# A probabilistic model for competitive binding of transcription factors

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One of the most important regulation steps of gene expression is transcriptional regulation, which is to a large extent controlled by transcription factors binding to DNA. Many models of transcription factor binding have been proposed but most of them model binding of a single transcription factor at a time. Existing prediction methods for multiple TFs base mainly on searching for clustered binding sites or cis-regulatory modules [1]. We have developed a probabilistic model that predicts simultaneously binding of several transcription factors. Our method considers the transcription factor binding process as a competition between factors which is realistic from the biological point of view. Modeling results show remarkable improvement compared to the cases where the individual prediction results of separate TF binding have been combined.

[1] Hannenhalli, S. (2008) Eukaryotic transcription factor binding sites--modeling and integrative search methods. Bioinformatics. 24,1325-1331.