STATS 507
Data Analysis in Python

Lecture 22: Advanced Command Line

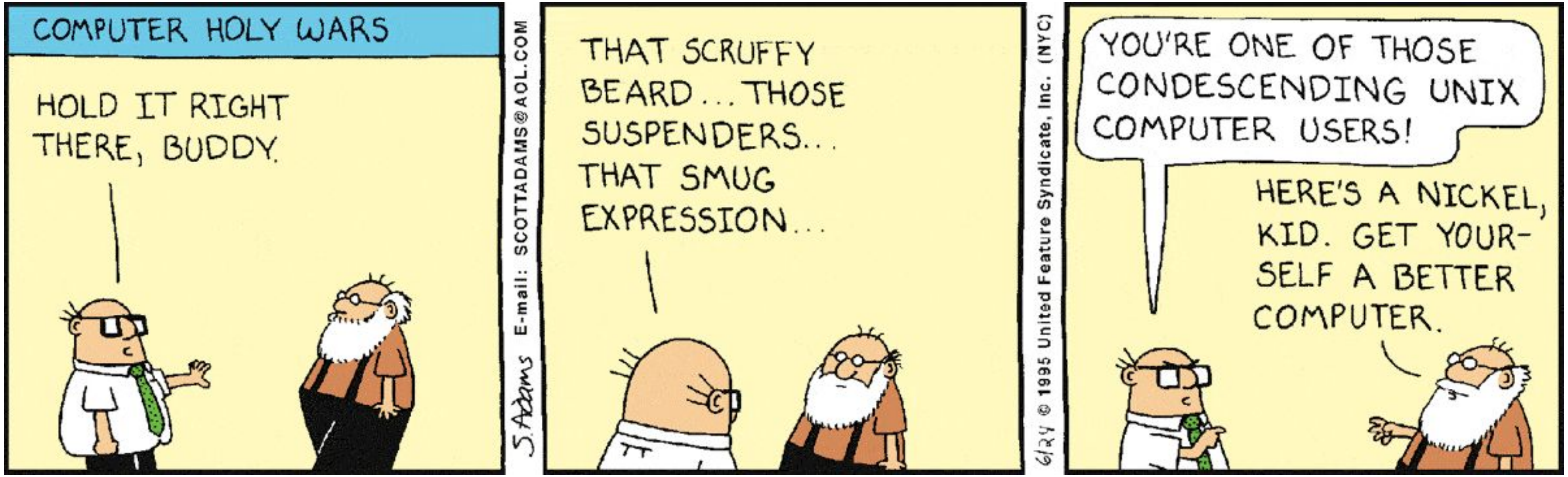
Why UNIX/Linux?

As a data scientist, you will spend **most** of your time dealing with data

Data sets never arrive “ready to analyze”

Cleaning data, fixing formatting, etc is 80% of the process

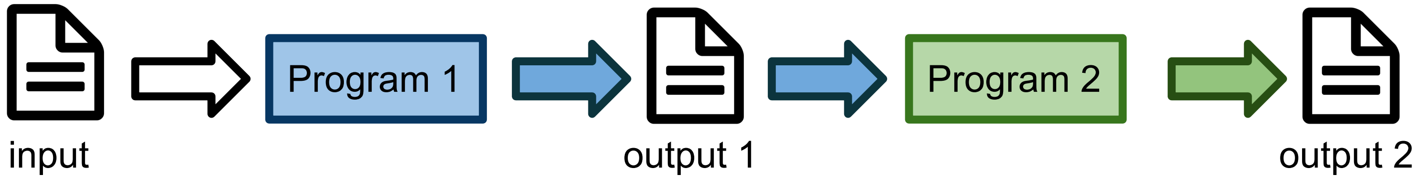
These “data wrangling” tasks are (often) best done on the command line



The Unix philosophy: do one thing well

1. Write programs that do one thing and do it well.
2. Write programs to work together.
3. Write programs to handle text streams, because that is a universal interface.

https://en.wikipedia.org/wiki/Unix_philosophy



Reminder: Basic concepts

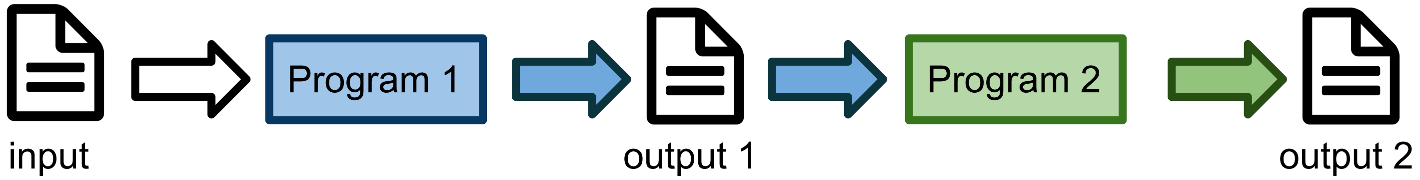
Shell : the program through which you interact with the computer.

provides the command line and facilitates typing commands and reading outputs.

Popular shells: bash (Bourne Again Shell), csh (C Shell), ksh (Korn Shell)

Redirect : take the output of one program and make it the input of another.

we'll see some simple examples in a few slides



stdin, stdout, stderr : three special "file handles"

for reading inputs from the shell (stdin)

and writing output to the shell (stderr for error messages, stdout other information).

