Postgraduate Seminar Series

Venue: Graduate Seminar Room
Date & Time: August 01, 2026 at 1:30 PM

Speaker Information

Al Imtiaz is a Ph.D. student in the Department of Computer Science and Engineering (CSE) at the Bangladesh University of Engineering and Technology (BUET), working in the field of Bioinformatics. He completed his B.Sc. in Computer Science and Engineering from the University of Information Technology and Sciences (UITS) in 2011, securing first place with a CGPA of 3.97, and earned his M.Sc. in Computer Science and Engineering from East West University in 2015. He was awarded the "Board of Trustee Gold Medal Award" at the second convocation of UITS in 2014. He has been serving as a faculty member in the Department of CSE at UITS since September 2012 . He has published more than 20 research articles in national and international journals and conferences. His research interests include Bioinformatics, Machine Learning, and IoT. He is currently pursuing his doctoral research under the supervision of Professor Dr. Mohammad Saifur Rahman. He will be speaking about his ongoing research in this talk.

Survival Prediction in Pancreatic Cancer: Insights and Limitations from Clinico-Genomic Integration

Despite advances in cancer genomics, pancreatic cancer remains one of the most lethal malignancies, with most patients diagnosed at advanced, inoperable stages. This study integrated clinical and somatic mutation data from TCGA and ICGC, yielding a harmonised dataset of 796 patients (discovery: n=597; validation: n=199). Of 43,871 genes, 24 with a mutation prevalence of at least 5% were selected for analysis. Mutation impact was assessed using SIFT, PolyPhen, and VEP, and missing data were imputed. Cox proportional hazards regression and twelve machine learning (ML) algorithms were applied to predict survival at multiple time points (6, 12, 24, and 36 months), with SMOTE used to address class imbalance. TP53 and HMCN1 mutations, particularly high-impact variants, were significantly associated with survival in multivariate hazard analysis, with HMCN1 reported here for the first time as an independent prognostic factor in pancreatic cancer. The best hazard model achieved AUROC values ranging from 0.51 to 0.63, while the top ML model, Multinomial Naïve Bayes, achieved an AUROC of 0.671 and an AUPR of 0.606. Both approaches struggled at shorter and longer intervals due to limited sample sizes and data imbalance. These results indicate that mutation data alone are insufficient for reliable survival prediction in pancreatic cancer. Incorporating multi-omics profiles, treatment history, and larger patient cohorts may substantially improve model accuracy in future work.