

# Basics of Unix

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# What do we learn today?

- Difference between absolute and relative
- Move around directory structure
- Create a new directory
- List and explore content of directories
- View plain text files
- To copy, move and rename files
- Work with compressed files
- Use variables and lists
- To download and install software

# Command line

To type commands (syntax):

```
name -flag(value) input > output
```

```
head -n20 file.txt > out.txt
```

What if I don't know?

```
man head  
head --help  
head -h
```

# 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

:

; semicolon

.

,

# hash

\_ underscore

- dash

\* asterisk

! exclamation mark

? question mark

& ampersand

@ at sign

' ' quotation mark single

" " quotation mark double

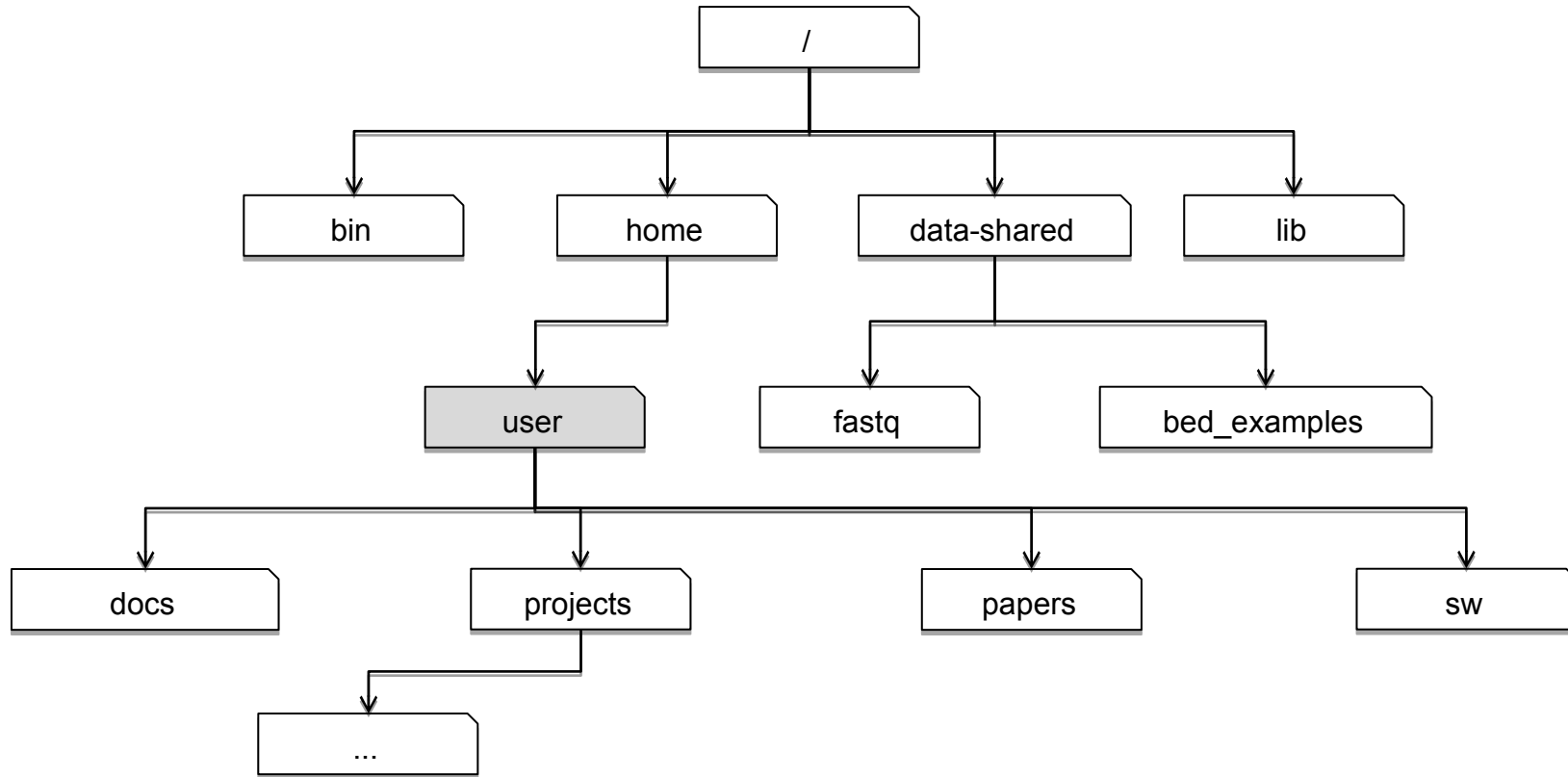
# screen

*Protection from unexpected connection drop outs*

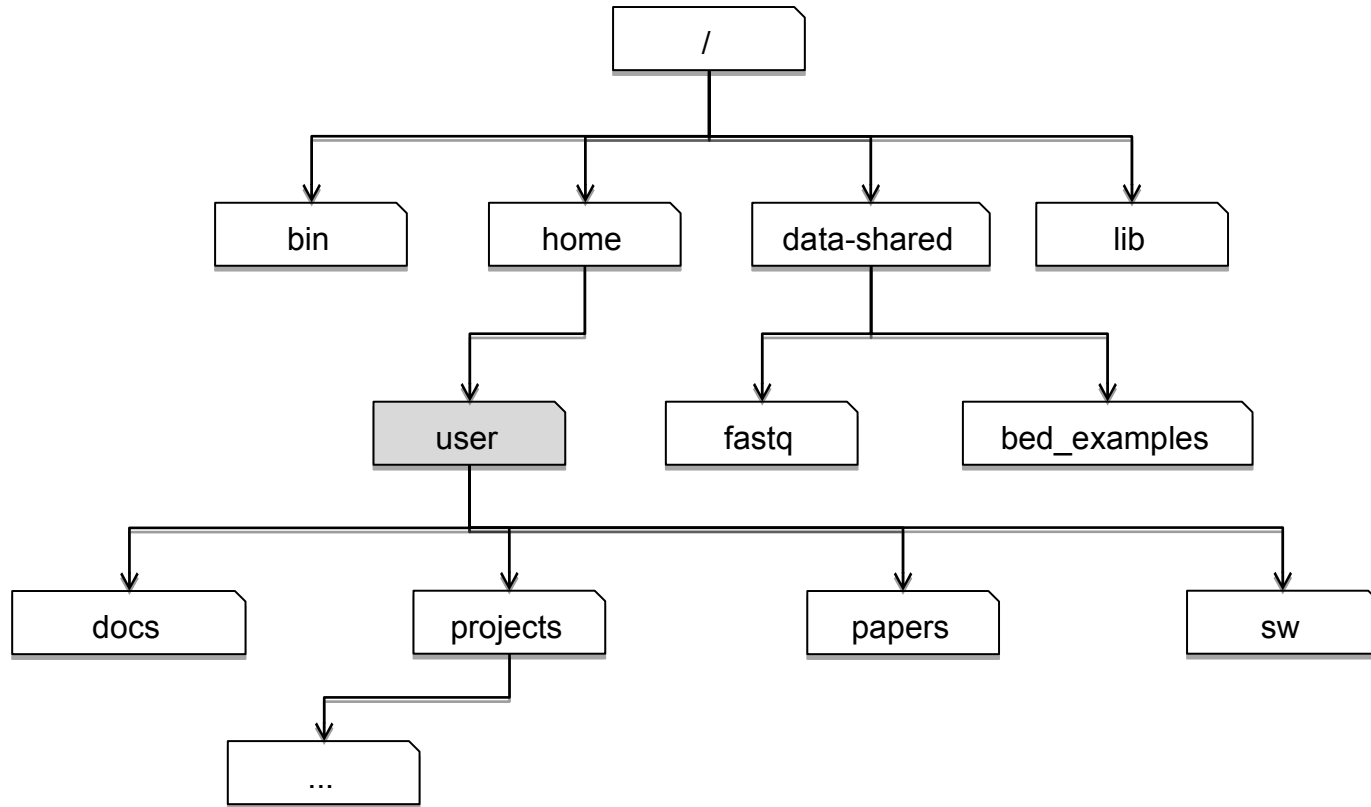
```
screen
screen -r
screen -ls
```

```
# inside screen
ctrl+a c      # new window
ctrl+a space  # switch between multiple windows
ctrl+a d      # detach from the screen
```