Special file handles: `stdin`, `stdout`, `stderr`

File handles are pointers to files

Familiar if you've programmed in C/C++

Similar: object returned by python `open()`

```
>>> f = open('workfile', 'w')
>>> print f
<open file 'workfile', mode 'w' at 80a0960>
```

By default, most command line programs

- take input from `stdin`
- Write output to `stdout`
- Write errors and status information to `stderr`

Special file handles: stdin, stdout, stderr

```
keith@Steinhaus:~$ echo "hello world."
hello world.
keith@Steinhaus:~$ echo "hello world." > myfile.txt
keith@Steinhaus:~$ cat myfile.txt
hello world.
keith@Steinhaus:~$ echo "!"
-bash: !: event not found
keith@Steinhaus:~$
```

`echo` sends its output to `stdout`, which is printed to the screen.

`echo` writes to `stdout`, which is redirected to the file `myfile.txt`.

`cat` writes the contents of `myfile.txt` to `stdout`, which is printed to the screen.

`bash` encounters an error, so it writes an error message to `stderr`. Both `stdout` and `stderr` are printed to the screen, but behave differently in other contexts.

Special file handles: stdin, stdout, stderr

```
keith@Steinhaus:~$ echo "hello world."
hello world.
keith@Steinhaus:~$ echo "hello world." > myfile.txt
keith@Steinhaus:~$ cat myfile.txt
hello world.
keith@Steinhaus:~$ echo "!"
-bash: !: event not found
keith@Steinhaus:~$
```

`echo` sends its output to `stdout`, which is printed to the screen.

`echo` writes to `stdout`, which is redirected to the file `myfile.txt`.

`cat` writes the contents of `myfile.txt` to `stdout`, which is printed to the screen.

`echo` encounters an error, so it writes an error message to `stderr`. Both `stdout` and `stderr` are printed to the screen, but behave differently in other contexts.

We haven't learned any programs that use `stdin`, yet, but we will in a few slides.

Reminder: redirections using >

Redirect sends output to a file instead of stdout

```
keith@Steinhaus:~$ echo -e  "hello\tworld." > myfile.txt
keith@Steinhaus:~$
```

Redirect tells the shell to send the output of the program on the “greater than” side to the file on the “lesser than” side. **This creates the file on the RHS, and overwrites the old file, if it already exists!**

Command line regexes: `grep`

`grep` is a command line regex tool

```
keith@Steinhaus:~$ grep 'hello' myfile.txt
hello world.
keith@Steinhaus:~$ grep 'goat' myfile.txt
keith@Steinhaus:~$
keith@Steinhaus:~$ cat myfile.txt | grep 'hello'
hello world.
keith@Steinhaus:~$
```

Searches for the string `hello` in the file `myfile.txt`, prints all matching lines to `stdout`.

String `goat` does not occur in `myfile.txt`, so no lines to print.

`grep` can also be made to search for a pattern in its `stdin`. This is our first example of a **pipe**.

This writes the contents of `myfile.txt` to the `stdin` of `grep`, which searches its `stdin` for the string `hello`

Command line regexes: `grep`

Command line regex tool

```
keith@Steinhaus:~$ grep 'hello' myfile.txt
hello world.
keith@Steinhaus:~$ grep 'goat' myfile.txt
keith@Steinhaus:~$
keith@Steinhaus:~$ cat myfile.txt | grep 'hello'
hello world.
keith@Steinhaus:~$
```

Searches for the string `hello` in the file `myfile.txt`, prints all matching lines to `stdout`.

String `goat` does not occur in `myfile.txt`, so no lines to print.

`grep` can also be made to search for a pattern in its `stdin`. This is our first example of a **pipe**.

Note: the `grep` pattern can also be a regular expression. Use `grep -E` to tell `grep` to use "extended regular expressions", which are (mostly) identical to those in Python `re`. See `man re_format` for more information.

Pipe (|) vs Redirect (>)

Pipe (|) reads the `stdout` from its left, and writes to `stdin` on its right.

Redirect (>) reads the `stdout` from its left and writes to a file on its right.

This is an important difference!

Warning: the example below is INCORRECT. It is an example of what NOT to do!

```
keith@Steinhaus:~$ cat myfile.txt > grep 'hello'
```

This writes the contents of `myfile.txt` to a file called `grep` and then `cat`s the file `‘hello’` to `stdout`, which is **not** what was intended.

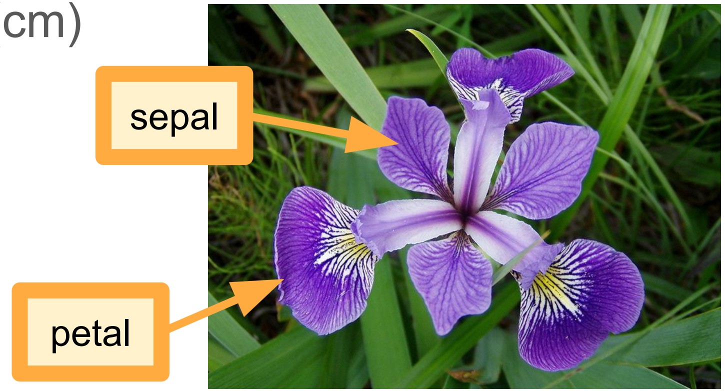
Running example: Fisher's Iris data set

Widely-used data set in machine learning

- Collected by E. Anderson, made famous by R. A. Fisher
- Three different species: *Iris setosa*, *Iris virginica* and *Iris versicolor*
- Each observation is a set of measurements of a flower:
  - Petal and sepal width and height (cm)
  - Along with species label

