xkcd

http://xkcd.com/208/

1. Regular expressions

2. sed

3. Editing Files

4. Shell loops

5. Shell scripts

Regular Expressions

Text often follows human conventions

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US: month-day-year

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Zip codes must be five digits long

Structure: certain number of columns or rows

Conventions can change: prior to 2000, dates were always 3 sets of two numbers

Regular Expressions, ctd.

If we can encode search context we can make much more powerful searches.

What sort of information would we like to specify?

Whether text is:

1. Composed of numbers
2. Composed of letter
3. A certain length
4. Full of spaces or tabs
5. First or last on the line

Regular Expressions, ctd.

Encoding	Modern Equivalent	Pattern Type
`.`		a single character
`.+`		one or more characters
`.*`		zero or more characters
`.?`		Maybe present
`^`		first on the line
`$`		last on the line
`[0-9]`	`\d`	digits
`[a-zA-Z]`	`\w`	letters
`' '`	`\s \t`	space
`{3}`		must be exactly 3 characters long
`{3,5}`		between 3-5 characters long
`[ACGT]`		a specific set of characters (a class)

Regular Expressions, ctd.

Expression	Regular Expression
341341	.....
	[0-9]+
julian catchen	[a-z]+ [a-z]+
541-485-5128	[0-9]{3}\-[0-9]{3}\-[0-9]{4}
	[0-9\-]+
June 3, 1978	[a-zA-Z]+ [0-9], [0-9]{4}
AGCCCCTAGGACTGAAATTCC	[ACGT]

Regular Expressions, ctd.

Expression	Regular Expression
`341341`	.....
	[0-9]+
`julian catchen`	[a-z]+ [a-z]+
`541-485-5128`	[0-9]{3}\-[0-9]{3}\-[0-9]{4}
	[0-9\-]+
`June 3, 1978`	[a-zA-Z]+ [0-9], [0-9]{4}
	[a-zA-Z]+ [0-9]+, [0-9]{4}
	[a-zA-Z]+ ?[0-9]?,? [0-9]{4}

1. Download and decompress the file:

   `http://creskolab.uoregon.edu/lund/record.tsv.gz`

2. Use grep and search the file for the different patterns above:

   `% grep -E "pattern" record.tsv`

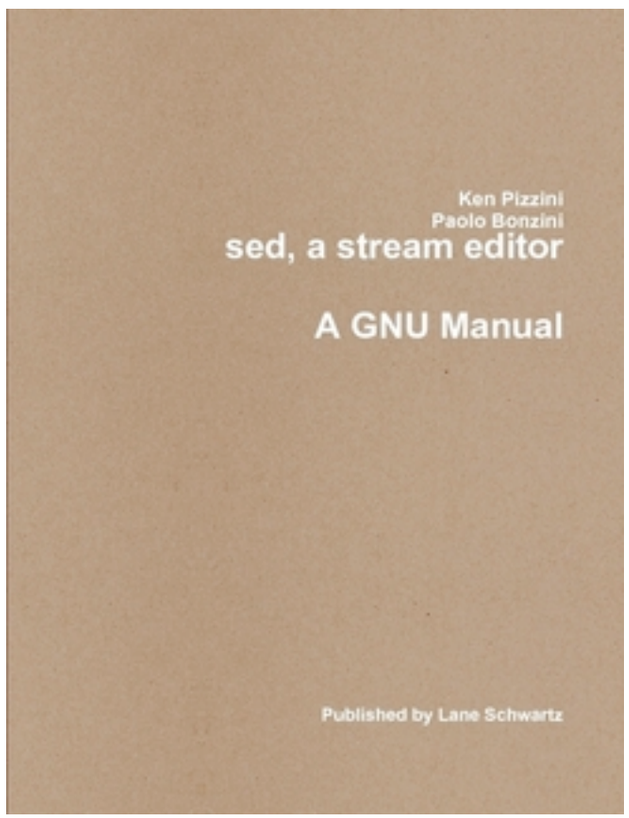
3. `cat` the file afterwards to examine what does and doesn't match with each pattern.