# Basic directory structure of unix

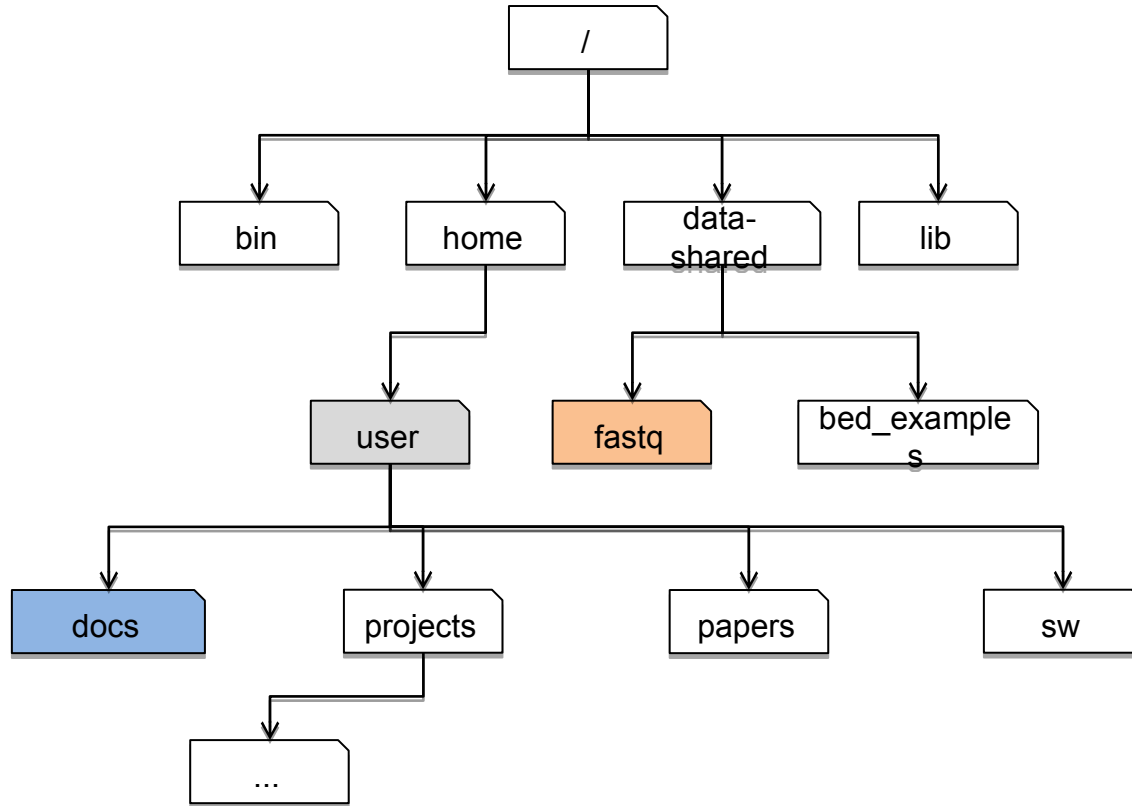


# Moving around



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

# Absolute vs. relative path

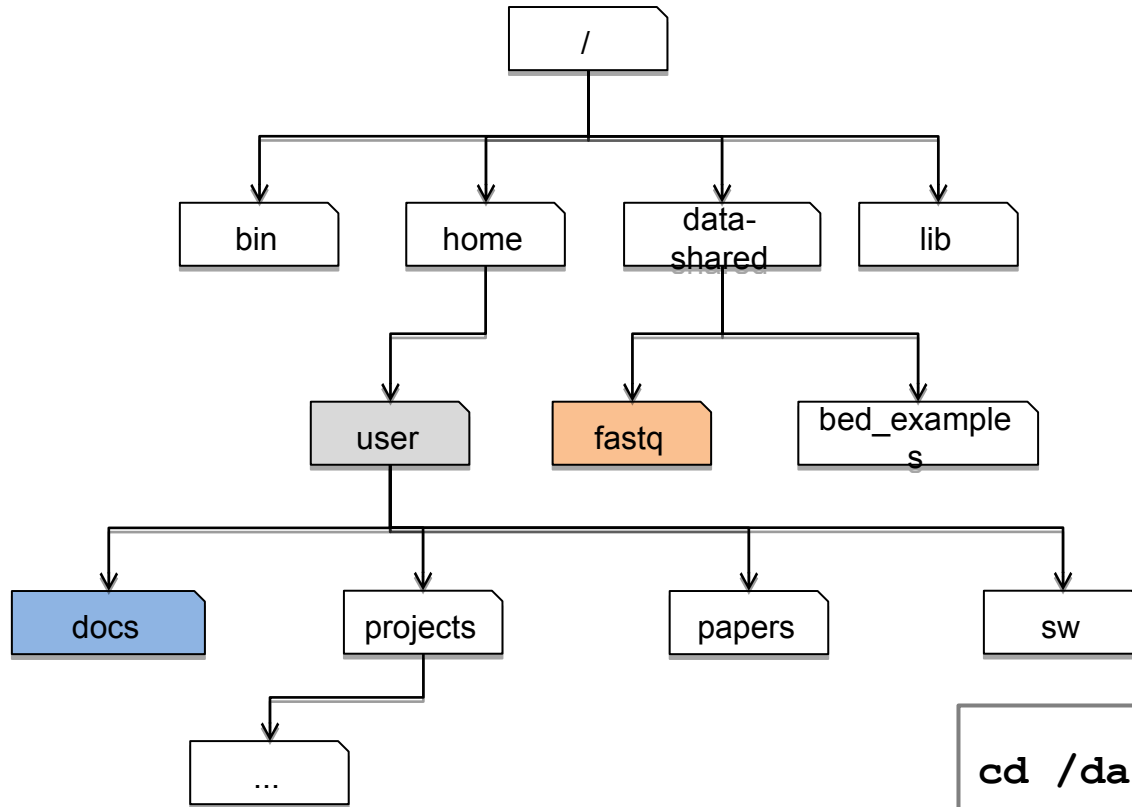


