

Workshop 1: Introduction to UNIX command-line

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Swiss Army knife" set of tools

Day 1

pwd - report your current directory

cd *<to where>* - change your current directory

ls *<directory>* -list contents of directory

cp *<old file>* *<new file>* - copy file

cp **-r** *<old dir>* *<new dir>* - copy a directory and its contents

mv *<old file/dir>* *<new file/dir>* - move (or rename)

rm *<file>* -delete a file

rm **-r** *<dir>* - remove a directory and its contents

mkdir *<new directory name>* -make a directory

Using hoffman2

- Log on to hoffman2:
 - `ssh myname@hoffman2.idre.ucla.edu`
- Request an interactive shell:
 - `qrsh -l i,time=3:00:00,h_data=2g`

You can make a “program” with the interactive shell script

Copy the working materials



```
[psscott17@login2 ~]$ git clone
```

```
https://github.com/p-scott17/Intro2Unix.git
```

```
Initialized empty Git repository in
/u/home/b/briggitta/code/W1.UNIX.command.line/.git/
remote: Counting objects: 88, done.
remote: Compressing objects: 100% (5/5), done.
remote: Total 88 (delta 0), reused 7 (delta 0), pack-reused 79
Unpacking objects: 100% (88/88), done.
```

<https://github.com/p-scott17/Intro2Unix.git>

Branch: master ▾ New pull request

Create new file Upload files Find file Clone or download

smangul1 organize slides and update workshopmaterials

figures	add figure from the UNIX paper
workshop.materials	organize slides and update workshopmaterials
workshop.slides	organize slides and update workshopmaterials
README.md	Update README.md

Clone with HTTPS ⓘ Use SSH

Use Git or checkout with SVN using the web URL.

<https://github.com/QCB-Collaboratory/>

Open in Desktop Download ZIP

<https://qcb.ucla.edu/collaboratory/workshops/introtounix/>

Working materials

- `cd Intro2Unix`
- `ls`

```
bwa_loop_pipe.sh  bwa_loop.sh  bwa.sh
day1_Unix_PAS_winter2020.pdf  day2_Unix_PAS_winter2020.pdf
day3_Unix_PAS_winter2020.pdfemp.txt      hg19.gtf
file_sed.txt    f.txt  numbers.txt    regex2.txt  regex_sort.txt
regex.txt  sales.txt  tobe.txt    toy3.reads.fastq
toy2.reads.fastq  toy.reads.fastq    toy.ref.fasta
    toy.ref.fasta.amb  toy.ref.fasta.ann    toy.ref.fasta.bwt
    toy.ref.fasta.pac  toy.ref.fasta.sa
```

Relative vs. absolute path

- A file or a directory can be referred to by
 - Relative path
 - **if you are at** `/u/home/p/pscott17/test/new/`
 - and you want `text.txt`
 - `../test.txt`
 - Absolute path
 - `/u/home/p/pscott17/test/test.txt`

**245 Highland Ave, Manhattan
Beach, California 90266**

Absolute



Relative



File permissions

- Each file in Unix has an associated permission level
- This allows the user to prevent others from reading/writing/executing their files or directories
- Use “`ls -l filename`” to find the permission level of that file
- There are 3 kinds of people in the world: **you** (user), **your friends** (group) and **the world** (others).

Permission levels

- “**r**” means “read only” permission
- “**w**” means “write” permission
- “**x**” means “execute” permission
 - In case of directory, “**x**” grants permission to list directory contents

File Permissions

```
-rw-r--r-- 1 pscott17 hbshaffe 72 Mar 11 14:22 large.txt  
-rw-r--r-- 1 pscott17 hbshaffe 263 Mar 11 15:18 new.tar  
-rw-r--r-- 1 pscott17 hbshaffe 13 Mar 11 15:27 test.txt  
drwxr-xr-x 2 pscott17 hbshaffe 4096 Mar 11 15:36 dfgdf
```



Type

User (you)



File Permissions

```
-rw-r--r-- 1 pscott17 hbshaffe 72 Mar 11 14:22 large.txt  
-rw-r--r-- 1 pscott17 hbshaffe 263 Mar 11 15:18 new.tar  
-rw-r--r-- 1 pscott17 hbshaffe 13 Mar 11 15:27 test.txt  
drwxr-xr-x 2 pscott17 hbshaffe4096 Mar 11 15:36 dfgdf
```



