Linux II and III

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Creating directories and files

- mkdir

```
milou-b: ~ $ cd course
-bash: cd: course: No such file or directory
milou-b: ~ $ mkdir course
milou-b: ~ $ cd course
```

Creating directories and files

- touch
  - if file does not exist, creates it with 0 size
  - if file exists, update its modification time

```
milou-b: ~/course $ touch a
milou-b: ~/course $ ls -l
total 0
-rw-rw-r-- 1 douglas douglas 0 Aug 24 11:00 a
milou-b: ~/course $ date
Sun Aug 24 11:01:01 CEST 2014
milou-b: ~/course $ touch a
milou-b: ~/course $ ls -l
total 0
-rw-rw-r-- 1 douglas_douglas 0 Aug 24 11:01 a
```

```
milou-b: ~/course $ touch b c d
milou-b: ~/course $ ls -l
total 0
-rw-rw-r-- 1 douglas douglas 0 Aug 24 11:01 a
-rw-rw-r-- 1 douglas douglas 0 Aug 24 11:03 b
-rw-rw-r-- 1 douglas douglas 0 Aug 24 11:03 c
-rw-rw-r-- 1 douglas douglas 0 Aug 24 11:03 d
```

Creating directories and files

- cat
  - con"cat"enate : dumps the contents of a file
  - can also be used to quickly create a short file

type this, then Return, then

Ctrl-D = EOF = "End Of File"

```
milou-b: ~/course $ cat > e
this is a short file
milou-b: ~/course $ cat e
this is a short file
milou-b: ~/course $ cat a
milou-b: ~/course $ ls -l
total 32
-rw-rw-r-- 1 douglas douglas  0 Aug 24 11:01 a
-rw-rw-r-- 1 douglas douglas  0 Aug 24 11:03 b
-rw-rw-r-- 1 douglas douglas  0 Aug 24 11:03 c
-rw-rw-r-- 1 douglas douglas  0 Aug 24 11:03 d
-rw-rw-r-- 1 douglas_douglas 21 Aug 24 13:14 e
```

Redirecting input: <

- *command* < file
  - give *command* input from 'file'
  - for *command*, input comes from 'standard input', 'stdin'

```
milou-b: ~/course $ cat < e
this is a short file
milou-b: ~/course $
```

  - for flexible commands, it is not quite the same as giving a file on the command line

```
milou-b: ~/course $ cat e
this is a short file
milou-b: ~/course $ cat e e
this is a short file
this is a short file
milou-b: ~/course $ cat e e e
this is a short file
this is a short file
this is a short file
milou-b: ~/course $
```

Redirecting input: <

- *command* < file
  - Files and stdin generally cannot be mixed using '<'

```
milou-b: ~/course $ cat e e < e
this is a short file
this is a short file
```

  - command line files can be more flexible

```
milou-b: ~/course $ cat > f
this file is a little longer
milou-b: ~/course $ cat f
this file is a little longer
milou-b: ~/course $ cat e f
this is a short file
this file is a little longer
```

  - Some commands understand the filename '-' to mean 'read from stdin'

```
milou-b: ~/course $ cat f - < e
this file is a little longer
this is a short file
milou-b: ~/course $
```

Here, cat first reads f, then reads stdin, which has e

Redirecting output: > and >>

- *command* > file
  - 'standard output, 'stdout', for *command* goes to 'file'

```
milou-b: ~/course $ cat e > ee
milou-b: ~/course $ cat ee
this is a short file
milou-b: ~/course $ ls -l e ee
-rw-rw-r-- 1 douglas douglas 21 Aug 24 13:14 e
-rw-rw-r-- 1 douglas douglas 21 Aug 24 17:00 ee
milou-b: ~/course $
```

- command >> file
  - ***appends*** stdout from *command* to 'file'

```
milou-b: ~/course $ cat f >> ee
milou-b: ~/course $ cat ee
this is a short file
this file is a little longer
milou-b: ~/course $ ls -l e f ee
-rw-rw-r-- 1 douglas douglas 21 Aug 24 13:14 e
-rw-rw-r-- 1 douglas douglas 50 Aug 24 17:04 ee
-rw-rw-r-- 1 douglas douglas 29 Aug 24 13:47 f
milou-b: ~/course $
```

