The Shell

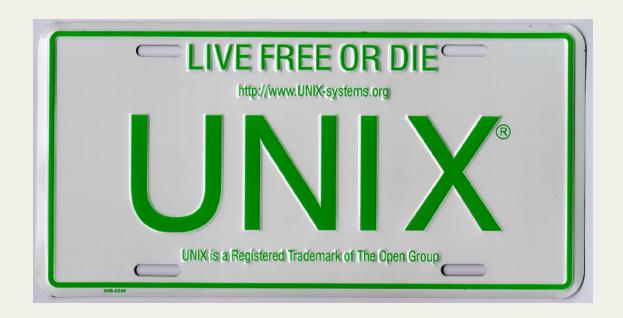


Mats Töpel

Department of Marine Sciences mats.topel@marine.gu.se

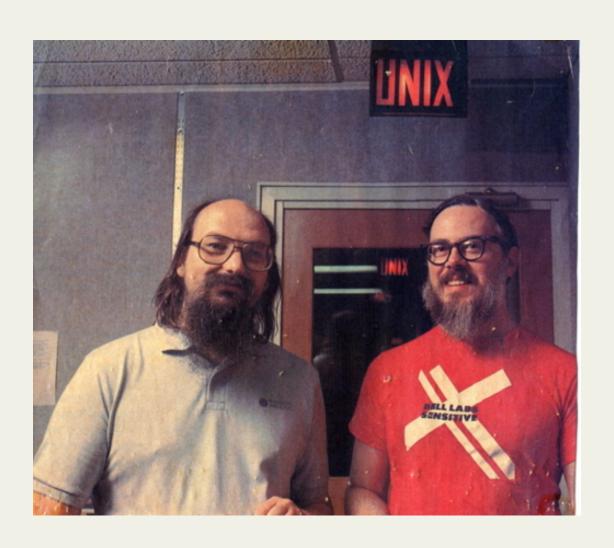
www.matstopel.se, @matstopel

UNIX?

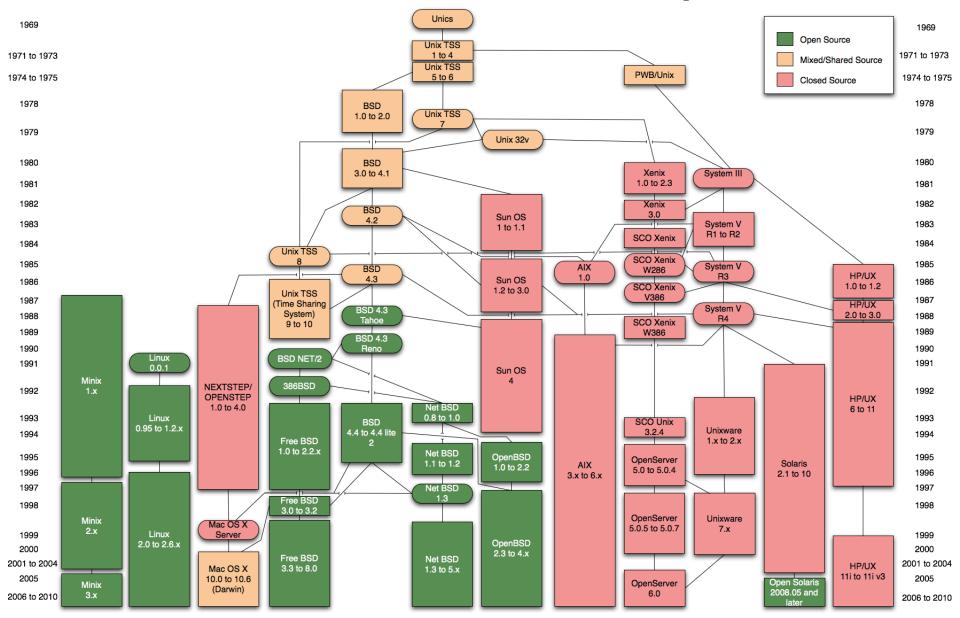


Terminal, shell, GNU/Linux, Mac OSX?

