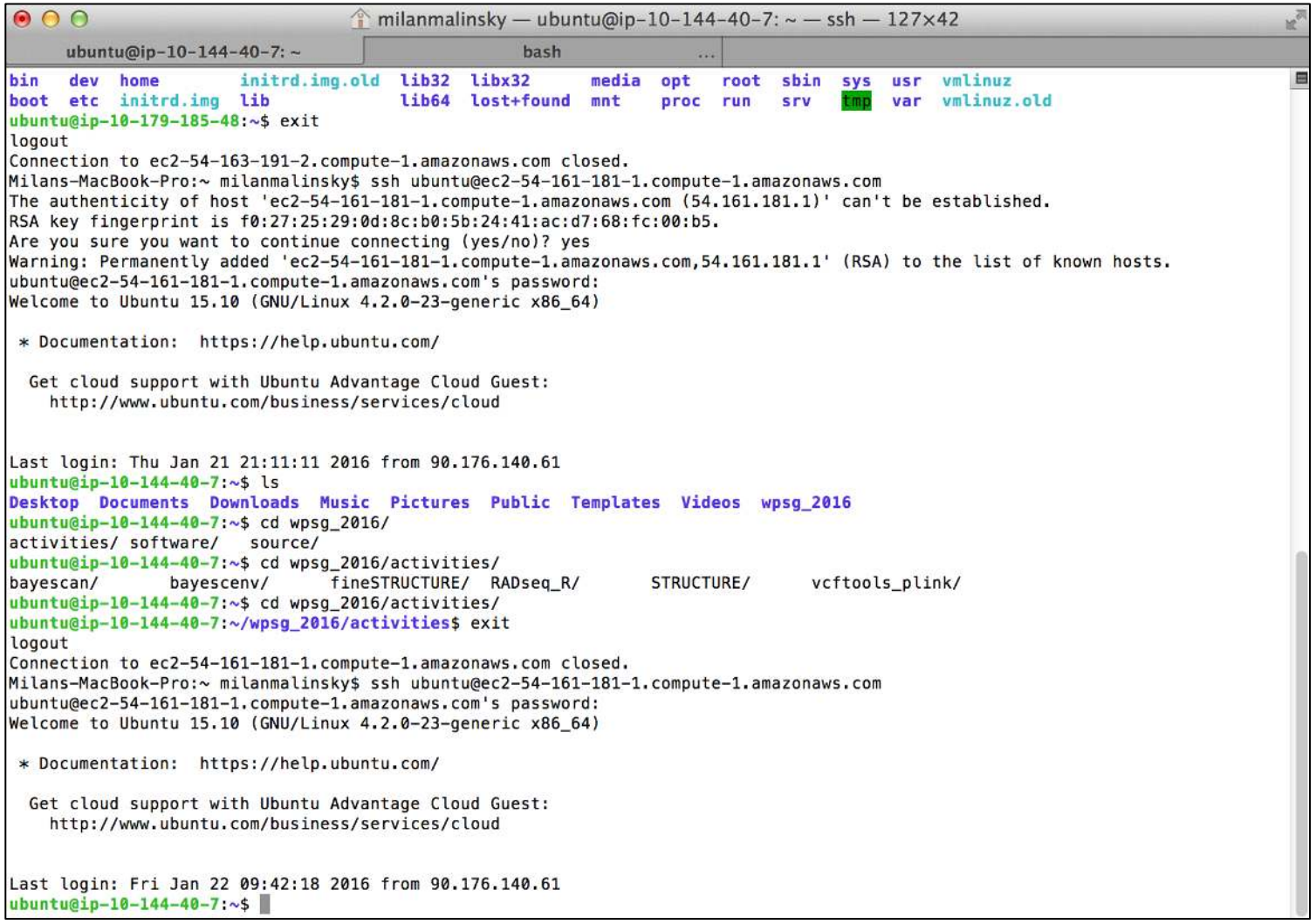
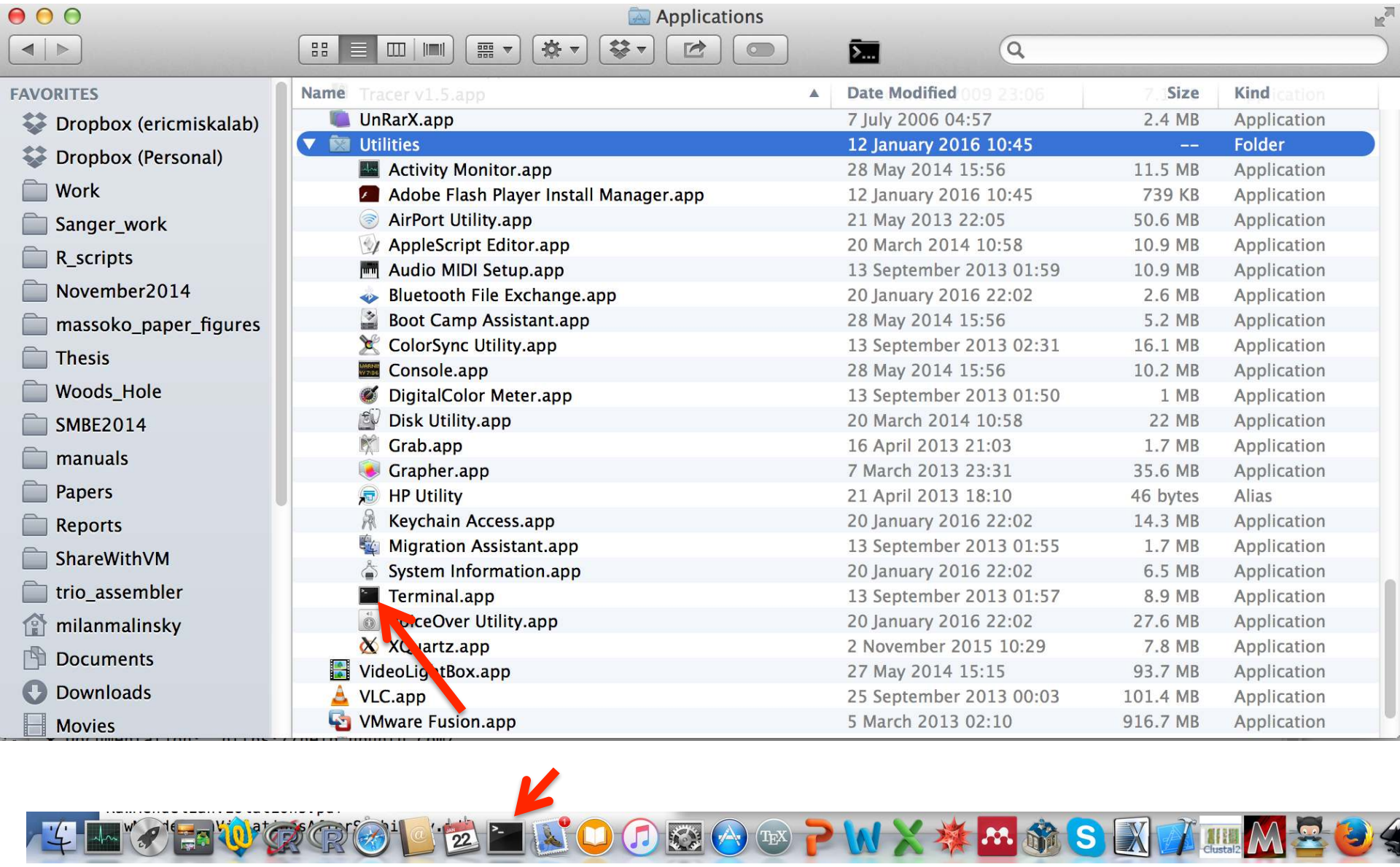
The UNIX terminal

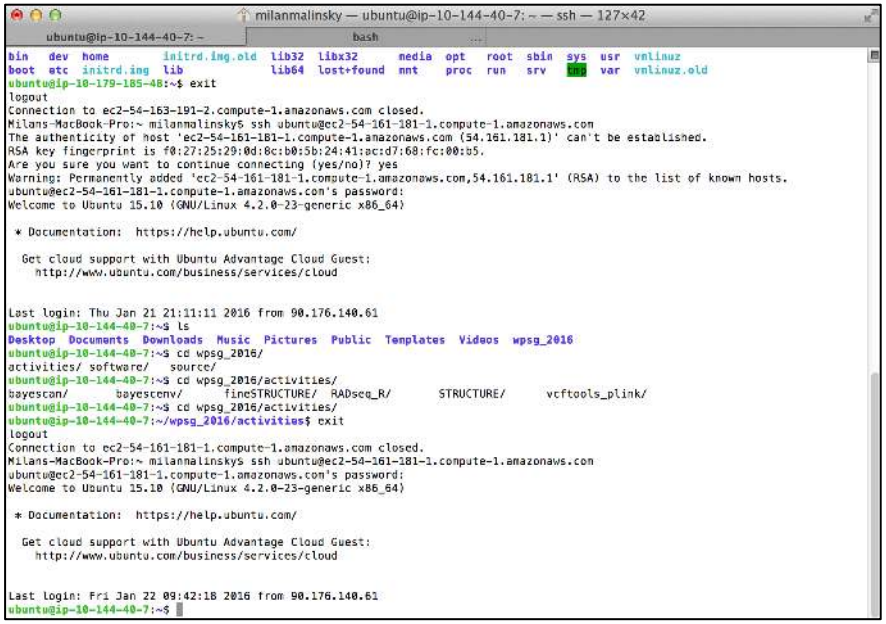


On the workshop desktop

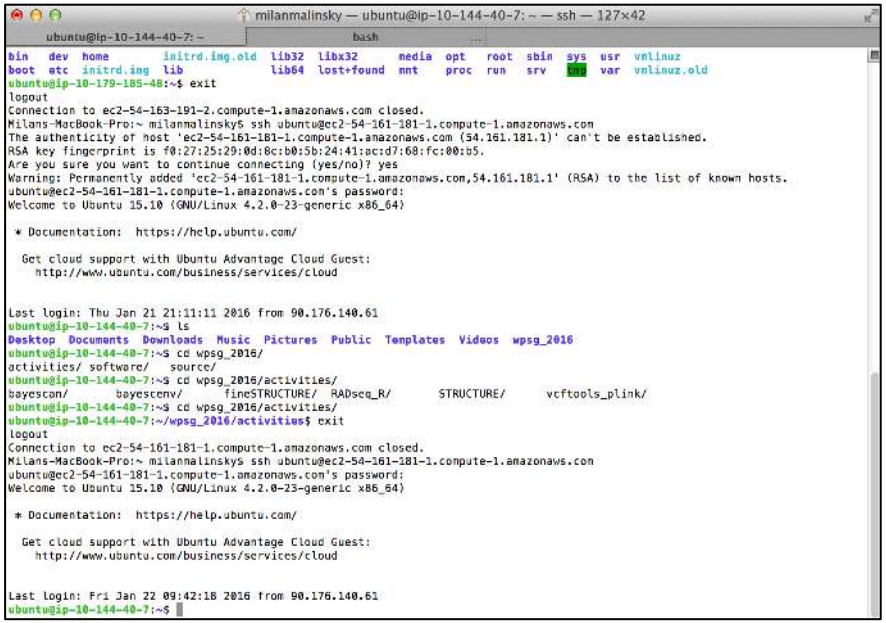
On a Mac computer



Why use something from the 1960s?



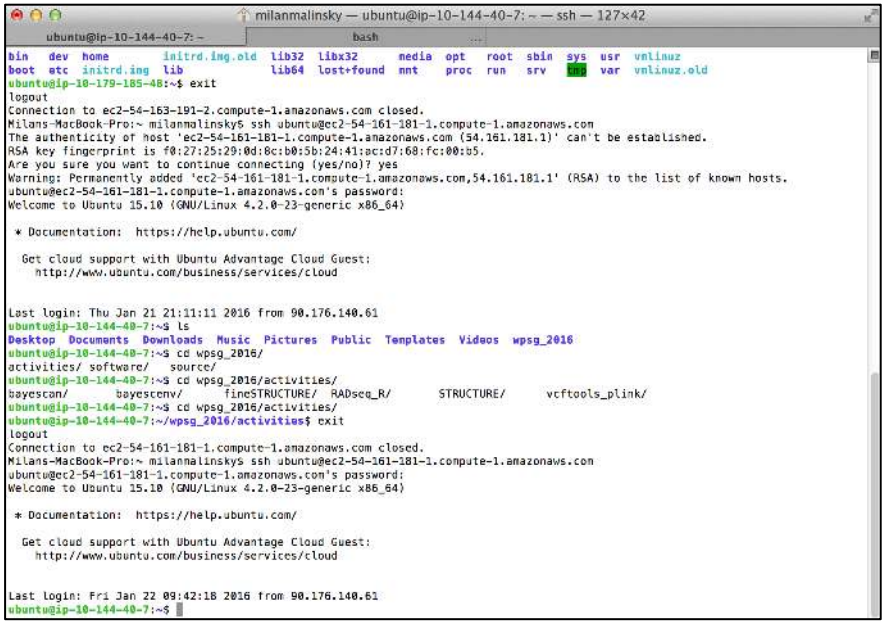
Why use something from the 1960s?



