Implementation and Management of MERFISH Spatial Transcriptomics in the SCOPE Core Facility

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Spatial transcriptomics is a method of mapping gene expression to physical location in tissue. A popular spatial transcriptomics technique is multiplexed error-robust fluorescence in situ hybridization (MERFISH). The Sanderson Center for Optical Experimentation (SCOPE) at UMass Chan Medical School was an early adopter of Vizgen's MERFISH technology for spatial transcriptomics, and has processed over 200 fresh frozen MERFISH samples of varying tissue types since 2021. Combined, these samples have produced 350 TB of data on Vizgen's Alpha and MERSCOPE platforms for both commercial and academic users. To manage MERFISH experiments, SCOPE technical staff have developed extensive workflows for project planning, sample handling, data storage, and data transfer. MERFISH samples are prepared in 2 -4 sample batches, with workflows adapted for different tissue types as needed. After the sample preparation process, there is a limited time window for a sample to be imaged before the sample expires. Depending on the sample's size and the number of gene probes used, a single sample can take 12 - 36 hours to image; as such, MERFISH sample batches must be carefully timed to ensure that preparation can take place efficiently and that all samples can be imaged before they expire. Data processing, archiving, and transfer to users poses an additional challenge, requiring additional management and tracking to ensure that users receive their results in a timely fashion. Due to this extensive sample preparation process and subsequent large data sets, core facilities operating MERFISH spatial transcriptomics services must thoroughly plan and budget for the infrastructure and workflows essential to successfully supporting users.