



## Seminar Presentation

### Predicting transcription factor binding sites using deep learning

#### Abstract

All cells that form various organs in our body have an identical genotype. Gene regulation occurs at various stages, including the genomic, transcriptomic, and proteomic levels. Specific regulatory mechanisms govern the activation or suppression of genes, depending on the proteins required for a particular phenotype. This process results in the cellular differentiation into distinct cell types. Transcriptional regulation is the cell's primary mode of controlling gene expression. Transcription factors (TFs) are proteins that recognize specific and short DNA sequences called transcription factor binding sites (TFBS) and bind to them. Identifying TFBS helps to understand the regulatory mechanisms that govern the transcriptional state of cells. Several experimental methods have been developed to identify TFBS. In the last decade with advances in omics technologies and the accumulation of omics data, some computational methods based on deep learning have been employed to identify TFBSs. In this review, we aim to give a brief overview of experimental and computational methods especially deep learning methods for TFBS prediction. Existing deep learning methods for identifying TFBS are based on a combination of convolutional neural network (CNN), Recurrent Neural Network (RNN), Long Short-Term Memory (LSTM), Bidirectional LSTM (Bi-LSTM), Autoencoder, and Attention mechanism. We introduce the architecture of each method and compare the results and differences between these models for TFBS prediction.

#### Presenter

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#### Instructor

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#### Date

30 January (10 bahman), 9:30 AM

#### Location (Physical and Online presentation)

Institute of Biochemistry and Biophysics. Amphitheater

<https://join.skype.com/AOch5b2nahlw>