Type



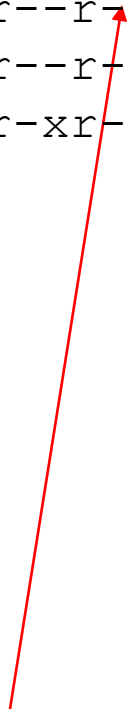
Group

File Permissions

```
-rw-r--r-- 1 pscott17 hbshaffe 72 Mar 11 14:22 large.txt  
-rw-r--r-- 1 pscott17 hbshaffe 263 Mar 11 15:18 new.tar  
-rw-r--r-- 1 pscott17 hbshaffe 13 Mar 11 15:27 test.txt  
drwxr-xr-x 2 pscott17 hbshaffe 4096 Mar 11 15:36 dfgdf
```



Type



“The World”

Command: chmod

- If you own the file, you can change it's permissions with "chmod"

– Syntax:

```
chmod [user/group/others/all]+-[permission] [file(s)]
```



```
[pscott17@login2 test]$ ls -l
drwxr-xr-x 3 pscott17 hbshaffe4096 Mar 11 15:23 archive
-rw-r--r-- 1 pscott17 hbshaffe 72 Mar 11 14:22 large.txt
-rw-r--r-- 1 pscott17 hbshaffe 263 Mar 11 15:18 new.tar
-rw-r--r-- 1 pscott17 hbshaffe 13 Mar 11 15:27 test.txt
[pscott17@login2 test]$ chmod g+w large.txt
[pscott17@login2 test]$ ls -l
drwxr-xr-x 3 pscott17 hbshaffe4096 Mar 11 15:23 archive
-rw-rw-r-- 1 pscott17 hbshaffe 72 Mar 11 14:22 large.txt
-rw-r--r-- 1 pscott17 hbshaffe 263 Mar 11 15:18 new.tar
-rw-r--r-- 1 pscott17 hbshaffe 13 Mar 11 15:27 test.txt
```

Redirection



- `program_a`
 - display `program_a`'s output at the terminal
- `program_a > file.txt`
 - `program_a`'s output is written to `file.txt`
 - “>” will **overwrite** any existing data in `file.txt`
- `program_a < input.txt`
 - `program_a` gets its input from a file called “`input.txt`”
- `program_a >> file.txt`
 - `program_a`'s output is **appended** to the end of `file.txt`

Let's practice!



```
[pscott17@login4 test]$ wc -l large.txt
300 large.txt
[pscott17@login4 test]$ wc -l large.txt > f_ls.txt
[pscott17@login4 test]$ head f_ls.txt
[pscott17@login4 test]$ ls > f_ls.txt
[pscott17@login4 test]$ head f_ls.txt
[pscott17@login4 test]$ head large.txt >> f_ls.txt
[pscott17@login4 test]$ head f_ls.txt
```

Pipeline

pipe character



- `program_a | program_b`
 - `program_a`'s output becomes `program_b`'s input
 - Analogous to

```
program_a > temp.txt
```

```
program_b < temp.txt
```

Command: **wc**

- To count the characters, words, and lines in a file use **wc**

```
wc <filename>
```

- The first column in the output is lines, the second is words, and the last is characters
- **-l** to count the lines

```
#lines      #words      #characters
    300      300      1092 large.txt
```


Let's practice!



```
[psscott17@login2 test]$ wc test.txt
```

```
300 300 1092 large.txt
```

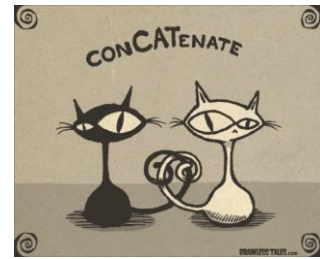
```
[psscott17@login2 test]$ wc -l test.txt
```

```
300 large.txt
```

```
[psscott17@login2 test]$ ls | wc -l
```

```
5
```

Command : **cat**



- Concatenate files together and displayed in the terminal.

```
cat <file1> <file2> ...
```

```
[pscott17@login2 test]$ cat large.txt f_ls.txt | wc -l
301
[pscott17@login2 test]$ cat large.txt test.txt > all.txt
[pscott17@login2 test]$ tail -n 3 all.txt
299
300
300 large.txt
```