Scripting: Write down a sequence of commands to perform a task

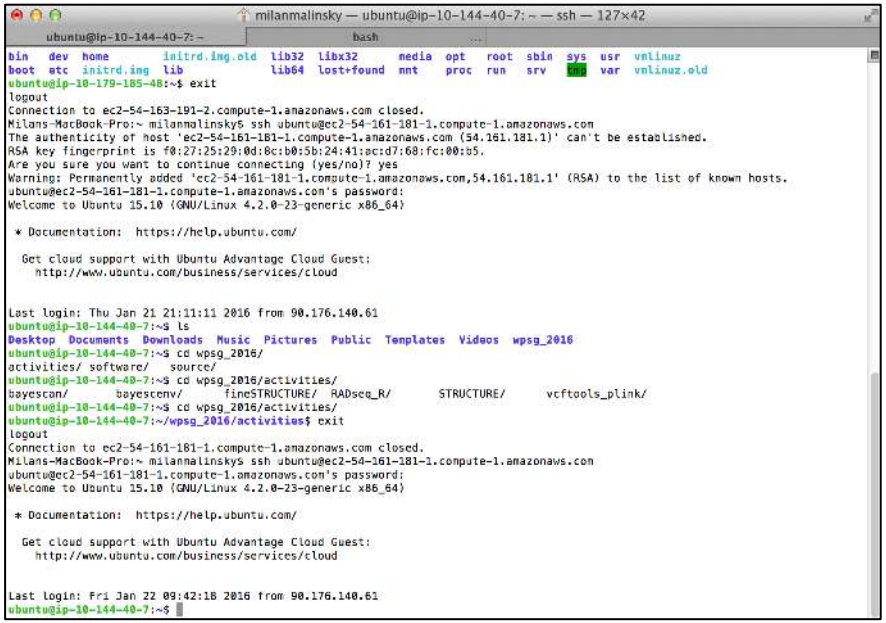
In genomics, a task almost always takes minutes, sometimes hours - not fun to sit and wait this long for the next mouse-click.

Why use something from the 1960s?



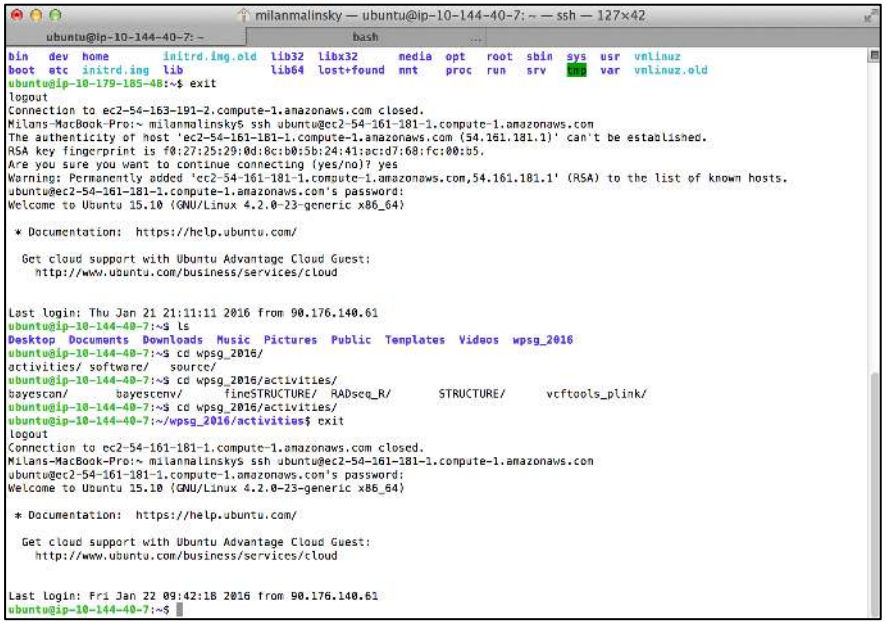
Scripting: Write down a sequence of commands to perform a task
In genomics, a task almost always takes minutes, sometimes hours - not fun to sit and wait this long for the next mouse-click.
Easy remote access: Running a real world genomics project on your own computer is impossible; you will usually access high performance compute facilities at your university.

Why use something from the 1960s?



Scripting: Write down a sequence of commands to perform a task
In genomics, a task almost always takes minutes, sometimes hours - not fun to sit and wait this long for the next mouse-click.
Easy remote access: Running a real world genomics project on your own computer is impossible; you will usually access high performance compute facilities at your university.
GUI for many programs not available: Genomics is a fast moving field and developing a graphical interface takes time and effort

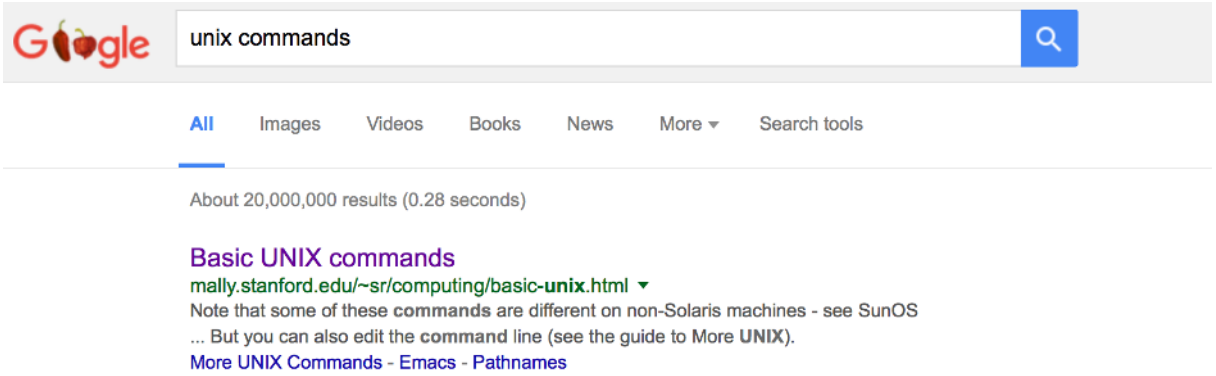
Why use something from the 1960s?



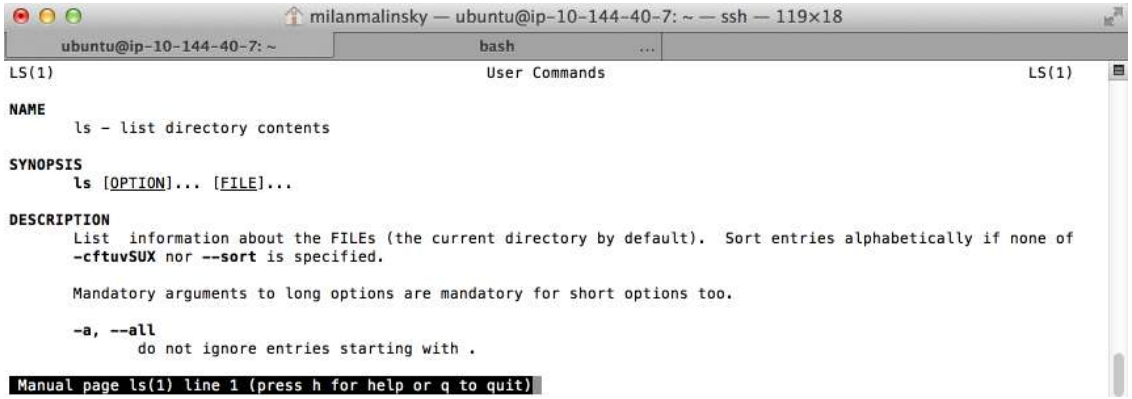
Scripting: Write down a sequence of commands to perform a task
In genomics, a task almost always takes minutes, sometimes hours - not fun to sit and wait this long for the next mouse-click.
Easy remote access: Running a real world genomics project on your own computer is impossible; you will usually access high performance compute facilities at your university.
GUI for many programs not available: Genomics is a fast moving field and developing a graphical interface takes time and effort
Powerful tools available in UNIX: enabling you to work through large amounts of files, data, and tasks quickly in an automated (programmatic) way

How to survive without 'seeing' your data, without pop-out menus, etc.?

1. Google: get a cheat-sheet with a list of possible commands:



2. Manual pages for each command: `ubuntu@ip-10-144-40-7:~$ man ls`



What do the `cp`, `vi`, and `awk` commands do? try: **`man cp, man vi, man awk`**

How to survive without 'seeing' your data, without pop-out menus, etc.?

3. Help: more concise than manual pages; describes different ways to run the program:

```
ubuntu@ip-10-144-40-7:~$ bcftools --help
```

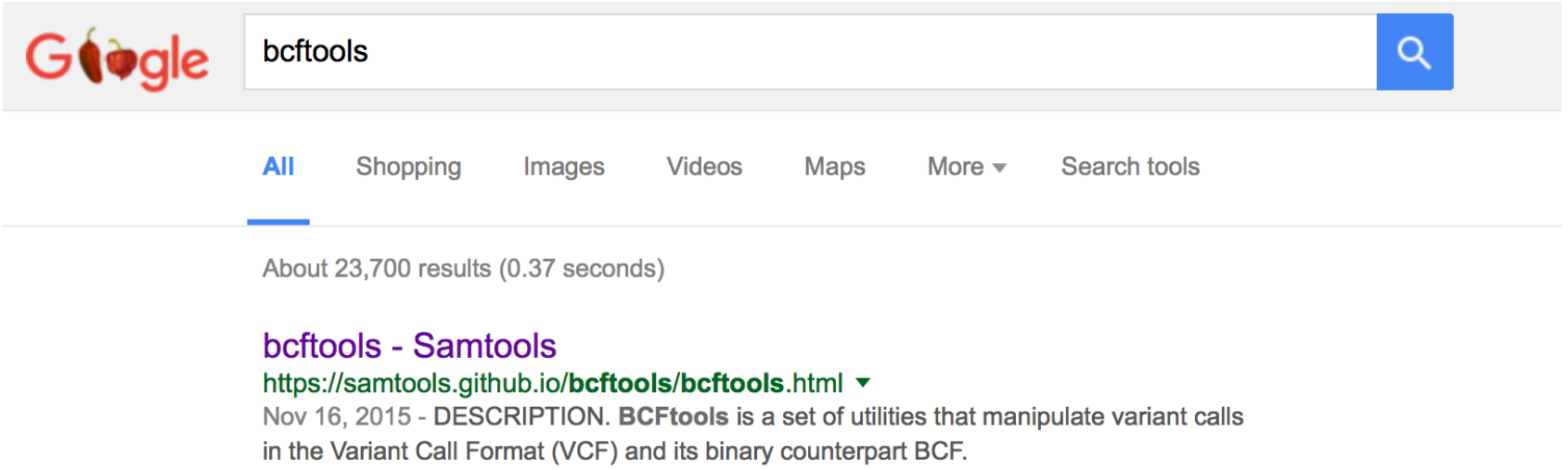
or

```
ubuntu@ip-10-144-40-7:~$ bcftools -h
```

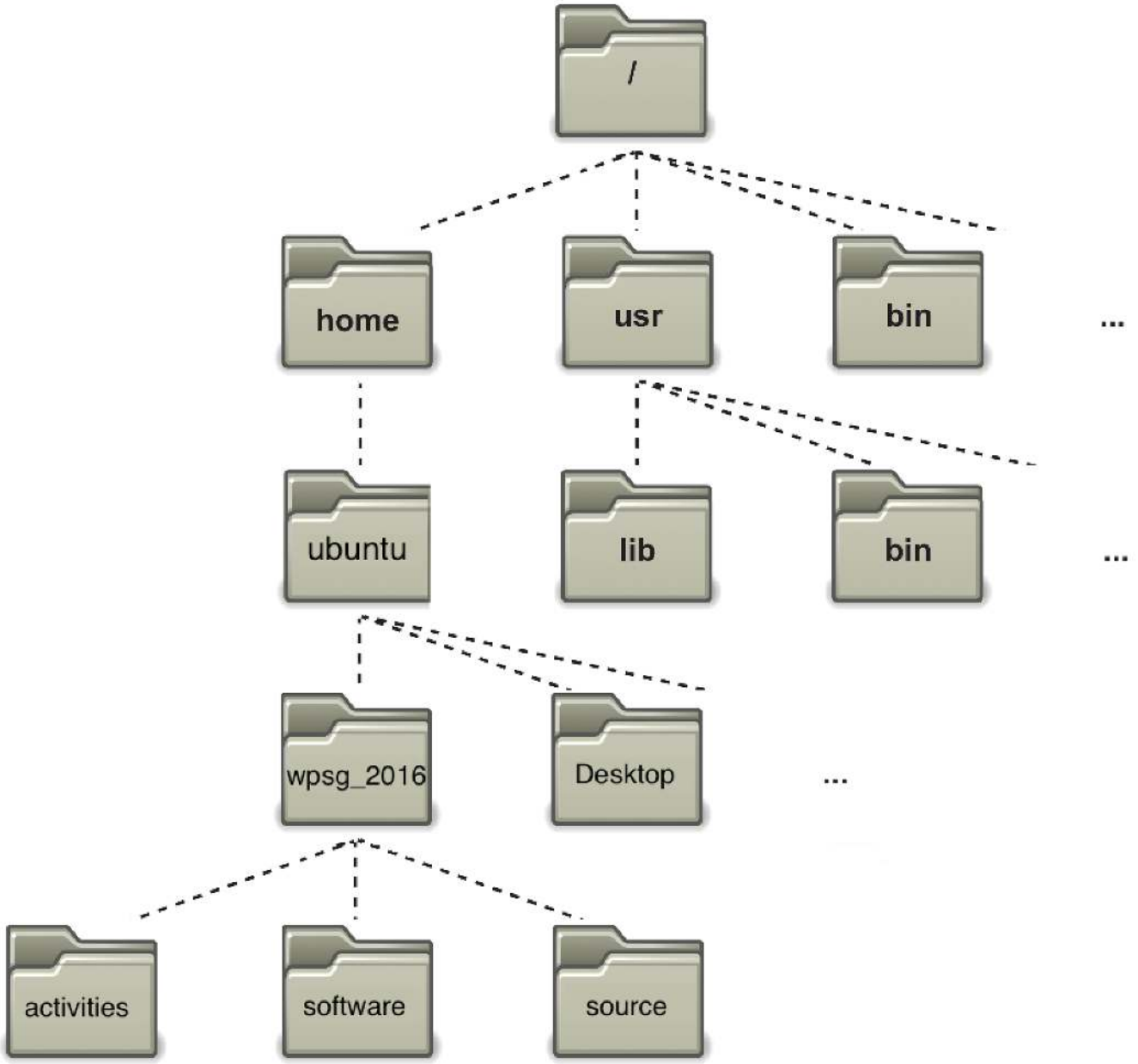
4. Genomics tools also usually have manual pages:

```
ubuntu@ip-10-144-40-7:~$ man bcftools
```

