

Biophysics: Can single cell gene expression help track cell lineages?

Single-cell genomics has recently emerged as a powerful tool for observing multicellular systems at a much higher level of resolution and depth than previously possible. High-throughput single-cell RNA sequencing techniques can simultaneously quantify expression levels of several thousands of genes within individual cells for tens of thousands of cells within a complex tissue. This has led to development of novel computational methods to analyze this high-dimensional data, investigating longstanding and fundamental questions regarding the granularity of cell types, the definition of cell states, and transitions from one cell type to another along developmental trajectories. The goal of this project is to outline this emerging field starting from the "input data" (e.g., quantifying transcription levels in single cells), which are then analyzed to define "identities" (e.g., cell types, states, and key genes) and to finally build "interactions" using models that can infer relations and transitions between cells.

Student will apply the current techniques to analyze single cell data to understand cardiac development in zebrafish. The main goal of the project is to classify cells from different time points during embryonic development and track cardiac precursor cells. Then identify important genes that define the cardiac lineages and suggest experiments to test predictions.

If interested, please contact me by email: goyal@physics.utoronto.ca or come by my office MP504 in the physics building. Check website for more details and other projects: <https://goyallab.wordpress.com>