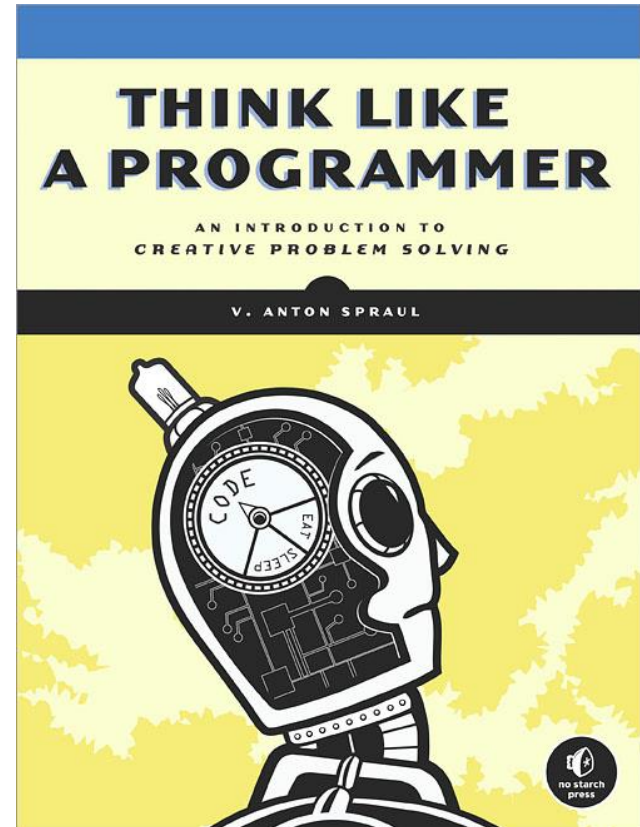
Directory

Find

- find **new** -name **test.txt** -type f

File

Tools for processing text files



Command : **grep**

- allows to search one file or multiple files for lines that contain a certain string
- g/re/p (globally search a regular expression and print)
- **grep** options
 - lines not containing the selected string (-v)
 - line numbers where the string occurs (-n)
 - number of lines containing the string (-c)
 - filenames where the string occurs (-l)
 - makes the match case-insensitive (-i)



Grep syntax treats the first argument as the pattern and the rest as filenames

Let's practice!



```
[pscott17@login4 test]$ grep "1" large.txt
```

```
1
```

```
10
```

```
...
```

```
19
```

```
[pscott17@login4 test]$ grep -n "1" large.txt
```

```
1:1
```

```
10:10
```

```
...
```

```
19:19
```

```
[pscott17@login4 test]$ grep -c "1" large.txt
```

```
138
```

```
[pscott17@login4 test]$ grep -l "1" large.txt f_ls.txt  
large.txt
```

```
[pscott17@login4 test]$ grep "1" large.txt f_ls.txt
```

```
large.txt:1
```

```
large.txt:10
```

```
...
```



Alternative? ←



Grep syntax treats the first argument as the pattern and the rest as filenames

Lines corresponding to chr2

```
[pscott17@login4 test]$ cd ~/Intro2Unix
[pscott17@login4 test]$ grep "chr2" hg19.gtf > chr2.txt
[pscott17@login4 test]$ tail -n 1 chr2.txt
chr21  hg19_knownGene  CDS 33066517  33066602  0.000000
      gene_id "uc002ypd.2"; transcript_id "uc002ypd.2";
```

Gtf file: The Gene transfer **format (GTF)** is a **file format** used to hold information about gene structure. It is a tab-delimited text **format** based on the general feature **format (GFF)**, but contains some additional conventions specific to gene information. (https://en.wikipedia.org/wiki/Gene_transfer_format)

Regular Expression

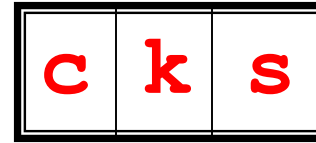


Regular Expression

/h[a4@]([c-<|(\k|\<)|(\k|\<)|(\k|\<))\s+\
((d|(\t|+|h))3ea4@)\s+p[1][a4@]n[3e][\t+] /i
(c)2006 FTS Conventures - www.ftskonventures.com

- A **regular expression** is a string that can be used to describe several sequences of characters.

regular expression →



UNIX Tools rocks.



↑
match

UNIX Tools sucks.



