(../02-filedir/index.html)

The Unix Shell (../)

(../04pipefil

# Working With Files and Directories



**Teaching:** 30 min **Exercises:** 20 min

#### Questions

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

#### **Objectives**

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

# Creating directories

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

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

Let's go back to our data-shell directory on the Desktop and use 1s -F to see what it contains:

\$ pwd

/Users/nelle/Desktop/data-shell

\$ 1s -F

creatures/ data/ molecules/ north-pacific-gyre/ notes.txt pizza.cfg solar.pdf writing/

# Create a directory

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

\$ 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:

\$ 1s -F

creatures/ data/ molecules/ north-pacific-gyre/ notes.txt pizza.cfg solar.pdf thesis/ writing/

# ★ 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.

#### A 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.

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/).

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

Commands treat names starting with - as options.

3. Stick with 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 quotes

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

ls -F thesis

## 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:

\$ cd thesis

\$ nano draft.txt

#### 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 Mac OS X), many programmers use Emacs (http://www.gnu.org/software/emacs/) or Vim (http://www.vim.org/) (both of which require more time to learn), or a graphical editor such as Gedit (http://projects.gnome.org/gedit/). On Windows, you may wish to use Notepad++ (http://notepad-plusplus.org/). 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. Once we're happy with our text, we can press Ctrl + 0 (press the Ctrl or Control key and, while holding it down, press the O key) to write our data to disk (we'll be asked what file we want to save this to: press Return to accept the suggested default of draft.txt ).

> GNU nano 2.0.6 File: draft.txt It's not "publish or perish" any more, it's "share and thrive".

Exit

WriteOut Justify

Read File Where Is

Prev Page Next Page Cut Text Cur Pos UnCut Text To Spell

Once our file is saved, we can use Ctrl-X to guit the editor and return to the shell.

## ★ 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 1s now shows that we have created a file called draft.txt:

\$ 1s

draft.txt

## Creating Files a Different Way

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

- \$ 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 1s -1 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 1s at the command line prompt. my\_file.txt can also be viewed in your GUI file explorer.
- 2. When you inspect the file with 1s -1, 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.

## ★ 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 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 whalesong, though it *might* cause the operating system to try to open it with a music player when someone double-clicks it.

# Moving files and directories

Returning to the data-shell directory,

cd ~/Desktop/data-shell/

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":

\$ 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, 1s shows us that thesis now contains one file called quotes.txt:

\$ 1s thesis

quotes.txt

One has to 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. An additional option, mv -i (or mv --interactive), can be used to make mv ask you for confirmation before overwriting.

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 just use 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.

\$ mv thesis/quotes.txt .

The effect is to move the file from the directory it was in to the current working directory. 1s now shows us that thesis is empty:

\$ 1s thesis

Further, 1s with a filename or directory name as an argument only lists that file or directory. We can use this to see that quotes.txt is still in our current directory:

\$ 1s quotes.txt

quotes.txt

# Moving to the Current Folder

After running the following commands, Jamie realizes that she put the files sucrose.dat and maltose.dat into the wrong folder:

\$ ls **-F** 

analyzed/ raw/

\$ ls -F analyzed

fructose.dat glucose.dat maltose.dat sucrose.dat

\$ cd raw,

Fill in the blanks to move these files to the current folder (i.e., the one she is currently in):

\$ mv \_\_\_/sucrose.dat \_\_\_/maltose.dat \_\_\_

Solution 
 □

\$ mv ../analyzed/sucrose.dat ../analyzed/maltose.dat .

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 1s with two paths as arguments — like most Unix commands, 1s can be given multiple paths at once:

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

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

We can also copy a directory and all its contents by using the recursive (https://en.wikipedia.org/wiki/Recursion) option -r , e.g. to back up a directory:

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

We can check the result by listing the contents of both the thesis and thesis\_backup directory:

## 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?

- cp statstics.txt statistics.txt
- 2. mv statstics.txt statistics.txt
- 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.

# Moving and Copying

What is the output of the closing 1s command in the sequence shown below?

