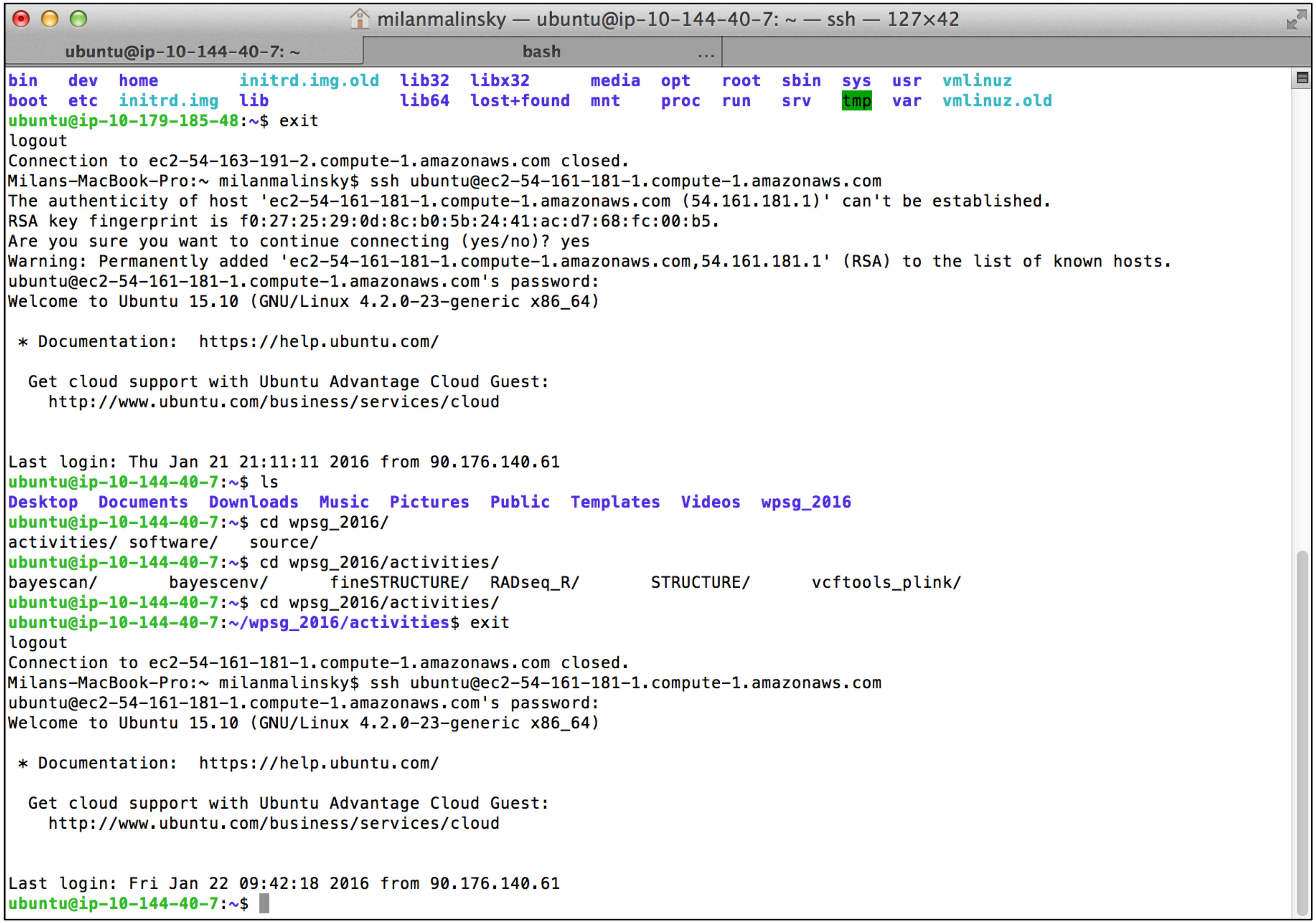
The UNIX terminal



```
bin   dev  home        initrd.img.old  lib32  libx32      media  opt   root  sbin  sys  usr  vmlinuz
boot  etc  initrd.img  lib             lib64  lost+found  mnt    proc  run   srv   tmp  var  vmlinuz.old
ubuntu@ip-10-179-185-48:~$ exit
logout
Connection to ec2-54-163-191-2.compute-1.amazonaws.com closed.
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RSA key fingerprint is f0:27:25:29:0d:8c:b0:5b:24:41:ac:d7:68:fc:00:b5.
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Last login: Thu Jan 21 21:11:11 2016 from 90.176.140.61
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Desktop  Documents  Downloads  Music  Pictures  Public  Templates  Videos  wpsg_2016
ubuntu@ip-10-144-40-7:~$ cd wpsg_2016/
activities/ software/   source/
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bayescan/       bayescenv/      fineSTRUCTURE/  RADseq_R/       STRUCTURE/      vcftools_plink/
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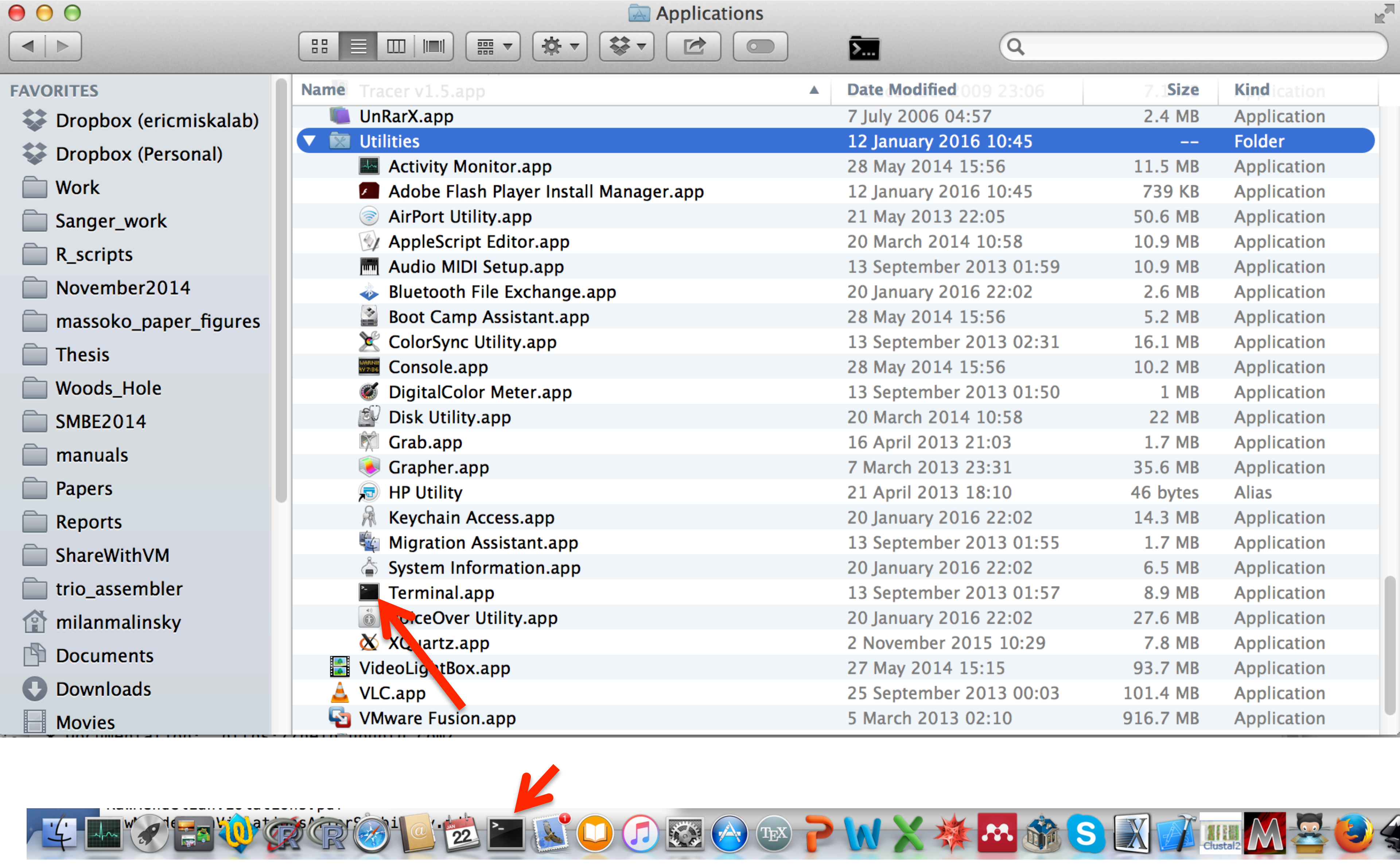
ubuntu@ip-10-144-40-7:~$ 
```

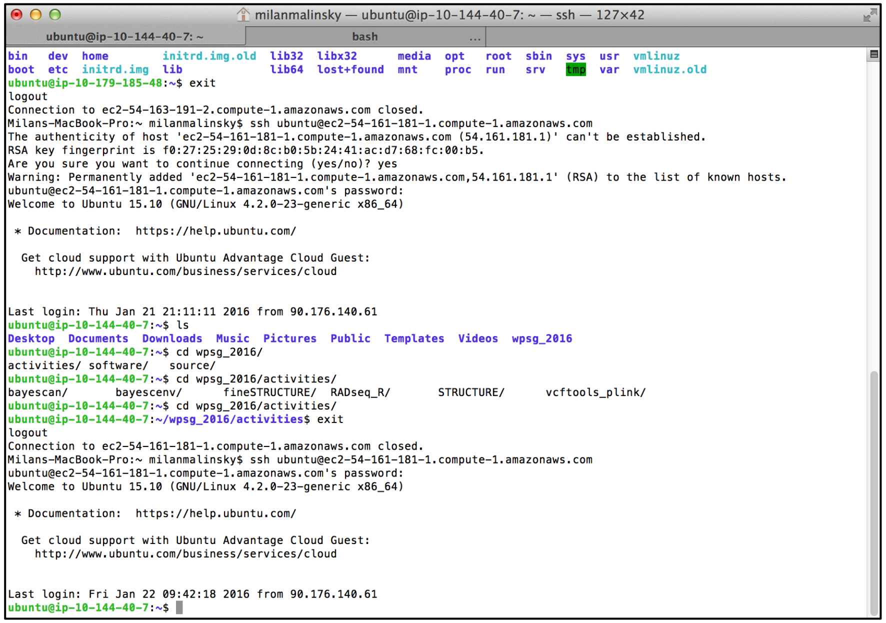
On the workshop desktop

On a Mac computer



Name	Date Modified	Size	Kind
UnRarX.app	7 July 2006 04:57	2.4 MB	Application
▼ Utilities	12 January 2016 10:45	--	Folder
Activity Monitor.app	28 May 2014 15:56	11.5 MB	Application
Adobe Flash Player Install Manager.app	12 January 2016 10:45	739 KB	Application
AirPort Utility.app	21 May 2013 22:05	50.6 MB	Application
AppleScript Editor.app	20 March 2014 10:58	10.9 MB	Application
Audio MIDI Setup.app	13 September 2013 01:59	10.9 MB	Application
Bluetooth File Exchange.app	20 January 2016 22:02	2.6 MB	Application
Boot Camp Assistant.app	28 May 2014 15:56	5.2 MB	Application
ColorSync Utility.app	13 September 2013 02:31	16.1 MB	Application
Console.app	28 May 2014 15:56	10.2 MB	Application
DigitalColor Meter.app	13 September 2013 01:50	1 MB	Application
Disk Utility.app	20 March 2014 10:58	22 MB	Application
Grab.app	16 April 2013 21:03	1.7 MB	Application
Grapher.app	7 March 2013 23:31	35.6 MB	Application
HP Utility	21 April 2013 18:10	46 bytes	Alias
Keychain Access.app	20 January 2016 22:02	14.3 MB	Application
Migration Assistant.app	13 September 2013 01:55	1.7 MB	Application
System Information.app	20 January 2016 22:02	6.5 MB	Application
Terminal.app	13 September 2013 01:57	8.9 MB	Application
VoiceOver Utility.app	20 January 2016 22:02	27.6 MB	Application
XQuartz.app	2 November 2015 10:29	7.8 MB	Application
VideoLightBox.app	27 May 2014 15:15	93.7 MB	Application
VLC.app	25 September 2013 00:03	101.4 MB	Application
VMware Fusion.app	5 March 2013 02:10	916.7 MB	Application

