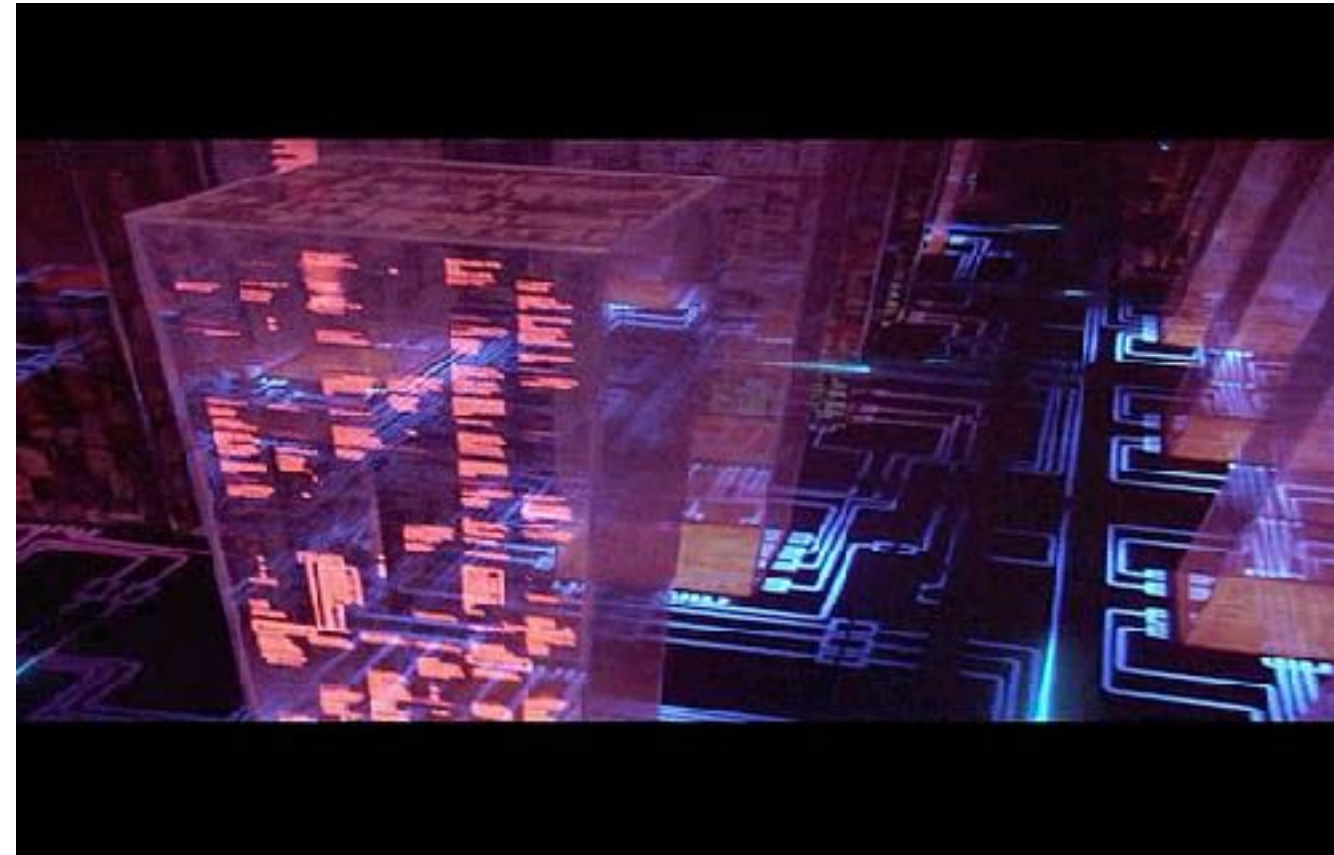


Tetrad computational bootcamp



Intro to computer architecture

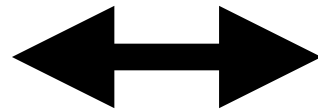


CPU

fast

small (< 1MB)

volatile

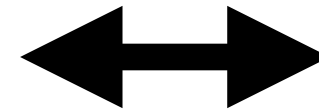


RAM
("memory")

