

## Summary of Lu Chen's research project

**Title:** Identification of biomarkers for immunotherapy response in hepatobiliary cancer using single-cell RNA sequencing data

**Background:** Hepatobiliary cancer is a significant contributor to cancer-related mortality worldwide, and despite the progress made in immunotherapy, the outlook for patients remains grim. Single-cell RNA sequencing (scRNA-seq) has emerged as a valuable tool for identifying the cellular diversity within tumors and may facilitate the discovery of potential biomarkers for predicting response to immunotherapy and prognosis. However, there is currently limited research on the application of scRNA-seq in the study of hepatobiliary cancer.

**Aims:** This study aims to identify prognostic and predictive biomarkers for immunotherapy response in hepatobiliary cancer using scRNA-seq data. Specifically, we will (1) identify cell types present in hepatobiliary cancer, (2) investigate the differences in gene expression between these cell types, (3) identify and validate differentially expressed genes associated with patient survival and immunotherapy responsiveness in two independent cohorts.

**Methodology:** Unsupervised clustering will be used to identify cell types in hepatobiliary cancer by using scRNA-seq data. Differential gene expression analysis will be performed to identify genes that are differentially expressed between cell types, and genes associated with patient survival and immunotherapy responsiveness will be identified. The prognostic potential of these genes will be validated in an independent cohort using qRT-PCR and immunohistochemistry.

**Timeframe:** This research project is expected to take 12 months. The first 3 months will be dedicated to obtaining scRNA-seq data and quality control checks. The next 3 months will focus on data preprocessing, including normalization and clustering. The following 3 months will be focused on differential gene expression analysis and clinical correlation analysis. The final 3 months will be dedicated to validating the identified genes' prognostic and immunotherapy responsiveness prediction potential in an independent cohort.