$ ls -FR ../project
```

OUTPUT

```
../project/:
data/  results/

../project/data:

../project/results:
```

CALLOUT

### TWO WAYS OF DOING THE SAME THING

Using the shell to create a directory is no different than using a file explorer. If you open the current directory using your operating system's graphical file explorer, the `thesis` directory will appear there too. While the shell and the file explorer are two different ways of interacting with the files, the files and directories themselves are the same.

CALLOUT

### 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.

1. 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. `north-pacific-gyre/` rather than `north pacific gyre/` ). To test this out, try typing `mkdir north pacific gyre` and see what directory (or directories!) are made when you check with `ls -F` .

2. Don't begin the name with `-` (dash).

Commands treat names starting with `-` as options.

3. Stick with lowercase letters, numbers, `.` (period or 'full stop'), `-` (dash) and `_` (underscore).

Many other characters have special meanings on the command line. We will learn about some of these during this lesson. There are special characters that can cause your command to not work as expected and can even result in data loss.

If you need to refer to names of files or directories that have spaces or other special characters, you should surround the name in single quotes ( `''` ).

It is often good practice to use all lowercase letters in names of files and directories; Windows and macOS file systems are typically case insensitive and therefore unable to distinguish between `thesis` and `Thesis` in the same directory.

## Create a text file

Let's change our working directory to `thesis` using `cd` , then run a text editor called Nano to create a file called `draft.txt` :

BASH

```bash
$ cd thesis
$ nano draft.txt
```

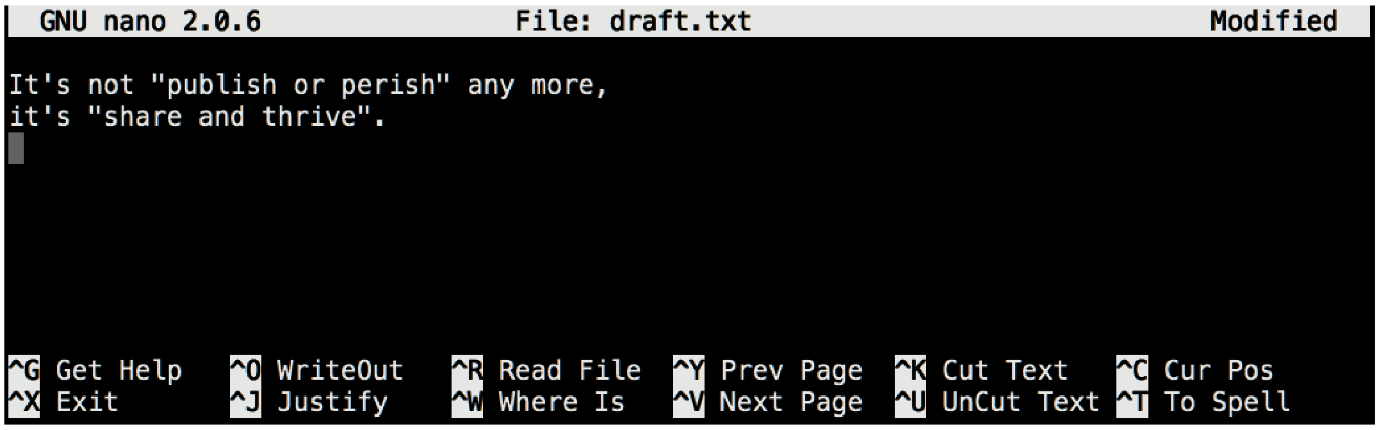
CALLOUT

### WHICH EDITOR?

When we say, ‘ `nano` is a text editor’ we really do mean ‘text’. It can only work with plain character data, not tables, images, or any other human-friendly media. We use it in examples because it is one of the least complex text editors. However, because of this trait, it may not be powerful enough or flexible enough for the work you need to do after this workshop. On Unix systems (such as Linux and macOS), many programmers use Emacs or Vim (both of which require more time to learn), or a graphical editor such as Gedit or VScode. On Windows, you may wish to use Notepad++. Windows also has a built-in editor called `notepad` that can be run from the command line in the same way as `nano` for the purposes of this lesson.

No matter what editor you use, you will need to know where it searches for and saves files. If you start it from the shell, it will (probably) use your current working directory as its default location. If you use your computer’s start menu, it may want to save files in your Desktop or Documents directory instead. You can change this by navigating to another directory the first time you ‘Save As…’

Let’s type in a few lines of text.



```
  GNU nano 2.0.6                File: draft.txt                        Modified

It's not "publish or perish" any more,
it's "share and thrive".


^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
```

Once we’re happy with our text, we can press `Ctrl` + `O` (press the `Ctrl` or `Control` key and, while holding it down, press the `O` key) to write our data to disk. We will be asked to provide a name for the file that will contain our text. Press `Return` to accept the suggested default of `draft.txt` .

Once our file is saved, we can use `Ctrl` + `X` to quit the editor and return to the shell.

CALLOUT

### CONTROL, CTRL, OR ^ KEY

The Control key is also called the 'Ctrl' key. There are various ways in which using the Control key may be described. For example, you may see an instruction to press the `Control` key and, while holding it down, press the `X` key, described as any of:

- `Control-X`
- `Control+X`
- `Ctrl-X`
- `Ctrl+X`
- `^X`
- `C-x`

In nano, along the bottom of the screen you'll see `^G Get Help ^O WriteOut`. This means that you can use `Control-G` to get help and `Control-O` to save your file.

`nano` doesn't leave any output on the screen after it exits, but `ls` now shows that we have created a file called `draft.txt`:

BASH

```bash
$ ls
```

OUTPUT

```
draft.txt
```

CHALLENGE

### CREATING FILES A DIFFERENT WAY

We have seen how to create text files using the `nano` editor. Now, try the following command:

BASH

```bash
$ touch my_file.txt
```

1. What did the `touch` command do? When you look at your current directory using the GUI file explorer, does the file show up?
2. Use `ls -l` to inspect the files. How large is `my_file.txt`?
3. When might you want to create a file this way?

Solution

1.
The `touch` command generates a new file called `my_file.txt` in your current directory. You can observe this newly generated file by typing `ls` at the command line prompt. `my_file.txt` can also be viewed in your GUI file explorer.

2.
When you inspect the file with `ls -l`, note that the size of `my_file.txt` is 0 bytes. In other words, it contains no data. If you open `my_file.txt` using your text editor it is blank.

3.
Some programs do not generate output files themselves, but instead require that empty files have already been generated. When the program is run, it searches for an existing file to populate with its output. The touch command allows you to efficiently generate a blank text file to be used by such programs.

DISCUSSION

### CREATING FILES A DIFFERENT WAY *(CONTINUED)*

To avoid confusion later on, we suggest removing the file you've just created before proceeding with the rest of the episode, otherwise future outputs may vary from those given in the lesson. To do this, use the following command:

BASH

```bash
$ rm my_file.txt
```

CALLOUT

### WHAT'S IN A NAME?

You may have noticed that all of Nelle's files are named 'something dot something', and in this part of the lesson, we always used the extension `.txt`. 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. 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, `.cfg` is a configuration file full of parameters for some program or other, `.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.

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.

## Moving files and directories

Returning to the `shell-lesson-data/exercise-data/writing` directory,

BASH

```
$ cd ~/Desktop/shell-lesson-data/exercise-data/writing
```

In our `thesis` directory we have a file `draft.txt` which isn't a particularly informative name, so let's change the file's name using `mv`, which is short for 'move':

BASH

```
$ mv thesis/draft.txt thesis/quotes.txt
```

The first argument tells `mv` what we're 'moving', while the second is where it's to go. In this case, we're moving `thesis/draft.txt` to `thesis/quotes.txt`, which has the same effect as renaming the file. Sure enough, `ls` shows us that `thesis` now contains one file called `quotes.txt`:

BASH

```
$ ls thesis
```

OUTPUT

```
quotes.txt
```

One must be careful when specifying the target file name, since `mv` will silently overwrite any existing file with the same name, which could lead to data loss. By default, `mv` will not ask for confirmation before overwriting files. However, an additional option, `mv -i` (or `mv --interactive`), will cause `mv` to request such confirmation.

Note that `mv` also works on directories.

Let's move `quotes.txt` into the current working directory. We use `mv` once again, but this time we'll use just the name of a directory as the second argument to tell `mv` that we want to keep the filename but put the file somewhere new. (This is why the command is called 'move'.) In this case, the directory name we use is the special directory name `.` that we mentioned earlier.

BASH

```
$ mv thesis/quotes.txt .
```

The effect is to move the file from the directory it was in to the current working directory. `ls` now shows us that `thesis` is empty:

BASH

```
$ ls thesis
```

OUTPUT

```
$
```

Alternatively, we can confirm the file `quotes.txt` is no longer present in the `thesis` directory by explicitly trying to list it:

BASH

```
$ ls thesis/quotes.txt
```

ERROR

```
ls: cannot access 'thesis/quotes.txt': No such file or directory
```

`ls` with a filename or directory as an argument only lists the requested file or directory. If the file given as the argument doesn't exist, the shell returns an error as we saw above. We can use this to see that `quotes.txt` is now present in our current directory:

BASH

```
$ ls quotes.txt
```

OUTPUT

```
quotes.txt
```

CHALLENGE

## MOVING FILES TO A NEW FOLDER

After running the following commands, Jamie realizes that she put the files `sucrose.dat` and `maltose.dat` into the wrong folder. The files should have been placed in the `raw` folder.

BASH

```
$ ls -F
 analyzed/ raw/
$ ls -F analyzed
fructose.dat glucose.dat maltose.dat sucrose.dat
$ cd analyzed
```

Fill in the blanks to move these files to the `raw/` folder (i.e. the one she forgot to put them in)

BASH

```
$ mv sucrose.dat maltose.dat ____/____
```

Solution

BASH

```
$ mv sucrose.dat maltose.dat ../raw
```

Recall that `..` refers to the parent directory (i.e. one above the current directory) and that `.` refers to the current directory.

## Copying files and directories

The `cp` command works very much like `mv`, except it copies a file instead of moving it. We can check that it did the right thing using `ls` with two paths as arguments — like most Unix commands, `ls` can be given multiple paths at once:

BASH

```
$ cp quotes.txt thesis/quotations.txt
$ ls quotes.txt thesis/quotations.txt
```

OUTPUT

```
quotes.txt   thesis/quotations.txt
```

We can also copy a directory and all its contents by using the recursive option `-r`, e.g. to back up a directory:

BASH

```
$ cp -r thesis thesis_backup
```

We can check the result by listing the contents of both the `thesis` and `thesis_backup` directory:

BASH

```
$ ls thesis thesis_backup
```

OUTPUT

```
thesis:
quotations.txt

thesis_backup:
quotations.txt
```

It is important to include the `-r` flag. If you want to copy a directory and you omit this option you will see a message that the directory has been omitted because `-r not specified`.

BASH

```
$ cp thesis thesis_backup
```

ERROR

```
cp: -r not specified; omitting directory 'thesis'
```

CHALLENGE

### RENAMING FILES

Suppose that you created a plain-text file in your current directory to contain a list of the statistical tests you will need to do to analyze your data, and named it `statstics.txt`

After creating and saving this file you realize you misspelled the filename! You want to correct the mistake, which of the following commands could you use to do so?

1. `cp statstics.txt statistics.txt`
2. `mv statstics.txt statistics.txt`
3. `mv statstics.txt .`
4. `cp statstics.txt .`

Solution

1. No. While this would create a file with the correct name, the incorrectly named file still exists in the directory and would need to be deleted.

2. Yes, this would work to rename the file.

3. No, the period(.) indicates where to move the file, but does not provide a new file name; identical file names cannot be created.

4. No, the period(.) indicates where to copy the file, but does not provide a new file name; identical file names cannot be created.

CHALLENGE

## MOVING AND COPYING

What is the output of the closing `ls` command in the sequence shown below?

BASH

```bash
$ pwd
```

OUTPUT

```
/Users/jamie/data
```

BASH

```bash
$ ls
```

OUTPUT

```
proteins.dat
```

BASH

```bash
$ mkdir recombined
$ mv proteins.dat recombined/
$ cp recombined/proteins.dat ../proteins-saved.dat
$ ls
```

1. `proteins-saved.dat recombined`
2. `recombined`
3. `proteins.dat recombined`
4. `proteins-saved.dat`

Solution

We start in the `/Users/jamie/data` directory, and create a new folder called `recombined`. The second line moves ( `mv` ) the file `proteins.dat` to the new folder ( `recombined` ). The third line makes a copy of the file we just moved. The tricky part here is where the file was copied to. Recall that `..` means 'go up a level', so the copied file is now in `/Users/jamie`. Notice that `..` is interpreted with respect to the current working directory, **not** with respect to the location of the file being copied. So, the only thing that will show using ls (in `/Users/jamie/data` ) is the recombined folder.

1. No, see explanation above. `proteins-saved.dat` is located at `/Users/jamie`
2. Yes
3. No, see explanation above. `proteins.dat` is located at `/Users/jamie/data/recombined`
4. No, see explanation above. `proteins-saved.dat` is located at `/Users/jamie`

## Removing files and directories

Returning to the `shell-lesson-data/exercise-data/writing` directory, let's tidy up this directory by removing the `quotes.txt` file we created. The Unix command we'll use for this is `rm` (short for 'remove'):

BASH

