INDRAPRASTHA INSTITUTE *of* INFORMATION TECHNOLOGY **DELHI**

Invitation to M.Tech. Thesis Defense of Debashish Mohanta : August 20, 2021 (Friday): 12.00-12.30 IST

In Partial Fulfilment of the Requirements for the Degree of

M.Tech. CB

Debashish Mohanta (MT19211)

Will defend her thesis

Title: "**Characterization of cell type boundaries using Spatial Transcriptomic studies**"

IIIT-D Faculty and Students are invited

Date: August 20, 2021 (Friday)
Time: 12.00-12.30 IST
Online over Google meet (https://meet.google.com/wex-drcf-tor)

Examiner:	Internal:	Arjun Ray
	~~External~~/Internal:	Gaurav Ahuja
	Advisor:	Debarka Sengupta

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Abstract

The tissue section development occurs due to cellular propagation which helps in defining the exoskeleton and the shape of the tissue and later defines the shape of an organ. Analyzing the factor which might control the stoppage of cellular propagation can help in finding relevance to the naturally occurring tissue and organ development mechanism in multicellular organisms. Since cellular heterogeneity defines the basis of all developments in a multicellular organism, by defining the heterogeneity of cells towards the boundary of a tissue section might help in defining their significant role in governing the size and shape of an organ.
We here did an extensive analysis for characterizing the properties and defining cell type of boundary cells using Spatial Transcriptomics studies. Single cell genomics was a barrier to analyze the specific boundary cells due to the loss of spatial information. Since, spatial transcriptomics provides quantitative gene expression data and visualization of the distribution of mRNAs within tissue sections, it gives us the chance to explore the properties of boundary cells by conserving their spatial information. By utilizing the concave hull algorithm, we selected the boundary cells based on their coordinate locations. Using the mouse brain as a study model we analyzed the properties of boundary cells and tried defining specific markers representing the boundary cells.
Through the analysis we were able to discover some key gene markers which were representing the boundary cells and validated our results, using Allen brain Atlas as reference. In order to signify the importance of boundary cell marker genes we explored their pathological inferences in various neurological disorders and found some promising results. Further analysis of these marker genes might give a valuable contribution to disease diagnostics.

Keywords: Spatial Transcriptomics, Boundary Cell, Single Cell Genomics.