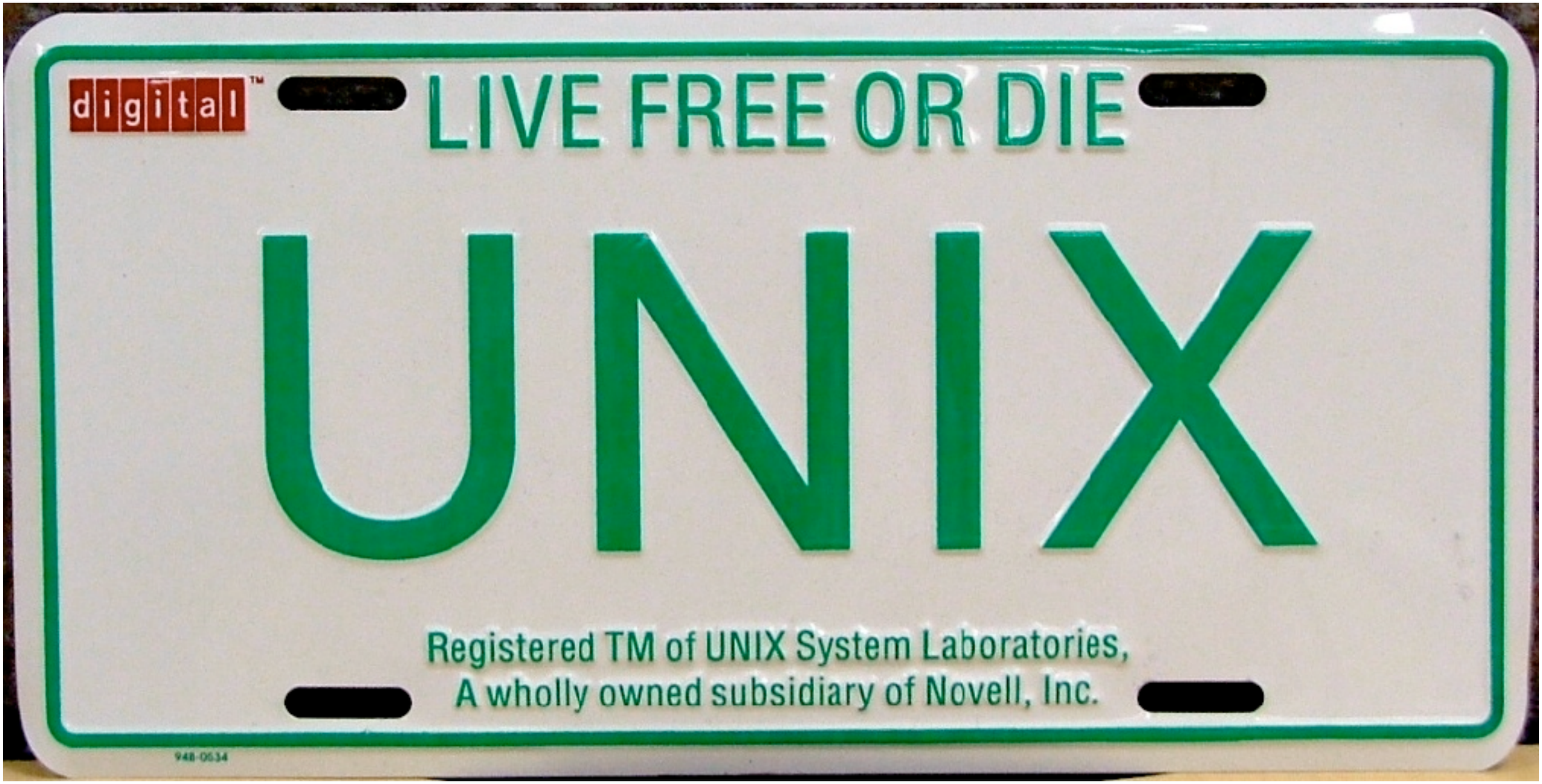
digital™
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UNIX
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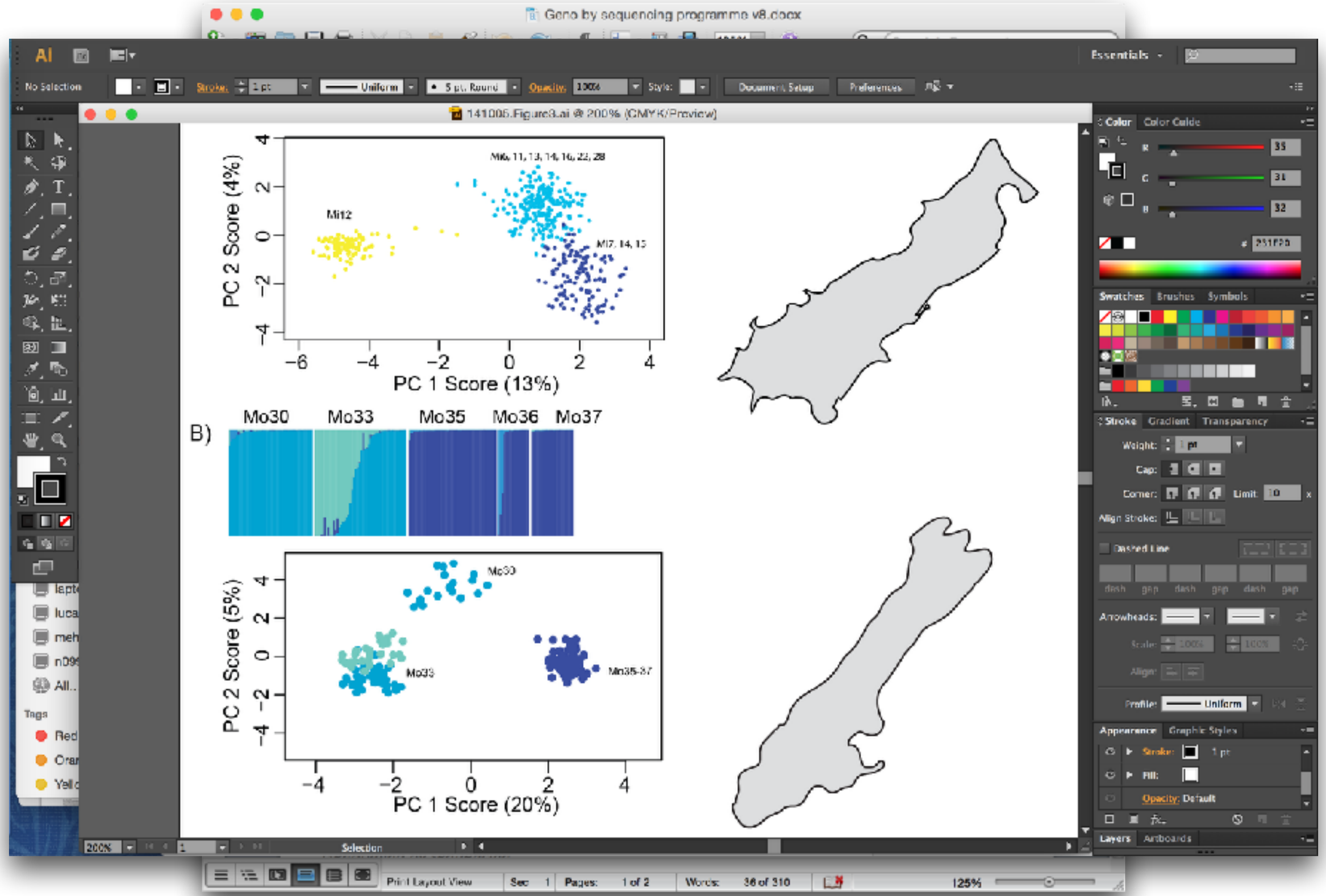
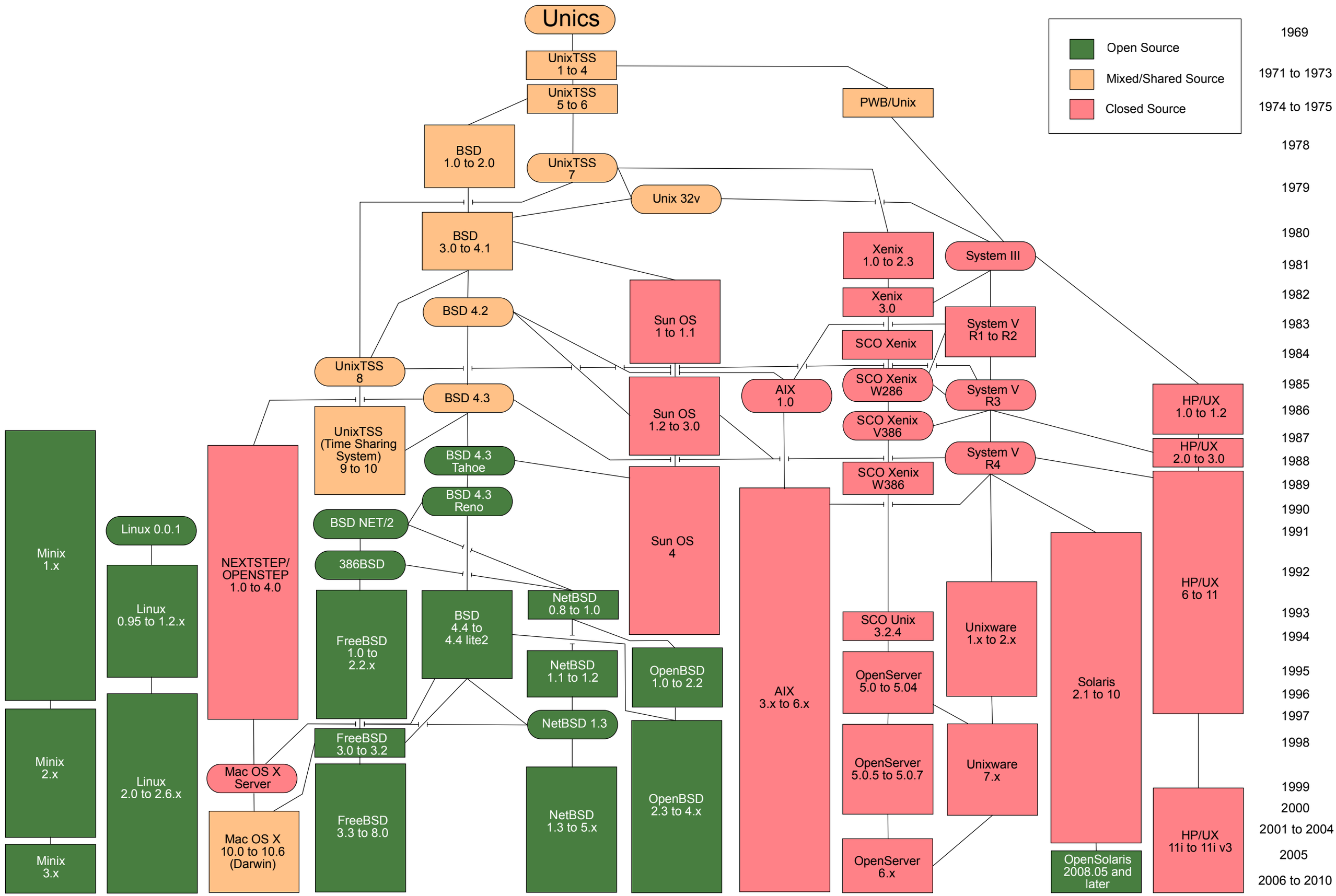
A wholly owned subsidiary of Novell, Inc.
948-0634


Gene by sequencing programme v8.docx
141006.Figure3.ai @ 200% (CMYK/Preview)
PC 2 Score (4%)
PC 1 Score (13%)
Mi12
Mi7, 14, 15
B)
Mo30
Mo33
Mo35
Mo36
Mo37
PC 2 Score (5%)
PC 1 Score (20%)
Mo30
Mo33
Mo35-37

Unix History



What computers can run Unix?

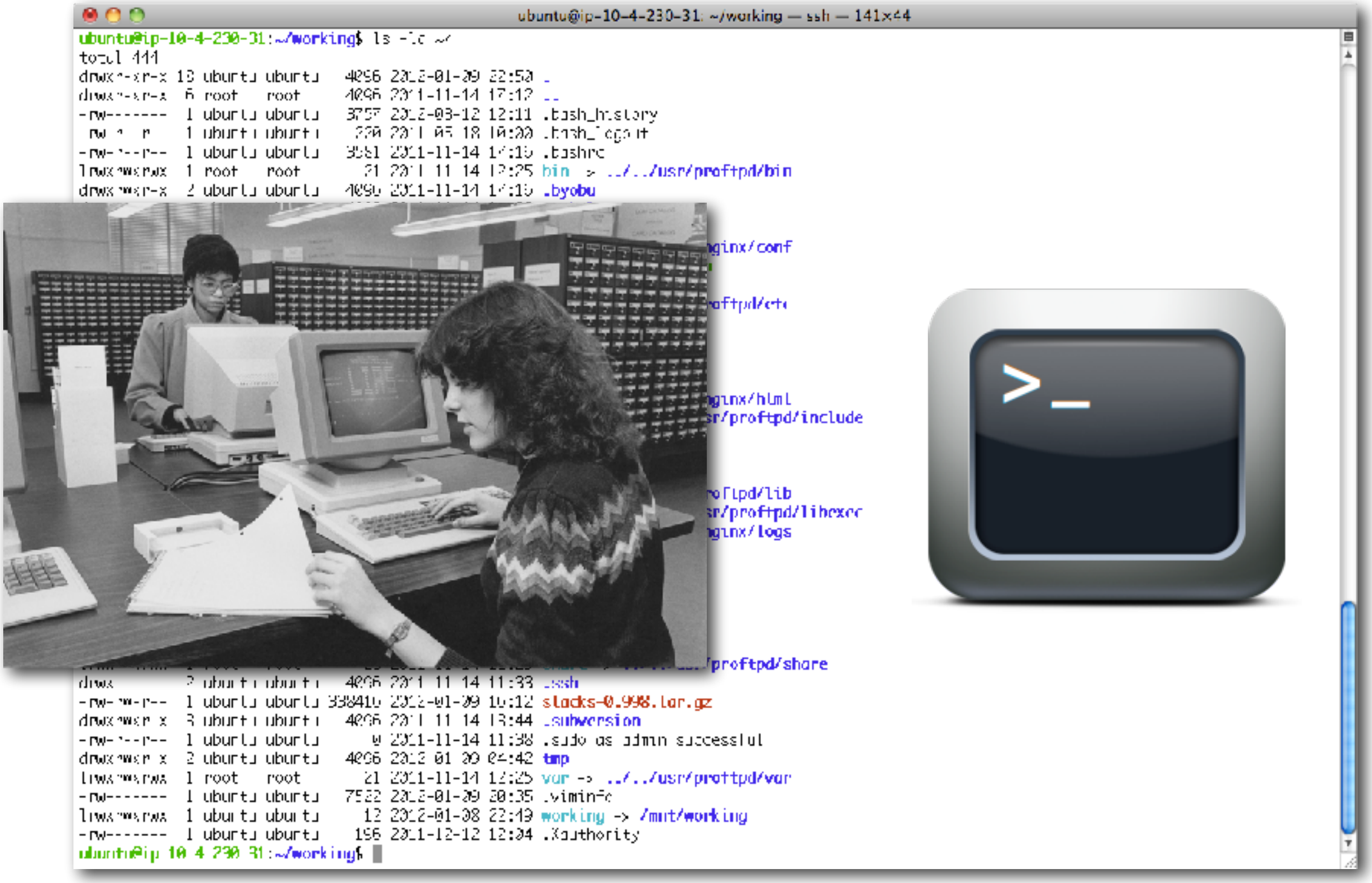
Apple OS X Macs

Wireless internet routers

Google's Android phones

Airplane entertainment systems

The Terminal Window



the shell, the prompt, the command line

The Terminal Window

```
ubuntu@ip-10-4-230-31: ~/working — ssh — 141x44
ubuntu@ip-10-4-230-31:~/working$ ls -lc ~/
total 444
drwx--xr-x 13 ubuntu ubuntu  4096 2012-01-09 22:50 .
drwx--xr-x  6 root   root    4096 2011-11-14 17:12 ..
-rw-------  1 ubuntu ubuntu  3757 2012-03-12 12:11 .bash_history
-rw-r--r--  1 ubuntu ubuntu   220 2011-05-18 10:00 .bash_logout
-rw-r--r--  1 ubuntu ubuntu  3561 2011-11-14 17:15 .bashrc
lrwxrwxrwx  1 root   root      21 2011-11-14 12:25 bin -> ../../usr/proftpd/bin
drwxrwxr-x  2 ubuntu ubuntu  4096 2011-11-14 17:15 .byobu
drwxrwxr-x  4 ubuntu ubuntu  4096 2011-11-14 14:33 .cabal
drwx------  5 ubuntu ubuntu  4096 2011-11-14 11:37 .cache
lrwxrwxrwx  1 root   root      30 2011-11-14 12:23 conf -> ../../usr/nginx/conf
-rwxrwxrwx  1 ubuntu ubuntu   993 2011-11-14 17:12 configure_freeux.sh
drwx------  3 ubuntu ubuntu  4096 2012-01-08 22:52 .emacs.d
lrwxrwxrwx  1 root   root      21 2011-11-14 12:25 etc -> ../../usr/proftpd/etc
drwx--xr-x  2 ubuntu ubuntu  4096 2011-11-14 12:51 .fontconfig
drwx------  2 ubuntu ubuntu  4096 2011-11-14 14:18 .gconf
drwx--xr-x  3 root   root    4096 2011-11-14 16:58 .gem
drwx------  2 ubuntu ubuntu  4096 2011-11-14 14:51 .gnupg
lrwxrwxrwx  1 root   root      20 2011-11-14 12:23 html -> ../../usr/nginx/html
lrwxrwxrwx  1 root   root      25 2011-11-14 12:25 include -> ../../usr/proftpd/include
drwxrwxr-x  7 ubuntu ubuntu  4096 2011-11-28 17:49 install
drwxrwxr-x  3 ubuntu ubuntu  4096 2011-11-14 12:27 .lein
-rw-------  1 ubuntu ubuntu    65 2011-11-14 13:07 .lesshst
lrwxrwxrwx  1 root   root      21 2011-11-14 12:25 lib -> ../../usr/proftpd/lib
lrwxrwxrwx  1 root   root      25 2011-11-14 12:25 libexec -> ../../usr/proftpd/libexec
lrwxrwxrwx  1 root   root      20 2011-11-14 12:23 logs -> ../../usr/nginx/logs
drwxrwxr-x  2 ubuntu ubuntu  4096 2011-11-14 12:51 .m2
drwxrwxr-x  2 ubuntu ubuntu  4096 2011-11-14 17:18 .matplotlib
-rw-------  1 ubuntu ubuntu  2964 2012-01-09 22:50 .mysql_history
-rw-r--r--  1 ubuntu ubuntu   675 2011-11-14 17:15 .profile
drwx--xr-x  2 root   root    4096 2011-11-14 12:25 sbin
-rw-rw-r--  1 ubuntu ubuntu     0 2011-11-14 11:37 .sudo_as_admin_successful
lrwxrwxrwx  1 root   root      23 2011-11-14 12:25 share -> ../../usr/proftpd/share
drwx------  2 ubuntu ubuntu  4096 2011-11-14 11:33 .ssh
-rw-rw-r--  1 ubuntu ubuntu 338416 2012-01-09 10:12 stacks-0.998.tar.gz
drwxrwxr-x  3 ubuntu ubuntu  4096 2011-11-14 13:44 .subversion
-rw-r--r--  1 ubuntu ubuntu     0 2011-11-14 11:38 .sudo_as_admin_successful
drwxrwxr-x  2 ubuntu ubuntu  4096 2012-01-09 04:42 tmp
lrwxrwxrwx  1 root   root      21 2011-11-14 12:25 var -> ../../usr/proftpd/var
-rw-------  1 ubuntu ubuntu  7522 2012-01-09 20:35 .viminfo
lrwxrwxrwx  1 ubuntu ubuntu    12 2012-01-08 22:49 working -> /mnt/working
-rw-------  1 ubuntu ubuntu   196 2011-12-12 12:04 .Xauthority
ubuntu@ip-10-4-230-31:~/working$
```