```bash
$ rm quotes.txt
```

We can confirm the file has gone using `ls`:

BASH

```bash
$ ls quotes.txt
```

ERROR

```
ls: cannot access 'quotes.txt': No such file or directory
```

CALLOUT

### DELETING IS FOREVER

The Unix shell doesn't have a trash bin that we can recover deleted files from (though most graphical interfaces to Unix do). Instead, when we delete files, they are unlinked from the file system so that their storage space on disk can be recycled. Tools for finding and recovering deleted files do exist, but there's no guarantee they'll work in any particular situation, since the computer may recycle the file's disk space right away.

CHALLENGE

### USING `rm` SAFELY

What happens when we execute `rm -i thesis_backup/quotations.txt`? Why would we want this protection when using `rm`?

Solution

OUTPUT

```
rm: remove regular file 'thesis_backup/quotations.txt'? y
```

The `-i` option will prompt before (every) removal (use `Y` to confirm deletion or `N` to keep the file). The Unix shell doesn't have a trash bin, so all the files removed will disappear forever. By using the `-i` option, we have the chance to check that we are deleting only the files that we want to remove.

If we try to remove the `thesis` directory using `rm thesis`, we get an error message:

BASH

```bash
$ rm thesis
```

ERROR

```
rm: cannot remove 'thesis': Is a directory
```

This happens because `rm` by default only works on files, not directories.

`rm` can remove a directory *and all its contents* if we use the recursive option `-r`, and it will do so *without any confirmation prompts*:

BASH

```bash
$ rm -r thesis
```

Given that there is no way to retrieve files deleted using the shell, `rm -r` *should be used with great caution* (you might consider adding the interactive option `rm -r -i`).

## Operations with multiple files and directories

Oftentimes one needs to copy or move several files at once. This can be done by providing a list of individual filenames, or specifying a naming pattern using wildcards. Wildcards are special characters that can be used to represent unknown characters or sets of characters when navigating the Unix file system.

CHALLENGE

## COPY WITH MULTIPLE FILENAMES

For this exercise, you can test the commands in the `shell-lesson-data/exercise-data` directory.

We have seen how `cp` behaves when given two arguments, but `cp` behaves differently when given three or more arguments. Let's try giving `cp` three arguments. In the example below, what does `cp` do when given several filenames and a directory name?

BASH

```
$ mkdir backup
$ cp creatures/minotaur.dat creatures/unicorn.dat backup/
```

In the example below, what does `cp` do when given three or more file names?

BASH

```
$ cd creatures
$ ls -F
```

OUTPUT

```
basilisk.dat  minotaur.dat  unicorn.dat
```

BASH

```
$ cp minotaur.dat unicorn.dat basilisk.dat
```

Solution

When `cp` is given two arguments and the second is a destination directory `cp` copies the files to the destination directory.

If given three or more arguments, `cp` throws an error such as the one below, because it is expecting a destination directory name as the last argument.

ERROR

```
cp: target 'basilisk.dat' is not a directory
```

## Using wildcards for accessing multiple files at once

**CALLOUT**

### WILDCARDS

`*` is a **wildcard**, which represents zero or more other characters. Let's consider the `shell-lesson-data/exercise-data/alkanes` directory: `*.pdb` represents `ethane.pdb`, `propane.pdb`, and every file that ends with '.pdb'. On the other hand, `p*.pdb` only represents `pentane.pdb` and `propane.pdb`, because the 'p' at the front can only represent filenames that begin with the letter 'p'.

`?` is also a wildcard, but it represents exactly one character. So `?ethane.pdb` could represent `methane.pdb` whereas `*ethane.pdb` represents both `ethane.pdb` and `methane.pdb`.

Wildcards can be used in combination with each other. For example, `???ane.pdb` indicates three characters followed by `ane.pdb`, giving `cubane.pdb ethane.pdb octane.pdb`.

When the shell sees a wildcard, it expands the wildcard to create a list of matching filenames *before* running the preceding command. As an exception, if a wildcard expression does not match any file, Bash will pass the expression as an argument to the command as it is. For example, typing `ls *.pdf` in the `alkanes` directory (which contains only files with names ending with `.pdb`) results in an error message that there is no file called `*.pdf`. However, generally commands like `wc` and `ls` see the lists of file names matching these expressions, but not the wildcards themselves. It is the shell, not the other programs, that expands the wildcards.

**CHALLENGE**

### LIST FILENAMES MATCHING A PATTERN

When run in the `alkanes` directory, which `ls` command(s) will produce this output?

```
ethane.pdb methane.pdb
```

1. `ls *t*ane.pdb`
2. `ls *t?ne.*`
3. `ls *t??ne.pdb`
4. `ls ethane.*`

Solution

The solution is `3.`

`1.` shows all files whose names contain zero or more characters (`*`) followed by the letter `t`, then zero or more characters (`*`) followed by `ane.pdb`. This gives `ethane.pdb methane.pdb octane.pdb pentane.pdb`.

`2.` shows all files whose names start with zero or more characters (`*`) followed by the letter `t`, then a single character (`?`), then `ne.` followed by zero or more characters (`*`). This will give us `octane.pdb` and `pentane.pdb` but doesn't match anything which ends in `thane.pdb`.

`3.` fixes the problems of option 2 by matching two characters (`??`) between `t` and `ne`. This is the solution.

`4.` only shows files starting with `ethane.`.

CHALLENGE

## MORE ON WILDCARDS

Sam has a directory containing calibration data, datasets, and descriptions of the datasets:

BASH

```
.
├── 2015-10-23-calibration.txt
├── 2015-10-23-dataset1.txt
├── 2015-10-23-dataset2.txt
├── 2015-10-23-dataset_overview.txt
├── 2015-10-26-calibration.txt
├── 2015-10-26-dataset1.txt
├── 2015-10-26-dataset2.txt
├── 2015-10-26-dataset_overview.txt
├── 2015-11-23-calibration.txt
├── 2015-11-23-dataset1.txt
├── 2015-11-23-dataset2.txt
├── 2015-11-23-dataset_overview.txt
├── backup
│   ├── calibration
│   └── datasets
└── send_to_bob
    ├── all_datasets_created_on_a_23rd
    └── all_november_files
```

Before heading off to another field trip, she wants to back up her data and send some datasets to her colleague Bob. Sam uses the following commands to get the job done:

BASH

```
$ cp *dataset* backup/datasets
$ cp ____calibration____ backup/calibration
$ cp 2015-____-____ send_to_bob/all_november_files/
$ cp ____ send_to_bob/all_datasets_created_on_a_23rd/
```

Help Sam by filling in the blanks.

The resulting directory structure should look like this

BASH

```
.
├── 2015-10-23-calibration.txt
├── 2015-10-23-dataset1.txt
├── 2015-10-23-dataset2.txt
├── 2015-10-23-dataset_overview.txt
├── 2015-10-26-calibration.txt
├── 2015-10-26-dataset1.txt
├── 2015-10-26-dataset2.txt
├── 2015-10-26-dataset_overview.txt
├── 2015-11-23-calibration.txt
├── 2015-11-23-dataset1.txt
├── 2015-11-23-dataset2.txt
├── 2015-11-23-dataset_overview.txt
├── backup
|   ├── calibration
|   │   ├── 2015-10-23-calibration.txt
|   │   ├── 2015-10-26-calibration.txt
|   │   └── 2015-11-23-calibration.txt
|   └── datasets
|       ├── 2015-10-23-dataset1.txt
|       ├── 2015-10-23-dataset2.txt
|       ├── 2015-10-23-dataset_overview.txt
|       ├── 2015-10-26-dataset1.txt
|       ├── 2015-10-26-dataset2.txt
|       ├── 2015-10-26-dataset_overview.txt
|       ├── 2015-11-23-dataset1.txt
|       ├── 2015-11-23-dataset2.txt
|       └── 2015-11-23-dataset_overview.txt
└── send_to_bob
    ├── all_datasets_created_on_a_23rd
    |   ├── 2015-10-23-dataset1.txt
    |   ├── 2015-10-23-dataset2.txt
    |   ├── 2015-10-23-dataset_overview.txt
    |   ├── 2015-11-23-dataset1.txt
    |   ├── 2015-11-23-dataset2.txt
    |   └── 2015-11-23-dataset_overview.txt
    └── all_november_files
        ├── 2015-11-23-calibration.txt
        ├── 2015-11-23-dataset1.txt
        ├── 2015-11-23-dataset2.txt
        └── 2015-11-23-dataset_overview.txt
```

Solution

BASH

```
$ cp *calibration.txt backup/calibration
$ cp 2015-11-* send_to_bob/all_november_files/
$ cp *-23-dataset* send_to_bob/all_datasets_created_on_a_23rd/
```

CHALLENGE

## ORGANIZING DIRECTORIES AND FILES

Jamie is working on a project, and she sees that her files aren't very well organized:

BASH

```
$ ls -F
```

OUTPUT

```
analyzed/  fructose.dat    raw/   sucrose.dat
```

The `fructose.dat` and `sucrose.dat` files contain output from her data analysis. What command(s) covered in this lesson does she need to run so that the commands below will produce the output shown?

BASH

```
$ ls -F
```

OUTPUT

```
analyzed/   raw/
```

BASH

```
$ ls analyzed
```

OUTPUT

```
fructose.dat    sucrose.dat
```

Solution

BASH

```
mv *.dat analyzed
```

Jamie needs to move her files `fructose.dat` and `sucrose.dat` to the `analyzed` directory. The shell will expand *.dat to match all .dat files in the current directory. The `mv` command then moves the list of .dat files to the 'analyzed' directory.

CHALLENGE

### REPRODUCE A FOLDER STRUCTURE

You're starting a new experiment and would like to duplicate the directory structure from your previous experiment so you can add new data.

Assume that the previous experiment is in a folder called `2016-05-18`, which contains a `data` folder that in turn contains folders named `raw` and `processed` that contain data files. The goal is to copy the folder structure of the `2016-05-18` folder into a folder called `2016-05-20` so that your final directory structure looks like this:

OUTPUT

```
2016-05-20/
└── data
    ├── processed
    └── raw
```

Which of the following set of commands would achieve this objective? What would the other commands do?

BASH

```bash
$ mkdir 2016-05-20
$ mkdir 2016-05-20/data
$ mkdir 2016-05-20/data/processed
$ mkdir 2016-05-20/data/raw
```

BASH

```bash
$ mkdir 2016-05-20
$ cd 2016-05-20
$ mkdir data
$ cd data
$ mkdir raw processed
```

BASH

```bash
$ mkdir 2016-05-20/data/raw
$ mkdir 2016-05-20/data/processed
```

BASH

```bash
$ mkdir -p 2016-05-20/data/raw
$ mkdir -p 2016-05-20/data/processed
```

BASH

```bash
$ mkdir 2016-05-20
$ cd 2016-05-20
$ mkdir data
$ mkdir raw processed
```

Solution

The first two sets of commands achieve this objective. The first set uses relative paths to create the top-level directory before the subdirectories.

The third set of commands will give an error because the default behavior of `mkdir` won't create a subdirectory of a non-existent directory: the intermediate level folders must be created first.

The fourth set of commands achieve this objective. Remember, the `-p` option, followed by a path of one or more directories, will cause `mkdir` to create any intermediate subdirectories as required.

The final set of commands generates the 'raw' and 'processed' directories at the same level as the 'data' directory.

## KEY POINTS

- `cp [old] [new]` copies a file.
- `mkdir [path]` creates a new directory.
- `mv [old] [new]` moves (renames) a file or directory.
- `rm [path]` removes (deletes) a file.
- `*` matches zero or more characters in a filename, so `*.txt` matches all files ending in `.txt` .
- `?` matches any single character in a filename, so `?.txt` matches `a.txt` but not `any.txt` .
- Use of the Control key may be described in many ways, including `Ctrl-X` , `Control-X` , and `^X` .
- The shell does not have a trash bin: once something is deleted, it's really gone.
- Most files' names are `something.extension` . The extension isn't required, and doesn't guarantee anything, but is normally used to indicate the type of data in the file.
- Depending on the type of work you do, you may need a more powerful text editor than Nano.

Content from Pipes and Filters

Last updated on 2025-07-25 | Edit this page

## OVERVIEW

### Questions

- How can I combine existing commands to produce a desired output?
- How can I show only part of the output?

### Objectives

- Explain the advantage of linking commands with pipes and filters.
- Combine sequences of commands to get new output
- Redirect a command's output to a file.
- Explain what usually happens if a program or pipeline isn't given any input to process.

Now that we know a few basic commands, we can finally look at the shell's most powerful feature: the ease with which it lets us combine existing programs in new ways. We'll start with the directory `shell-lesson-data/exercise-data/alkanes` that contains six files describing some simple organic molecules. The `.pdb` extension indicates that these files are in Protein Data Bank format, a simple text format that specifies the type and position of each atom in the molecule.

BASH

```bash
$ ls
```

OUTPUT

```
cubane.pdb    methane.pdb    pentane.pdb
ethane.pdb    octane.pdb     propane.pdb
```

Let's run an example command:

BASH