sed, a stream editor

Program 1

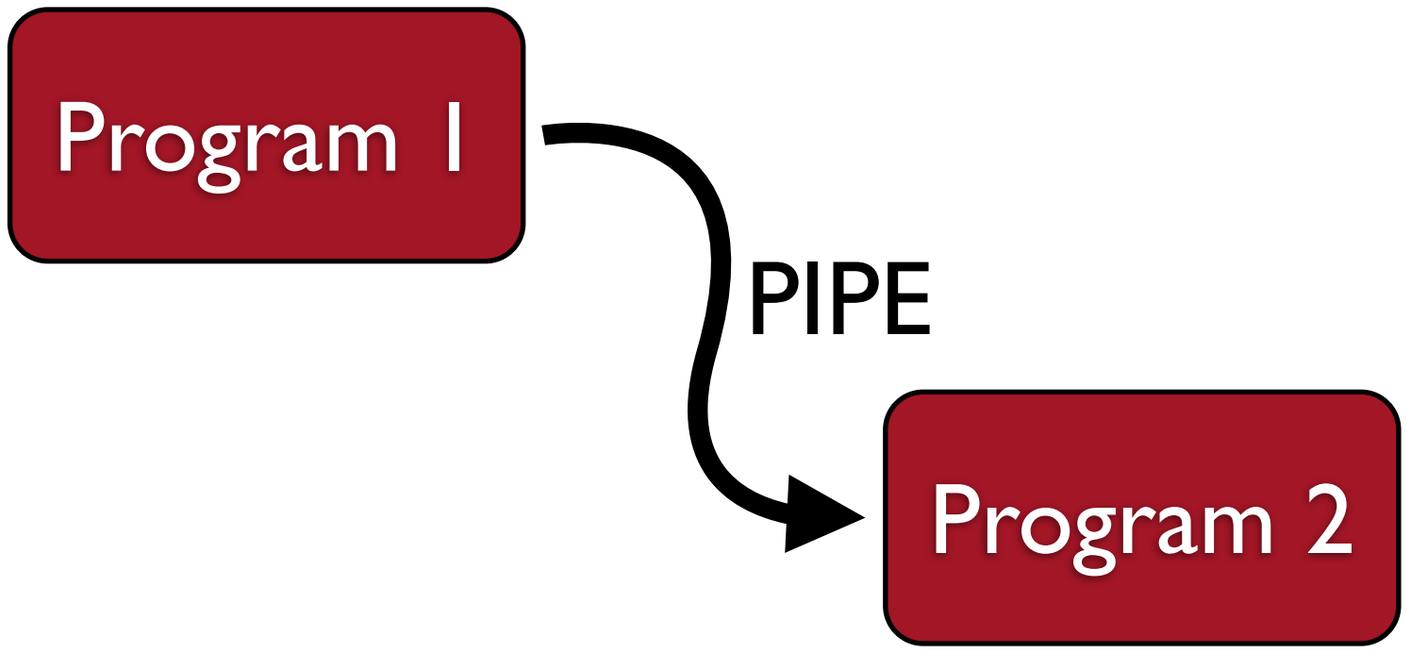
Program 2

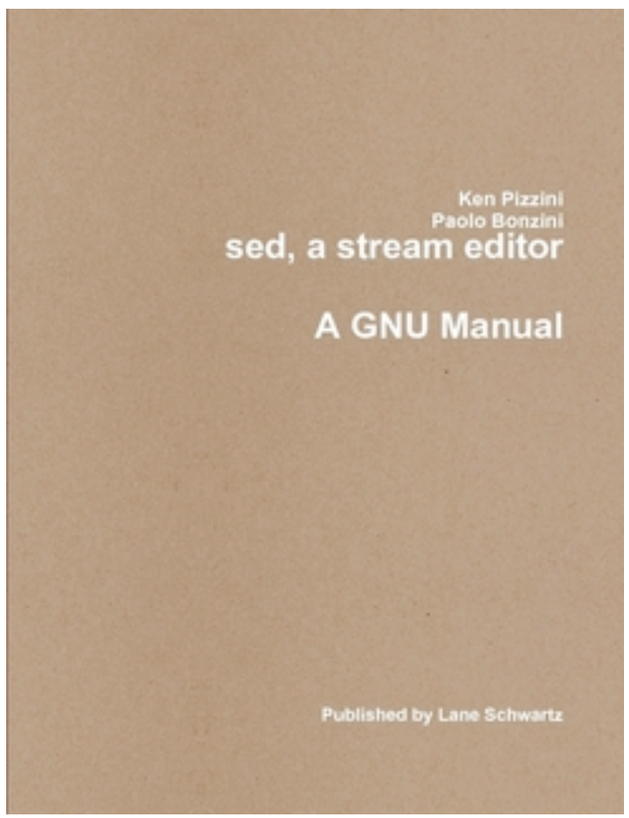
Program 3



Search and replace on data flowing through the pipe (a stream)

