Development of Innovative Analytic Methods for Single-cell Data

Dr Chen Jinmiao
Project Leader
Single-cell Analysis & Bioinformatics
Singapore Immunology Network (SIgN)
A*STAR, Singapore

Abstract
Single-cell analysis technologies such as single-cell RNA-sequencing and high dimensional mass cytometry allow for measurements of cellular heterogeneity with unprecedented dimensionality. However, analysis and interpretation of high-dimensional single-cell data remains challenging with existing methods. My lab (single-cell computational/system immunology lab) currently focuses on developing innovative analytic methodologies for single-cell data, with the aim of studying cellular diversity, cell lineage, cell-cell interaction, cell movement and rare cell populations. We have recently developed cytofkit: an R/Bioconductor package for an integrated mass cytometry data analysis pipeline [2, 4, 5]. Cytofkit integrates state-of-the-art bioinformatics methods and in-house novel algorithms for data visualization via dimensionality reduction (PCA, t-SNE, ISOMAP, diffusion map), automated subset identification via clustering (DensVM, flowSOM, Rphenograph, ClusterX) as well as inference of inter-subset relatedness. Moreover, we have developed a novel method named Mpath for constructing multi-branching cell lineages from single-cell data [1]. Applied to single-cell RNA-sequencing data of myeloid progenitors, Mpath constructed novel and refined models of myeloid lineages and identified putative early regulators of myeloid development.

Selected Publications for Reference
4. Michael T Wong1*, Jinmiao Chen1*, Siriram Narayanan1, Wenyu Lin1, Rosslyn Anicete2, Henry Tan Kun Kiang2, Maria Alicia Curotto De LaFaille1, Michael Poidinger1, Evan W. Newell. "Mapping the diversity and phenotypic progression of follicular helper T cells in human blood and tonsils using high dimensional mass cytometry analysis", Cell Reports, Volume 11, Issue 11, p1822-1833, 2015 (co-first author)