

**Imaging and Sequencing Analysis of Cellular Regulation and Communication within Spatial Context in Cancer Tissue**

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# Thesis abstract:

Cells in the multicellular organisms can perform the cross communication at molecular level to coordinate higher biology functions. Cellular interaction is a mechanism that one cells can influence the behaviour of itself of other cells through signalling molecule to coordinate biological processes. Due to the heterogeneity in cancer, malignant tumours often comprise of multiple layers of cell-cell interaction. Studies have shown that cancer cells can develop the mutations to supress immune responses through cellular interaction to foster tumorigenesis and metastasis. By studying cell-cell interaction in cancer, we can systematically understand the behaviours of cancer cells and unravel the complexity of the crosstalk between cancer-immune cells. Besides, there are thousands of cells signalling molecules that have been identified as the possible communication tools. Experimentally iterate through each individual signalling molecule is prohibitively expensive. Therefore, thesis will focus about developing computation analysis for cell-cell interaction in cancer.

On the other hand, tumour growth and cancer metastasis are a location-dependent events. The heterogeneity of the cancer tumour is the central issues that hinders successful cancer treatment. Therefore, the ability to capture the genes and/or proteins expression of cells within the spatial context is essential in studying cell-cell communication in cancer. The past few years have witnessed an unprecedented development of the state-of-the-art spatial-omics technologies including spatial transcriptomic and proteomic. While there already several cell-cell interaction inference packages that have been developed for single-cell RNA sequencing data, there still limited number of packages