```bash
$ wc cubane.pdb
```

OUTPUT

```
20  156 1158 cubane.pdb
```

`wc` is the 'word count' command: it counts the number of lines, words, and characters in files (returning the values in that order from left to right).

If we run the command `wc *.pdb`, the `*` in `*.pdb` matches zero or more characters, so the shell turns `*.pdb` into a list of all `.pdb` files in the current directory:

BASH

```bash
$ wc *.pdb
```

OUTPUT

```
  20  156   1158   cubane.pdb
  12  84    622    ethane.pdb
   9  57    422    methane.pdb
  30  246   1828   octane.pdb
  21  165   1226   pentane.pdb
  15  111   825    propane.pdb
 107  819   6081   total
```

Note that `wc *.pdb` also shows the total number of all lines in the last line of the output.

If we run `wc -l` instead of just `wc`, the output shows only the number of lines per file:

BASH

```bash
$ wc -l *.pdb
```

OUTPUT

```
 20  cubane.pdb
 12  ethane.pdb
  9  methane.pdb
 30  octane.pdb
 21  pentane.pdb
 15  propane.pdb
107  total
```

The `-m` and `-w` options can also be used with the `wc` command to show only the number of characters or the number of words, respectively.

CALLOUT

### WHY ISN'T IT DOING ANYTHING?

What happens if a command is supposed to process a file, but we don't give it a filename? For example, what if we type:

BASH

```
$ wc -l
```

but don't type `*.pdb` (or anything else) after the command? Since it doesn't have any filenames, `wc` assumes it is supposed to process input given at the command prompt, so it just sits there and waits for us to give it some data interactively. From the outside, though, all we see is it sitting there, and the command doesn't appear to do anything.

If you make this kind of mistake, you can escape out of this state by holding down the control key ( `Ctrl` ) and pressing the letter `C` once: `Ctrl` + `C` . Then release both keys.

## Capturing output from commands

Which of these files contains the fewest lines? It's an easy question to answer when there are only six files, but what if there were 6000? Our first step toward a solution is to run the command:

BASH

```
$ wc -l *.pdb > lengths.txt
```

The greater than symbol, `>` , tells the shell to **redirect** the command's output to a file instead of printing it to the screen. This command prints no screen output, because everything that `wc` would have printed has gone into the file `lengths.txt` instead. If the file doesn't exist prior to issuing the command, the shell will create the file. If the file exists already, it will be silently overwritten, which may lead to data loss. Thus, **redirect** commands require caution.

`ls lengths.txt` confirms that the file exists:

BASH

```
$ ls lengths.txt
```

OUTPUT

```
lengths.txt
```

We can now send the content of `lengths.txt` to the screen using `cat lengths.txt`. The `cat` command gets its name from 'concatenate' i.e. join together, and it prints the contents of files one after another. There's only one file in this case, so `cat` just shows us what it contains:

BASH

```bash
$ cat lengths.txt
```

OUTPUT

```
  20  cubane.pdb
  12  ethane.pdb
   9  methane.pdb
  30  octane.pdb
  21  pentane.pdb
  15  propane.pdb
 107  total
```

CALLOUT

### OUTPUT PAGE BY PAGE

We'll continue to use `cat` in this lesson, for convenience and consistency, but it has the disadvantage that it always dumps the whole file onto your screen. More useful in practice is the command `less` (e.g. `less lengths.txt`). This displays a screenful of the file, and then stops. You can go forward one screenful by pressing the spacebar, or back one by pressing `b`. Press `q` to quit.

## Filtering output

Next we'll use the `sort` command to sort the contents of the `lengths.txt` file. But first we'll do an exercise to learn a little about the sort command:

CHALLENGE

### WHAT DOES `sort -n` DO?

The file `shell-lesson-data/exercise-data/numbers.txt` contains the following lines:

```
10
2
19
22
6
```

If we run `sort` on this file, the output is:

OUTPUT

```
10
19
2
22
6
```

If we run `sort -n` on the same file, we get this instead:

OUTPUT

```
2
6
10
19
22
```

Explain why `-n` has this effect.

Solution

The `-n` option specifies a numerical rather than an alphanumerical sort.

We will also use the `-n` option to specify that the sort is numerical instead of alphanumerical. This does *not* change the file; instead, it sends the sorted result to the screen:

BASH

```
$ sort -n lengths.txt
```

OUTPUT

```
  9  methane.pdb
 12  ethane.pdb
 15  propane.pdb
 20  cubane.pdb
 21  pentane.pdb
 30  octane.pdb
107  total
```

We can put the sorted list of lines in another temporary file called `sorted-lengths.txt` by putting `> sorted-lengths.txt` after the command, just as we used `> lengths.txt` to put the output of `wc` into `lengths.txt`. Once we've done that, we can run another command called `head` to get the first few lines in `sorted-lengths.txt`:

BASH

```
$ sort -n lengths.txt > sorted-lengths.txt
$ head -n 1 sorted-lengths.txt
```

OUTPUT

```
  9  methane.pdb
```

Using `-n 1` with `head` tells it that we only want the first line of the file; `-n 20` would get the first 20, and so on. Since `sorted-lengths.txt` contains the lengths of our files ordered from least to greatest, the output of `head` must be the file with the fewest lines.

CALLOUT

## REDIRECTING TO THE SAME FILE

It's a very bad idea to try redirecting the output of a command that operates on a file to the same file. For example:

BASH

```
$ sort -n lengths.txt > lengths.txt
```

Doing something like this may give you incorrect results and/or delete the contents of `lengths.txt`.

CHALLENGE

## WHAT DOES `>>` MEAN?

We have seen the use of `>`, but there is a similar operator `>>` which works slightly differently. We'll learn about the differences between these two operators by printing some strings. We can use the `echo` command to print strings e.g.

BASH

```
$ echo The echo command prints text
```

OUTPUT

```
The echo command prints text
```

Now test the commands below to reveal the difference between the two operators:

BASH

```
$ echo hello > testfile01.txt
```

and:

BASH

```
$ echo hello >> testfile02.txt
```

Hint: Try executing each command twice in a row and then examining the output files.

Solution

In the first example with `>`, the string 'hello' is written to `testfile01.txt`, but the file gets overwritten each time we run the command.

We see from the second example that the `>>` operator also writes 'hello' to a file (in this case `testfile02.txt`), but appends the string to the file if it already exists (i.e. when we run it for the second time).

CHALLENGE

### APPENDING DATA

We have already met the `head` command, which prints lines from the start of a file. `tail` is similar, but prints lines from the end of a file instead.

Consider the file `shell-lesson-data/exercise-data/animal-counts/animals.csv` . After these commands, select the answer that corresponds to the file `animals-subset.csv` :

BASH

```
$ head -n 3 animals.csv > animals-subset.csv
$ tail -n 2 animals.csv >> animals-subset.csv
```

1. The first three lines of `animals.csv`
2. The last two lines of `animals.csv`
3. The first three lines and the last two lines of `animals.csv`
4. The second and third lines of `animals.csv`

Solution

Option 3 is correct. For option 1 to be correct we would only run the `head` command. For option 2 to be correct we would only run the `tail` command. For option 4 to be correct we would have to pipe the output of `head` into `tail -n 2` by doing `head -n 3 animals.csv | tail -n 2 > animals-subset.csv`

## Passing output to another command

In our example of finding the file with the fewest lines, we are using two intermediate files `lengths.txt` and `sorted-lengths.txt` to store output. This is a confusing way to work because even once you understand what `wc` , `sort` , and `head` do, those intermediate files make it hard to follow what's going on. We can make it easier to understand by running `sort` and `head` together:

BASH

```
$ sort -n lengths.txt | head -n 1
```

OUTPUT

```
  9  methane.pdb
```

The vertical bar, `|` , between the two commands is called a **pipe**. It tells the shell that we want to use the output of the command on the left as the input to the command on the right.

This has removed the need for the `sorted-lengths.txt` file.

## Combining multiple commands

Nothing prevents us from chaining pipes consecutively. We can for example send the output of `wc` directly to `sort`, and then send the resulting output to `head`. This removes the need for any intermediate files.

We'll start by using a pipe to send the output of `wc` to `sort`:

BASH

```
$ wc -l *.pdb | sort -n
```

OUTPUT

```
  9 methane.pdb
 12 ethane.pdb
 15 propane.pdb
 20 cubane.pdb
 21 pentane.pdb
 30 octane.pdb
107 total
```

We can then send that output through another pipe, to `head`, so that the full pipeline becomes:

BASH

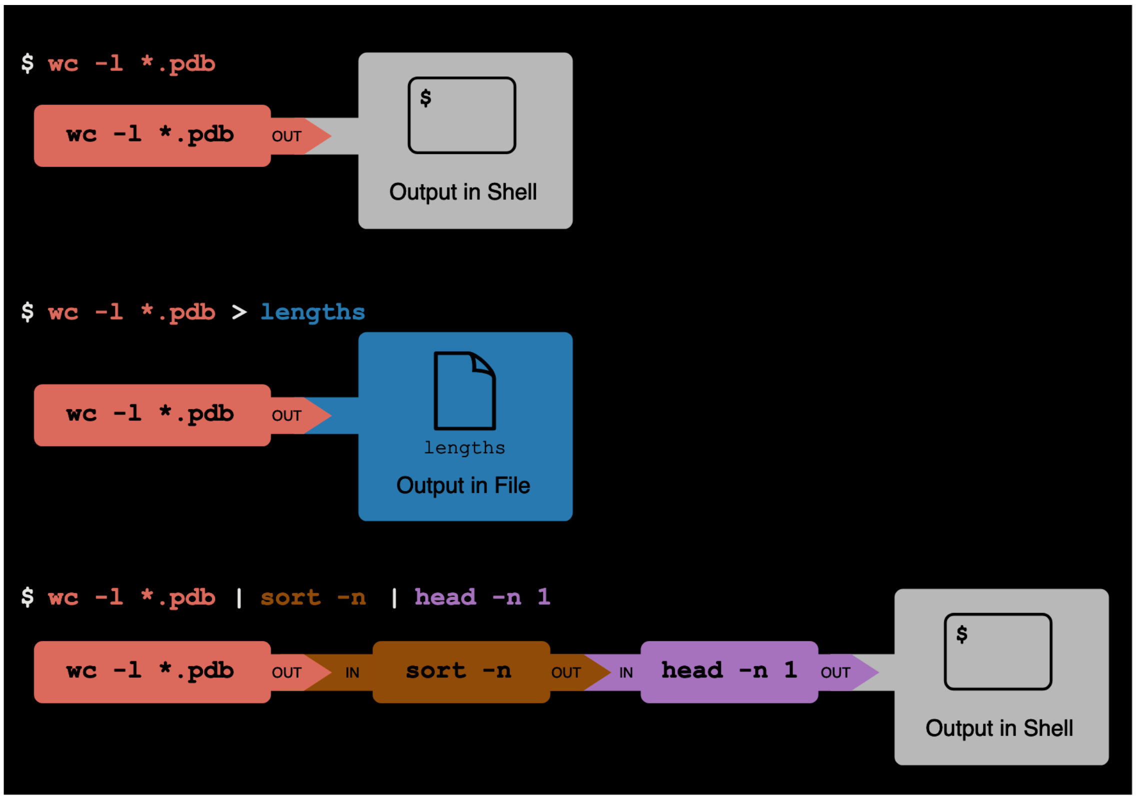
```
$ wc -l *.pdb | sort -n | head -n 1
```

OUTPUT

```
  9  methane.pdb
```

This is exactly like a mathematician nesting functions like *log(3x)* and saying 'the log of three times *x*'. In our case, the algorithm is 'head of sort of line count of `*.pdb`'.

The redirection and pipes used in the last few commands are illustrated below:



CHALLENGE

### PIPING COMMANDS TOGETHER

In our current directory, we want to find the 3 files which have the least number of lines. Which command listed below would work?

1. `wc -l * > sort -n > head -n 3`
2. `wc -l * | sort -n | head -n 1-3`
3. `wc -l * | head -n 3 | sort -n`
4. `wc -l * | sort -n | head -n 3`

Solution

Option 4 is the solution. The pipe character `|` is used to connect the output from one command to the input of another. `>` is used to redirect standard output to a file. Try it in the `shell-lesson-data/exercise-data/alkanes` directory!

## Tools designed to work together

This idea of linking programs together is why Unix has been so successful. Instead of creating enormous programs that try to do many different things, Unix programmers focus on creating lots of simple tools that each do one job well, and that work well with each other. This programming model is called 'pipes and filters'. We've already seen pipes; a **filter** is a program like `wc` or `sort` that transforms a stream of input into a stream of output. Almost all of the standard Unix tools can work this way. Unless told to do otherwise, they read from standard input, do something with what they've read, and write to standard output.

The key is that any program that reads lines of text from standard input and writes lines of text to standard output can be combined with every other program that behaves this way as well. You can *and should* write your programs this way so that you and other people can put those programs into pipes to multiply their power.

CHALLENGE

## PIPE READING COMPREHENSION

A file called `animals.csv` (in the `shell-lesson-data/exercise-data/animal-counts` folder) contains the following data:

```
2012-11-05,deer,5
2012-11-05,rabbit,22
2012-11-05,raccoon,7
2012-11-06,rabbit,19
2012-11-06,deer,2
2012-11-06,fox,4
2012-11-07,rabbit,16
2012-11-07,bear,1
```

What text passes through each of the pipes and the final redirect in the pipeline below? Note, the `sort -r` command sorts in reverse order.

BASH

```bash
$ cat animals.csv | head -n 5 | tail -n 3 | sort -r > final.txt
```

Hint: build the pipeline up one command at a time to test your understanding

Solution

The `head` command extracts the first 5 lines from `animals.csv`. Then, the last 3 lines are extracted from the previous 5 by using the `tail` command. With the `sort -r` command those 3 lines are sorted in reverse order. Finally, the output is redirected to a file: `final.txt`. The content of this file can be checked by executing `cat final.txt`. The file should contain the following lines:

```
2012-11-06,rabbit,19
2012-11-06,deer,2
2012-11-05,raccoon,7
```

## CHALLENGE

### PIPE CONSTRUCTION

For the file `animals.csv` from the previous exercise, consider the following command:

BASH

```bash
$ cut -d , -f 2 animals.csv
```

The `cut` command is used to select or 'cut out' certain sections of each line in the file for further processing while leaving the original file unchanged. By default, `cut` expects the lines to be separated into columns by a `Tab` character. A character used in this way is called a **delimiter**.
In the example above we use the `-d` option to specify the comma as our delimiter character instead of `Tab`. We have also used the `-f` option to specify that we want to extract the second field (column). This gives the following output:

OUTPUT

```
deer
rabbit
raccoon
rabbit
deer
fox
rabbit
bear
```

The `uniq` command filters out adjacent matching lines in a file. How could you extend this pipeline (using `uniq` and another command) to find out what animals the file contains (without any duplicates in their names)?

Solution

BASH

```bash
$ cut -d , -f 2 animals.csv | sort | uniq
```

CHALLENGE

### WHICH PIPE?

The file `animals.csv` contains 8 lines of data formatted as follows:

OUTPUT

```
2012-11-05,deer,5
2012-11-05,rabbit,22
2012-11-05,raccoon,7
2012-11-06,rabbit,19
...
```

The `uniq` command has a `-c` option which gives a count of the number of times a line occurs in its input. Assuming your current directory is `shell-lesson-data/exercise-data/animal-counts`, what command would you use to produce a table that shows the total count of each type of animal in the file?

1. `sort animals.csv | uniq -c`
2. `sort -t, -k2,2 animals.csv | uniq -c`
3. `cut -d, -f 2 animals.csv | uniq -c`
4. `cut -d, -f 2 animals.csv | sort | uniq -c`
5. `cut -d, -f 2 animals.csv | sort | uniq -c | wc -l`

Solution

Option 4 is the correct answer. If you have difficulty understanding why, try running the commands, or sub-sections of the pipelines (make sure you are in the `shell-lesson-data/exercise-data/animal-counts` directory).

## Nelle’s Pipeline: Checking Files

Nelle has run her samples through the assay machines and created 17 files in the `north-pacific-gyre` directory described earlier. As a quick check, starting from the `shell-lesson-data` directory, Nelle types:

BASH

```
$ cd north-pacific-gyre
$ wc -l *.txt
```

The output is 18 lines that look like this:

OUTPUT

```
300 NENE01729A.txt
300 NENE01729B.txt
300 NENE01736A.txt
300 NENE01751A.txt
300 NENE01751B.txt
300 NENE01812A.txt
... ...
```

Now she types this:

BASH

```
$ wc -l *.txt | sort -n | head -n 5
```

OUTPUT

```
 240 NENE02018B.txt
 300 NENE01729A.txt
 300 NENE01729B.txt
 300 NENE01736A.txt
 300 NENE01751A.txt
```

Whoops: one of the files is 60 lines shorter than the others. When she goes back and checks it, she sees that she did that assay at 8:00 on a Monday morning — someone was probably in using the machine on the weekend, and she forgot to reset it. Before re-running that sample, she checks to see if any files have too much data:

BASH

```
$ wc -l *.txt | sort -n | tail -n 5
```

OUTPUT

```
 300 NENE02040B.txt
 300 NENE02040Z.txt
 300 NENE02043A.txt
 300 NENE02043B.txt
5040 total
```

Those numbers look good — but what's that 'Z' doing there in the third-to-last line? All of her samples should be marked 'A' or 'B'; by convention, her lab uses 'Z' to indicate samples with missing information. To find others like it, she does this:

BASH

```
$ ls *Z.txt
```

OUTPUT

```
NENE01971Z.txt    NENE02040Z.txt
```

Sure enough, when she checks the log on her laptop, there's no depth recorded for either of those samples. Since it's too late to get the information any other way, she must exclude those two files from her analysis. She could delete them using `rm`, but there are actually some analyses she might do later where depth doesn't matter, so instead, she'll have to be careful later on to select files using the wildcard expressions `NENE*A.txt NENE*B.txt` .

CHALLENGE

### REMOVING UNNEEDED FILES

Suppose you want to delete your processed data files, and only keep your raw files and processing script to save storage. The raw files end in `.dat` and the processed files end in `.txt` . Which of the following would remove all the processed data files, and *only* the processed data files?

1. `rm ?.txt`
2. `rm *.txt`
3. `rm * .txt`
4. `rm *.*`

Solution

1. This would remove `.txt` files with one-character names
2. This is the correct answer
3. The shell would expand `*` to match everything in the current directory, so the command would try to remove all matched files and an additional file called `.txt`
4. The shell expands `*.*` to match all filenames containing at least one `.` , including the processed files ( `.txt` ) *and* raw files ( `.dat` )

KEY POINTS

- `wc` counts lines, words, and characters in its inputs.
- `cat` displays the contents of its inputs.
- `sort` sorts its inputs.
- `head` displays the first 10 lines of its input by default without additional arguments.
- `tail` displays the last 10 lines of its input by default without additional arguments.
- `command > [file]` redirects a command's output to a file (overwriting any existing content).
- `command >> [file]` appends a command's output to a file.
- `[first] | [second]` is a pipeline: the output of the first command is used as the input to the second.
- The best way to use the shell is to use pipes to combine simple single-purpose programs (filters).

Content from Loops

Last updated on 2025-08-20 | Edit this page

## OVERVIEW

### Questions

- How can I perform the same actions on many different files?

## Objectives

- Write a loop that applies one or more commands separately to each file in a set of files.
- Trace the values taken on by a loop variable during execution of the loop.
- Explain the difference between a variable's name and its value.
- Explain why spaces and some punctuation characters shouldn't be used in file names.
- Demonstrate how to see what commands have recently been executed.
- Re-run recently executed commands without retyping them.

**Loops** are a programming construct which allow us to repeat a command or set of commands for each item in a list. As such they are key to productivity improvements through automation. Similar to wildcards and tab completion, using loops also reduces the amount of typing required (and hence reduces the number of typing mistakes).

Suppose we have several hundred genome data files named `basilisk.dat`, `minotaur.dat`, and `unicorn.dat`. For this example, we'll use the `exercise-data/creatures` directory which only has three example files, but the principles can be applied to many many more files at once.

The structure of these files is the same: the common name, classification, and updated date are presented on the first three lines, with DNA sequences on the following lines. Let's look at the files:

BASH

```bash
$ head -n 5 basilisk.dat minotaur.dat unicorn.dat
```

We would like to print out the classification for each species, which is given on the second line of each file. For each file, we would need to execute the command `head -n 2` and pipe this to `tail -n 1`. We'll use a loop to solve this problem, but first let's look at the general form of a loop, using the pseudo-code below:

BASH

```bash
# The word "for" indicates the start of a "For-loop" command
for thing in list_of_things
#The word "do" indicates the start of job execution list
do
    # Indentation within the loop is not required, but aids legibility
    operation_using/command $thing
# The word "done" indicates the end of a loop
done
```

and we can apply this to our example like this:

BASH

```bash
$ for filename in basilisk.dat minotaur.dat unicorn.dat
> do
>     echo $filename
>     head -n 2 $filename | tail -n 1
> done
```

OUTPUT

```
basilisk.dat
CLASSIFICATION: basiliscus vulgaris
minotaur.dat
CLASSIFICATION: bos hominus
unicorn.dat
CLASSIFICATION: equus monoceros
```

**CALLOUT**

### FOLLOW THE PROMPT

The shell prompt changes from `$` to `>` and back again as we were typing in our loop. The second prompt, `>`, is different to remind us that we haven't finished typing a complete command yet. A semicolon, `;`, can be used to separate two commands written on a single line.

When the shell sees the keyword `for`, it knows to repeat a command (or group of commands) once for each item in a list. Each time the loop runs (called an iteration), an item in the list is assigned in sequence to the **variable**, and the commands inside the loop are executed, before moving on to the next item in the list. Inside the loop, we call for the variable's value by putting `$` in front of it. The `$` tells the shell interpreter to treat the variable as a variable name and substitute its value in its place, rather than treat it as text or an external command.

In this example, the list is three filenames: `basilisk.dat`, `minotaur.dat`, and `unicorn.dat`. Each time the loop iterates, we first use `echo` to print the value that the variable `$filename` currently holds. This is not necessary for the result, but beneficial for us here to have an easier time to follow along. Next, we will run the `head` command on the file currently referred to by `$filename`. The first time through the loop, `$filename` is `basilisk.dat`. The interpreter runs the command `head` on `basilisk.dat` and pipes the first two lines to the `tail` command, which then prints the second line of `basilisk.dat`. For the second iteration, `$filename` becomes `minotaur.dat`. This time, the shell runs `head` on `minotaur.dat` and pipes the first two lines to the `tail` command, which then prints the second line of `minotaur.dat`. For the third iteration, `$filename` becomes `unicorn.dat`, so the shell runs the `head` command on that file, and `tail` on the output of that. Since the list was only three items, the shell exits the `for` loop.

**CALLOUT**

### SAME SYMBOLS, DIFFERENT MEANINGS

Here we see `>` being used as a shell prompt, whereas `>` is also used to redirect output. Similarly, `$` is used as a shell prompt, but, as we saw earlier, it is also used to ask the shell to get the value of a variable.

If the *shell* prints `>` or `$` then it expects you to type something, and the symbol is a prompt.

If *you* type `>` or `$` yourself, it is an instruction from you that the shell should redirect output or get the value of a variable.

When using variables it is also possible to put the names into curly braces to clearly delimit the variable name: `$filename` is equivalent to `${filename}`, but is different from `${file}name`. You may find this notation in other people's programs.

We have called the variable in this loop `filename` in order to make its purpose clearer to human readers. The shell itself doesn't care what the variable is called; if we wrote this loop as:

BASH

```
$ for x in basilisk.dat minotaur.dat unicorn.dat
> do
>     head -n 2 $x | tail -n 1
> done
```

or:

BASH

```
$ for temperature in basilisk.dat minotaur.dat unicorn.dat
> do
>     head -n 2 $temperature | tail -n 1
> done
```

it would work exactly the same way. *Don't do this.* Programs are only useful if people can understand them, so meaningless names (like `x`) or misleading names (like `temperature`) increase the odds that the program won't do what its readers think it does.

In the above examples, the variables ( `thing` , `filename` , `x` and `temperature` ) could have been given any other name, as long as it is meaningful to both the person writing the code and the person reading it.

Note also that loops can be used for other things than filenames, like a list of numbers or a subset of data.

CHALLENGE

## WRITE YOUR OWN LOOP

How would you write a loop that echoes all 10 numbers from 0 to 9?

Solution

BASH

```
$ for loop_variable in 0 1 2 3 4 5 6 7 8 9
> do
>     echo $loop_variable
> done
```

OUTPUT

```
0
1
2
3
4
5
6
7
8
9
```

Alternatively, try replacing the enumeration of integers `0 1 2 3 4 5 6 7 8 9` by `{0..9}` to obtain an identical output.

CHALLENGE

## VARIABLES IN LOOPS

This exercise refers to the `shell-lesson-data/exercise-data/alkanes` directory. `ls *.pdb` gives the following output:

OUTPUT

```
cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
```

What is the output of the following code?

BASH

```bash
$ for datafile in *.pdb
> do
>     ls *.pdb
> done
```

Now, what is the output of the following code?

BASH

```bash
$ for datafile in *.pdb
> do
>     ls $datafile
> done
```

Why do these two loops give different outputs?

Solution

The first code block gives the same output on each iteration through the loop. Bash expands the wildcard `*.pdb` within the loop body (as well as before the loop starts) to match all files ending in `.pdb` and then lists them using `ls`. The expanded loop would look like this:

BASH

```bash
$ for datafile in cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
> do
>     ls cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
> done
```

OUTPUT

```
cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
cubane.pdb  ethane.pdb  methane.pdb  octane.pdb  pentane.pdb  propane.pdb
```

The second code block lists a different file on each loop iteration. The value of the `datafile` variable is evaluated using `$datafile`, and then listed using `ls`.

OUTPUT

```
cubane.pdb
ethane.pdb
methane.pdb
octane.pdb
pentane.pdb
propane.pdb
```

CHALLENGE

### LIMITING SETS OF FILES

What would be the output of running the following loop in the `shell-lesson-data/exercise-data/alkanes` directory?

BASH

