# Incorporating Spatial Transcriptome Data into Ligand-Receptor Analyses to Discover Regional Activation in Cells

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***Abstract***— Interactions between receptors and ligands are crucial for many essential biological processes, including neurotransmission and metabolism. Ligand-receptor analyses that examine cell behavior and interactions often utilize cell type-specific RNA expressions from single-cell RNA sequencing (scRNA-seq) data. Using CellPhoneDB, a public repository consisting of ligands, receptors, and ligand-receptor interactions, there was exploration of the cell-cell interactions in a specific scRNA-seq dataset from kidney tissue and portrayed the results with dot plots and heat maps. Depending on the type of cell, each were aligned to a ligand-receptor pair with the interacting cell type, and calculated the *a positori* probabilities of these associations, with corresponding *P* values reflecting average expression values between the triads and their significance. By performing an interaction analysis, comparing the reactions it was discovered that a significant interaction for myeloid and T-cell ligand-receptor pairs, including those between Secreted Phosphoprotein 1 (SPP1) and Fibronectin 1 (FN1), which is consistent with previous findings. As a next step, potential laboratory methods were explored to incorporate spatial transcriptome data into ligand-receptor analyses to allow for the derivation of more information from similar ligand-receptor-cell interactions. An effective protocol would involve a filtration step where cell types would be filtered out depending on which ligand-receptor pair is activated in that part of the tissue, as well as the incorporation of the CellPhoneDB data in a streamlined workflow pipeline. It was believed this would reveal where in the cell various ligands and receptors are interacting with different cell types, allowing one to more easily identify which cells are being impacted and why, for the purpose of disease treatment. The hope is this new computational method utilizing spatially explicit ligand-receptor association data can be used to uncover previously unknown specific interactions within kidney tissue.

**Biography**
Eric Bang has worked with the Broad Institute of MIT and Harvard Sean is passionate about bioinformatics and hopes to conduct more research in the field.

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