

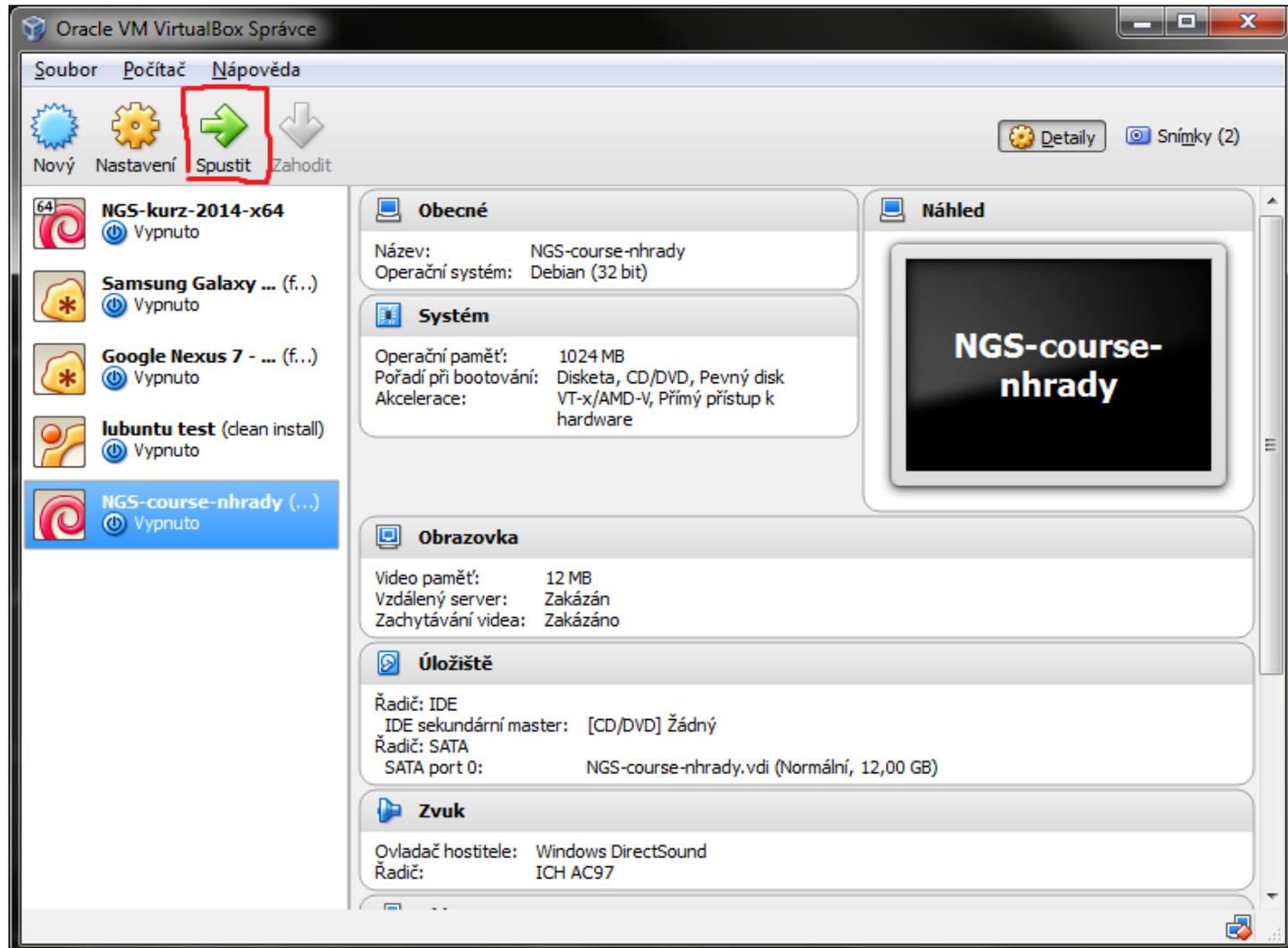
# Unix - Basics

Course on Unix and Genomic Data  
Prague, January 2016

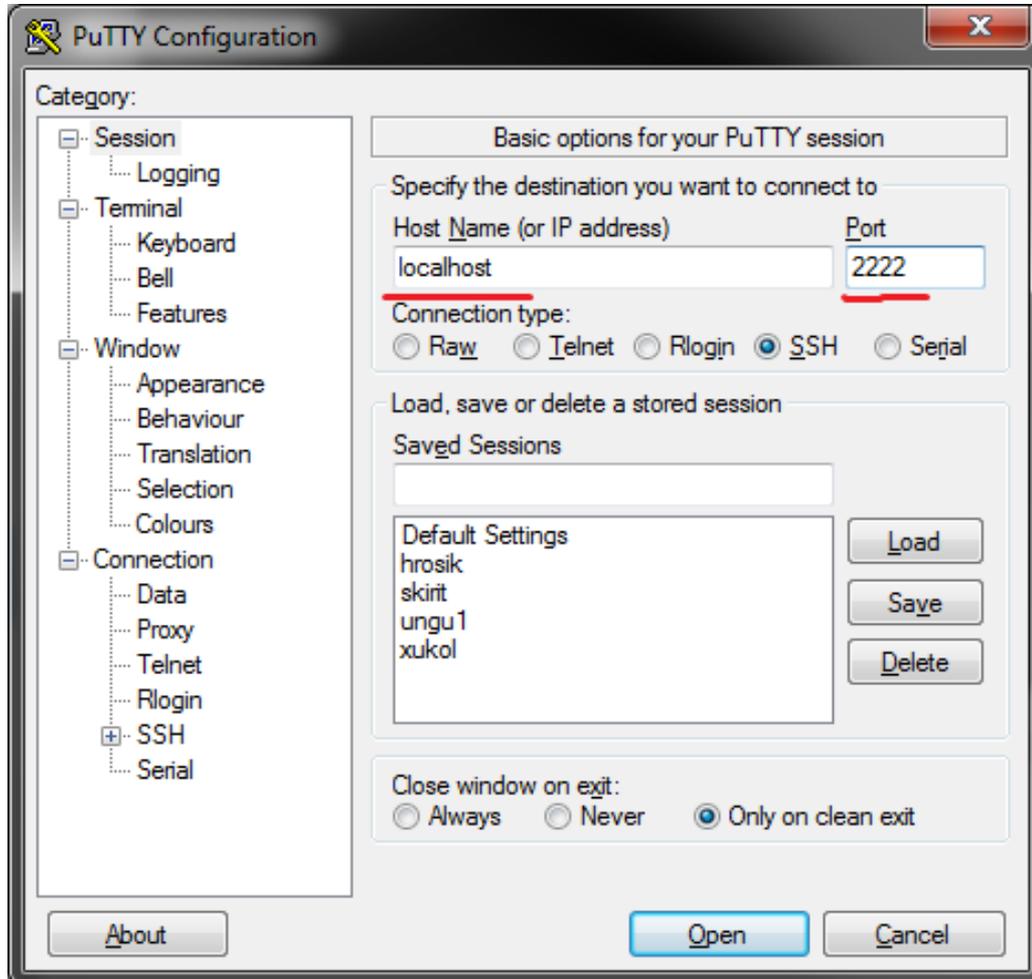
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<http://ngs-course.readthedocs.org/en/praha-january-2016/>

# Start Virtual Machine



# Get connected: PuTTY



OS X/Linux (command line):

```
ssh -p 2222 user@localhost
```

```
user@localhost:~$
```

*This is where all begins...*

# Command line

To type commands (syntax):

```
name (-flag(=flag-parameter)) (input) (output)
```

```
head -n 20 file.txt > file-out.txt
```

\*\* man command || google it

# Take a break and check your keyboard

[ ] - squared brackets

{ } - curly brackets

< > - angle brackets (smaller-than,  
bigger-than sign)

( ) - parentheses

~ - tilde

/ - slash

\ - back slash

| - pipe

^ - caret

\$ - dollar sign

:

;

.

