Docket #: S20-075

Determining Spatial Accumulation of Signaling Molecules within Tissue Samples

Researchers at Stanford have developed a method for spatially modeling signaling molecules and cell types to identify cell-cell signaling pathways. The method aligns multiplexed imaging data to resolve the positioning information of multiple cell types and single cell transcriptomics data. The software is capable of projecting the expression of mRNAs within the tissue at a higher resolution than current spatial transcriptomics approaches. The researchers have captured 25 cell types in muscle tissue and single cell spatial information; moreover, they have curated a database of ~2000 signaling proteins and molecules, along with their estimated diffusion constants to predict the accumulation of these signaling molecules within the tissue based on expression level and positioning of source cells. This allows the algorithm to calculate the potential effect of ligands on each cell type of interest and enables more accurate predictions of cell-cell signaling -- thus representing a potent drug discovery tool.

Related Technologies:
Stanford docket S20-173 - Methods for Composing High Dimensional Fluorescence Microscopy Images in Subpixel Resolution
This invention describes a software suite for correcting fluorescence images generated from widefield or confocal microscopes, enabling efficient and highly accurate registration and stitching of these images. A comprehensive, optimized software package suitable for biology labs, pharmaceutical companies, and microscope companies.

Stage of Development
The researchers have used the algorithm to identify previously validated signaling molecules that regulate muscle stem cells during muscle regeneration, providing proof-of-concept for the discovery of ligands and growth factors that influence

critical cell types.

Applications

- Drug discovery
- Spatial transcriptomics
- Disease mechanisms
- Cell-cell signaling
- High dimenstional imaging

Advantages

- Unbiased discovery tool
- Predicts spatial accumulation of growth factors and ligands (difficult to determine using traditional approaches of immunohistochemistry and mass spectrometry)
- Fewer false positive predictions of signaling molecules
- Aligns protein expression data to mRNA expression

Patents

- Published Application: WO2021174210
- Published Application: 20230088271

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