***Single cell analysis - exercise***

Use google colab (<https://colab.research.google.com/>) to open the file *Example Notebook.py* available under the title **Single Cell Tutorial** in folder **10 Single Cell RNA Sequencing**.

The file you will open contains both text and commands, that you can run one after the other by clicking on the little arrow on the left of each command section.

This exercise is intended as a starting tutorial to analyse single cell data. You can always ask questions about the analysis process and clarifications about the code.

In the **first session** of breakout room exercise, you should be able to read notes and run the commands from the beginning of the tutorial to the end of the preprocessing part (including dimensionality reduction), and be able to discuss it when we meet.

In the **second session** of breakout room exercise, you should be able to read notes and run the commands until the end of the clustering and cluster assignment, and be able to discuss it when we meet.

In the **third session** of breakout room exercise, you should be able to read notes and run all the remaining commands until the end, and be able to discuss it when we meet.

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When you are at home, and if you are excited about it, you can choose if you want to dig more and tweak some parameters. For example you can:

1. change the choice of filtering cells and genes and try to redo the clustering and cell classification on your own.
2. Change the parameters in the commands for the cell fate analysis, and look if you can see new potential cell fates showing up.
3. Isolate the somatic cells in the dataset after clustering, and doing an enrichment analysis for the differentially expressed genes of each cluster

You can also download the python notebook files for the scanpy tutorials on the scanpy homepage, and run those in google colab ☺