Make it comfortable to work in:

- Resize the window
- Change your font size
- Open multiple terminal windows

Grab File Edit Capture Window Help

catchen@Whitaker.local:/Users/catchen/hg/stacks — bash — 181×39

```
  Processes:      868
  Usage of /:     85% of 917G
  Memory usage:   78%
  Users:          2
  IP address for eth0 is 128.223.42.74

[catchen@genome]:~% ls
aori_test/                  clone/                      groupIV_contigs.tsv         mst_test/                   seqs/
abyss-1.3.4/                cl_test/                    groupIX_contigs.tsv         Music/                      seqs.tar.gz
abyss-1.3.4.tar.gz          coord_test/                 groupXII_contigs.tsv        Mus_musculus.GRCm38.68.spliceSites  shenhua/
adapter/                    corr/                       gtff_backup/                NACAn_allgeno.tsv           shell/
aj/                         count-genome-len.pl*        gztest/                     Nescent/                    simison/
allpathslg-41370.tar.gz     courses/                    hans/                       Nescent.tar.gz              south/
allpathslg-44683.tar.gz     dania_sexdet_radtags-sep_29_2011.tsv.gz  harriet/                    palm/                       sparsehash-2.0.2.tar.gz
allpathslg-44837.tar.gz     dave/                       hashtest/                   parallel-20130522/          sql.bak/
ALLPATHS-LG.test_genome/    denovo_map.log              Homo_sapiens.GRCh37.72.pep.all.fa  parallel-latest.tar         src.bak/
ash.py*                     Desktop/                    hsu/                        pdtoolkit-3.16/             ss_test/
ash.py~                     Documents/                  ids.txt                     pdf.tgz                     stacks-0.997.tar.gz
ash.sum                     Downloads/                  kfilter_test/               petest/                     Stickleback1.0.agp
batch_1.fst_9-12.tsv        emily/                      ktree/                      pe_test/                    structure_test/
batch_1.fst_9-12.tsv.new    erica/                      ktreetest/                  phase.2.1.1.linux/          tau-2.20.3/
batch_1.fst_9-12.tsv.old    fance_radtags.genotype_corrections.tsv.gz  ktree.tgz                   phase.2.1.1.linux.tar.gz    tau.tgz
batch_1_ids.txt             fastphase_finalliklihoods   ld_test/                    php.bak/                    Templates/
batch_1.summbots_1.csv      fastPHASE_Linux*            LICENCE*                    phylip-3.695/               test.genome.tar.gz
ben/                        faststructure/              Mail/                       phylip-3.695.tar.gz         test.png
bentley/                    gac_gen_broads1_e64.coords  mancor_test/                Pictures/                   thom/
bi510/                      gac_map_test/               mario/                      plink-1.07-src.zip          ustacks_test/
blair/                      Gasterosteus_aculeatus_assembly.agp  marine/                     plink-1.07-x86_64.zip       vcf_test/
bptest/                     Gasterosteus_aculeatus.BROAD51.68.gtf  markos/                     plink.log                   velvet_1.2.08.tgz
broad/                      genepop/                    megan/                      process_radtags_test/       Videos/
build_tags.sh*              gmap-gsnap-2013-11-27.tar.gz  megan2/                     Public/                     working/
build_tags.sh~*             gnuplot-4.6.4/              mi12_vs_mi12-sympatric.tsv  research6                   yan/
catalog_test/               gnuplot-4.6.4.tar.gz        mitch/                      rom/
catchen_ecz.per             group1_contigs.tsv          model_test/                 sascha/
[catchen@genome]:~% emacs /var/www/creskolab/stacks/index.php
[catchen@genome]:~% exit
logout
Connection to genome.uoregon.edu closed.
[catchen@Whitaker]:~/hg/stacks%
```

```
[catchen@Whitaker]:~/hg/stacks% hg pull
warning: bitbucket.org certificate with fingerprint 24:9c:45:8b:9c:ac:ba:55:4e:01:6d:58:ff:e4:28:7d:2a:14:ae:3b not verified (check hostfingerprints or web.cacerts config setting)
http authorization required
realm: Bitbucket.org HTTP
user: jcatchen
password:
warning: bitbucket.org certificate with fingerprint 24:9c:45:8b:9c:ac:ba:55:4e:01:6d:58:ff:e4:28:7d:2a:14:ae:3b not verified (check hostfingerprints or web.cacerts config setting)
pulling from https://jcatchen%bitbucket.org/jcatchen/stacks
warning: bitbucket.org certificate with fingerprint 24:9c:45:8b:9c:ac:ba:55:4e:01:6d:58:ff:e4:28:7d:2a:14:ae:3b not verified (check hostfingerprints or web.cacerts config setting)
warning: bitbucket.org certificate with fingerprint 24:9c:45:8b:9c:ac:ba:55:4e:01:6d:58:ff:e4:28:7d:2a:14:ae:3b not verified (check hostfingerprints or web.cacerts config setting)
searching for changes
warning: bitbucket.org certificate with fingerprint 24:9c:45:8b:9c:ac:ba:55:4e:01:6d:58:ff:e4:28:7d:2a:14:ae:3b not verified (check hostfingerprints or web.cacerts config setting)
adding changesets
adding manifests
adding file changes
added 1 changesets with 1 changes to 1 files
warning: bitbucket.org certificate with fingerprint 24:9c:45:8b:9c:ac:ba:55:4e:01:6d:58:ff:e4:28:7d:2a:14:ae:3b not verified (check hostfingerprints or web.cacerts config setting)
(run 'hg update' to get a working copy)
[catchen@Whitaker]:~/hg/stacks% hg update
1 files updated, 0 files merged, 0 files removed, 0 files unresolved
[catchen@Whitaker]:~/hg/stacks%
```

Macintosh HD
499.42 GB, 332.89 GB free

awk_test
2 items

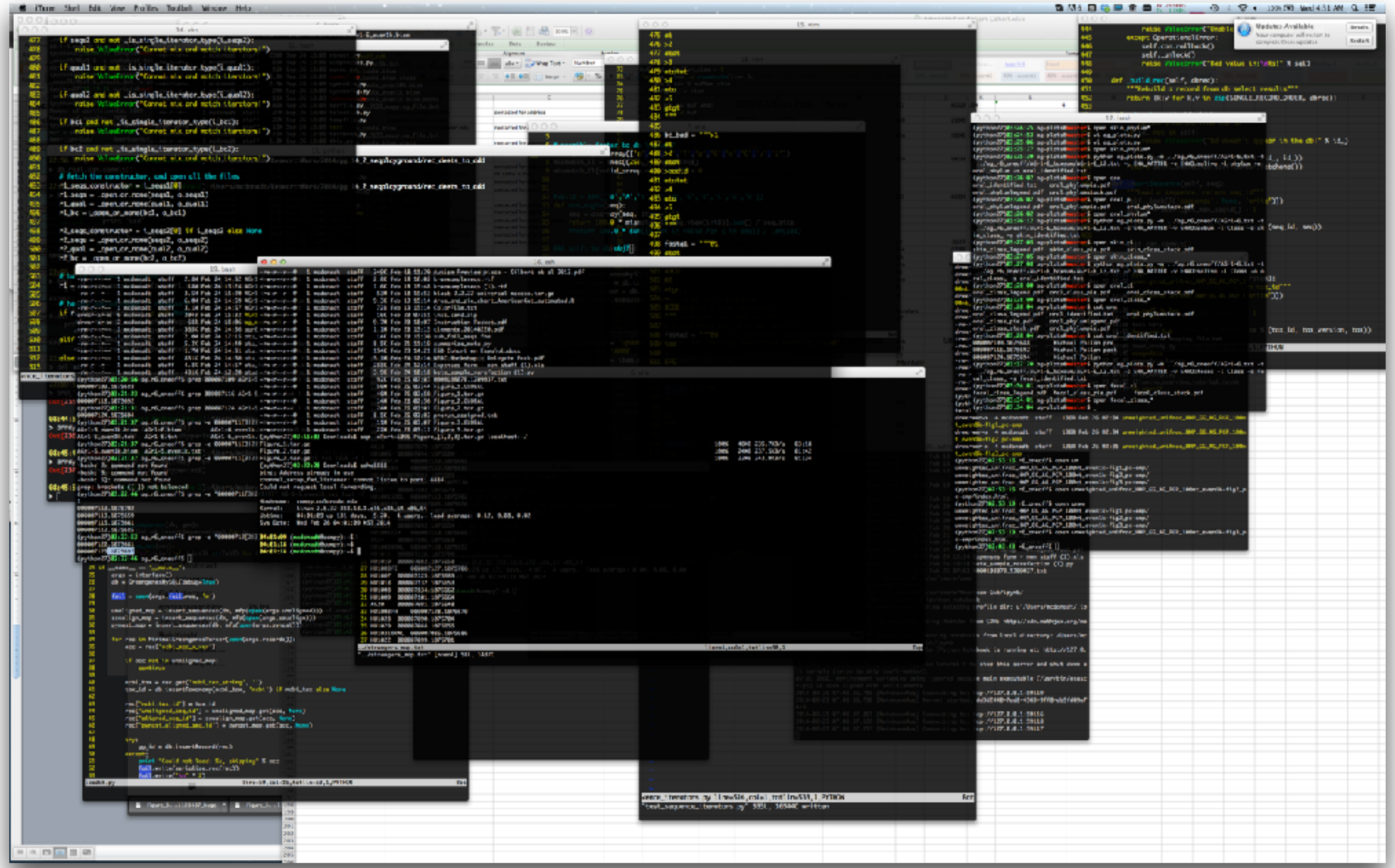
metapop_commands.txt

scan.stacks

vStacks.app.zip
285 KB

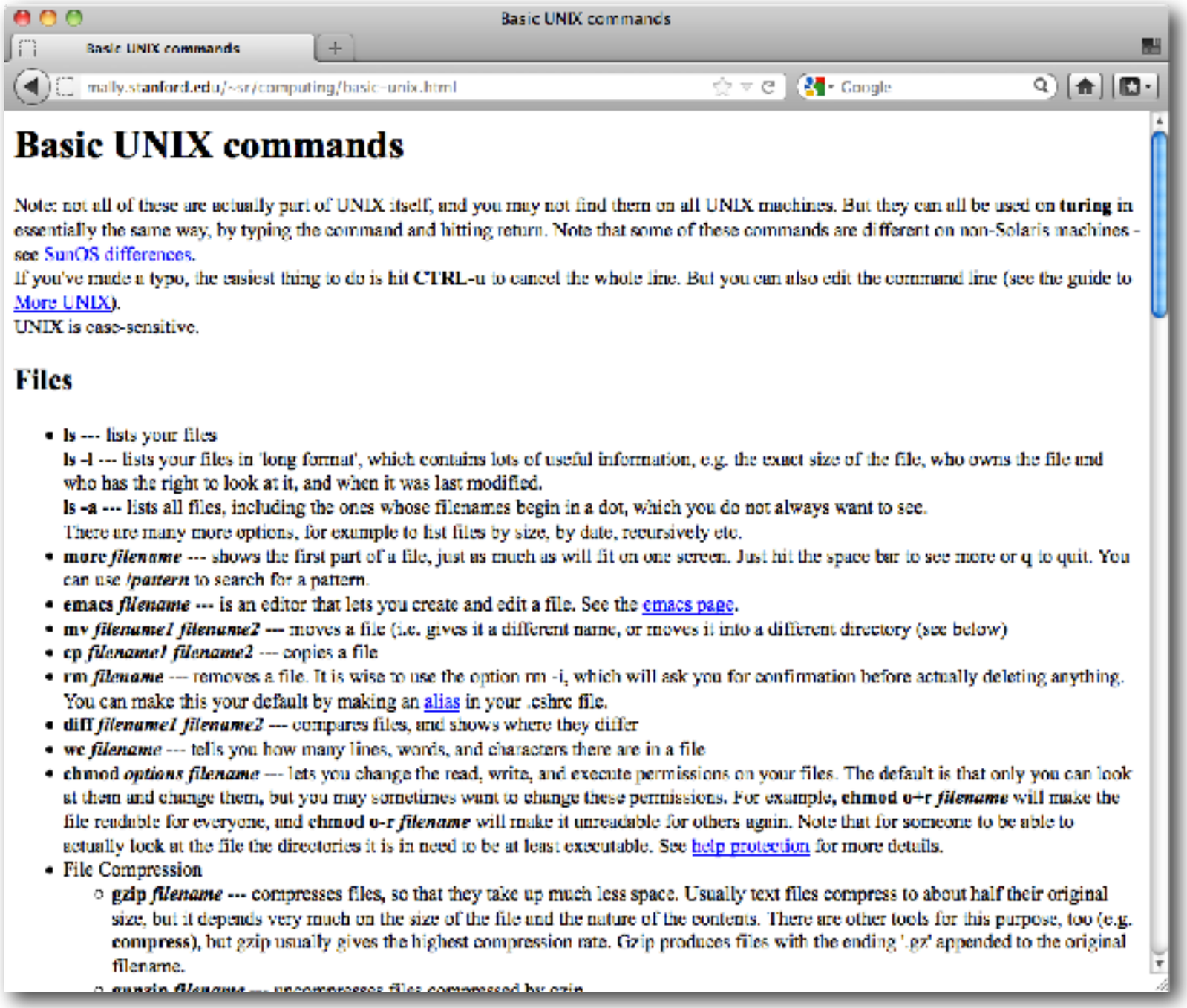
scan_stacks
77 items

10.tar.gz ustacks*
11.tar.gz vStacks/
12.tar.gz
13.tar.gz



Obtain a cheat sheet

google “unix commands”



Basic UNIX commands

Basic UNIX commands

mally.stanford.edu/~sr/computing/basic-unix.html

Google

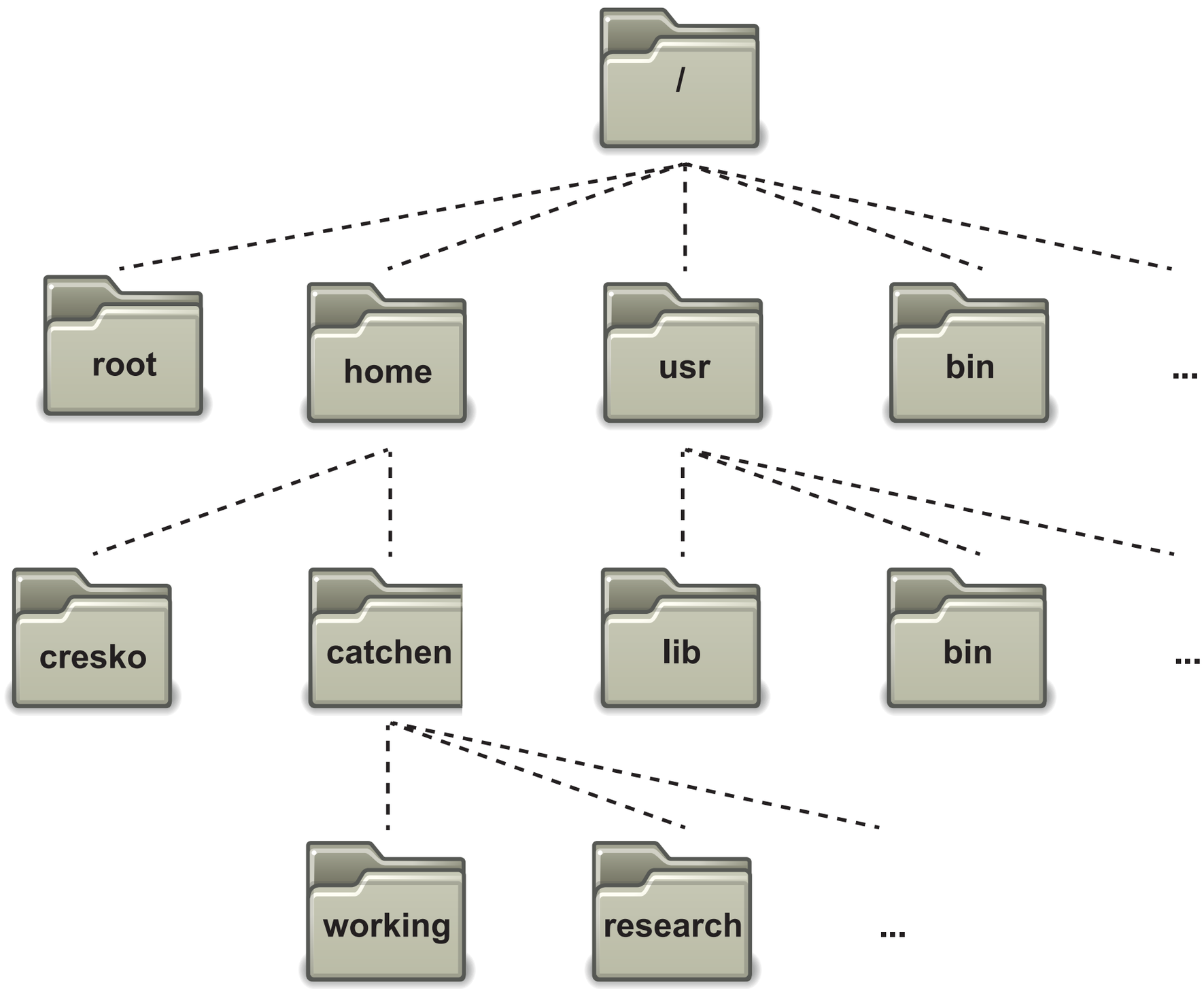
Basic UNIX commands

Note: not all of these are actually part of UNIX itself, and you may not find them on all UNIX machines. But they can all be used on **turing** in essentially the same way, by typing the command and hitting return. Note that some of these commands are different on non-Solaris machines - see SunOS differences.
If you've made a typo, the easiest thing to do is hit **CTRL-u** to cancel the whole line. But you can also edit the command line (see the guide to More UNIX).
UNIX is case-sensitive.

