

# Linux Exercise

## Exercise 1: First Linux commands

- Open terminal
- List content in current directory
- Navigate to the directory called *student*
- List content in *student*

### Useful examples:

```
List content  
ls  
  
List content with more details  
ls -l  
  
Change directory (move "down")  
cd student/  
  
Change directory (move "up")  
cd ../
```

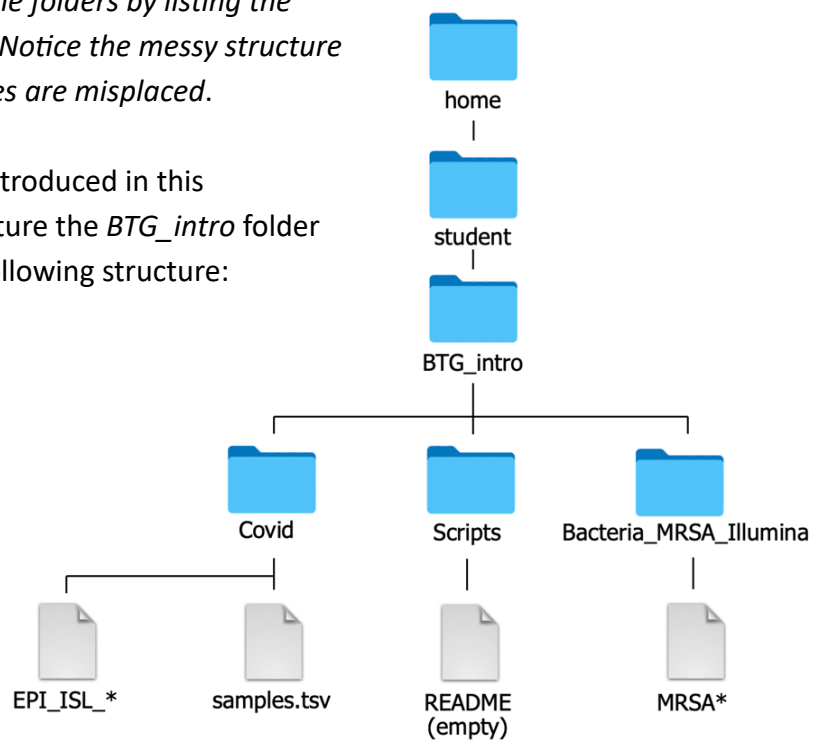
## Exercise 2: Working with compressed files

- Decompress the file called *BTG\_intro.zip*
- List content in *BTG\_intro*

## Exercise 3: Organizing directories

- Observe the structure of the folders by listing the content of the subfolders. Notice the messy structure and observe how some files are misplaced.

By using the commands introduced in this exercise (page 2), re-structure the *BTG\_intro* folder so the directory has the following structure:



### Useful examples:

```
Linux
Create a file called test.txt
touch test.txt

Move test.fastq.gz two levels "up" and into a directory called reads
mv test.fastq.gz ../../reads/

Create a directory called test
mkdir test

Remove directory called test including all its content
rm test

Rename folder called wrong_name to right_name
mv wrong_name right_name

Move all files ending with .fasta to test/reads
mv *.fast test/reads/
```

### Exercise 4: View files

- Navigate to `/home/student/BTG_intro/Bacteria_MRSA_Illumina/` and choose a file to explore for exercises 4-6.
- Display the content of one of the files by using the following commands:
  - `cat`
  - `less` (exit view by pressing "q")

### Exercise 5: grep is a powerful tool

- Display the header names in your file by using `grep`  
*hint: use ">" (quotations are very important)*
- Save the header names in a file called `header_names.txt`  
*hint: it is not necessary to make a header\_names.txt prior to this exercise*
- Display the content of `header_names.txt`
- Display the line count, word count, and character count for `header_names.txt` and note the number of headers  
*Hint: use `wc`.*
- Append the headers of another fasta file to `header_names.txt`. Repeat exercise 5d.

### Useful examples:

```
Linux
Search and match "pattern" in test.fasta
grep "pattern" test.fasta

Search and match "pattern" in test.fasta and save output in example.txt
grep "pattern" test.fasta > example.txt

Search and match "pattern" in test.fasta and append output to example.txt
grep "pattern" test.fasta >> example.txt
```

### Exercise 5: Linux is merciless

Let's see what happens if we forget quotations around the grep pattern:

- f. Copy and run the following command from the directory where header\_names.txt is located: `grep > header_names.txt`
- g. Display the content of header\_names.txt  
`grep` will not view `>` as a pattern to search for as `>` in itself, is a Linux command. Thus, `grep` will search for nothing, find nothing, and overwrite the current content of header\_names.txt with this nothing. There is **no** magic undo button in Linux.
- h. Remove header\_names.txt

### Exercise 6

Just like we can redirect or append the output to a file, we can also redirect the output of a command into another by using pipe `|`.

- a. By combining `ls`, `wc` and pipe, count the number of files in *BTG/Bacteria\_MRSA\_Illumina*
- b. Get the word count of your fasta file  
We do not learn much from this.
- c. By combining `grep`, `wc` and pipe `|`, count the number of sequence headers in the fasta file

### Useful examples:

```
Search and match "2021" in samples.tsv and display first 2 lines Linux  
grep 2021 samples.tsv | head -n 2
```