## Exercise:

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



# Absolute vs. relative path

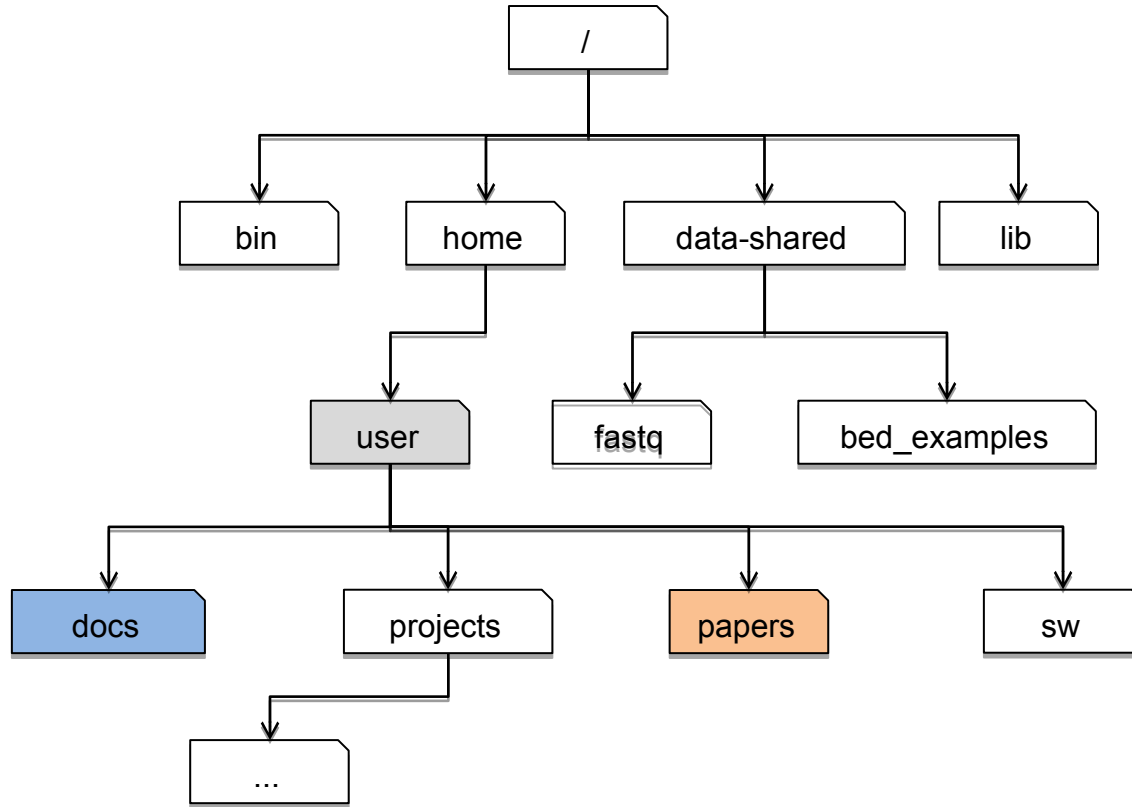


## Exercise:

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

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