Why use something from the 1960s?



```
bin   dev  home        initrd.img.old  lib32  libx32      media  opt   root  sbin  sys  usr  vmlinuz
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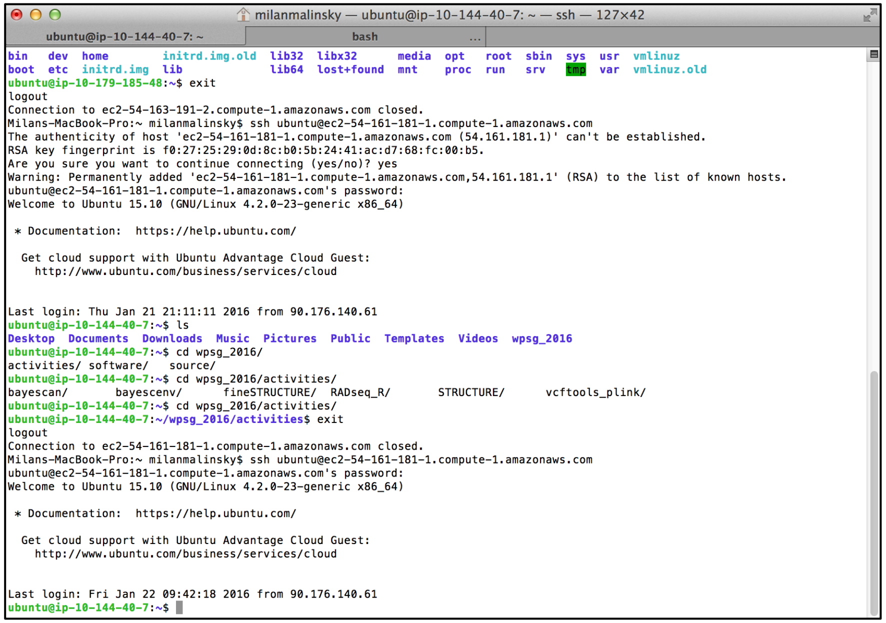

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bin   dev  home        initrd.img.old  lib32  libx32      media  opt   root  sbin  sys  usr  vmlinuz
boot  etc  initrd.img  lib             lib64  lost+found  mnt    proc  run   srv   tmp  var  vmlinuz.old
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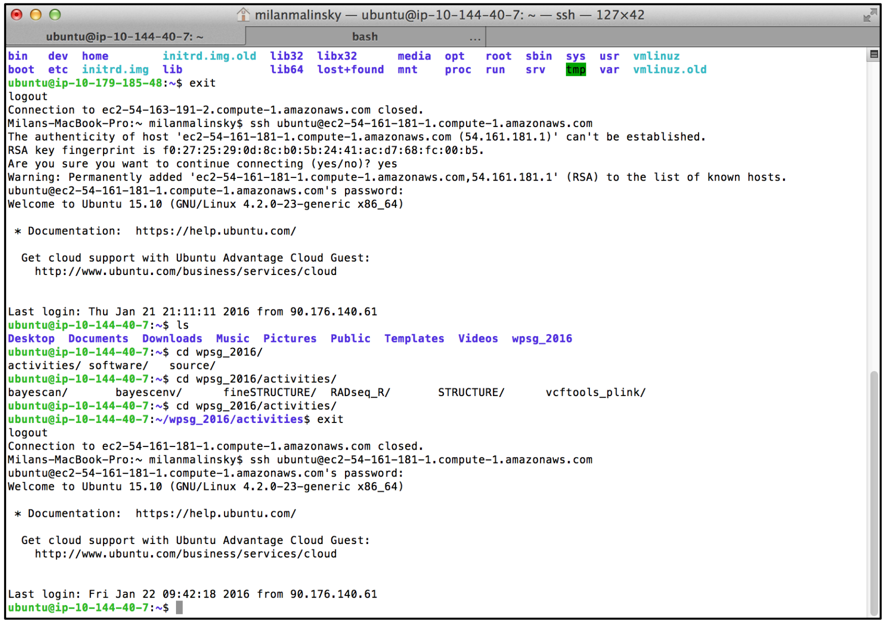

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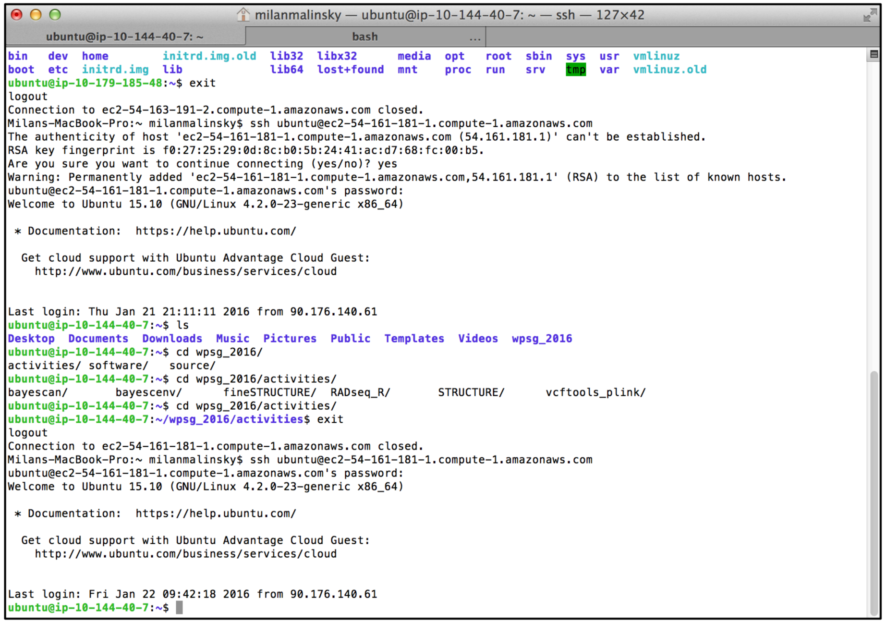

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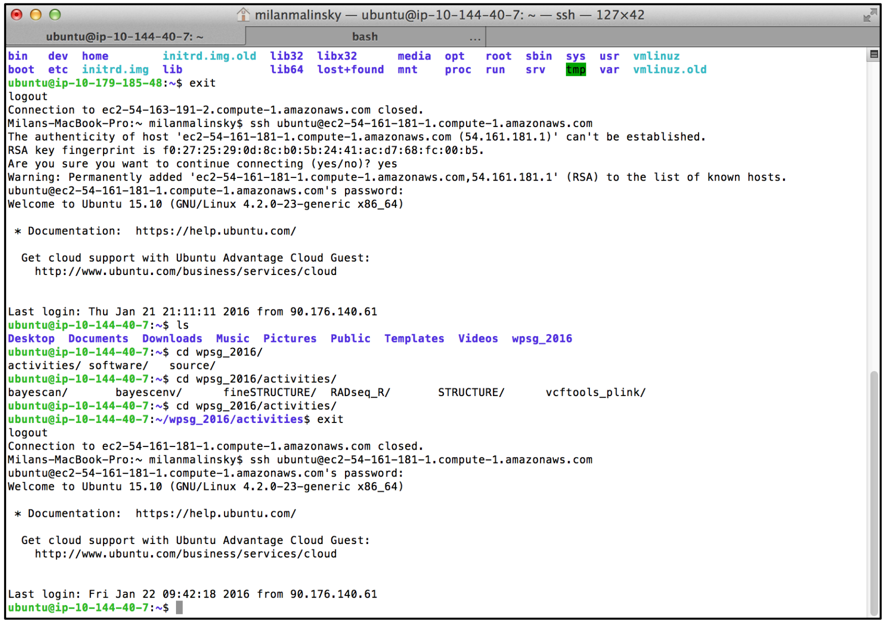

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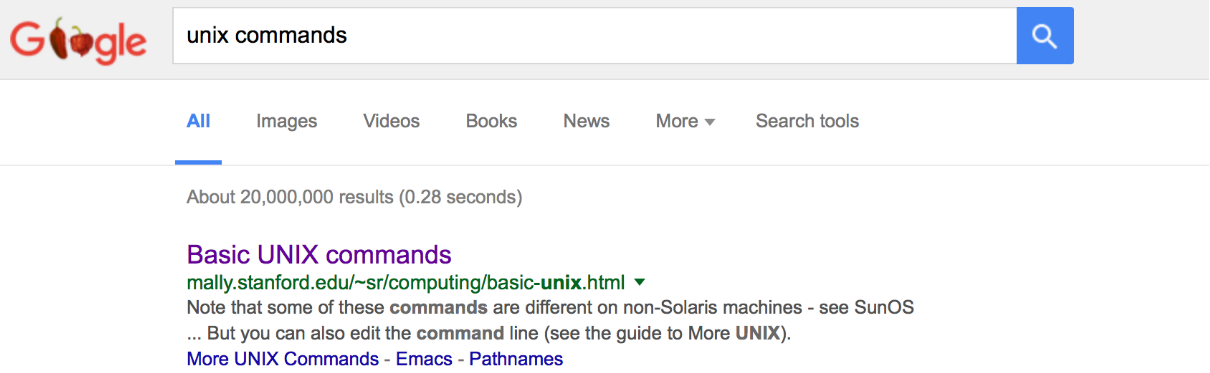
Powerful tools available in UNIX: enabling you to work through large amounts of files, data, and tasks quickly in an automated (programmatic) way

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

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

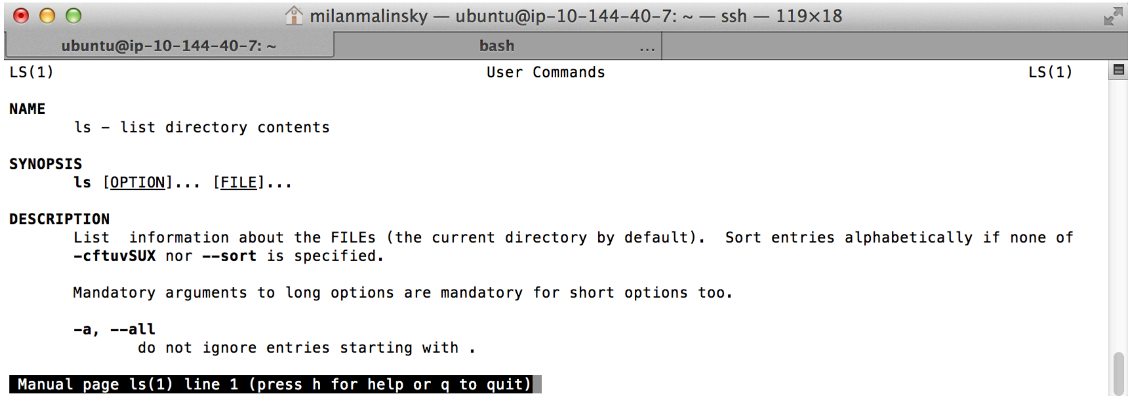


About 20,000,000 results (0.28 seconds)

Basic UNIX commands
mally.stanford.edu/~sr/computing/basic-**unix**.html
Note that some of these **commands** are different on non-Solaris machines - see SunOS
... But you can also edit the **command** line (see the guide to More **UNIX**).
More UNIX Commands - Emacs - Pathnames

2. Manual pages for each command:

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



```
LS(1)                                   User Commands                                   LS(1)

NAME
       ls - list directory contents

SYNOPSIS
       ls [OPTION]... [FILE]...

DESCRIPTION
       List  information about the FILEs (the current directory by default).  Sort entries alphabetically if none of
       -cftuvSUX nor --sort is specified.

       Mandatory arguments to long options are mandatory for short options too.

       -a, --all
              do not ignore entries starting with .

 Manual page ls(1) line 1 (press h for help or q to quit)
```

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
```