5. Google again:



UNIX directory structure

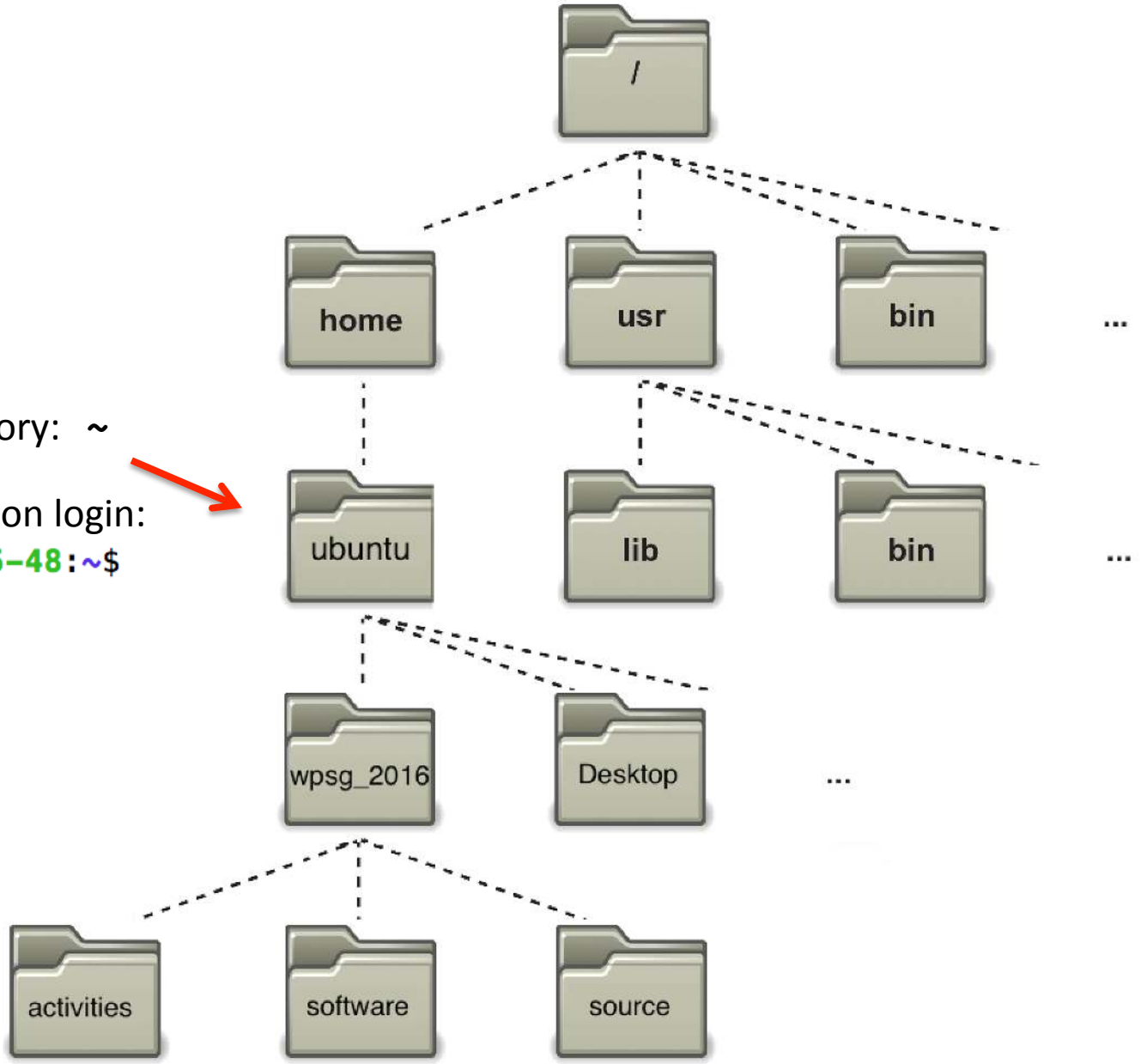


UNIX directory structure

Home Directory: ~

That's where you are upon login:

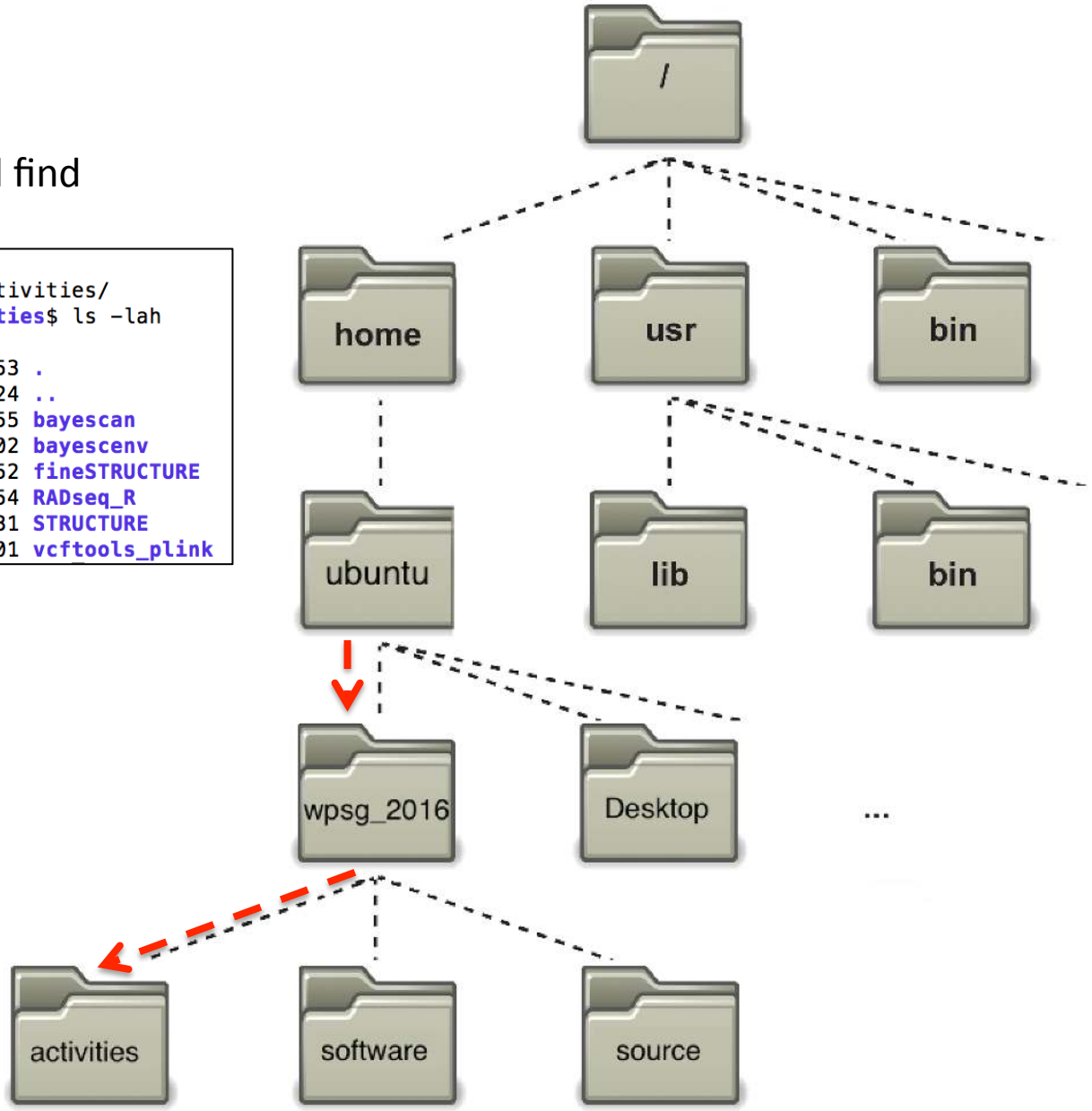
```
ubuntu@ip-10-179-185-48:~$
```



UNIX directory structure

Go to the 'activities' folder and find what is in there:

```
ubuntu@ip-10-179-185-48:~$ cd wpsg_2016/
ubuntu@ip-10-179-185-48:~/wpsg_2016$ cd activities/
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ ls -lah
total 32K
drwxrwxr-x 8 ubuntu ubuntu 4.0K Jan 21 11:53 .
drwxrwxr-x 5 ubuntu ubuntu 4.0K Jan 19 23:24 ..
drwxrwxr-x 4 ubuntu ubuntu 4.0K Jan 21 11:55 bayescan
drwxrwxr-x 6 ubuntu ubuntu 4.0K Jan 21 12:02 bayescenv
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 20 17:52 fineSTRUCTURE
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 11:54 RADseq_R
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 15:31 STRUCTURE
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 17:01 vcftools_plink
```



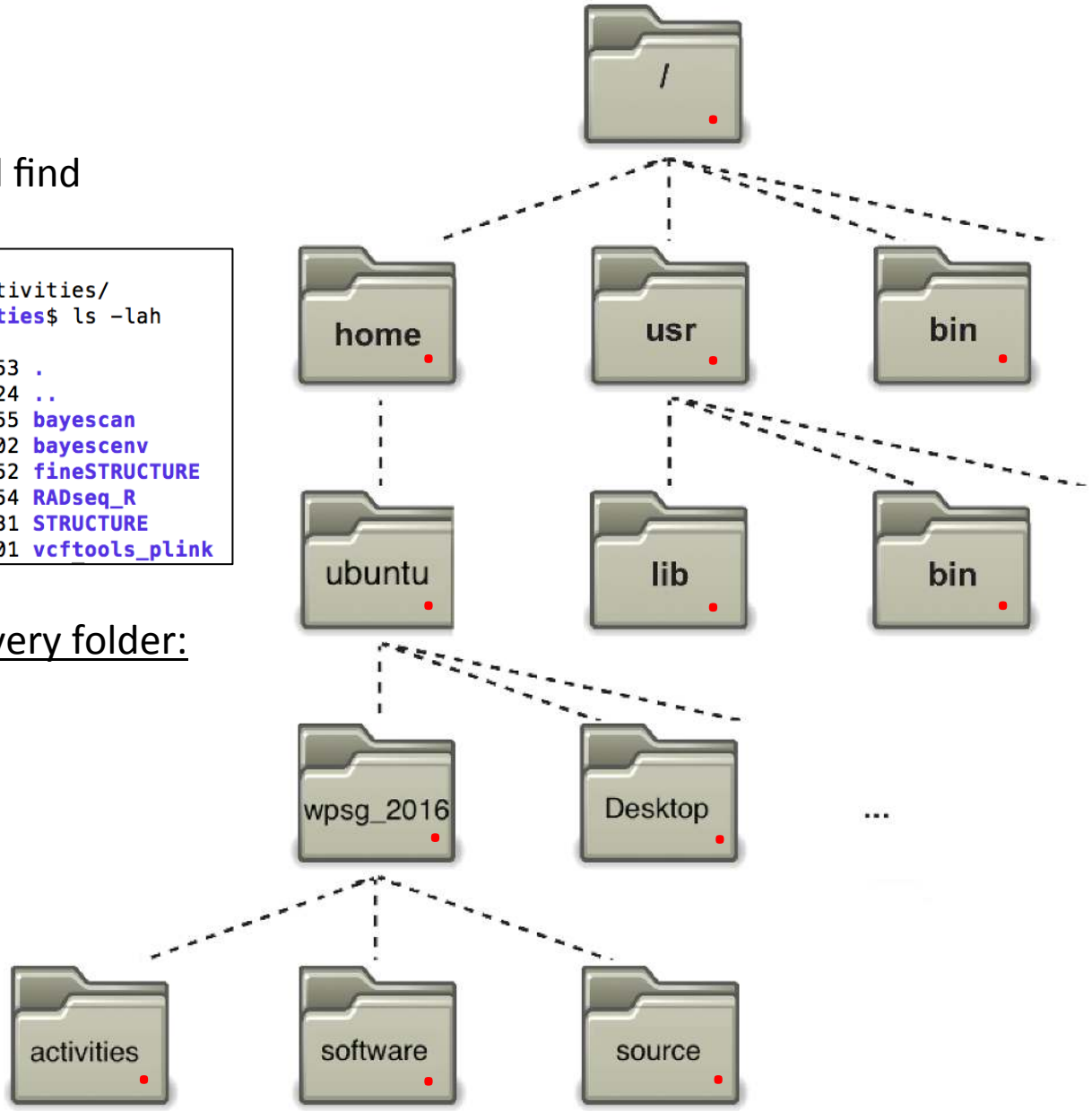
UNIX directory structure

Go to the 'activities' folder and find what is in there:

```
ubuntu@ip-10-179-185-48:~$ cd wpsg_2016/
ubuntu@ip-10-179-185-48:~/wpsg_2016$ cd activities/
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ ls -lah
total 32K
drwxrwxr-x 8 ubuntu ubuntu 4.0K Jan 21 11:53 .
drwxrwxr-x 5 ubuntu ubuntu 4.0K Jan 19 23:24 ..
drwxrwxr-x 4 ubuntu ubuntu 4.0K Jan 21 11:55 bayescan
drwxrwxr-x 6 ubuntu ubuntu 4.0K Jan 21 12:02 bayescenv
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 20 17:52 fineSTRUCTURE
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 11:54 RADseq_R
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 15:31 STRUCTURE
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 17:01 vcftools_plink
```