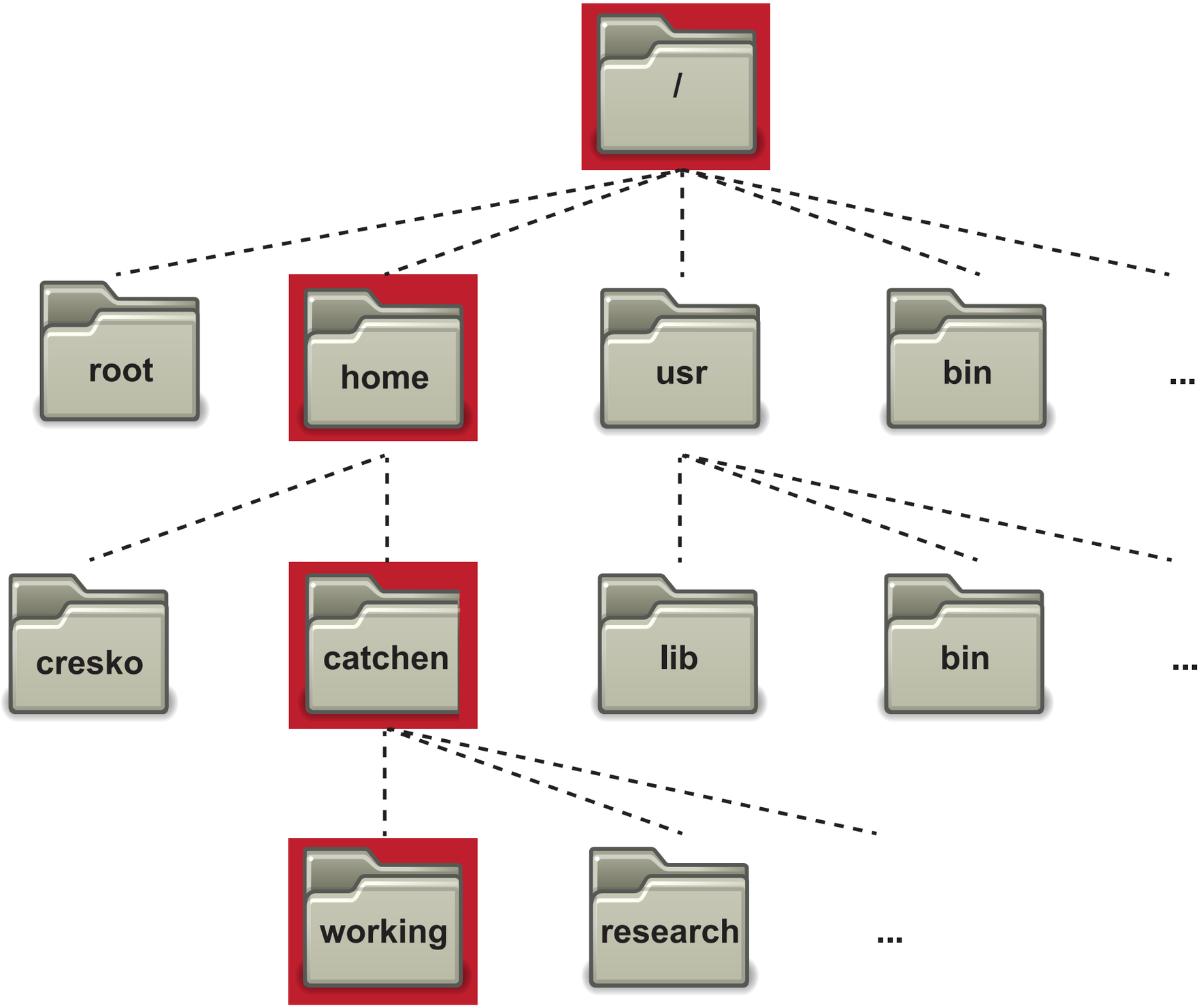
Files

- **ls** --- lists your files
  ls -l --- lists your files in 'long format', which contains lots of useful information, e.g. the exact size of the file, who owns the file and who has the right to look at it, and when it was last modified.
  ls -a --- lists all files, including the ones whose filenames begin in a dot, which you do not always want to see.
  There are many more options, for example to list files by size, by date, recursively etc.
- **more *filename*** --- shows the first part of a file, just as much as will fit on one screen. Just hit the space bar to see more or **q** to quit. You can use */pattern* to search for a pattern.
- **emacs *filename*** --- is an editor that lets you create and edit a file. See the emacs page.
- **mv *filename1 filename2*** --- moves a file (i.e. gives it a different name, or moves it into a different directory (see below)
- **cp *filename1 filename2*** --- copies a file
- **rm *filename*** --- removes a file. It is wise to use the option rm -i, which will ask you for confirmation before actually deleting anything. You can make this your default by making an alias in your .cshrc file.
- **diff *filename1 filename2*** --- compares files, and shows where they differ
- **wc *filename*** --- tells you how many lines, words, and characters there are in a file
- **chmod *options filename*** --- lets you change the read, write, and execute permissions on your files. The default is that only you can look at them and change them, but you may sometimes want to change these permissions. For example, **chmod o+r *filename*** will make the file readable for everyone, and **chmod o-r *filename*** will make it unreadable for others again. Note that for someone to be able to actually look at the file the directories it is in need to be at least executable. See help protection for more details.
- File Compression
  - **gzip *filename*** --- compresses files, so that they take up much less space. Usually text files compress to about half their original size, but it depends very much on the size of the file and the nature of the contents. There are other tools for this purpose, too (e.g. **compress**), but gzip usually gives the highest compression rate. Gzip produces files with the ending '.gz' appended to the original filename.
  - **gunzip *filename*** --- uncompresses files compressed by gzip

In UNIX everything is a file organized in a hierarchy



Paths



/home/catchen/working

Create a series of directories

```
ubuntu@ip-10-4-193-188:~$ mkdir shell
ubuntu@ip-10-4-193-188:~$ cd shell
ubuntu@ip-10-4-193-188:~/shell$ mkdir research
ubuntu@ip-10-4-193-188:~/shell$ ls
research
ubuntu@ip-10-4-193-188:~/shell$ cd research/
ubuntu@ip-10-4-193-188:~/shell/research$ mkdir seq
ubuntu@ip-10-4-193-188:~/shell/research$ ls
seq
ubuntu@ip-10-4-193-188:~/shell/research$ cd seq/
ubuntu@ip-10-4-193-188:~/shell/research/seq$ mkdir radtags
ubuntu@ip-10-4-193-188:~/shell/research/seq$ cd radtags/
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ ls
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ ls -la
total 8
drwxrwxr-x 2 ubuntu ubuntu 4096 2012-03-06 23:08 .
drwxrwxr-x 3 ubuntu ubuntu 4096 2012-03-06 23:08 ..
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ pwd
/home/ubuntu/shell/research/seq/radtags
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$
```

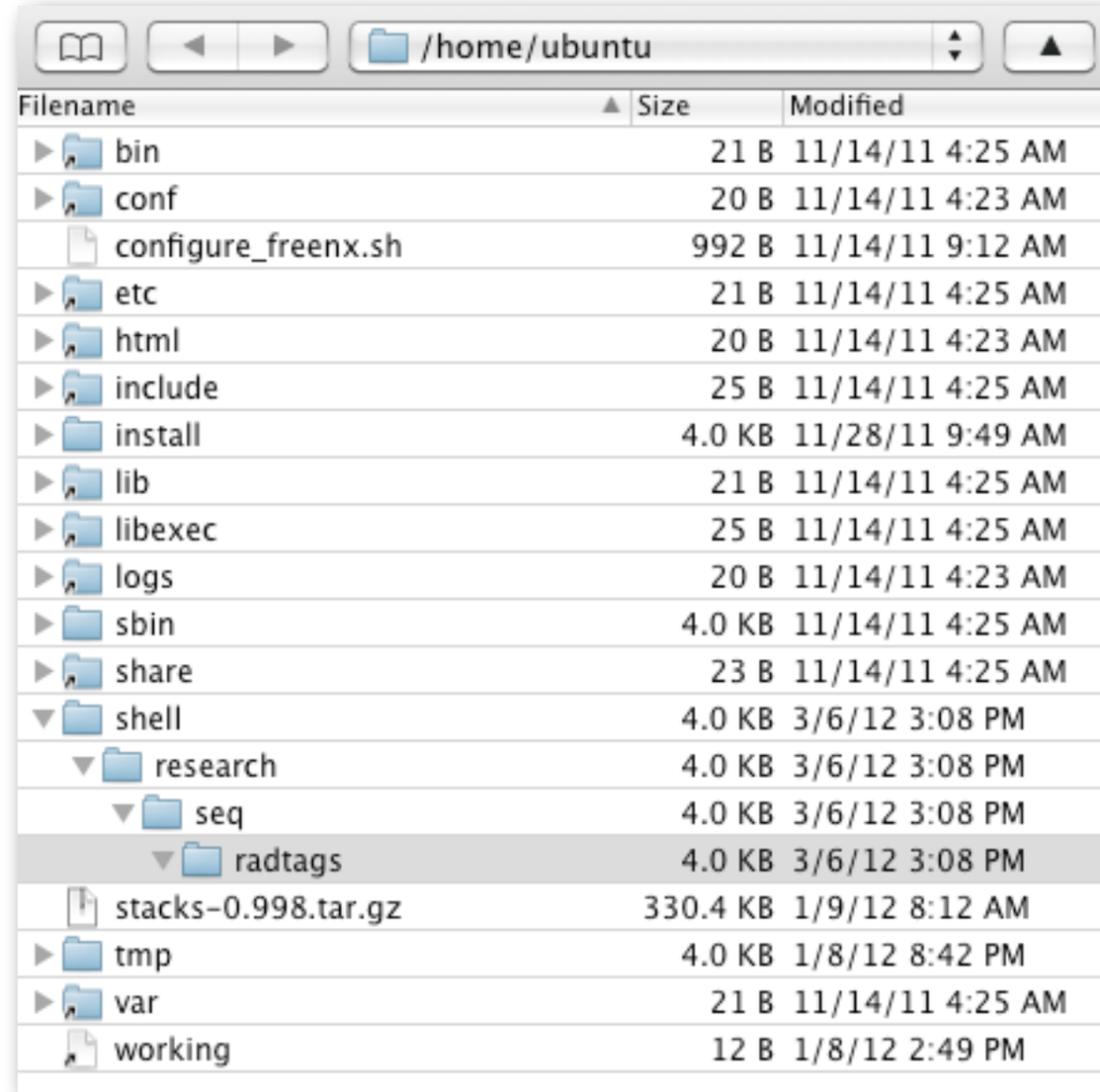
```
% mkdir shell        % cd shell        % ls
```

Paths, cont

This shell view of the nested directories shell, research, seq, and radtags…..

```
ubuntu@ip-10-4-193-188:~$ mkdir shell
ubuntu@ip-10-4-193-188:~$ cd shell
ubuntu@ip-10-4-193-188:~/shell$ mkdir research
ubuntu@ip-10-4-193-188:~/shell$ ls
research
ubuntu@ip-10-4-193-188:~/shell$ cd research/
ubuntu@ip-10-4-193-188:~/shell/research$ mkdir seq
ubuntu@ip-10-4-193-188:~/shell/research$ ls
seq
ubuntu@ip-10-4-193-188:~/shell/research$ cd seq/
ubuntu@ip-10-4-193-188:~/shell/research/seq$ mkdir radtags
ubuntu@ip-10-4-193-188:~/shell/research/seq$ cd radtags/
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ ls
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ ls -la
total 8
drwxrwxr-x 2 ubuntu ubuntu 4096 2012-03-06 23:08 .
drwxrwxr-x 3 ubuntu ubuntu 4096 2012-03-06 23:08 ..
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ pwd
/home/ubuntu/shell/research/seq/radtags
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$
```

…. is equivalent to this GUI view of the same directories

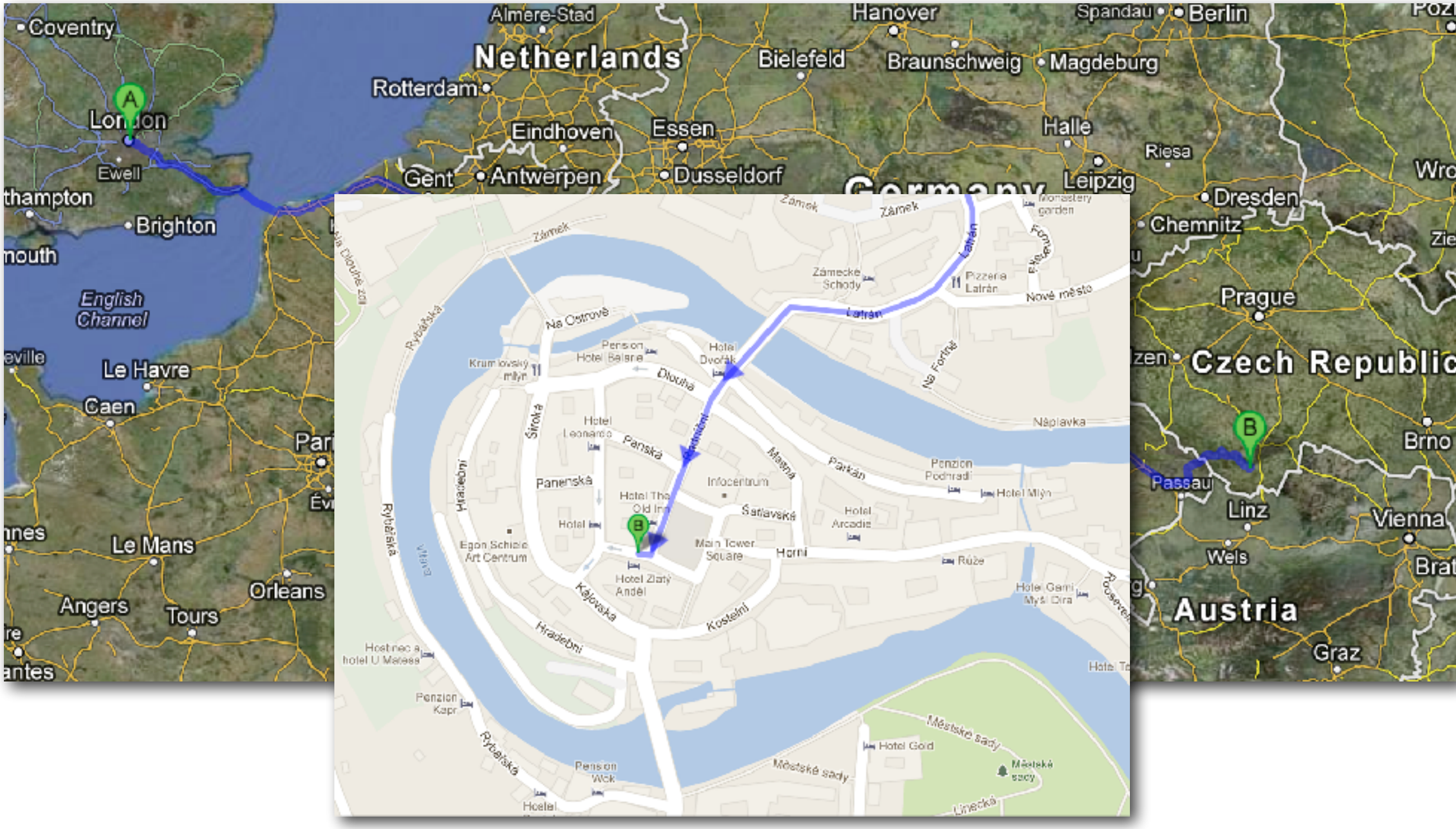


And the `radtags` directory is uniquely identified by its path:

`/home/ubuntu/shell/research/seq/radtags`

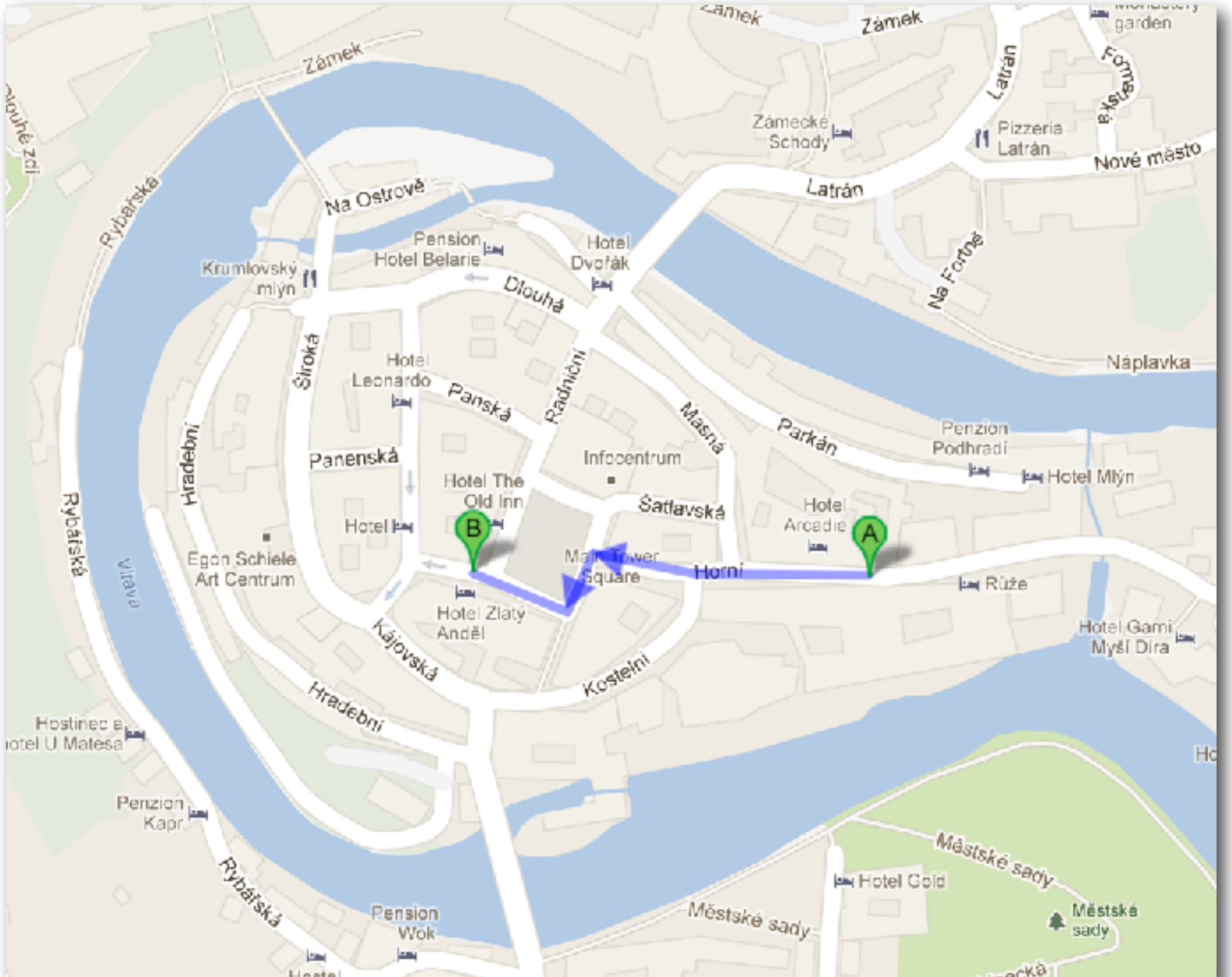
Absolute and relative paths

How do I get to the Hotel Zlaty Andel?

