

Half-Day Short-Course

Bioinformatics and statistics for Next Generation Sequencing data analysis

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Thanks to recent technological advances, it is now possible to measure thousands of gene expression profiles in individual cells. Until very recently, the equipment, cost and time needed to perform single-cell transcriptomics have limited their application to a few selected studies. All of this has changed thanks to novel time and cost-effective strategies to obtain RNA-seq libraries for thousands of cells in a single experiment using microfluidics (Drop-seq and DropIn).

This short course will briefly introduce the technology to generate single-cell transcriptomic data, the challenges in dealing with this new type of data and how to practically analyse and visualise the data using the R programming environment.

Prerequisite

Participants are invited to bring along their own laptop with R with the following packages (seurat, Rtsne, uwot) for hands-on training.