Two special 'files' present in every folder:

1) dot - means 'this directory'



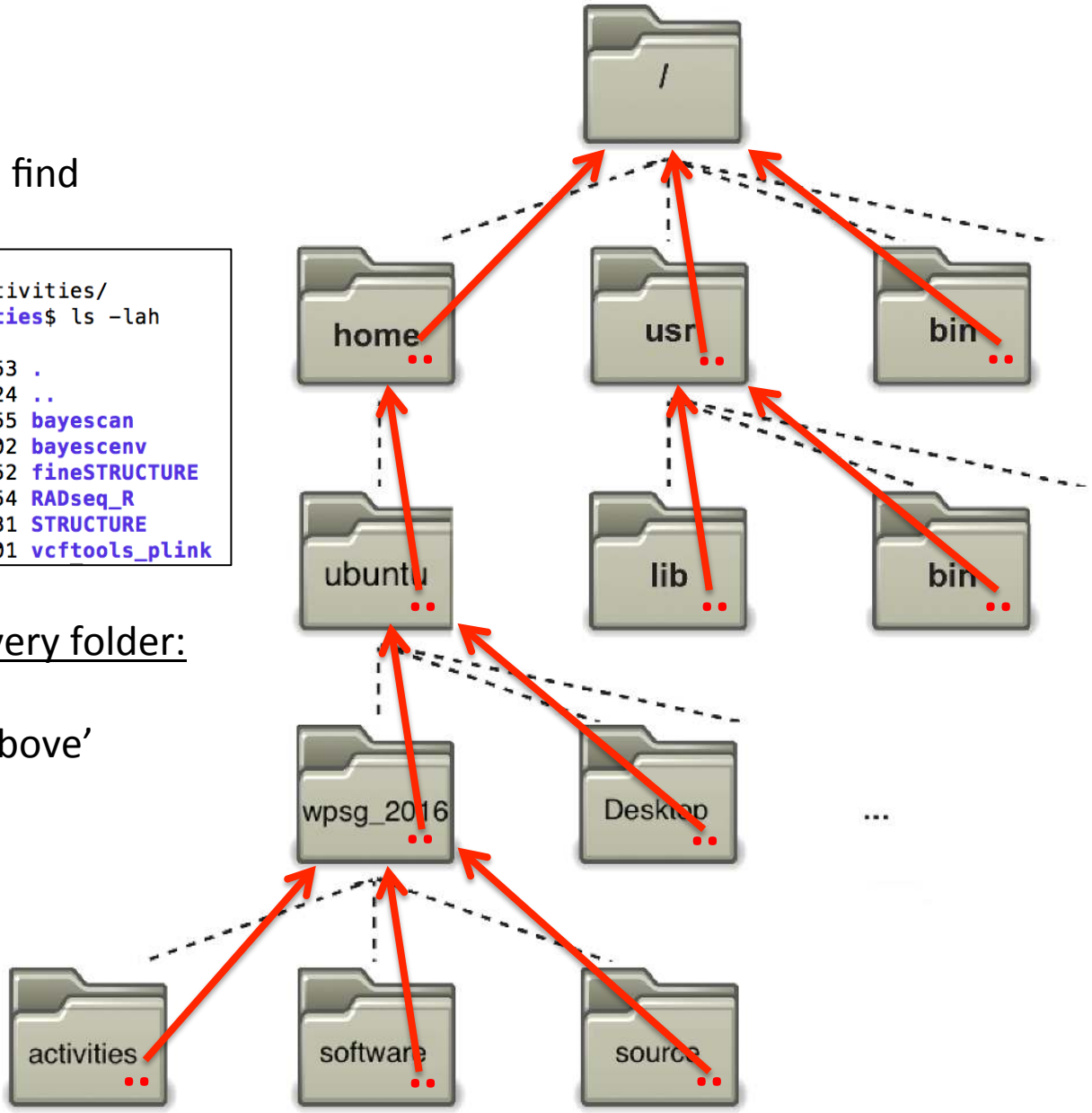
UNIX directory structure

Go to the 'activities' folder and find what is in there:

```
ubuntu@ip-10-179-185-48:~$ cd wpsg_2016/
ubuntu@ip-10-179-185-48:~/wpsg_2016$ cd activities/
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ ls -lah
total 32K
drwxrwxr-x 8 ubuntu ubuntu 4.0K Jan 21 11:53 .
drwxrwxr-x 5 ubuntu ubuntu 4.0K Jan 19 23:24 ..
drwxrwxr-x 4 ubuntu ubuntu 4.0K Jan 21 11:55 bayescan
drwxrwxr-x 6 ubuntu ubuntu 4.0K Jan 21 12:02 bayescenv
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 20 17:52 fineSTRUCTURE
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 11:54 RADseq_R
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 15:31 STRUCTURE
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 17:01 vcftools_plink
```

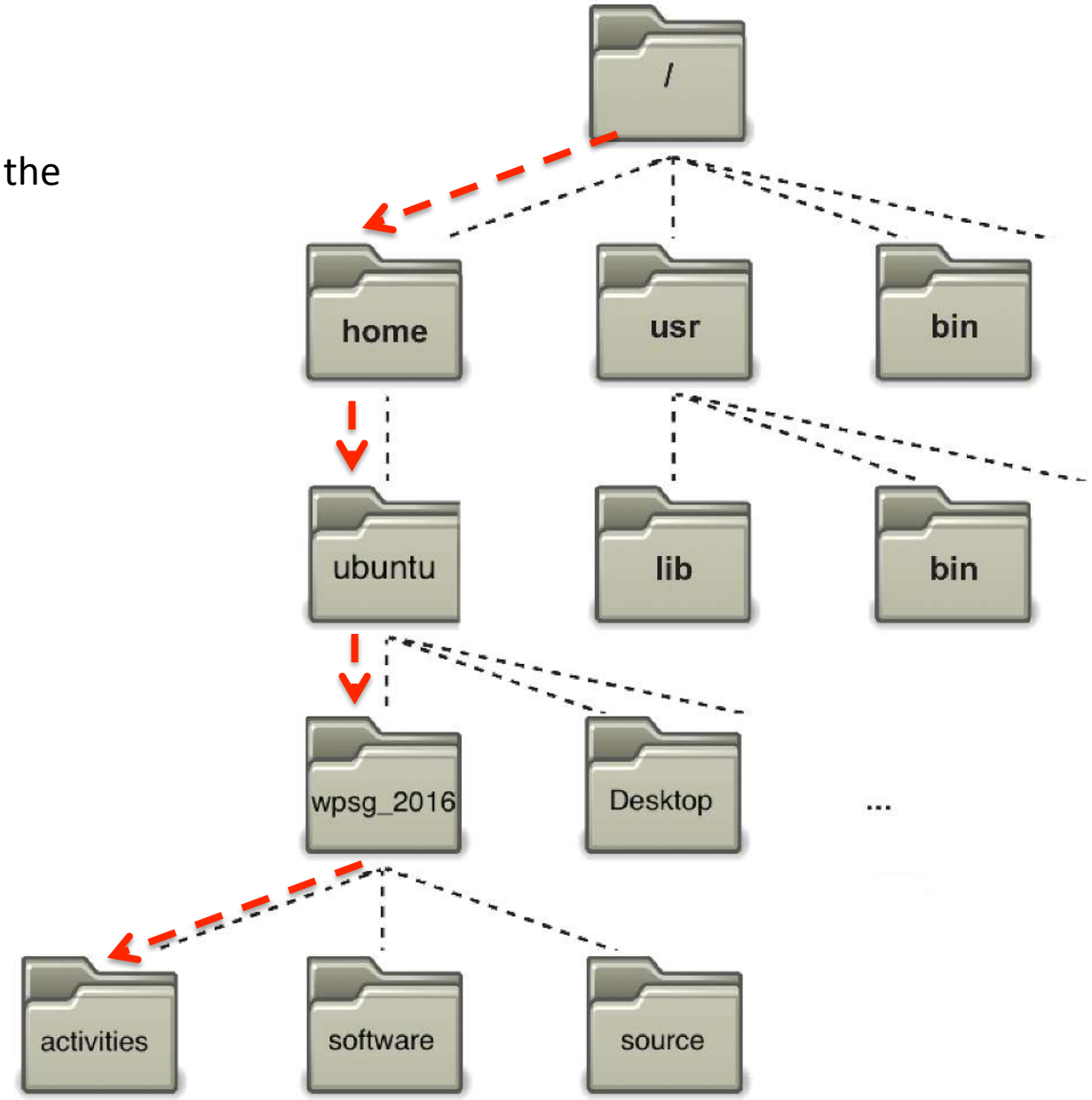
Two special 'files' present in every folder:

1) dot - means 'this directory'
2) dot dot - mean 'directory above'



UNIX directory structure

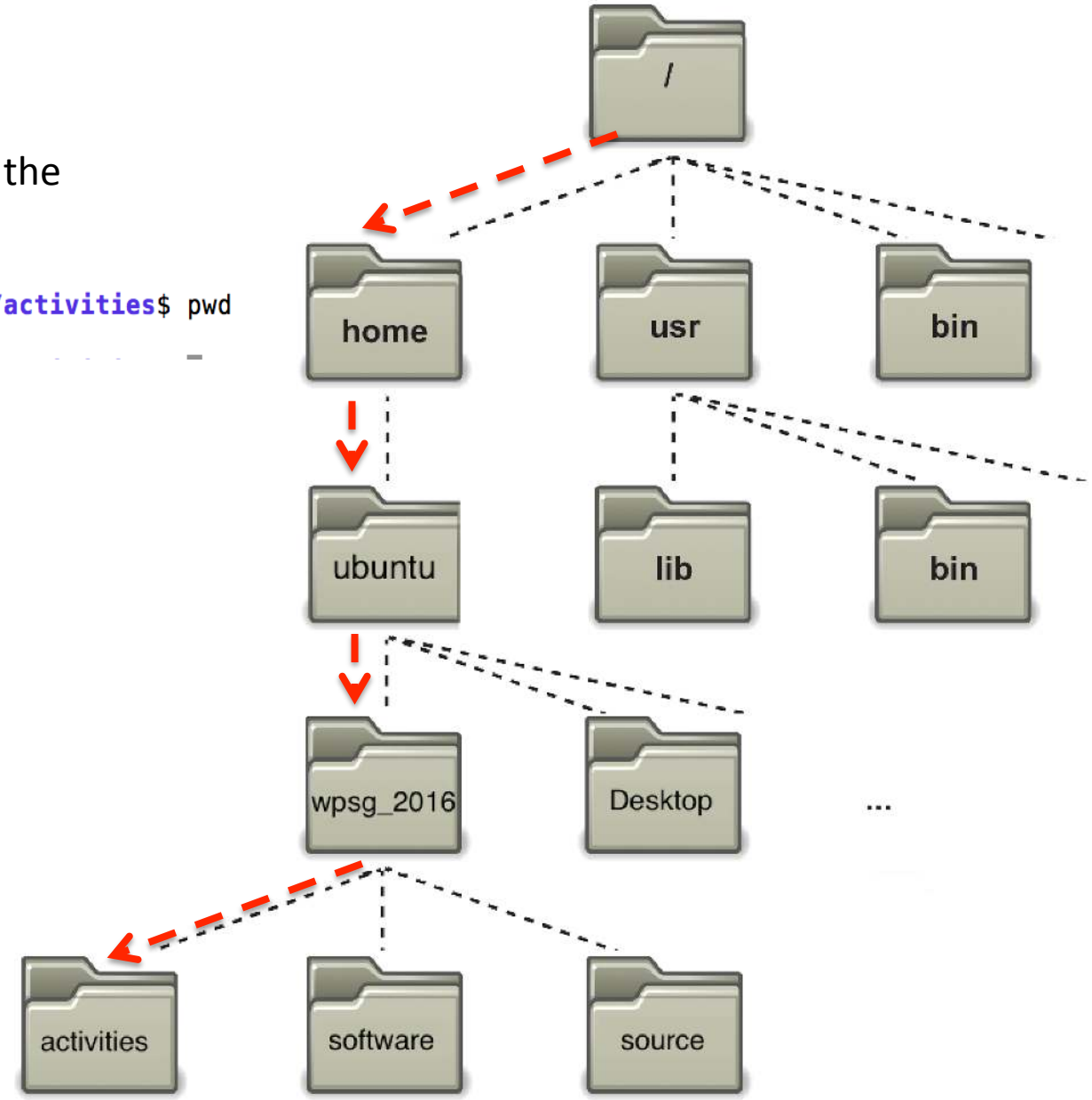
What is the ‘absolute path’ to the activities folder?