>10x slower

medium (~10GB)

volatile



Hard Drive
("disk")

>100-1000x slower

large (>1TB)

"permanent"

Serial vs parallel vs vector processing

| | **2 | | |
|---|-----|---|----|
| 1 | 1*1 | = | 1 |
| 2 | 2*2 | = | 4 |
| 3 | 3*3 | = | 9 |
| 4 | 4*4 | = | 16 |
| 5 | 5*5 | = | 25 |
| 6 | 6*6 | = | 36 |
| 7 | 7*7 | = | 49 |
| 8 | 8*8 | = | 64 |

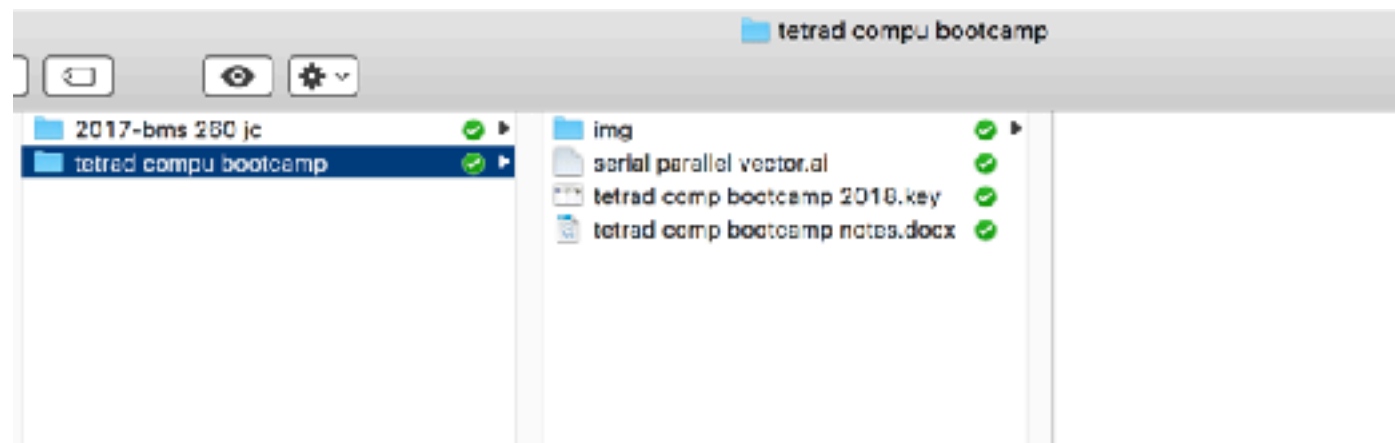
One CPU: total time = 8 units

“serial processing”

What is an operating system?