Connecting stdout to stdin with the pipe: |

Swedish Mac: Alt-7

- *command1* | *command2*
  - stdout of *command1* is connected to stdin of *command2*

```
milou-b: ~/course $ cat f ee | cat > ff
milou-b: ~/course $ cat ff
this file is a little longer
this is a short file
this file is a little longer
milou-b: ~/course $ cat f | wc -l
1
milou-b: ~/course $ cat ee | wc -l
2
milou-b: ~/course $ cat ff | wc -l
3
```

- 'wc -l' counts the number of lines in stdin, or a file or set of files, and prints the result to stdout
- 'wc' counts the number of lines, words and characters

```
milou-b: ~/course $ cat ff | wc
       3      17      79
```

The "other" output: standard error, 'stderr'

- Commands which use pipes or redirect stdout may still produce output to the terminal:

```
milou-b: ~/course $ bwa mem -a -E3 -t 8 ref.fa reads.fq | samtools view -Sb - > aln.bam
[M::main_mem] read 32 sequences (4916 bp)...
[M::mem_process_seqs] Processed 32 reads in 0.014 CPU sec, 0.005 real sec
[main] Version: 0.7.10-r789
[main] CMD: bwa mem -a -E3 -t 8 ref.fa[samopen] SAM header is present: 1 sequences.
 reads.fq
[main] Real time: 0.056 sec; CPU: 0.019 sec
```

- This is a second output stream: standard error, 'stderr'
- Not all tools use it
- To capture standard error, use **2>** (for stdout, **1>** equals **>**)

```
milou-b: ~/course $ bwa mem -a -E3 -t 8 ref.fa reads.fq 2> bwa.stderr | samtools view
-Sb - > aln.bam
[samopen] SAM header is present: 1 sequences.
milou-b: ~/course $ bwa mem -a -E3 -t 8 ref.fa reads.fq 2> bwa.stderr | samtools view
-Sb - > aln.bam 2> samtools.stderr
milou-b: ~/course $
```

Putting stderr together with stdout

- To capture *all* output of a command, not just stdout or stderr
- Reassign stderr to be directed to stdout (or vice versa) and then capture the combined output stream

command > file **2>&1** To append: >> file 2>&1

  - when directing to a file, order is important: 2>&1 *after* >file

- When piping between tools, this is usually not a good idea because downstream tools usually expect one output stream or the other, but not both

```
milou-b: ~/course $ bwa mem -a -E3 -t 8 ref.fa reads.fq 2>&1 | samtools view -Sb - > aln.bam
[samopen] no @SQ lines in the header.
[sam_read1] missing header? Abort!
milou-b: ~/course $
```

This sends both stdout and stderr through the pipe.

With Bash 4+, you can use '&>' and '&>>' to redirect/append both to a file, and '|&' as a pipe that redirects both, but these are not portable so don't use them.

Shell wildcards: ? *

- Using wildcards, filenames can be specified using expressions
- 0, 1 or more than 1 filename may match the expression
- Bash wildcards are similar but not identical to grep, sed, etc.

```
milou2: ~/course $ ls
a  b  c  d  e  ee  f  ff
```

- '?' matches any 1 character

```
milou2: ~/course $ ls ?
*  a  b  c  d  e  f
milou2: ~/course $ ls f?
ff
```

- '*' matches 0 or more of any character

```
milou2: ~/course $ ls e*
e  ee
milou2: ~/course $ ls *
*  a  b  c  d  e  ee  f  ff
```

Quote to match literally:

```
milou2: ~/course $ touch "*"
milou2: ~/course $ ls "*"
*
```

Shell wildcards: character groups with [ ] - ^

- You can specify character groups using **[ ] - ^**

```
milou2: ~/course $ ls
*  a  b  c  d  e  ee  f  ff
```

Match specific character: **[a]** Two characters: **[af]** Range: **[a-f]**

```
milou2: ~/course $ ls [a]
a
milou2: ~/course $ ls [af]
a  f
milou2: ~/course $ ls [a-f]
a  b  c  d  e  f
milou2: ~/course $ ls [a-f]?
ee  ff
```

Anything but specific characters: **[^a]** **[^a-d]**

```
milou2: ~/course $ ls [^a]
*  b  c  d  e  f
milou2: ~/course $ ls [^a-d]
*  e  f
milou2: ~/course $ ls [^a-d]?
ee  ff
```

Shell wildcards: groups of terms using { , }

- You can specify term groups using **{ , }**

```
milou-b: ~/course $ ls
a  b  c  d  e  ee  f  ff
```