,

# - hash

\_ - underscore

- - dash

\* - asterisk

! - exclamation mark

? - question mark

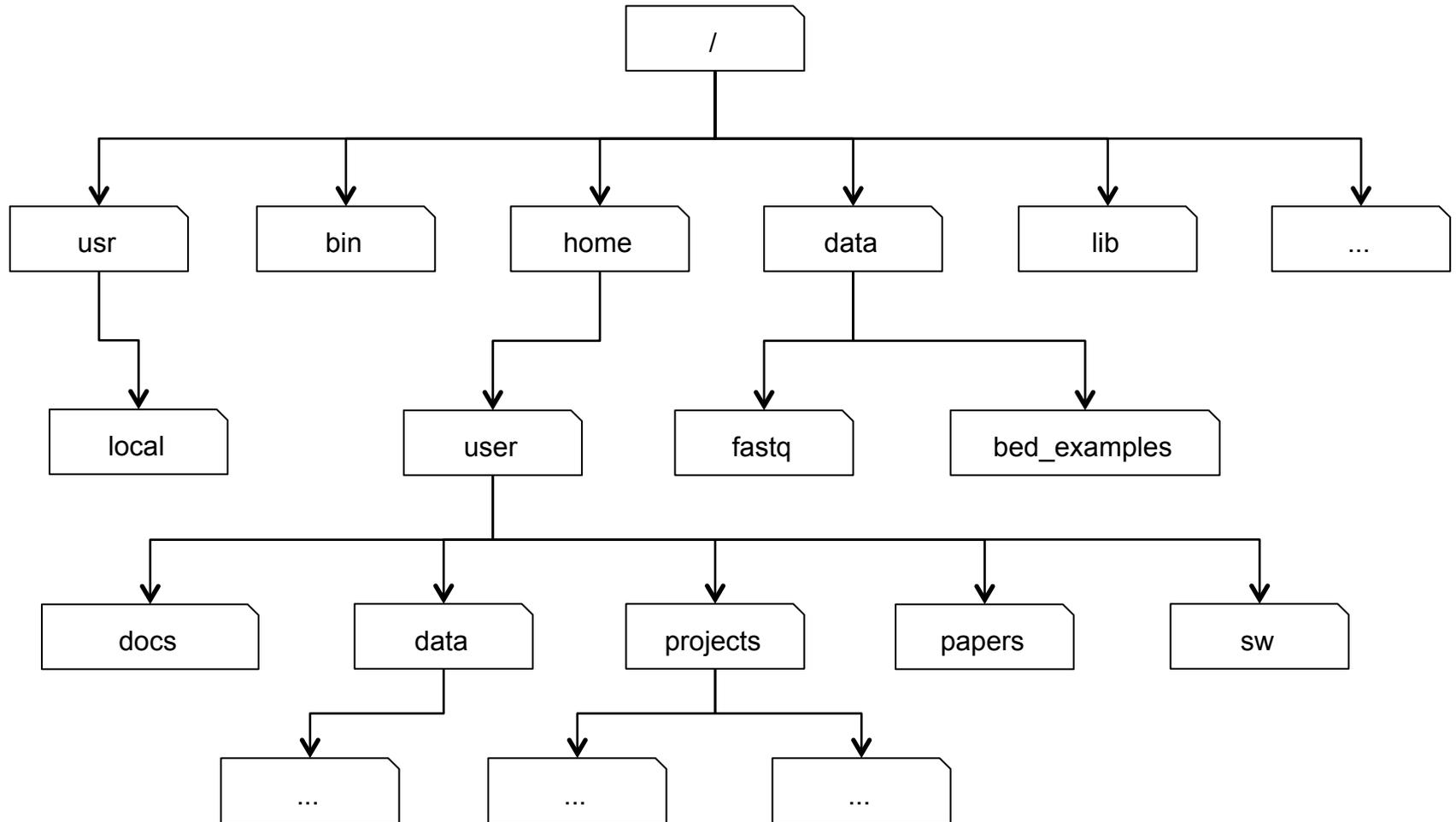
& - ampersand

@ - at sign

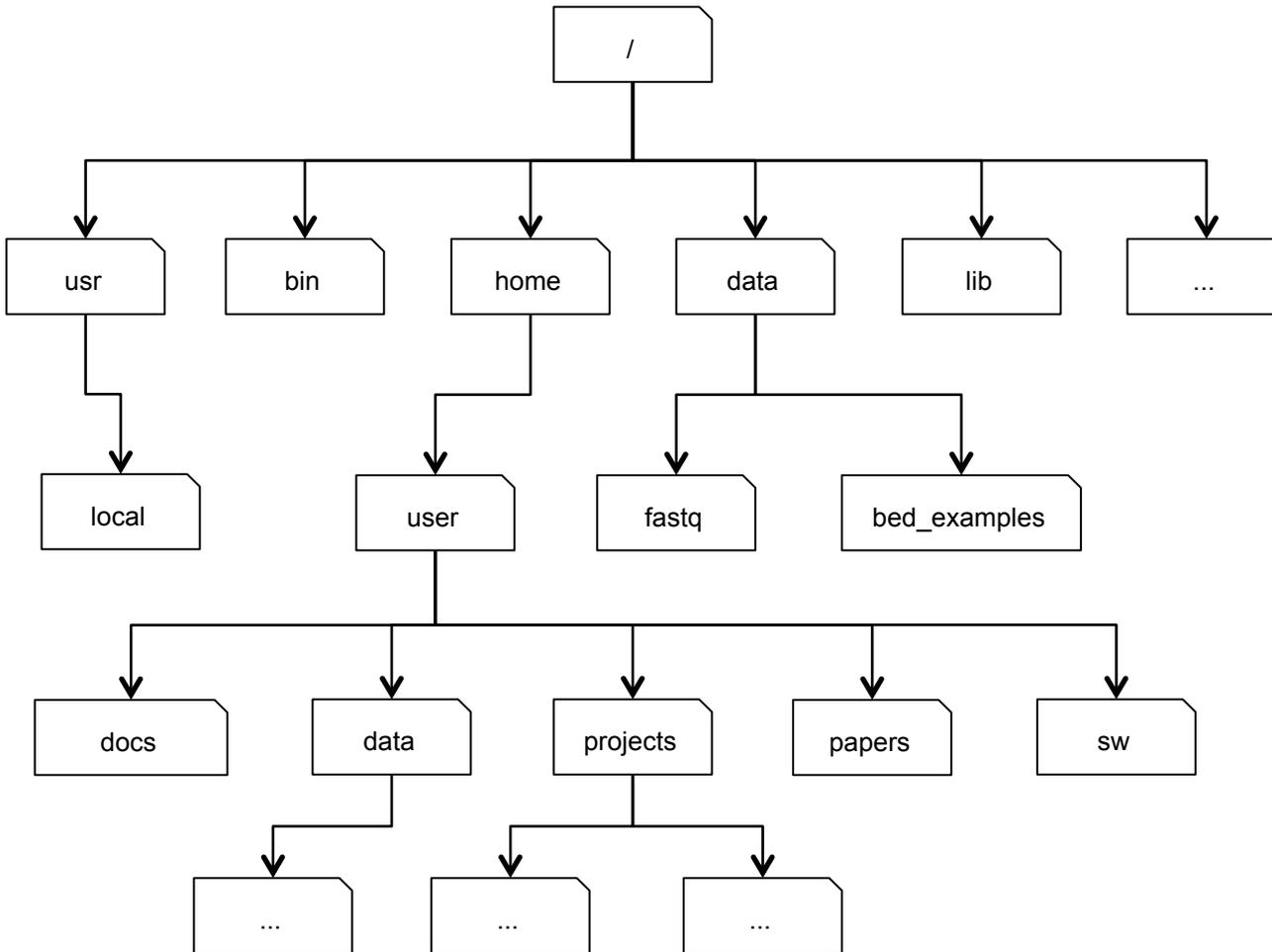
