

# *New:* Shiny application for single cell mRNAseq data analysis for biologists

**A novel data analysis tool for investigating the complexity of mRNA expression at single cell level**

A major bottleneck in the initial steps of single cell RNA seq data analysis is initial processing of data, which is highly time-consuming since it requires a lot of interaction between the end-user and the bioinformatician. The CB UTechS has developed a Shiny tool (scShinyHub) that allows biologists to intuitively and autonomously perform cell and gene selection in the process of single cell mRNA sequencing data analysis.

The scShinyHub is a new addition to analysis tools already available to the community on the CB UTechS analysis computers. The tool is modular and easily extendable, such that individual needs can be addressed rapidly.

*Individualized support with the downstream steps of scRNAseq analysis is provided by the CB UTechS/C3BI bioinformatician.*

The scShinyHub tool is hosted and maintained on a dedicated computer within the CB UTechS compute resources, located in the CFJ-Aquarium and accessible to the user community upon a dedicated training.

***Location:*** Institut Pasteur, CFJ Building, ***Room:*** Aquarium

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