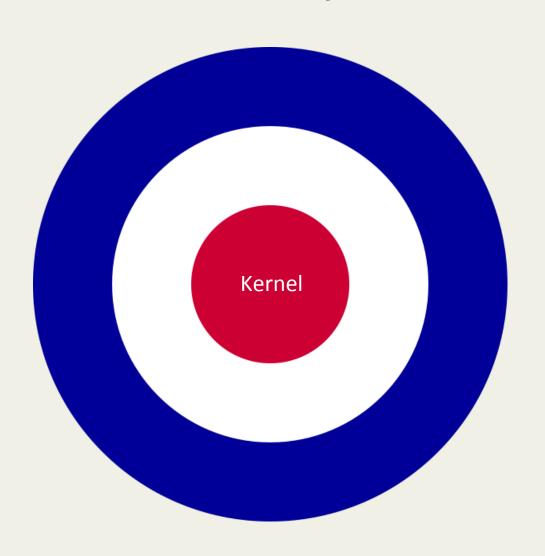
Ken Tompson & Dennis Rithcie

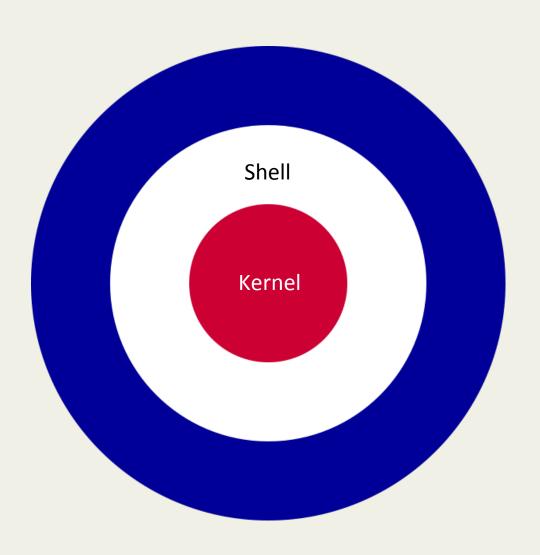


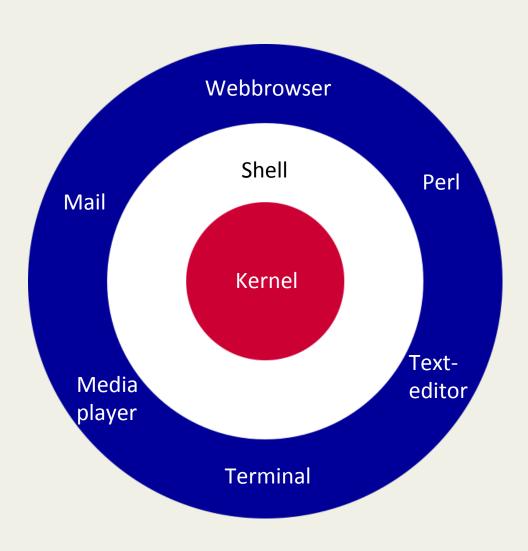
Evolution of UNIX-like systems



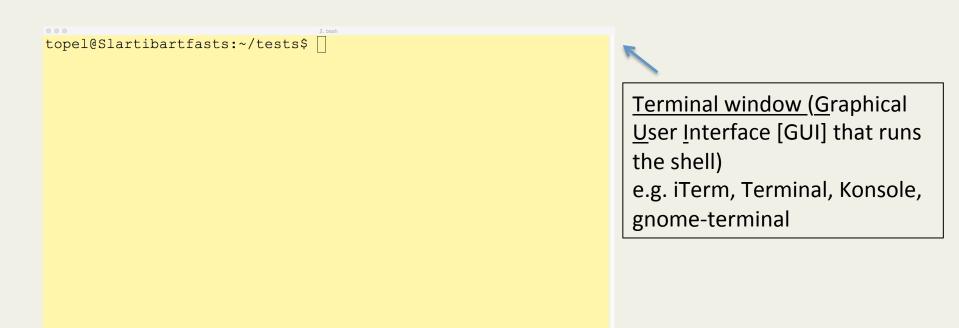




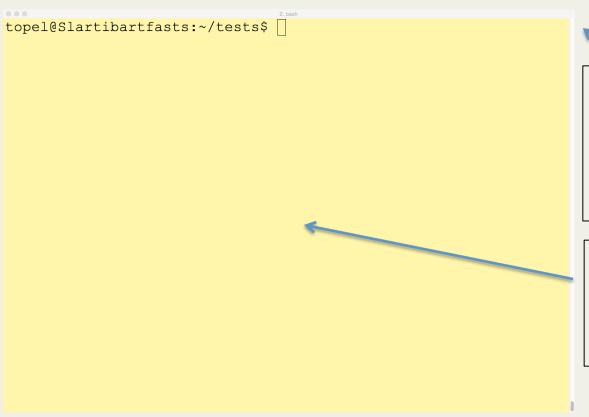




(virtual) Terminal vs. shell vs. bash



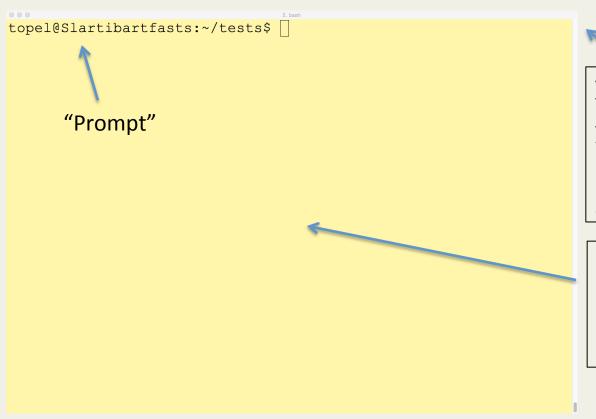
(virtual) Terminal vs. shell vs. bash



<u>Terminal window (Graphical</u>
<u>User Interface [GUI] that runs</u>
the shell)
e.g. iTerm, Terminal, Konsole,
gnome-terminal

<u>The shell</u> (a.k.a <u>Comand Line</u> <u>Interface [CLI]</u>. Program that starts other programs) e.g. bash, sh, tcsh

(virtual) Terminal vs. shell vs. bash



<u>Terminal window (Graphical</u>
<u>User Interface [GUI] that runs</u>
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e.g. iTerm. Terminal Konsole

e.g. iTerm, Terminal, Konsole, gnome-terminal

<u>The shell</u> (a.k.a <u>Comand Line</u> <u>Interface</u> [CLI]. Program that starts other programs) e.g. <u>bash</u>, sh, tcsh

UNIX. Why so successful?

- Do one thing and do it good
- Don't be "chatty"

Do one thing and do it good

ls [List files and directories]

rm [Remove files]

mkdir [Create directories]

wc [Count words, lines and characters]

- Do one thing and do it good
- Don't be "chatty"

```
Is [Only outputs the <u>names</u> of files and dir's]
```

rm [Will remove a file without any warning]

- Do one thing and do it good