There must be at least two terms: **{e,f}**

```
milou-b: ~/course $ ls {e,f}
e  f
```

Terms can contain wildcards: **{c,??}**

```
milou-b: ~/course $ ls {c,??}
c  ee  ff
```

Using terms can save a lot of typing:

```
milou-b: ~ $ cp /some/really/long/directory/run-1.{log,out,err,pdf,sh} .
```

Man(ual) pages

- Uncertain about a command, or want to know what more it can do?
- Type 'man *command*'

- man wc

```
WC(1)                          User Commands                          WC(1)

NAME
       wc - print newline, word, and byte counts for each file

SYNOPSIS
       wc [OPTION]... [FILE]...
       wc [OPTION]... --files0-from=F

DESCRIPTION
       Print  newline,  word, and byte counts for each FILE, and a total line if more than
       one FILE is specified.  With no FILE, or when FILE is -, read standard input.

       -c, --bytes
              print the byte counts

       -m, --chars
              print the character counts

       -l, --lines
              print the newline counts

       --files0-from=F
              read input from the files specified by NUL-terminated names in file F; If  F
              is - then read names from standard input

       -L, --max-line-length
              print the length of the longest line

       -w, --words
              print the word counts

       --help display this help and exit

       --version
              output version information and exit

AUTHOR
       Written by Paul Rubin and David MacKenzie.
```

Man pipes output through 'less', press SPACE to continue, 'q' at any time to quit, and 'h' to get help on searching, etc.

Finding patterns: grep

- 'grep' is a very useful command that finds patterns
- Patterns can be literal ('My name is Uppmax') or can be regular expressions ('My [a-z]\+ is Uppmax')
- Wildcards are regular expressions too, but in grep you can do a lot more
  - many tutorials available online
  - same syntax is also used in 'sed' and 'awk' and (a slight variant) 'perl'
  - we will only use a tiny bit of what is available

How many sequences in a sequence file?

- Get example Fasta and FastQ files

```
rackham3: ~/course $ cp /proj/g2020002/labs/linux2_additional-files/*.{fa,fq} .
rackham3: ~/course $ ls
a  b  c  d  e  ee  f  ff  reads.fq  ref.fa
```

- Looking at their formats...

```
rackham3: ~/course $ head -n 4 ref.fa reads.fq
==> ref.fa <==
>seq1
TGGCTCCTTTTGGTGTCAGTTGACTTGACTGGGCGGGTCCAATATCAATTGGGGCCTTTC
TGCCTTTTGGGCGGTCAGGTCTACCGGTTGTGAGGGGTGGCTTTCAACAATCTCAAAAGT
ATTTTCTGAAGACAGTTCTACTGGCTGGCTTCGCCGGCTGTAGACTGAATAACTAAAGAC

==> reads.fq <==
@UQNPK:00025:00052
GAAGAACGCAGCGAA
+
BB?BB@CCCCCCBCC
```

- Lines holding Fasta sequence names begin with '>'
- ... FastQ ... begin with '@'

How many sequences: name lines begin with > or @

- 'at beginning of line' is indicated with '^'
- 'at end of line' is indicated with '$'
- The regular expression should be single- or double-quoted so bash does not become confused (we will be using '>' !)

```
milou2: ~/course $ grep '^>' ref.fa
>seq1
>seq2
>seq3
>seq4
>seq5
>seq6
>seq7
milou2: ~/course $ grep '^>' ref.fa | wc -l
7
```

- How would you do this to count FastQ reads?
- Can you think of another way to count FastQ with 'wc -l'?

Extracting pieces of output or files

- What if we want just the sequence names?

```
milou2: ~/course $ grep '^>' ref.fa
>seq1
>seq2
>seq3
>seq4
>seq5
>seq6
>seq7
```

- 'cut' the sequence names out by (c)olumn!

```
milou2: ~/course $ grep '^>' ref.fa | cut -c2-
seq1
seq2
seq3
seq4
seq5
seq6
seq7
```

```
milou2: ~/course $ grep '^>' ref.fa | cut -c4-5
q1
q2
q3
q4
q5
q6
q7
```

Find the line of a specific sequence

- 'grep -n' includes line (n)umbers

```
milou2: ~/course $ grep -n '^>seq1$' ref.fa
1:>seq1
```