' - quotation mark single

" - quotation mark double

# Basic Structure

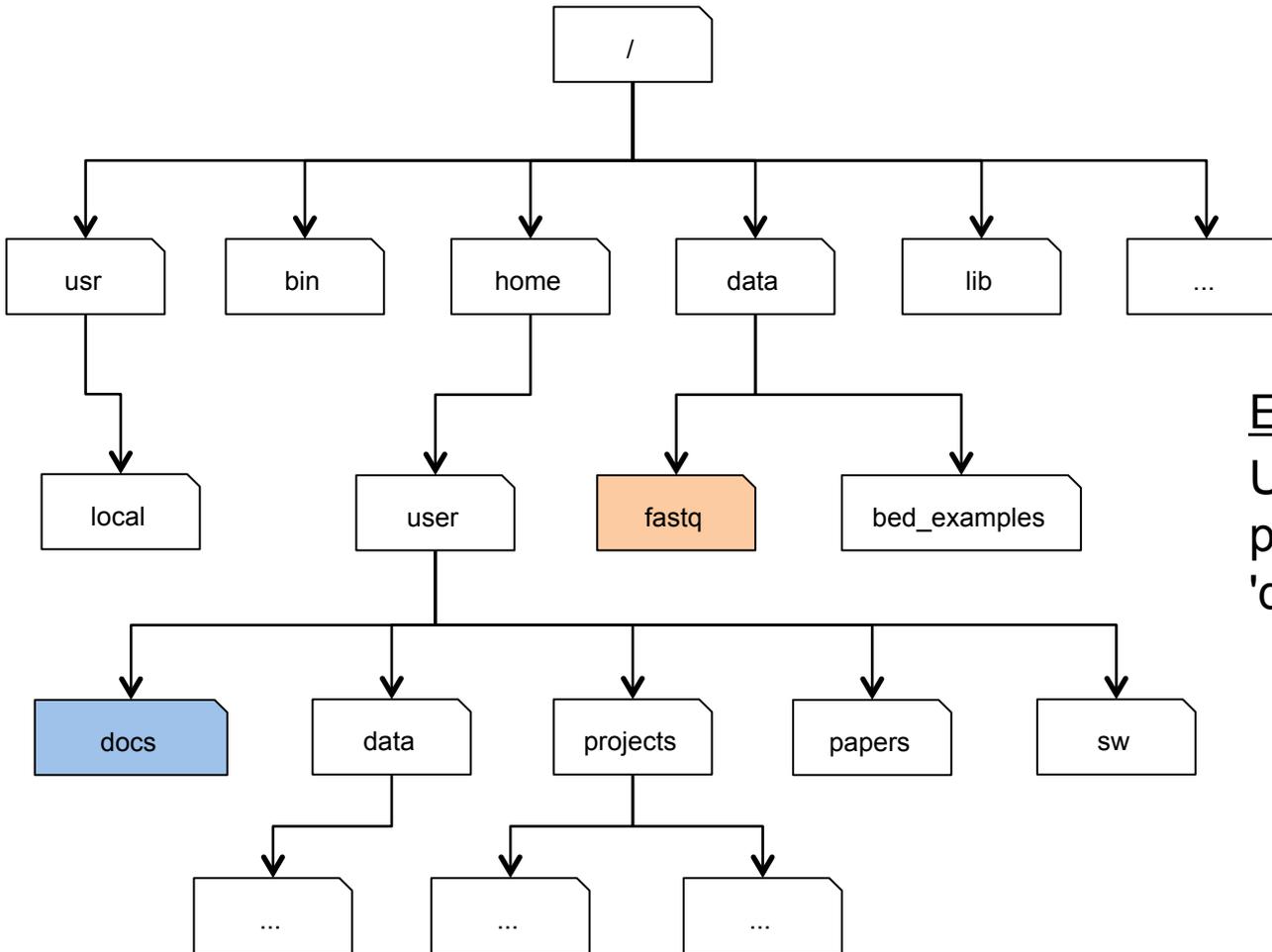


# Moving Around



```
pwd
ls
ls ~
ls /
ls ..
ls ../..
