Postgraduate Seminar Series
Venue: Graduate Seminar Room

Speaker Information

Mohammad Nuwaisir Rahman (Std No. 0422052121) is a full time M.Sc. student in the department of CSE, BUET. He completed his undergraduate studies from BUET in 2022. His research interest lies in the Spatial Transcriptomics, Computational Modeling, Application of Machine Learning of Bioinformatics. He is currently doing his postgraduate thesis under the supervision of Dr. Mohammad Saifur Rahman. He will be speaking about his ongoing research in this talk.

IDENTIFICATION OF PATHOLOGICALLY REMODELED SPATIAL TRANSCRIPTOMICS TISSUE REGIONS BY CONSTRUCTING AN OPTIMAL TRANSPORT PLAN

The impact of pathological events on tissue regions often manifests with spatial variability. Comprehensive quantification of pathological effects and a nuanced understanding of the underlying spatial variability mechanisms are essential for identifying suitable therapeutic targets. To address these challenges, Spatial Transcriptomics (ST) is a valuable technology, providing spatially resolved gene expression values. However, the utilization of the potential within ST datasets requires suitable methods. Here we introduce SPaSE (Spatially-resolved Pathology ScorE), designed to quantify pathological effects within an ST tissue sample incorporating an optimal transport problem formulation between the pathologically impacted and control reference ST samples, considering both gene expression and spatial spot locations. The scores generated by SPaSE exhibit comparable effectiveness to other methods that leverage orthogonal single-nucleus data as well as prior biological knowledge for inferring distinct cardiac zones in post-MI (myocardial infarction) mouse hearts. Notably, our findings underscore the predictive nature of gene expressions in delineating the pathological state of tissue regions, providing spatial and temporal insights into the post-MI niche. We anticipate SPaSE to serve as a valuable tool for comprehending and quantifying pathological changes in spatiotemporal ST data. Moreover, it holds the potential to identify pathology-specific signature genes, offering insights into diverse post-MI processes.