- Don't be "chatty"

```
Is [Only outputs the <u>names</u> of files and dir's]
```

rm [Will remove a file without any warning]

This behavior can be modified using options a.k.a. "flags"

ls

```
topel@Slartibartfasts:~/tests$ ls
alignment.aln
               ebooks.txt
                               python
                                                sequences.fasta
                               rasberrypi
clear
               make
                                                speciesgeocoder
topel@Slartibartfasts:~/tests$
```

```
topel@Slartibartfasts:~/tests$ ls
alignment.aln
               ebooks.txt
                            python
                                             sequences.fasta
                                             speciesgeocoder
clear
               make
                              rasberrypi
topel@Slartibartfasts:~/tests$ ls -l
total 40
            1 topel staff 1254 Aug 31 10:54 alignment.aln
-rw-r--r--
                             68 Aug 31 11:16 clear
            2 topel staff
drwxr-xr-x
-rw-r--r 1 topel staff 9537 Aug 31 10:53 ebooks.txt
            8 topel staff 272 May 23 2014 make
drwxr-xr-x
drwxr-xr-x 4 topel staff 136 Jun 12 2014 python
            3 topel staff 102 Sep 13 2014 rasberrypi
drwxr-xr-x
-rw-r--r-- 1 topel staff
                           3179 Aug 31 10:51 sequences.fasta
drwxr-xr-x 24 topel staff 816 Jul 17 2014 speciesgeocoder
topel@Slartibartfasts:~/tests$
```

