

Virtual Meet on **MEDICAL ONCOLOGY AND TUMOUR CELLS**

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Reconstruction of cell spatial organization based on ligand-receptor mediated self-assembly**Xianwen Ren, Guojie Zhong, Qiming Zhang, Lei Zhang, Yujie Sun and Zemin Zhang***Peking University, Beijing, China*

Single-cell RNA sequencing (scRNA-seq) has revolutionized transcriptomic studies by providing unprecedented cellular and molecular throughputs, but spatial information of individual cells is lost during tissue dissociation. While imaging-based technologies such as in situ sequencing show great promise, technical difficulties currently limit their wide usage. Since cellular spatial organization is inherently encoded by cell identity and can be reconstructed, at least in part, by ligand-receptor interactions, here we present CSOmap, a computational strategy to infer cellular interaction from scRNA-seq. We show that CSOmap can successfully recapitulate the spatial organization of tumor microenvironments for multiple cancers, and reveal molecular determinants of cellular interactions. Further, CSOmap readily and enable in silico simulates molecular and cellular perturbation of genes or cell types to gain novel biological insights, especially into how immune cells interact in the tumor microenvironment. CSOmap can be widely applicable to interrogate cellular organizations based on scRNA-seq data for various tissues in diverse systems.

Biography

Xianwen Ren has his expertise in bioinformatics algorithm development in leveraging power inherent in omics data for improving the health and wellbeing. The recent bioinformatics algorithm he developed creates new pathways for investigating the cellular and molecular mechanisms of tumor immune microenvironment in mediating immunotherapies. Based on single-cell RNA-seq data and human ligand-receptor Interactome data, he has developed a bioinformatics algorithm named as CSOmap to successfully reconstruct cellular spatial organizations, which has been validated on a diverse set of organs and tumors. In particular, CSOmap enables in silico gene overexpression/depletion and adoptive cell transfer/depletion to characterize the corresponding spatial changes, which is insightful to identify critical drug targets.

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