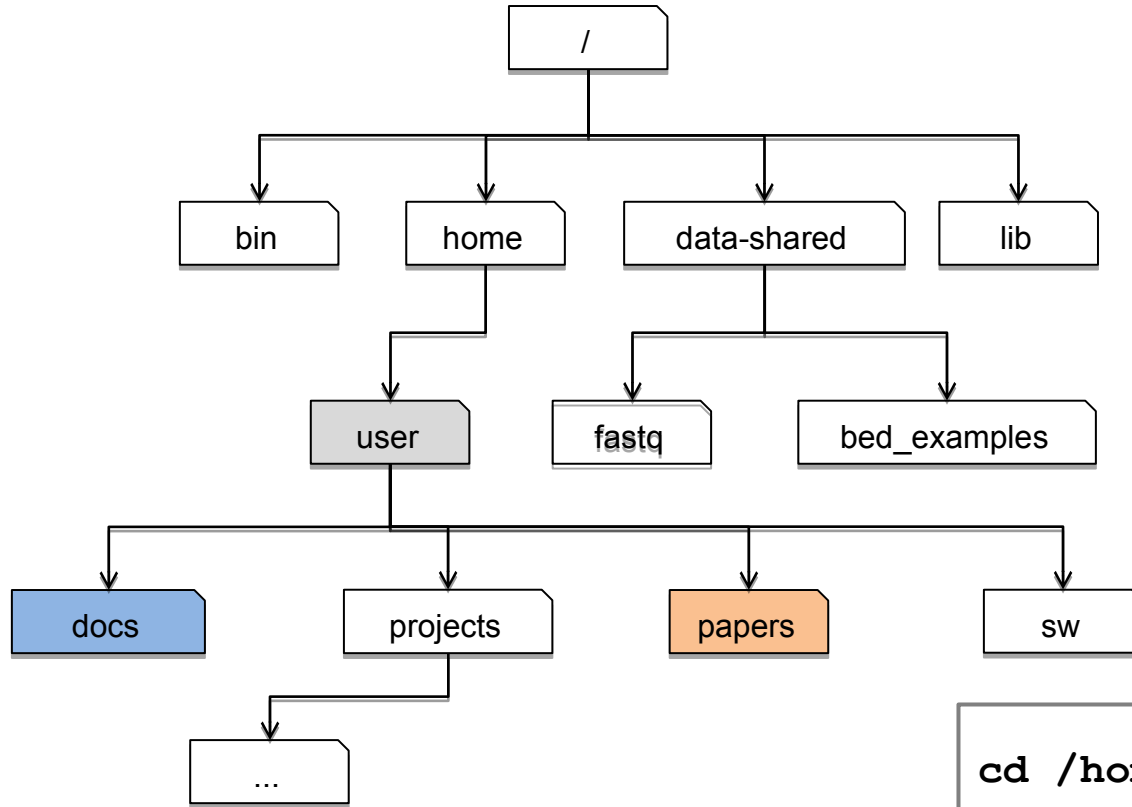
# Absolute vs. relative path



## 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
```

# Moving and copying files or directories

*Try these tools to:*

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