Common tasks:

- clustering, classification



Available at UCI ML Repository: https://archive.ics.uci.edu/ml/datasets/Iris

Downloading the data

Following the download link on UCI ML repo leads to this index page

Index of /ml/machine-learning-databases/iris

Name	Last modified	Size	Description
Parent Directory		-	
Index	03-Dec-1996 04:01	105	
bezdekIris.data	14-Dec-1999 12:12	4.4K	
iris.data	08-Mar-1993 16:27	4.4K	
iris.names	11-Jul-2000 21:30	2.9K	

Apache/2.2.15 (CentOS) Server at archive.ics.uci.edu Port 443

> What's the difference between these two files? The documentation actually doesn't say.

Downloading the data

Create a project directory and `cd` into it.

Move the data files from downloads folder to project directory. Not mandatory, just convenient!

```
keith@Steinhaus:~$ mkdir demodir
keith@Steinhaus:~$ cd demodir
keith@Steinhaus:~/demodir$ mv ~/Downloads/iris.data .
keith@Steinhaus:~/demodir$ mv ~/Downloads/bezdekIris.data .
keith@Steinhaus:~/demodir$ ls
bezdekIris.data  iris.data   myfile.txt
keith@Steinhaus:~/demodir$ ls -l
total 40
-rw-r--r--@ 1 keith  staff  4551 Nov  15 13:47 bezdekIris.data
-rw-r--r--@ 1 keith  staff  4551 Nov  15 13:47 iris.data
-rw-r--r--@ 1 keith  staff    13 Nov   2 12:56 myfile.txt
keith@Steinhaus:~/demodir$
```

Files are there, now.

From `man ls`:
-l (The lowercase letter “ell”.) List in long format. (See below.) If the output is to a terminal, a total sum for all the file sizes is output on a line before the long listing.

Comparing files: `diff`

`diff` takes two files and compares them line by line

By default, prints only the lines that differ:

```
keith@Steinhaus:~/demodir$ diff iris.data bezdekIris.data
35c35
< 4.9,3.1,1.5,0.1,Iris-setosa
---
> 4.9,3.1,1.5,0.2,Iris-setosa
38c38
< 4.9,3.1,1.5,0.1,Iris-setosa
---
> 4.9,3.6,1.4,0.1,Iris-setosa
keith@Steinhaus:~/demodir$
```

`XcY` means `X`th line in `FILE1` was replaced by `Y`th line in `FILE2`

< : lines from `FILE1`

> : lines from `FILE2`

Comparing files: `diff`

So, the two files differ in precisely two lines…

What's up with that?

```
keith@Steinhaus:~/demodir$ diff iris.data bezdekIris.data
35c35
< 4.9,3.1,1.5,0.1,Iris-setosa
---
> 4.9,3.1,1.5,0.2,Iris-setosa
38c38
< 4.9,3.1,1.5,0.1,Iris-setosa
---
> 4.9,3.6,1.4,0.1,Iris-setosa
keith@Steinhaus:~/demodir$
```

From UCI Documentation:
This data differs from the data presented in Fisher's article (identified by Steve Chadwick, spchadwick '@' espeedaz.net). The 35th sample should be: 4.9,3.1,1.5,0.2,"Iris-setosa" where the error is in the fourth feature. The 38th sample: 4.9,3.6,1.4,0.1,"Iris-setosa" where the errors are in the second and third features.

Comparing files: `diff`

So `bezdekIris.data` is a corrected version of `iris.data`. That's nice of them!

So, the two files differ in precisely two lines…

What's up with that?

```
keith@Steinhaus:~/demodir$ diff iris.data bezdekIris.data
35c35
< 4.9,3.1,1.5,0.1,Iris-setosa
---
> 4.9,3.1,1.5,0.2,Iris-setosa
38c38
< 4.9,3.1,1.5,0.1,Iris-setosa
---
> 4.9,3.6,1.4,0.1,Iris-setosa
keith@Steinhaus:~/demodir$
```

From UCI Documentation:
This data differs from the data presented in Fisher's article (identified by Steve Chadwick, spchadwick '@' espeedaz.net). The 35th sample should be: 4.9,3.1,1.5,0.2,"Iris-setosa" where the error is in the fourth feature. The 38th sample: 4.9,3.6,1.4,0.1,"Iris-setosa" where the errors are in the second and third features.

Comparing files: `diff`

Often useful: get the diff of two files and save it to another file

```
keith@Steinhaus:~/demodir$ diff iris.data bezdekIris.data > diff.txt
keith@Steinhaus:~/demodir$ cat diff.txt
35c35
< 4.9,3.1,1.5,0.1,Iris-setosa
---
> 4.9,3.1,1.5,0.2,Iris-setosa
38c38
< 4.9,3.1,1.5,0.1,Iris-setosa
---
> 4.9,3.6,1.4,0.1,Iris-setosa
keith@Steinhaus:~/demodir$
```

Before we go on...