```bash
$ for filename in c*
> do
>     ls $filename
> done
```

1. No files are listed.
2. All files are listed.
3. Only `cubane.pdb` , `octane.pdb` and `pentane.pdb` are listed.
4. Only `cubane.pdb` is listed.

Solution

4 is the correct answer. `*` matches zero or more characters, so any file name starting with the letter c, followed by zero or more other characters will be matched.

CHALLENGE

### LIMITING SETS OF FILES *(CONTINUED)*

How would the output differ from using this command instead?

BASH

```bash
$ for filename in *c*
> do
>     ls $filename
> done
```

1. The same files would be listed.
2. All the files are listed this time.
3. No files are listed this time.
4. The files `cubane.pdb` and `octane.pdb` will be listed.
5. Only the file `octane.pdb` will be listed.

Solution

4 is the correct answer. `*` matches zero or more characters, so a file name with zero or more characters before a letter c and zero or more characters after the letter c will be matched.

CHALLENGE

## SAVING TO A FILE IN A LOOP - PART ONE

In the `shell-lesson-data/exercise-data/alkanes` directory, what is the effect of this loop?

BASH

```bash
for alkanes in *.pdb
do
    echo $alkanes
    cat $alkanes > alkanes.pdb
done
```

1. Prints `cubane.pdb` , `ethane.pdb` , `methane.pdb` , `octane.pdb` , `pentane.pdb` and `propane.pdb` , and the text from `propane.pdb` will be saved to a file called `alkanes.pdb` .
2. Prints `cubane.pdb` , `ethane.pdb` , and `methane.pdb` , and the text from all three files would be concatenated and saved to a file called `alkanes.pdb` .
3. Prints `cubane.pdb` , `ethane.pdb` , `methane.pdb` , `octane.pdb` , and `pentane.pdb` , and the text from `propane.pdb` will be saved to a file called `alkanes.pdb` .
4. None of the above.

Solution

1. The text from each file in turn gets written to the `alkanes.pdb` file. However, the file gets overwritten on each loop iteration, so the final content of `alkanes.pdb` is the text from the `propane.pdb` file.

CHALLENGE

## SAVING TO A FILE IN A LOOP - PART TWO

Also in the `shell-lesson-data/exercise-data/alkanes` directory, what would be the output of the following loop?

BASH

```bash
for datafile in *.pdb
do
    cat $datafile >> all.pdb
done
```

1. All of the text from `cubane.pdb` , `ethane.pdb` , `methane.pdb` , `octane.pdb` , and `pentane.pdb` would be concatenated and saved to a file called `all.pdb` .
2. The text from `ethane.pdb` will be saved to a file called `all.pdb` .
3. All of the text from `cubane.pdb` , `ethane.pdb` , `methane.pdb` , `octane.pdb` , `pentane.pdb` and `propane.pdb` would be concatenated and saved to a file called `all.pdb` .
4. All of the text from `cubane.pdb` , `ethane.pdb` , `methane.pdb` , `octane.pdb` , `pentane.pdb` and `propane.pdb` would be printed to the screen and saved to a file called `all.pdb` .

Solution

3 is the correct answer. `>>` appends to a file, rather than overwriting it with the redirected output from a command. Given the output from the `cat` command has been redirected, nothing is printed to the screen.

Let's continue with our example in the `shell-lesson-data/exercise-data/creatures` directory. Here's another example:

BASH

```bash
$ for filename in *.dat
> do
>     echo $filename
>     head -n 100 $filename | tail -n 20
> done
```

The shell starts by expanding `*.dat` to create the list of files it will process. The **loop body** then executes two commands for each of those files. In the first command, `$filename` is expanded to the name of the file, so `echo $filename` prints the name of the file. Then, the `head` and `tail` combination selects lines 81-100 from whatever file is being processed (assuming the file has at least 100 lines).

CALLOUT

## SPACES IN NAMES

Spaces are used to separate the elements of the list that we are going to loop over. If one of those elements contains a space character, we need to surround it with quotes, and do the same thing to our loop variable. Suppose our data files are named:

```
red dragon.dat
purple unicorn.dat
```

To loop over these files, we would need to add double quotes like so:

BASH

```bash
$ for filename in "red dragon.dat" "purple unicorn.dat"
> do
>     head -n 100 "$filename" | tail -n 20
> done
```

It is simpler to avoid using spaces (or other special characters) in filenames.

The files above don't exist, so if we run the above code, the `head` command will be unable to find them; however, the error message returned will show the name of the files it is expecting:

ERROR

```
head: cannot open ‘red dragon.dat' for reading: No such file or directory
head: cannot open ‘purple unicorn.dat' for reading: No such file or directory
```

Try removing the quotes around `$filename` in the loop above to see the effect of the quote marks on spaces. Note that we get a result from the loop command for unicorn.dat when we run this code in the `creatures` directory:

OUTPUT

```
head: cannot open ‘red' for reading: No such file or directory
head: cannot open ‘dragon.dat' for reading: No such file or directory
head: cannot open ‘purple' for reading: No such file or directory
CGGTACCGAA
AAGGGTCGCG
CAAGTGTTCC
...
```

We would like to modify each of the files in `shell-lesson-data/exercise-data/creatures` , but also save a version of the original files. We want to copy the original files to new files named `original-basilisk.dat` and `original-unicorn.dat` , for example. We can't use:

BASH

```bash
$ cp *.dat original-*.dat
```

because that would expand to:

BASH

```bash
$ cp basilisk.dat minotaur.dat unicorn.dat original-*.dat
```

This wouldn't back up our files, instead we get an error:

ERROR

```
cp: target `original-*.dat' is not a directory
```

This problem arises when `cp` receives more than two inputs. When this happens, it expects the last input to be a directory where it can copy all the files it was passed. Since there is no directory named `original-*.dat` in the `creatures` directory, we get an error.

Instead, we can use a loop:

BASH

```bash
$ for filename in *.dat
> do
>     cp $filename original-$filename
> done
```

This loop runs the `cp` command once for each filename. The first time, when `$filename` expands to `basilisk.dat` , the shell executes:

BASH

```bash
cp basilisk.dat original-basilisk.dat
```

The second time, the command is:

BASH

```bash
cp minotaur.dat original-minotaur.dat
```

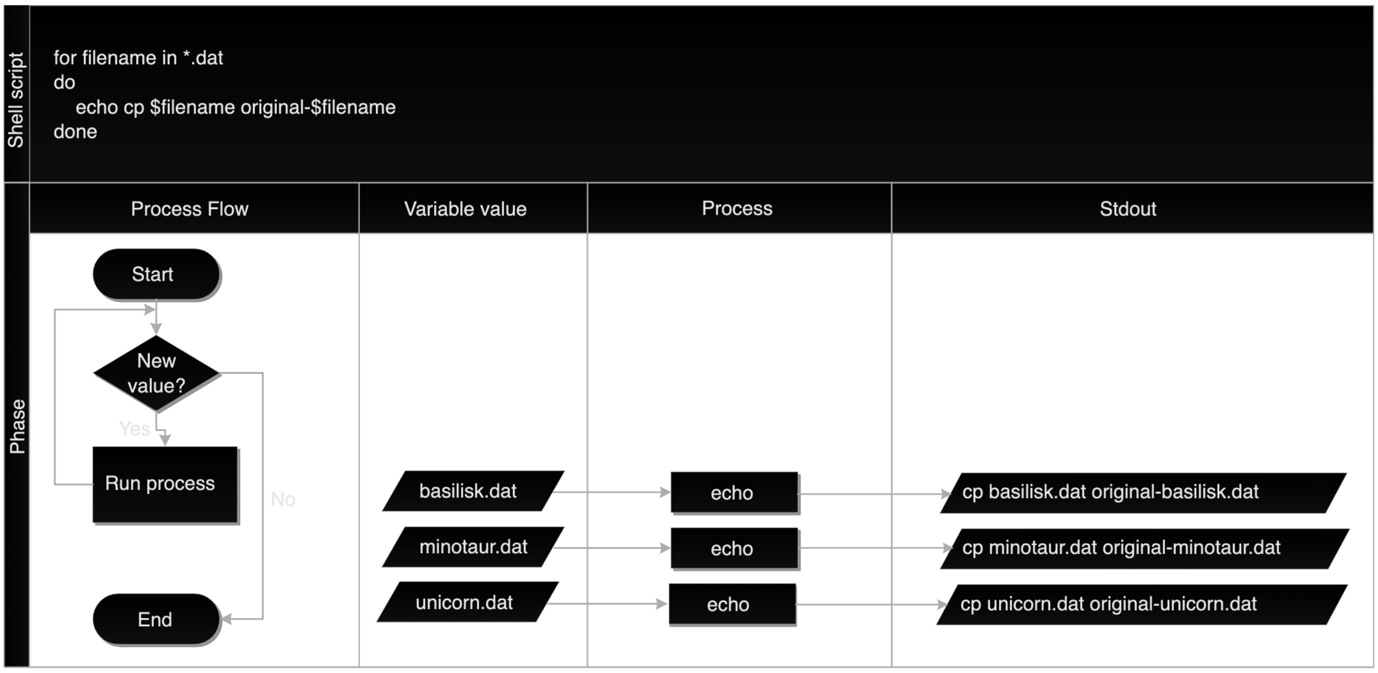
The third and last time, the command is:

BASH

```bash
cp unicorn.dat original-unicorn.dat
```

Since the `cp` command does not normally produce any output, it's hard to check that the loop is working correctly. However, we learned earlier how to print strings using `echo` , and we can modify the loop to use `echo` to print our commands without actually executing them. As such we can check what commands *would be* run in the unmodified loop.

The following diagram shows what happens when the modified loop is executed and demonstrates how the judicious use of `echo` is a good debugging technique.



## Nelle's Pipeline: Processing Files

Nelle is now ready to process her data files using `goostats.sh` — a shell script written by her supervisor. This calculates some statistics from a protein sample file and takes two arguments:

1. an input file (containing the raw data)
2. an output file (to store the calculated statistics)

Since she's still learning how to use the shell, she decides to build up the required commands in stages. Her first step is to make sure that she can select the right input files — remember, these are ones whose names end in 'A' or 'B', rather than 'Z'. Moving to the `north-pacific-gyre` directory, Nelle types:

BASH

```
$ cd
$ cd Desktop/shell-lesson-data/north-pacific-gyre
$ for datafile in NENE*A.txt NENE*B.txt
> do
>     echo $datafile
> done
```

OUTPUT

```
NENE01729A.txt
NENE01736A.txt
NENE01751A.txt

...
NENE02040B.txt
NENE02043B.txt
```

Her next step is to decide what to call the files that the `goostats.sh` analysis program will create. Prefixing each input file's name with 'stats' seems simple, so she modifies her loop to do that:

BASH

```
$ for datafile in NENE*A.txt NENE*B.txt
> do
>     echo $datafile stats-$datafile
> done
```

OUTPUT

```
NENE01729A.txt stats-NENE01729A.txt
NENE01736A.txt stats-NENE01729A.txt
NENE01751A.txt stats-NENE01729A.txt
...
NENE02040B.txt stats-NENE02040B.txt
NENE02043B.txt stats-NENE02043B.txt
```

She hasn't actually run `goostats.sh` yet, but now she's sure she can select the right files and generate the right output filenames.

Typing in commands over and over again is becoming tedious, though, and Nelle is worried about making mistakes, so instead of re-entering her loop, she presses ↑ . In response, the shell redisplays the whole loop on one line (using semi-colons to separate the pieces):

BASH

```
$ for datafile in NENE*A.txt NENE*B.txt; do echo $datafile stats-$datafile; done
```

Using the ← , Nelle navigates to the `echo` command and changes it to `bash goostats.sh` :

BASH

```
$ for datafile in NENE*A.txt NENE*B.txt; do bash goostats.sh $datafile stats-$datafile; done
```

When she presses `Enter` , the shell runs the modified command. However, nothing appears to happen — there is no output. After a moment, Nelle realizes that since her script doesn't print anything to the screen any longer, she has no idea whether it is running, much less how quickly. She kills the running command by typing `Ctrl` + `C` , uses ↑ to repeat the command, and edits it to read:

BASH

```
$ for datafile in NENE*A.txt NENE*B.txt; do echo $datafile;
bash goostats.sh $datafile stats-$datafile; done
```

CALLOUT

### BEGINNING AND END

We can move to the beginning of a line in the shell by typing `Ctrl` + `A` and to the end using `Ctrl` + `E` .

When she runs her program now, it produces one line of output every five seconds or so:

OUTPUT

```
NENE01729A.txt
NENE01736A.txt
NENE01751A.txt
...
```

1518 times 5 seconds, divided by 60, tells her that her script will take about two hours to run. As a final check, she opens another terminal window, goes into `north-pacific-gyre`, and uses `cat stats-NENE01729B.txt` to examine one of the output files. It looks good, so she decides to get some coffee and catch up on her reading.

CALLOUT

### THOSE WHO KNOW HISTORY CAN CHOOSE TO REPEAT IT

Another way to repeat previous work is to use the `history` command to get a list of the last few hundred commands that have been executed, and then to use `!123` (where '123' is replaced by the command number) to repeat one of those commands. For example, if Nelle types this:

BASH