Is -I

```
topel@Slartibartfasts:~/tests$ ls
alignment.aln
               ebooks.txt
                            python
                                             sequences.fasta
clear
               make
                             rasberrypi
                                             speciesgeocoder
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           1 topel staff
                           3179 Aug 31 10:51 sequences.fasta
drwxr-xr-x 24 topel staff 816 Jul 17 2014 speciesgeocoder
topel@Slartibartfasts:~/tests$
```

File permissions (more on this later)

```
topel@Slartibartfasts:~/tests$ ls
alignment.aln
               ebooks.txt
                            python
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topel@Slartibartfasts:~/tests$ ls -l
total 40
            1 topel staff
                           1254 Aug 31 10:54 alignment.aln
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            2 topel staff
                             68 Aug 31 11:16 clear
drwxr-xr-x
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                           9537 Aug 31 10:53 ebooks.txt
drwxr-xr-x 8 topel staff
                           272 May 23 2014 make
drwxr-xr-x 4 topel staff 136 Jun 12 2014 python
drwxr-xr-x 3 topel staff 102 Sep 13 2014 rasberrypi
           1 topel staff
-rw-r--r--
                           3179 Aug 31 10:51 sequences.fasta
           24 topel staff
                           816 Jul 17 2014 speciesgeocoder
drwxr-xr-x
topel@Slartibartfasts:~/tests$
```

User and group that owns the file

```
topel@Slartibartfasts:~/tests$ ls
alignment.aln
               ebooks.txt
                               python
                                               sequences.fasta
                                               speciesgeocoder
clear
               make
                               rasberrypi
topel@Slartibartfasts:~/tests$ ls -l
total 40
            1 topel staff
                            1254 Aug 31 10:54 alignment.aln
-rw-r--r--
                              68 Aug 31 11:16 clear
            2 topel staff
drwxr-xr-x
            1 topel staff 9537 Aug 31 10:53 ebooks.txt
-rw-r--r--
            8 topel staff
                             272 May 23 2014 make
drwxr-xr-x
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                             102 Sep 13 2014 rasberrypi
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            3 topel staff
-rw-r--r--
            1 topel staff
                            3179 Aug 31 10:51 sequences.fasta
drwxr-xr-x 24 topel staff
                             816 Jul 17 2014 speciesgeocoder
topel@Slartibartfasts:~/tests$
                    File size in bytes
```

```
topel@Slartibartfasts:~/tests$ ls
alignment.aln
               ebooks.txt
                              python
                                              sequences.fasta
                                              speciesgeocoder
clear
               make
                              rasberrypi
topel@Slartibartfasts:~/tests$ ls -l
total 40
            1 topel staff 1254 Aug 31 10:54 alignment.aln
-rw-r--r--
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-rw-r--r--
            1 topel staff
                           3179 Aug 31 10:51 sequences.fasta
drwxr-xr-x 24 topel staff
                            816 Jul 17 2014 speciesgeocoder
topel@Slartibartfasts:~/tests$
                      Modification date
```

```
topel@Slartibartfasts:~/tests$ ls
alignment.aln
               ebooks.txt
                              python
                                              sequences.fasta
clear
               make
                                              speciesgeocoder
                              rasberrypi
topel@Slartibartfasts:~/tests$ ls -1
total 40
            1 topel staff 1254 Aug 31 10:54 alignment.aln
-rw-r--r--
            2 topel staff
                             68 Aug 31 11:16 clear
drwxr-xr-x
            1 topel staff 9537 Aug 31 10:53 ebooks.txt
-rw-r--r--
            8 topel staff 272 May 23 2014 make
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-rw-r--r--
            1 topel staff
                           3179 Aug 31 10:51 sequences.fasta
drwxr-xr-x 24 topel staff
                            816 Jul 17 2014 speciesgeocoder
topel@Slartibartfasts:~/tests$
```

