Regulation of gene expression includes a variety of mechanisms to increase or decrease specific gene products. Gene expression can be regulated at any stage from transcription to post-transcription and it's essential to almost all living organisms, as it increases the versatility and adaptability by allowing the cell to express the needed proteins.

In this dissertation, we comprehensively studied the gene regulation from both transcriptional and post-transcriptional points of view. Transcriptional regulation is by which cells regulate the transcription from DNA to RNA, thereby directing gene activity. Transcriptional factors (TFs) play a very important role in transcriptional regulation and they are proteins that bind to specific DNA sequences (regulatory elements) to regulate the gene expression. Current studies on TF binding are still very limited and thus, it leaves much to be improved in understanding the TF binding mechanism. To fill this gap, we proposed a variety of computational methods for predicting TF binding elements, which have been proved to be more efficient and accurate compared with other existing tools such as DREME and RSAT peaks-motif. On the other hand, studying only the transcriptional gene regulation is not enough for a comprehensive understanding. Therefore, we also studied the gene regulation at the post-transcriptional level. MicroRNAs (miRNAs) are believed to post-transcriptionally regulate the expression of thousands of target mRNAs, yet the miRNA binding mechanism is still not well understood. In this dissertation, we explored both the traditional and novel features of miRNA-binding and proposed several computational models for miRNA target prediction. The developed tools outperformed the traditional microRNA target prediction methods (e.g miRanda and TargetScan) in terms of prediction accuracy (precision, recall) and time efficiency.

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The public is welcome to attend.