- for all matches

```
milou2: ~/course $ grep -n '^>' ref.fa
1:>seq1
11:>seq2
19:>seq3
26:>seq4
34:>seq5
43:>seq6
52:>seq7
```

- Only line numbers? 'cut' a (f)ield using a (d)elimiter

```
milou2: ~/course $ grep -n '^>' ref.fa | cut -f1 -d':'
1
11
19
26
34
43
52
```

What if we only want the line number for the last sequence?

```
milou2: ~/course $ grep -n '^>' ref.fa | cut -f1 -d':' | tail -n 1
52
```

Some differences with grep patterns

- '.' means any character, equivalent to '?' in the shell
- '*' means '0 or more of the *previous* character'
- '.*' is equivalent to '*' in the shell

Some grep patterns can be specified more simply by providing the −P option ('grep −P' for (P)erl style patterns)

- '+' means '1 or more of the *previous* character' ('\+' w/o −P)
- Terms are easier, too

```
rackham3: ~/course $ grep '^>\(seq1\|seq7\)$' ref.fa
>seq1
>seq7

rackham3: ~/course $ grep -P '^>(seq1|seq7)$' ref.fa
>seq1
>seq7
```

Other grep options

- grep -i : (i)gnore case in expression

```
milou2: ~/course $ grep -i 'SEQ1' ref.fa
>seq1
```

- grep -v : in(v)ert match, lines that do not match expression

```
milou2: ~/course $ grep -i 'SEQ[1-5]' ref.fa | grep -v '[457]'
>seq1
>seq2
>seq3
```

- grep -F : (F)ixed expression, ignore wildcards

```
milou2: ~/course $ ls
*  a  b  c  d  e  ee  f  ff  reads.fq  ref.fa
milou2: ~/course $ ls -l | grep -F '*'
-rw-rw-r-- 1 douglas douglas    0 Aug 25 15:11 *
milou2: ~/course $ ls -l "*"
-rw-rw-r-- 1 douglas douglas 0 Aug 25 15:11 *
```

- grep --color : use color in output

```
milou2: ~/course $ grep -i --color 'SEQ[^2-6]' ref.fa
>seq1
>seq7
```

Just a few more grep options

- grep -c : only print a (c)ount of the matching lines

```
milou2: ~/course $ grep -c '^>' ref.fa
7
milou2: ~/course $ grep -cv '^>' ref.fa
52
```

- grep -m *N* : stop output after *N* (m)atches

```
milou2: ~/course $ grep -m 1 'q[367]' ref.fa
>seq3
```

- grep -H : include the filename (default with >1 file)

```
milou2: ~/course $ grep -Hn --color 'q[14]' ref.fa
ref.fa:1:>seq1
ref.fa:26:>seq4
milou2: ~/course $ cat ref.fa | grep -Hn --color 'q[14]'
(standard input):1:>seq1
(standard input):26:>seq4
```

sorry, no mnemonic

- grep -l, -L : only print fi(l)enames containing/(L)acking match

```
milou2: ~/course $ grep -l 'seq1$' ref.fa reads.fq
ref.fa
milou2: ~/course $ grep -L 'seq1$' ref.fa reads.fq
reads.fq
```

The last grep options, seriously

- grep -B *N* : include *N* lines (B)efore the match in output
- grep -A *N* : include *N* lines (A)fter the match in output

```
milou2: ~/course $ grep -B 1 '^>seq2$' ref.fa
TGTGCAGGACGCC
>seq2
milou2: ~/course $ grep -A 3 '^@UQNPK:00685:00805$' reads.fq
@UQNPK:00685:00805
GAAGGATCATTGAATCTATCGTGCA
+
1=<>;??9895442444:4444999
```

- Just the sequence of that read? The quality string? The name of the next read?

```
milou2: ~/course $ grep -A 1 '^@UQNPK:00685:00805$' reads.fq | tail -n 1
GAAGGATCATTGAATCTATCGTGCA
milou2: ~/course $ grep -A 3 '^@UQNPK:00685:00805$' reads.fq | tail -n 1
1=<>;??9895442444:4444999
milou2: ~/course $ grep -A 4 '^@UQNPK:00685:00805$' reads.fq | tail -n 1
@UQNPK:01060:00786
```

```
milou2: ~/course $ grep '^>' ref.fa | grep -A 1 '^>seq3$' | tail -n 1
>seq4
```

Bash $(…)