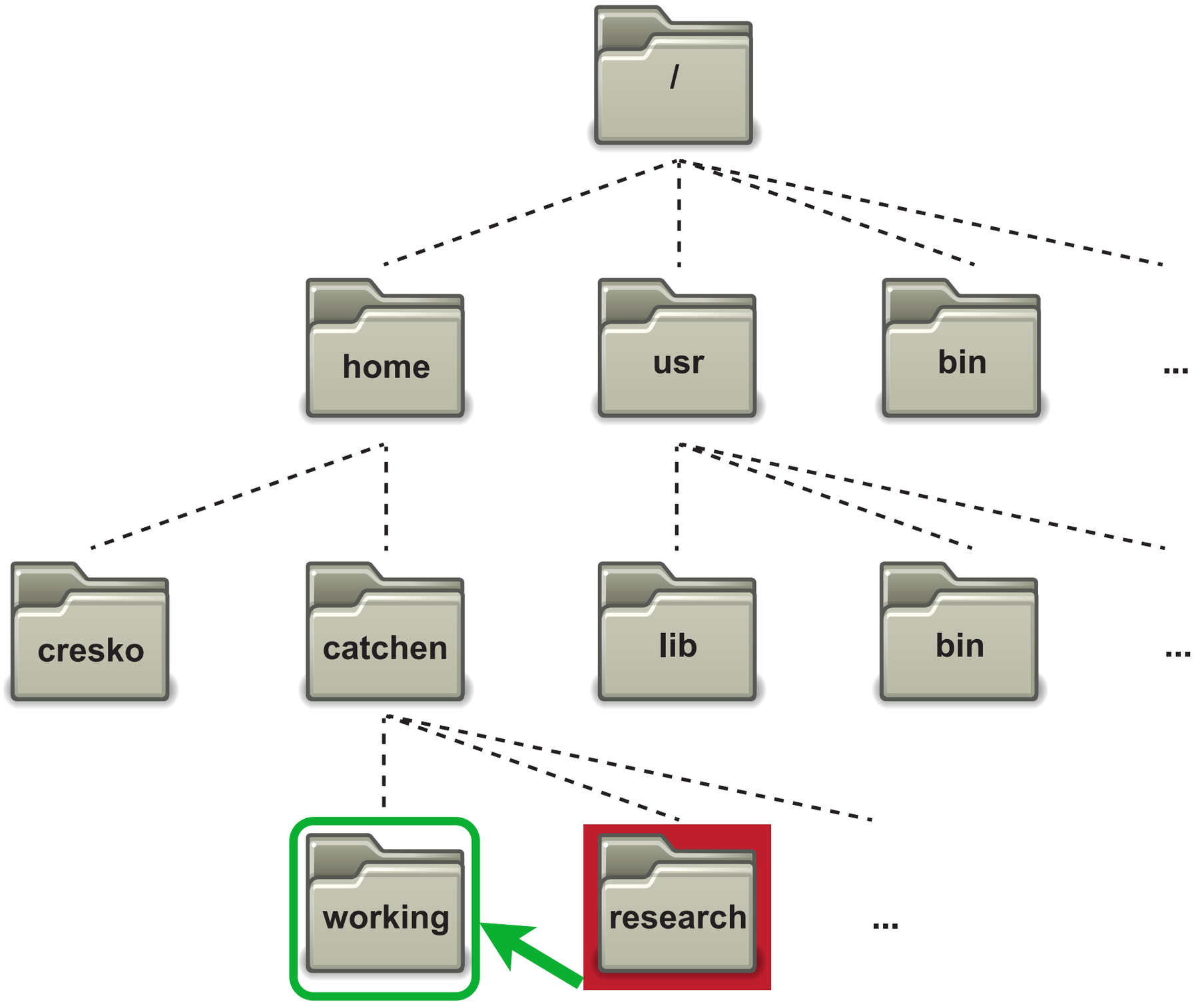


Absolute and relative paths

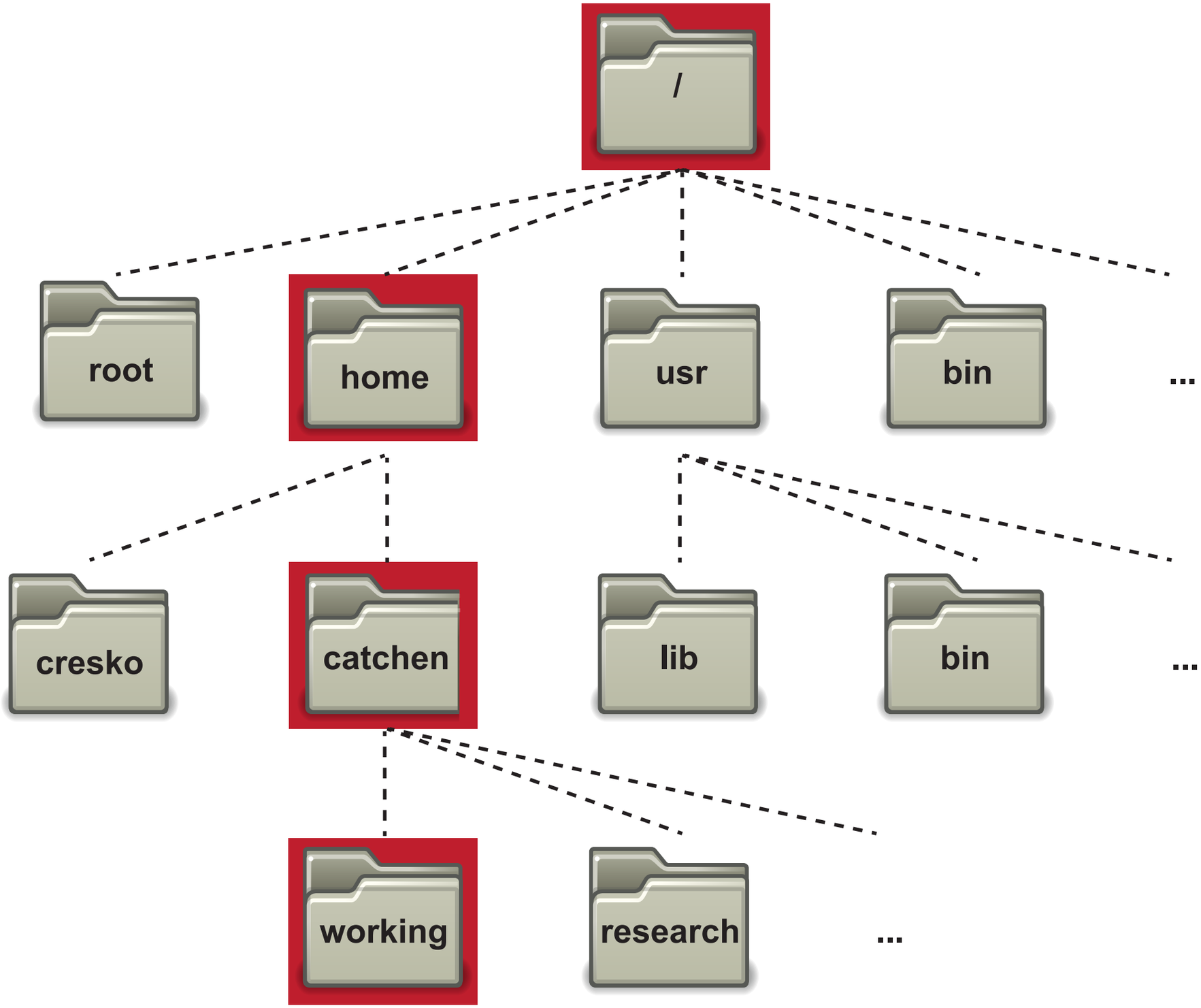
How do I get to the Hotel Zlaty Andel?