Finder vs the terminal

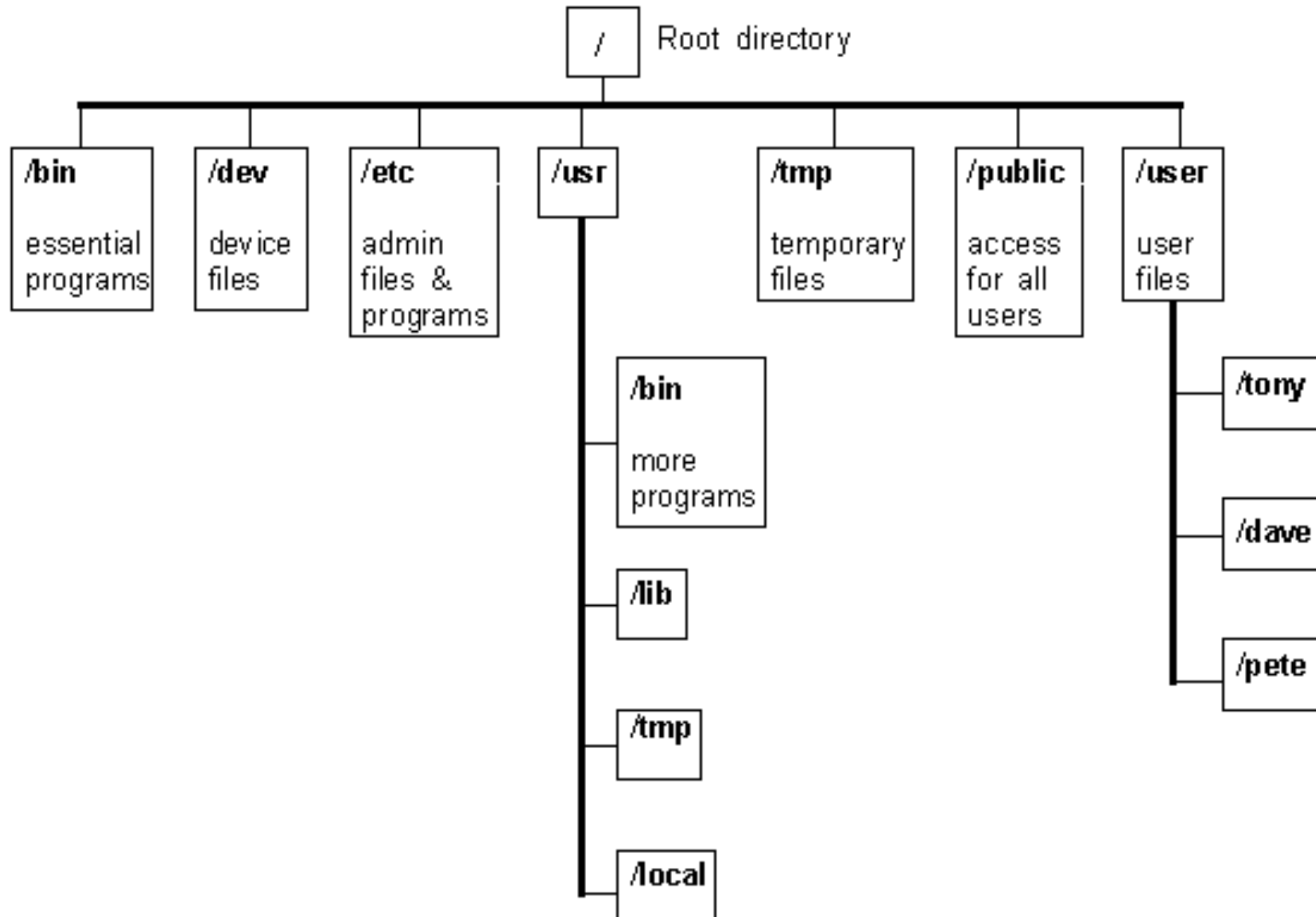


```
Terminal — -zsh — 107x44
[snf@snf-iMac prof/teaching/tetrad compu bootcamp]$ ls
img 'serial parallel vector.ai' 'tetrad comp bootcamp 2018.key' 'tetrad comp bootcamp notes.docx'
[snf@snf-iMac prof/teaching/tetrad compu bootcamp]$
```

Macintosh HD > Users > snf > Dropbox > prof > teaching > tetrad compu bootcamp

```
Terminal — -zsh — 107x44
[[snf@snf-iMac prof/teaching/tetrad compu bootcamp]$ pwd
/Users/snf/Dropbox/prof/teaching/tetrad compu bootcamp
[snf@snf-iMac prof/teaching/tetrad compu bootcamp]$
```

The linux/UNIX/BSD/OSX file system



Command line bootcamp

http://rik.smith-unna.com/command_line_bootcamp/

For more on using the command line

<http://rescuedbycode.com/linux-bootcamp>

[http://korflab.ucdavis.edu/Unix and Perl/current.html](http://korflab.ucdavis.edu/Unix_and_Pperl/current.html)

<http://www.tldp.org/LDP/GNU-Linux-Tools-Summary/html/GNU-Linux-Tools-Summary.html>

Exercise 1

Navigate to `/usr/share/calendar/`

What are the contents of the file `calendar.lotr`?

