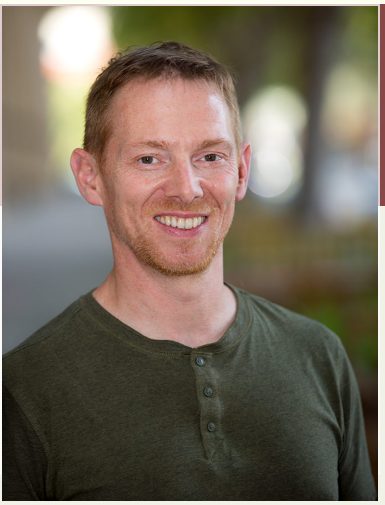
GENETICS, BIOINFORMATICS & SYSTEMS BIOLOGY COLLOQUIUM

THURSDAY, June 3rd
12:00-1:00 PM
Held on Zoom

Click Here for Zoom Link!
Meeting Password: Genetics



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Stanford University

Atlas of Clinically Distinct Cell States and Cellular Ecosystems Across Human Solid Tumors

Determining how cells vary with their local signaling environment and organize into distinct cellular communities is critical for understanding processes as diverse as development, aging, and cancer. We have developed EcoTyper, a new machine learning framework for large-scale identification and validation of cell states and multicellular communities from bulk, single-cell, and spatially-resolved gene expression data. When applied to 12 major cell lineages across nearly 6,000 tumor specimens from 16 types of human carcinoma, EcoTyper identified 69 transcriptionally-defined cell states. Most cell states were specific to neoplastic tissue, ubiquitous across tumor types, and significantly prognostic. By analyzing cell state co-occurrence patterns, we discovered 10 clinically-distinct multicellular communities with unexpectedly strong conservation, including four with unique myeloid and stromal elements, one enriched in normal tissue, and two associated with early cancer development. This work elucidates fundamental units of cellular organization in human carcinoma and provides a framework for large-scale profiling of cellular ecosystems in any tissue.

Faculty Host: Jill Mesirov

Presented by:

IGM Institute for Genomic Medicine

UC San Diego Bioinformatics & Systems Biology

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Organization Committee: J. Gleeson, F. Furnari, A. Majithia, T. Gaasterland
GBSBC Seminar Coordinators: R. White

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