

**Invitation to M.Tech. Thesis Defense of Arpit Mathur: December 19, 2022 (Monday): 05:30 PM-06:00 PM IST**

In Partial Fulfilment of the Requirements for the Degree of

**M.Tech. CB**

**Arpit Mathur (MT20328)**

Will defend her thesis

**Title: “Finding Unique Pattern in Transcriptome and Epigenome of Cancer Cells”**

IIIT-D Faculty and Students are invited

**Date: December 19, 2022 (Monday)
Time:** **05:30 PM-06:00 PM IST**

**Meeting Link:** [**http://meet.google.com/tat-yday-tan**](http://meet.google.com/tat-yday-tan)

**Examiner: Internal:   Arjun Ray**

**~~External~~/Internal: Tarini Shankar Ghosh**

**Advisor: Vibhor Kumar**

**Co-Advisor NA**

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**Abstract**

Studying Chromatin Architecture is paramount to an understanding about cells and nuclei in disease and normal state. With recent advances in genomic technologies and computational power, new domains like Topologically associated domains (TAD) have been discovered. Studying TAD in the context of cancer cells gives insights into how chromatin folding relates to the survival of the patient. Exploiting chromatin interactions from the lens of enhancer-gene interactions is of cardinal value since identifying specific chromatin interactions (enhancer-gene pairs) in disease state cells which are etiology pairs for the disease, and using genomic editing technologies to knockdown these pairs, could be a potential precise and accurate model to beat disease cells, especially cancer cells. Our study is divided into two parts; in the first part, we build a method to understand TAD biology and its implication in estimating patient survival. In the second part of our study, we modified a previously proposed method scEChiA to detect enhancer-gene pairs interactions in cancer-specific cells using using RNA-seq profiles. We further validates the predicted interactions with 4D genome and Activity by Contact (ABC) databases.

Identification of specific TAD, which is most surviving in cancer cell lines, and understanding its underlying biology gives a new definition of TAD property and function. Chromatin interaction results from scEChiA along pipelined developed algorithms give enhancer-gene, enhancer-enhancer, and gene-gene interactions, which could be a database for potential target whose knockdown could be a potential cure to cancer cells.