cd
cd ~
cd /
cd ..
```

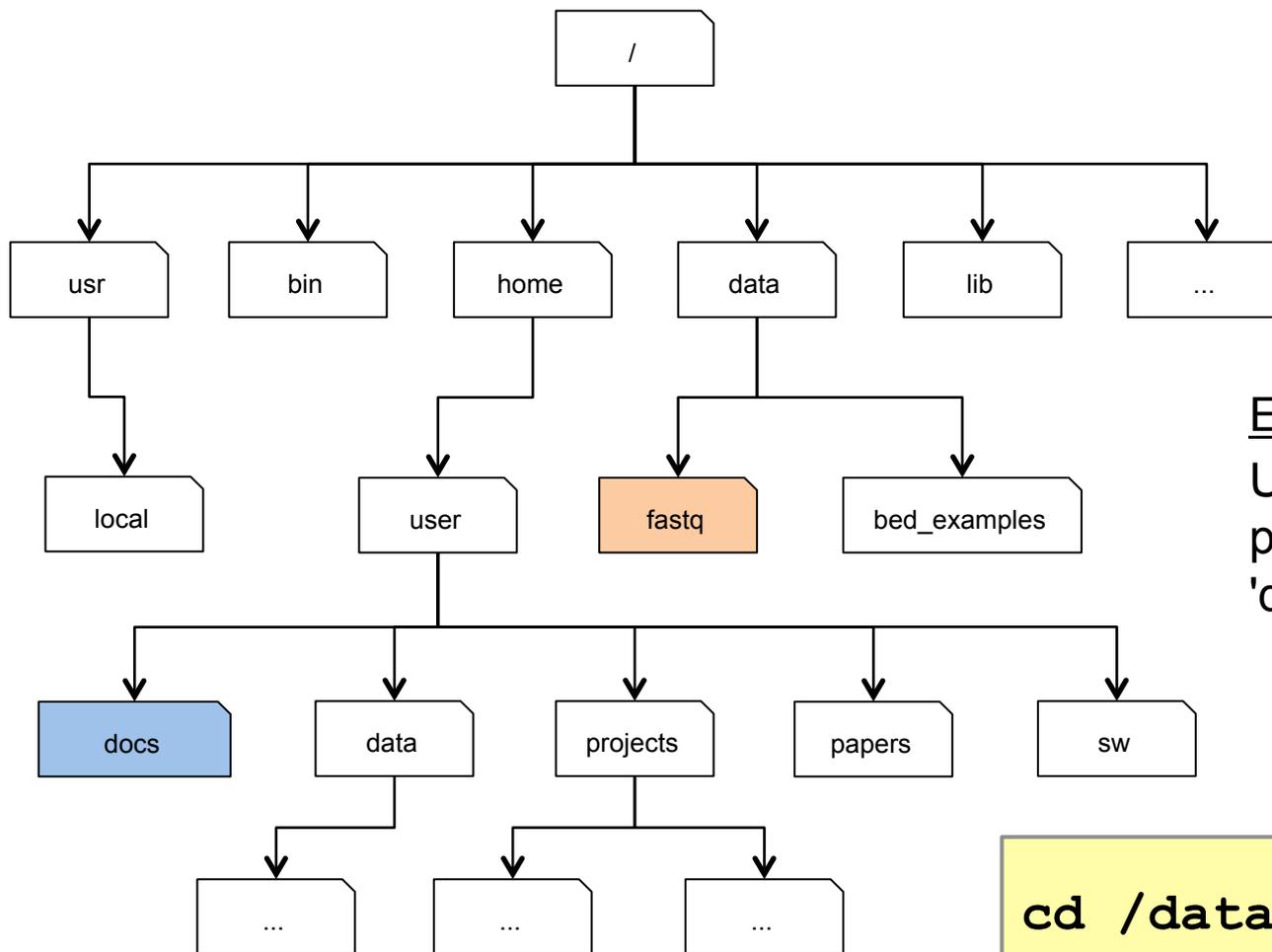
# Absolute vs. Relative Path



## Exercise:

Use absolute and relative path in to move from 'docs' (blue) to 'fastq' (red)