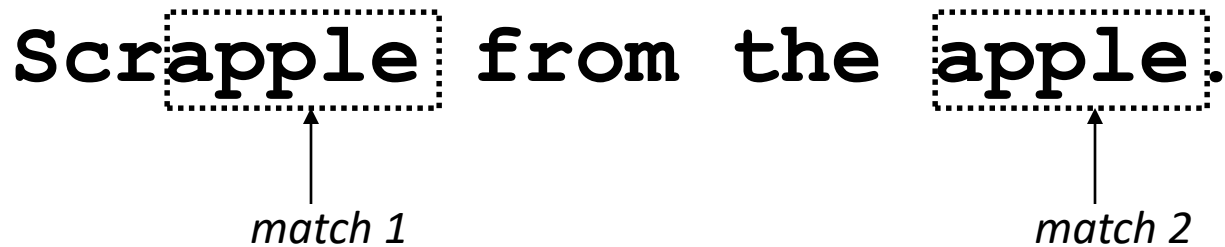
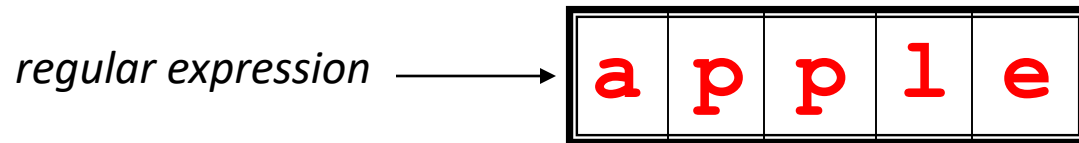
↑
match

UNIX Tools are okay.

no match

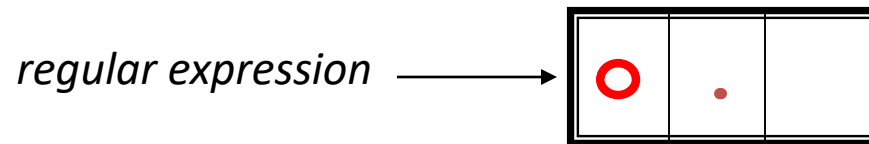
Regular Expressions

- A regular expression can match a string in more than one place.



Regular Expressions

- The `.` regular expression can be used to match any character.



For me to fool **o**with.

match 1 *match 2*

The image shows the sentence 'For me to fool with.' in a monospace font. The first letter 'F' and the first letter 'o' are enclosed in dashed rectangular boxes. Below the 'F' box is an upward-pointing arrow labeled 'match 1'. Below the 'o' box is an upward-pointing arrow labeled 'match 2'.

Character Classes

- Character classes `[]` can be used to match any specific set of characters.

regular expression →

b	[eor]	a	t
----------	--------------	----------	----------

beat

match 1

a

brat

match 2

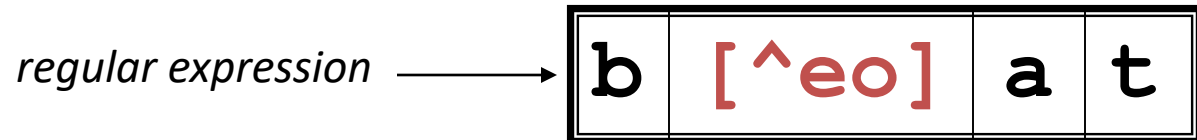
on a

boat

match 3

Negated Character Classes

- Character classes can be negated with the `[^]` syntax.



beat a **brat** on a boat

↑
match

Let's practice!



```
[psscott17@login4 intro2unix]$ grep "boat" regex.txt  
[psscott17@login4 intro2unix]$ grep "b[eor]at" regex.txt  
[psscott17@login4 intro2unix]$ grep "b.at" regex.txt  
[psscott17@login4 intro2unix]$ grep "b[^eor]at" regex.txt  
[psscott17@login4 intro2unix]$ grep "b[^eor]" regex.txt
```

More About Character Classes

- `[aeiou]` will match any of the characters **a**, **e**, **i**, **o**, or **u**
- `[kK]orn` will match **korn** or **Korn**
- Ranges can also be specified in character classes
 - `[1-9]` is the same as `[123456789]`
 - `[abcde]` is equivalent to `[a-e]`
 - You can also combine multiple ranges
 - `[abcde123456789]` is equivalent to `[a-e1-9]`
 - Note that the **-** character has a special meaning in a character class **but only** if it is used within a range, `[-123]` would match the characters **-**, **1**, **2**, or **3**

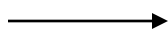
Alphanumeric characters

- Alphanumeric characters
 - [a-zA-Z]
 - **[[:alpha:]]**
- Digits
 - **[0-9]**
 - [[:digit:]]
- Alphanumeric characters
 - [a-zA-Z0-9]
 - **[[:alnum:]]**