sed, a stream editor

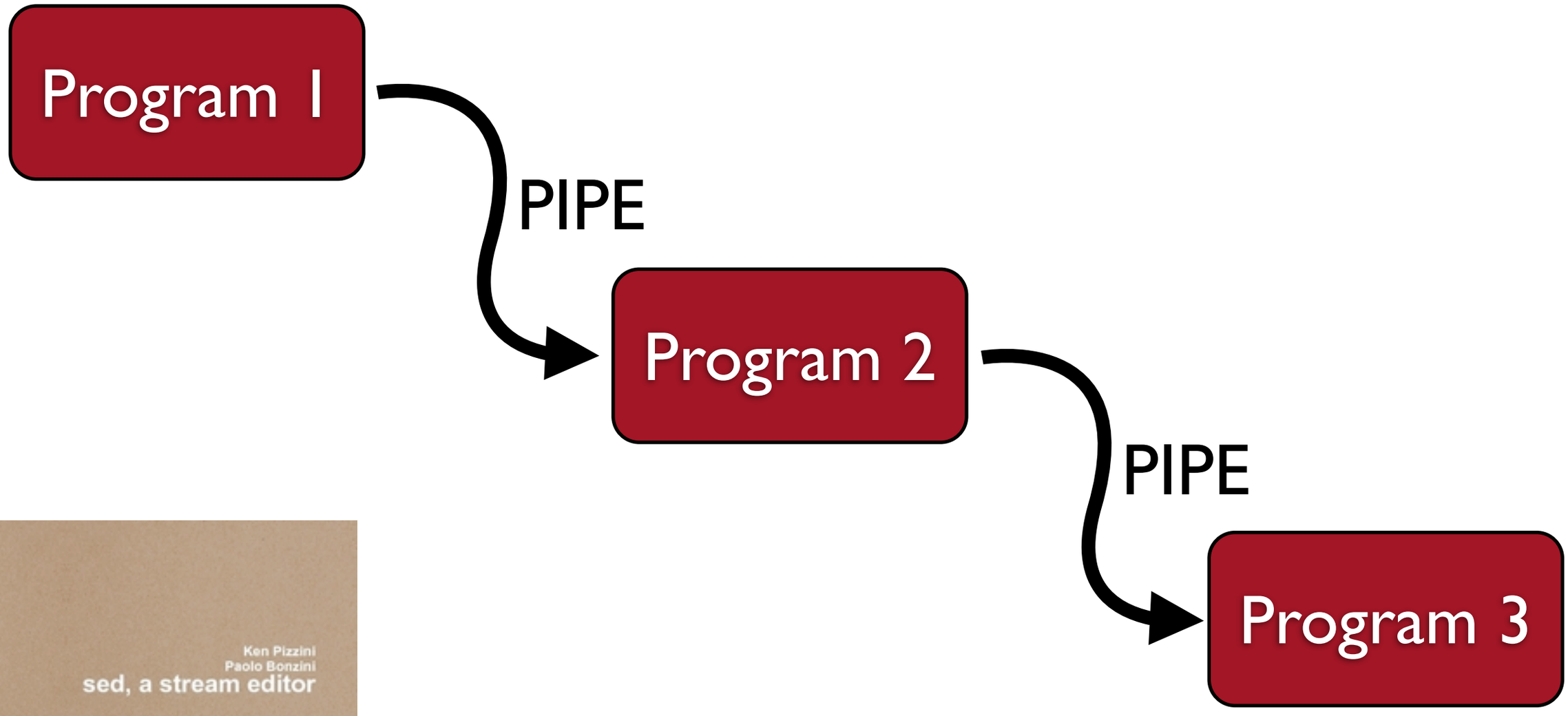


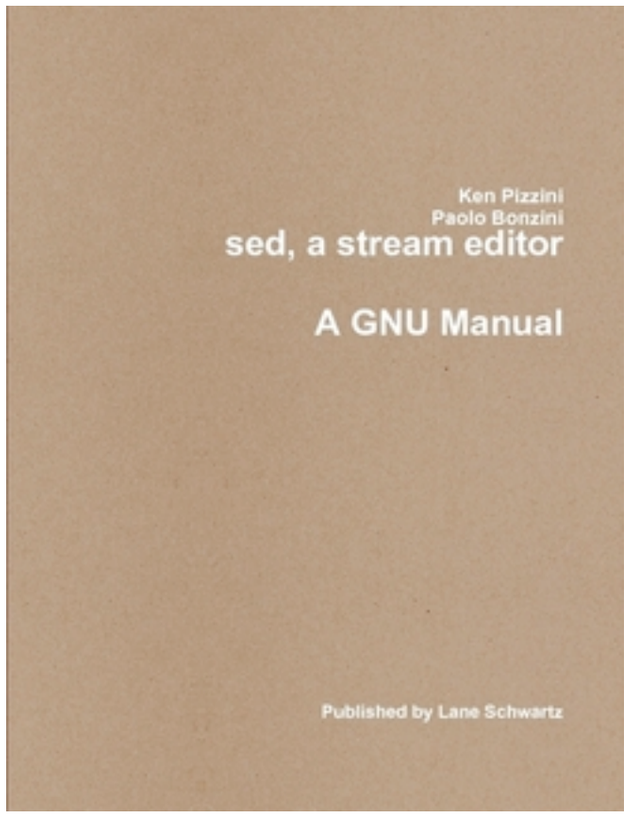


Program 3

Search and replace on data flowing through the pipe (a stream)

sed, a stream editor





Search and replace on data flowing through the pipe (a stream)

sed, a stream editor, ctd.

`s/pattern/replace/`

Two new encodings:

Record a match: `(pattern)`

Back references: `\1 \2 \3`

```
% sed -E 's/[a-z]+ [a-z]+/foo/'
```

sed, a stream editor, ctd.

s/pattern/replace/

```
% cat record.tsv | sed -E 's/[a-z]+ [a-z]+/foo/'

% cat record.tsv | sed -E 's/([a-z]+) [a-z]+/\1/'

% cat record.tsv | sed -E 's/[0-9]+//'

% cat record.tsv | sed -E 's/[0-9]+//g'

% cat record.tsv | sed -E 's/^[0-9]+    //'
```

sed, a stream editor, ctd.

`s/pattern/replace/`

Create a complex command:

```
% cd samples
% ls -1
fish_001.tags.tsv
fish_003.tags.tsv
fish_004.tags.tsv
fish_005.tags.tsv

% ls -1 | sed -E 's/^(fish_[0-9]+\.tags)\.tsv/mv \1\.tsv \1.loc/'
```

fish_310.tags.tsv.gz

`http://creskolab.uoregon.edu/lund/fish_310.tags.tsv.gz`

`ls`
`gunzip`
`man`
`more`
`cat`
`wc`
`head`
`cut`
`grep`
`sed`
`tr`
`>`
`|`

1. Decompress the file
2. Extract out the consensus sequences (2,191 sequences)
3. Extract out the ID and sequence for each consensus
4. Use sed to reverse the columns

   sed -E "s/^([0-9]+) ([ACGTN]+)/\2 \1/"
5. Use sed/tr to convert to a FASTA file

   sed -E "s/^([0-9]+) ([ACGTN]+)/>\1|\2/"

   use tr to replace the "|" character with a new line "\n"

1. use ctrl-v tab to get a literal tab on the command line

Editing on UNIX

Emacs

Richard Stallman - 1976
Founded GNU Project

Vi

Bill Joy - 1976
BSD/Sun Microsystems

Download example file using `wget`

Decompress the file in your home directory.

`http://creskolab.uoregon.edu/lund/manifesto.gz`

```
% emacs <filename>

% emacs /absolute/path/to/file

% emacs ../../../relative/path/to/file

% emacs file1 /path/file2 ../../file3
```

Command mode versus **Text-entry mode**

Your mouse cannot help you! (mostly.)