Filenames

- Do one thing and do it good
- Don't be chatty
- Redirect ">", append ">>" and pipe "|"

- Do one thing and do it good
- Don't be chatty
- Redirect ">", append ">>" and pipe "|"
 - Output from a program can be saved in a new file...

ls > my_file.txt

- Do one thing and do it good
- Don't be chatty
- Redirect ">", append ">>" and pipe "|"
 - Output from a program can be saved in a new file...
 - >> ...or appended to an existing file...

ls -la >> my_file.txt

(include "all" files, also those that are hidden)

cat my_file.txt

(this command will show the content of "my_file.txt")

- Do one thing and do it good
- Don't be chatty
- Redirect ">", append ">>" and pipe "|"
 - Output from a program can be saved in a new file...
 - >> ...or appended to an existing file...
 - ...or sent to another program.

How many files?

ls -a | wc -l

How many sequences in a file?

The fasta file format

>otToc34

MSDEEYSEDEYVSSEGEGAEGRDVEPQAQQAAPVLGPKEWVGLSSMPAATQQALLETLGK KANAAGEKVVNERPWLTDMVGTMVEMACAKESYEYDHKKAGKKLDPNNKYKIWMLPLFLF QAFVLRPLMIGQIRRDIRKSDEDKKKKSARPAPKK

>cmToc34

MDSETPTKNEAEQRASPDRTGQVTQRPVSLFRKNGTFAYPLEDSDVYEEQVLALEDVPEP TAQAILRLALAAERQGVPRLRFLVVGAPGVGKSSLINTLLNENLCSVSAWERGTKNAQVC ARQVDSVVIEFIDTPGIAPCRRSGLEASRRQVQRLRKLLDARGADEHPYLRSFHAILYVM RLDDTRPDLVDYHNWKVLMEFF

The fasta file format

>otToc34

MSDEEYSEDEYVSSEGEGAEGRDVEPQAQQAAPVLGPKEWVGLSSMPAATQQALLETLGK KANAAGEKVVNERPWLTDMVGTMVEMACAKESYEYDHKKAGKKLDPNNKYKIWMLPLFLF QAFVLRPLMIGQIRRDIRKSDEDKKKKSARPAPKK

>cmToc34

MDSETPTKNEAEQRASPDRTGQVTQRPVSLFRKNGTFAYPLEDSDVYEEQVLALEDVPEP TAQAILRLALAAERQGVPRLRFLVVGAPGVGKSSLINTLLNENLCSVSAWERGTKNAQVC ARQVDSVVIEFIDTPGIAPCRRSGLEASRRQVQRLRKLLDARGADEHPYLRSFHAILYVM RLDDTRPDLVDYHNWKVLMEFF

UNIX design strategy

grep ">" my_seq-file.fst | wc -l

UNIX design strategy

grep ">" my_seq-file.fst | wc -l grep -c ">" my_seq-file.fst

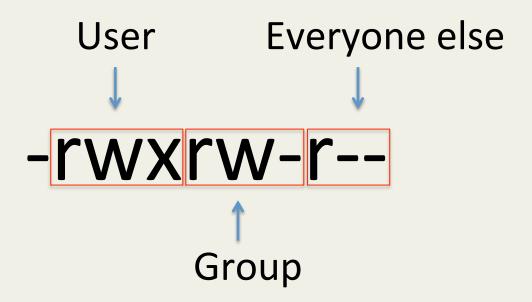
```
topel@Slartibartfasts:~/tests$ ls
alignment.aln
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-rw-r--r--
          1 topel staff
                           3179 Aug 31 10:51 sequences.fasta
drwxr-xr-x 24 topel staff 816 Jul 17 2014 speciesgeocoder
topel@Slartibartfasts:~/tests$
```

File permissions (more on this now)

-rwxrw-r--

-rwxrw-r--

r = read w = write x = execute



r = read w = write x = execute



Type (file, link, directory etc.)

