

Title: Machine Learning in Single-cell Genomics

Speaker: Prof. Hamim Zafar

Date: Wednesday, 28th September, 2022

Time: 6:00 PM

Venue: L18

Abstract:

Recent advances in high-throughput sequencing technologies have vastly expanded the scale and complexity of biological datasets. This increasing complexity have resulted in a growing use of machine learning models in genomics to build informative and predictive models of the underlying biological processes. Exploration of biological systems and processes often requires the development of unsupervised learning algorithms.

In this talk, we will discuss such unsupervised learning algorithms (MARGARET) for inferring single-cell trajectory and fate mapping for diverse dynamic cellular processes. MARGARET reconstructs complex trajectory topologies using a deep unsupervised metric learning and a graph-partitioning approach based on a novel connectivity measure, automatically detects terminal cell states, and generalizes the quantification of fate plasticity for complex topologies.

Bio:

Dr. Hamim Zafar completed his Ph.D. in 2018 from the Department of Computer Science at Rice University, USA in the field of Computational Biology. He joined IIT Kanpur as a joint faculty in CSE and BSBE in 2018. He took a year-long break for pursuing Lane Fellowship in the Computational Biology Department at Carnegie Mellon University, USA, and resumed his position at IIT Kanpur in 2019. His research interests include computational biology, probabilistic models, and single-cell omics. He is currently the recipient of Har Gobind Khorana-Innovative Young Biotechnologist Award from DBT and he has also been selected for the Wellcome Trust/DBT India Alliance Early Career Fellowship.