- $(< **file**) replaces the whole $(…) with the contents of **file**
- $(*command*) replaces $(…) with the output of *command*

```
milou-b: ~/course $ cat > filelist
c
e
ff
milou-b: ~/course $ grep -n 'longer' $(< filelist)
ff:1:this file is a little longer
ff:3:this file is a little longer
milou-b: ~/course $ grep -n 'longer' $(cat filelist)
ff:1:this file is a little longer
ff:3:this file is a little longer
milou-b: ~/course $ grep -n 'longer' $(grep '[ef]' filelist)
ff:1:this file is a little longer
ff:3:this file is a little longer
```

```
milou-b: ~/course $ for F in $(cat filelist) ; do
> grep -Hn 'longer' "$F"
> done
ff:1:this file is a little longer
ff:3:this file is a little longer
```

Bash <(…) : anonymous named pipe

Also called *process substitution*

- <(*somecommand*) creates a temporary file containing the output of *somecommand*

- Useful for creating temporary files that don't use extra space
  - for example, do some preliminary processing before use, such as sort:

```
diff <(sort file1.txt) <(sort file2.txt)
```

  - removing blank and whitespace-only lines before processing:

```
somecommand <(grep -v '^\s*$' file.txt)
```

  - decompressing files for commands that don't handle compressed files

```
bwa mem ref.fa <(xzcat r1.fq.xz) <(xzcat r2.fq.xz) | ...
```

Augmenting your environment: .bashrc

- Wherever you are, save your position with 'pushd .' and cd to your home directory. See the directory stack with 'dirs'

```
milou2: ~/course $ pushd .
~/course ~/course
milou2: ~/course $ cd
milou2: ~ $ dirs
~ ~/course
milou2: ~ $ dirs -v
 0  ~
 1  ~/course
```

- Edit the '.bashrc' configuration file with nano, add the line

```
alias rm='rm -i'
```

A similar line may already be there, check first!

- Move back to previous location with 'popd'

```
milou2: ~ $ popd
~/course
milou2: ~/course $ dirs
~/course
```

Load an UPPMAX module with some tools

- the tinyutils module provides several useful tools
- search for module versions with **module spider**

```
rackham3: ~/course $ module spider tinyutils
```

- load the module with **module load**

```
rackham3: ~/course $ module load tinyutils/1.4
rackham3: ~/course $ which hist
/sw/apps/tinyutils/1.4/rackham/hist
rackham3: ~/course $ which table
/sw/apps/tinyutils/1.4/rackham/table
```

OR: Fetch the github repository with the tools

- URL: https://github.com/douglasgscofield/tinyutils

```
milou2: ~/course $ git clone https://github.com/douglasgscofield/tinyutils.git
Initialized empty Git repository in /pica/h1/douglas/course/tinyutils/.git/
remote: Counting objects: 231, done.
remote: Total 231 (delta 0), reused 0 (delta 0), pack-reused 231
Receiving objects: 100% (231/231), 44.84 KiB, done.
Resolving deltas: 100% (167/167), done.
milou2: ~/course $ ls -l tinyutils/
total 768
-rw-rw-r-- 1 douglas douglas 18027 Oct 19 12:06 LICENSE
-rw-rw-r-- 1 douglas douglas  2682 Oct 19 12:06 Makefile
-rw-rw-r-- 1 douglas douglas  5671 Oct 19 12:06 README.md
-rwxrwxr-x 1 douglas douglas  1458 Oct 19 12:06 boolify
-rwxrwxr-x 1 douglas douglas  1036 Oct 19 12:06 cumsum
-rwxrwxr-x 1 douglas douglas  1079 Oct 19 12:06 diffs
-rwxrwxr-x 1 douglas douglas  1065 Oct 19 12:06 div
-rwxrwxr-x 1 douglas douglas  2483 Oct 19 12:06 hist
-rwxrwxr-x 1 douglas douglas  1915 Oct 19 12:06 inrange
-rwxrwxr-x 1 douglas douglas   713 Oct 19 12:06 len
-rwxrwxr-x 1 douglas douglas   999 Oct 19 12:06 log
-rwxrwxr-x 1 douglas douglas  1005 Oct 19 12:06 log10
-rwxrwxr-x 1 douglas douglas   983 Oct 19 12:06 max
-rwxrwxr-x 1 douglas douglas   958 Oct 19 12:06 mean
-rwxrwxr-x 1 douglas douglas  1967 Oct 19 12:06 median
-rwxrwxr-x 1 douglas douglas   983 Oct 19 12:06 min
-rwxrwxr-x 1 douglas douglas   999 Oct 19 12:06 mult
-rwxrwxr-x 1 douglas douglas   741 Oct 19 12:06 ncol
-rwxrwxr-x 1 douglas douglas   997 Oct 19 12:06 range
-rwxrwxr-x 1 douglas douglas  1028 Oct 19 12:06 round
-rwxrwxr-x 1 douglas douglas  1275 Oct 19 12:06 stripfilt
-rwxrwxr-x 1 douglas douglas   951 Oct 19 12:06 sum
-rwxrwxr-x 1 douglas douglas  2118 Oct 19 12:06 table
drwxrwxr-x 2 douglas douglas  2048 Oct 19 12:06 tests
```

