Duke Molecular Genomics core

10x Genomics Xenium data analysis

BASIC

- Imaging
- Transcript decoding
- Cell segmentation
- Cell transcript assignment (cell count)
- Deliverable files include the following: image files, matrix files, cell and transcript info files.

ADVANCED

- QC analysis – filtering outliers
- Normalization
- Unsupervised clustering
- Gene expression plots (All genes)
- Using reference single cell data - SpaceXR Seurat wrapper
- Comparative analysis between regions/samples to find DEG.
- GSEA and volcano plots for DEGs
- Deliverable files include the following: Clustering UMAP/Spatial plots, QC plots, cell count info in csv and bar graph, heatmap of top 10 genes per cluster, differential gene expression results per cluster in csv and between regions of interest (ROI) if comparing two ROIs, avg gene expression per cluster in csv, genes expression in feature,violin and spatial plots for all genes in the panel. UMAP/spatial plots from cell type prediction, Volcano and pathway plots from DEG results.

OTHER ANALYSES

- Neighborhood enrichment analysis (Squidpy)
- Co-occurrence probability analysis (Squidpy)
- Gene spatial correlation analysis (Squidpy)
- Cell- cell interaction analysis (stLearn)
- Spatial trajectory inference (stLearn)
- Tissue Domain Identification (Bansky)

IMPORTANT!

- It is your responsibility to store your data long term.
- You will receive a link with your raw sequencing data. <u>You must download it by the deadline listed in the email.</u>
- Basic analysis results will be shared either via Duke OneDrive, 10X cloud or using sftp download option from temp directory. Advanced analysis and other analysis results would be shared via Duke Box or email. <u>You must download your files within two weeks of receipt.</u>
- Any analysis requested after initial basic and advanced analysis requires submission of a new service request.