Paths

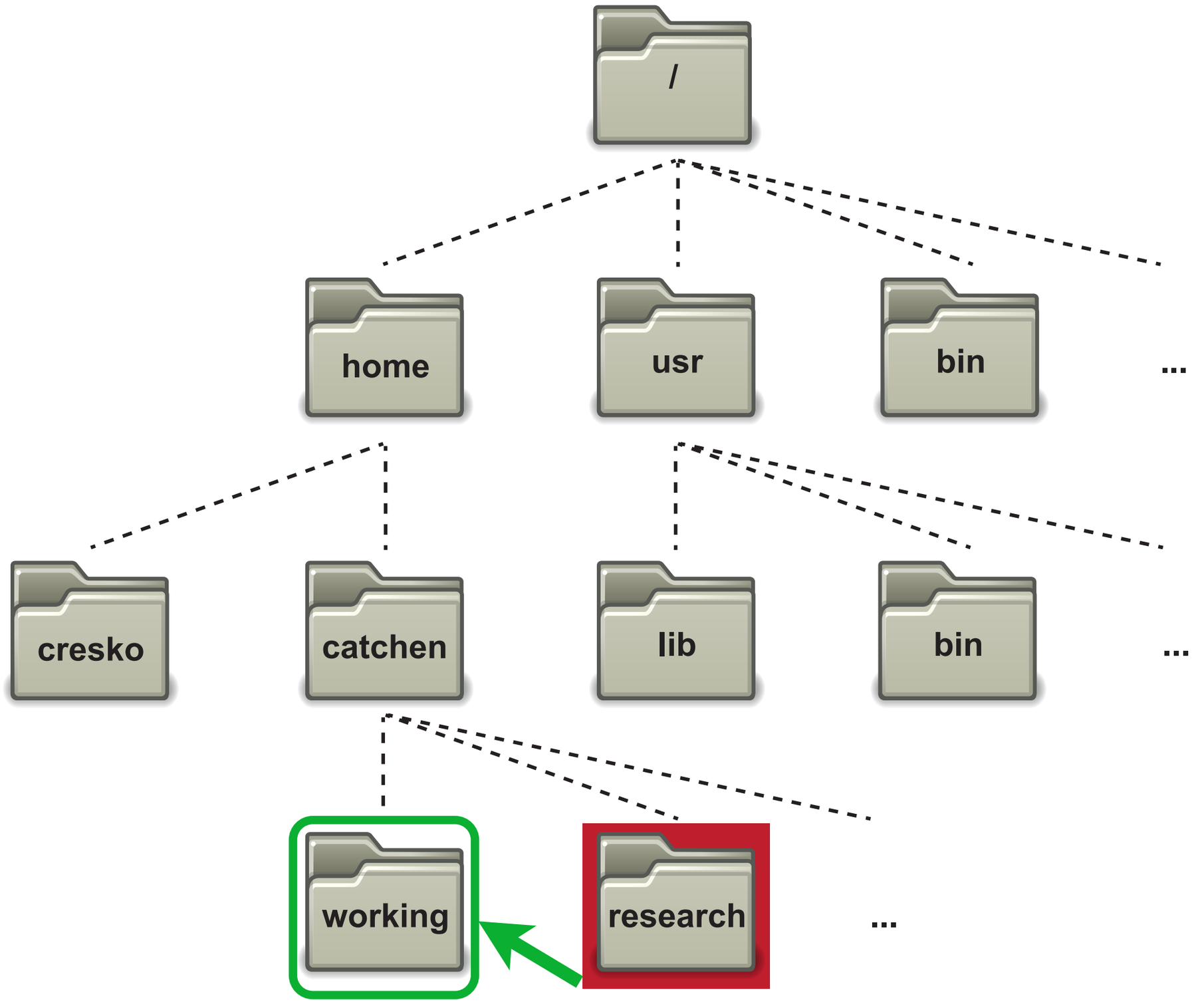


Absolute Path

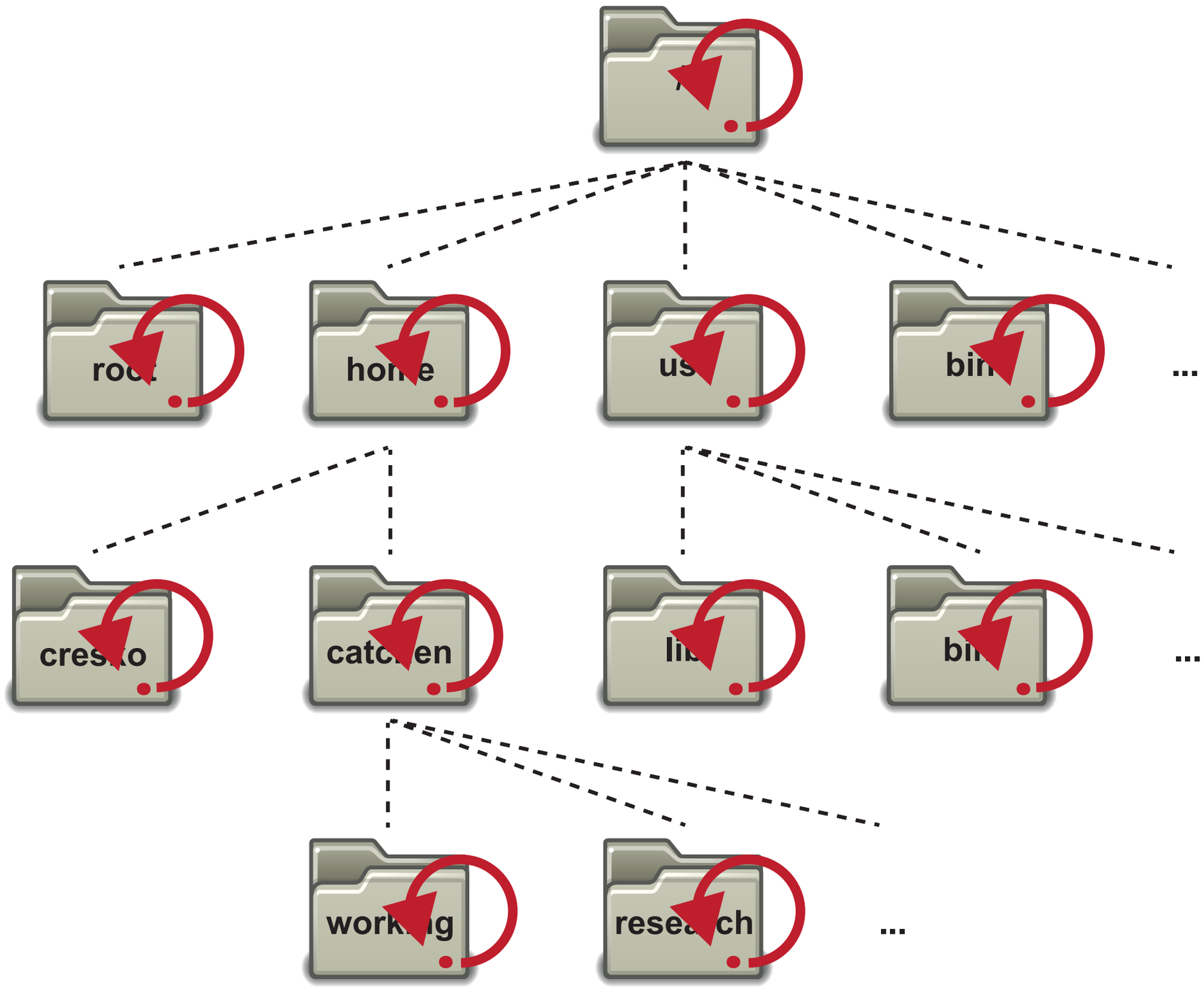


/home/catchen/working

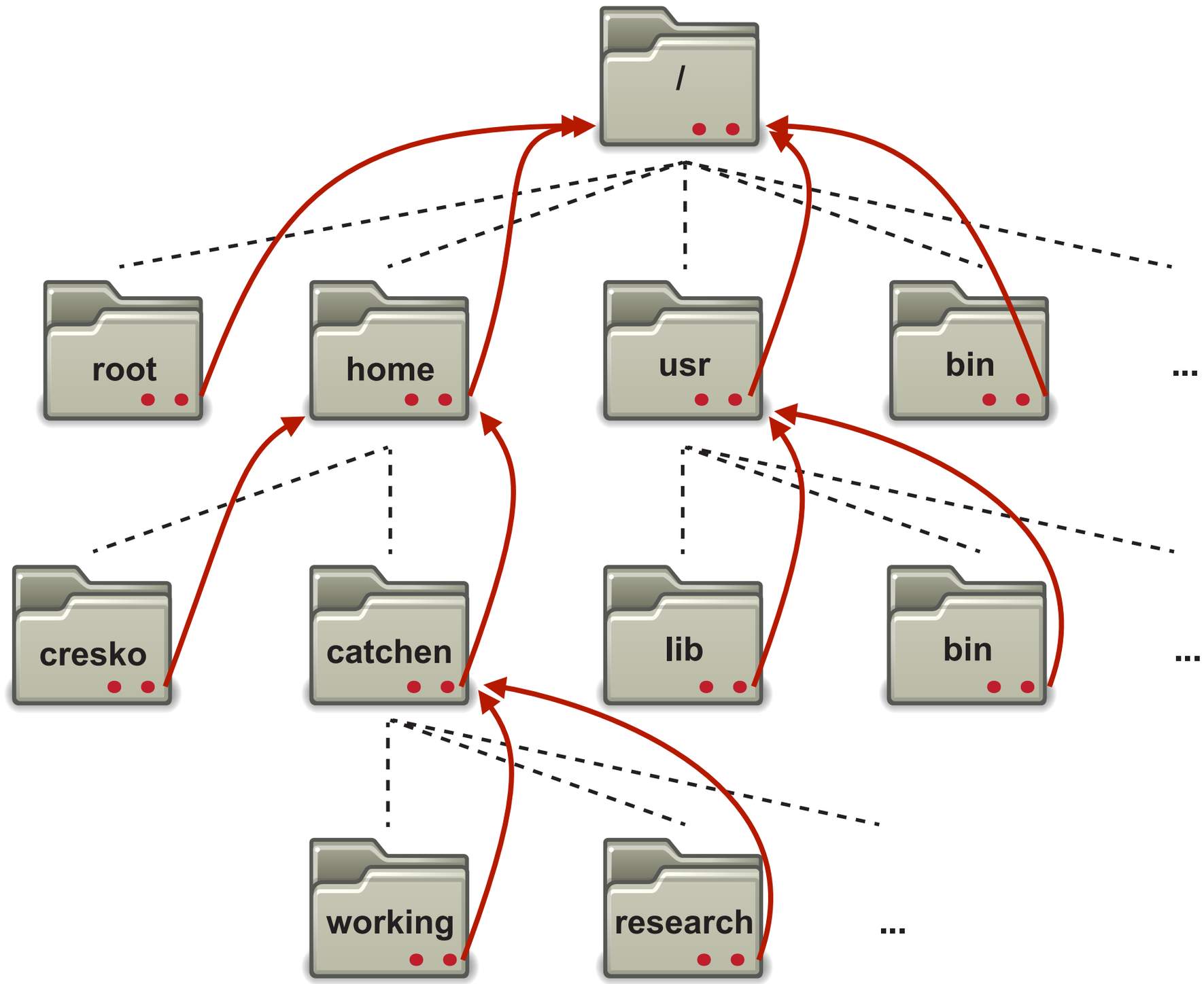
Relative Path?



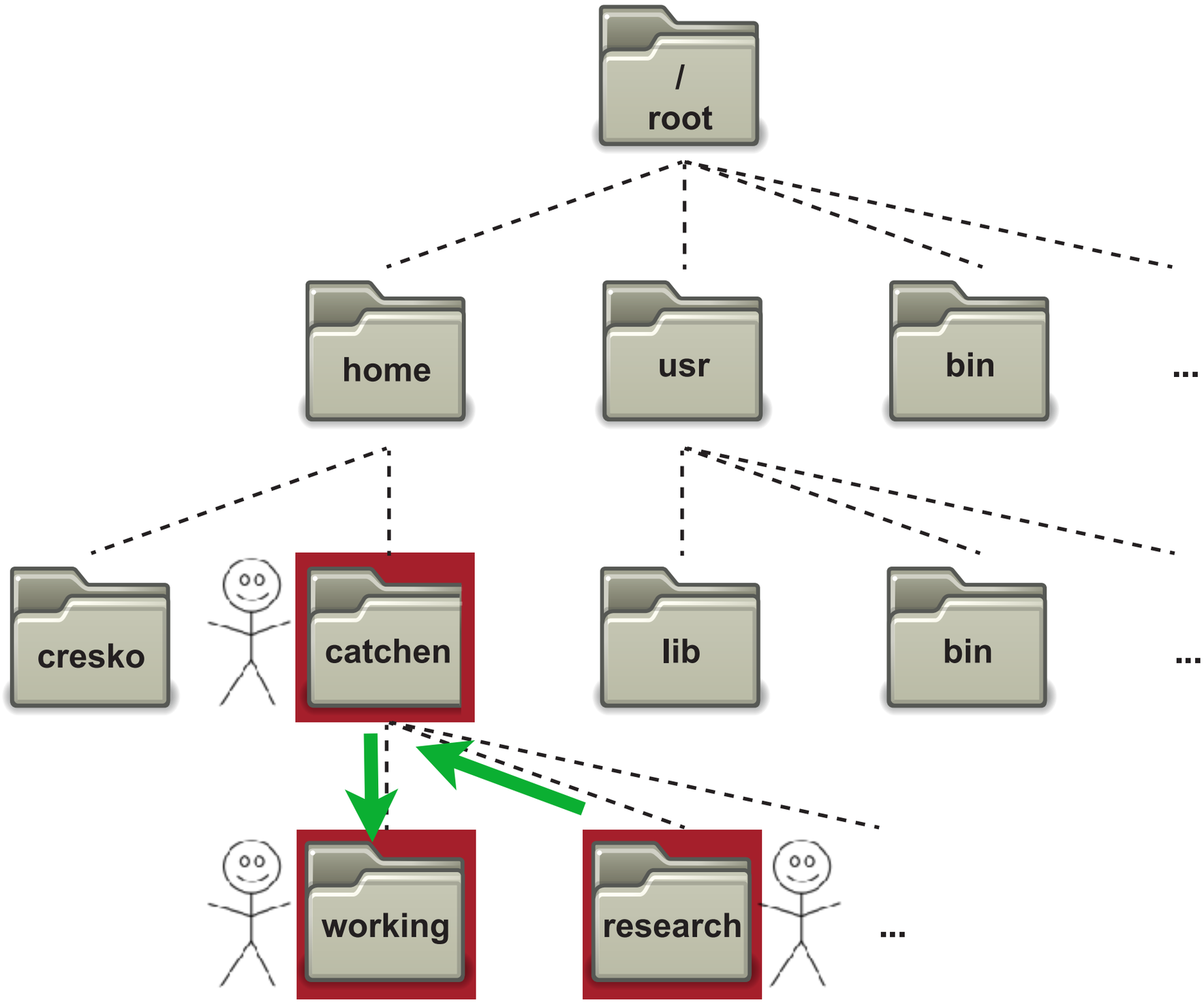
Special files -- ‘*dot*’



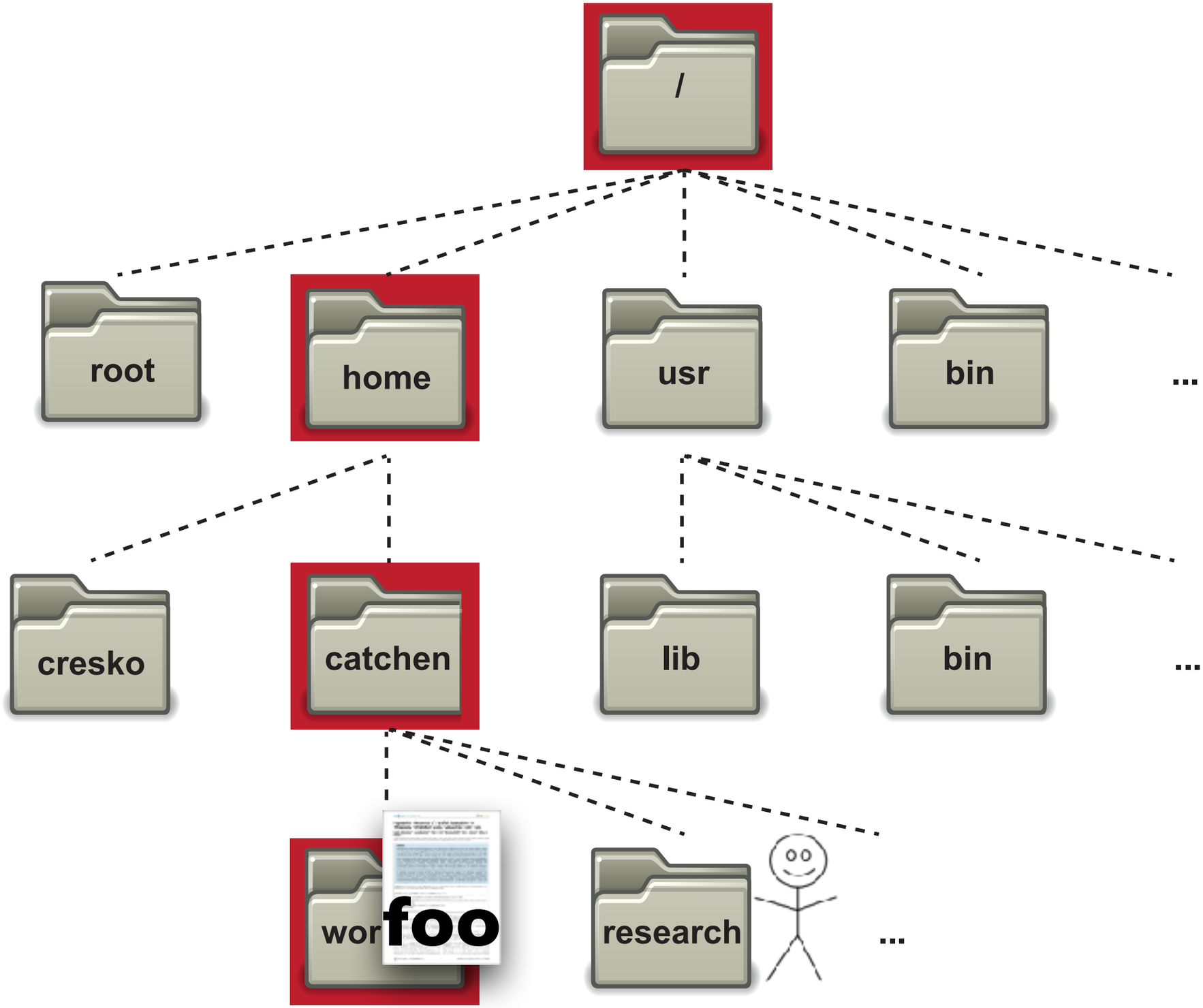
Special files -- '*dot dot*'



Relative Path

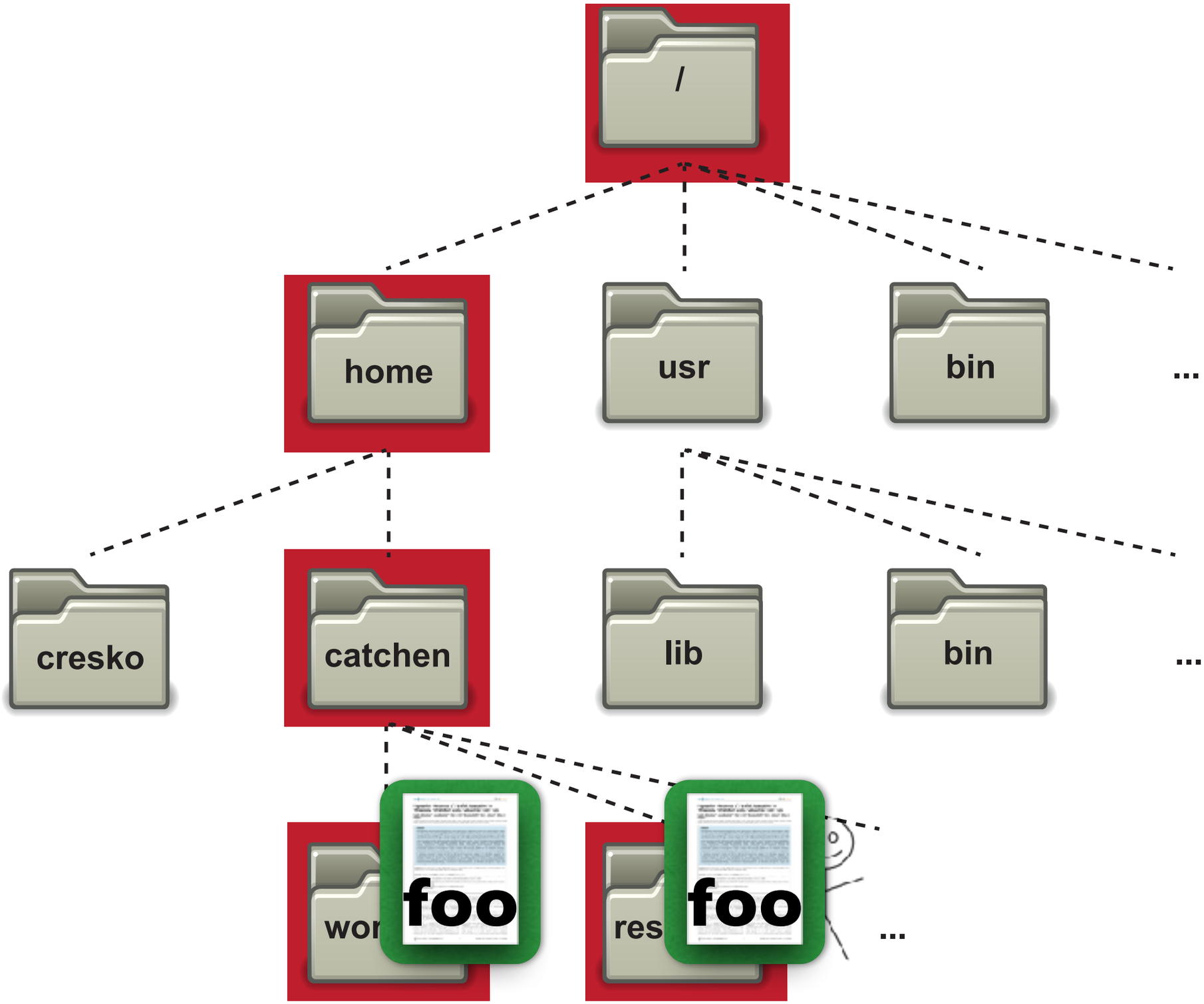



```
../working
```



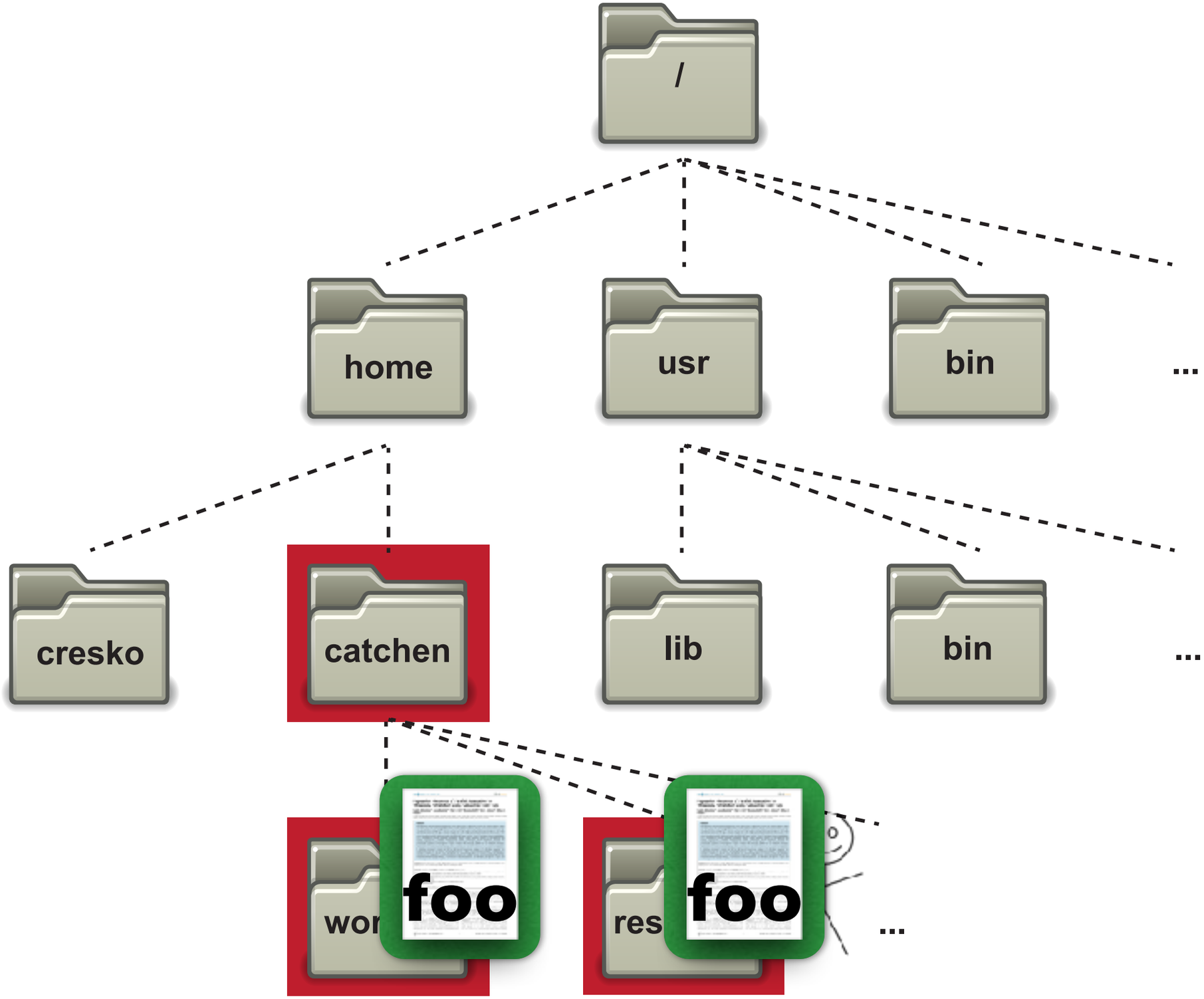
Absolute Path: **`/home/catchen/working/foo`**

