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Poster presentation

Prediction and evolution of transcription factors and their evolutionary families in prokaryotes

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Transcription factors (TFs) play an important role in the genetic regulation of transcription in response to internal and external cellular stimulus even in a simple bacterium like *Escherichia coli* [1]. However little is known about their functional roles, expression dynamics and evolutionary scenarios on a large scale, even in a well studied model organisms. In this short tutorial, I will first talk about the prediction of transcription factors, which form the core of the regulatory repertoires in prokaryotes, responsible for controlling the expression of genes/transcription units by binding to their cis-regulatory regions. I will present different commonly used sequenced-based approaches to predict TFs in prokarya and discuss a simple rule of thumb to identify the putative regulatory role played by a TF based on its protein sequence alone [2-6]. I will discuss on some important properties of prokaryotic TFs which distinguish them apart from rest of the protein coding genes. The second part of the talk would concentrate on the evolutionary conservation of TFs and TF families across genomes and the implications of the observations on the phenotypic adaptation of species to different niches [3,7,8]. Finally, I will discuss some future perspectives in this area of research.

References

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