\$ pwd

/Users/jamie/data

\$ 1s

proteins.dat

- \$ mkdir recombine
- \$ mv proteins.dat recombine/
- \$ cp recombine/proteins.dat ../proteins-saved.dat
- \$ 1s
- 1. proteins-saved.dat recombine
- 2. recombine
- 3. proteins.dat recombine
- 4. proteins-saved.dat

## Solution



We start in the <code>/Users/jamie/data</code> directory, and create a new folder called <code>recombine</code>. The second line moves ( <code>mv</code> ) the file <code>proteins.dat</code> to the new folder ( <code>recombine</code> ). 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 <code>/Users/jamie</code>. Notice that .. is interpreted with respect to the current working directory, <code>not</code> with respect to the location of the file being copied. So, the only thing that will show using Is (in <code>/Users/jamie/data</code>) is the recombine 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/recombine
- 4. No, see explanation above. proteins-saved.dat is located at /Users/jamie

# Removing files and directories

Returning to the data-shell 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'):

\$ rm quotes.txt

We can confirm the file has gone using 1s:

\$ 1s quotes.txt

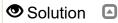
ls: cannot access 'quotes.txt': No such file or directory

# ★ 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.

## ✓ Using rm Safely

What happens when we execute rm -i thesis\_backup/quotations.txt? Why would we want this protection when using rm?



\$ 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:

\$ rm thesis

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:

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.

## Copy with Multiple Filenames

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

In the example below, what does cp do when given several filenames and a directory name?

- \$ mkdir backup
- \$ cp amino-acids.txt animals.txt backup/

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

\$ 1s -F

amino-acids.txt animals.txt backup/ elements/ morse.txt pdb/ planets.txt salmon.txt sunspot.txt

\$ cp amino-acids.txt animals.txt morse.txt

# Solution 🖪

If given more than one file name followed by a directory name (i.e. the destination directory must be the last argument), cp copies the files to the named directory.

If given three file names, cp throws an error such as the one below, because it is expecting a directory name as the last argument.

cp: target 'morse.txt' is not a directory

# Using wildcards for accessing multiple files at once

#### ★ Wildcards

- \* is a **wildcard**, which matches zero or more characters. Let's consider the data-shell/molecules directory: \*.pdb matches ethane.pdb , propane.pdb , and every file that ends with '.pdb'. On the other hand, p\*.pdb only matches pentane.pdb and propane.pdb , because the 'p' at the front only matches filenames that begin with the letter 'p'.
- ? is also a wildcard, but it matches exactly one character. So ?ethane.pdb would match methane.pdb whereas \*ethane.pdb matches both ethane.pdb , and methane.pdb .

Wildcards can be used in combination with each other e.g. ???ane.pdb matches 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 command that was asked for. 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 1s \*.pdf in the molecules 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 1s see the lists of file names matching these expressions, but not the wildcards themselves. It is the shell, not the other programs, that deals with expanding wildcards, and this is another example of orthogonal design.

## List filenames matching a pattern

When run in the molecules directory, which 1s 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.\*

# 

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. .

#### 

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

```
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:

```
$ 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

```
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
         L__ 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
  $ 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/
```

#### Organizing Directories and Files

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

\$ 1s -F

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?

\$ 1s **-F** 

analyzed/ raw/

\$ 1s analyzed

fructose.dat sucrose.dat

Solution

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.

#### 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-data folder into a folder called 2016-05-20 so that your final directory structure looks like this:

```
2016-05-20/

— data

— processed
— raw
```

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

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

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

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

$ mkdir 2016-05-20/data/processed

$ mkdir 2016-05-20/data/processed

$ mkdir 2016-05-20
$ mkdir 2016-05-20
$ mkdir ata
$ mkdir ata
$ mkdir ata
$ 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 <code>mkdir</code> won't create a subdirectory of a non-existant directory: the intermediate level folders must be created first.

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.





Copyright © 2018–2019 The Carpentries (https://carpentries.org/)
Copyright © 2016–2018 Software Carpentry Foundation (https://software-carpentry.org)

Edit on GitHub (https://github.com/neurodatascience/shell-novice/edit/gh-pages/\_episodes/03-create.md) / Contributing (https://github.com/neurodatascience/shell-novice/blob/gh-pages/CONTRIBUTING.md) / Source (https://github.com/neurodatascience/shell-novice/) / Cite (https://github.com/neurodatascience/shell-novice/blob/gh-pages/CITATION) / Contact (mailto:team@carpentries.org)

Using The Carpentries style (https://github.com/carpentries/styles/) version 9.5.2 (https://github.com/carpentries/styles/releases/tag/v9.5.2).