

**Invitation to M.Tech. Thesis Defense of Nikita Gupta: February 12, 2020 (Wednesday): 14.00-15.00 IST**

In Partial Fulfillment of the Requirements for the Degree of

**M.Tech. CB**

**Nikita Gupta (MT16127)**

Will defend her thesis

**Title: "Acquiring metabolic insights from embryonic stem cells scRNAseq data"**

IIIT-D Faculty and Students are invited

**Date: February 12, 2020 (Wednesday)**

**Time: 14.00-15.00 IST**

**Place: CB Meeting Room (3rd Floor, R&D Building)**

<b>Examiner:</b>	<b>Internal:</b>	<b>Debarka Sengupta</b>
	<b>External/Internal:</b>	<b>Vibhor Kumar</b>
	<b>Advisor:</b>	<b>Ganesh Bagler(IIITD), Abhishek Jha (Elucidata)</b>

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**Abstract**

"RNA plays a key role in the expression and regulation of genes. With the advent of single cell technology, scRNA sequencing is widely adopted for characterising unique cell types, identifying rare cellular populations, investigating genetic relationship, and tracking the progression of cellular lineages during the development process. However, processing and analysing huge scRNA data demands a tailor-fit computational pipeline, dependent on the nature of the data. A gold standard computational tool for scRNA-seq data is yet to be developed. To overcome these challenges, a computation pipeline has been developed. The pipeline combines robust features of single-cell data analyses (like noise removal, identification of variable genes, dimensionality reduction, differential expression calculation and intuitive visualisations) with a network-based approach developed by Abhishek et al to reduce the bias of already known canonical metabolic pathway knowledge and find new metabolic rewiring modules. The pipeline can be used for developing, refining and validating metabolic hypotheses. Stem cells are found to play a primary role in cell therapies and regenerative medicines. This has generated a tremendously growing interest in the mechanisms underlying these magical cells. Researchers are showing keen interest in the mechanisms dictating self-renewal, potency and plasticity of stem cells. Therefore the developed pipeline was used to find metabolic insights from three scRNA datasets. Coherent metabolic findings were reported from two similar scRNA datasets. Additionally, the insights drawn from the pipeline were also consistent with the published literature. Thus, validating the accuracy of the pipeline. The pipeline also highlighted novel metabolic insights, opening up an innovative direction for studying various stages of stem cell differentiation and distinct cellular populations with confidence and ease."