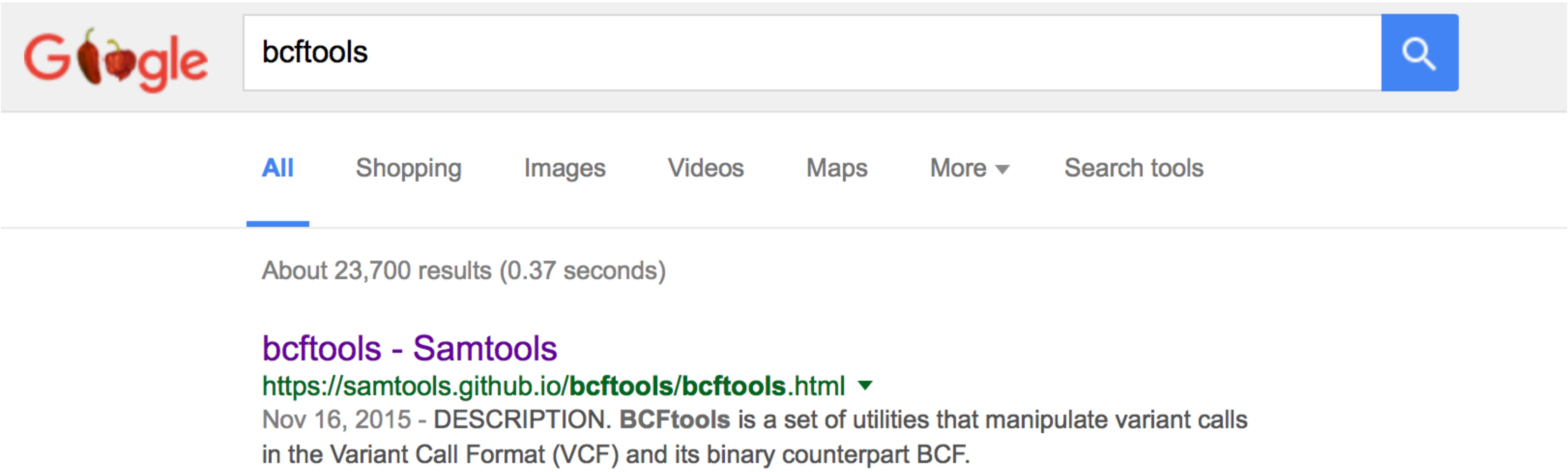
or

```
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:



bcftools

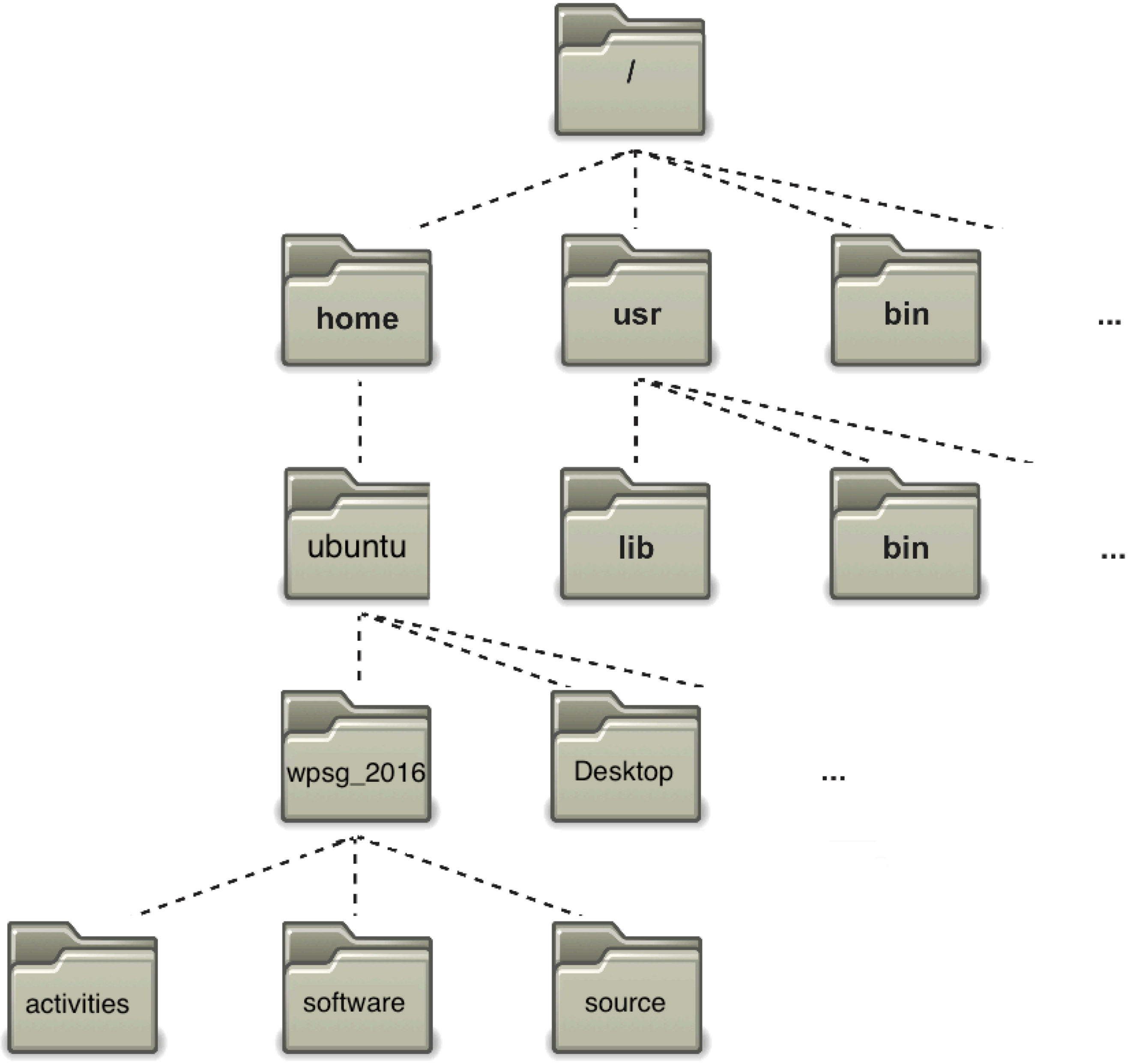
About 23,700 results (0.37 seconds)

bcftools - Samtools

https://samtools.github.io/**bcftools**/**bcftools**.html

Nov 16, 2015 - DESCRIPTION. **BCFtools** is a set of utilities that manipulate variant calls in the Variant Call Format (VCF) and its binary counterpart BCF.

UNIX directory structure



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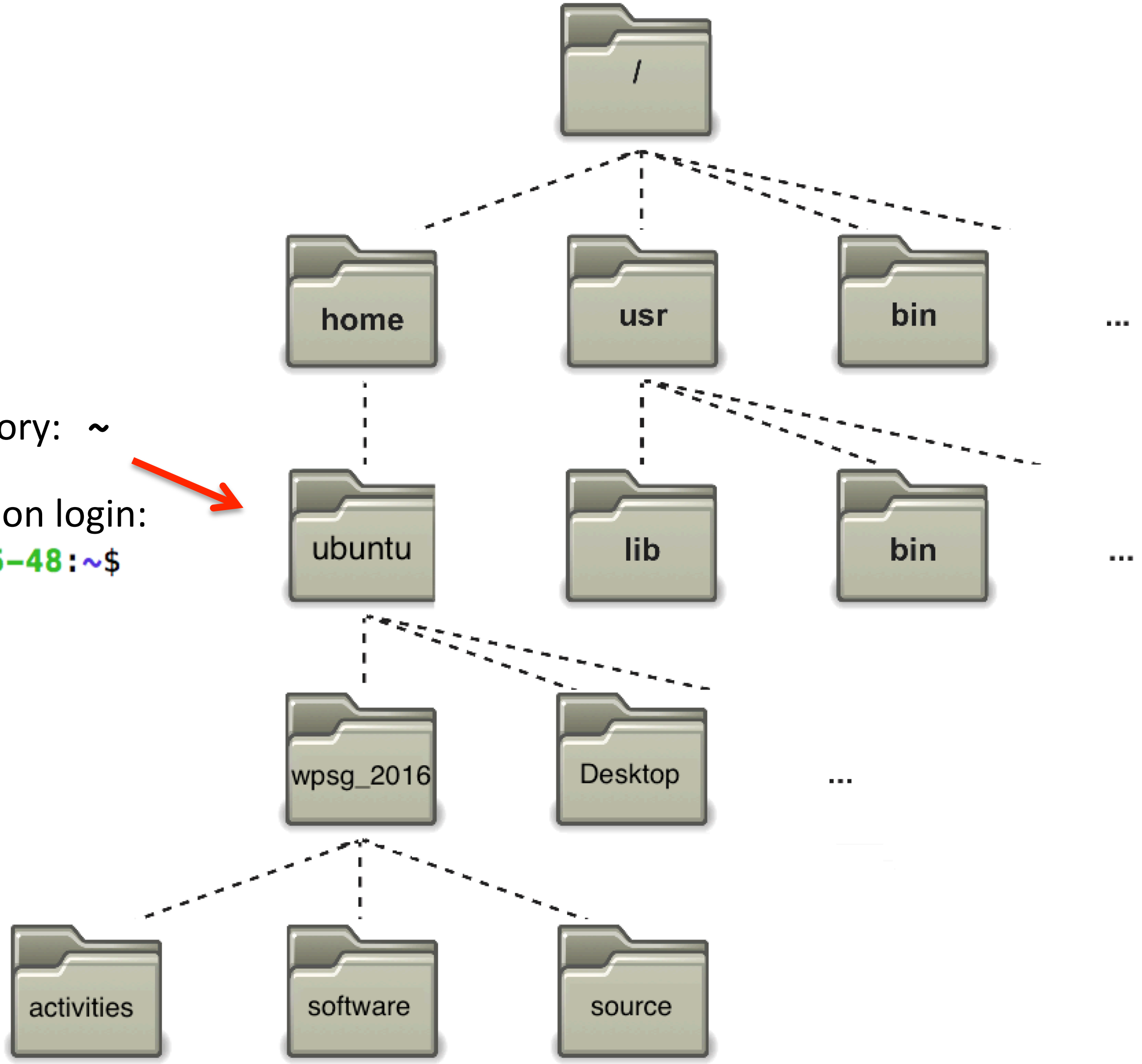


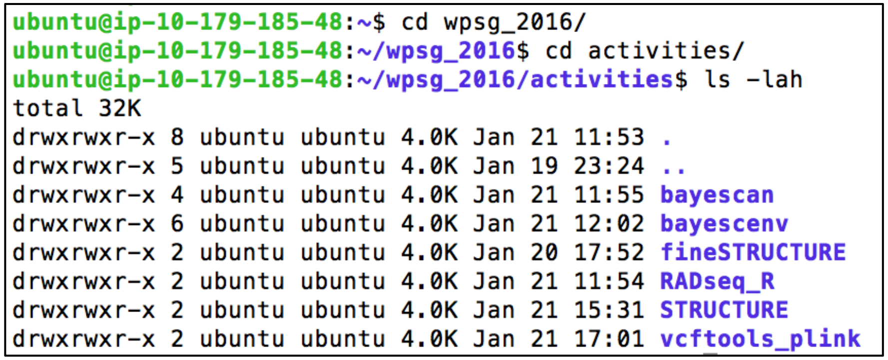
Home Directory: ~

That’s where you are upon login:

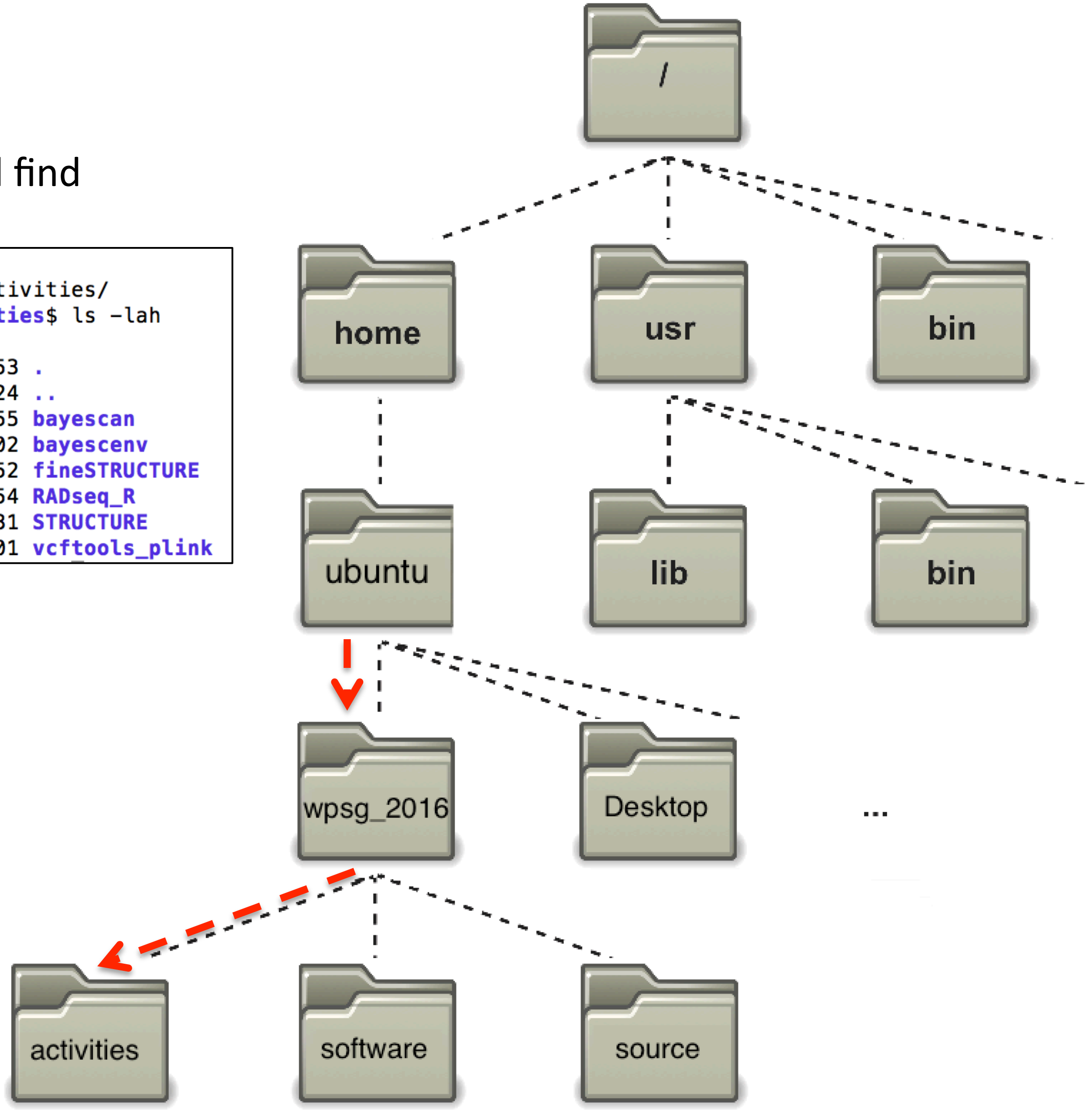
```
ubuntu@ip-10-179-185-48:~$
```

UNIX directory structure

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

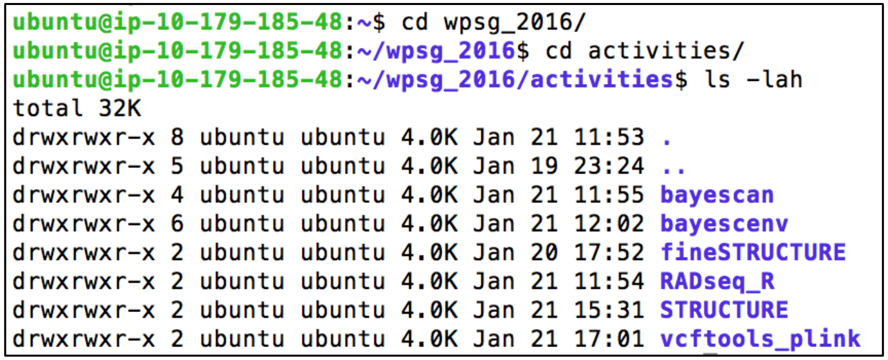


```
ubuntu@ip-10-179-185-48:~$ cd wpsg_2016/
ubuntu@ip-10-179-185-48:~/wpsg_2016$ cd activities/
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ ls -lah
total 32K
drwxrwxr-x 8 ubuntu ubuntu 4.0K Jan 21 11:53 .
drwxrwxr-x 5 ubuntu ubuntu 4.0K Jan 19 23:24 ..
drwxrwxr-x 4 ubuntu ubuntu 4.0K Jan 21 11:55 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

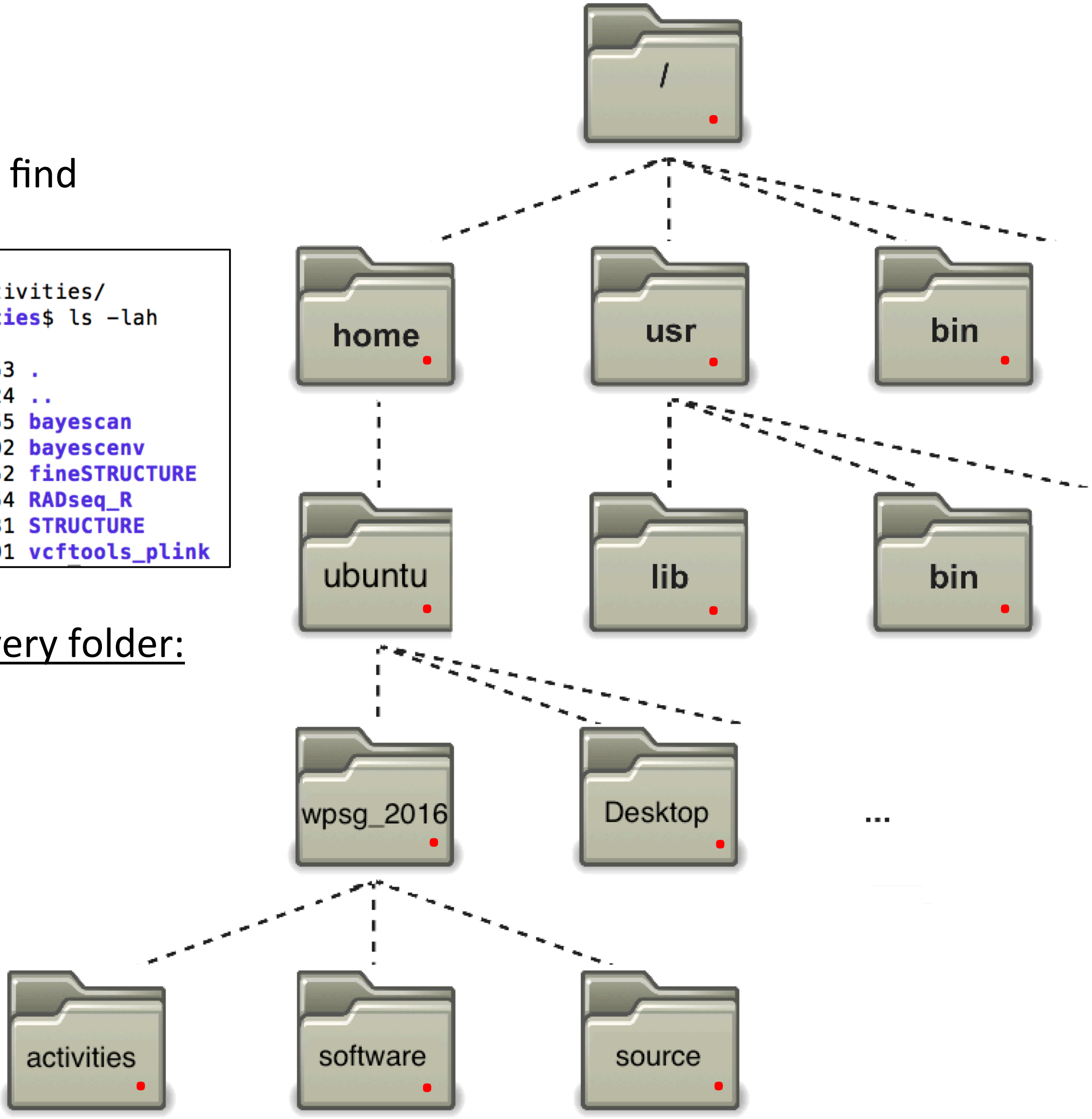
Go to the ‘activities’ folder and find what is in there:



```
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
```

