Prediction of the gene transcription dynamics based on the structure of regulatory sequences

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***Short Abstract* — Gene transcription is a highly dynamic process taking place in all living cells. The transcription process comprises of several stages, during which transcription factors interact with DNA sequence leading to the formation of a preinitiation complex. Rate of this process may be enhanced or modified by mechanisms that are still not fully understood. It is likely that the differences in transcription timing are reflected in differences in the structure of regulatory sequences, such as promoter region or 3'UTR. Recent studies show that genes having different transcription dynamics patterns show significant differences in the structure of their promoter region and stability of transcribed mRNA. Better understanding of transcription dynamics and ability to predict rate of transcription provides support for more precise modeling of cell response to a given stimuli.**

***Keywords* — Gene regulation, transcription dynamics, 3'UTR, promoter region, ARE, transcription factors**

I. Introduction

TRANSCRIPTION is a crucial step in the process of gene expression and it's regulation. The transcription process comprises of several stages, during which regulatory proteins such as basal transcription factors interact with DNA sequence leading to the formation of a preinitiation complex. Rate of this process, which is considered as the primary step of transcription, may be altered by participation of additional regulatory elements. Transcriptional activity and gene regulation is possible due to the recruitment of specific regulatory complexes to target genes. Although binding sites for basal transcription machinery are rather well identified by basal transcription factors, finding active gene-specific transcription factors binding sites (TFBS) using computational methods is more complicated as transcription factors widely bind to spurious sites [1,2].

In the work of Tian et al.[3] NF-κB dependent genes were categorized into groups based on the time of their transcriptional response. Similar dynamics patterns were observed in the work of Hao and Baltimore [4]. It is not obvious what mechanism is responsible for segregation of the genes' into several transcription dynamics groups. The Similarity of these two experiments led us to seek a correlation between promoter structure, and the occurrence of ARE elements in the 3 'UTR sequence. For promoter region this might concern differences in number and type of TFBS as well as for the putative cofactors [5-7].

Despite extensive studies carried out in this field the precise nature of transcriptional gene regulation and dynamics is still not fully understood.

II. Conclusion

In our recent studies we have computationally analyzed the structure of regulatory regions in the NF-κB dependent genes belonging to the Early, Middle, Late and Paradox groups [8]. We have found that genes belonging to different transcription dynamics categories show different characteristics in structure of the promoter region and in the 3'UTR. The most differences have been found among the Early and the Late groups. To validate this computational approach to the gene transcription dynamics, we applied this method to larger group of genes. Based on the structure of regulatory sequences we tried to predict the type of transcription dynamics and compare it with experimental data.

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