Emacs commands start with either **ctrl** or **meta** (esc-x)

The **Mark**

1. No mouse, so we need a way to indicate/highlight regions of text.
2. `ctrl-space` sets the mark
3. Use the arrow keys to highlight a region of text
4. Issue a command, e.g. copy/paste, or just press the space bar to unhighlight

Useful Emacs commands

`ctrl-x ctrl-s`	save file
`ctrl-x ctrl-f`	open a new file
`ctrl-space`	set the mark
`esc w`	copy highlighted text
`ctrl-w`	cut highlighted text
`ctrl-y`	paste text
`ctrl-x u`	undo
`ctrl-x b`	switch to another file (buffer)
`ctrl-s`	search for text
`esc %`	search and replace text
`ctrl-]`	quit current command
`ctrl-v`	page-down
`esc v`	page-up
`esc g g`	goto line
`ctrl-x ctrl-c`	quit emacs

manifesto.gz

1. Start emacs, opening `manifesto`
2. Copy the title and paste it one line below.
3. Search for the term '`GNU`', how many instances can you find?
4. Search/replace the phrase '`free software`' with '`proprietary software`'. How many instances did you replace?
5. Now, undo the replacements so that we remain `free`
6. Cut out the first paragraph of text.
7. Open a new file, `manifesto2`, paste the paragraph, save, quit emacs, view the file with `more`

One “dumb” question.

Download the example file using `wget`

1. Visit in your web browser:

`http://creskolab.uoregon.edu/stacks/`

2. Right click on the "Download Stacks" link and select "Copy Link Location" (or a similar variant)

3. Paste the link into the terminal and use `wget` to fetch it. Untar and decompress the archive.

File Permissions, Users+Groups

```
ubuntu@ip-10-4-193-188:~$ tar xfz stacks-0.998.tar.gz
ubuntu@ip-10-4-193-188:~$ cd stacks-0.998/
ubuntu@ip-10-4-193-188:~/stacks-0.998$ ls -la
total 500
drwxrwxr-x  7 ubuntu ubuntu   4096 2012-01-09 22:24 .
drwxr-xr-x 20 ubuntu ubuntu   4096 2012-03-06 23:20 ..
-rw-rw-r--  1 ubuntu ubuntu  35863 2012-01-07 03:11 aclocal.m4
-rwxr-xr--  1 ubuntu ubuntu    186 2011-02-03 05:27 autogen.sh
-rw-r--r--  1 ubuntu ubuntu  15209 2012-01-07 03:23 ChangeLog
drwxrwxr-x  2 ubuntu ubuntu   4096 2012-01-09 22:24 config
-rw-rw-r--  1 ubuntu ubuntu   3288 2012-01-07 03:14 config.h.in
-rwxr-xr-x  1 ubuntu ubuntu 207941 2012-01-07 03:11 configure
-rw-r--r--  1 ubuntu ubuntu    948 2012-01-07 02:51 configure.ac
-rw-r--r--  1 ubuntu ubuntu   9498 2011-02-03 05:27 INSTALL
-rw-r--r--  1 ubuntu ubuntu  35147 2011-02-03 05:27 LICENSE
-rw-r--r--  1 ubuntu ubuntu   7956 2012-01-07 03:11 Makefile.am
-rw-rw-r--  1 ubuntu ubuntu 141976 2012-01-07 03:12 Makefile.in
drwxrwxr-x  3 ubuntu ubuntu   4096 2012-01-09 22:24 php
-rw-r--r--  1 ubuntu ubuntu   4204 2011-10-10 04:56 README
drwxrwxr-x  2 ubuntu ubuntu   4096 2012-01-09 22:24 scripts
drwxrwxr-x  2 ubuntu ubuntu   4096 2012-01-09 22:24 sql
drwxrwxr-x  2 ubuntu ubuntu   4096 2012-01-09 22:24 src
ubuntu@ip-10-4-193-188:~/stacks-0.998$
```

