

DBDS Workshop in Biostatistics

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(In Person, MSOB x303 (**preferred**) & Virtual access Password: 210310)

DATE:	May 5, 2022
TIME:	1:30-2:50pm
TITLE:	Demystifying stem cell hierarchies and clinically distinct cellular ecosystems in cancer
SPEAKER:	Aaron Matthew Newman , Assistant Professor of Biomedical Data Science, Stanford University

Abstract:

Abstract: Just as normal cell types are ultimately derived from stem cells, increasing evidence suggests that human tumors arise from cancer stem cells, which have been implicated in tumor development, resistance to therapy, relapse, and metastasis. Despite their importance, our fundamental understanding of cancer stem cells remains incomplete, and therapies that target these cells are largely lacking. While single-cell RNA sequencing (scRNA-seq) has become a powerful approach for characterizing cellular differentiation hierarchies from human tissue specimens, most computational methods for scRNA-seq-based trajectory inference require either (1) prior knowledge of the starting point (and thus, direction) of the biological process or (2) systems with continuous, short-term developmental processes (such as those that occur during embryogenesis). In this talk, I will describe our efforts to predict single-cell developmental states from scRNA-seq data without the need for prior knowledge or continuous cell fate transitions. I will then present methods for quantifying tumor cellular composition and expression from bulk genomic data, enabling cell profiling at a scale that is not currently achievable with scRNA-seq alone. Finally, I will describe recent work focused on modeling spatially-defined tumor cellular ecosystems, with implications for delineating the signaling networks that sustain unique cancer stem cell states and their surrounding microenvironments.

Pre-read information/References:

- [Gulati/Sikandar et al.](#), Single-cell transcriptional diversity is a hallmark of developmental potential, *Science* 2020
- [Newman et al.](#), Determining cell type abundance and expression from bulk tissues with digital cytometry, *Nature Biotechnology* 2019
- [Luca/Steen et al.](#), Atlas of clinically distinct cell states and ecosystems across human solid tumors, *Cell* 2021



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