

# BASH!



# BASH: Flag Formats

- Each of the following is a common flag format:
  - `--flag-name` or `-flagname`
  - `-f -l -n`
  - `-fln`
  - `--output my_filename.txt`
  - `--strand forward`

# BASH: Navigating Directories

- What would each of the following commands do?

`cd .`

`cd /`

`cd /home/cpalmer`

`cd ../../`

`cd ~`

`cd ~/Documents/..`

`cd`

`cd ..`

# BASH: Extracting Files

zip files (.zip)	unzip
tar archives (.tar)	untar (or tar x)
gzip files (.gz, .tar.gz, .tgz)	gunzip or gzip -d; tar xzvf
bzip2 files (.bz2, .tar.bz2)	bunzip2 or bzip2 -d; tar xjvf
xz files (.xz, .tar.xz)	unxz or xz -d; tar xJvf
rar files (.rar, possibly in pieces)	unrar (often absent in terminal)

# R!



# R: Variable Assignment

- Try changing the value of the variable **x** to 5. What happens to **number**?
- Now try changing the value of the variable **y** to contain the value 10. What do you need to do, to update the variable **number**?

# R: Data Types

<b>numeric</b>	any numerical value
<b>character</b>	text values, denoted by quotes ("" ) around value
<b>integer</b>	integer numbers (e.g. 2L, the L indicating to R that it's an integer
<b>logical</b>	TRUE, FALSE: the Boolean data type
<b>complex</b>	complex numbers with real and imaginary parts (1+4i)
<b>raw</b>	will not discuss today

# R: Aggregating Vectors

- Create a vector of numeric and character values by *combining* the two vectors that we just created (**glengths** and **species**). Assign the combined vector to a new variable called **combined**. *Hint: you will need to use the combine `c()` function to do this.*
- Print the **combined** vector in the console. What looks different compared to the original vectors?



# R: Categorical Data

- Let's say that in our experimental analyses, we are working with three different sets of cells: normal, cells knocked out for geneA, and cells overexpressing geneA. There are three replicates for each celltype.

```
samplegroup <- c("CTL", "CTL", "CTL", "KO", "KO", "KO", "OE", "OE", "OE")
```

- Create a vector **samplegroup** using the code above. This vector will contain nine elements: 3 control ("CTL") samples, 3 knockout ("KO") samples, and 3 overexpressing ("OE") samples
- Turn **samplegroup** into a factor data structure.