It’s a good habit to **always look at the data.** Go exploring!

```
keith@Steinhaus:~/demodir$ head bezdekIris.data
5.1,3.5,1.4,0.2,Iris-setosa
4.9,3.0,1.4,0.2,Iris-setosa
4.7,3.2,1.3,0.2,Iris-setosa
4.6,3.1,1.5,0.2,Iris-setosa
5.0,3.6,1.4,0.2,Iris-setosa
5.4,3.9,1.7,0.4,Iris-setosa
4.6,3.4,1.4,0.3,Iris-setosa
5.0,3.4,1.5,0.2,Iris-setosa
4.4,2.9,1.4,0.2,Iris-setosa
4.9,3.1,1.5,0.1,Iris-setosa
keith@Steinhaus:~/demodir$
```

Before we go on...

It’s a good habit to **always look at the data.** Go exploring!

```
keith@Steinhaus:~/demodir$  head -n 70 bezdekIris.data | tail
5.0,2.0,3.5,1.0,Iris-versicolor
5.9,3.0,4.2,1.5,Iris-versicolor
6.0,2.2,4.0,1.0,Iris-versicolor
6.1,2.9,4.7,1.4,Iris-versicolor
5.6,2.9,3.6,1.3,Iris-versicolor
6.7,3.1,4.4,1.4,Iris-versicolor
5.6,3.0,4.5,1.5,Iris-versicolor
5.8,2.7,4.1,1.0,Iris-versicolor
6.2,2.2,4.5,1.5,Iris-versicolor
5.6,2.5,3.9,1.1,Iris-versicolor
keith@Steinhaus:~/demodir$
```

Before we go on...

It's a good habit to **always look at the data.** Go exploring!

```
keith@Steinhaus:~/demodir$ tail bezdekIris.data
6.9,3.1,5.1,2.3,Iris-virginica
5.8,2.7,5.1,1.9,Iris-virginica
6.8,3.2,5.9,2.3,Iris-virginica
6.7,3.3,5.7,2.5,Iris-virginica
6.7,3.0,5.2,2.3,Iris-virginica
6.3,2.5,5.0,1.9,Iris-virginica
6.5,3.0,5.2,2.0,Iris-virginica
6.2,3.4,5.4,2.3,Iris-virginica
5.9,3.0,5.1,1.8,Iris-virginica

keith@Steinhaus:~/demodir$
```

Species types are contiguous in the file. That means if we are going to, for example, make a train/dev/test split, we can't just take the first and second halves of the file!

File contains a trailing newline. We'll probably want to remove that!

Counting: `wc`

`wc` counts the number of lines, words, and bytes in a file or in `stdin`

- Prints result to `stdout`

```
keith@Steinhaus:~/demodir$ wc bezdekIris.data
     151  150  4551 bezdekIris.data
keith@Steinhaus:~/demodir$ cat bezdekIris.data | wc
     151  150  4551
keith@Steinhaus:~/demodir$ cat bezdekIris.data | wc -l
     151
keith@Steinhaus:~/demodir$ cat bezdekIris.data | wc -w
     150
keith@Steinhaus:~/demodir$ cat bezdekIris.data | wc -c
     4551
keith@Steinhaus:~/demodir$
```

Note: a word is a group of one or more non-whitespace characters.

Counting: `wc`

`wc` counts the number of lines, wo

Prints result to `stdout`

```
keith@Steinhaus:~/demodir$ wc bezdekIris.data
     151  150  4551 bezdekIris.data
keith@Steinhaus:~/demodir$ cat bezdekIris.data | wc
     151  150  4551
keith@Steinhaus:~/demodir$ cat bezdekIris.data | wc -l
     151
keith@Steinhaus:~/demodir$ cat bezdekIris.data | wc -w
     150
keith@Steinhaus:~/demodir$ cat bezdekIris.data | wc -c
     4551
keith@Steinhaus:~/demodir$
```

Test your understanding: we saw using `head` and `tail` that each line is a single word (group of non-whitespace characters), so number of words should be same as number of lines. Why isn't that the case?

Note: a word is a group of one or more non-whitespace characters.

Making small changes: `tr`

> **From the man page:** The `tr` utility copies the standard input to the standard output with substitution or deletion of selected characters.

Right now, `bezdekIris.data` is comma-separated.

What if I want to make it tab-separated, instead?

`tr` is a good tool for the job

```
keith@Steinhaus:~/demodir$ cat bezdekIris.data | tr ',' '\t' > iris.tsv
keith@Steinhaus:~/demodir$ head -n 5 iris.tsv
5.1     3.5     1.4     0.2     Iris-setosa
4.9     3.0     1.4     0.2     Iris-setosa
4.7     3.2     1.3     0.2     Iris-setosa
4.6     3.1     1.5     0.2     Iris-setosa
5.0     3.6     1.4     0.2     Iris-setosa
keith@Steinhaus:~/demodir$
```

> Replace commas with tabs. So we turn a comma-separated (.csv) file into a tab-separated (.tsv) file.

Making small changes: `tr`

From the man page: The `tr` utility copies the standard input to the standard output with substitution or deletion of selected characters.

```
keith@Steinhaus:~/demodir$ cat bezdekIris.data | tr '.,' ',\t' > iris_euro.tsv
keith@Steinhaus:~/demodir$ head iris_euro.tsv
5,1	3,5	1,4	0,2	Iris-setosa
4,9	3,0	1,4	0,2	Iris-setosa
4,7	3,2	1,3	0,2	Iris-setosa
4,6	3,1	1,5	0,2	Iris-setosa
5,0	3,6	1,4	0,2	Iris-setosa
5,4	3,9	1,7	0,4	Iris-setosa
4,6	3,4	1,4	0,3	Iris-setosa
5,0	3,4	1,5	0,2	Iris-setosa
4,4	2,9	1,4	0,2	Iris-setosa
4,9	3,1	1,5	0,1	Iris-setosa
keith@Steinhaus:~/demodir$
```

Turn decimal points into decimal commas, change from comma-separated to tab-separated.