File Permissions, Users+Groups

rwxrwxr-x

111111101

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File Permissions, Users+Groups

```
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Owner	Group	Other
rwx	rwx	r-x
111	111	101

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```

File Permissions, Users+Groups

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```

Owner	Group	Other
rwx	rwx	r-x
111	111	101
7	7	5

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drwxrwxr-x  2 ubuntu              22:24 src
ubuntu@ip-10-4-193-18
```
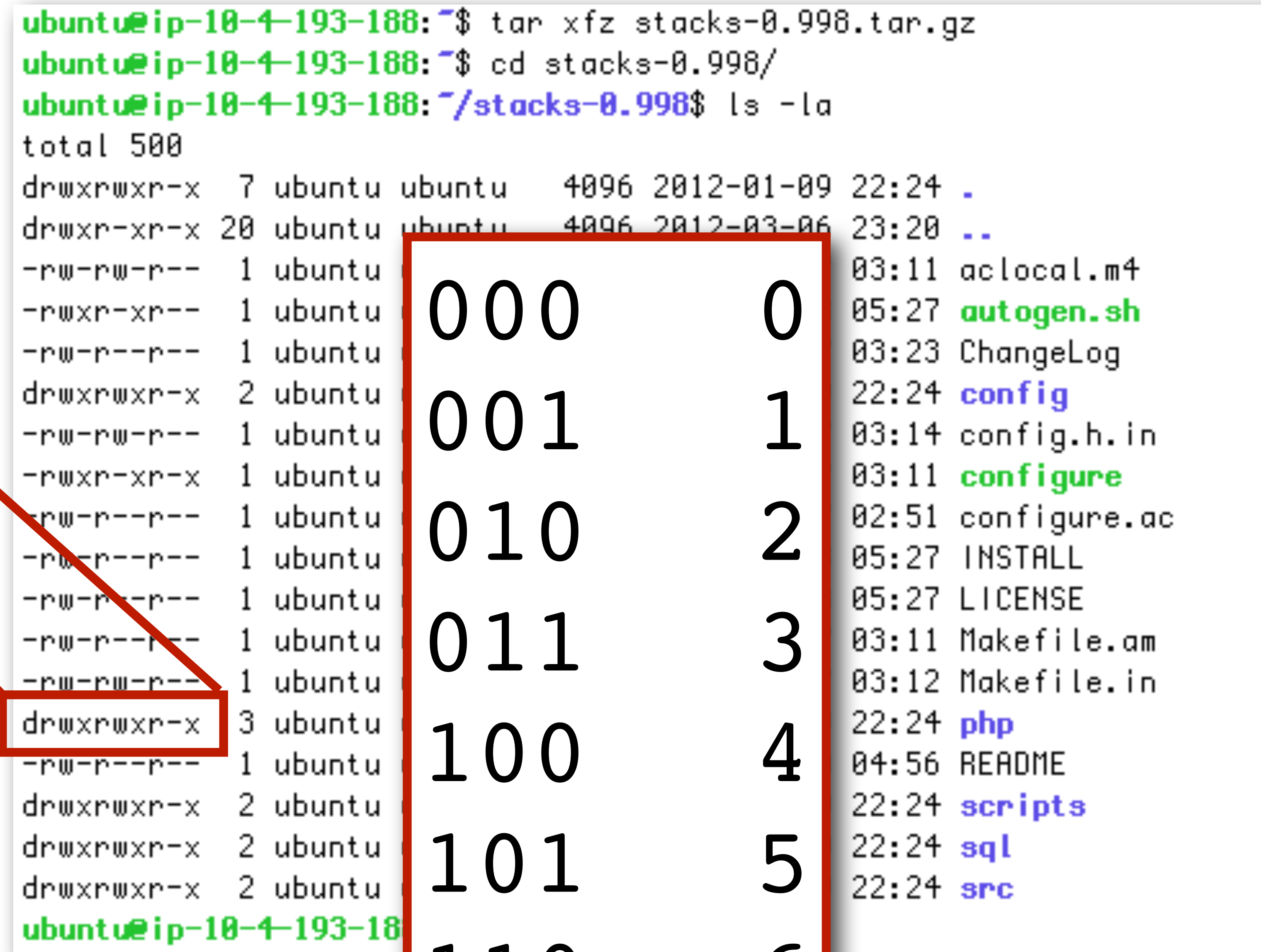

000	0
001	1
010	2
011	3
100	4
101	5
110	6
111	7

File Permissions, Users+Groups

```
rwxrwxr-x
111111101
```



000	0
001	1
010	2
011	3
100	4
101	5
110	6
111	7

Owner	Group	Other
rwx	rwx	r-x
111	111	101
7	7	5

`chmod 777 README`   `chmod 644 README`   `chmod 600 README`

What is a variable?

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What is a variable, ctd.

1. A variable can have almost any name:
    - `foo`
    - `bar`
    - `cats`
    - `line`

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2. You assign it a value like this:
   - `foo=32`
   - `bar=27.4938193`
   - `cats="LOLzzzz"`
   - `line="sample_01.fq"`

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3. You refer to it using a dollar sign:
   - `$foo`
   - `${foo}`

What is a variable, ctd.