UNIX directory structure

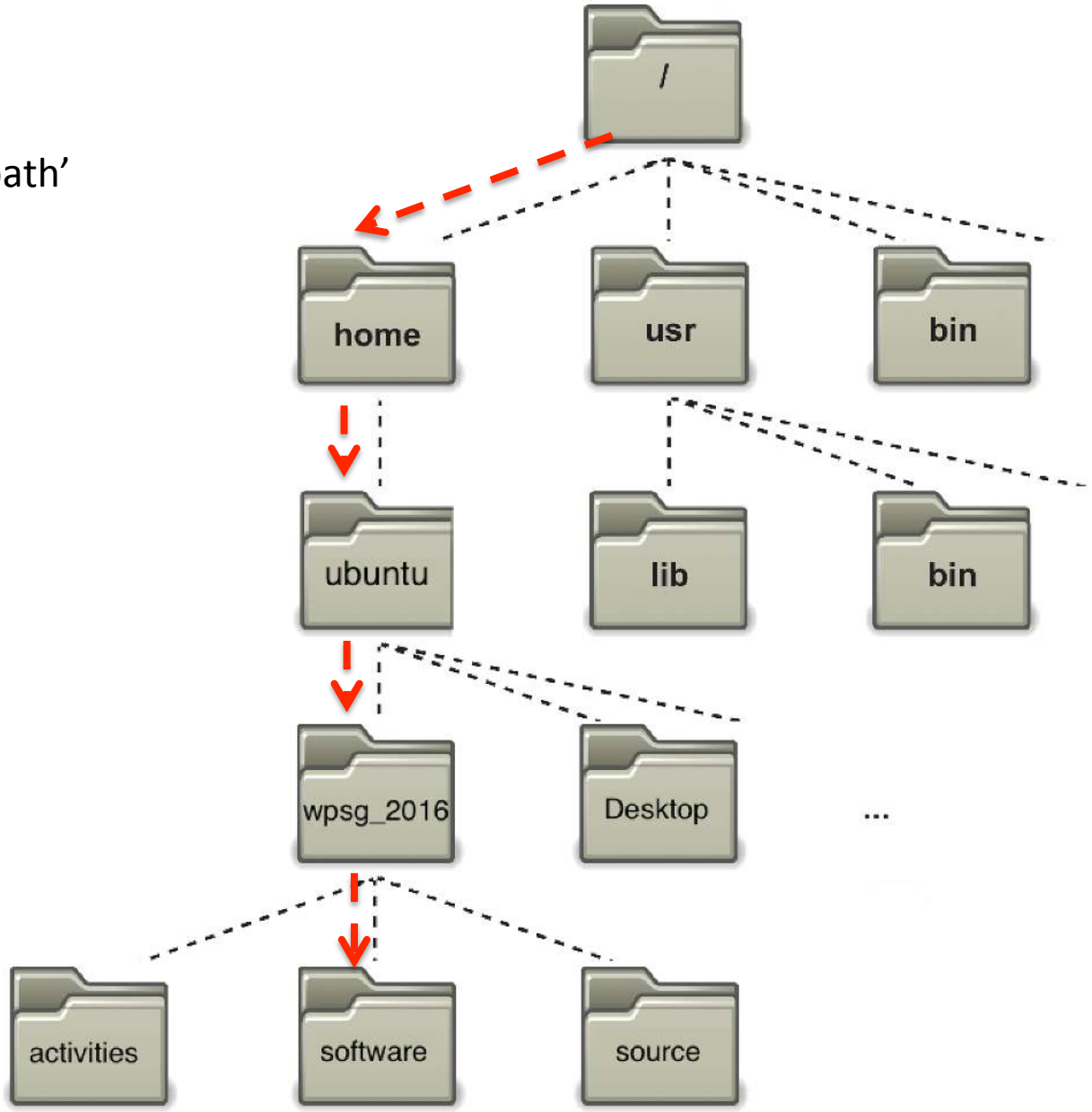
What is the ‘absolute path’ to the activities folder?

```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ pwd
/home/ubuntu/wpsg_2016/activities
```



UNIX directory structure

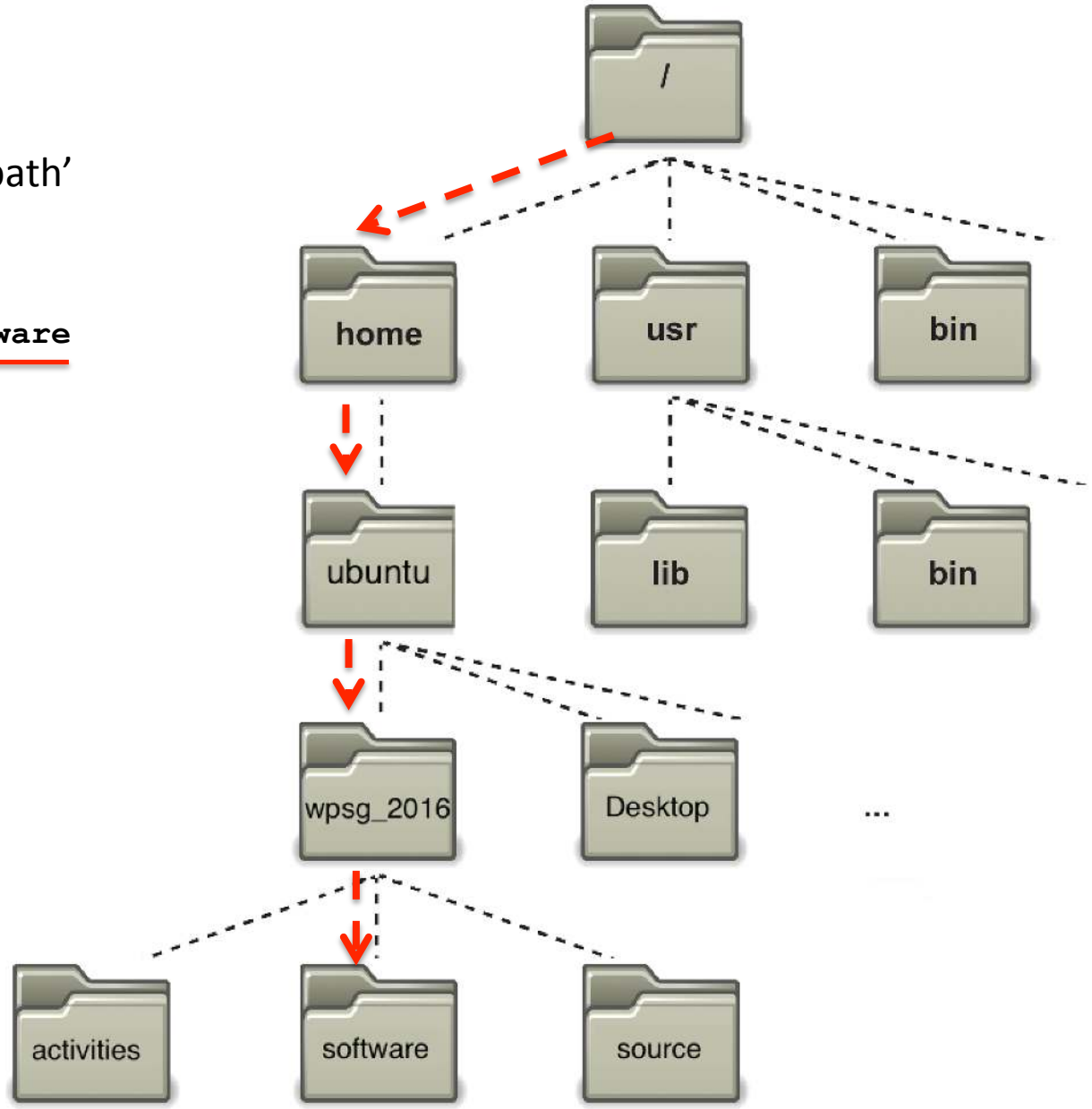
What would be the ‘absolute path’ to the ‘software’ folder?



UNIX directory structure

What would be the 'absolute path' to the 'software' folder?

`/home/ubuntu/wpsg_2016/software`

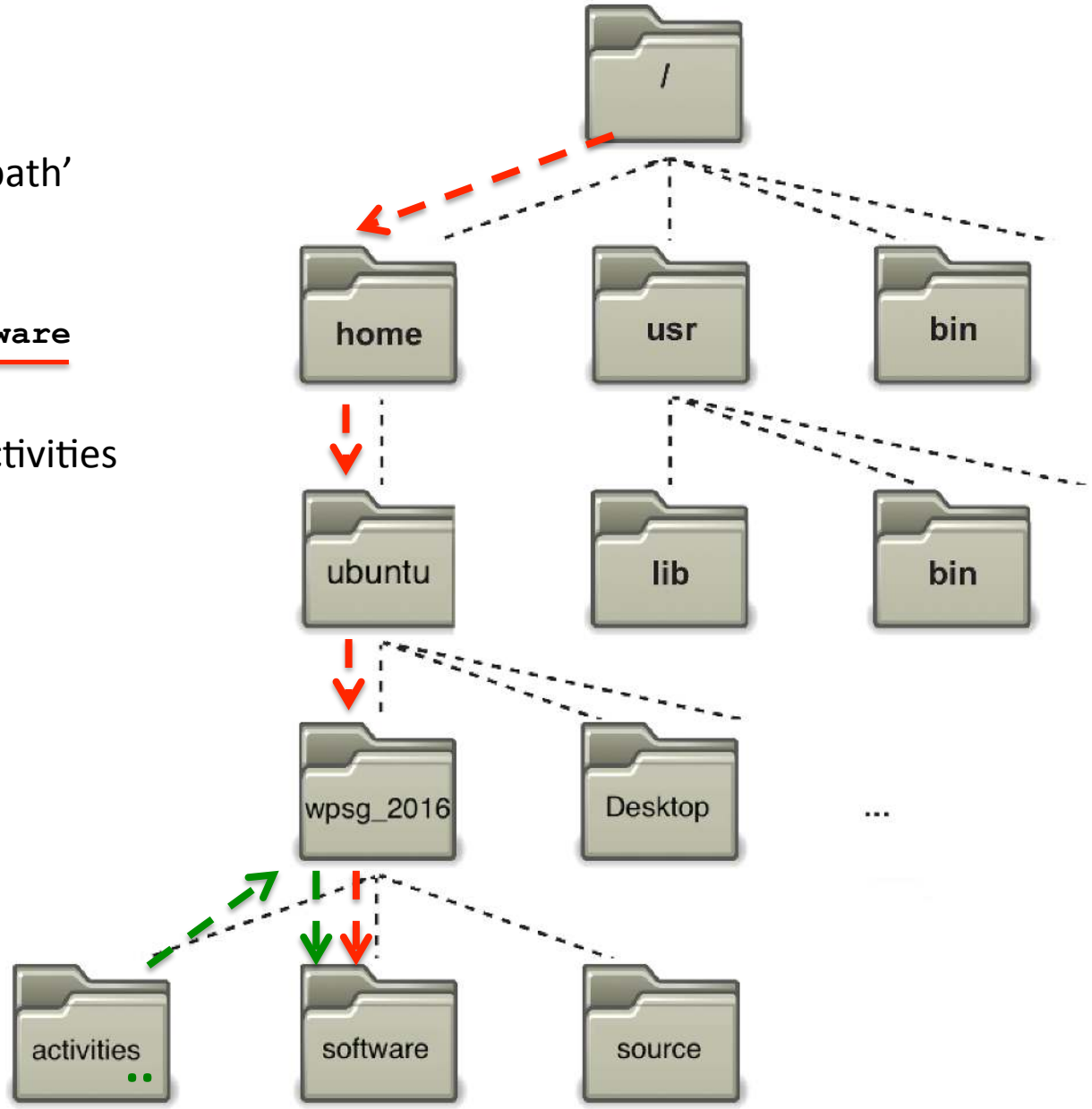


UNIX directory structure

What would be the 'absolute path' to the 'software' folder?

`/home/ubuntu/wpsg_2016/software`

And 'relative path' from the activities folder to the software folder?



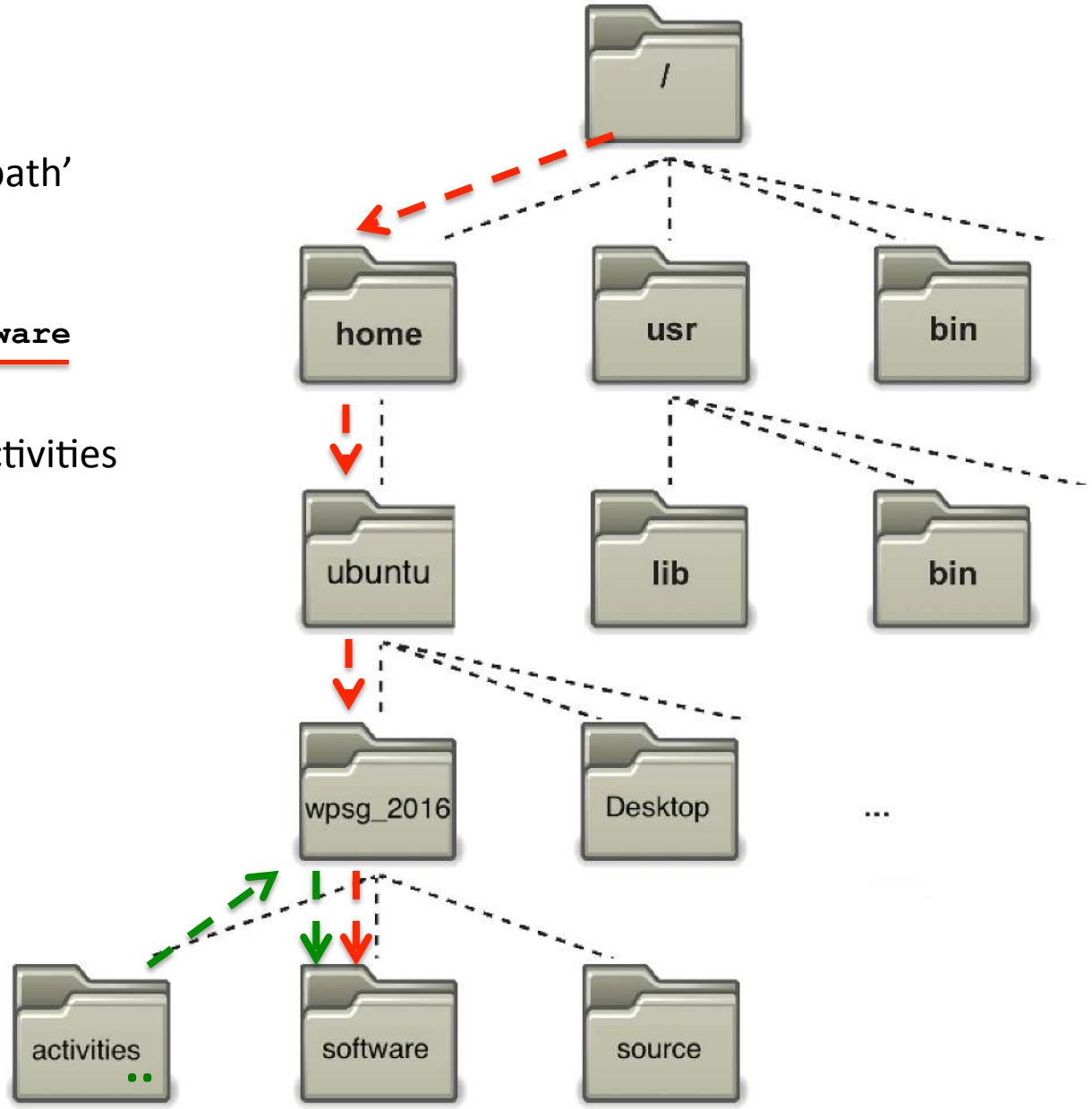
UNIX directory structure

What would be the 'absolute path' to the 'software' folder?