Note: `tr 'abc' 'xyz'` turns all `a` into `x`, `b` into `y`, `c` into `z`. Importantly, `tr 'ab' 'bc'` turns `a` to `b` and `b` to `c`, but no `a` turns into `c`. `tr` doesn't "apply the transformation twice"

Picking out columns: `cut`

I want to make a new data set: **only** petal data and species

Could load everything into spreadsheet and edit there, or...

Attribute Information:
1. sepal length in cm
2. sepal width in cm
3. petal length in cm
4. petal width in cm
5. class:
-- Iris Setosa
-- Iris Versicolour
-- Iris Virginica

```
keith:~/demodir$ cat bezdekIris.data | cut -d ',' -f 3,4,5 > petal.data
keith:~/demodir$ head -n 3 petal.data
1.4,0.2,Iris-setosa
1.4,0.2,Iris-setosa
1.3,0.2,Iris-setosa
keith:~/demodir$ head -n 3 bezdekIris.data
5.1,3.5,1.4,0.2,Iris-setosa
4.9,3.0,1.4,0.2,Iris-setosa
4.7,3.2,1.3,0.2,Iris-setosa
keith:~/demodir$
```

Columns **d**elimited by `','`
Pick out **f**ields 3,4 and 5.
Equivalent command:
`cut -d ',' -f 3-5`

Picking out columns: `cut`

What if I want to split the attributes into their own files?

Attribute Information:
1. sepal length in cm
2. sepal width in cm
3. petal length in cm
4. petal width in cm
5. class:
-- Iris Setosa
-- Iris Versicolour
-- Iris Virginica

```
keith:~/demodir$ cat bezdekIris.data | cut -d ',' -f 1 > sepal_len.data
keith:~/demodir$ cat bezdekIris.data | cut -d ',' -f 2 > sepal_wid.data
keith:~/demodir$ cat bezdekIris.data | cut -d ',' -f 3 > petal_len.data
keith:~/demodir$ cat bezdekIris.data | cut -d ',' -f 4 > petal_wid.data
keith:~/demodir$ cat bezdekIris.data | cut -d ',' -f 5 > species.data
keith:~/demodir$
```

Aggregation: `paste` and `lam`

Okay, I changed my mind. I want to put the five separate files back together!

```
keith:~/demodir$ paste sepal_len.data sepal_wid.data petal_len.data
petal_wid.data species.data > pasted.data
keith:~/demodir$ diff pasted.data iris.tsv
151c151
<
---
>
keith:~/demodir$
```

Recall that last line was blank, so we have some strange behavior here.

`paste` (from the man page): concatenates the corresponding lines of the given input files, replacing all but the last file's newline characters with a single tab character, and writes the resulting lines to standard output.

Aggregation: `paste` and `lam`

`lam` (from the man page): copies the named files side by side onto the standard output.

Okay, I changed my mind. I want to put the five separate files back together!

```
keith:~/demodir$ lam sepal_len.data -s ',' sepal_wid.data -s ','
petal_len.data -s ',' petal_wid.data -s ',' species.data  | head -n 3
5.1,3.5,1.4,0.2,Iris-setosa
4.9,3.0,1.4,0.2,Iris-setosa
4.7,3.2,1.3,0.2,Iris-setosa
keith:~/demodir$ lam sepal_len.data -s ',' sepal_wid.data -s ','
petal_len.data -s ',' petal_wid.data -s ',' species.data | tail -n 3
6.2,3.4,5.4,2.3,Iris-virginica
5.9,3.0,5.1,1.8,Iris-virginica
,,,,
keith:~/demodir$
```

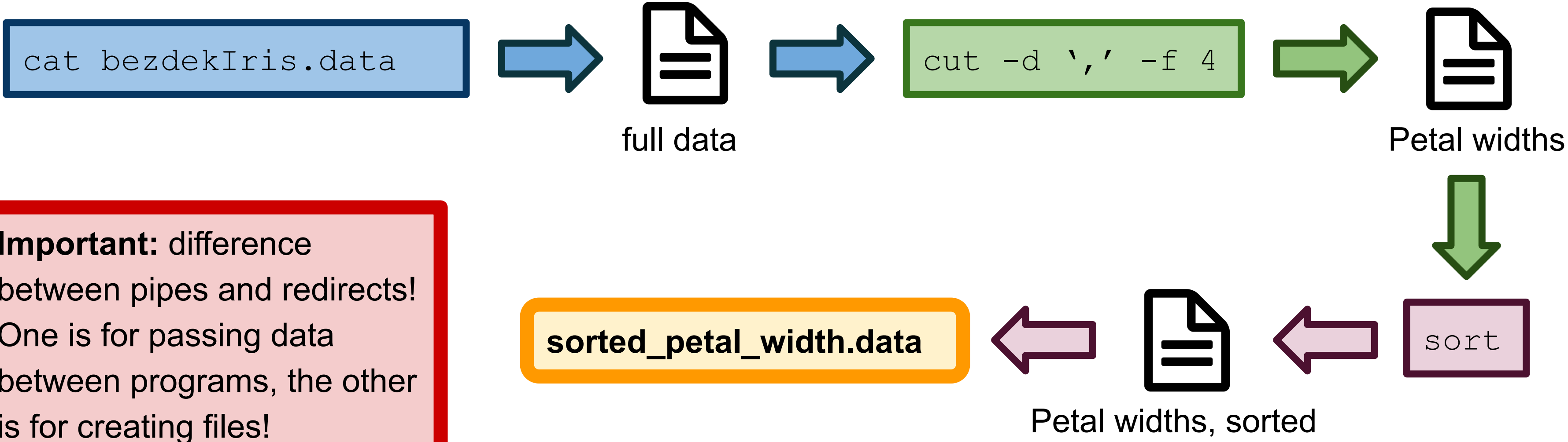
Have to specify a separator character with `-s` everywhere I want one.