How long are my fasta sequences?

- Use the ‘fastalength’ tool from the exonerate module
  - `module load bioinfo-tools`
  - `module load exonerate`

```
milou-b: ~/course $ module load bioinfo-tools exonerate
milou-b: ~/course $ fastalength ref.fa
493 seq1
368 seq2
356 seq3
364 seq4
461 seq5
468 seq6
383 seq7
```

What is the total length? Mean? Median?

- That's what tinyutils are for

```
milou-b: ~/course $ fastalength ref.fa | cut -f1 -d' '
493
368
356
364
461
468
383
milou-b: ~/course $ fastalength ref.fa | cut -f1 -d' ' | sum
2893
milou-b: ~/course $ fastalength ref.fa | cut -f1 -d' ' | mean
413.286
milou-b: ~/course $ fastalength ref.fa | cut -f1 -d' ' | median
368
milou-b: ~/course $ fastalength ref.fa | cut -f1 -d' ' | max
493
milou-b: ~/course $ fastalength ref.fa | cut -f1 -d' ' | min
356
```

What is the length distribution of my reads?

- With a bit of awk (or the `len` tinyutil) to get lengths of lines

```
milou-b: ~/course $ grep '^[ACGTN]\+$' reads.fq | head -n 3
GAAGAACGCAGCGAA
GAAGAACGCAGCGAA
GAAGGATCATTGAATCTATCGTGCATCGATGAAGAACGCAGCGAA
milou-b: ~/course $ grep '^[ACGTN]\+$' reads.fq | awk '{ print length($0) }' | head -n 3
15
15
45
milou-b: ~/course $ grep '^[ACGTN]\+$' reads.fq | len | head -n 3
15
15
45
milou-b: ~/course $ grep '^[ACGTN]\+$' reads.fq | len | table
45      7
46      1
19      1
37      1
47      2
22      1
15      25
25      1
milou-b: ~/course $ grep '^[ACGTN]\+$' reads.fq | len | table | sort
15      25
19      1
22      1
25      1
37      1
45      7
46      1
47      2
```

Using 'find' to search a directory tree

- **find** *location list-of-file-attributes optional-actions*

```
rackham3: ~/course $ mkdir directory
rackham3: ~/course $ mv ? ?? directory/
rackham3: ~/course $ find . -name d
./directory/d
rackham3: ~/course $ find . -name '??'
./directory/ee
./directory/ff
rackham3: ~/course $ find . -iname B -ls
470961739    0 -rw-rw-r--   1 douglas  douglas         0 Jan 13 14:29 ./directory/b
rackham3: ~/course $ find . -type d
.
./directory
rackham3: ~/course $ find . -type f -name '*.fa' -exec grep '^>seq3$' {} \;
>seq3
rackham3: ~/course $ find . -type f -name '*.fa' -exec grep -Hn '^>seq3$' {} \;
./ref.fa:19:>seq3
```

Most wildcards work, use within quotes

The `-iname` option is case-insensitive and `-ls` runs '`ls -l`' on each file

Look for specific type of file

Run commands on found files

- Other options for size, ownership, modification times, etc.
- See the (long) man page and online tutorials for more

Create symbolic links to clear things up

- Use 'ln -s' … do not forget the '-s' !
- Symbolic links indicate the location of another file/directory

```
milou-b: ~/course $ ln -s f sf
milou-b: ~/course $ ls -li f sf
1105098318 -rw-rw-r-- 1 douglas douglas 22 Jan 27  2015 f
1915648234 lrwxrwxrwx 1 douglas douglas  1 Aug 22 11:37 sf -> f
```