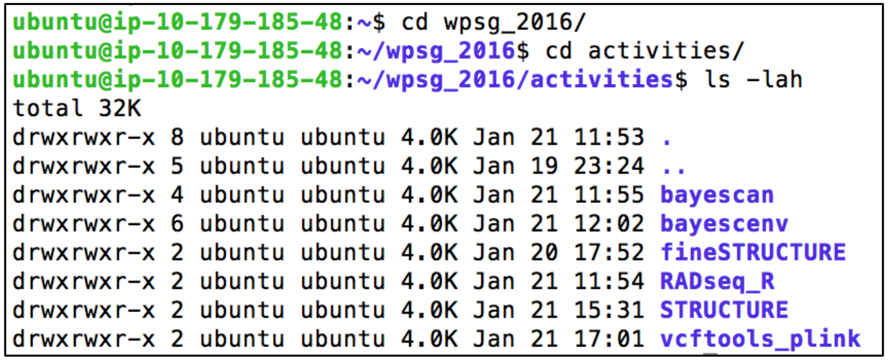
<u>Two special ‘files’ present in every folder:</u>

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
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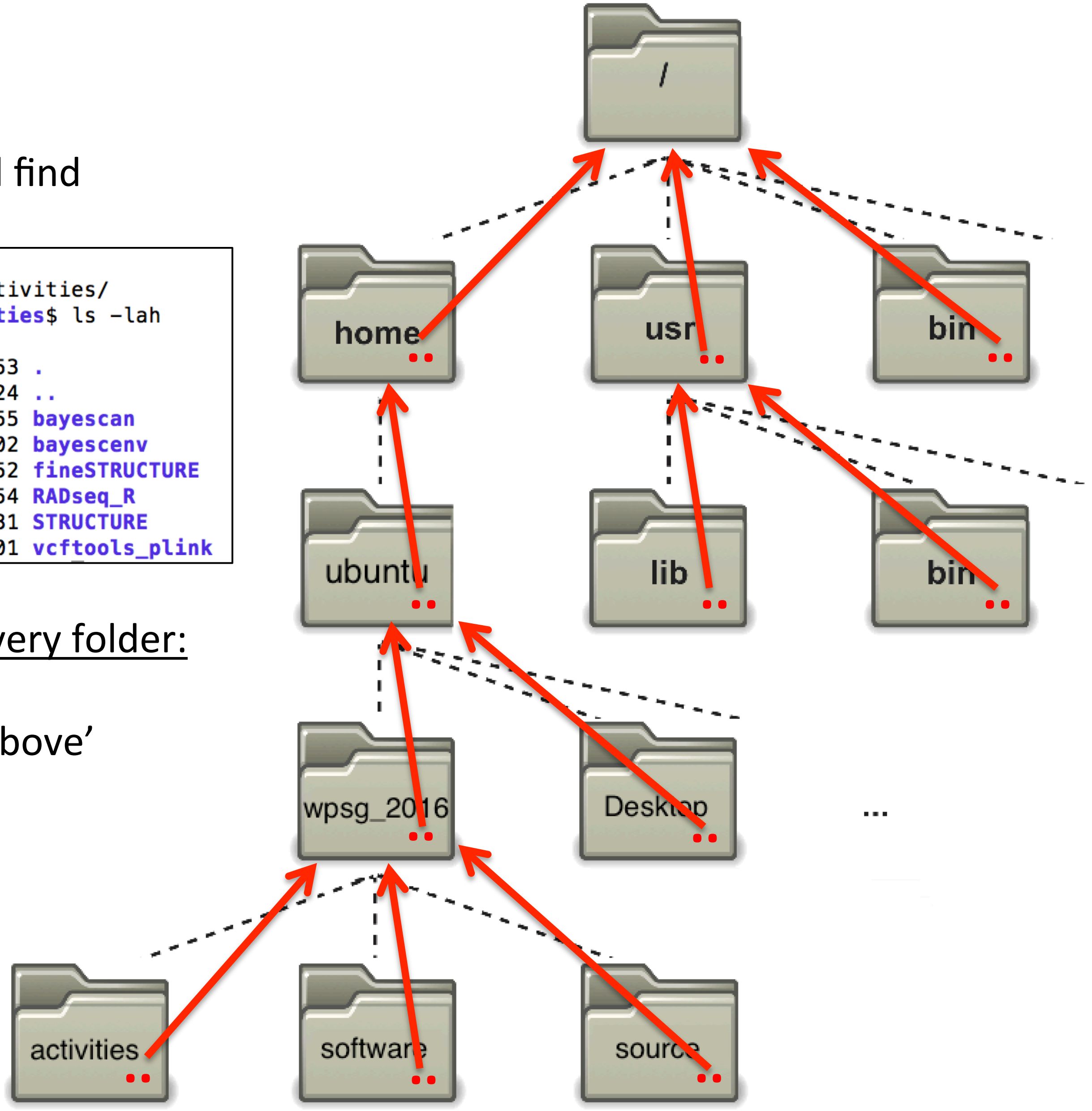
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 15:31 STRUCTURE
drwxrwxr-x 2 ubuntu ubuntu 4.0K Jan 21 17:01 vcftools_plink
```

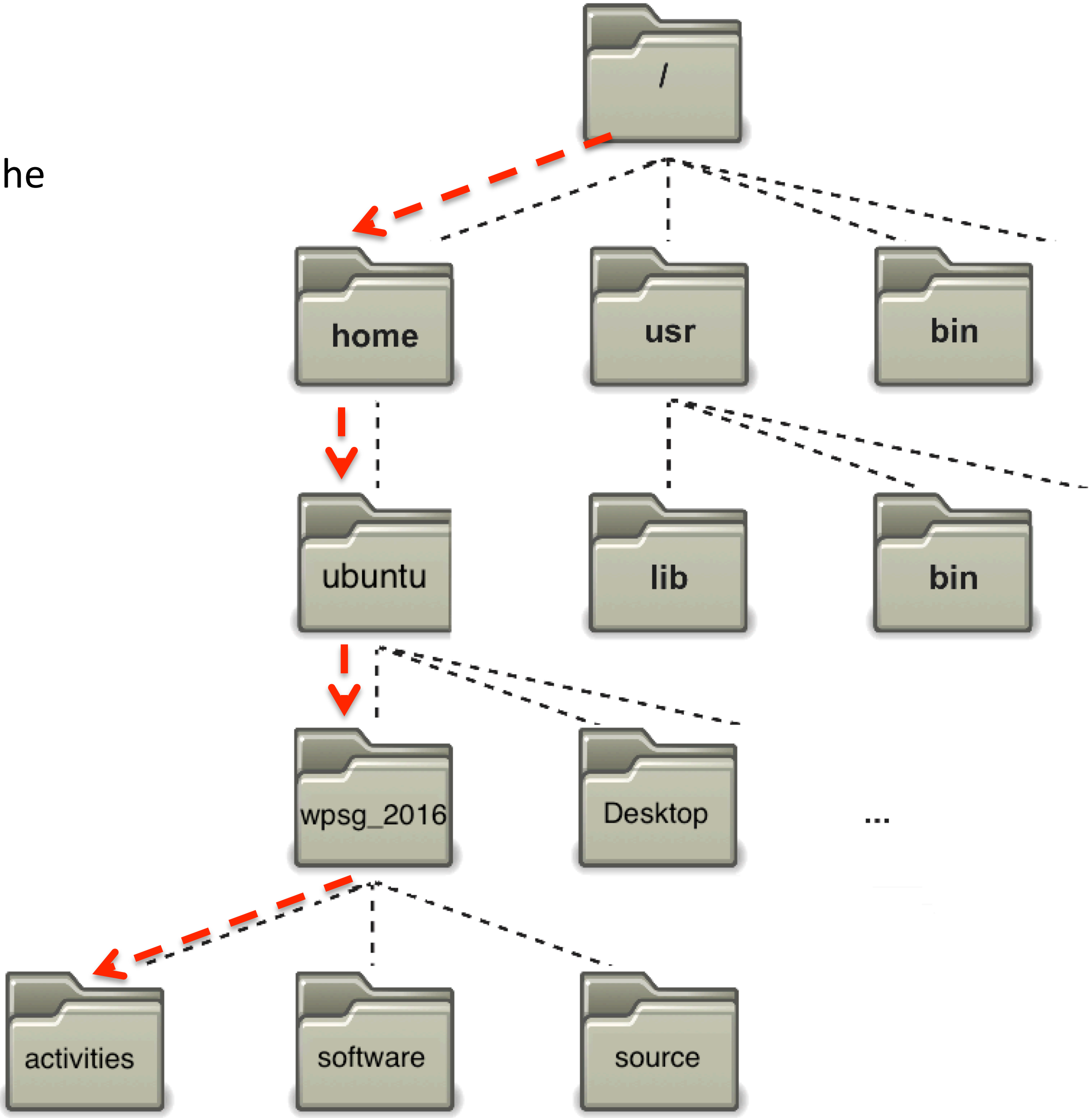
Two special ‘files’ present in every folder:

1) dot - means ‘this directory’
2) dot dot - mean ‘directory above’



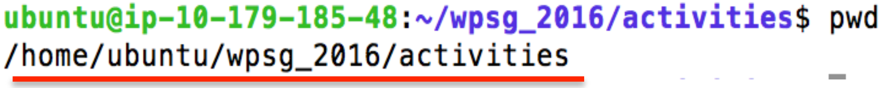
UNIX directory structure

What is the 'absolute path' to the activities folder?

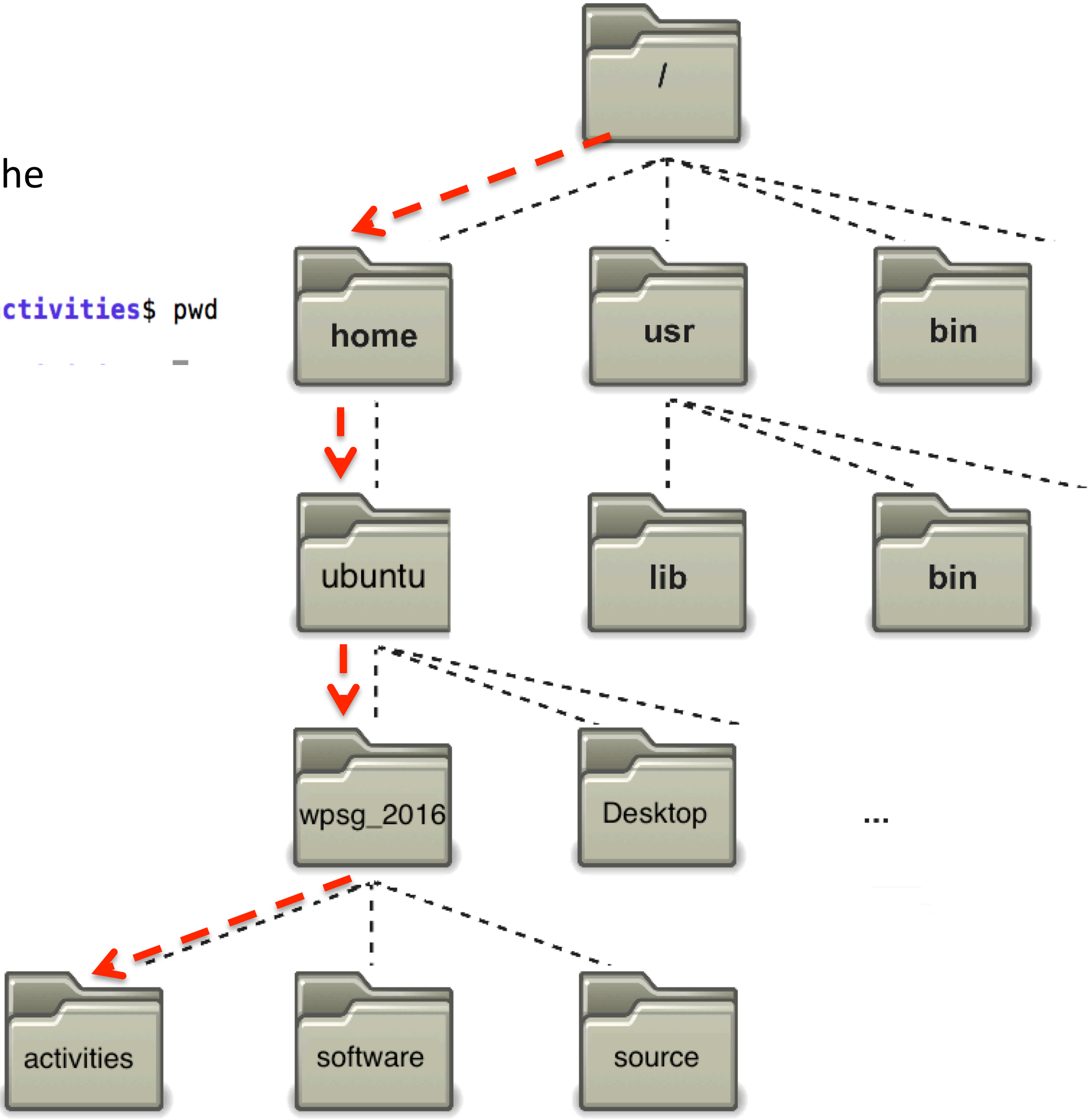


UNIX directory structure

What is the 'absolute path' to the activities folder?

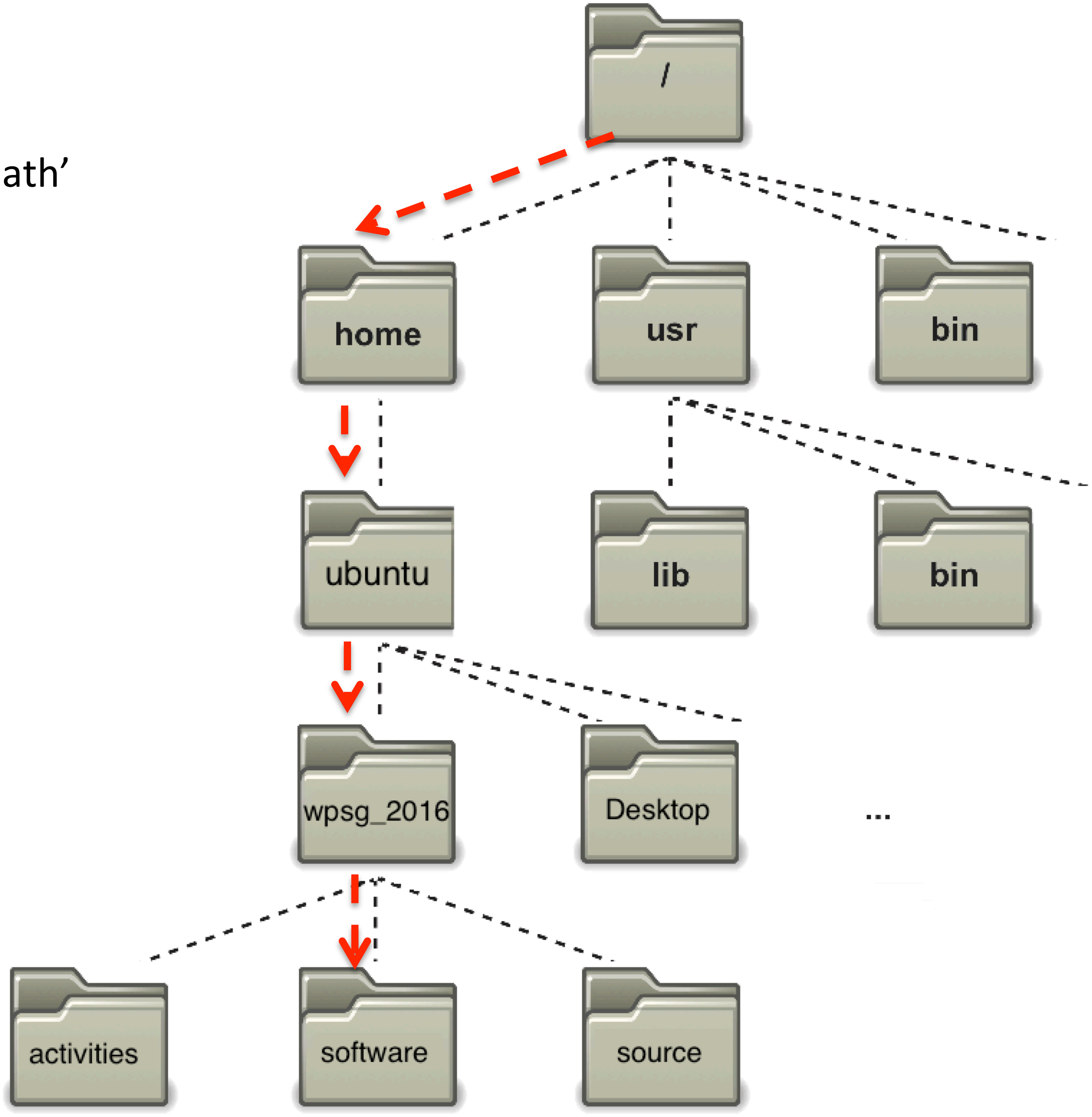


