Biomedical Informatics Grand Rounds

Wednesday, April 24, 2024
3:00 pm – 4:00 pm

Clustering-Independent Estimation of Cell Abundances in Bulk Tissues using Single-Cell RNA-seq Data

Pablo Gonzalez-Cámara, Ph.D.
Assistant Professor of Genetics,
University of Pennsylvania, Perelman School of Medicine, Philadelphia, NY

Location: MART 7M-0602
Remote Access
Join Zoom Meeting https://stonybrook.zoom.us/j/95617197636?pwd=KytzZ2pVRG9SZGpKZUtpNXJISjNjZz09
Meeting ID: 956 1719 7636 Passcode: 924293

Bio: Pablo G. Cámara is an Assistant Professor of Genetics at the University of Pennsylvania and a faculty member of the Penn Institute for Biomedical Informatics and the Center for AI and Data Science for Integrated Diagnostics. He received a Ph.D. in Theoretical Physics in 2006 from Universidad Autónoma de Madrid. He performed research in string theory for several years, with postdoctoral appointments at Ecole Polytechnique, the European Organization for Nuclear Research (CERN), and the University of Barcelona. In 2014, his research shifted to address problems in quantitative biology. A characteristic of his current research is the incorporation of concepts from applied topology and metric geometry into the toolbox of computational biology and their application to questions in single-cell biology and population genetics.

Currently his lab focuses on three different areas of activity:
1. The development of geometry- and topology-based algorithms for the integration and analysis of single-cell multi-omics, cytometry, and imaging data of tissues.
2. Their application to the study of the cellular ecosystem, oncogenic pathways, and immuno-regulatory mechanisms of glioma.
3. Their application to the functional characterization of chimeric antigen receptor (CAR) T cell immunotherapies.

Abstract: Single-cell RNA sequencing has transformed the study of biological tissues by enabling transcriptomic characterizations of their constituent cell states. Computational methods for gene expression deconvolution use this information to infer the cell composition of related tissues profiled at the bulk level. However, current deconvolution methods are restricted to discrete cell types and have limited power to make inferences about continuous cellular processes like cell differentiation or immune cell activation. In this talk, I will discuss ConDecon, an approach for inferring the likelihood for each cell in a reference single-cell dataset to be present in a tissue that has been profiled at the bulk level, without relying on cluster labels or cell-type specific gene expression signatures. ConDecon makes use of the space of gene rank correlations to approximate the space of cell abundances. We will demonstrate the utility of this approach using gene expression data of pediatric ependymal tumors, where we uncover the implication of GPNMB-high microglia in the mesenchymal transformation of these tumors.

Educational Objectives:

1. Learn more about applications of Next Generation Sequencing in translational research.
2. Teaching future researchers and computational biologists on new techniques in deconvolution methods.
3. Follow through an application of the bioinformatic methodology on patient tumor data and discoveries that were found.

Disclosure Statement: The faculty and planners have no relevant financial relationship with ineligible companies, whose primary business is producing, marketing, selling, reselling, or distributing health care products used by or on patients.

Continuing Medical Education Credits: The School of Medicine, State University of New York at Stony Brook, is accredited by the Accreditation Council for Continuing Medical Education to provide continuing medical education for physicians. The School of Medicine, State University of New York at Stony Brook designates this live activity for a maximum of **1** ***AMA PRA Category 1 Credits™.*** Physicians should only claim credit commensurate with the extent of their participation in the activity.