

عنوان مقاله:

The Role of Tumor Microenvironment Communication in Cancer Progression Using Single-Cell RNA Sequencing: A System Level Study

محل انتشار:

اولین همایش بین المللی و دهمین همایش ملی بیوانفورماتیک ایران (سال: 1400)

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خلاصه مقاله:

Tumor microenvironments are complex ecosystems comprised of cancer cells, infiltrating immune cells, and other cell types. Diverse cell types interact with each other and collectively create complex networks of intercellular and intracellular signals. In fact, these networks determine cancer progression as well as response to therapy. Recent advances in single-cell transcriptomics have laid the foundations for studying tumors at the microscopic resolution. This technology provides a compelling strategy to fill gaps in knowledge of human tumors and uncover complex networks between diverse cell types in a tumor ecosystem. In this study, we proposed a framework to explore the molecular mechanisms in different stage of cancer by integrating single-cell RNA-sequencing (scRNA-seq) data and a multi-layer network that integrate information from different levels. The heterogeneous multi-layered network provides a great way to represent the biological system's hierarchy: from gene to cellular function and final phenotype. It allows to uncover novel relations between biological entities on a microscopic view. The pipeline was applied to glioma scRNA-seq data and complex network analysis (topology and functional analysis) of the different networks from different cancer stages revealed important signaling module, important ligand-receptor connection, and most significant ligand – receptor-TF axis. Differential network analysis between stage III and IV glioma discovered the most important nodes and edges in the rewiring of interactions. In addition, hidden hierarchies in data have been revealed by heterogeneous multi-layered network models.

کلمات کلیدی:

Tumor microenvironment; complex networks; heterogeneous multi-layered network; scRNA-seq

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