‘Hard links’ (ln *without* -s) are rarely necessary

- Hard links are truly another name for the same file

```
milou-b: ~/course $ ln f hf
milou-b: ~/course $ ls -li f hf sf
1105098318 -rw-rw-r-- 2 douglas douglas 22 Jan 27  2015 f
1105098318 -rw-rw-r-- 2 douglas douglas 22 Jan 27  2015 hf
1915648234 lrwxrwxrwx 1 douglas douglas  1 Aug 22 11:37 sf -> f
milou-b: ~/course $ rm f
rm: remove regular file `f'? y
milou-b: ~/course $ ls -li f hf sf
ls: cannot access f: No such file or directory
1105098318 -rw-rw-r-- 1 douglas douglas 22 Jan 27  2015 hf
1915648234 lrwxrwxrwx 1 douglas douglas  1 Aug 22 11:37 sf -> f
milou-b: ~/course $ mv hf f
milou-b: ~/course $ ls -li f hf sf
ls: cannot access hf: No such file or directory
1105098318 -rw-rw-r-- 1 douglas douglas 22 Jan 27  2015 f
1915648234 lrwxrwxrwx 1 douglas douglas  1 Aug 22 11:37 sf -> f
```

Manipulating names in bash

- *name*=**value** assigns **value** to *name*
- $*name* and ${*name*} produce the value of *name*
- ${*name*} can be useful in some contexts
  - ${*name*}_suffix prefixes the value of *name* to ‘_suffix’
  - $name_suffix looks in *name_suffix* for a value
- ${*name*%**pattern**} removes **pattern** from end of *name*
  - F=file.fa; echo ${F%.fa} produces ‘file’
  - F=f.file.fa; echo ${F%%.*} produces ‘f’
- ${*name*#**pattern**} removes **pattern** from beginning of *name*
  - F=/home/douglas/file.fa; echo ${F#*/} produces ‘home/douglas/file.fa’
  - F=/home/douglas/file.fa; echo ${F##*/} produces ‘file.fa’
- How might one get just the directory part?

Manipulating names in bash

- Save a result to a filename with a modified suffix

```
milou-b: ~/course $ F=ref.fa; grep -c '^>' "$F" > ${F%.fa}.count
milou-b: ~/course $ cat ref.count
7
```

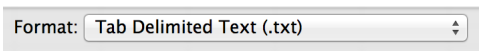
- basename and dirname can also be helpful to get filenames and directory names

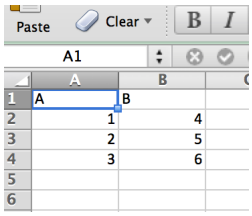
```
milou-b: ~/course $ F=/home/douglas/file.fa
milou-b: ~/course $ basename $F
file.fa
milou-b: ~/course $ dirname $F
/home/douglas
```

- 'man basename' and 'man dirname'

File conversions

- Mac, Windows and Linux text files use different line endings
  - Linux: Linefeed
  - Mac: Carriage-return
  - Windows: Carriage-return + Linefeed






```
rackham3: ~/course $ cp /proj/g2020002/labs/linux2_additional-files/Workbook1.txt .
rackham3: ~/course $ cat Workbook1.txt
3       6rackham3: ~/course $
rackham3: ~/course $ dos2unix Workbook1.txt
dos2unix: converting file Workbook1.txt to Unix format ...
rackham3: ~/course $ cat Workbook1.txt
3       6rackham3: ~/course $
rackham3: ~/course $ mac2unix Workbook1.txt
mac2unix: converting file Workbook1.txt to Unix format ...
rackham3: ~/course $ cat Workbook1.txt
A       B
1       4
2       5
3       6rackham3: ~/course $
```

Collecting multiple files into one: `tar`

- a cluster of options specifies the mode, compression, other options, and the output file into which files are collected.
  - -c creates a file; no compression, or z j J to specify compression format

```
rackham3: ~/course $ tar -cvf t.tar ?
B
C
D
a
b
c
d
e
f
t
rackham3: ~/course $ tar -czf t.tar.gz ?
rackham3: ~/course $ tar -cjf t.tar.bz2 ?
rackham3: ~/course $ tar -cJf t.tar.xz ?
rackham3: ~/course $ ls -l t.tar*
-rw-rw-r-- 1 douglas douglas 10240 Jan 20 12:29 t.tar
-rw-rw-r-- 1 douglas douglas   259 Jan 20 12:29 t.tar.bz2
-rw-rw-r-- 1 douglas douglas   243 Jan 20 12:29 t.tar.gz
-rw-rw-r-- 1 douglas douglas   272 Jan 20 12:29 t.tar.xz
```