# Absolute vs. Relative Path



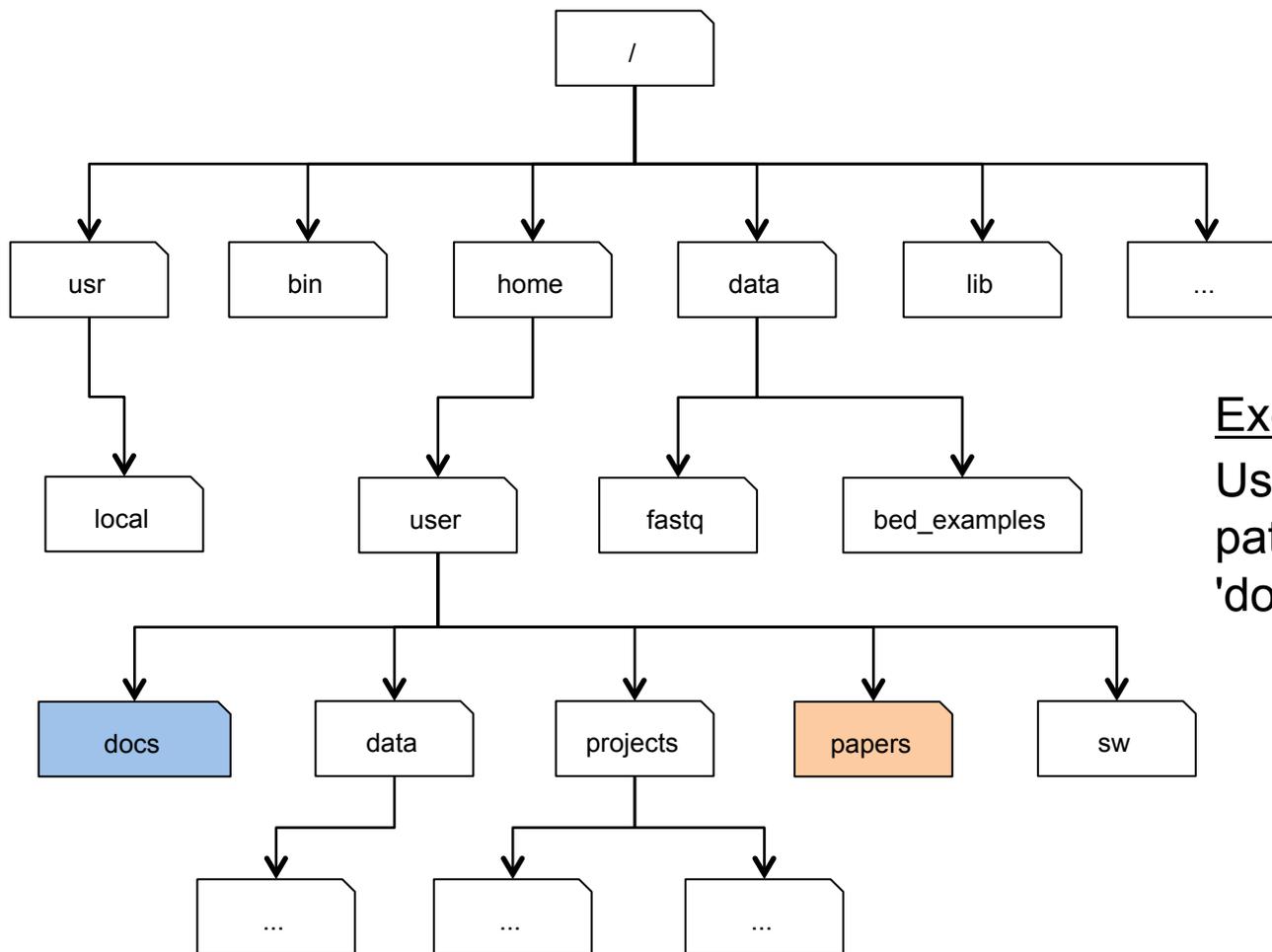
## Exercise:

Use absolute and relative path in to move from 'docs' (blue) to 'fastq' (red)

```
cd /data/fastq
```

```
cd ../../../../data/fastq
```