Relative Path: **`../working/foo`**



Absolute Path: **`/home/catchen/working/foo`**

Absolute Path: **`/home/catchen/research/foo`**



Relative Path: `../working/foo`

Relative Path: `./foo`

Absolute and relative paths

```
ubuntu@ip-10-4-193-188:~$ mkdir shell
ubuntu@ip-10-4-193-188:~$ cd shell
ubuntu@ip-10-4-193-188:~/shell$ mkdir research
ubuntu@ip-10-4-193-188:~/shell$ ls
research
ubuntu@ip-10-4-193-188:~/shell$ cd research/
ubuntu@ip-10-4-193-188:~/shell/research$ mkdir seq
ubuntu@ip-10-4-193-188:~/shell/research$ ls
seq
ubuntu@ip-10-4-193-188:~/shell/research$ cd seq/
ubuntu@ip-10-4-193-188:~/shell/research/seq$ mkdir radtags
ubuntu@ip-10-4-193-188:~/shell/research/seq$ cd radtags/
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ ls
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ ls -la
total 8
drwxrwxr-x 2 ubuntu ubuntu 4096 2012-03-06 23:08 .
drwxrwxr-x 3 ubuntu ubuntu 4096 2012-03-06 23:08 ..
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$ pwd
/home/ubuntu/shell/research/seq/radtags
ubuntu@ip-10-4-193-188:~/shell/research/seq/radtags$
```

Special Files

dot

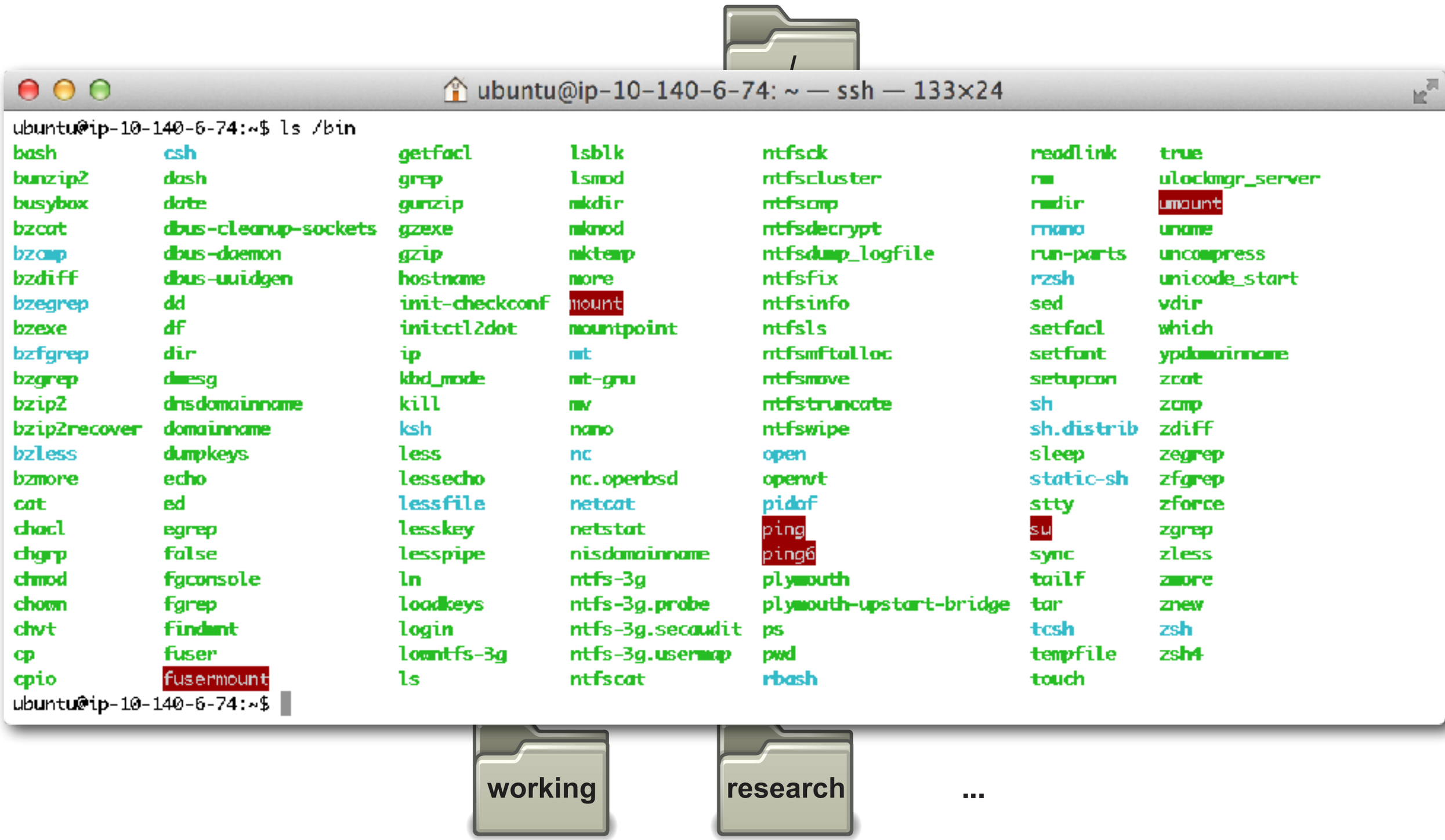
dot dot

```
% ls .
```

```
% ls ..
```

```
% ls ../../
```

Binary programs - ls, cp, mkdir, etc.



% ls /bin

Relative and absolute paths

A shortcut to your ‘home’, tilde:

~

Moving through the filesystem:

cd

Knowing where you are:

pwd

```
% ls ~/
```

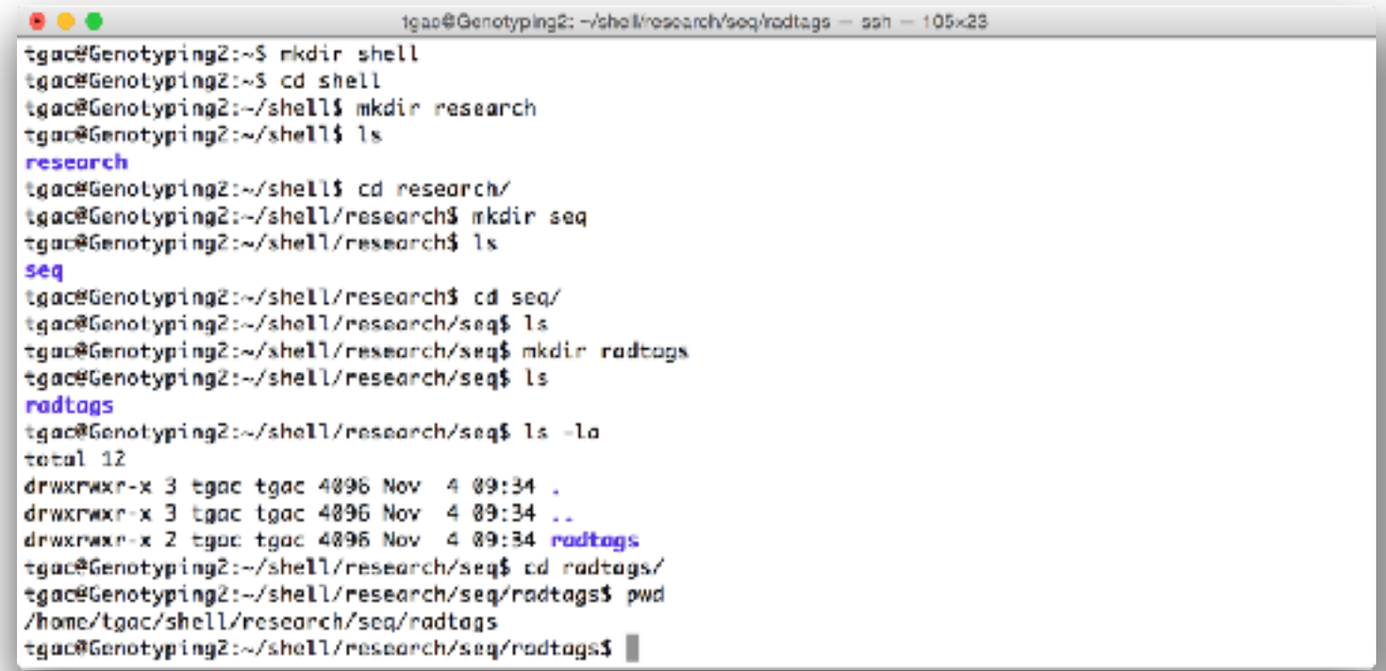
```
% cd ~/
```

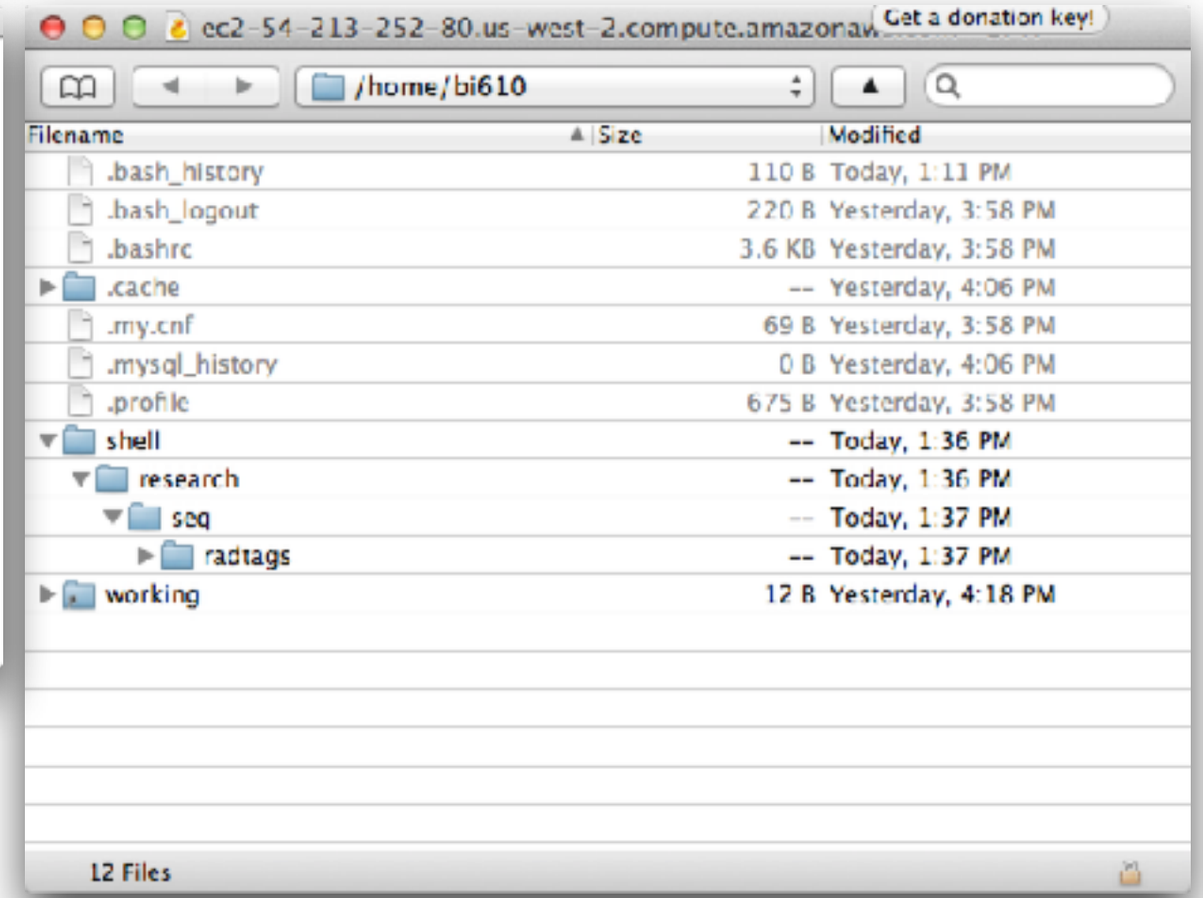
```
% cd
```

```
% pwd
```

Relative and absolute paths

`/home/tgac/shell/research/seq/radtags`






```
% ls .                % ls ..                % ls ../../
% cd ~/               % cd shell/research    % pwd
```

Are you typing? You're doing it wrong.

Tab-completion:

- Tab once to complete uniquely
- Tab twice to see all possible completions

Up-arrow:

- Previous commands can be found by pressing "up-arrow"

'history'

```
bi610@ip-172-31-17-121: /etc — ssh — 92×40
bi610@ip-172-31-17-121:~/shell/research/seq/radtags$ cd /etc/
bi610@ip-172-31-17-121:/etc$ ls -l
total 868
-rw-r--r-- 1 root root   15070 Apr  4 04:30 a2ps.cfg
-rw-r--r-- 1 root root    2563 Apr  4 04:30 a2ps-site.cfg
drwxr-xr-x 3 root root    4096 Apr 16 18:26 acpi
-rw-r--r-- 1 root root    2981 Apr 16 18:25 adduser.conf
-rw-r--r-- 1 root root      10 Apr 16 18:27 adjtime
drwxr-xr-x 2 root root    4096 Jun 20 22:23 alternatives
drwxr-xr-x 8 root root    4096 Jun 20 21:30 apache2
drwxr-xr-x 3 root root    4096 Apr 16 18:25 apm
drwxr-xr-x 3 root root    4096 Apr 16 18:26 apparmor
drwxr-xr-x 8 root root    4096 Jun 19 22:10 apparmor.d
drwxr-xr-x 3 root root    4096 Jun 19 22:00 apport
drwxr-xr-x 6 root root    4096 Apr 16 18:27 apt
-rw-r----- 1 root daemon   144 Oct 21  2013 at.deny
-rw-r--r-- 1 root root    2177 Apr  9 01:03 bash.bashrc
-rw-r--r-- 1 root root      45 Mar 22 20:57 bash_completion
drwxr-xr-x 2 root root    4096 Jun 20 21:44 bash_completion.d
-rw-r--r-- 1 root root     356 Jan  1  2012 bindresvport.blacklist
-rw-r--r-- 1 root root     321 Apr 16 16:07 blkid.conf
lrwxrwxrwx 1 root root      15 Jun  3 20:54 blkid.tab -> /dev/.blkid.tab
drwxr-xr-x 2 root root    4096 Apr 16 18:26 byobu
drwxr-xr-x 3 root root    4096 Apr 16 18:25 ca-certificates
-rw-r--r-- 1 root root    7464 Apr 16 18:26 ca-certificates.conf
drwxr-xr-x 2 root root    4096 Apr 16 18:26 calendar
drwxr-s--- 2 root dip     4096 Apr 16 18:26 chatscripts
drwxr-xr-x 4 root root    4096 Apr 16 18:27 cloud
drwxr-xr-x 2 root root    4096 Apr 16 18:25 console-setup
drwxr-xr-x 2 root root    4096 Jun 19 22:10 cron.d
drwxr-xr-x 2 root root    4096 Jun 19 22:10 cron.daily
drwxr-xr-x 2 root root    4096 Apr 16 18:25 cron.hourly
drwxr-xr-x 2 root root    4096 Apr 16 18:25 cron.monthly
-rw-r--r-- 1 root root     722 Feb  9  2013 crontab
drwxr-xr-x 2 root root    4096 Jun 20 22:23 cron.weekly
-rw-r--r-- 1 root root      54 Apr 16 18:26 crypttab
drwxr-xr-x 4 root root    4096 Apr 16 18:26 dbus-1
-rw-r--r-- 1 root root    2969 Feb 23 14:30 debconf.conf
-rw-r--r-- 1 root root      11 Feb 20 02:43 debian_version
drwxr-xr-x 3 root root    4096 Jun 20 22:23 default
```

```
% cd /etc
% ls c <tab>
```

```
% pwd
% ls c <tab><tab>
```

Three variants to `ls`

`ls -l`	`ls -la`	`ls -lh`
provides a *long* listing	includes *all* files, even hidden files	displays file sizes in *human* readable numbers

Four ways to view a text file

`more`	`head`	`tail`	`cat`
view a text file one screen full at a time	view the top 15 lines of a file	view the last 15 lines of a file	spit the whole file at once
space-bar: scroll q: quit	-n num controls the number of lines	-n num controls the number of lines	

Explore the file hierarchy

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 the root, what directories do you see?
4. Move back home, what are three ways to move home from the root?

Copy example files

Return to the directory in your home called ‘shell’.