Recall that the last line is blank, which `lam` handles as required, but here's a good reason to have removed that blank line sooner.

Sorting: `sort`

`sort` reads from stdin, sorts the lines, and sends the result to stdout.

```
keith:~$ cat bezdekIris.data | cut -d ',' -f 4 | sort > sorted_petal_width.data
keith:~$
```



Important: difference between pipes and redirects! One is for passing data between programs, the other is for creating files!

Sorting: `sort`

```
keith:~$ cat bezdekIris.data | cut -d ',' -f 4 | sort > sorted_petal_width.data
keith:~$ head -n 8 sorted_petal_width.data

0.1
0.1
0.1
0.1
0.1
0.2
0.2
keith:~$ tail -n 2 sorted_petal_width.data
2.5
2.5
keith:~$
```

Blank line is still giving us trouble!

Editing text streams: `sed`

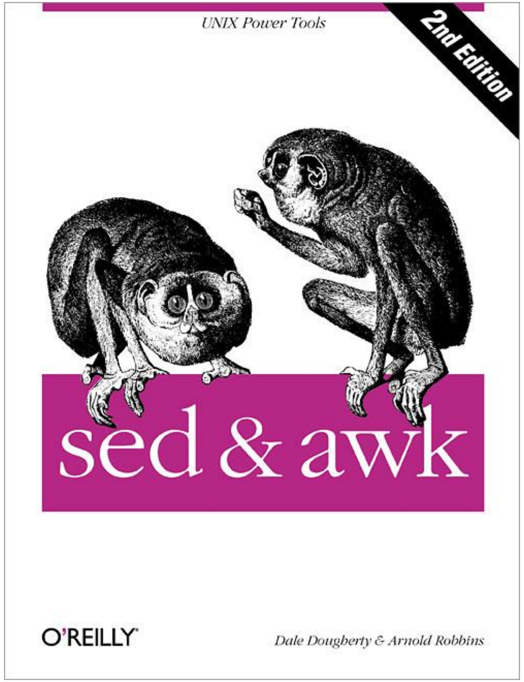
`sed` is short for **stream editor**

One of the most powerful and versatile UNIX tools

Commonly paired with `awk`

small command line language for string processing

Has lots of features, so we'll focus on one: **substitutions**




```
keith:~$ echo "hello world" | sed 's/hello/goodbye/g'
goodbye world
```

`s` for substitute

Replace this...

...with this.

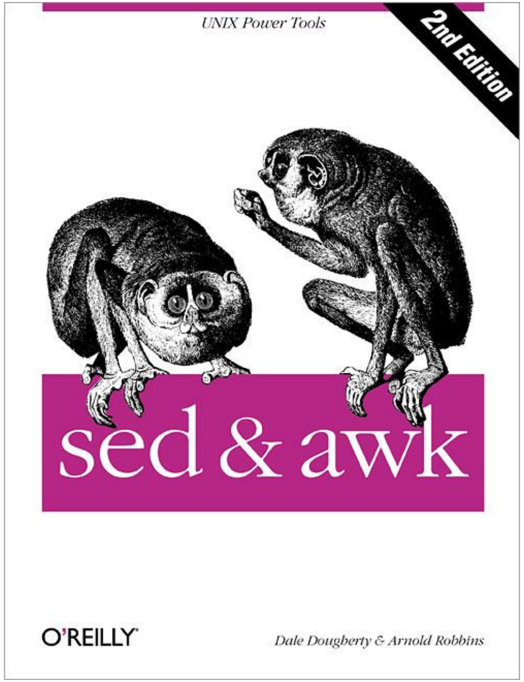
`g` for globally, meaning everywhere in the input.

