"Big data modeling of cell-microbe social networks"

The Lau lab considers every one of the 30 plus trillion cells in the body to be unique, thus, utilizes state-of-the art technologies to profile tissues at the single-cell resolution. Resulting "big data" consisting of thousands of data points and dimensions are analyzed by data science-driven computational techniques to determine:

- how altering different cell types in the gut influences the cell-microbiome ecosystem of Inflammatory Bowel Disease

- how interactions between the gut microbiome and epithelial cells contribute to benign colonic polyps progressing to colon cancer

- how the origins of colon cancer stem cells affect the progression of cancer and responses to therapies

- how different mutations affecting the same pathway can lead to different outcomes depending on the cellular ecosystem