Variables often have types, depending on the language

integer	`1, 2, 3, 4, 5...` `-1, -2, -3, -4, -5...`
float (double)	`3.141592653589790`
string (of characters)	`“My dog is Billy”`

What is a variable, ctd.

1. Try it out: set a variable on the command line:
    - `foo=32`
2. Display the value the variable holds:
    - `echo $foo`
3. Set a new value and display it:
    - `foo="The cat likes thai food"`
    - `echo $foo`

Shell Loops

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My favorite command: `ls -1`

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while read line; do **`command $line`**; done

Shell Loops

My favorite command: `ls -1`

while read line; do **`command $line`**; done

Pipe `ls -1` to a `while` loop and watch magic happen

samples.tar.gz

1. Expand the archive: **`tar -xvf`**

```
fish_001.tags.tsv
fish_003.tags.tsv
fish_004.tags.tsv
fish_005.tags.tsv
```

2. Move into the samples directory
3. Execute a command that can identify the consensus sequences in this file.
4. Try out the `ls -1` command
5. Combine parts 3 and 4 with a while loop to count the number of consensus sequences in each file

```
4
5
4
6
```

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```
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while read line; do **`command $line`**; done

Shell Scripts

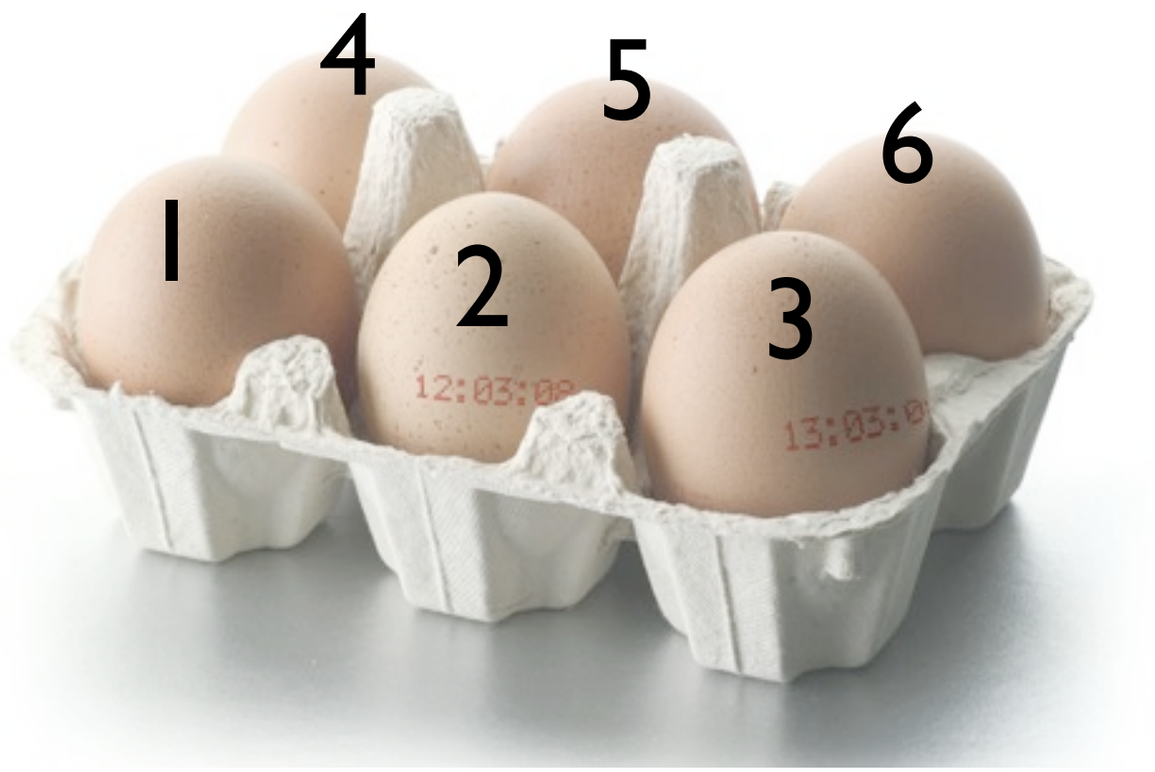
1. Anything you can do on the shell can be placed in a shell script
2. Shell scripts often end in the suffix ".sh"
3. Shell scripts must be executable (`chmod 755`)
4. *Comments* can be written in scripts with a "#"
5. Variables can be used to shorten long paths
6. Shell loops can be used to process lots of files
7. "\" can be used to wrap long commands across multiple lines
8. #!/bin/bash must be the first line - specifies interpreter

Shell Scripts, ctd.