```bash
$ history | tail -n 5
```

OUTPUT

```
456  for datafile in NENE*A.txt NENE*B.txt; do   echo $datafile stats-$datafile; done
457  for datafile in NENE*A.txt NENE*B.txt; do echo $datafile stats-$datafile; done
458  for datafile in NENE*A.txt NENE*B.txt; do bash goostats.sh $datafile stats-$datafile; done
459  for datafile in NENE*A.txt NENE*B.txt; do echo $datafile; bash goostats.sh $datafile
stats-$datafile; done
460  history | tail -n 5
```

then she can re-run `goostats.sh` on the files simply by typing `!459`.

CALLOUT

### OTHER HISTORY COMMANDS

There are a number of other shortcut commands for getting at the history.

- `Ctrl` + `R` enters a history search mode 'reverse-i-search' and finds the most recent command in your history that matches the text you enter next. Press `Ctrl` + `R` one or more additional times to search for earlier matches. You can then use the left and right arrow keys to choose that line and edit it then hit `Return` to run the command.
- `!!` retrieves the immediately preceding command (you may or may not find this more convenient than using `↑`)
- `!$` retrieves the last word of the last command. That's useful more often than you might expect: after `bash goostats.sh NENE01729B.txt stats-NENE01729B.txt`, you can type `less !$` to look at the file `stats-NENE01729B.txt`, which is quicker than doing `↑` and editing the command-line.

CHALLENGE

## DOING A DRY RUN

A loop is a way to do many things at once — or to make many mistakes at once if it does the wrong thing. One way to check what a loop *would* do is to `echo` the commands it would run instead of actually running them.

Suppose we want to preview the commands the following loop will execute without actually running those commands:

BASH

```
$ for datafile in *.pdb
> do
>     cat $datafile >> all.pdb
> done
```

What is the difference between the two loops below, and which one would we want to run?

BASH

```
# Version 1
$ for datafile in *.pdb
> do
>     echo cat $datafile >> all.pdb
> done
```

BASH

```
# Version 2
$ for datafile in *.pdb
> do
>     echo "cat $datafile >> all.pdb"
> done
```

Solution

The second version is the one we want to run. This prints to screen everything enclosed in the quote marks, expanding the loop variable name because we have prefixed it with a dollar sign. It also *does not* modify nor create the file `all.pdb`, as the `>>` is treated literally as part of a string rather than as a redirection instruction.

The first version appends the output from the command `echo cat $datafile` to the file, `all.pdb`. This file will just contain the list; `cat cubane.pdb`, `cat ethane.pdb`, `cat methane.pdb` etc.

Try both versions for yourself to see the output! Be sure to open the `all.pdb` file to view its contents.

CHALLENGE

### NESTED LOOPS

Suppose we want to set up a directory structure to organize some experiments measuring reaction rate constants with different compounds *and* different temperatures. What would be the result of the following code:

BASH

```bash
$ for species in cubane ethane methane
> do
>     for temperature in 25 30 37 40
>     do
>         mkdir $species-$temperature
>     done
> done
```

Solution

We have a nested loop, i.e. contained within another loop, so for each species in the outer loop, the inner loop (the nested loop) iterates over the list of temperatures, and creates a new directory for each combination.

Try running the code for yourself to see which directories are created!

## KEY POINTS

- A `for` loop repeats commands once for every thing in a list.
- Every `for` loop needs a variable to refer to the thing it is currently operating on.
- Use `$name` to expand a variable (i.e., get its value). `${name}` can also be used.
- Do not use spaces, quotes, or wildcard characters such as '*' or '?' in filenames, as it complicates variable expansion.
- Give files consistent names that are easy to match with wildcard patterns to make it easy to select them for looping.
- Use the up-arrow key to scroll up through previous commands to edit and repeat them.
- Use `Ctrl + R` to search through the previously entered commands.
- Use `history` to display recent commands, and `![number]` to repeat a command by number.

Content from Shell Scripts

Last updated on 2023-08-05 | Edit this page

## OVERVIEW

### Questions

- How can I save and re-use commands?

## Objectives

- Write a shell script that runs a command or series of commands for a fixed set of files.
- Run a shell script from the command line.
- Write a shell script that operates on a set of files defined by the user on the command line.
- Create pipelines that include shell scripts you, and others, have written.

We are finally ready to see what makes the shell such a powerful programming environment. We are going to take the commands we repeat frequently and save them in files so that we can re-run all those operations again later by typing a single command. For historical reasons, a bunch of commands saved in a file is usually called a **shell script**, but make no mistake — these are actually small programs.

Not only will writing shell scripts make your work faster, but also you won't have to retype the same commands over and over again. It will also make it more accurate (fewer chances for typos) and more reproducible. If you come back to your work later (or if someone else finds your work and wants to build on it), you will be able to reproduce the same results simply by running your script, rather than having to remember or retype a long list of commands.

Let's start by going back to `alkanes/` and creating a new file, `middle.sh` which will become our shell script:

BASH

```bash
$ cd alkanes
$ nano middle.sh
```

The command `nano middle.sh` opens the file `middle.sh` within the text editor 'nano' (which runs within the shell). If the file does not exist, it will be created. We can use the text editor to directly edit the file by inserting the following line:

```
head -n 15 octane.pdb | tail -n 5
```

This is a variation on the pipe we constructed earlier, which selects lines 11-15 of the file `octane.pdb`. Remember, we are *not* running it as a command just yet; we are only incorporating the commands in a file.

Then we save the file (`Ctrl-O` in nano) and exit the text editor (`Ctrl-X` in nano). Check that the directory `alkanes` now contains a file called `middle.sh`.

Once we have saved the file, we can ask the shell to execute the commands it contains. Our shell is called `bash`, so we run the following command:

BASH

```bash
$ bash middle.sh
```

OUTPUT

```
ATOM      9  H           1      -4.502   0.681   0.785  1.00  0.00
ATOM     10  H           1      -5.254  -0.243  -0.537  1.00  0.00
ATOM     11  H           1      -4.357   1.252  -0.895  1.00  0.00
ATOM     12  H           1      -3.009  -0.741  -1.467  1.00  0.00
ATOM     13  H           1      -3.172  -1.337   0.206  1.00  0.00
```

Sure enough, our script's output is exactly what we would get if we ran that pipeline directly.

CALLOUT

### TEXT VS. WHATEVER

We usually call programs like Microsoft Word or LibreOffice Writer “text editors”, but we need to be a bit more careful when it comes to programming. By default, Microsoft Word uses `.docx` files to store not only text, but also formatting information about fonts, headings, and so on. This extra information isn’t stored as characters and doesn’t mean anything to tools like `head`, which expects input files to contain nothing but the letters, digits, and punctuation on a standard computer keyboard. When editing programs, therefore, you must either use a plain text editor or be careful to save files as plain text.

What if we want to select lines from an arbitrary file? We could edit `middle.sh` each time to change the filename, but that would probably take longer than typing the command out again in the shell and executing it with a new file name. Instead, let’s edit `middle.sh` and make it more versatile:

BASH

```
$ nano middle.sh
```

Now, within “nano”, replace the text `octane.pdb` with the special variable called `$1`:

```
head -n 15 "$1" | tail -n 5
```

Inside a shell script, `$1` means ‘the first filename (or other argument) on the command line’. We can now run our script like this:

BASH

```
$ bash middle.sh octane.pdb
```

OUTPUT

```
ATOM      9  H           1      -4.502   0.681   0.785  1.00  0.00
ATOM     10  H           1      -5.254  -0.243  -0.537  1.00  0.00
ATOM     11  H           1      -4.357   1.252  -0.895  1.00  0.00
ATOM     12  H           1      -3.009  -0.741  -1.467  1.00  0.00
ATOM     13  H           1      -3.172  -1.337   0.206  1.00  0.00
```

or on a different file like this:

BASH

```
$ bash middle.sh pentane.pdb
```

OUTPUT

```
ATOM      9  H           1       1.324   0.350  -1.332  1.00  0.00
ATOM     10  H           1       1.271   1.378   0.122  1.00  0.00
ATOM     11  H           1      -0.074  -0.384   1.288  1.00  0.00
ATOM     12  H           1      -0.048  -1.362  -0.205  1.00  0.00
ATOM     13  H           1      -1.183   0.500  -1.412  1.00  0.00
```

CALLOUT

## DOUBLE-QUOTES AROUND ARGUMENTS

For the same reason that we put the loop variable inside double-quotes, in case the filename happens to contain any spaces, we surround `$1` with double-quotes.

Currently, we need to edit `middle.sh` each time we want to adjust the range of lines that is returned. Let's fix that by configuring our script to instead use three command-line arguments. After the first command-line argument ( `$1` ), each additional argument that we provide will be accessible via the special variables `$1` , `$2` , `$3` , which refer to the first, second, third command-line arguments, respectively.

Knowing this, we can use additional arguments to define the range of lines to be passed to `head` and `tail` respectively:

BASH

```
$ nano middle.sh
```

```
head -n "$2" "$1" | tail -n "$3"
```

We can now run:

BASH

```
$ bash middle.sh pentane.pdb 15 5
```

OUTPUT

```
ATOM      9  H           1       1.324   0.350  -1.332  1.00  0.00
ATOM     10  H           1       1.271   1.378   0.122  1.00  0.00
ATOM     11  H           1      -0.074  -0.384   1.288  1.00  0.00
ATOM     12  H           1      -0.048  -1.362  -0.205  1.00  0.00
ATOM     13  H           1      -1.183   0.500  -1.412  1.00  0.00
```

By changing the arguments to our command, we can change our script's behaviour:

BASH

```
$ bash middle.sh pentane.pdb 20 5
```

OUTPUT

```
ATOM     14  H           1      -1.259   1.420   0.112  1.00  0.00
ATOM     15  H           1      -2.608  -0.407   1.130  1.00  0.00
ATOM     16  H           1      -2.540  -1.303  -0.404  1.00  0.00
ATOM     17  H           1      -3.393   0.254  -0.321  1.00  0.00
TER      18              1
```

This works, but it may take the next person who reads `middle.sh` a moment to figure out what it does. We can improve our script by adding some **comments** at the top:

BASH

```
$ nano middle.sh
```

```
# Select lines from the middle of a file.
# Usage: bash middle.sh filename end_line num_lines
head -n "$2" "$1" | tail -n "$3"
```

A comment starts with a `#` character and runs to the end of the line. The computer ignores comments, but they're invaluable for helping people (including your future self) understand and use scripts. The only caveat is that each time you modify the script, you should check that the comment is still accurate. An explanation that sends the reader in the wrong direction is worse than none at all.

What if we want to process many files in a single pipeline? For example, if we want to sort our `.pdb` files by length, we would type:

BASH

```
$ wc -l *.pdb | sort -n
```

because `wc -l` lists the number of lines in the files (recall that `wc` stands for 'word count', adding the `-l` option means 'count lines' instead) and `sort -n` sorts things numerically. We could put this in a file, but then it would only ever sort a list of `.pdb` files in the current directory. If we want to be able to get a sorted list of other kinds of files, we need a way to get all those names into the script. We can't use `$1` , `$2` , and so on because we don't know how many files there are. Instead, we use the special variable `$@` , which means, 'All of the command-line arguments to the shell script'. We also should put `$@` inside double-quotes to handle the case of arguments containing spaces ( `"$@"` is special syntax and is equivalent to `"$1"` `"$2"` …).

Here's an example:

BASH

```
$ nano sorted.sh
```

```
# Sort files by their length.
# Usage: bash sorted.sh one_or_more_filenames
wc -l "$@" | sort -n
```

BASH

```
$ bash sorted.sh *.pdb ../creatures/*.dat
```

OUTPUT

```
9 methane.pdb
12 ethane.pdb
15 propane.pdb
20 cubane.pdb
21 pentane.pdb
30 octane.pdb
163 ../creatures/basilisk.dat
163 ../creatures/minotaur.dat
163 ../creatures/unicorn.dat
596 total
```

CHALLENGE

### LIST UNIQUE SPECIES

Leah has several hundred data files, each of which is formatted like this:

```
2013-11-05,deer,5
2013-11-05,rabbit,22
2013-11-05,raccoon,7
2013-11-06,rabbit,19
2013-11-06,deer,2
2013-11-06,fox,1
2013-11-07,rabbit,18
2013-11-07,bear,1
```

An example of this type of file is given in `shell-lesson-data/exercise-data/animal-counts/animals.csv` .

We can use the command `cut -d , -f 2 animals.csv | sort | uniq` to produce the unique species in `animals.csv` . In order to avoid having to type out this series of commands every time, a scientist may choose to write a shell script instead.

Write a shell script called `species.sh` that takes any number of filenames as command-line arguments and uses a variation of the above command to print a list of the unique species appearing in each of those files separately.

Solution

BASH

```
# Script to find unique species in csv files where species is the second data field
# This script accepts any number of file names as command line arguments

# Loop over all files
for file in $@
do
    echo "Unique species in $file:"
    # Extract species names
    cut -d , -f 2 $file | sort | uniq
done
```

Suppose we have just run a series of commands that did something useful — for example, creating a graph we'd like to use in a paper. We'd like to be able to re-create the graph later if we need to, so we want to save the commands in a file. Instead of typing them in again (and potentially getting them wrong) we can do this:

BASH

