

**Invitation to M.Tech. Thesis Defense of** **Chandan Saini: May 21, 2023 (Sunday):** **11:00 AM – 11:30 AM IST**

In Partial Fulfillment of the Requirements for the Degree of

**M.Tech. CB**

**Chandan Saini (MT20337)**

Will defend his thesis

**Title: “Deicphering Heterogeneous structure using Cryo-electron microscopic images”**

IIIT-D Faculty and Students are invited

**Date: May 21, 2023 (Sunday)  
Time:** **11:00 AM – 11:30 AM IST**

**Meeting Link:** [**https://meet.google.com/edp-jqnz-jdc**](https://meet.google.com/edp-jqnz-jdc)

**Examiner: Internal:   Arul N Murugan**

**~~External~~/Internal: Tavpritesh Sethi**

**Advisor: Vibhor Kumar**

**Co-Advisor NA**

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**Abstract**

The cryo-electron microscopy (cryo-EM) technique allows the capture 2D projection images of three-dimensional (3-D) volumes of biological structures, revealing their inherent heterogeneity arising from structural flexibility, conformational changes, and the presence of distinct functional states. This variability can be influenced by factors such as ligand binding, conformational rearrangements, and variations in subunit composition. Accurate identification and understanding of this heterogeneity play a pivotal role in unraveling the intricate structure-function relationships that govern biological processes and facilitating the development of targeted therapeutic interventions.

To address the heterogeneity challenge in cryo-EM, numerous computational approaches have been developed. These methods aim to extract distinct conformations from heterogeneous datasets, enabling the resolution of underlying structural variability. By generating high-resolution 3-D reconstructions of individual states within a heterogeneous sample, these approaches unveil hidden details and provide deeper mechanistic insights.

In this research project, our objective was to identify the flexible and fixed regions of the LDL protein. We employed principal component analysis based on the singular value decomposition (SVD) algorithm, which enhances the resolution of the 3-D volume and facilitates the classification of 2-D images using EMAN2. Through multiple iterations of refinement, our study successfully obtained different 3-D volumes with improved resolution. Further analysis identified two highly variable principal components, allowing us to distinguish between the fixed and variable parts of the protein structure.