Installing programs: bioconda (for linux/OSX)

Install Anaconda:

https://repo.anaconda.com/archive/Anaconda3-5.2.0-MacOSX-x86_64.pkg

```
[[snf@snf-iMac ~]$ which conda  
/Users/snf/anaconda3/bin/conda
```

<https://bioconda.github.io/>

```
conda config --add channels defaults  
conda config --add channels conda-forge  
conda config --add channels bioconda
```

```
[[snf@snf-iMac ~]$ conda search star  
Loading channels: done  
# Name          Version          Build    Channel  
star            2.4.0j           0        bioconda  
star            2.4.0j           1        bioconda  
star            2.5.0c           0        bioconda  
star            2.5.1b           0        bioconda  
star            2.5.2a           0        bioconda  
star            2.5.2b           0        bioconda  
star            2.5.3a           0        bioconda  
star            2.5.4a           0        bioconda  
star            2.6.0b           0        bioconda  
star            2.6.0c           0        bioconda  
star            2.6.0c           1        bioconda  
star            2.6.1a           1        bioconda
```

Installing programs: bioconda

```
[[snf@snf-iMac ~]$ conda install star
```

```
Solving environment: done
```

```
## Package Plan ##
```

```
environment location: /Users/snf/miniconda3
```

```
added / updated specs:
```

```
- star
```

```
The following packages will be downloaded:
```

| package | build | | |
|---------------------------|------------|--------|-------------|
| conda-4.5.11 | py36_0 | 625 KB | conda-forge |
| certifi-2018.8.24 | py36_1 | 139 KB | conda-forge |
| ca-certificates-2018.8.24 | ha4d7672_0 | 136 KB | conda-forge |
| star-2.6.1a | 1 | 1.7 MB | bioconda |
| openssl-1.0.2p | h470a237_0 | 3.3 MB | conda-forge |
| Total: | | 5.9 MB | |

```
[[snf@snf-iMac ~]$ which STAR  
/Users/snf/miniconda3/bin/STAR
```

conda install -y fastp pysam samtools

```
[[snf@snf-iMac ~]$ conda list | grep -e pysam -e samtools -e fastp -e star  
fastp          0.19.3          hd28b015_0      bioconda  
pysam          0.14.1          py36hae42fb6_1  bioconda  
samtools       1.7             1              bioconda  
star           2.6.1a          1              bioconda
```

Installing programs in the terminal

Programs you install for yourself go in `~/src`

Programs you install for everyone typically go in `/usr` or `/usr/local`

Programs bioconda installs go in `~/anaconda3/bin/`

(remember: `~` is your home directory)

Exercise 2

kallisto is an alignment-free RNA-seq quantification tool

use conda to install kallisto

Exercise 3

Navigate to the newly-installed kallisto directory

Find "run_test.sh"

Run it (**source**)

Remote access: ssh, scp, wget, ftp

```
ssh snf@brubeck.ucsf.edu
```

```
scp snf@brubeck.ucsf.edu:file ~
```

```
scp snf@brubeck.ucsf.edu:file .
```

```
wget https://repo.anaconda.com/archive/Anaconda3-5.2.0-MacOSX-  
x86_64.pkg
```

Please run these to install lftp:

```
conda install -y lftp
```

```
cd ~/miniconda3/lib
```

```
ln -s libtinfo.dylib libtinfo.6.dylib
```

```
lftp ftp.ensembl.org
```


Exercise 4: download some gene annotations

```
lftp ftp.ensembl.org
```

```
download the release 93 gff3 for Homo sapiens  
chromosome 1
```