```bash
$ history | tail -n 5 > redo-figure-3.sh
```

The file `redo-figure-3.sh` now contains:

```
297 bash goostats.sh NENE01729B.txt stats-NENE01729B.txt
298 bash goodiff.sh stats-NENE01729B.txt /data/validated/01729.txt > 01729-differences.txt
299 cut -d ',' -f 2-3 01729-differences.txt > 01729-time-series.txt
300 ygraph --format scatter --color bw --borders none 01729-time-series.txt figure-3.png
301 history | tail -n 5 > redo-figure-3.sh
```

After a moment's work in an editor to remove the serial numbers on the commands, and to remove the final line where we called the `history` command, we have a completely accurate record of how we created that figure.

CHALLENGE

### WHY RECORD COMMANDS IN THE HISTORY BEFORE RUNNING THEM?

If you run the command:

BASH

```bash
$ history | tail -n 5 > recent.sh
```

the last command in the file is the `history` command itself, i.e., the shell has added `history` to the command log before actually running it. In fact, the shell *always* adds commands to the log before running them. Why do you think it does this?

Solution

If a command causes something to crash or hang, it might be useful to know what that command was, in order to investigate the problem. Were the command only be recorded after running it, we would not have a record of the last command run in the event of a crash.

In practice, most people develop shell scripts by running commands at the shell prompt a few times to make sure they're doing the right thing, then saving them in a file for re-use. This style of work allows people to recycle what they discover about their data and their workflow with one call to `history` and a bit of editing to clean up the output and save it as a shell script.

## Nelle's Pipeline: Creating a Script

Nelle's supervisor insisted that all her analytics must be reproducible. The easiest way to capture all the steps is in a script.

First we return to Nelle's project directory:

BASH

```
$ cd ../../north-pacific-gyre/
```

She creates a file using `nano` ...

BASH

```
$ nano do-stats.sh
```

...which contains the following:

BASH

```
# Calculate stats for data files.
for datafile in "$@"
do
    echo $datafile
    bash goostats.sh $datafile stats-$datafile
done
```

She saves this in a file called `do-stats.sh` so that she can now re-do the first stage of her analysis by typing:

BASH

```
$ bash do-stats.sh NENE*A.txt NENE*B.txt
```

She can also do this:

BASH

```
$ bash do-stats.sh NENE*A.txt NENE*B.txt | wc -l
```

so that the output is just the number of files processed rather than the names of the files that were processed.

One thing to note about Nelle's script is that it lets the person running it decide what files to process. She could have written it as:

BASH

```
# Calculate stats for Site A and Site B data files.
for datafile in NENE*A.txt NENE*B.txt
do
    echo $datafile
    bash goostats.sh $datafile stats-$datafile
done
```

The advantage is that this always selects the right files: she doesn't have to remember to exclude the 'Z' files. The disadvantage is that it *always* selects just those files — she can't run it on all files (including the 'Z' files), or on the 'G' or 'H' files her colleagues in Antarctica are producing, without editing the script. If she wanted to be more adventurous, she could modify her script to check for command-line arguments, and use `NENE*A.txt NENE*B.txt` if none were provided. Of course, this introduces another tradeoff between flexibility and complexity.

CHALLENGE

## VARIABLES IN SHELL SCRIPTS

In the `alkanes` directory, imagine you have a shell script called `script.sh` containing the following commands:

BASH

```
head -n $2 $1
tail -n $3 $1
```

While you are in the `alkanes` directory, you type the following command:

BASH

```
$ bash script.sh '*.pdb' 1 1
```

Which of the following outputs would you expect to see?

1. All of the lines between the first and the last lines of each file ending in `.pdb` in the `alkanes` directory
2. The first and the last line of each file ending in `.pdb` in the `alkanes` directory
3. The first and the last line of each file in the `alkanes` directory
4. An error because of the quotes around `*.pdb`

Solution

The correct answer is 2.

The special variables `$1`, `$2` and `$3` represent the command line arguments given to the script, such that the commands run are:

BASH

```
$ head -n 1 cubane.pdb ethane.pdb octane.pdb pentane.pdb propane.pdb
$ tail -n 1 cubane.pdb ethane.pdb octane.pdb pentane.pdb propane.pdb
```

The shell does not expand `'*.pdb'` because it is enclosed by quote marks. As such, the first argument to the script is `'*.pdb'` which gets expanded within the script by `head` and `tail`.

CHALLENGE

## FIND THE LONGEST FILE WITH A GIVEN EXTENSION

Write a shell script called `longest.sh` that takes the name of a directory and a filename extension as its arguments, and prints out the name of the file with the most lines in that directory with that extension. For example:

BASH

```bash
$ bash longest.sh shell-lesson-data/exercise-data/alkanes pdb
```

would print the name of the `.pdb` file in `shell-lesson-data/exercise-data/alkanes` that has the most lines.

Feel free to test your script on another directory e.g.

BASH

```bash
$ bash longest.sh shell-lesson-data/exercise-data/writing txt
```

Solution

BASH

```bash
# Shell script which takes two arguments:
#    1. a directory name
#    2. a file extension
# and prints the name of the file in that directory
# with the most lines which matches the file extension.

wc -l $1/*.$2 | sort -n | tail -n 2 | head -n 1
```

The first part of the pipeline, `wc -l $1/*.$2 | sort -n`, counts the lines in each file and sorts them numerically (largest last). When there's more than one file, `wc` also outputs a final summary line, giving the total number of lines across *all* files. We use `tail -n 2 | head -n 1` to throw away this last line.

With `wc -l $1/*.$2 | sort -n | tail -n 1` we'll see the final summary line: we can build our pipeline up in pieces to be sure we understand the output.

CHALLENGE

## SCRIPT READING COMPREHENSION

For this question, consider the `shell-lesson-data/exercise-data/alkanes` directory once again. This contains a number of `.pdb` files in addition to any other files you may have created. Explain what each of the following three scripts would do when run as `bash script1.sh *.pdb`, `bash script2.sh *.pdb`, and `bash script3.sh *.pdb` respectively.

BASH

```bash
# Script 1
echo *.*
```

BASH

```bash
# Script 2
for filename in $1 $2 $3
do
    cat $filename
done
```

BASH

```bash
# Script 3
echo $@.pdb
```

Solution

In each case, the shell expands the wildcard in `*.pdb` before passing the resulting list of file names as arguments to the script.

Script 1 would print out a list of all files containing a dot in their name. The arguments passed to the script are not actually used anywhere in the script.

Script 2 would print the contents of the first 3 files with a `.pdb` file extension. `$1`, `$2`, and `$3` refer to the first, second, and third argument respectively.

Script 3 would print all the arguments to the script (i.e. all the `.pdb` files), followed by `.pdb`. `$@` refers to *all* the arguments given to a shell script.

OUTPUT

```
cubane.pdb ethane.pdb methane.pdb octane.pdb pentane.pdb propane.pdb.pdb
```

CHALLENGE

## DEBUGGING SCRIPTS

Suppose you have saved the following script in a file called `do-errors.sh` in Nelle's `north-pacific-gyre` directory:

BASH

```bash
# Calculate stats for data files.
for datafile in "$@"
do
    echo $datfile
    bash goostats.sh $datafile stats-$datafile
done
```

When you run it from the `north-pacific-gyre` directory:

BASH

```bash
$ bash do-errors.sh NENE*A.txt NENE*B.txt
```

the output is blank. To figure out why, re-run the script using the `-x` option:

BASH

```bash
$ bash -x do-errors.sh NENE*A.txt NENE*B.txt
```

What is the output showing you? Which line is responsible for the error?

Solution

The `-x` option causes `bash` to run in debug mode. This prints out each command as it is run, which will help you to locate errors. In this example, we can see that `echo` isn't printing anything. We have made a typo in the loop variable name, and the variable `datfile` doesn't exist, hence returning an empty string.

KEY POINTS

- Save commands in files (usually called shell scripts) for re-use.
- `bash [filename]` runs the commands saved in a file.
- `$@` refers to all of a shell script's command-line arguments.
- `$1`, `$2`, etc., refer to the first command-line argument, the second command-line argument, etc.
- Place variables in quotes if the values might have spaces in them.
- Letting users decide what files to process is more flexible and more consistent with built-in Unix commands.

Content from Finding Things

Last updated on 2025-08-06 | Edit this page

## OVERVIEW

### Questions

- How can I find files?
- How can I find things in files?

### Objectives

- Use `grep` to select lines from text files that match simple patterns.
- Use `find` to find files and directories whose names match simple patterns.
- Use the output of one command as the command-line argument(s) to another command.
- Explain what is meant by 'text' and 'binary' files, and why many common tools don't handle the latter well.

In the same way that many of us now use 'Google' as a verb meaning 'to find', Unix programmers often use the word 'grep'. 'grep' is a contraction of 'global/regular expression/print', a common sequence of operations in early Unix text editors. It is also the name of a very useful command-line program.

`grep` finds and prints lines in files that match a pattern. For our examples, we will use a file that contains three haiku taken from a 1998 competition in *Salon* magazine (Credit to authors Bill Torcaso, Howard Korder, and Margaret Segall, respectively. See Haiku Error Messages archived Page 1 and Page 2 .). For this set of examples, we're going to be working in the writing subdirectory:

BASH

```bash
$ cd
$ cd Desktop/shell-lesson-data/exercise-data/writing
$ cat haiku.txt
```

OUTPUT

```
The Tao that is seen
Is not the true Tao, until
You bring fresh toner.

With searching comes loss
and the presence of absence:
"My Thesis" not found.

Yesterday it worked
Today it is not working
Software is like that.
```

Let's find lines that contain the word 'not':

BASH

```bash
$ grep not haiku.txt
```

OUTPUT

```
Is not the true Tao, until
"My Thesis" not found
Today it is not working
```

Here, `not` is the pattern we're searching for. The grep command searches through the file, looking for matches to the pattern specified. To use it type `grep`, then the pattern we're searching for and finally the name of the file (or files) we're searching in.

The output is the three lines in the file that contain the letters 'not'.

By default, grep searches for a pattern in a case-sensitive way. In addition, the search pattern we have selected does not have to form a complete word, as we will see in the next example.

Let's search for the pattern: 'The'.

BASH

```
$ grep The haiku.txt
```

OUTPUT

```
The Tao that is seen
"My Thesis" not found.
```

This time, two lines that include the letters 'The' are outputted, one of which contained our search pattern within a larger word, 'Thesis'.

To restrict matches to lines containing the word 'The' on its own, we can give `grep` the `-w` option. This will limit matches to word boundaries.

Later in this lesson, we will also see how we can change the search behavior of grep with respect to its case sensitivity.

BASH

```
$ grep -w The haiku.txt
```

OUTPUT

```
The Tao that is seen
```

Note that a 'word boundary' includes the start and end of a line, so not just letters surrounded by spaces. Sometimes we don't want to search for a single word, but a phrase. We can also do this with `grep` by putting the phrase in quotes.

BASH

```
$ grep -w "is not" haiku.txt
```

OUTPUT

```
Today it is not working
```

We've now seen that you don't have to have quotes around single words, but it is useful to use quotes when searching for multiple words. It also helps to make it easier to distinguish between the search term or phrase and the file being searched. We will use quotes in the remaining examples.

Another useful option is `-n`, which numbers the lines that match:

BASH

```
$ grep -n "it" haiku.txt
```

OUTPUT

```
5:With searching comes loss
9:Yesterday it worked
10:Today it is not working
```

Here, we can see that lines 5, 9, and 10 contain the letters ‘it’.

We can combine options (i.e. flags) as we do with other Unix commands. For example, let’s find the lines that contain the word ‘the’. We can combine the option `-w` to find the lines that contain the word ‘the’ and `-n` to number the lines that match:

BASH

```
$ grep -n -w "the" haiku.txt
```

OUTPUT

```
2:Is not the true Tao, until
6:and the presence of absence:
```

Now we want to use the option `-i` to make our search case-insensitive:

BASH

```
$ grep -n -w -i "the" haiku.txt
```

OUTPUT

```
1:The Tao that is seen
2:Is not the true Tao, until
6:and the presence of absence:
```

Now, we want to use the option `-v` to invert our search, i.e., we want to output the lines that do not contain the word ‘the’.

BASH

```
$ grep -n -w -v "the" haiku.txt
```

OUTPUT

```
1:The Tao that is seen
3:You bring fresh toner.
4:
5:With searching comes loss
7:"My Thesis" not found.
8:
9:Yesterday it worked
10:Today it is not working
11:Software is like that.
```

If we use the `-r` (recursive) option, `grep` can search for a pattern recursively through a set of files in subdirectories.

Let's search recursively for `Yesterday` in the `shell-lesson-data/exercise-data/writing` directory:

BASH

```
$ grep -r Yesterday .
```

OUTPUT

```
./LittleWomen.txt:"Yesterday, when Aunt was asleep and I was trying to be as still as a
./LittleWomen.txt:Yesterday at dinner, when an Austrian officer stared at us and then
./LittleWomen.txt:Yesterday was a quiet day spent in teaching, sewing, and writing in my
./haiku.txt:Yesterday it worked
```

`grep` has lots of other options. To find out what they are, we can type:

BASH