```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ pwd
/home/ubuntu/wpsg_2016/activities
```



UNIX directory structure

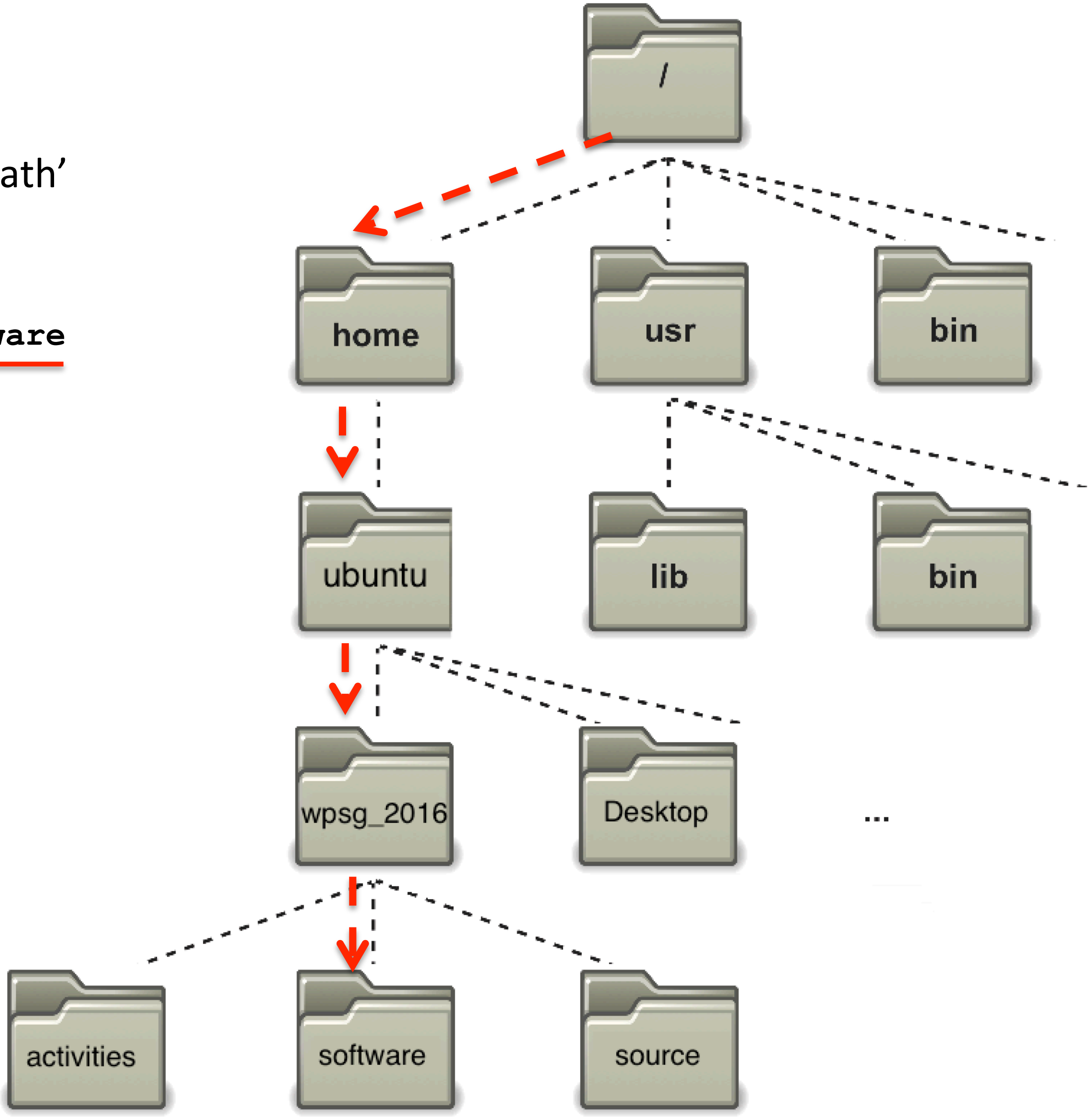
What would be the ‘absolute path’ to the ‘software’ folder?



UNIX directory structure

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

`/home/ubuntu/wpsg_2016/software`

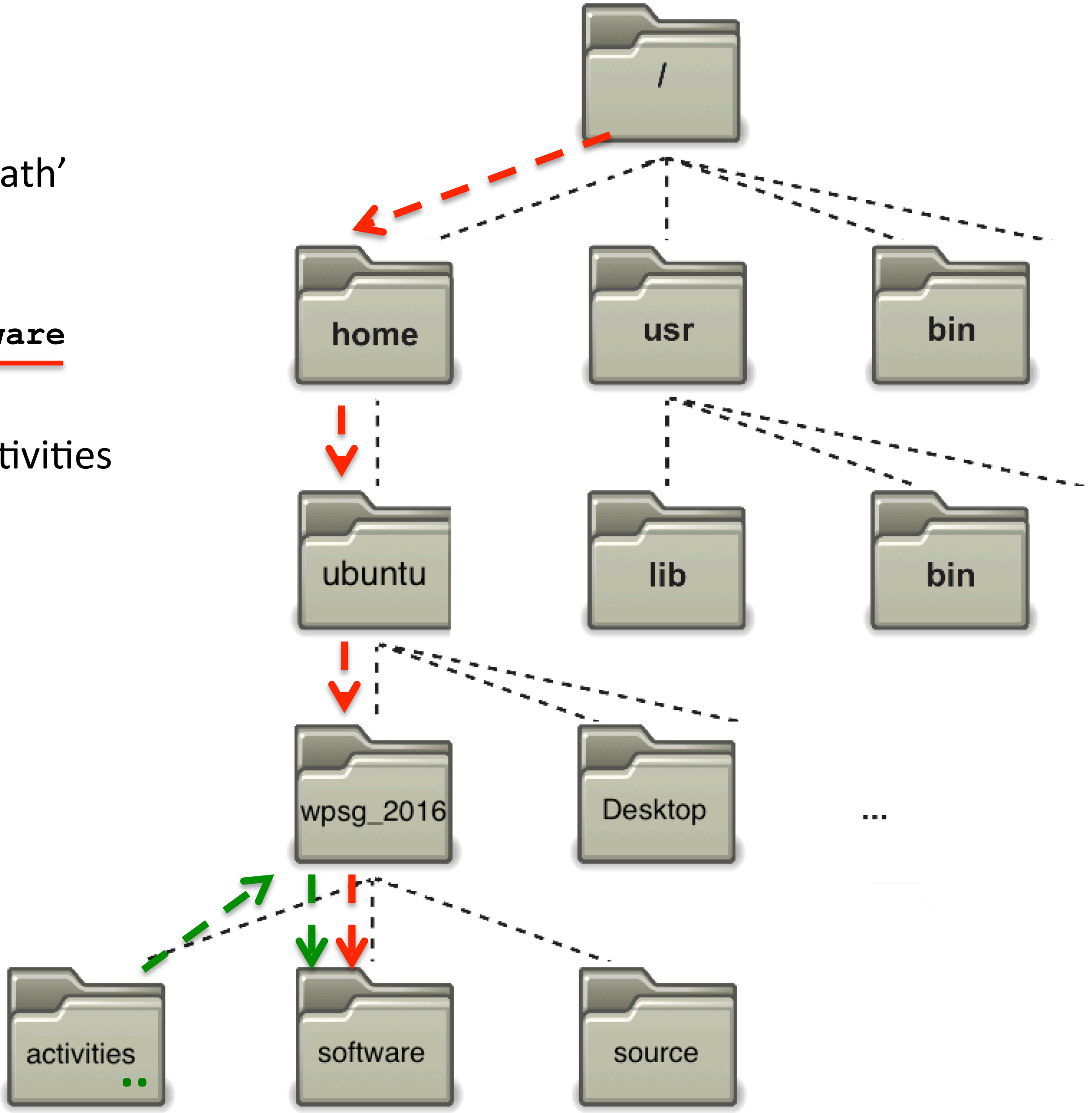


UNIX directory structure

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?



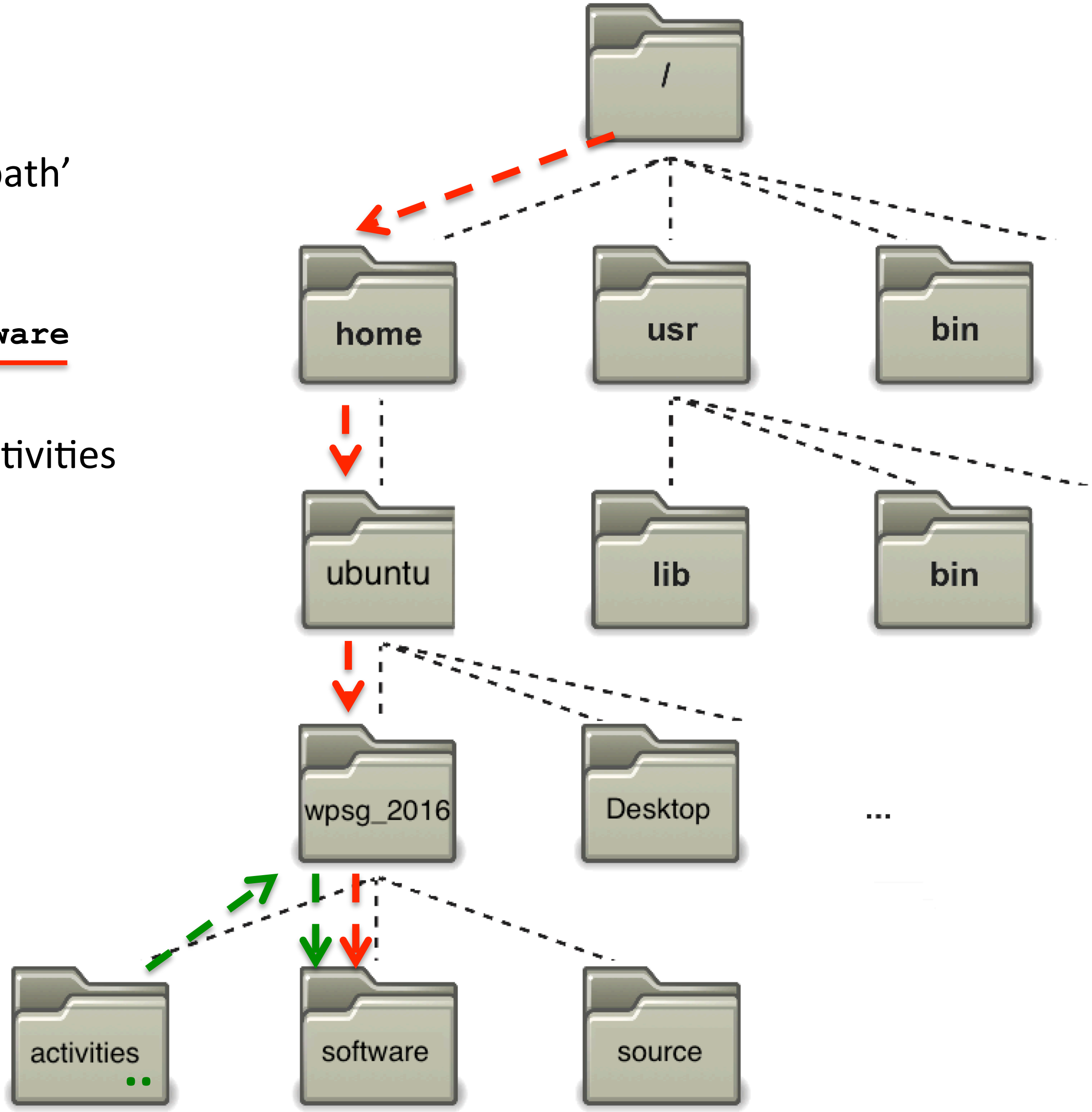
UNIX directory structure

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

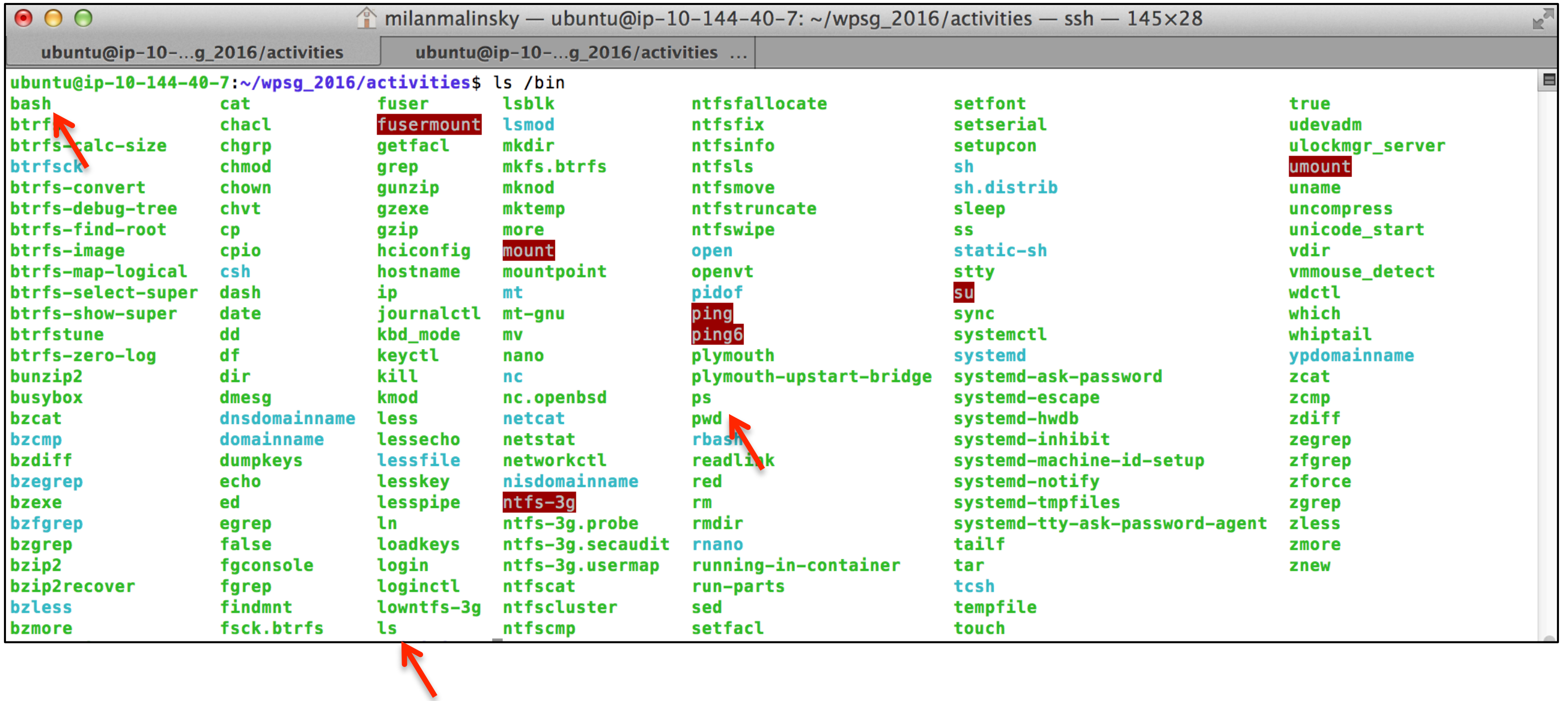
`/home/ubuntu/wpsg_2016/software`

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

`../software`



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



