Exploring immune cell states in cancer and infection; New methods for single-cell data science

Different subtypes of lymphocytes and myeloid cells infiltrate tumors and contribute or interfere with cancer progression and cancer therapy. Identification of these cancer-associated immune cell states in individual patients is fundamental to reveal mechanisms of primary and acquired resistance, to identify biomarkers of response and design improved therapies.

Single-cell technologies have recently opened a unique opportunity to explore the immune response at a resolution and scale that seemed inconceivable only ten years ago. Single-cell omics analysis of cancer patients’ biopsies is rapidly expanding. However, while the resolution at which we can now profile cellular states has increased dramatically, biological interpretation of these data remains a major challenge in the field. In particular, computational methods to accurately interpret single-cell data in the context of previous studies and prior knowledge are currently lacking.

I will discuss about some of the current challenges in single-cell data science, and present the single-cell analysis tools we are developing to interpret immunological states across individuals and tissues, in health and disease. I will focus on the construction of reference transcriptional atlases to summarize knowledge from multiple studies, and how they can be used to interpret T cell immune responses.

We envision that meta-analyses of single-cell omics data from patients and mouse models will be fundamental to understand the cellular mechanisms of cancer therapy resistance, to identify biomarkers of response for clinical decision support and to identify novel therapeutic opportunities.

Date: Monday, April 11th, 2022
Time: 16:15 h – 17:15 h
Room: https://unibas.zoom.us/j/64509967057?pwd=N1hCaVJbUFJuU0tEN1dia2hHVUFtZz09
(meeting ID: 645 0996 7057, pass code: FS-2022)
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