TSV file:
~/unix/batch_1.genotypes_1.loc.gz

FASTQ file:
~/unix/s_1_sequence.txt.gz

Tar Archive:
~/unix/samples.tar.gz

What is a tar archive?

tar = tape archive

Compress / Decompress

`gzip` / `gunzip`

batch_1.genotypes_1.loc.gz

s_1_sequence.txt.gz

Gzipped Tar archive

`tar xvfz`

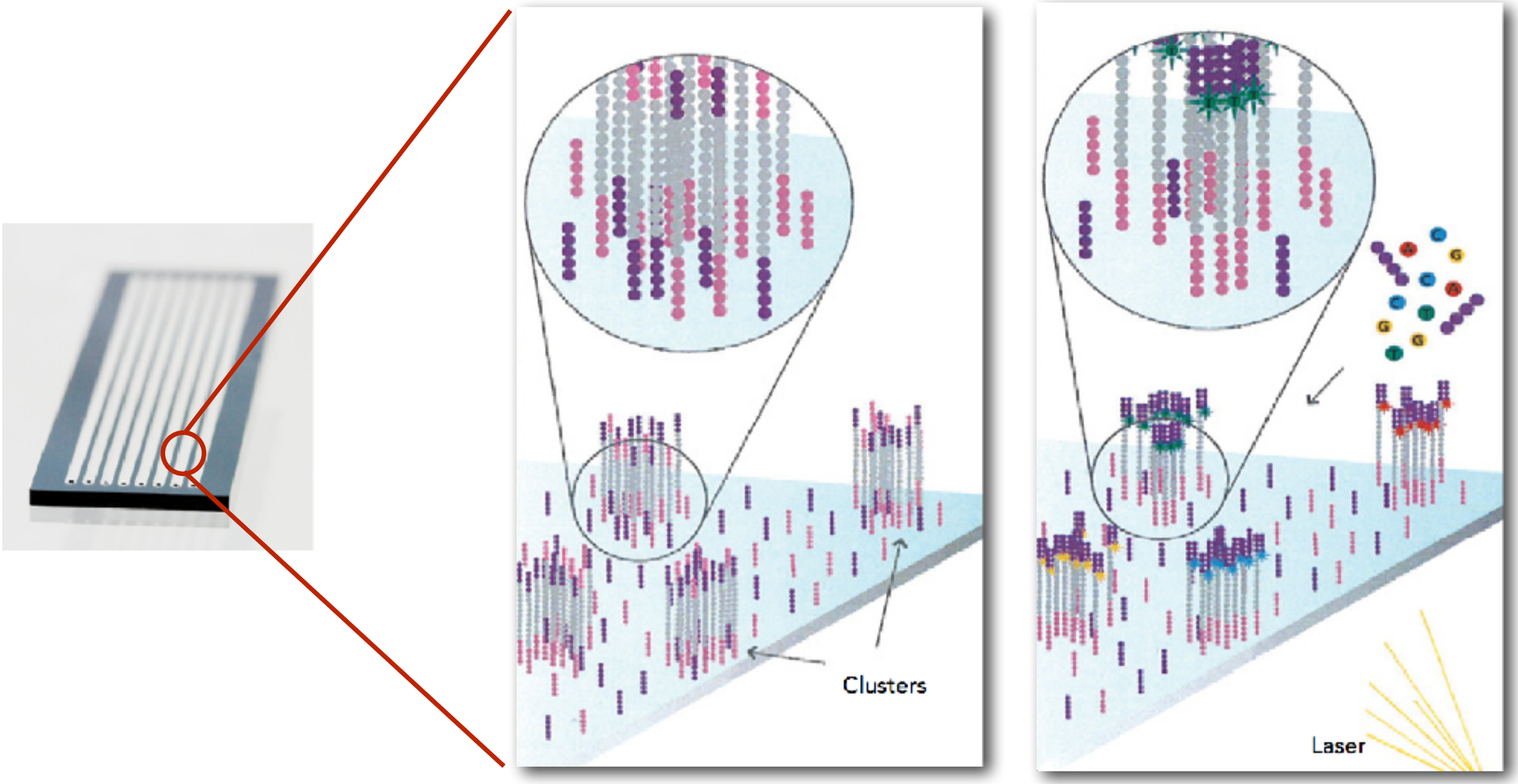
samples.tar.gz

Tar archive

`tar xvf`

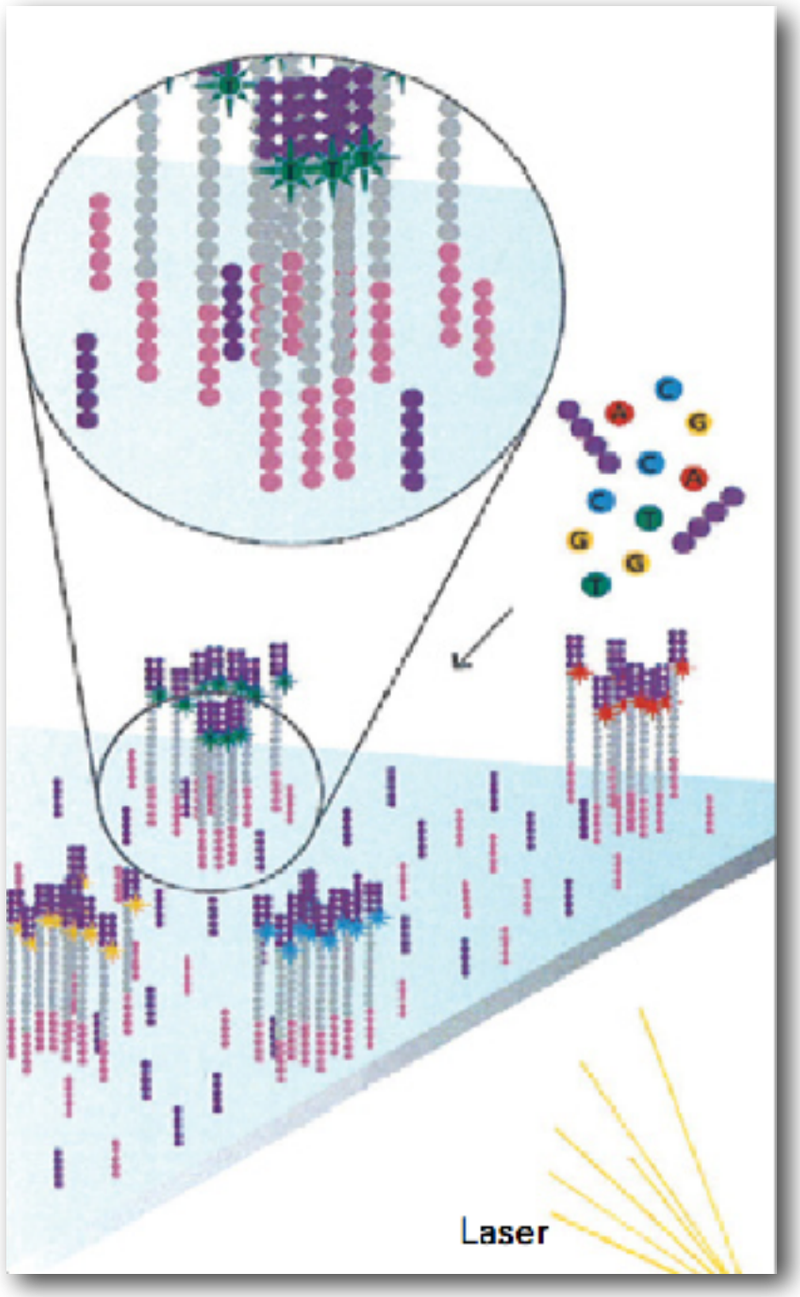
samples.tar

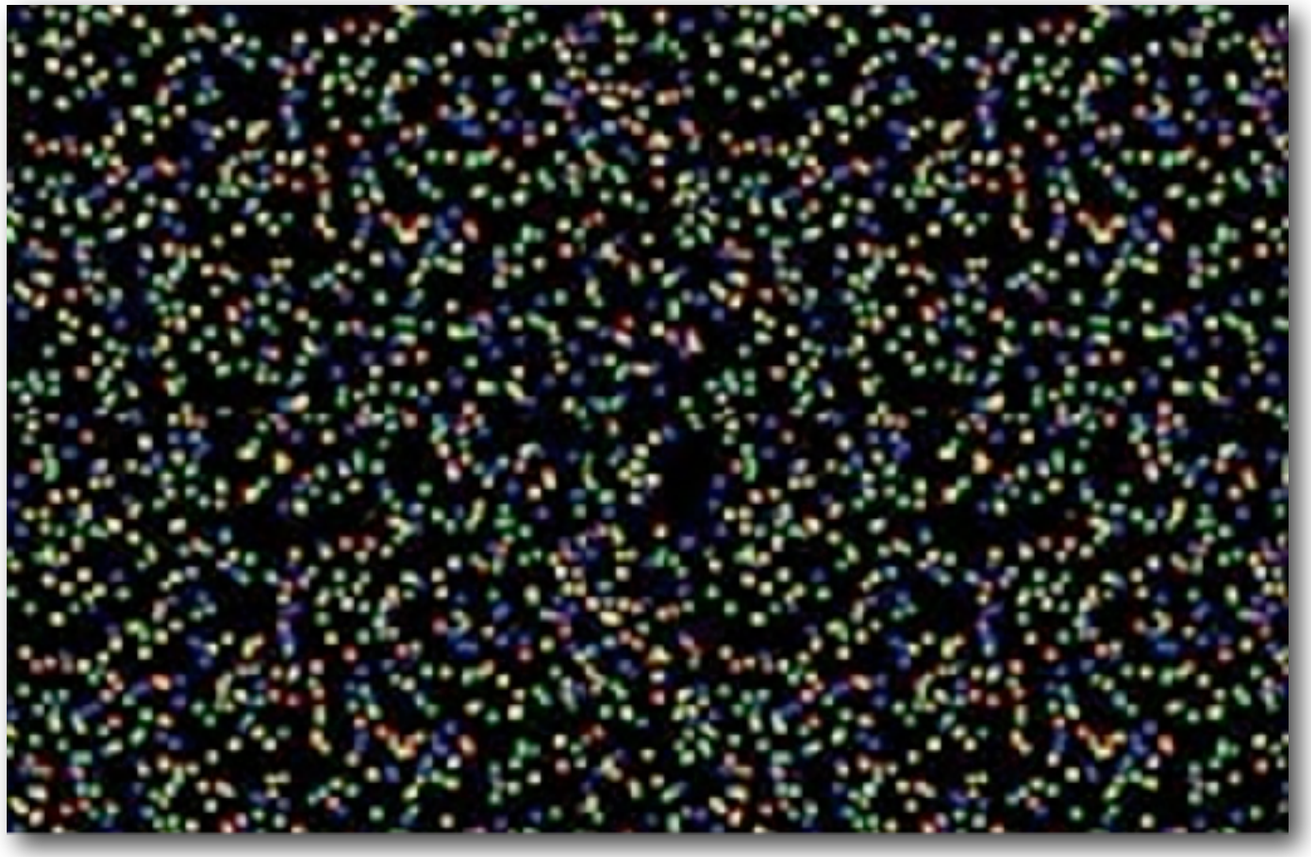
Sequencing on Illumina's Flow cell



Source: Illumina Publication 770-2007-002 01May07

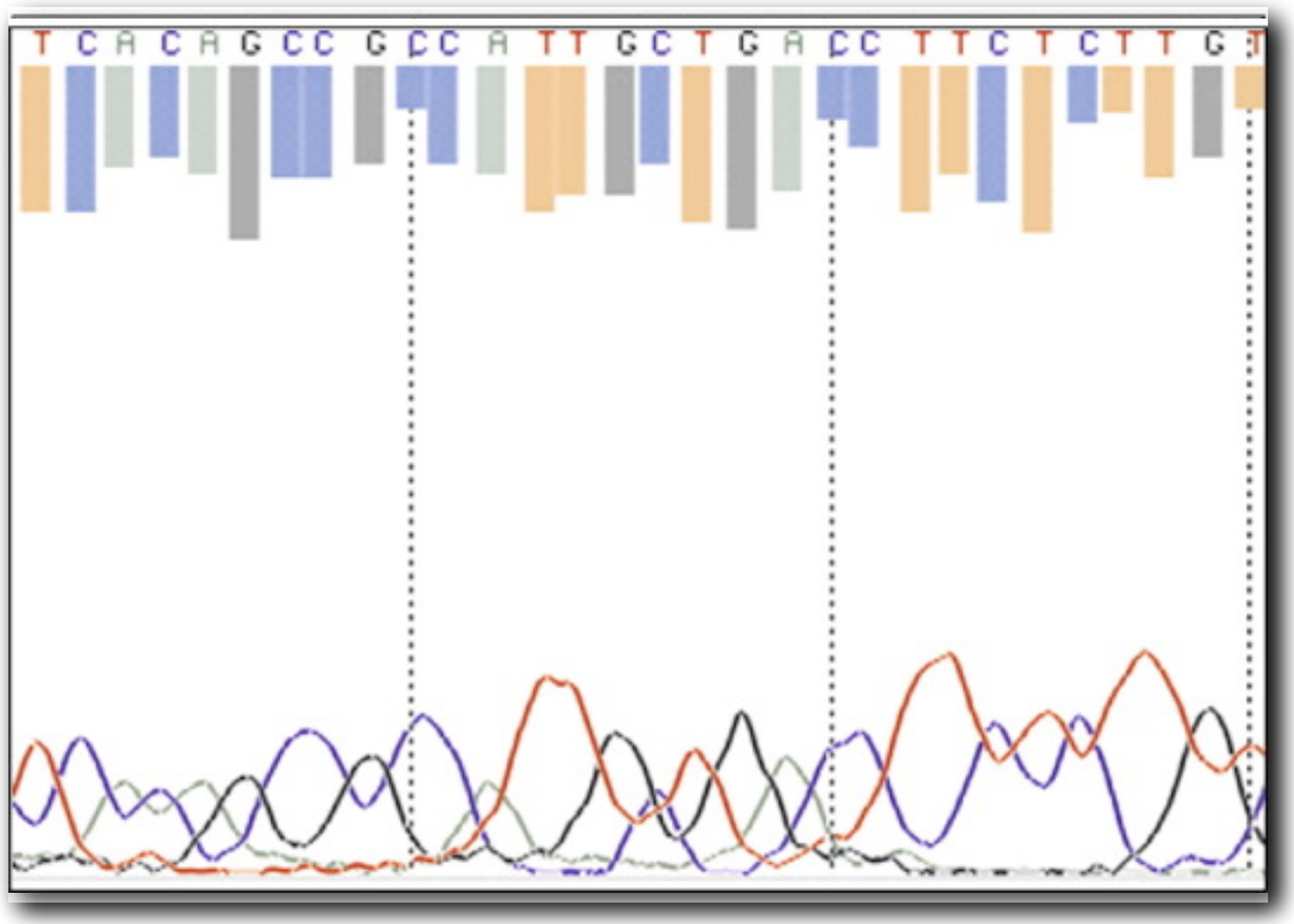
Sequencing on Illumina's Flow cell, ctd.





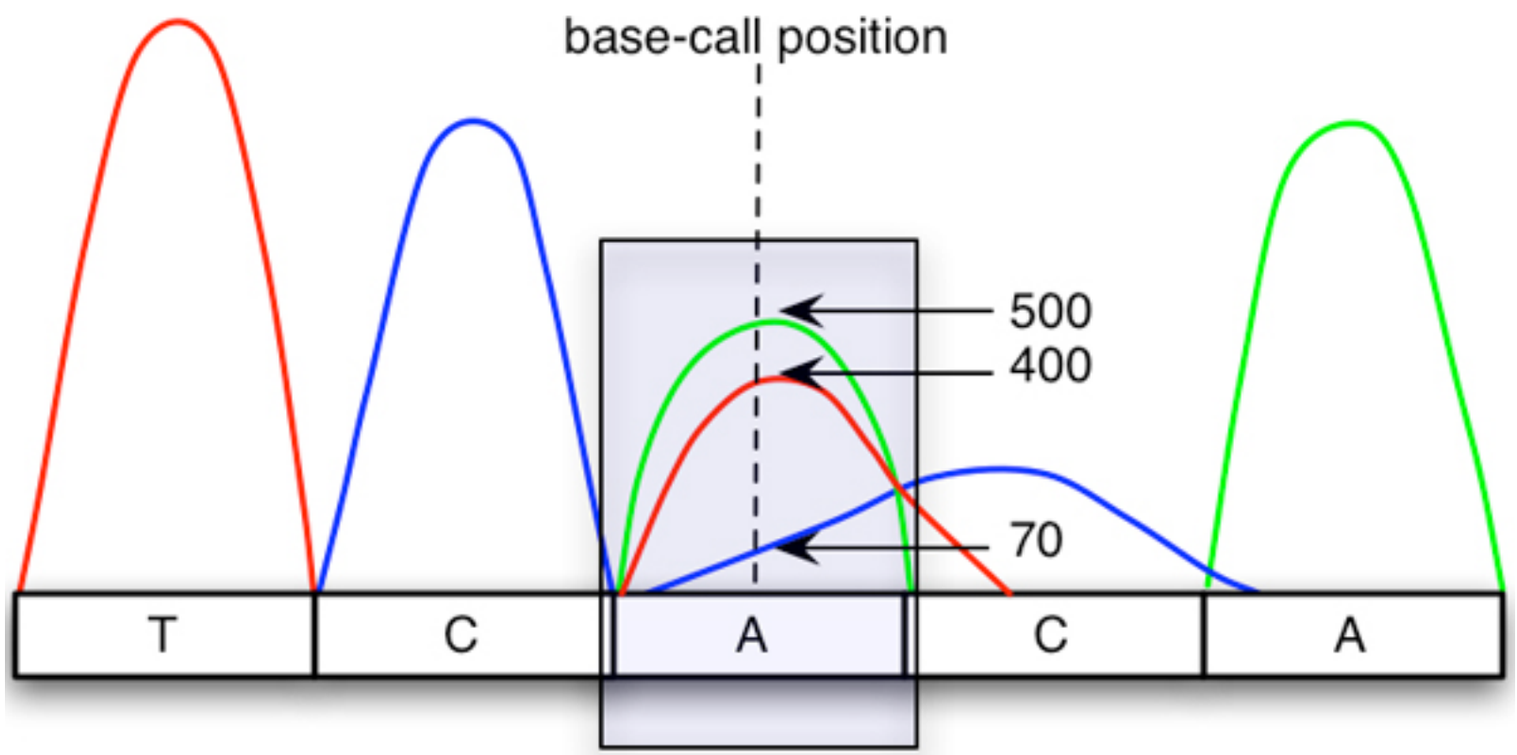
Source: Illumina Publication 770-2007-002 01May07

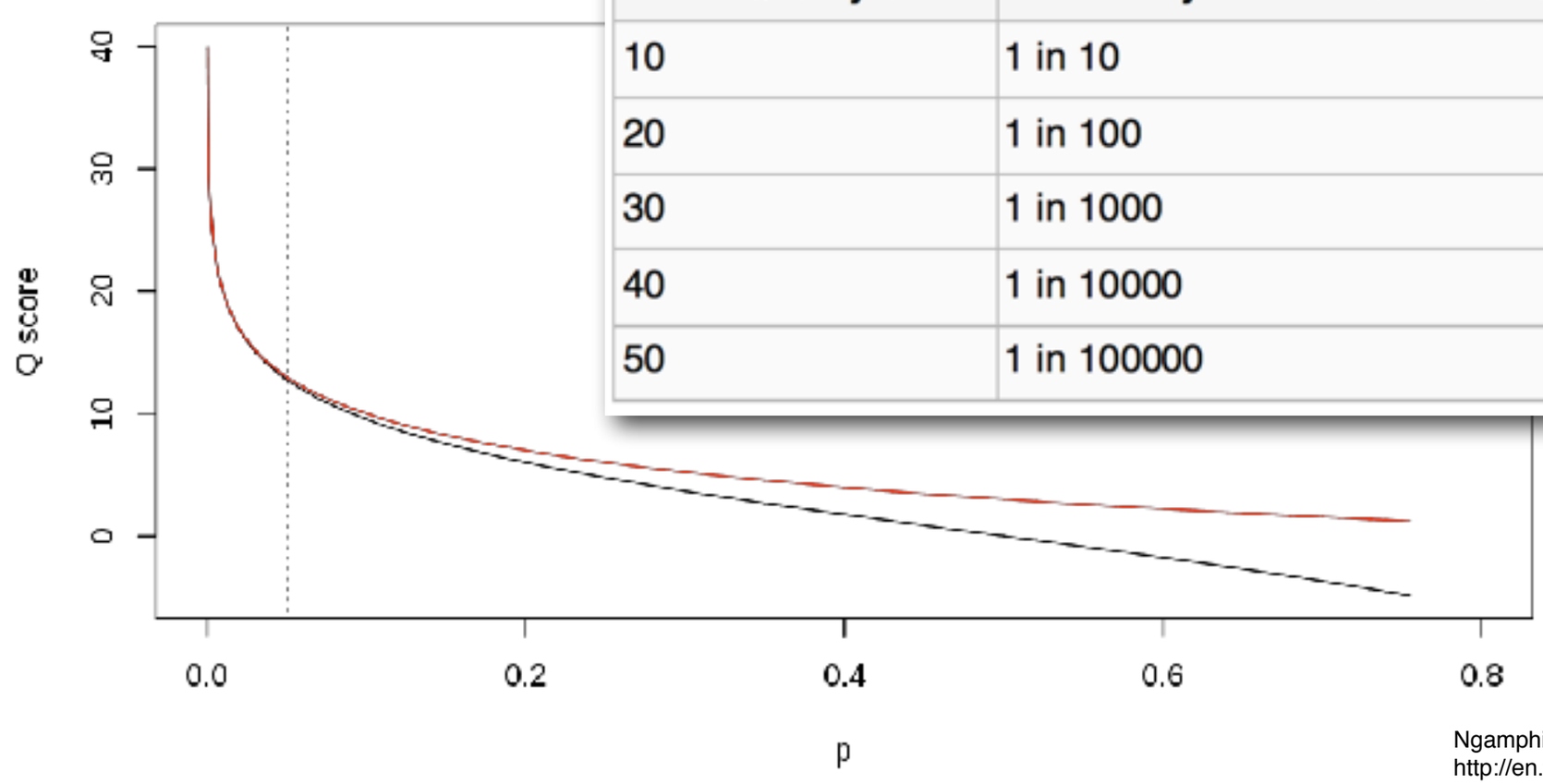
Sequencing on Illumina's Flow cell, ctd.