Editing text streams: `sed`

`sed` commands can include regular expressions

```
keith:~$ echo "a aa aaa" | sed 's/a*/b/g'
b b b
```

`'*'` Works like in Python `re`



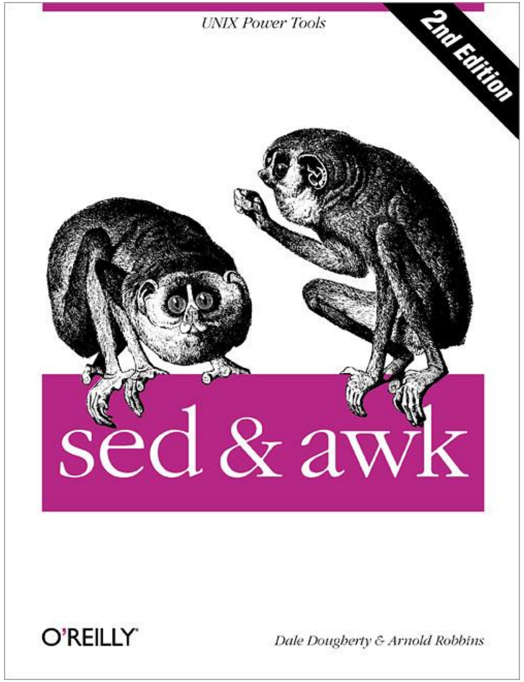
Editing text streams: `sed`

`sed` commands can include regular expressions

```
keith:~$ echo "a aa aaa" | sed 's/a*/b/g'
b b b
```

`'*'` Works like in Python `re`

Test your understanding: is the `sed` regex matcher greedy?



Editing text streams: `sed`

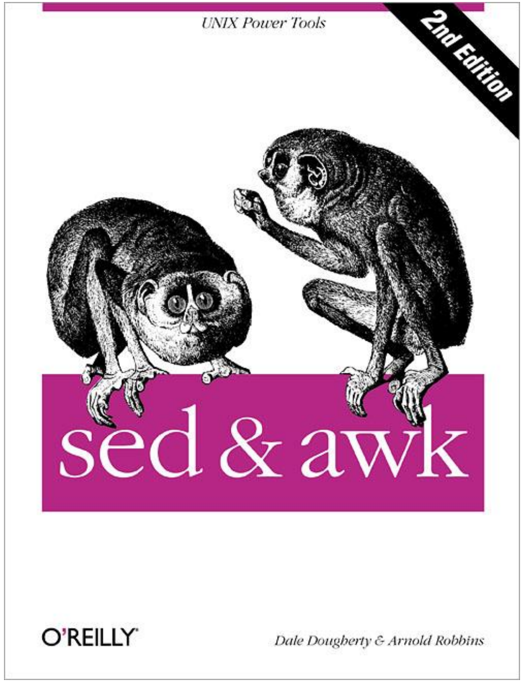
`sed` commands can include regular expressions

```
keith:~$ echo "a aa aaa" | sed 's/a*/b/g'
b b b
```

'*' Works like in Python `re`

Test your understanding: is the `sed` * operator greedy?

Answer: yes! If it were lazy, above would output just a mess of 'b's



Editing text streams: sed

sed commands can include regular expressions

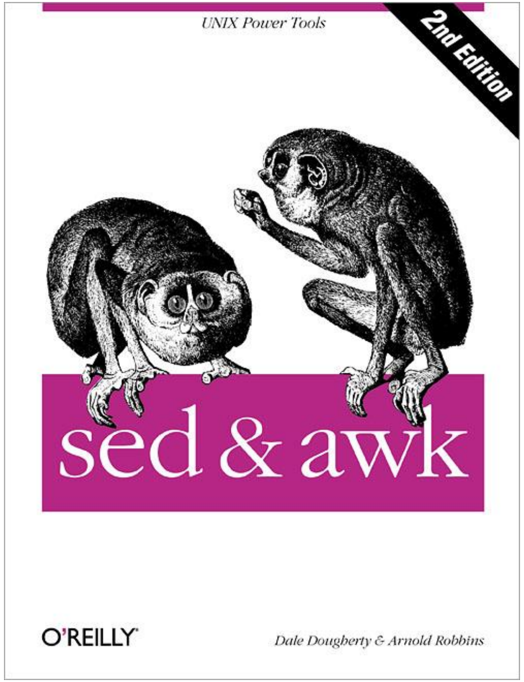
```
keith:~$ echo "a aa aaa" | sed 's/a*/b/g'
b b b
```

'*' Works like in Python re

Test your understanding: is the sed * operator greedy?

Answer: yes! If it were lazy, above would output just a mess of 'b's

As promised, most of your knowledge of regexes in Python re package will transfer directly to sed, as well as other tools (e.g., grep and perl)



Editing text streams: `sed`

`sed` commands can include regular expressions

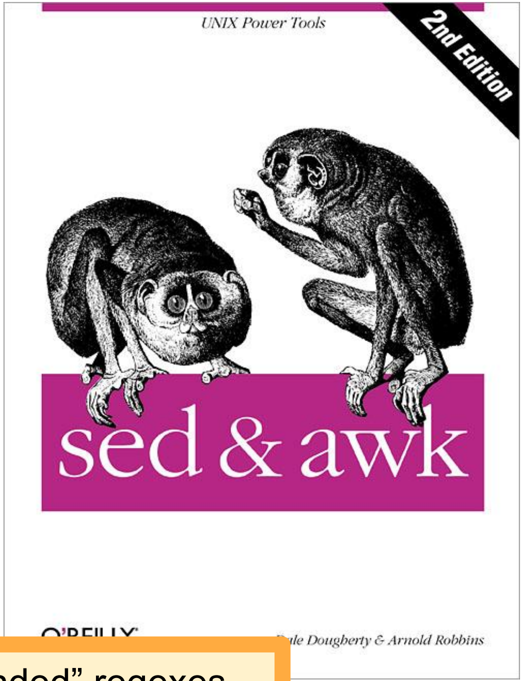
```
keith:~$ echo "a aa aaa" | sed 's/a*/b/g'
b b b
```