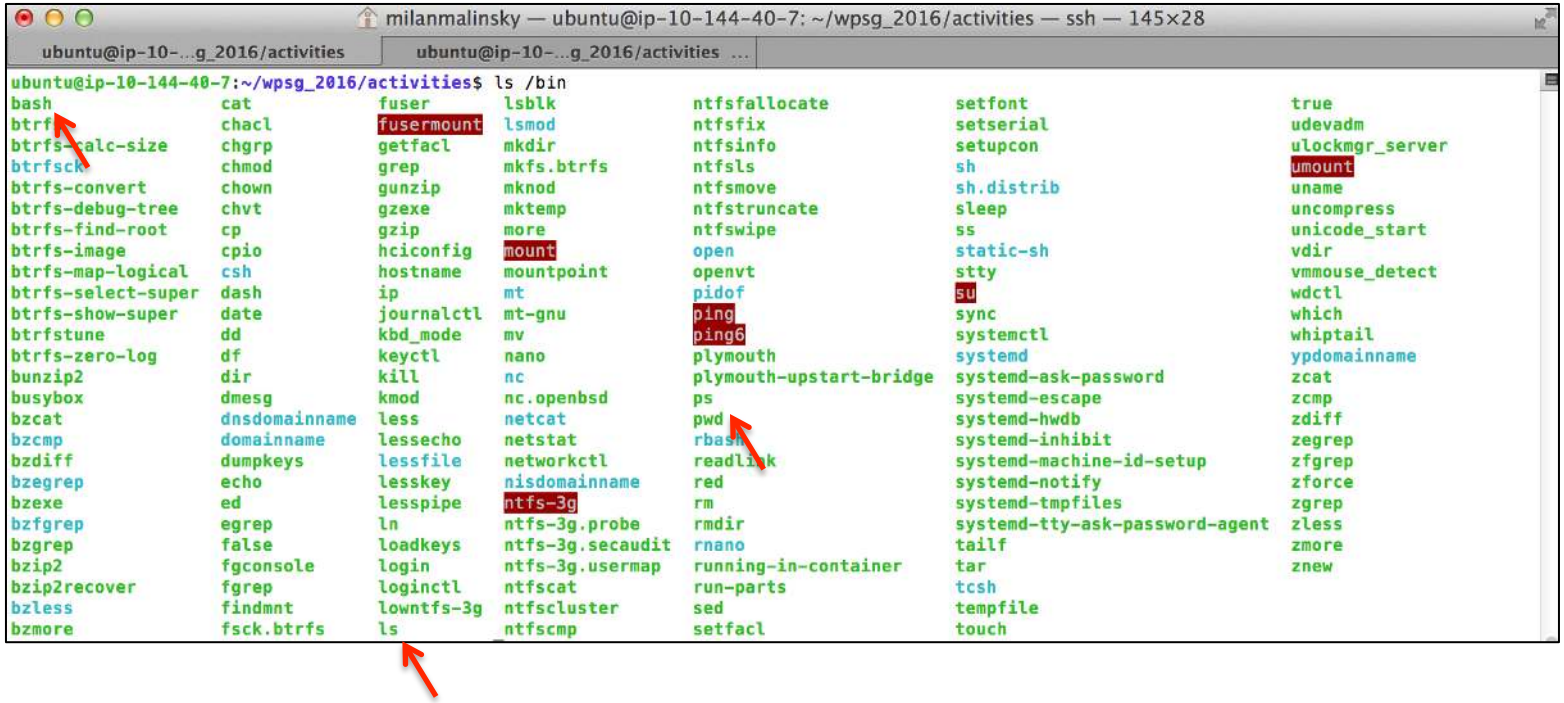
`/home/ubuntu/wpsg_2016/software`

And 'relative path' from the activities folder to the software folder?

`../software`



Many ‘programs’ are in the **`/bin`** folder



You have already seen some in action:

- **`cd`** – Change directory (part of the ‘**`bash`**’ program)
- **`ls`** – List directory contents
- **`pwd`** – Know where you are (‘print working directory’)

A few ways to view a text file:

`less`	`head`	`tail`	`cat`
view a text file one screen-full at a time	view the top 10 lines of a file	view the bottom 10 lines of a file	print the whole file at once on screen
space-bar: scroll q: quit	`-n num` option controls the number of lines	`-n num` option controls the number of lines	

Exercise 1: Navigating the file system and some UNIX system files

1. Move to the directory **`/etc`**

- What is the first line of the file '**`hosts`**' in the directory **`/etc`**?
- What is the relative file path to get to **`/var/log`** from here? What is the absolute path?

2. Move to the directory **`/var/log`**

- What is the contents on line 73 of the '**`dpkg.log`**' file?
- Without changing directories, what is the second line of the '**`cpuinfo`**' file in the **`/proc`** directory?
- What is the command to read this file with a relative path?
- An absolute path?

3.Move back to your home folder (remember **~**), what directories do you see?

Helpful features to save you typing:

1. Tab completion
   - <tab> once to complete a 'word' uniquely
   - <tab><tab> twice to show all possible completions
2. Up-arrow (history)
   - Show previous commands

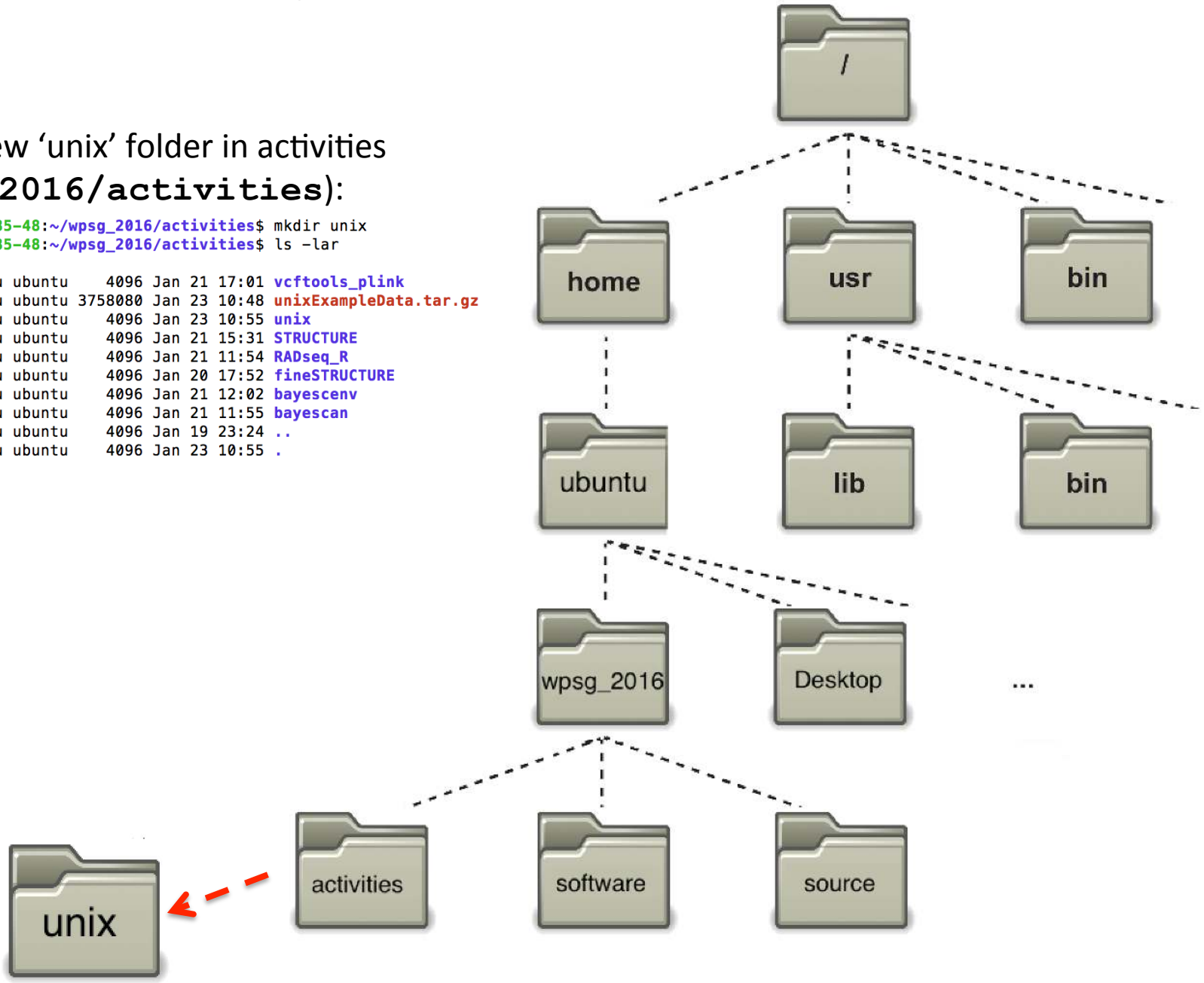
Try:

```
1. cd /etc
2. ls
3. cd c<tab><tab>
4. cd cal<tab>
```

UNIX directory structure

Create a new 'unix' folder in activities (**~/wpsg_2016/activities**):

```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ mkdir unix
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ ls -lar
total 3708
drwxrwxr-x 2 ubuntu ubuntu    4096 Jan 21 17:01 vcftools_plink
-rw-r--r-- 1 ubuntu ubuntu 3758080 Jan 23 10:48 unixExampleData.tar.gz
drwxrwxr-x 2 ubuntu ubuntu    4096 Jan 23 10:55 unix
drwxrwxr-x 2 ubuntu ubuntu    4096 Jan 21 15:31 STRUCTURE
drwxrwxr-x 2 ubuntu ubuntu    4096 Jan 21 11:54 RADseq_R
drwxrwxr-x 2 ubuntu ubuntu    4096 Jan 20 17:52 fineSTRUCTURE
drwxrwxr-x 6 ubuntu ubuntu    4096 Jan 21 12:02 bayescenv
drwxrwxr-x 4 ubuntu ubuntu    4096 Jan 21 11:55 bayescan
drwxrwxr-x 5 ubuntu ubuntu    4096 Jan 19 23:24 ..
drwxrwxr-x 9 ubuntu ubuntu    4096 Jan 23 10:55 .
```



Extracting example data into the new **`unix`** folder:

The example data are in the following compressed tar file:
`~/wpsg_2016/activities/unixExampleData.tar.gz`

What is a tar archive?

When you download programs for UNIX, they often come in tar files.

Genomics data is normally stored compressed to save on disk space/ costs.

tar = tape archive

Extracting example data into the new **`unix`** folder:

The example data are in the following compressed tar file:
`~/wpsg_2016/activities/unixExampleData.tar.gz`

`gzip/gunzip`	`tar -xvzf`	`tar -xvf`	`bgzip`
compress/ decompress a file	extract a gzipped tar archive like **`unixExampleData.tar.gz`**	extract an uncompressed tar archive like **`unixExampleData.tar`**	another compression algorithm you will come across in genomics

Extracting example data into the new **`unix`** folder:

The example data are in the following compressed tar file:
`~/wpsg_2016/activities/unixExampleData.tar.gz`

```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ cd unix/
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ tar -xvzf ../unixExampleData.tar.gz
exampleVariants.vcf.gz
examplesGenomeSeqence.fastq.gz
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ ls -lah
total 3.6M
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 23 11:29 .
drwxrwxr-x 9 ubuntu ubuntu 4.0K Jan 23 11:01 ..
-rw-r----- 1 ubuntu ubuntu 3.6M Jan 22 19:35 examplesGenomeSeqence.fastq.gz
-rw-r----- 1 ubuntu ubuntu 7.1K Jan 22 20:00 exampleVariants.vcf.gz
```

The **`unixExampleData`** archive contains two compressed files:

1) **`examplesGenomeSeqence.fastq.gz`**
   - output from a genome sequencer - Illumina type
2) **`exampleVariants.vcf.gz`**
   - a file with variants (differences) from the reference genome

Working with the sequence file:

The FASTQ format:

```
@HS22_09582:8:1105:9492:70247#84/1
GAGAATCTCATCCACATCACAGGCTATATTGGCCCCAGCCAGGCAGCGGGGGTAAAATCCTCTTGCATGCCTGATCCACCCCTGGCATGCATCTACTGAT
+
B?CFDFGEFFEGEFGGFFIFEEGICCDFFGJFGFGEFFEHFFEGHEEGFGFG?GFFFGGGDGFGEFFHFBGGFFEGFDFFHFGEFGGBFFFDFFGEEFCE
```

