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Course:

Analysis of single-cell RNA-seq data

Speaker: Simone MARINI, PhD

Department of Computational Medicine and Bioinformatics
University of Michigan

Learning Objectives:

The attendee will learn the basic principles of single-cell RNA sequencing technologies, and how to conduct a typical analysis of single cell RNA-sequencing data. She will learn to perform quality control; to handle outlier; to perform data enrichment; to isolate and label cell populations; to find statistically significant biomarkers; and to communicate results by visualizing informative and convincing figures.

Abstract:

Single cell RNA-sequencing (scRNA-seq) is providing an unprecedented granularity in the study of tissues and diseases. Once we abandon the assumption of a sample composed of average cells, with an average gene expression, the full heterogeneity of the different cells composing a tissue can emerge. Isolating specific expression profiles, usually through unsupervised clustering, it is therefore possible to characterize different cell populations or states (for example, separating stromal from immune cells). Once isolated, these populations can be further clustered in a nested fashion, to let sub-population emerge (for example, characterizing M1 versus M2 macrophages). In turn, these cell populations offer a tremendous potential to characterize prognostic or diagnostic biomarkers, unveiling molecular aberrations by comparing tissue under different conditions. Cell composition, i.e., the relative proportion of different cell types, constitutes a first example of these biomarkers. Another example of biomarkers are cell states, i.e., altered regulatory programs with identified cell types as the cells adapt to transient environmental changes, such as senescent phenotypes. A third biomarker example comes from gene expression, as scRNA-seq allows the detection of signals from rare cells. In contrast, a faint signal would be impossible to detect via bulk tissue RNA-seq, as it would get diluted by averaging it over the whole sample expression. Furthermore, it will be possible to decouple a gene signal in the sample down to the different contributions of diverse cell populations.We expect the biomarkers from scRNA-seq analysis to be adopted in the future clinical practice, especially to characterize profiles of precision or personalized medicine. Despite the temptations offered by of-the-shelf, one-solution-fits-all scRNA-seq approaches and pipelines, extracting and interpreting this kind of data comes with some caveats and peculiarities. In this workshop, we will learn how to conduct a scRNA-seq data analysis, and we will address pitfalls and problems with real-data examples.

20/12/2018
21/12/2018
14.00 - 18.00

Aula D8, Dipartimento di Ingegneria
Industriale e dell'Informazione
Università degli Studi di Pavia
Via Ferrata 5, Pavia