MicroTAS 2021 Workshop 5 Information

WORKSHOP TITLE: Single-Cell Data Analytics

PRESENTER AFFILIATION:

Federica Caselli, University of Rome Tor Vergata, Italy (http://dicii.uniroma2.it/caselli)
Topic - Inline signal analysis for phenotypic recognition

Bo Wang, Stanford University. (https://bioengineering.stanford.edu/person/bo-wang)
Topic - Single-cell transcriptomic analysis

Carlos Honrado, University of Virginia, Charlottesville
(https://scholar.google.co.in/citations?hl=en&user=V0W-I7oAAAAJ)
Topic - Machine learning for automated impedance-based phenotypic classification

WORKSHOP DESCRIPTION:

In the last two decades, emerging techniques for single-cell biophysical phenotyping are altering our understanding of cells, tissues and biosystems. This workshop will focus on tools for inline phenotypic recognition, machine learning for automated phenotypic classification, and single-cell transcriptomic analysis.

OVERVIEW OF MATERIAL TO BE COVERED AND WHAT ATTENDEES CAN EXPECT TO TAKE AWAY FROM THE WORKSHOP:

This workshop will describe the tools along three related topics:

(i) Signal analysis for biophysical cytometry (Federica Caselli): In the last two decades, different techniques for single-cell biophysical phenotyping have been developed, which are changing the way we look at single cells. Alongside the increase in single-cell data made available by such techniques, there is the need to develop novel signal processing approaches to effectively extract the valuable phenotypic information embedded in the measured signals/images. In this talk, I will first provide a comprehensive overview of the available techniques for biophysical cytometry (including impedance-based and image-based flow cytometry), with an emphasis on the relevant datatype and information content. I will discuss stat-of-the-art signal-processing approaches, along with associated challenges and emerging trends. Second, I will present two case studies: (i) the use of neural networks for high-speed processing of multi-frequency single-cell electrical fingerprints, which opens opportunities for inline recognition and sorting; (ii) the development of multimodal approaches that combine information of different nature (e.g., electrical signals and optical images) to increase phenotypic classification accuracy.

(ii) Single-cell transcriptomic analysis (Bo Wang): The newfound ability to characterize cellular heterogeneity at single-cell resolution has encouraged broad efforts to construct transcriptomic maps of cell types and cell states from a wide variety of tissues, organs, and organisms. However, the deeper we delve into the more uncharted biomedical territories, the more challenging the data analysis and interpretation become. This talk will provide a guided tour in two major areas of single-cell analysis. First, I will provide a

comprehensive overview of state-of-the-art methods for dimensionality reduction, which is the first key step for most single-cell data analysis pipeline. I will discuss quantitative metrics that allow rigorous benchmarking and prospective method selection for specific datasets. Second, I will focus on the recently emerging frontier of single-cell analysis that maps datasets across species. Such analysis can facilitate the transfer of knowledge between organisms. I will present examples how such comparisons can advance our understanding of the conservation and diversification of cell types across evolution.

(iii) Machine learning for automated phenotypic classification (Carlos Honrado): The quantification of phenotypic heterogeneity is significant to understand biological function and to address the needs of precision medicine. Over the last decade, microfluidic impedance cytometry has carved a niche within this broader need by enabling quantification of subpopulations based on their electrical physiology. However, as high-dimensional data becomes increasingly available, the identification of subpopulations by manual gating becomes impractical and automated data-driven clustering and classification strategies are required. This talk will first provide an overview of recent implementations of machine learning-based data analysis methods on impedance cytometry data, with a brief contextualization of the techniques and methods implemented. Second, the talk will focus on case studies exploring the application of these methods in the stratification of cellular heterogeneity, based on their electrophysiology, within the broader context of drug assessment research and personalized medicine.

WHO SHOULD ATTEND:
PhD students, post-docs, and researchers interested in state-of-the-art data analytics approaches for single-cell phenotypic and transcriptomic analysis.

PARTICIPANTS WILL NEED THE FOLLOWING:
For those attending in-person, a laptop or iPad with headphones are required.