1. Decompress the file
2. Count the number of reads
   - **`wc -l examplesGenomeSeqence.fastq`**
   - **`grep "@HS" examplesGenomeSeqence.fastq`**
   - **`grep -c "@HS" examplesGenomeSeqence.fastq`**
   - **`grep -v "@HS" examplesGenomeSeqence.fastq`**
   - **`grep -v -c "@HS" examplesGenomeSeqence.fastq`**
3. Print and count reads with undetermined bases in them:
   - **`grep ”N" examplesGenomeSeqence.fastq`**
   - **`grep -c ”N" examplesGenomeSeqence.fastq`**

Working with the VCF variants file:

The VCF file (without a header) is a text file with **<tab>** separated columns:

- columns 1-8: information about a variant (location, alleles, quality scores, filtering, etc.)
- columns 9 onwards: information about the genotypes (variants) present in each individual

Working with the VCF variants file:

The VCF file (without a header) is a text file with **<tab>** separated columns:

- columns 1-8: information about a variant (location, alleles, quality scores, filtering, etc.)
- columns 9 onwards: information about the genotypes (variants) present in each individual

There is a lot of information, especially in the INFO and FORMAT columns: you are going to find what some of these things mean tomorrow and during the rest of the course. But if you can't wait, the formal specification is here: http://www.1000genomes.org/wiki/analysis/variant%20call%20format/vcf-variant-call-format-version-41

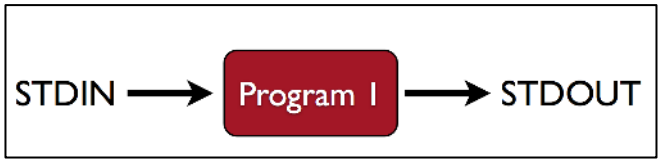
Working with the VCF variants file:

The VCF file (without a header) is a text file with **<tab>** separated columns:

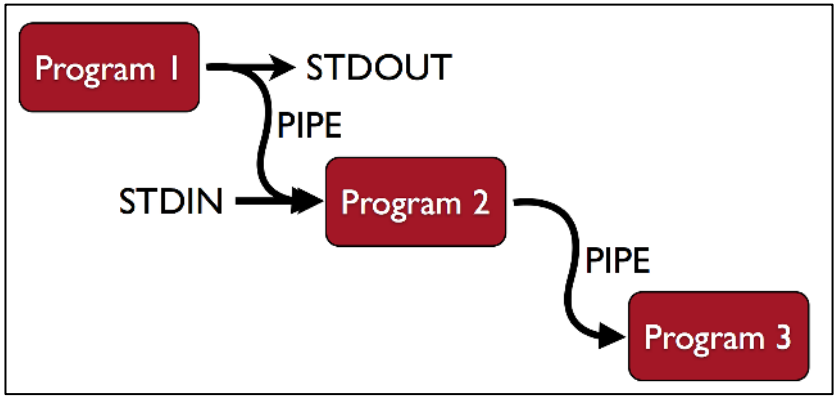
- columns 1-8: information about a variant (location, alleles, quality scores, filtering, etc.)
- columns 9 onwards: information about the genotypes (variants) present in each individual

We will use one of UNIX's cool features: Pipes

So far we have been doing this:



Now we are going to learn to link multiple UNIX programs:



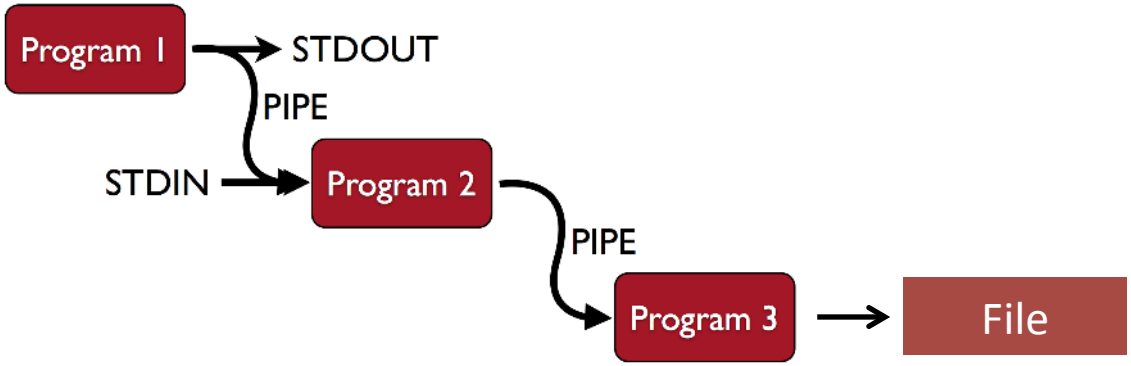
Working with the VCF variants file:

The VCF file (without a header) is a text file with **<tab>** separated columns:

- columns 1-8: information about a variant (location, alleles, quality scores, filtering, etc.)
- columns 9 onwards: information about the genotypes (variants) present in each individual

1. Decompress the file
2. Have a look at the file
   - **`less exampleVariants.vcf`**
   - **`less -S exampleVariants.vcf`**
3. Find out how many chromosomes there are:
   - **`cut -f 1 exampleVariants.vcf`**
   - **`cut -f 1 exampleVariants.vcf | uniq`**
   - Make sure you know what **`cut -f`** does! Try **`cut -f 2`**
   - **`man uniq`** (see what **`uniq`** does)
4. Find how many variants have a "**`T`**" as the reference allele (fourth column):
   - **`cut -f 4 exampleVariants.vcf`**
   - **`cut -f 4 exampleVariants.vcf | grep "T"`**
   - **`cut -f 4 exampleVariants.vcf | grep -o "T"`**
   - **`cut -f 4 exampleVariants.vcf | grep -o "T" | wc -l`**
   - **`man grep`** (see what the **`-o`** option does)

Working with the VCF variants file:



5. Capture the genotype information for the first three individuals into a different file:
   - **`cut -f 10-12 exampleVariants.vcf > threeGenotypes.txt`**
6. Remove the newly created file:
   - **`rm threeGenotypes.txt`**

!!!There is **NO** undo button, no trash can**!!!!**

Once deleted a file is lost forever (or at least you'd need professional data recovery)

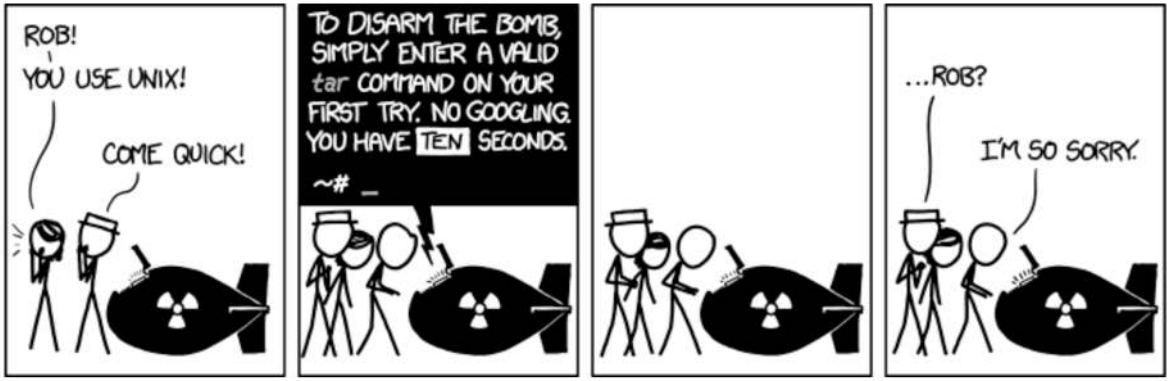
- **`rm -i exampleVariants.vcf`** (then press **`n`** and enter)

```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ rm -i exampleVariants.vcf
rm: remove regular file 'exampleVariants.vcf'? n
```

Using a second set of example data:

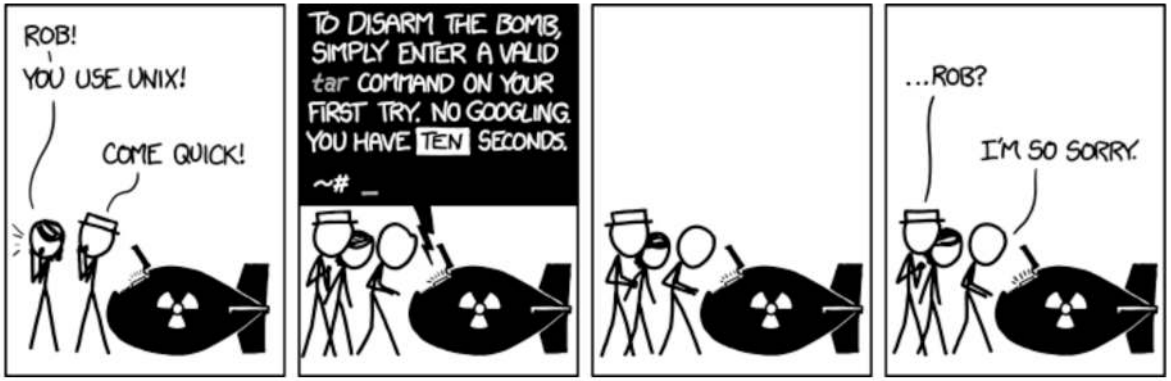
The example data are in the following compressed tar file:

`~/wpsg_2016/activities/unixExampleData2.tar.gz`



Using a second set of example data:

The example data are in the following compressed tar file:
`~/wpsg_2016/activities/unixExampleData2.tar.gz`



The **`unixExampleData2`** archive contains 11 uncompressed fasta sequence files:

```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ tar -xvzf ../unixExampleData2.tar.gz
scaffold_600.fa
scaffold_601.fa
scaffold_602.fa
scaffold_603.fa
scaffold_604.fa
scaffold_605.fa
scaffold_606.fa
scaffold_607.fa
scaffold_608.fa
scaffold_609.fa
scaffold_610.fa
```

Using a second set of example data:

The example data are in the following compressed tar file:
`~/wpsg_2016/activities/unixExampleData2.tar.gz`

Each file contains a header line (starts with **>**) and then a lot of sequence:

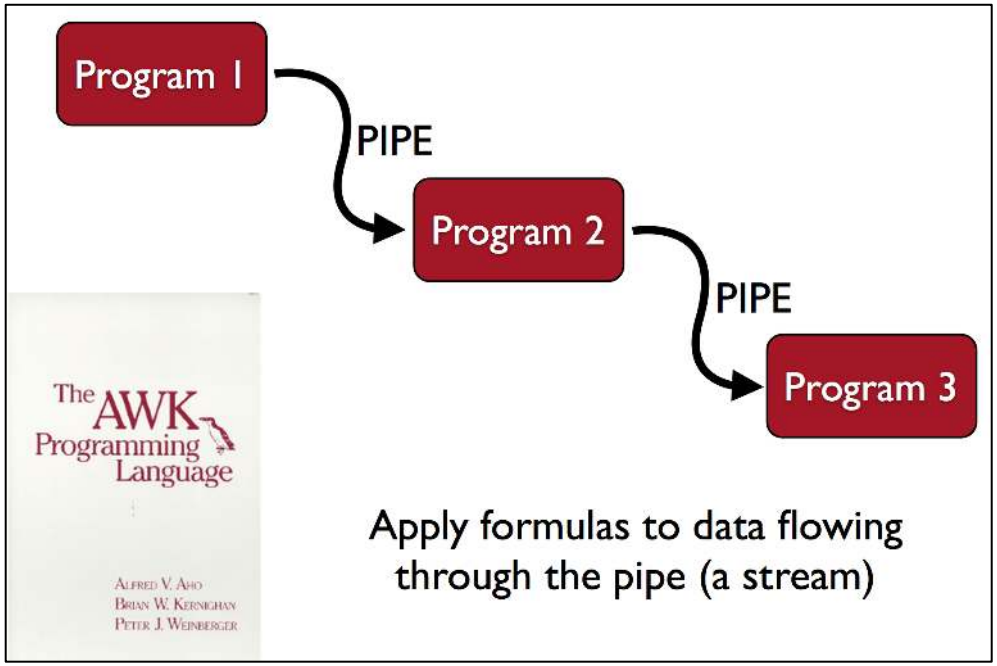
```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ less scaffold_600.fa

>scaffold_600
TATATATATATATATATATATATATATATATCTGACAATACTATAATATTGGCCATATTATATTTACATTACCACAGTGA
GATGACTTTAGTCTCATGAACAACATAACAACATTAACTAGTTGTTATTTGCTAACTAATCTTAAATGACTGTTCAGCAC
AGAAATGAAGCCCAACAATCATGTTCTACAGTCCCGTGGTCTCAGCCTCAGATACTCAACTAATCAAGGTGATGTCATGA
CAAAATGAATGACCAACAAAACATTTTTCTCCTTCATTTCTGTCAAACAAAGCTGTATGTAACGTGTCTCGTGGTTAGTA
TCATGGTTGCTAGGCAACGGAGGCTAGACCATCCCATTTCACAAGCCTCGCACTTCCGGCCTTAGCGGTCTTTAAGTACG
CGGCCCGTGAGGACTGGCTCACGGGCTGCAGACCCTGAATTGGGATACAGACTAGAAGCTATTGATGCGCTTTTTGATGA
CGTCTTTTCTGACGTCGACGTCTCGAGATCTGGCCATACCACGAAAAAACACTAAGGCTCTCAAGACTGCTAACATCTAC
AACCGATTGAAACTGCTAACTTGATTTTGGCTCTTGCAAACTTTTGTTTATTTATGTTCCCCTTAATTTATTTTATTTTT
TGTACTCACTTTTGTCTCACTGTCCTTGTCACTCTCTCTGTTCCTCATTGTACTACCACAATGTTATATTTTATGTGATT
CCTGTTTTACTTGACTGTATGTCTAAAATGTGATAAATAAAGTTTAAAAAAAAAATCTGGCCATACCACGTGACAAATTT
```

How would you:

1) find the length of the DNA sequence in each file?
2) edit the header line of each file to read "**`chromosome_`**" instead of "**`scaffold_`**"?
3) What if you had 3000 such files?