Anchors

- Anchors are used to match at the beginning or end of a line (or both).
- ^ means beginning of the line
- \$ means end of the line

regular expression

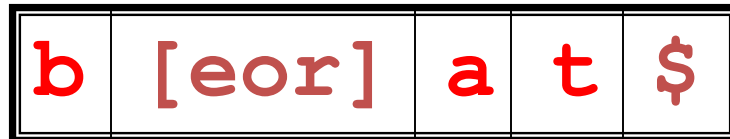


beat

a brat on a boat

match

regular expression



beat a brat on a **boat**

match

^word\$

^\$

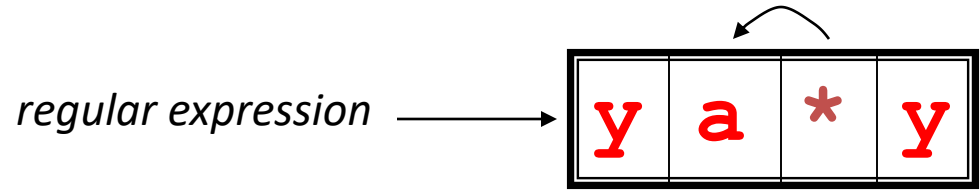
Let's practice!



```
grep "[Aa]1" regex2.txt
grep "^[Aa]1" regex2.txt
grep "[Aa][0-9]$" regex2.txt
grep "[0-9]" regex2.txt
grep "[[:alnum:]]" regex2.txt
grep "[[:alpha:]]" regex2.txt
```

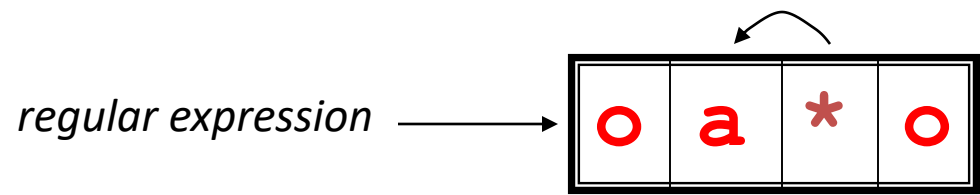
Repetition operators

- The * (asterisk) matches the zero or more occurrences of the **preceding** character



I got mail, yaaaaaaaaay!

↑
match



For me to fool with.

↑
match

. *

Special characters

- `\s` space
- `\t` tab
- `\s+` many spaces
- `\t\t` two adjacent tabs

Lines corresponding to chr2

```
[pscott17@login4 test]$ grep "chr2" hg19.gtf > chr2.txt  
[pscott17@login4 test]$ tail -n 1 chr2.txt  
chr21 hg19_knownGene CDS 33066517 33066602 0.000000  
gene_id "uc002ypd.2"; transcript_id "uc002ypd.2";
```

Lines corresponding to chr2

```
grep "chr2\s" hg19.gtf > chr2.gtf
```

Or more specific:

```
grep "^chr2\s" hg19.gtf > chr2.gtf
```


Repetition operators

*	Zero or more...
?	Zero or one... (i.e. optional element)
+	One or more...
{ x }	x instance of...
{ x,y }	between x and y instances of...
{ x, }	at least x instances of...
r1 r2	regular expressions r1 or r2

-E

grep -E <pattern> <filename>

Let's practice!



```
grep -E "a1|b1" regex2.txt
```

Alternative
←



Let's practice!



```
grep -E "a1|b1" regex2.txt  
grep "[ab]1" regex2.txt
```

Alternative
←



Repetition operators

- If you want to group part of an expression so that `*` or `{ }` applies to more than just the previous character, use `()` notation
- Subexpressions are treated like a single character
 - `a*` matches 0 or more occurrences of `a`
 - `abc*` matches `ab`, `abc`, `abcc`, `abccc`, ...
 - `(abc)*` matches `abc`, `abcabc`, `abcabcabc`, ...
 - `(abc){2,3}` matches `abcabc` or `abcabcabc`

Let's practice!



```
grep -E "a+" regex2.txt
grep -E "a{3}" regex2.txt
grep -E "a{2,3}" regex2.txt
grep -E "a{2}" regex2.txt
grep -E "(abc)*" regex2.txt
grep -E "(abc)+" regex2.txt
grep -E "(abc){2}" regex2.txt
grep -E "[[:alpha:]]{3}" regex2.txt
grep -E "[[:alpha:]][0-9]{2}" regex2.txt
grep -E "([[:alpha:]][0-9]){2}" regex2.txt
grep -E "[[:alpha:]][0-9]sa" regex2.txt
```

?