What is an array?

Shell Scripts, ctd.

What is an array?



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Shell Scripts, ctd.

What is an array?

1. A variable can have almost any name:
    - `foo`
    - `bar`
    - `cats`
    - `line`

2. You assign it a value like this:

    - ```
      foo="progeny_10.fa
      progeny_11.fa
      progeny_12.fa
      progeny_13.fa
      progeny_14.fa
      progeny_15.fa"
      ```
      ```

Shell Scripts, ctd.

```
[catchen@genome]:~/research/seq/dre_hap% more build_tags.sh
#!/bin/bash

ROOT=$HOME/research/seq
bin=$ROOT/radtags/stacks/trunk/
src=$ROOT/dre_hap
db=dre_hap_radtags
batch_id=1
date=2011-05-17
desc="Danio rerio haploid map"

cd $bin
nice -n 19 $bin/scripts/denovo_map.pl -m 3 -B $db -b $batch_id -t -a $date -D "$desc" -e $bin -T 40 \
  -o $src/nstacks \
  -p $src/samples/female.fq \
  -r $src/samples/progeny_01.fq \
  -r $src/samples/progeny_02.fq \
  -r $src/samples/progeny_03.fq \
  -r $src/samples/progeny_05.fq \
  -r $src/samples/progeny_06.fq \
  -r $src/samples/progeny_08.fq \
  -r $src/samples/progeny_09.fq \
  -r $src/samples/progeny_10.fq \
  -r $src/samples/progeny_13.fq \
  -r $src/samples/progeny_14.fq \
  -r $src/samples/progeny_16.fq \
  -r $src/samples/progeny_17.fq \
  -r $src/samples/progeny_18.fq \
  -r $src/samples/progeny_19.fq \
  -r $src/samples/progeny_20.fq \
  -r $src/samples/progeny_23.fq \
  -r $src/samples/progeny_24.fq \
  -r $src/samples/progeny_25.fq \
  -r $src/samples/progeny_27.fq \
  -r $src/samples/progeny_33.fq \
  -r $src/samples/progeny_34.fq \
  -r $src/samples/progeny_35.fq \
  -r $src/samples/progeny_36.fq \
  -r $src/samples/progeny_37.fq \
  -r $src/samples/progeny_38.fq
```

Shell Scripts, ctd.

catchen@genome.uoregon.edu:/home/catchen — ssh — 178×47

```
File Edit Options Buffers Tools Sh-Script Help
#!/bin/bash

ROOT=$HOME
src=$ROOT/research/seq/or_phylo
bwa_db=$ROOT/research/bwa/gac_gen_broads1_e64
bowtie_db=$ROOT/research/bowtie/gac_gen_broads1_e64
bin=$ROOT/research/stacks/trunk

files="stl_1274.31
stl_1274.32
stl_1274.33
stl_1274.34
stl_1274.35
stl_1274.36
stl_1274.37
stl_1274.38
stl_1274.39
"

#
# Align with GSnap
#
for file in $files
do
   echo $file >> aligned/gsnap.log
   gsnap -t 24 -n 1 --quiet-if-excessive --terminal-threshold=10  -A sam -m 5 -i 2 -d gac_gen_broads1_e64 \
         -D /home/catchen/research/gsnap/gac_gen_broads1_e64 $src/samples/${file}.fq > $src/aligned/${file}.sam 2>> $src/aligned/gsnap.log
done

-UU-:----F1  build_tags.sh   All L29    (Shell-script[bash])----------
Wrote /home/catchen/build_tags.sh
```

Advanced Bash-Scripting Guide

http://tldp.org/LDP/abs/html/

Download example file using `wget`

Untar the file in your home directory.

`http://creskolab.uoregon.edu/lund/seqs.tar.gz`

Shell Scripts, ctd.

`http://creskolab.uoregon.edu/lund/seqs.tar.gz`

1. Move into the seqs directory
2. Use `ls -1` and a shell loop to count the number of lines in each file
3. Use a shell loop to concatenate the files into a single file, use the >> operator to redirect the output
4. Count the lines in the final file, make sure they match
5. Create a shell script to do all of the above.