Exercises of lesson 2

1. Download fastqc and run it by line command on the bulk RNAseq example and the R2 of the single cell experiment.
2. Use chmod to make fastqc executable
3. Discuss the differences in results generated by a bulk and single cell RNAseq QC
4. Install multiQC (https://multiqc.info) or use the docker container (https://multiqc.info/docs/#using-the-docker-container)
5. Use multiQC function on the dataset provided on the moodle (dataset1).

The bulkRNAseq file is the dataset0, while the scRNA experiment is the file present in lesson 1. To solve these exercises, create a folder called "lesson2" and put all the files in it. Then, download fastqc and copy and paste the folder containing the data of fastqc in both the folders on which I will work. To run fastqc, I have to move in the fastqc folder and put the full path of the file, otherwise it does not work! I run the same command for both files:

Now, to run multiqc on dataset1, I have to move it in the same folder (lesson2) and run it on the docker. Docker ps -a allows me to see the containers → docker logs *docker container* → docker run -t ewels/multiqc → docker run -tv C:/Users/cauci/Desktop/lesson2/dataset1:/usr/src/multiqc ewels/multiqc