Find the length of the DNA sequence in each file:

One solution is to use `awk` :




```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ man awk

GAWK(1)                                                    Utility Commands                                                    GAWK(1)

NAME
       gawk - pattern scanning and processing language

SYNOPSIS
       gawk [ POSIX or GNU style options ] -f program-file [ -- ] file ...
       gawk [ POSIX or GNU style options ] [ -- ] program-text file ...

DESCRIPTION
       Gawk  is  the  GNU Project's implementation of the AWK programming language.  It conforms to the definition of the language in the POSIX 1003.1 Standard.  This
       version in turn is based on the description in The AWK Programming Language, by Aho, Kernighan, and Weinberger.  Gawk provides the additional features found in
       the current version of Brian Kernighan's awk and a number of GNU-specific extensions.

       The  command  line  consists of options to gawk itself, the AWK program text (if not supplied via the -f or --file options), and values to be made available in
       the ARGC and ARGV pre-defined AWK variables.
```

awk, a stream programming language

```
pattern {action}
```

1. Awk is column (*field*) aware:

   `$0` - the whole line
   `$1` - column one
   `$2` - column two
   …

2. `pattern` can be any logical statement:

   `$3 > 0` - if column 3 is greater than 0
   `$1 == 32` - if column 1 equals 32
   `$1 == $3` - if column 1 equals column 3
   `$1 == "consensus"` - if column 1 contains the string, "consensus"

If pattern is true, everything in {…} is executed

awk, a stream programming language

```
pattern {action}
```

Apply action to every line

```
{action}
```

Execute action once at start

```
BEGIN {action} pattern {action}
```

Execute action once at end

```
pattern {action} END {action}
```

```
BEGIN {action} pattern {action} END {action}
```

awk, a stream programming language

```
pattern {action1; action2; action3}
```

1. Built in variables

```
NR - number of records seen so far (aka line number)
NF - number of fields in the current record
FILENAME - name of the current file being read
```

2. Built in functions

```
length(x) - length of the field
print(x)  - print a field
rand()    - generate a random number
sqrt(x)   - calculate square root of x
sub(x, y) - substitute s for r in $0
```

3. User defined variables

```
increment: n  = n + 1
multiply:  n += $2 * $3
```

Find the length of the DNA sequence in each file:

Find the length of the DNA sequence in file **`scaffold_600.fa:`**

```
awk 'NR > 1 { total=total+length($0)} END{print(total)}' scaffold_600.fa
```

do not count the first line

always add the line length to **`total`**

- What is the answer?
- How would you do this for 3000 files?

Find the length of the DNA sequence in each file:

Find the length of the DNA sequence in file **`scaffold_600.fa:`**

```
awk 'NR > 1 { total=total+length($0)} END{print(total)}' scaffold_600.fa
```

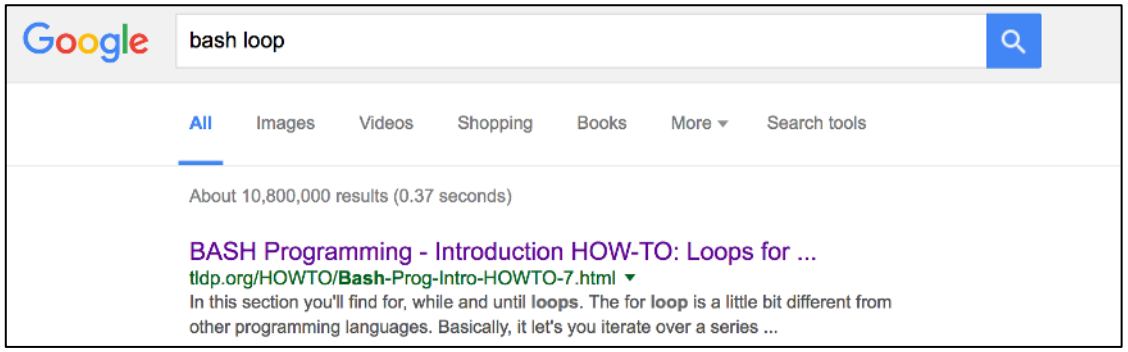
do not count the first line

always add the line length to **`total`**

- What is the answer?
- How would you do this for 3000 files?

Answer:

a shell loop



Find the length of the DNA sequence in each file:

Find the length of the DNA sequence in files **`scaffold_600.fa`** through to **`scaffold_610.fa:`**

- **`for i in {600..610}; do echo scaffold_${i}.fa; done`**

a shell variable

using the variable

Find the length of the DNA sequence in each file:

Find the length of the DNA sequence in files **`scaffold_600.fa`** through to **`scaffold_610.fa`:**

- `for i in {600..610}; do echo scaffold_${i}.fa; done`

a shell variable

using the variable

The solution is:

```
for i in {600..610}; do
echo scaffold_${i}.fa
awk 'NR > 1 { total=total+length($0)} END{print(total)}' scaffold_${i}.fa
done
```

Or, say if you want to omit `scaffold_605`, one alternative is:

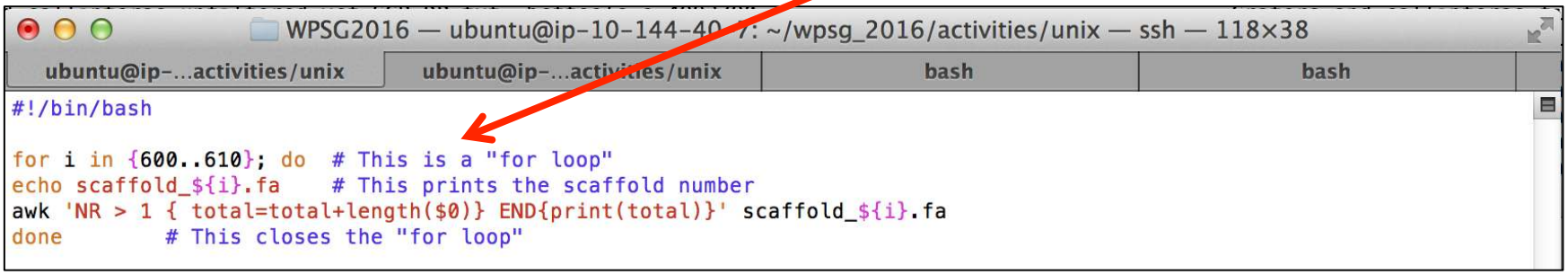
```
for i in 600 601 602 603 604 606 607 608 609 610}; do
echo scaffold_${i}.fa
awk 'NR > 1 { total=total+length($0)} END{print(total)}' scaffold_${i}.fa
done
```

But how do you write it all on one line?

Shell scripting

- Anything you can do on the shell can be placed in a shell script
- Shell scripts often end in the suffix "**.sh**"
- Comments can be written in scripts with a "**#**"
- **#!/bin/bash** must be the first line - specifies interpreter

comments in blue



Shell scripting

Emacs

Richard Stallman - 1976
Founded GNU Project

Vi

Bill Joy - 1976
BSD/Sun Microsystems

```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ man vi

VIM(1)                                  General Commands Manual                                 VIM(1)

NAME
       vim - Vi IMproved, a programmers text editor
```

Shell scripting

- **`vi <filename>`**
- **`vi /absolute/path/to/file`**
- **`vi ../../../relative/path/to/file`**

Command mode versus **Text-entry mode**

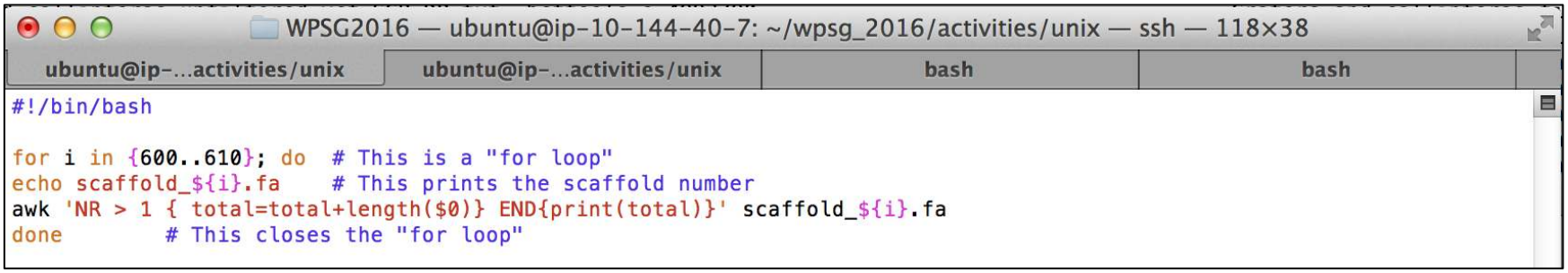
Your mouse cannot help you!

vi commands start with a colon " : "

Shell scripting

Do the following:

1. **`vi printLengths.sh`**
2. **Enter the Text-entry mode by pressing the "i" key**
3. **Write the script (the comments are optional)**

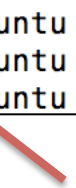


4. **exit the text-entry mode by pressing <esc>**
5. **Use the command `:w` to save (write) the file**
6. **Use the command `:q` to exit `vi`**

Get a cheat-sheet for **`vi`**, e.g.:
http://www.digilife.be/quickreferences/QRC/vi%20Quick%20Reference.pdf
A detailed guide to bash scripting:
http://tldp.org/LDP/abs/html/

Shell scripting

```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ ls -lah
total 500K
drwxrwxr-x  2 ubuntu ubuntu 4.0K Jan 24 00:29 .
drwxrwxr-x 12 ubuntu ubuntu 4.0K Jan 23 22:59 ..
-rw-rw-r--  1 ubuntu ubuntu  238 Jan 24 00:16 printLengths.sh
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:38 scaffold_600.fa
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:39 scaffold_601.fa
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:39 scaffold_602.fa
```

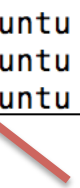


file permissions

Owner	Group	Others
rw-	rw-	r--

Shell scripting

```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ ls -lah
total 500K
drwxrwxr-x  2 ubuntu ubuntu 4.0K Jan 24 00:29 .
drwxrwxr-x 12 ubuntu ubuntu 4.0K Jan 23 22:59 ..
-rw-rw-r--  1 ubuntu ubuntu  238 Jan 24 00:16 printLengths.sh
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:38 scaffold_600.fa
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:39 scaffold_601.fa
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:39 scaffold_602.fa
```



file permissions

Owner	Group	Others
`rw-`	`rw-`	`r--`

Shell scripts must be executable: `chmod +x printLengths.sh`

```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ chmod +x printLengths.sh
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ ls -lah
total 500K
drwxrwxr-x  2 ubuntu ubuntu 4.0K Jan 24 00:29 .
drwxrwxr-x 12 ubuntu ubuntu 4.0K Jan 23 22:59 ..
-rwxrwxr-x  1 ubuntu ubuntu  238 Jan 24 00:16 printLengths.sh
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:38 scaffold_600.fa
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:39 scaffold_601.fa
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:39 scaffold_602.fa
```

Script/program execution and $PATH

Now you should be able to execute your script:

`./printLengths.sh`

executing in this folder (remember, a dot "`.`" means 'this folder')

`printLengths.sh`

will not work

`~/wpsg_2016/activities/unix` **is not in your PATH**

Script/program execution and $PATH

Now you should be able to execute your script:

`./printLengths.sh`

executing in this folder (remember, a dot " **.** " means 'this folder')

`printLengths.sh`

will not work

`~/wpsg_2016/activities/unix` **is not in your PATH**

```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ echo $PATH
/home/ubuntu/wpsg_2016/software/beast/bin:/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/usr/games:/usr
/local/games:/usr/lib/jvm/java-8-oracle/bin:/usr/lib/jvm/java-8-oracle/db/bin:/usr/lib/jvm/java-8-oracle/jre/bin
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ PATH=$PATH:~/wpsg_2016/activities/unix
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ echo $PATH
/home/ubuntu/wpsg_2016/software/beast/bin:/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/usr/games:/usr
/local/games:/usr/lib/jvm/java-8-oracle/bin:/usr/lib/jvm/java-8-oracle/db/bin:/usr/lib/jvm/java-8-oracle/jre/bin:/home
/ubuntu/wpsg_2016/activities/unix
```

Type:

`PATH=$PATH:~/wpsg_2016/activities/unix`

and try again:

`printLengths.sh`

Script/program execution and $PATH

Now you should be able to execute your script:

`./printLengths.sh`

executing in this folder (remember, a dot " **.** " means 'this folder')

`printLengths.sh`

will not work

`~/wpsg_2016/activities/unix` **is not in your PATH**

```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ echo $PATH
/home/ubuntu/wpsg_2016/software/beast/bin:/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/usr/games:/usr
/local/games:/usr/lib/jvm/java-8-oracle/bin:/usr/lib/jvm/java-8-oracle/db/bin:/usr/lib/jvm/java-8-oracle/jre/bin
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ PATH=$PATH:~/wpsg_2016/activities/unix
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ echo $PATH
/home/ubuntu/wpsg_2016/software/beast/bin:/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/usr/games:/usr
/local/games:/usr/lib/jvm/java-8-oracle/bin:/usr/lib/jvm/java-8-oracle/db/bin:/usr/lib/jvm/java-8-oracle/jre/bin:/home
/ubuntu/wpsg_2016/activities/unix
```

Type the above and try again:

`printLengths.sh`

All the software you use during this workshop has already been put in your PATH so you don't have to search for the folders where it is stored.