- `grep -E "[0-9]{3}[-]{0,1}[0-9]{3}[-]{0,1}[0-9]{4}" f.txt`

sed : a “stream editor”



- A non-interactive text editor
- Routine editing tasks
 - find, replace, delete, append, insert
- Input text flows through the program, is modified, and is directed to standard output.

```
sed [options] commands [file-to-edit]
```

Why use sed?



- Sed is designed to be especially useful in three cases:
 - files are too large for interactive editing
 - editing is too complicated for regular text editors
 - multiple editing in one pass

sed : Substitute command **s**

```
sed 's/old_word/new_word/' [file-to-edit]
```

To bee, or not to bee

```
sed 's/bee/be/' tobe.txt
```

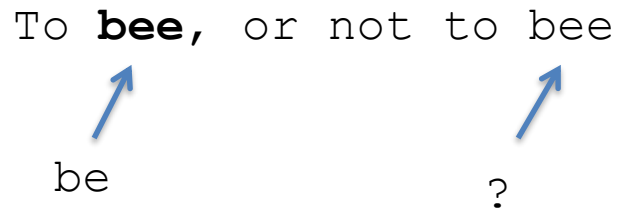


To be, or not to **bee**

sed : **g** - Global replacement

- Normally, substitutions apply to only the first match in the string.

To **bee**, or not to bee



The diagram illustrates the concept of global replacement. It shows the string "To **bee**, or not to bee". Below the word "bee" is the text "be", and below the comma is a question mark "?". Two blue arrows point upwards from "be" and "?" to the "bee" in the original string, indicating that both "be" and "?" are potential matches for the substitution pattern.

- To apply the substitution to **all** matches in the string use "**g**" options

```
sed 's/bee/be/g' tobe.txt
```

Edit matched text

- Put parentheses around the matched text:

```
sed -E 's/<pattern>/ (&) /' annoying.txt
```

Let's practice!



```
To bee, or not to bee
less tobe.txt
sed 's/bee/be/' tobe.txt
To be, or not to bee
sed 's/bee/be/g' tobe.txt
To be, or not to be
```

```
sed 's/seven/nine/g' file_sed.txt | sed 's/nine/two/g'
sed 's/a/o/g' file_sed.txt
sed 's/^and/or/' file_sed.txt
sed 's/s.../xxxxx/g' file_sed.txt
sed 's/ago$/ago!/' file_sed.txt
```

```
sed 's/[12]/3/g' regex2.txt
sed 's/[[alpha:]]/B/g' regex2.txt
sed -E 's/[[alnum:]]{2}/(&)/g' regex2.txt
```



Don't read and write the same file!

- `sed 's/seven/nine/g' sed_file.txt >sed_file.txt`



Redirections are done by the shell, before the command runs. This means that the shell is told to write the file before **sed** gets a chance to read it. There is no way around this if you are using shell redirection.

Delete lines with sed

- Remove the 3rd line:
 - `sed '3d' fileName.txt`
- Remove the line containing the string "awk":
 - `sed '/awk/d' filename.txt`
- Remove the last line:
 - `sed '$d' filename.txt`

Let's practice!



```
sed '3d' regex2.txt  
sed '/a/d' regex2.txt  
sed '/[0-9]/d' regex2.txt  
sed '$d' regex2.txt
```

Summary

file permissions

cat

wc

>, >>, <

pipeline

ln -s

grep

regex

Set up the alias for Mac OS/linux

- Go to home directory ON YOUR COMPUTER: `cd ~`
- Open file `.bash_profile`: `nano .bash_profile`
- Add in the end of the file:


```
alias hoffman='pscott17@hoffman2.idre.ucla.edu'
```
- Restart the session



Run from the local session of the terminal. To open a local session : **Control-T**

Set up the alias for Cygwin



- Go to home directory :
 - This PC / Windows (C:) / Cygwin64 / etc
- Open file **ssh_config** in text editor
- Add in the end of the file:
- Host hoffman

```
HostName hoffman2.idre.ucla.edu
Port 22
User username
```
- Restart the session



Run from the local session of the terminal. To open a local session : **Control-T**