Protein copy number distributions for a self-regulating gene in the presence of decoy binding sites

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Keywords: stochastic gene expression; bursting; decoy binding sites; bimodality

A single transcription factor may interact with a multitude of targets on the genome, some of which are at gene promoters, others being part of DNA repeat elements. Being sequestered at binding sites, protein molecules can be prevented from partaking in other pathways, specifically, from regulating the expression of the very gene that encodes them. Acting as decoys at the expense of the autoregulatory loop, the binding sites can have a profound impact on protein abundance — on its mean as well as on its cell-to-cell variability. In order to quantify this impact, we study in this paper a mathematical model for pulsatile expression of a transcription factor that autoregulates its expression and interacts with decoys. We determine the exact stationary distribution for protein abundance at the single-cell level, showing that in the case of non-cooperative positive autoregulation, the distribution can be bimodal, possessing a basal expression mode and a distinct, up-regulated, mode. Bimodal protein distributions are more feasible if the rate of degradation is the same irrespective of whether protein is bound or not. Contrastingly, the presence of decoy binding sites which protect the protein from degradation reduces the availability of the bimodal scenario.

The talk presents results which have been published in [1].

References

[1] P. Bokes, A. Singh (2015), *Protein Copy Number Distributions for a Self-Regulating Gene in the Presence of Decoy Binding Sites*, PLoS ONE **10**(3) e0120555.