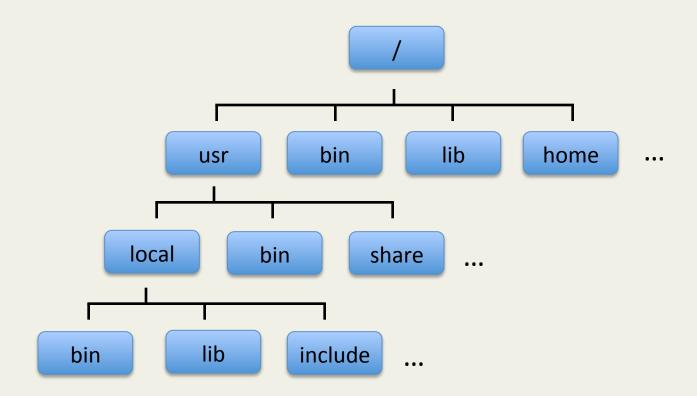
r = read w = write x = execute

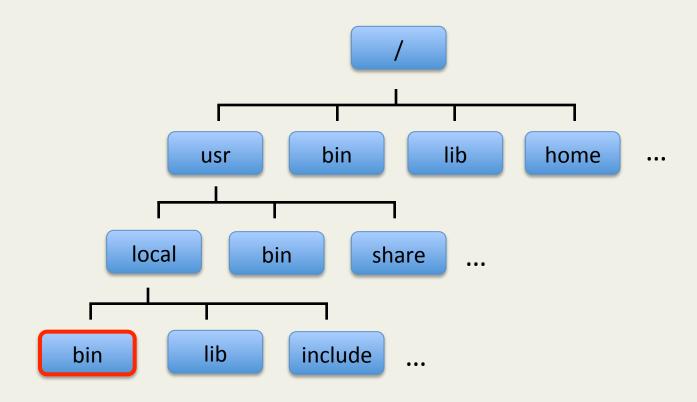
 File permissions can be changed using the command "chmod"

The command...