Source: Kim, et al. doi:10.1016/j.pnsc.2007.12.011

Phred Quality Score





Phred Quality Score	Probability of incorrect base call	Base call accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1000	99.9%
40	1 in 10000	99.99%
50	1 in 100000	99.999%

Ngamphiw, et al. doi:10.1186/1471-2105-9-S12-S9
http://en.wikipedia.org/wiki/FASTQ_format

The FASTQ File Format

FASTA

```
>chromosome7
TTTGTCTGCAGGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATTTT
ACATACTGCAGGGTCAGGAGGATTATCTCCTCTGCAAGGTAACGCCTGCTGTAACCGTTGTTCTTCATCCTTTT
CCTAACTGCAGGGCTGTCTTGTCAGGTCTGACAAGACATATGCAGGGCTCAATTTGAGATAATTGCTCAATATA
```

FASTQ

```
@Sequence_137
TTTGTCTGCAGGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATTTT
+Sequence_137
<?@DDDDDHFHHFBB@GGIACFHGGHBGHGCDHBEAHACHI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA
```

```
@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTTGTCTGCAGGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATTTT
+
<?@DDDDDHFHHFBB@GGIACFHGGHBGHGCDHBEAHACHI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA
```

http://4toc.com/fb/FBHelp/gfx/AppF_ASCIITable.png

ASCII Code

0	<NUL>	32	<SPC>	64	@	96	`	128	Ä	160	†	192	¿	224	‡
1	<SOH>	33	!	65	A	97	a	129	Å	161	°	193	¡	225	·
2	<STX>	34	"	66	B	98	b	130	Ç	162	¢	194	¬	226	‚
3	<ETX>	35	#	67	C	99	c	131	É	163	£	195	√	227	„
4	<EOT>	36	$	68	D	100	d	132	Ñ	164	§	196	ƒ	228	‰
5	<ENQ>	37	%	69	E	101	e	133	Ö	165	•	197	≈	229	Â
6	<ACK>	38	&	70	F	102	f	134	Ü	166	¶	198	Δ	230	Ê
7	<BEL>	39	'	71	G	103	g	135	á	167	ß	199	«	231	Á
8	<BS>	40	(	72	H	104	h	136	à	168	®	200	»	232	Ë
9	<TAB>	41	)	73	I	105	i	137	â	169	©	201	…	233	È
10	<LF>	42	*	74	J	106	j	138	ä	170	™	202		234	Í
11	<VT>	43	+	75	K	107	k	139	ã	171	´	203	À	235	Î
12	<FF>	44	,	76	L	108	l	140	å	172	¨	204	Ã	236	Ï
13	<CR>	45	-	77	M	109	m	141	ç	173	≠	205	Õ	237	Ì
14	<SO>	46	.	78	N	110	n	142	é	174	Æ	206	Œ	238	Ó
15	<SI>	47	/	79	O	111	o	143	è	175	Ø	207	œ	239	Ô
16	<DLE>	48	0	80	P	112	p	144	ê	176	∞	208	–	240	
17	<DC1>	49	1	81	Q	113	q	145	ë	177	±	209	—	241	Ò
18	<DC2>	50	2	82	R	114	r	146	í	178	≤	210	“	242	Ú
19	<DC3>	51	3	83	S	115	s	147	ì	179	≥	211	”	243	Û
20	<DC4>	52	4	84	T	116	t	148	î	180	¥	212	‘	244	Ù
21	<NAK>	53	5	85	U	117	u	149	ï	181	µ	213	’	245	ı
22	<SYN	54	6	86	V	118	v	150	ñ	182	∂	214	÷	246	ˆ
23	<ETB>	55	7	87	W	119	w	151	ó	183	∑	215	◊	247	˜
24	<CAN>	56	8	88	X	120	x	152	ò	184	∏	216	ÿ	248	¯
25	<EM>	57	9	89	Y	121	y	153	ô	185	π	217	Ÿ	249	˘
26	<SUB>	58	:	90	Z	122	z	154	ö	186	∫	218	/	250	˙
27	<ESC>	59	;	91	[	123	{	155	õ	187	ª	219	€	251	°
28	<FS>	60	<	92	\	124	|	156	ú	188	º	220	‹	252	¸
29	<GS>	61	=	93	]	125	}	157	ù	189	Ω	221	›	253	˝
30	<RS>	62	>	94	^	126	~	158	û	190	æ	222	fi	254	˛
31	<US>	63	?	95	_	127	<DEL>	159	ü	191	ø	223	fl	255	ˇ

8 bits = 2^8 combinations = 256

0	1	1	1	1	0	0	1

$0x2^7+1x2^6+1x2^5+1x2^4+1x2^3+0x2^2+0x2^1+1x2^0 = 121 =$ **y**

$1x10^2+2x10^1+1x10^0 = 121 =$ **y**

The FASTQ File Format, ctd

```
@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTTGTCTGCAGGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATTTT
+
<?@DDDDDHFHHFBB@GGIACFHGGHBGHGCDHBEAHACHI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA
```

Quality Scores

```
  SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS.......................................................
  ........................XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX......................
  ..............................IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII......................
  ................................JJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJ......................
 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL.......................................................
 !"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKLMNOPQRSTUVWXYZ[\]^_`abcdefghijklmnopqrstuvwxyz{|}~
 |                         |    |        |                              |                     |
33                        59   64       73                            104                   126

S - Sanger        Phred+33,  raw reads typically (0, 40)
X - Solexa        Solexa+64, raw reads typically (-5, 40)
I - Illumina 1.3+ Phred+64,  raw reads typically (0, 40)
J - Illumina 1.5+ Phred+64,  raw reads typically (3, 40)
   with 0=unused, 1=unused, 2=Read Segment Quality Control Indicator (bold)
   (Note: See discussion above).
L - Illumina 1.8+ Phred+33,  raw reads typically (0, 41)
```

ASCII values $33 - 73 = 0 - 40$

'F' = 70 70 - 33 = **37**

http://en.wikipedia.org/wiki/FASTQ_format

The FASTQ File Format, ctd

```
@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTTGTCTGCAGGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATTTT
+
<?@DDDDDHFHHFBB@GGIACFHGGHBGHGCDHBEAHACHI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA
```

70 - 33 = 37

Phred Quality Score	Probability of incorrect base call	Base call accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1000	99.9%
40	1 in 10000	99.99%
50	1 in 100000	99.999%

http://en.wikipedia.org/wiki/Phred_quality_score

Count raw reads:

```
wc -l s_1_sequence.txt

grep "@" s_1_sequence.txt
grep -c "@" s_1_sequence.txt

grep -v "@" s_1_sequence.txt
grep -v -c "@" s_1_sequence.txt
```

Count reads with barcode:

```
grep -c "^CGATA" s_1_sequence.txt
```

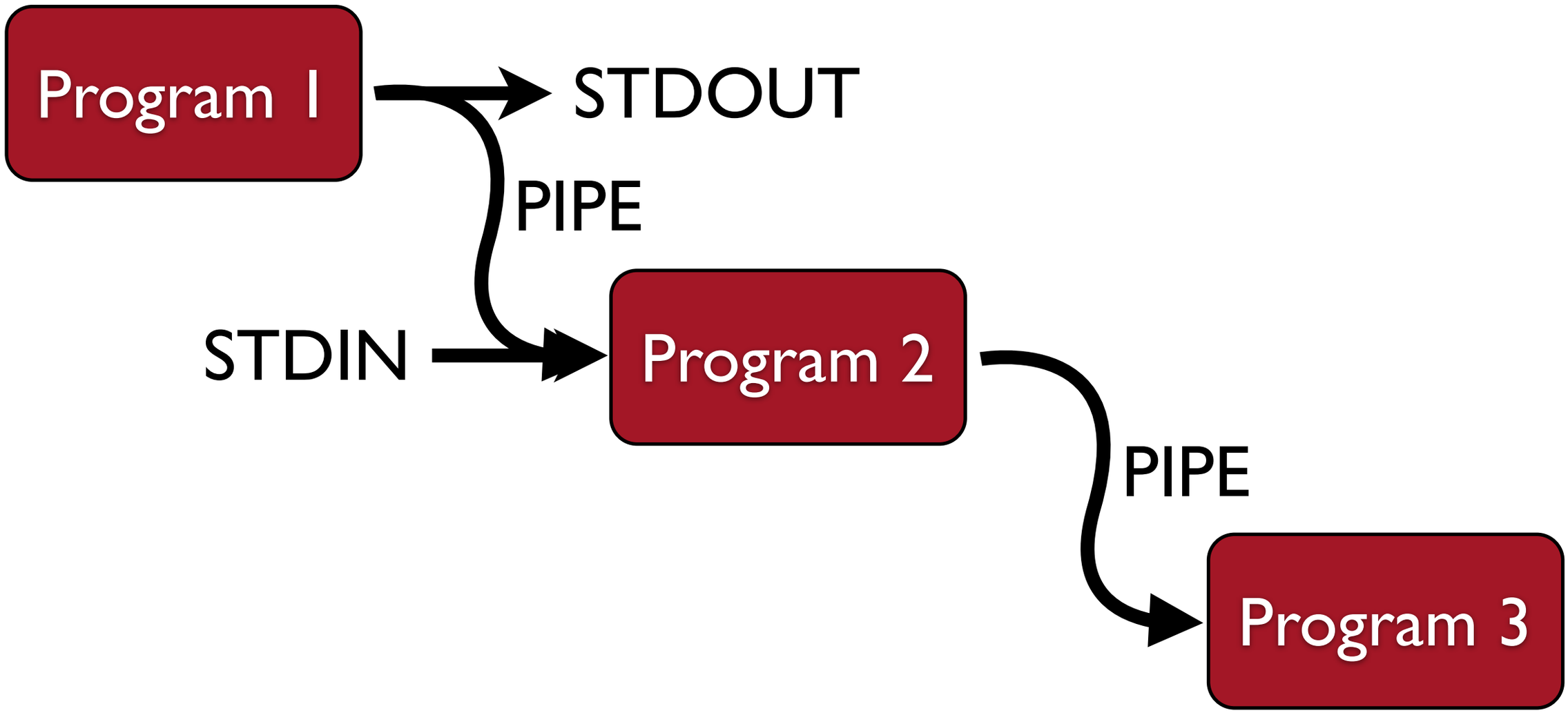
Special Files

STDIN, STDOUT, STDERR

The Shell's Killer App: **Pipes**

The Shell's Killer App: **Pipes**, ctd.

The Shell's Killer App: **Pipes**, ctd.



So what is the purpose of the program **`cat`**?

cut

```
cut -f 10 batch_1.genotypes_1.loc
```

cut, capture the output

```
cut -f 1-10 batch_1.genotypes_1.loc > genos
```

cut, pipe the output to grep

```
cut -f 2 batch_1.genotypes_1.loc | grep -c "nnxnp"
```

```
cut -f 1-10,15,17 batch_1.genotypes_1.loc | grep "nnxnp" > genos2
```

Examine a marker, translating the output

```
cat batch_1.genotypes_1.loc | tr "     " "," | grep "^96053"
```

s_1_sequence.txt.gz

Decompress the file

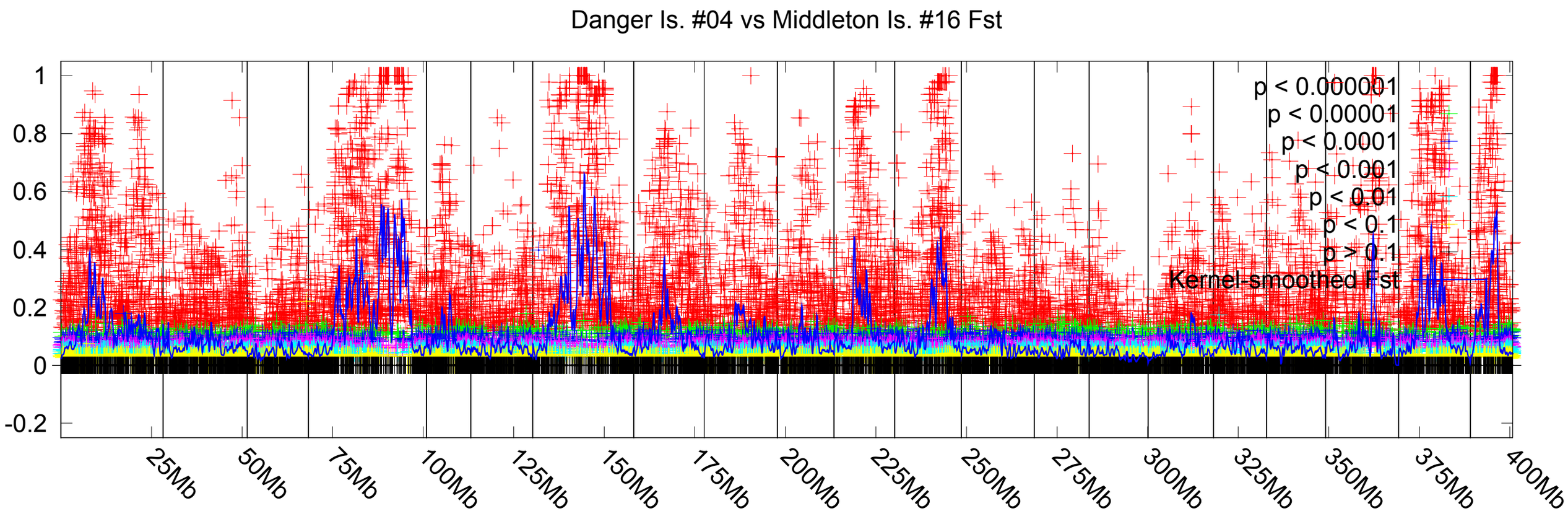
1. Count the number of raw reads (250,000)
2. Count the number of reads with barcode `CGATA` (19,501)
3. Capture all FASTQ records for `ACCAT` into a file called sample_01.fq (you should get 18352 records, 73408 lines)
4. Determine the count of all barcodes in the file

```
286 CTAGT
7900 TCAGA
10659 ACTGC
10931 TGACC
11536 GAGAT
11871 CTGAA
14409 CGGCG
14508 TGGTT
18226 GAAGC
18352 ACCAT
18375 TCGAG
19501 CGATA
23012 AATTT
26336 GCATT
31136 CTAGG
```

`ls`
`gunzip`
`man`
`more`
`cat`
`wc`
`head`
`cut`
`grep`
`sort`
`uniq`
`>`
`|`

1. Use **`head`** when building a command, **`cat`** once the command is working
2. Look at the **-n** option for the **head** command, the **-l** option for **wc**
3. The "^" character means "must occur at beginning of line" in a grep search
4. Look at the **grep** options: **-c**, **-v, -A**, **-B**
5. Read the man pages for **sort** and **uniq** to learn how to combine them

Problem Set #1



# Batch ID	Locus ID		Pop 1 ID	Pop 2 ID	Chr	BP	Column	Overall Pi	Fst	Fisher's P	Odds Ratio
2	7894	2	3	groupI	11832	19	0.428182	-0.0076252913	0.191294		0.687192
2	7896	2	3	groupI	11900	83	0.328622	0.1775694587	4.35747e-08		5.44667
2	9611	2	3	groupI	49756	48	0.090426	-0.1127451906	0.00109115		0.0898072
2	9611	2	3	groupI	49765	57	0.0132887	-0.1522407447	0.518395		0.493113
2	9611	2	3	groupI	49766	58	0.0133776	-0.1563725438	0.520033		0.501401
...											
2	7083	2	3	groupIX	20172984	57	0.0480227	-0.1249752728	0.0230205		0.152263
2	7083	2	3	groupIX	20173004	77	0.0181808	-0.1405892833	0.27288		0.355556
2	7083	2	3	groupIX	20173016	89	0.0424072	-0.1243625038	0.0442229		0.17037
2	7083	2	3	groupIX	20173018	91	0.148072	0.2305903127	2.24832e-07		13.2936
2	7084	2	3	groupIX	20172960	29	0.388239	-0.0102170169	0.307185		0.758001
2	7084	2	3	groupIX	20172995	64	0.368259	-0.0130602425	0.233889		0.70084
2	7084	2	3	groupIX	20173013	82	0.0121578	-0.1359057575	0.51309		0.46472