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# From Protein-DNA Binding to Spatial Transcriptomics: Machine Learning Models of Transcriptional Regulation at Multiple Scales

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Md. Abul Hassan Samee is an assistant professor in the Department of Molecular Physiology and Biophysics at Baylor College of Medicine. His research integrates algorithms, machine learning, and comparative genomics to reveal the molecular mechanisms underlying transcriptional regulation. Dr. Samee received his Ph.D. in computer science from the University of Illinois Urbana-Champaign (2008-15), and did his post-doctoral research as a Bioinformatics Fellow in the Gladstone Institutes at University of California San Francisco (2015-19). Dr. Samee is the recipient of the International Fulbright Science and Technology Fellowship, the MAVIS Future Faculty Fellowship (UIUC), and the Gladstone Institutes Award for Scientific Leadership.

## **Abstract**

Proper regulation of gene transcription is critical to all forms of life and at all stages of development. Disruption in transcriptional regulation is a hallmark of many diseases, including cancer and neuropsychiatric disorders. While the key information for transcriptional regulation is encoded in our genome, the process is characterized by “many moving parts” functioning at different scales. In this talk, we will present our recent algorithms on understanding the mechanisms of the three main components of transcriptional regulation: protein-DNA binding, protein-polymerase interaction, and intercellular communication.

**When:** [Saturday, 3<sup>rd</sup> October, 2020 \(8:00 PM\)](#)

**Where:** [Online. Zoom Meeting ID: 650 7876 2959, Password: 948829](#)

**Organized by** BUET ACM Chapter, Dept. of CSE, BUET.