Single-Cell Core
Associate Director of Spatial Transcriptomics
Harvard Medical School

Since its inception in 2016, the Single-Cell Core (SCC) at Harvard Medical School (HMS) has been instrumental in a wide variety of breakthrough discoveries by members of the HMS community by providing expert advice and access for the design and execution of state-of-the-art single-cell genomics assays. To expand the offerings of this core and continue to provide access to the latest cutting-edge advances in single-cell and transcriptomic methods, the SCC is seeking an Associate Director of Spatial Transcriptomics, who will be responsible for incorporating into the SCC recent and novel approaches to spatially resolved transcriptomics and guiding their use within the HMS community.

Single-cell genomic methods, such as single-cell RNA sequencing, have emerged as indispensable and powerful tools for addressing a broad range of biological questions, from basic developmental biology to disease phenotyping and pathway discovery. Yet, the required dissociation of cells prior to capture and characterization largely discards important information regarding the spatial organization of cells within tissues and of molecules, such as RNAs, within cells. In turn, this spatial context is essential to the understanding of many biological questions.

Over the past few years, a suite of spatial transcriptomics technologies have emerged that aim to retain or restore this critical spatial context in genomics-scale measurements. Such technologies incorporate a variety of approaches, from spatial capture methods--in which spatially arrayed barcodes are incorporated into RNA molecules prior to sequencing--or image-based methods--in which unique fluorescence barcodes are generated from individual molecules within intact cells and tissues and these barcodes are used to identify and localize hundreds to thousands of different RNAs. These technologies have complementary strengths with spatial capture methods providing untargeted measures of expressed RNAs but at modest resolution and sensitivity and image-based methods providing sub-cellular resolution with high sensitivity but of targeted sets of RNAs. New approaches are continually being introduced, and early-stage technologies are now becoming commercially available. Excitingly, this emerging suite of technologies promises new biological breakthroughs in a broad range of systems and questions.

Position Summary
The Associate Director (AD) of Spatial Transcriptomics will be charged with making available key spatial transcriptomic technologies for members of the HMS community through the SCC. This AD will be tasked with gaining a deep working knowledge of both spatial capture methodologies—Visium and Stereo-seq—as well as a leading image-based method—MERFISH—and leveraging these experiences to provide guidance to members of the HMS community on experimental design, the preparation of diverse sample types, measurement optimization, and spatial data interpretation and analysis. This AD will also be tasked with maintaining a working knowledge of this rapidly developing field and guiding the adoption of future spatial transcriptomic technologies by the SCC. The AD will join the dynamic team at the SCC and coordinate these efforts with the SCC Director and staff.

Leveraging the embedded expertise in spatial transcriptomics at HMS, this AD will train with the laboratory of Dr. Jeffrey Moffitt, a co-inventor of MERFISH and emerging leader in the field of spatial transcriptomics, and will receive additional scientific guidance, training, and support from the Core Director, core staff, and Dr. Allon Klein, the founder of the SCC and a leader in single-cell genomics.

Key Responsibilities:

- Collaborate with the Director to manage the daily operations and long-term strategy of the SCC.
- Consult with a wide range of research groups on how to design and conduct successful spatial transcriptomics experiments using commercial and in-house technologies.
- Hands-on implementation of spatial transcriptomics experiments, from sample handling to data distribution.
- Experimental evaluation of new spatial transcriptomics applications to determine whether they are appropriate to be incorporated into the SCC.
- Carry out training and outreach to the local biomedical research community
- Present results from core work at local, national and international meetings.
- Document and communicate results and progress to the SCC Scientific Advisory Board.
- Supervise/mentor staff and students in basic laboratory techniques.
- Collaborate with the sequencing and bioinformatics cores for analysis and troubleshooting.

Position Requirements

In addition to a desire to work at the cutting-edge of single-cell transcriptomics, qualified candidates should have

- A PhD in Molecular Biology, Genetics, Biochemistry, Cell Biology, Bioengineering, Biophysics or other related fields with at least 1-year experience in relevant areas of research (postdoctoral experience counts).
- A clear understanding of basic molecular biology techniques (e.g., DNA/RNA purification, PCR/RT-PCR amplification), some experience in microscopy (e.g. light microscopy, immunofluorescence etc.), and cell or tissue biology (e.g. tissue culture, or histology, etc)
- The ability to work well in a team
- Excellent organizational skill and attention to detail
- Strong communication and interpersonal skills

Suggested Requirements
Prior experience in any of the following topics would be beneficial but is not considered required

- Knowledge in genomic data analysis in R or Python environments, including but not limited to single cell analysis in Seurat or Scanpy
- Single-cell genomic data collection, including on platforms such as 10X Chromium
- RNA in situ methods, such as single-molecule fluorescence in situ hybridization (FISH) or RNAscope
- Preparation methods associated with tissue sectioning, including cryosectioning or the sectioning of formalin-fixed paraffin embedded (FFPE) samples
- Spatial transcriptomics methods, including spatial capture methods, such as Visium or GeoMx, or image-based methods, such as MERFISH

EEO Statement
We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability status, protected veteran status, gender identity, sexual orientation, pregnancy and pregnancy-related conditions, or any other characteristic protected by law.

Please send your CV and cover letter to Mandovi_Chatterjee@hms.harvard.edu and mention Position #P0025393 in the subject line.