'*' Works like in Python `re`

Basic syntax of `sed` `s` commands:
`sed 's/regexp/replacement/flags'`

To use "extended" regexes, need to give `-E` flag.

```
keith:~$ echo "a aa aaa" | sed -E 's/a+/b/g'
b b b
keith:~$
```



Editing text streams: `sed`

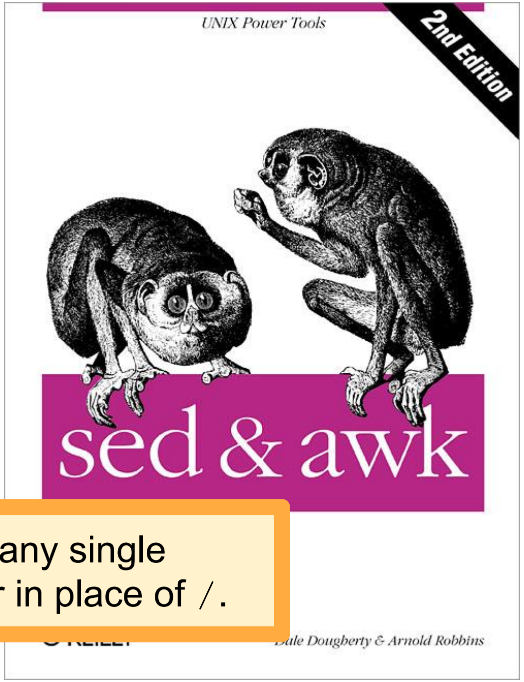
Basic syntax of `sed s` commands:
`sed 's/regexp/replacement/flags'`

```
keith:~$ echo "a aa aaa" | sed -E 's/a+/b/g'
b b b
keith:~$ echo "a aa aaa" | sed -E 's|a+|b|g'
b b b
keith:~$ echo "a| aa| aaa| aaaa" | sed -E 's/a+\|/b/g'
b b b aaaa
keith:~$
```

Can use any single character in place of `/`.

Special characters have to be escaped.

All the power of Python regexes, but with the convenience of the command line! And we're only barely scratching the surface: https://www.gnu.org/software/sed/manual/html_node/index.html#Top



Basic Shell Scripting

Bash (and other shells) support scripting

Useful for automating repetitive tasks:

E.g., Renaming files; processing files in batches

The Bash command line supports its own programming language

Has variables, conditionals, for-loops, etc.

We'll only scratch the surface of this, here. See, for example, the Linux Documentation Project (TLDP, www.tldp.org) or *Learning the Bash Shelll* by C. Newham for more.

Basic Shell Scripting

Variable assignment in bash is of the form
`VARIABLE=[value]`
Note that there should be NO spaces between the variable name and the assignment operator and between the assignment operator and the value.

```
keith:~$ MYVAR='cat dog bird goat'
keith:~$ echo $MYVAR
cat dog bird goat
keith:~$ FILENAME="myfile.txt"
keith:~$ echo "here is some text" > $FILENAME
keith:~$ cat $FILENAME
here is some text
keith:~$ echo FILENAME
FILENAME
keith:~$
```

To retrieve the value of a variable, prepend it with a dollar sign `$`.

Once `FILENAME` has a value, we can treat it just as though we were writing the actual name of a file in its place.

Common error: forgetting to prepend with a dollar sign `$`.

Basic Shell Scripting

For loops take the form

```
for vname in <set>; do <expr>; done
```

```
keith:~$ MYVAR='cat dog bird goat'
keith:~$ for s in $MYVAR; do echo $s; done
cat
dog
bird
goat
keith:~$ for x in `echo "1 2 3 4 5"`; do echo "$x" > ${x}.txt; done
keith:~$ ls
1.txt    2.txt    3.txt    4.txt    5.txt    myfile.txt
keith:~$
```

Enclosing in backticks (`) turns the output of the expression to a string-like expression that can be assigned to a variable or iterated over.

Enclosing a variable in curly braces is a good habit when putting a variable in a longer string. Prevents ambiguity of `$x.txt` or `$xfile.txt` vs `${x}file.txt`.

Basic Shell Scripting

```
keith:~$ for x in `echo "1 2 3 4 5"`; do echo "$x" > ${x}.txt; done
keith:~$ ls
1.txt    2.txt    3.txt    4.txt    5.txt    myfile.txt
keith:~$ for f in `ls .`; do echo -n "${f} : "; cat $f; done
1.txt : 1
2.txt : 2
3.txt : 3
4.txt : 4
5.txt : 5
myfile.txt : here is some text
keith:~$
```

This line lists each file in the current directory along with its contents.

Basic Shell Scripting

```
keith:~$ for x in `echo "1 2 3 4 5"`; do echo "$x" > ${x}.txt; done
keith:~$ ls
1.txt    2.txt    3.txt    4.txt    5.txt    myfile.txt
keith:~$ for f in `ls .`; do echo -n "${f} : "; cat $f; done
1.txt : 1
2.txt : 2
3.txt : 3
4.txt : 4
5.txt : 5
myfile.txt : here is some text
keith:~$
```

This line lists each file in the current directory along with its contents.

Lots more tools available (not in this lecture):
More syntax: conditionals, while-loops, etc.
Scripts: put a sequence of commands into a file and run it from the command line.