`tar -cvf t.tar ?`
- `-c` create new
- `v` verbose option
- `f t.tar` create the file t.tar
- `?` list of files to be included in the created file

`tar -czf t.tar.gz ?`
- `z` created file is gzip-compressed

`tar -cjf t.tar.bz2 ?`
- `j` created file is bzip2-compressed

`tar -cJf t.tar.xz ?`
- `J` created file is xz-compressed

Verbose and compression options can both be included: `tar -cvzf t.tar.gz ?`

List the contents of a tarfile: `tar -t`

- compression format is autodetected

```
rackham3: ~/course $ tar -tf t.tar
B
C
D
a
b
c
d
e
f
t
rackham3: ~/course $ tar -tvf t.tar.bz2
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 B
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 C
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 D
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 a
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 b
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 c
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 d
-rw-rw-r-- douglas/douglas  21 2020-08-26 09:23 e
-rw-rw-r-- douglas/douglas  29 2020-08-26 09:23 f
-rw-rw-r-- douglas/douglas  21 2020-08-26 09:23 t
rackham3: ~/course $ tar -tvf t.tar.xz B a z
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 B
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 a
tar: z: Not found in archive
tar: Exiting with failure status due to previous errors
```

`tar -tf t.tar.bz2`
- `-t` list contents
- `v` detailed listing
- `f t.tar.bz2` use tarfile t.tar.bz2

If a name or names are given after the name of the tarfile, only those files are shown in the list

Extract the contents of a tarfile: `tar -x`

- compression format is autodetected

```
rackham3: ~/course $ mkdir extract
rackham3: ~/course $ cd extract
rackham3: ~/course/extract $ tar -xvf ../t.tar.gz
B
C
D
a
b
c
d
e
f
t
rackham3: ~/course/extract $ ls
B  C  D  a  b  c  d  e  f  t
rackham3: ~/course/extract $ tar -xvvf ../t.tar.gz
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 B
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 C
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 D
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 a
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 b
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 c
-rw-rw-r-- douglas/douglas   0 2020-08-26 09:23 d
-rw-rw-r-- douglas/douglas  21 2020-08-26 09:23 e
-rw-rw-r-- douglas/douglas  29 2020-08-26 09:23 f
-rw-rw-r-- douglas/douglas  21 2020-08-26 09:23 t
```

`tar -xvf t.tar.gz`

- `-x` extract contents
- `v` show list of files as extracted
- `f t.tar.gz` extract from t.tar.gz

If a name or names are given after the name of the tarfile, only those files are extracted from the tarfile

Using two v characters 'vv' shows a detailed list of files while extracting

Computing and verifying checksums

- A 'short' number calculated while reading the contents of a file
- The checksums for files that differ by a little differ by a lot
- If a downloaded file has a checksum, check it!

```
rackham3: ~/course $ cat e
this is a short file
rackham3: ~/course $ cat e1
this is a shirt file
rackham3: ~/course $ md5sum e > e.md5
rackham3: ~/course $ cat e.md5
a7499c996564a448b368fe716d8e9dec  e
rackham3: ~/course $ md5sum e1 > e1.md5
rackham3: ~/course $ cat e1.md5
e5fe8beffb5de4ea0b9ad7e0a002a9c1  e1
rackham3: ~/course $ md5sum -c e.md5 e1.md5
e: OK
e1: OK
```

`md5sum file`

calculates MD5 (32-byte) checksum for `file` (without file, reads stdin)

`md5sum -c file.md5`

verifies MD5 checksums for files and checksums contained in `file.md5`

Other programs calculate other checksums: SHA256, SHA512, etc.

```
rackham3: ~/course $ sha256sum e
fe70698e2af77a74a77321bed21cdf02f67d1edbcaf10fc25ea3a6a4743bf432  e
rackham3: ~/course $ sha512sum e
8bb1ea7ca3810f375835b78bba40980c94ddcc2e9234e78682ee6466339ae5087a7f667bcf45c26a1cf1daef6a264e45fe986680a004124f9fdb9cb53eb19cbc  e
```