```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities$ ls /bin
bash                cat            fuser       lsblk             ntfsfallocate            setfont                         true
btrfs               chacl          fusermount  lsmod             ntfsfix                  setserial                       udevadm
btrfs-calc-size     chgrp          getfacl     mkdir             ntfsinfo                 setupcon                        ulockmgr_server
btrfsck             chmod          grep        mkfs.btrfs        ntfsls                   sh                              umount
btrfs-convert       chown          gunzip      mknod             ntfsmove                 sh.distrib                      uname
btrfs-debug-tree    chvt           gzexe       mktemp            ntfstruncate             sleep                           uncompress
btrfs-find-root     cp             gzip        more              ntfswipe                 ss                              unicode_start
btrfs-image         cpio           hciconfig   mount             open                     static-sh                       vdir
btrfs-map-logical   csh            hostname    mountpoint        openvt                   stty                            vmmouse_detect
btrfs-select-super  dash           ip          mt                pidof                    su                              wdctl
btrfs-show-super    date           journalctl  mt-gnu            ping                     sync                            which
btrfstune           dd             kbd_mode    mv                ping6                    systemctl                       whiptail
btrfs-zero-log      df             keyctl      nano              plymouth                 systemd                         ypdomainname
bunzip2             dir            kill        nc                plymouth-upstart-bridge  systemd-ask-password            zcat
busybox             dmesg          kmod        nc.openbsd        ps                       systemd-escape                  zcmp
bzcat               dnsdomainname  less        netcat            pwd                      systemd-hwdb                    zdiff
bzcmp               domainname     lessecho    netstat           rbash                    systemd-inhibit                 zegrep
bzdiff              dumpkeys       lessfile    networkctl        readlink                 systemd-machine-id-setup        zfgrep
bzegrep             echo           lesskey     nisdomainname     red                      systemd-notify                  zforce
bzexe               ed             lesspipe    ntfs-3g           rm                       systemd-tmpfiles                zgrep
bzfgrep             egrep          ln          ntfs-3g.probe     rmdir                    systemd-tty-ask-password-agent  zless
bzgrep              false          loadkeys    ntfs-3g.secaudit  rnano                    tailf                           zmore
bzip2               fgconsole      login       ntfs-3g.usermap   running-in-container     tar                             znew
bzip2recover        fgrep          loginctl    ntfscat           run-parts                tcsh
bzless              findmnt        lowntfs-3g  ntfscluster       sed                      tempfile
bzmore              fsck.btrfs     ls          ntfscmp           setfacl                  touch
```

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

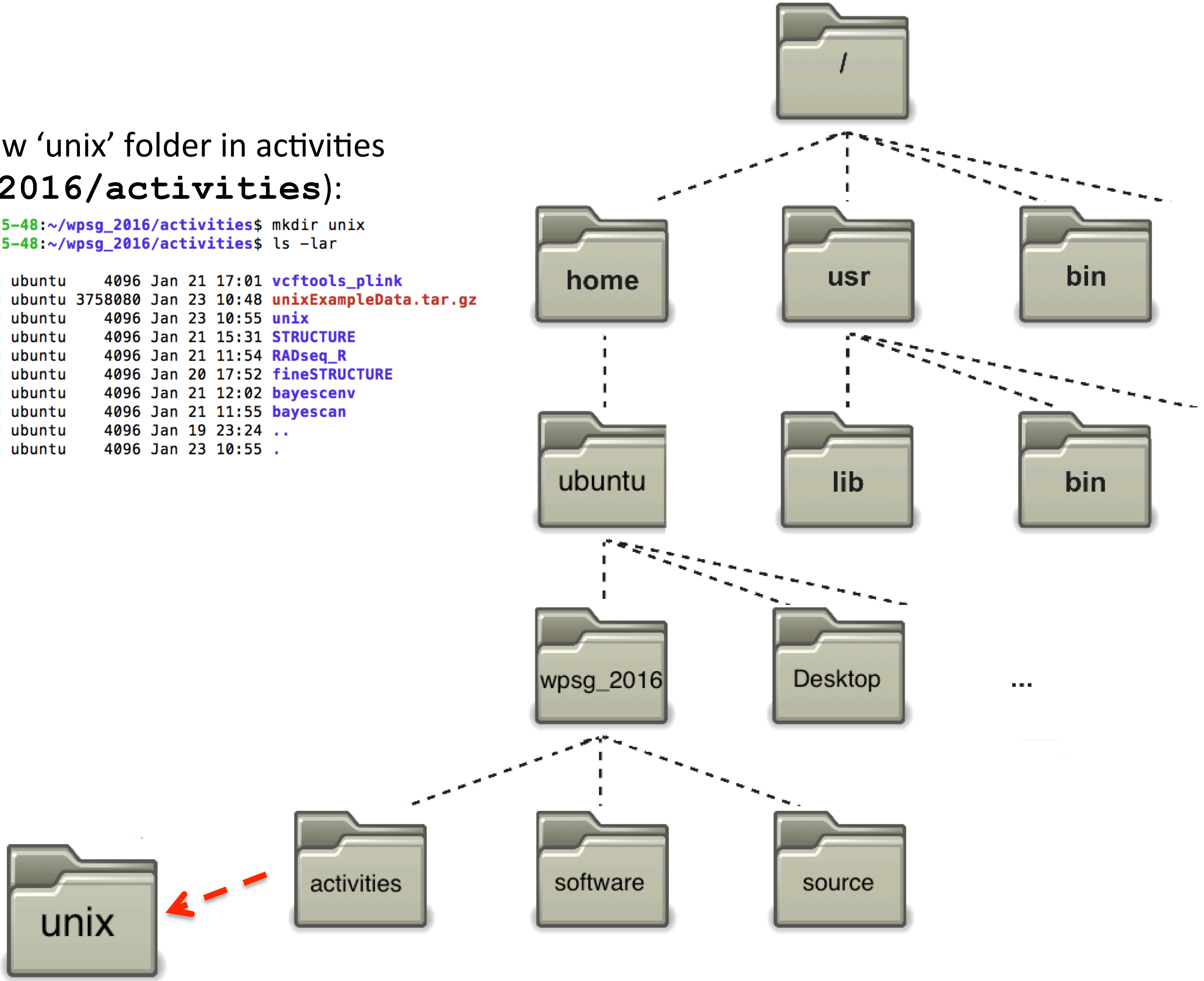
Try:

```
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

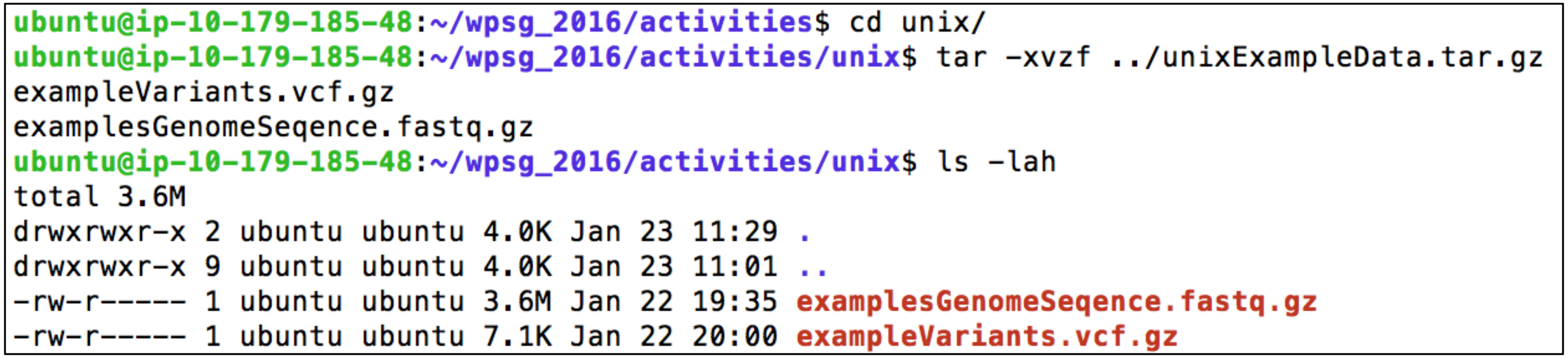
Extracting example data into the new **`unix`** folder:

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`



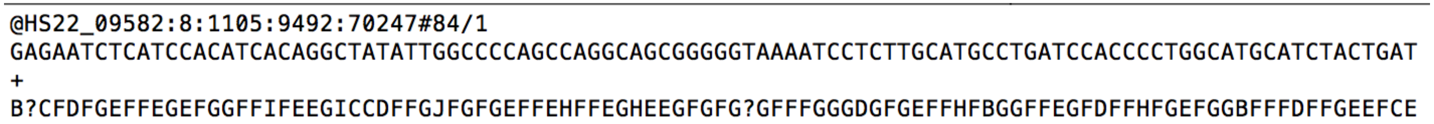
```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities$ cd unix/
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ tar -xvzf ../unixExampleData.tar.gz
exampleVariants.vcf.gz
examplesGenomeSeqence.fastq.gz
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ ls -lah
total 3.6M
drwxrwxr-x 2 ubuntu ubuntu 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:

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- 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

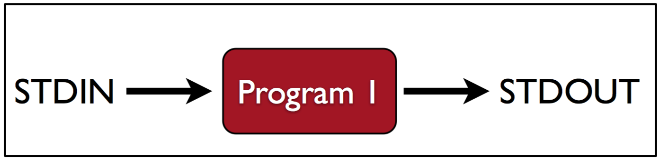
Working with the VCF variants file:

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

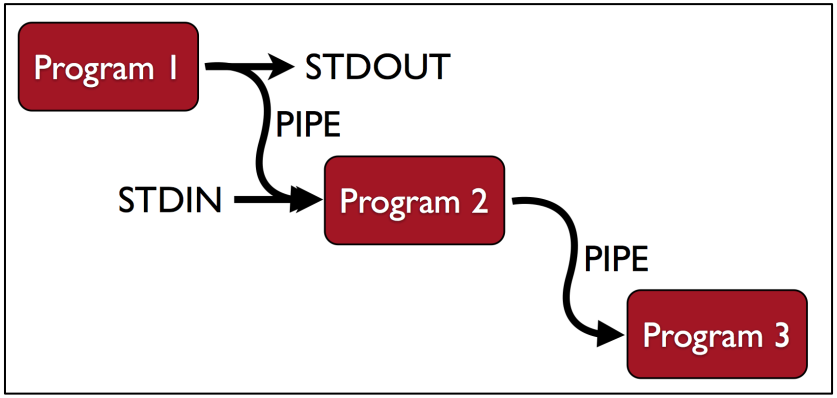
We will use one of UNIX's cool features: Pipes

So far we have been doing this:



STDIN → Program 1 → STDOUT

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



Program 1 → STDOUT

PIPE

STDIN → Program 2

PIPE

Program 3

Working with the VCF variants file:

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

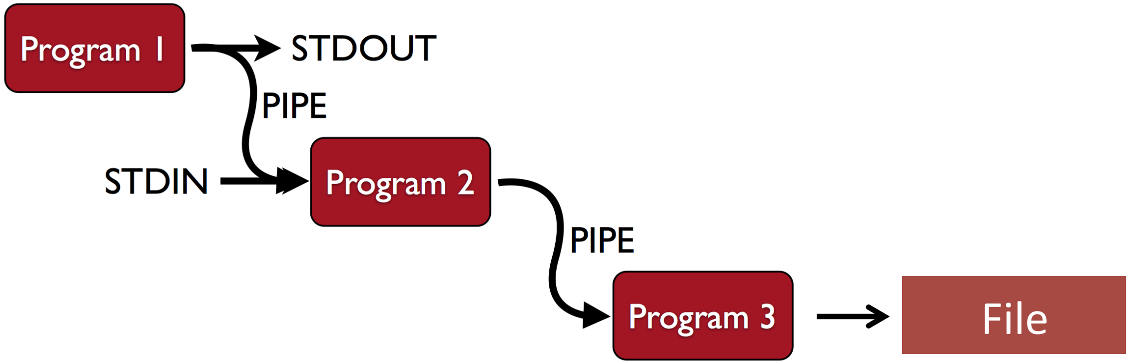
- columns 1-8: information about a variant (location, alleles, quality scores, filtering, etc.)
- columns 9 onwards: information about the genotypes (variants) present in each individual

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:

   a pipe

    - `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:

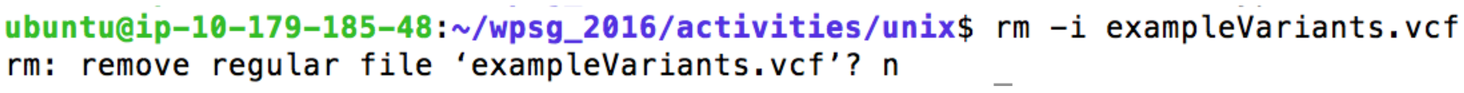


5. Capture the genotype information for the first three individuals into a different file:
   - `cut -f 10-12 exampleVariants.vcf > threeGenotypes.txt`
6. Remove the newly created file:
   - `rm threeGenotypes.txt`

!!!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)

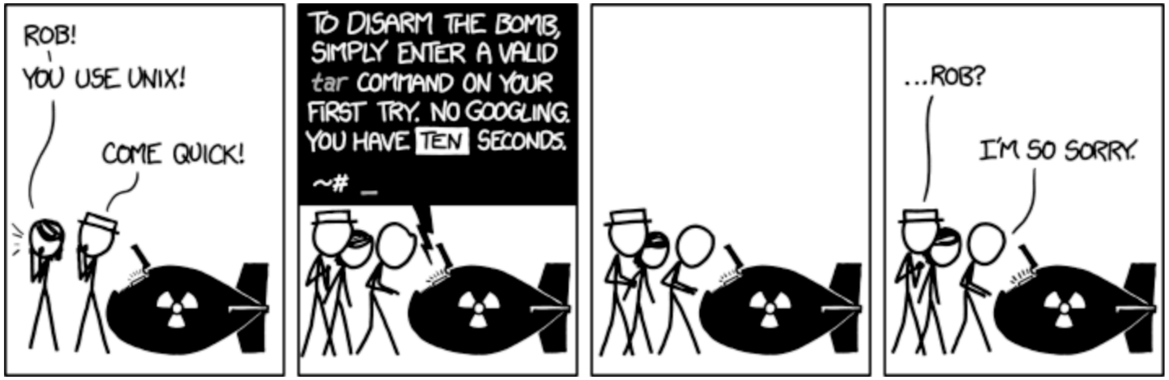


```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ rm -i exampleVariants.vcf
rm: remove regular file ‘exampleVariants.vcf’? n
```

Using a second set of example data:

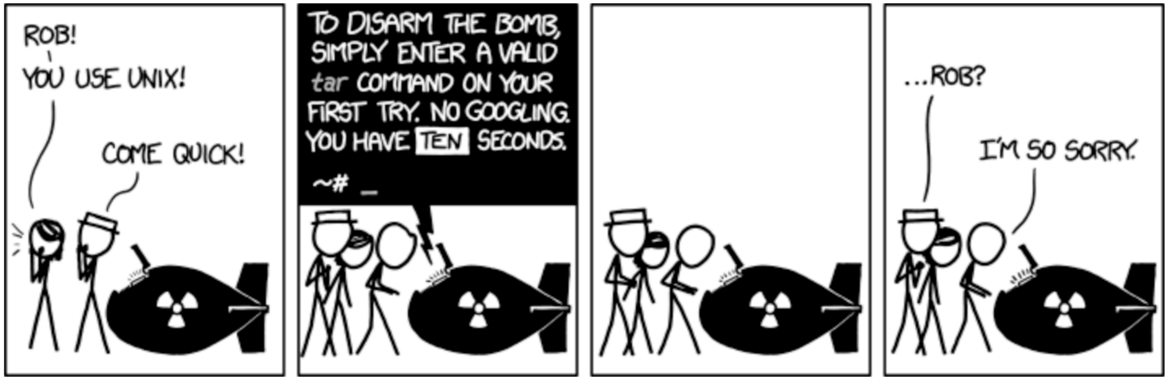
The example data are in the following compressed tar file:

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

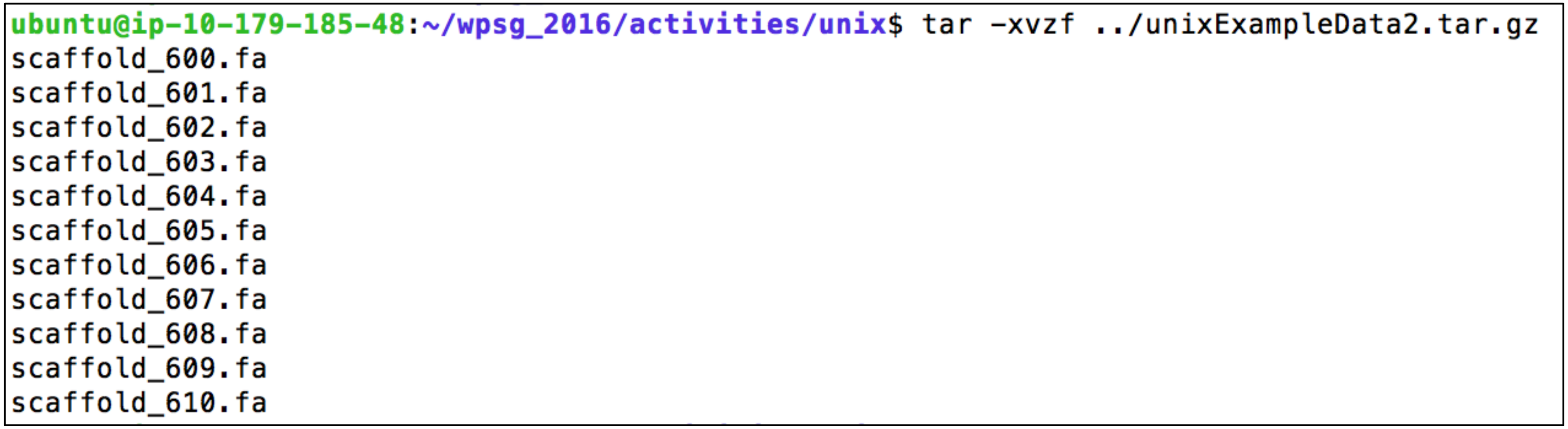


Using a second set of example data:

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:

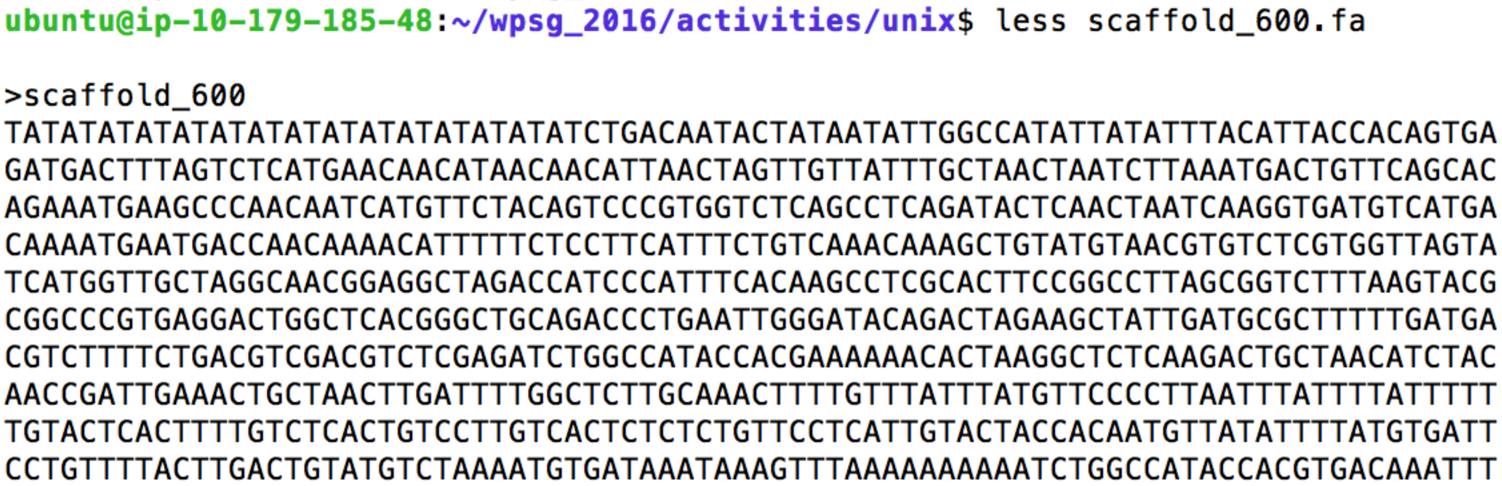


```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ tar -xvzf ../unixExampleData2.tar.gz
scaffold_600.fa
scaffold_601.fa
scaffold_602.fa
scaffold_603.fa
scaffold_604.fa
scaffold_605.fa
scaffold_606.fa
scaffold_607.fa
scaffold_608.fa
scaffold_609.fa
scaffold_610.fa
```

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:



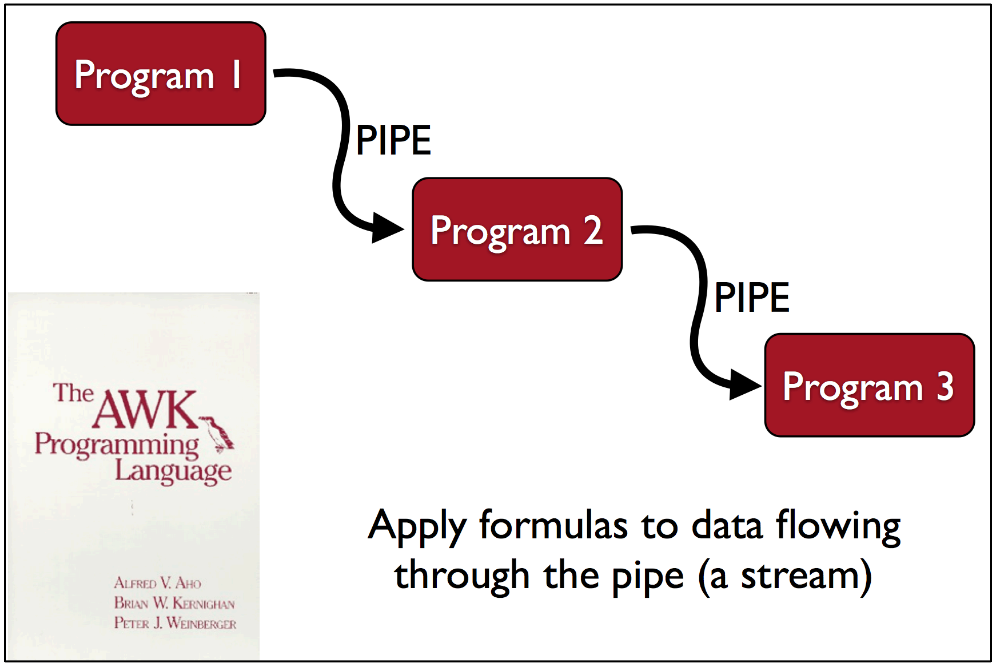
```
ubuntu@ip-10-179-185-48:~/wpsg_2016/activities/unix$ less scaffold_600.fa

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

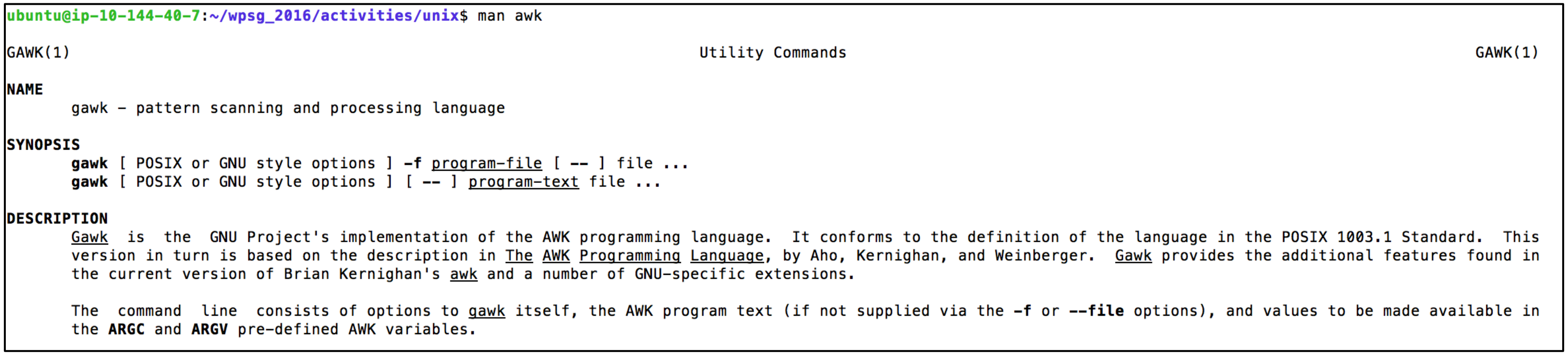
How would you:
1) find the length of the DNA sequence in each file?
2) edit the header line of each file to read "**`chromosome_`**" instead of "**`scaffold_`**"?
3) What if you had 3000 such files?