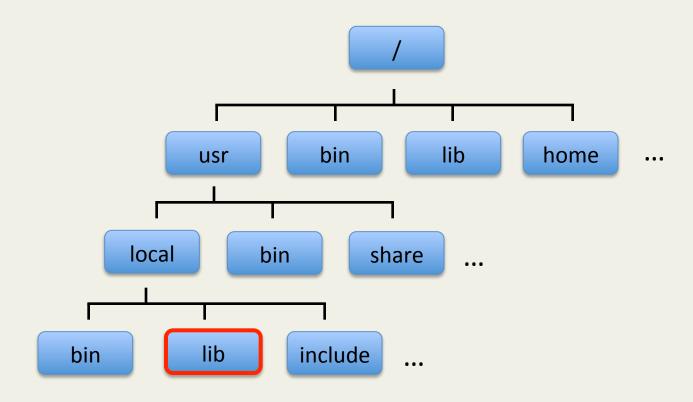
chmod +x my_file.txt

...will make "my_file.txt" executable



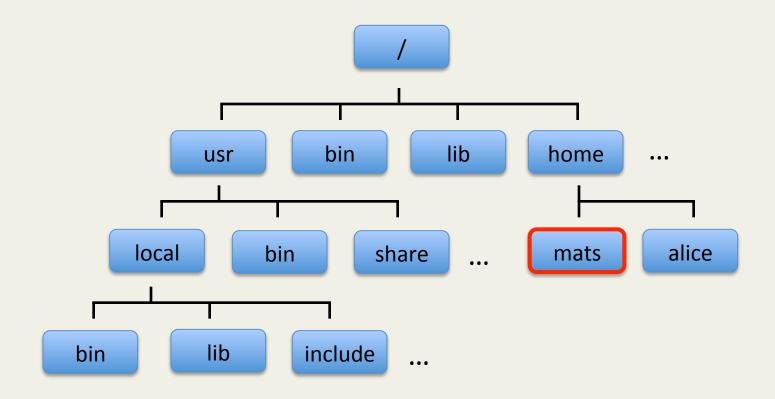


/usr/local/bin

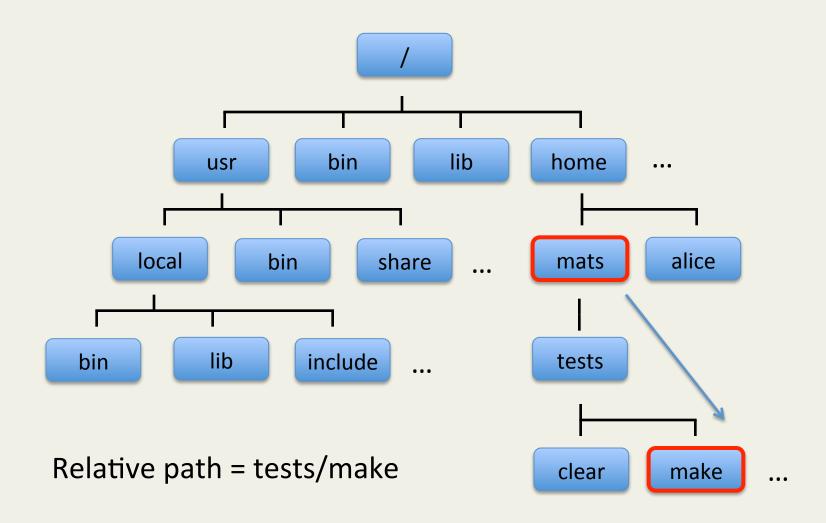


/usr/local/lib

cd /usr/local/bin



/home/mats = ~



cd tests/make

Putting it all together!

Writing a program

- A program is a set of instructions collected in a file
- This file is executable
- The file usually contains information about which programing language the instructions are written in (the shebang)

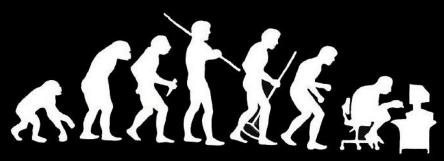
how_many_files.sh

- 1. #!/bin/bash
- 2. Is -a | wc -l

covgc_plot.sh

(by Alvar Almstedt)

```
#!/bin/bash
SMRT_JOB_NUM=$1
OUT PREFIX=$2
echo "Creating symlink and copying assembly..."
In -s /data01/smrtanalysis/userdata/jobs/016/$SMRT JOB NUM/data/aligned reads.bam
cp /data01/smrtanalysis/userdata/jobs/016/$SMRT_JOB_NUM/data/polished_assembly.fasta.gz ./
echo "Symlink created and assembly copied..."
gunzip polished assembly.fasta.gz
echo "Assembly gunzipped..."
echo "Commencing generation of coverage file..."
genomeCoverageBed -ibam aligned reads.bam -d > $OUT PREFIX.coverage
echo "Coverage file generated..."
echo "Cutting..."
cut -f 1,3 $OUT PREFIX.coverage > cut $OUT PREFIX.coverage
echo "Cut made..."
echo "Launching contig average coverage.py..."
contig average coverage.py cut $OUT PREFIX.coverage > cut $OUT PREFIX.avg.coverage
echo "Average calculated..."
echo "Deleting..."
rm $OUT PREFIX.coverage
rm cut $OUT PREFIX.coverage
echo "Intermediary files removed..."
echo "Formatting fasta file headers..."
sed 's/|quiver//g' polished assembly.fasta > temp && mv temp polished assembly.fasta
echo "Headers formatted..."
echo "Launching fasta analyzer.py"
fasta_analyzer.py -cg polished_assembly.fasta cut_$OUT_PREFIX.avg.coverage
```



Something, somewhere went terribly wrong

Thank you for your attention!

Albiorix

Address: albiorix.bioenv.gu.se

Exercises:

https://github.com/The-Bioinformatics-Group/Learning_Unix/wiki/Learn-Unix-with-applications-to-NGS-data

Bash on Windows computers

I suggest you use the mobaxterm program. Go to ...

http://mobaxterm.mobatek.net/download-home-edition.html

...and download the portable edition.

Suggested additional tutorials

To start with:

 Do tutorial One, Two, Three, Four, Five [up to 5.2] (and optionally Six) at

http://www.ee.surrey.ac.uk/Teaching/Unix/

Codecademy

 https://www.codecademy.com/en/courses/learn-thecommand-line

For experienced users:

https://wikis.utexas.edu/display/bioiteam/Shell+Script