



# St. Jude BioHackathon

## **Title**

Visualizing spatial transcriptomic data from serial sections in 3-dimensional space

## **Category**

Processing Pipelines And Methods

## **Challenge**

Spatial transcriptomics (2020 Nature Method of the Year) maps RNA expression data to a physical location on a tissue section. This methodology has enhanced our ability to decipher the complex biological processes occurring at the ~cell and tissue level during development, tissue injury, infection and cancer. However, a section is only one thin plane of the larger tissue. Existing analysis tools have no way of integrating multi-layered spatial data (similar to a confocal z stack), limiting the impact of spatially-resolved transcriptomics. A way to normalize between slices and collate them to view the dataset in 3-dimensional space would be extremely used.

## **Benefit**

The Thomas Lab has, and will continue to use, spatial transcriptomics to interrogate immune responses to infection (influenza) and cancer. Given the development of the Center for Spatial Transcriptomics at St. Jude, this solution would be highly valuable to researchers across St. Jude, allowing users to visually interrogate expression of a tissue in 3 dimensions.

## **Helpful Tools, Packages, or Software**

SpaceRanger (10X Genomics)

## **Test Data**

<https://www.10xgenomics.com/resources/datasets>