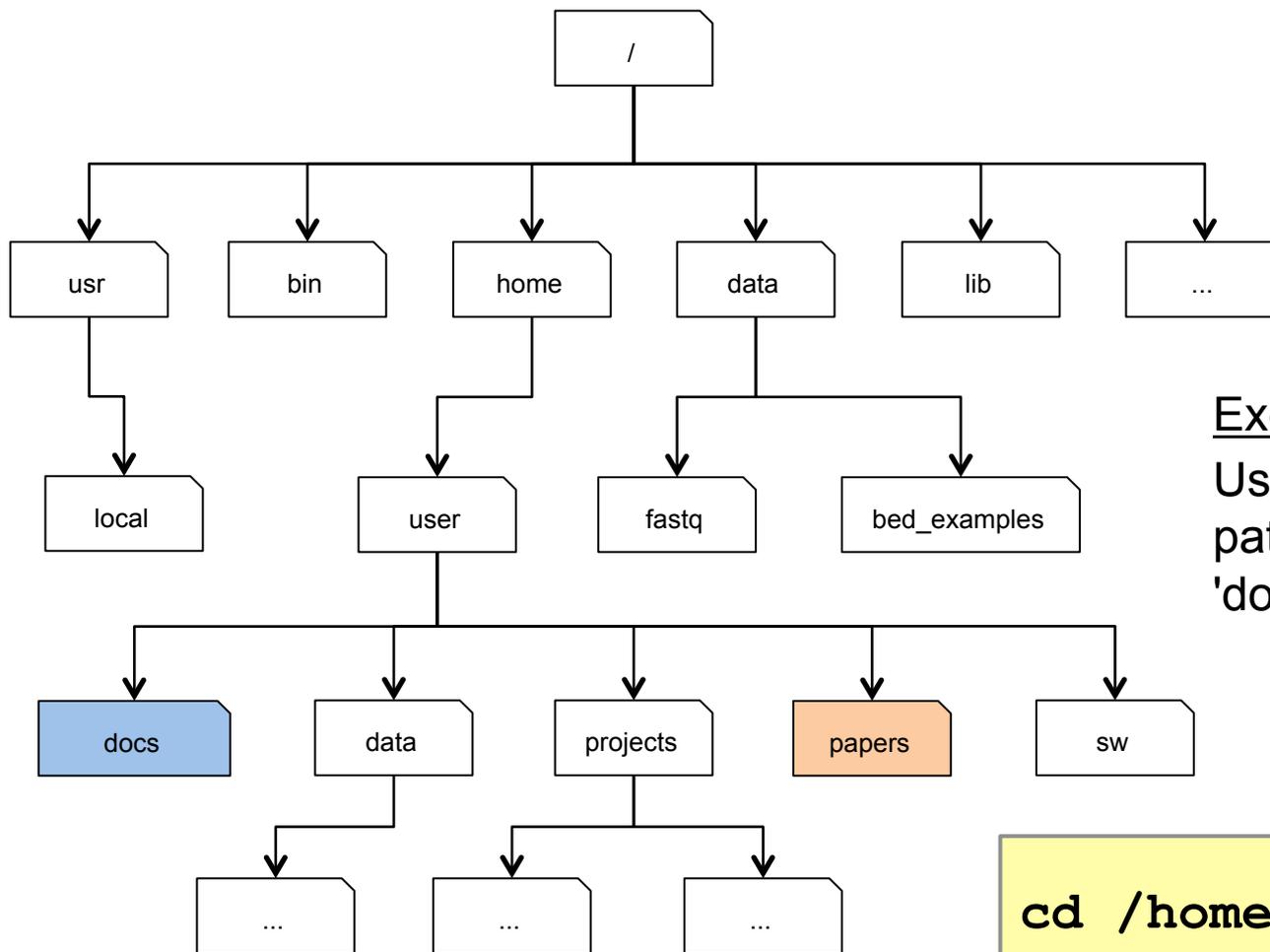
# Absolute vs. Relative Path



## Exercise:

Use absolute and relative path in to move from 'docs' (blue) to 'projects' (red)

# Absolute vs. Relative Path



## Exercise:

Use absolute and relative path in to move from 'docs' (blue) to 'projects' (red)

```
cd /home/user/projects  
cd ../projects
```

# Directory content and its size, disc usage

```
cd /data
```

```
ls -shaR # list content of a directory
```

```
du -sh # disc usage (by directory)
```

```
df -h # disc free
```

```
ls | wc -l # what does this command do?
```

```
locate # find a file/program
```

# Moving/coping files/directories

```
touch # make empty file
mv # move/rename files
cp (-r) # copy files (-r directories)
mkdir (-p) # make directory (-p subdirectory)
rm (-r) # remove file (-r non-empty directory)
ln -s # make a symbolic link
```