```
$ grep --help
```

OUTPUT

```
Usage: grep [OPTION]... PATTERN [FILE]...
Search for PATTERN in each FILE or standard input.
PATTERN is, by default, a basic regular expression (BRE).
Example: grep -i 'hello world' menu.h main.c

Regexp selection and interpretation:
  -E, --extended-regexp     PATTERN is an extended regular expression (ERE)
  -F, --fixed-strings       PATTERN is a set of newline-separated fixed strings
  -G, --basic-regexp        PATTERN is a basic regular expression (BRE)
  -P, --perl-regexp         PATTERN is a Perl regular expression
  -e, --regexp=PATTERN      use PATTERN for matching
  -f, --file=FILE           obtain PATTERN from FILE
  -i, --ignore-case         ignore case distinctions
  -w, --word-regexp         force PATTERN to match only whole words
  -x, --line-regexp         force PATTERN to match only whole lines
  -z, --null-data           a data line ends in 0 byte, not newline

Miscellaneous:
...         ...         ...
```

CHALLENGE

## USING `grep`

Which command would result in the following output:

OUTPUT

```
and the presence of absence:
```

1. `grep "of" haiku.txt`
2. `grep -E "of" haiku.txt`
3. `grep -w "of" haiku.txt`
4. `grep -i "of" haiku.txt`

Solution

The correct answer is 3, because the `-w` option looks only for whole-word matches. The other options will also match 'of' when part of another word.

CALLOUT

## WILDCARDS

`grep` 's real power doesn't come from its options, though; it comes from the fact that patterns can include wildcards. (The technical name for these is **regular expressions**, which is what the 're' in 'grep' stands for.) Regular expressions are both complex and powerful; if you want to do complex searches, please look at the lesson on our website. As a taster, we can find lines that have an 'o' in the second position like this:

BASH

```
$ grep -E "^.o" haiku.txt
```

OUTPUT

```
You bring fresh toner.
Today it is not working
Software is like that.
```

We use the `-E` option and put the pattern in quotes to prevent the shell from trying to interpret it. (If the pattern contained a `*`, for example, the shell would try to expand it before running `grep`.) The `^` in the pattern anchors the match to the start of the line. The `.` matches a single character (just like `?` in the shell), while the `o` matches an actual 'o'.

CHALLENGE

### TRACKING A SPECIES

Leah has several hundred data files saved in one directory, each of which is formatted like this:

```
2012-11-05,deer,5
2012-11-05,rabbit,22
2012-11-05,raccoon,7
2012-11-06,rabbit,19
2012-11-06,deer,2
2012-11-06,fox,4
2012-11-07,rabbit,16
2012-11-07,bear,1
```

She wants to write a shell script that takes a species as the first command-line argument and a directory as the second argument. The script should return one file called `<species>.txt` containing a list of dates and the number of that species seen on each date. For example using the data shown above, `rabbit.txt` would contain:

```
2012-11-05,22
2012-11-06,19
2012-11-07,16
```

Below, each line contains an individual command, or pipe. Arrange their sequence in one command in order to achieve Leah's goal:

BASH

```bash
cut -d : -f 2
>
|
grep -w $1 -r $2
|
$1.txt
cut -d , -f 1,3
```

Hint: use `man grep` to look for how to grep text recursively in a directory and `man cut` to select more than one field in a line.

An example of such a file is provided in `shell-lesson-data/exercise-data/animal-counts/animals.csv`

Solution

```
grep -w $1 -r $2 | cut -d : -f 2 | cut -d , -f 1,3 > $1.txt
```

Actually, you can swap the order of the two cut commands and it still works. At the command line, try changing the order of the cut commands, and have a look at the output from each step to see why this is the case.

You would call the script above like this:

BASH

```
$ bash count-species.sh bear .
```

CHALLENGE

## LITTLE WOMEN

You and your friend, having just finished reading *Little Women* by Louisa May Alcott, are in an argument. Of the four sisters in the book, Jo, Meg, Beth, and Amy, your friend thinks that Jo was the most mentioned. You, however, are certain it was Amy. Luckily, you have a file `LittleWomen.txt` containing the full text of the novel ( `shell-lesson-data/exercise-data/writing/LittleWomen.txt` ). Using a `for` loop, how would you tabulate the number of times each of the four sisters is mentioned?

Hint: one solution might employ the commands `grep` and `wc` and a `|` , while another might utilize `grep` options. There is often more than one way to solve a programming task, so a particular solution is usually chosen based on a combination of yielding the correct result, elegance, readability, and speed.

Solution

```
for sis in Jo Meg Beth Amy
do
    echo $sis:
    grep -ow $sis LittleWomen.txt | wc -l
done
```

Alternative, slightly inferior solution:

```
for sis in Jo Meg Beth Amy
do
    echo $sis:
    grep -ocw $sis LittleWomen.txt
done
```

This solution is inferior because `grep -c` only reports the number of lines matched. The total number of matches reported by this method will be lower if there is more than one match per line.

Perceptive observers may have noticed that character names sometimes appear in all-uppercase in chapter titles (e.g. 'MEG GOES TO VANITY FAIR'). If you wanted to count these as well, you could add the `-i` option for case-insensitivity (though in this case, it doesn't affect the answer to which sister is mentioned most frequently).

While `grep` finds lines in files, the `find` command finds files themselves. Again, it has a lot of options; to show how the simplest ones work, we'll use the `shell-lesson-data/exercise-data` directory tree shown below.

OUTPUT

```
.
├── animal-counts/
│   └── animals.csv
├── creatures/
│   ├── basilisk.dat
│   ├── minotaur.dat
│   └── unicorn.dat
├── numbers.txt
├── alkanes/
│   ├── cubane.pdb
│   ├── ethane.pdb
│   ├── methane.pdb
│   ├── octane.pdb
│   ├── pentane.pdb
│   └── propane.pdb
└── writing/
    ├── haiku.txt
    └── LittleWomen.txt
```

The `exercise-data` directory contains one file, `numbers.txt` and four directories: `animal-counts`, `creatures`, `alkanes` and `writing` containing various files.

For our first command, let's run `find .` (remember to run this command from the `shell-lesson-data/exercise-data` folder).

BASH

```
$ find .
```

OUTPUT

```
.
./writing
./writing/LittleWomen.txt
./writing/haiku.txt
./creatures
./creatures/basilisk.dat
./creatures/unicorn.dat
./creatures/minotaur.dat
./animal-counts
./animal-counts/animals.csv
./numbers.txt
./alkanes
./alkanes/ethane.pdb
./alkanes/propane.pdb
./alkanes/octane.pdb
./alkanes/pentane.pdb
./alkanes/methane.pdb
./alkanes/cubane.pdb
```

As always, the `.` on its own means the current working directory, which is where we want our search to start. `find` 's output is the names of every file **and** directory under the current working directory. This can seem useless at first but `find` has many options to filter the output and in this lesson we will discover some of them.

The first option in our list is `-type d` that means 'things that are directories'. Sure enough, `find` 's output is the names of the five directories (including `.` ):

BASH

```
$ find . -type d
```

OUTPUT

```
.
./writing
./creatures
./animal-counts
./alkanes
```

Notice that the objects `find` finds are not listed in any particular order. If we change `-type d` to `-type f` , we get a listing of all the files instead:

BASH

```
$ find . -type f
```

OUTPUT

```
./writing/LittleWomen.txt
./writing/haiku.txt
./creatures/basilisk.dat
./creatures/unicorn.dat
./creatures/minotaur.dat
./animal-counts/animals.csv
./numbers.txt
./alkanes/ethane.pdb
./alkanes/propane.pdb
./alkanes/octane.pdb
./alkanes/pentane.pdb
./alkanes/methane.pdb
./alkanes/cubane.pdb
```

Now let's try matching by name:

BASH

```
$ find . -name *.txt
```

OUTPUT

```
./numbers.txt
```

We expected it to find all the text files, but it only prints out `./numbers.txt`. The problem is that the shell expands wildcard characters like `*` *before* commands run. Since `*.txt` in the current directory expands to `./numbers.txt`, the command we actually ran was:

BASH

```
$ find . -name numbers.txt
```

`find` did what we asked; we just asked for the wrong thing.

To get what we want, let's do what we did with `grep`: put `*.txt` in quotes to prevent the shell from expanding the `*` wildcard. This way, `find` actually gets the pattern `*.txt`, not the expanded filename `numbers.txt`:

BASH

```
$ find . -name "*.txt"
```

OUTPUT

```
./writing/LittleWomen.txt
./writing/haiku.txt
./numbers.txt
```

CALLOUT

### LISTING VS. FINDING

`ls` and `find` can be made to do similar things given the right options, but under normal circumstances, `ls` lists everything it can, while `find` searches for things with certain properties and shows them.

As we said earlier, the command line's power lies in combining tools. We've seen how to do that with pipes; let's look at another technique. As we just saw, `find . -name "*.txt"` gives us a list of all text files in or below the current directory. How can we combine that with `wc -l` to count the lines in all those files?

The simplest way is to put the `find` command inside `$()` :

BASH

```bash
$ wc -l $(find . -name "*.txt")
```

OUTPUT

```
  21022 ./writing/LittleWomen.txt
     11 ./writing/haiku.txt
      5 ./numbers.txt
  21038 total
```

When the shell executes this command, the first thing it does is run whatever is inside the `$()` . It then replaces the `$()` expression with that command's output. Since the output of `find` is the three filenames `./writing/LittleWomen.txt` , `./writing/haiku.txt` , and `./numbers.txt` , the shell constructs the command:

BASH

```bash
$ wc -l ./writing/LittleWomen.txt ./writing/haiku.txt ./numbers.txt
```

which is what we wanted. This expansion is exactly what the shell does when it expands wildcards like `*` and `?` , but lets us use any command we want as our own 'wildcard'.

It's very common to use `find` and `grep` together. The first finds files that match a pattern; the second looks for lines inside those files that match another pattern. Here, for example, we can find txt files that contain the word "searching" by looking for the string 'searching' in all the `.txt` files in the current directory:

BASH

```bash
$ grep "searching" $(find . -name "*.txt")
```

OUTPUT

```
./writing/LittleWomen.txt:sitting on the top step, affected to be searching for her book, but was
./writing/haiku.txt:With searching comes loss
```

CHALLENGE

## MATCHING AND SUBTRACTING

The `-v` option to `grep` inverts pattern matching, so that only lines which do *not* match the pattern are printed. Given that, which of the following commands will find all .dat files in `creatures` except `unicorn.dat`? Once you have thought about your answer, you can test the commands in the `shell-lesson-data/exercise-data` directory.

1. `find creatures -name "*.dat" | grep -v unicorn`
2. `find creatures -name *.dat | grep -v unicorn`
3. `grep -v "unicorn" $(find creatures -name "*.dat")`
4. None of the above.

Solution

Option 1 is correct. Putting the match expression in quotes prevents the shell expanding it, so it gets passed to the `find` command.

Option 2 also works in this instance because the shell tries to expand `*.dat` but there are no `*.dat` files in the current directory, so the wildcard expression gets passed to `find`. We first encountered this in episode 3.

Option 3 is incorrect because it searches the contents of the files for lines which do not match 'unicorn', rather than searching the file names.

CALLOUT

## BINARY FILES

We have focused exclusively on finding patterns in text files. What if your data is stored as images, in databases, or in some other format?

A handful of tools extend `grep` to handle a few non text formats. But a more generalizable approach is to convert the data to text, or extract the text-like elements from the data. On the one hand, it makes simple things easy to do. On the other hand, complex things are usually impossible. For example, it's easy enough to write a program that will extract X and Y dimensions from image files for `grep` to play with, but how would you write something to find values in a spreadsheet whose cells contained formulas?

A last option is to recognize that the shell and text processing have their limits, and to use another programming language. When the time comes to do this, don't be too hard on the shell. Many modern programming languages have borrowed a lot of ideas from it, and imitation is also the sincerest form of praise.

The Unix shell is older than most of the people who use it. It has survived so long because it is one of the most productive programming environments ever created — maybe even *the* most productive. Its syntax may be cryptic, but people who have mastered it can experiment with different commands interactively, then use what they have learned to automate their work. Graphical user interfaces may be easier to use at first, but once learned, the productivity in the shell is unbeatable. And as Alfred North Whitehead wrote in 1911, 'Civilization advances by extending the number of important operations which we can perform without thinking about them.'

## CHALLENGE

### `find` PIPELINE READING COMPREHENSION

Write a short explanatory comment for the following shell script:

BASH

```bash
wc -l $(find . -name "*.dat") | sort -n
```

Solution

1. Find all files with a `.dat` extension recursively from the current directory
2. Count the number of lines each of these files contains
3. Sort the output from step 2. numerically

## KEY POINTS

- `find` finds files with specific properties that match patterns.
- `grep` selects lines in files that match patterns.
- `--help` is an option supported by many bash commands, and programs that can be run from within Bash, to display more information on how to use these commands or programs.
- `man [command]` displays the manual page for a given command.
- `$([command])` inserts a command's output in place.