```
touch # make empty file(s)
```

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

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

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

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

# Viewing plain text file content

```
less -SN
```

```
tail -n8
```

```
head -n8
```

```
cat
```

```
nano
```

# Work with compressed data

```
# only gzipped (only one file)
```

```
gunzip file.gz
```

```
# view content of a compressed file
```

```
zcat fastq.gz | less
```

```
# gzipped tarball archive
```

```
tar -xzvf fastq.tar.gz
```

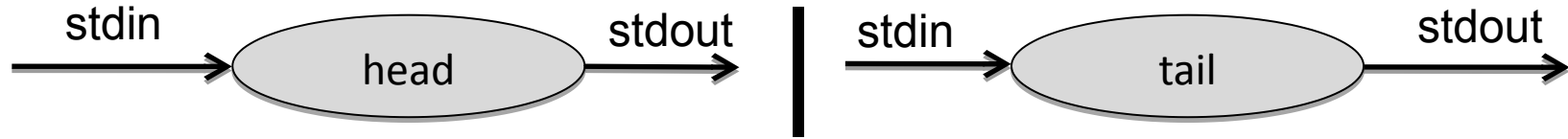
# Exercise

*Prepare FASTQ data file:*

```
# go to home directory
cd
# make a new dir
mkdir projects/fastq && cd projects/fastq
# copy a fastq tarball to the new dir
cp /data-shared/fastq/fastq.tar.gz .
# decompress files
tar -zxvf fastq.tar.gz
# list files
ls -sh
```

# Pipes '|'

*Chaining standard input and output:*



```
head -8 HRTMUOC01.RL12.00.fastq | tail -4 | less
```

*# Neater way to structure pipelines*

```
< HRTMUOC01.RL12.00.fastq head -8 | tail -4 | less
```



# Globbing & wildcards (\*, ?, [class])

*What if I need to choose multiple files?*

```
cd ~/projects/fastq
```

```
ls *.fastq # choose all fastq files
```

```
ls HRTMUOC01.RL12.0?.fastq # one character
```

```
ls HRTMUOC01.RL12.0[1-9].fastq # one numerical character
```

# Exercise

*How many reads are in all fastq files?*

```
cd ~/projects/fastq  
cat *.fastq | wc -l
```

```
expr XXXX / 4 ## Or  
echo $( (XXXX/4) )
```

# Variables

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

```
CPU=4
```

```
echo $CPU
```

```
FILE=~/projects/fastq/HRTMUOC01.RL12.00.fastq
```

```
echo $FILE
```

# Loops

*Loop over set of parameter values*

```
PARAM=${0..9}
```

```
for v in $PARAM
```

```
do
```

```
    echo $v;
```

```
Done
```

```
# one line syntax
```

```
For v in $PARAM; do echo $v; done
```

# Installing software in Unix

- *The easiest way is to use package manager (apt-get)*

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

# Installing software in Unix

- *Otherwise we have to download the source code and compile it on its own (canonical way in Unix):*

```
# Downloading compressed source code
```

```
wget -O - ..url.. | tar xvz
```

```
# Cloning from Git repository
```

```
git clone ..url..
```

```
# Compilation of binaries
```

```
cd ...directory..
```

```
./configure
```

```
make
```

```
sudo make install
```

# bedtools2

- *See our website*

```
# Download the compressed source code
```

```
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
```

```
# Or clone Git repository
```

```
git clone https://github.com/arq5x/bedtools2
```

```
# Compile binaries
```

```
cd bedtools2
```

```
make
```

# What we learned today?

- Difference between absolute and relative
- Move around directory structure
- Create a new directory
- List and explore content of directories
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- Read compressed files
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- To download and install software



*That's all for today...*

# File size and permissions: `ls`

```
ls -a  
ls -sh  
ls -ll
```

TODO: FINISH PERMISSIONS