Find the length of the DNA sequence in each file:

One solution is to use `awk` :



Apply formulas to data flowing through the pipe (a stream)



```
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`**:

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awk 'NR > 1 { total=total+length($0)} END{print(total)}' scaffold_600.fa
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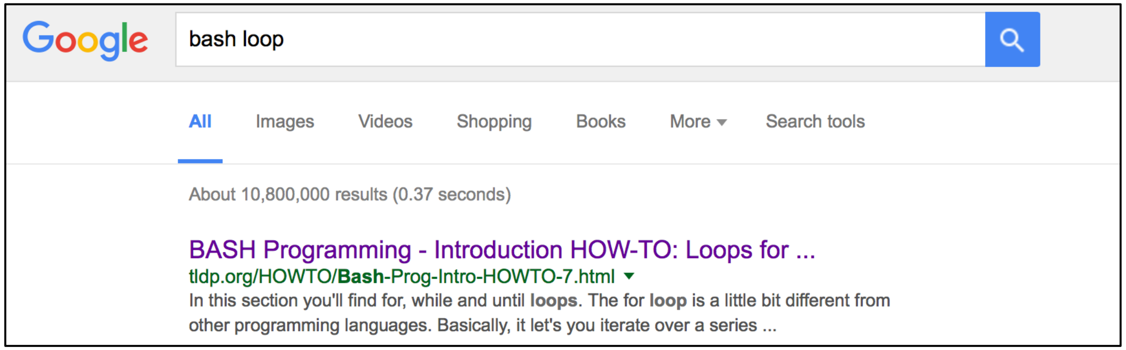
always add the line length to **`total`**

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

Answer:

a shell loop



About 10,800,000 results (0.37 seconds)

BASH Programming - Introduction HOW-TO: Loops for ...
tldp.org/HOWTO/**Bash**-Prog-Intro-HOWTO-7.html
In this section you'll find for, while and until **loops**. The for **loop** is a little bit different from other programming languages. Basically, it let's you iterate over a series ...

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:

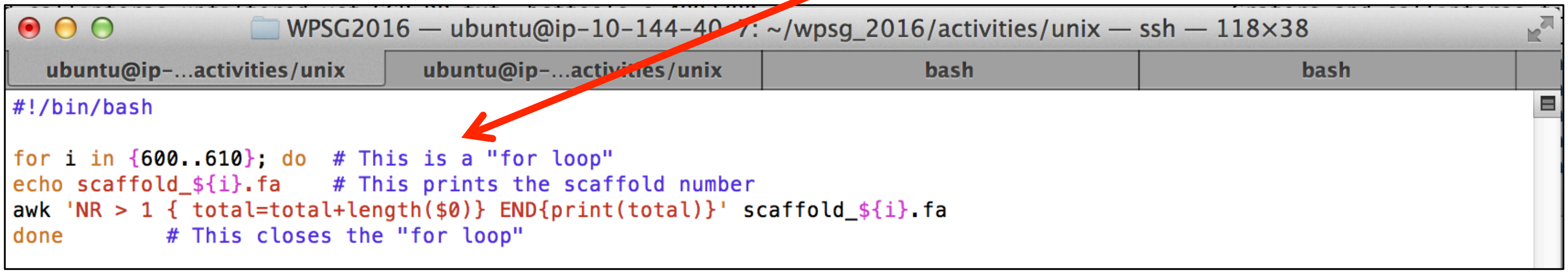
```
for i in 600 601 602 603 604 606 607 608 609 610}; do
echo scaffold_${i}.fa
awk 'NR > 1 { total=total+length($0)} END{print(total)}' scaffold_${i}.fa
done
```

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



```
#!/bin/bash

for i in {600..610}; do  # This is a "for loop"
echo scaffold_${i}.fa    # This prints the scaffold number
awk 'NR > 1 { total=total+length($0)} END{print(total)}' scaffold_${i}.fa
done         # This closes the "for loop"
```

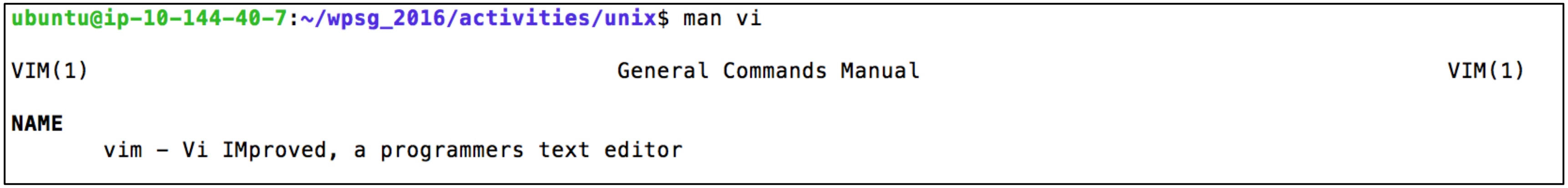
Shell scripting

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**

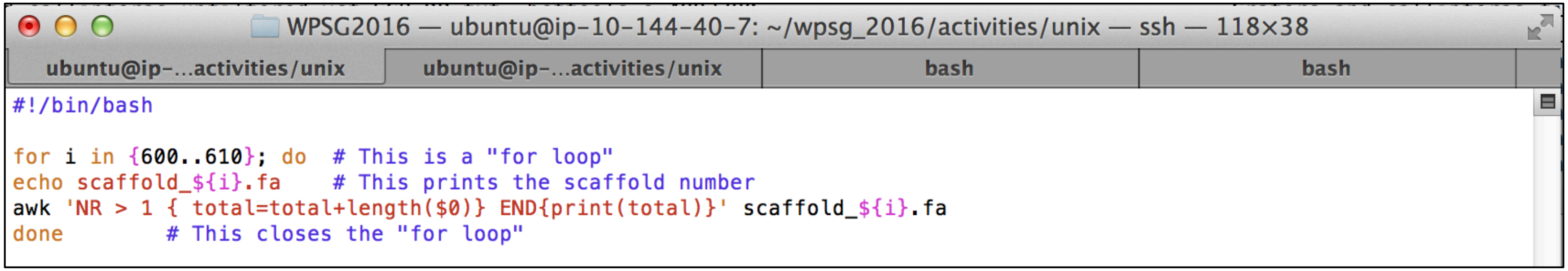
Your mouse cannot help you!

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)**



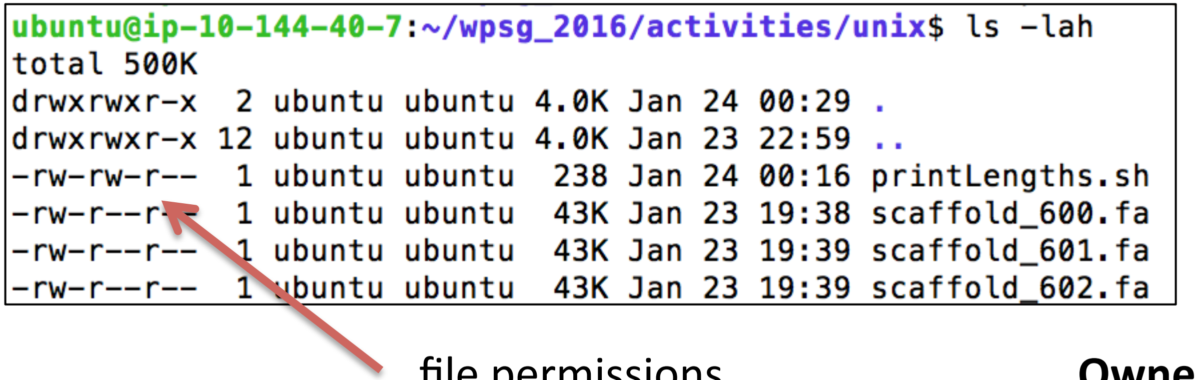
```
#!/bin/bash

for i in {600..610}; do  # This is a "for loop"
echo scaffold_${i}.fa    # This prints the scaffold number
awk 'NR > 1 { total=total+length($0)} END{print(total)}' scaffold_${i}.fa
done         # This closes the "for loop"
```

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

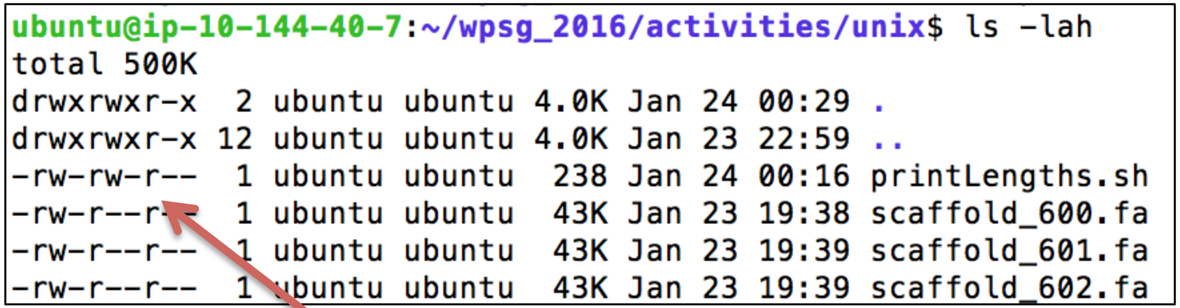


```
ubuntu@ip-10-144-40-7:~/wpsg_2016/activities/unix$ ls -lah
total 500K
drwxrwxr-x  2 ubuntu ubuntu 4.0K Jan 24 00:29 .
drwxrwxr-x 12 ubuntu ubuntu 4.0K Jan 23 22:59 ..
-rw-rw-r--  1 ubuntu ubuntu  238 Jan 24 00:16 printLengths.sh
-rw-r--r--  1 ubuntu ubuntu  43K Jan 23 19:38 scaffold_600.fa
-rw-r--r--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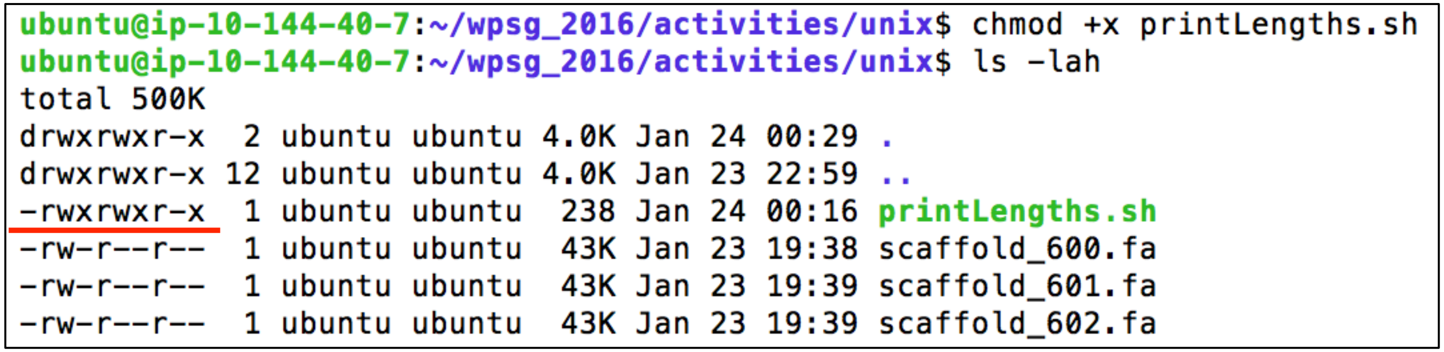
```

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
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```

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:

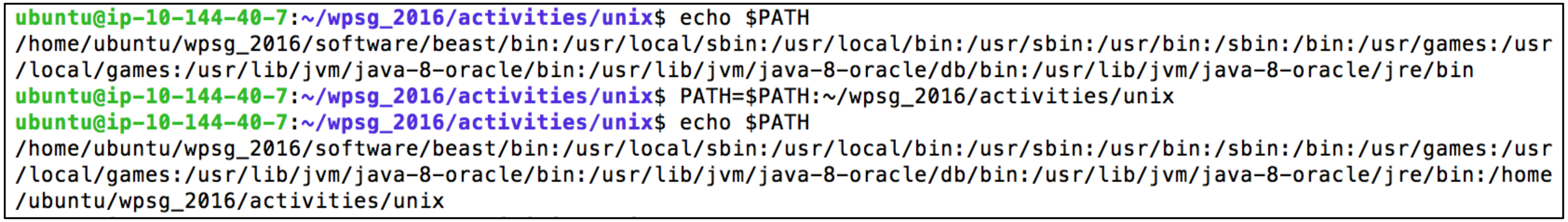
`./printLengths.sh`

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:

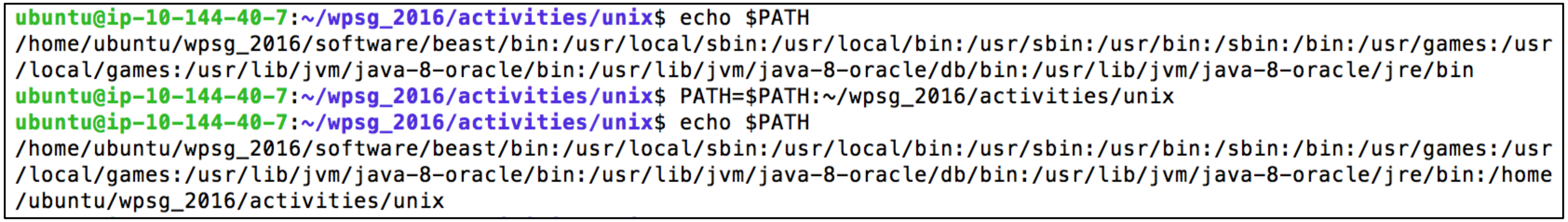
`./printLengths.sh`

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.