# From Bench Backlog to Breakthrough: How Bridge Informatics Accelerated Spatial Transcriptomics Analysis

**CASE STUDY**

## SITUATION

- A pharmaceutical company sought to understand immune reactions after pathogen exposure and unveil the spatial signature of immune cell subtype involvement to pinpoint potential targets for therapeutic treatments.
- Client's research and development (R&D) team conducted extensive experiments that resulted in identifying a list of potential gene biomarkers.
- An investigative transcriptomic experiment was designed to find additional targets in an unbiased way and to further verify the relationship of the markers previously found by R&D to the corresponding patho/physiological pathways.

- Client's Bioinformatics Scientist and Principal Scientist attempted to conduct their analysis internally before realizing that it would take months for their small team to complete it. Moreover, the Principal Scientist was planning to perform spatial transcriptomics and integrate it with their existing transcriptomic data but was not fully certain which spatial technology platform would be suitable for their objective
- Client was referred to Bridge Informatics (BI) when looking for an experienced outsourcing partner to quickly conduct the spatial transcriptomics analysis, integrate with existing transcriptomic and visualize the results.

## AT-A-GLANCE

- A pharmaceutical company sought to understand immune reactions after pathogen exposure.
- They needed to identify spatial immune cell subtype involvement for potential therapeutic targets.
- Bridge Informatics was approached for quick analysis and integration of spatial transcriptomics data.

## STRATEGY & PROCESS

Within a week, BI's data scientists proposed and began executing on a statement of work in line with Client's delivery timeline, which included:

- Conducting a detailed review of various spatial omics technologies, including hybridization-based (e.g., MERFISH), barcode-based (e.g., SlideTag, Slide-seq), and spot-based methods (e.g., Visium, Xenium), exploring the advantages and disadvantages of each technology to determine suitability.
- Pre-processing spatial transcriptomics data to account for variations in detection efficiency and background noise specific to each spatial technology.
- Performing dimensional reduction and spatial clustering to identify distinct spatial gene expression patterns and cellular composition within the tissue context.
- Implementing cell-type annotation using reference-free and/or reference-based methods.
- Transferring labels from Client's transcriptomic data and checking the quality of cell type annotation.
- Conducting downstream analysis in spatial data, including differential gene expression within cell types across conditions.
- Identifying spatially variable genes, spatial gene set enrichment analysis, pathway analysis (using KEGG and Reactome) to interpret biological pathways influenced by spatial variability.
- Performing cell proximity and niche analysis to understand cellular microenvironments and the functional dynamics that occur in situ, which can be crucial for deciphering complex biological processes and disease mechanisms.
- Investigating cell-cell communication with spatial resolution through ligand-receptor interactions.
- Creating spatial maps and detailed visualizations to illustrate findings.
- Listing candidate genes in a spatially informed manner for further validation through in situ hybridization or immunohistochemistry.
- Assisting in integrating spatial transcriptomics data with other omics data types to provide a comprehensive view of the molecular and cellular landscape, aiding in a multi-omic integration approach.

## RESULTS

- Within two months of receiving the sequencing data from Client, BI conducted the analysis, integrated the data, and summarized the most compelling findings, which included:
  - Specific immune cell subtypes are present in certain spatial niches within the tissue following pathogen exposure.
  - The characterization of specific molecular pathways mediated by these immune cell subtypes illuminated several intricate molecular interactions key to Client's pathway of interest. This illuminated the intricate molecular interactions for the Client.
- Following comprehensive presentations, both Client's Bioinformatics Scientist and Principal Scientist could quickly extract the insight and postulate the mechanisms underlying disease progression and pathogenesis.
- BI educated Client's Bioinformatics Scientist and Principal Scientist on the very specific spatial transcriptomics analysis workflows and the corresponding visualizations to prepare them to present the analysis to their non-technical coworkers.

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