# Moving/coping files/directories - Exercise

*Try these tools to:*

- make new files/(sub)directories
- move/rename them
- remove them

```
touch # make empty file
```

```
mv # move/rename files
```

```
cp (-r) # copy files (-r directories)
```

```
mkdir (-p) # make directory (-p subdirectory)
```

```
rm (-r) # remove file (-r non-empty directory)
```

# Moving/coping files/directories - Exercise

*Prepare FASTQ data:*

```
cd ~  
mkdir -p data/fastq  
sudo cp -r /data/fastq/fastq.tar.gz data/fastq/.  
ls data/fastq
```

# Uncompressing data

```
tar -xzvf data/fastq/fastq.tar.gz # tarball  
archive + gzip
```

```
gunzip file.gz # only gzipped
```

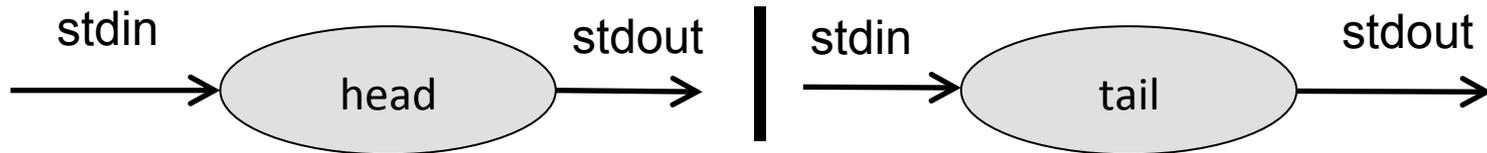
# Viewing plain text file content

```
less -SN  
tail -n 8  
head -n 8  
cat  
nano
```

\*\* TAB completion

# Pipes '|'

*Chaining standard input and output:*



```
head -n 8 data/fastq/HRTMUOC01.RL12.00.fastq | \  
tail -n 4 | less
```

```
< data/fastq/HRTMUOC01.RL12.00.fastq head -n8 | \  
tail -n4 | less
```

# Pipes '|' - Exercise

*How many reads are there?*

```
cd ~  
cat data/fastq/HRTMUOC01.RL12.00.fastq | wc -l  
expr XXXX / 4
```

# Globbering

*What if I need to choose multiple files?*

```
cd ~  
cat data/fastq/HRTMUOC01.RL12.*.fastq | wc -l  
expr XXXX / 4
```

```
cat data/fastq/HRTMUOC01.RL12.0?.fastq | wc -l  
expr XXXX / 4
```

# Producing Lists

```
cd ~  
mkdir data2 && cd data2  
touch file-{1..12}.txt  
ls
```

# Producing Lists

*Try these examples below:*

```
touch file-0{1..9}.txt file-{10..20}.txt
```

```
touch 0{1..9}-{a..f}.txt {10..20}-{a..f}.txt
```

```
touch 0{1..9}-{jan,feb,mar}.txt {10..20}-  
{jan,feb,mar}.txt
```

# Variables

*Variable: storage location paired with an associated symbolic name*

```
CPU=4
```

```
echo $CPU
```

```
FILE=data/fastq/HRTMUOC01.RL12.00.fastq
```

```
echo $FILE
```

```
FILES=`ls data/fastq/*.fastq`
```

```
echo $FILES
```

```
** echo '$FILE'
```

# Loops

*Repeat a command (set of commands) multiple times:*

```
FILE=`ls data/fastq/*.fastq`  
  
for i in $FILE  
do  
    echo $i  
done
```

# Loops

*Repeat a command (set of commands) multiple times:*

```
FILE=`ls data/fastq/*.fastq`  
  
for i in $FILE  
do  
    head -n 1 $i | wc -c  
done
```

# Multiple Windows in Unix

*Yes, you can have them...*

*+ protection from unexpected network fails*

```
screen  
screen -ls  
screen -r XXXX.NNNNNN.XXXX  
screen -X -S XXXX.NNNNNN.XXXX quit
```

```
ctrl+a c  
ctrl+a space  
ctrl+a d
```

# Installing Software in Unix

- *The easiest way is to use package manager (apt-get)*
- *Otherwise one needs to download the source code and compile it on its own (canonical way in Unix):*

```
wget -O - ..url.. | tar xvz
cd ..unpacked directory..
./configure # configuration of MAKE file based
on the OS
make # actual compilation of source code
sudo make install # installation of binaries
```

# htop

- *Package manager*

```
sudo apt-get install htop
```

# bedtools2

- *wget*

```
wget https://github.com/arq5x/bedtools2/  
releases/download/v2.25.0/bedtools-2.25.0.tar.gz  
tar -zxvf bedtools-2.25.0.tar.gz  
cd bedtools2  
make
```

\*\* if you need the most recent (development) version – use 'git clone'

*That's all for today...*