

Genetic Switches between two population with regards to mRNA and proteins

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Abstract

As Arc, one virus-like gene, crucial for learning and memory, was discovered by researchers in neurological disorders fields, Arc mRNA's single directed path and allowing protein binding regional restrictively is a potential investigation on helping shuttle toxic proteins responsible for some diseases related to memory deficiency. To study especially the transform between mRNA and proteins, the switching function of the phenotypes, 'normals' multiplying populations and 'persisters', resilient to stress instead of multiplying is of our interest. Mean time to switching (MTS) is calculated explicitly quantifying the switching process in statistical methods combining Hamiltonian Markov Chain. The model derived from predator and prey with type II functional response studies the mechanism of normals with intrinsic rate of increase and the persisters with the instantaneous discovery rate and converting coefficients. During solving the results, since the numeric method is applied for the 2D approximation of Hamiltonian with intrinsic noise induced switching combining geometric minimum action method. The MTS, trajectories and Hamiltonian dynamics demonstrate the practical and robust advantages of our model on interpreting the switching process of genes (IGFs, Hax Arcs and etc.) with respects to memory deficiency in aging process which can be useful in further drug efficiency test and disease curing.

1 Introduction

In cell biology, non-equilibrium stochastic process is of interest since the observation of experimental results are becoming of higher resolution, studying the molecules both with imaging and expression data are often conducted in both single and population (thousand) order, which basically described in stochastic process whether on a discrete or continuous scale with status changes either genotypically or phenotypically. Many problems are thus studied related to status switching, including cell regulatory networks[1], signal response on excitability and inhibition[2], (convincing by translational and transcriptional burst of expression for instances.), metastability among populations, (binding of ligands and proteins, forming of polymerases and etc.). In this paper, we focus on the interaction among genes, mRNA, proteins and etc. To be more specific, while the switching problem among molecules can be studied on genotype, including sequencing for single RNA, alignments and binding considering codons and etc, we stay on the switching with expression (concentration) only, which is simplified as modified population problem using Lotka-Volterra equations[3] of two populations only. Thus, rather than the competitor model(for instances, cell bifurcations.), we applied simulation of switching on predator model. The model is based on the following basic assumptions: Prey population(promoters) is fed with enough food all the time while the predator population of the predator(the persisters) depends on the size

of prey(promoters).In our paper, we mainly study the interaction of DNA and its interaction with the associated proteins.(Clinical data of Hax1 and HS_1 is downloaded from Ensembl gene database[4]). On one hand, the switching model is calculated under the large deviation theory(LDT)[5] combining the least actions. The Markov chain[6] consider the states of the 2D coordinates (x,y) of mRNA numbers and protein numbers referencing the distribution of x , which follows the order $O(1)$ while P_x follows the time scale on $O(1/\varepsilon)$ and guaranteeing the variant of LDT hold with the transform of the expressions in single population. Only considering the process of diffusion case, we study the binding of hax1 with simple switching between on and off status under its interaction with HS_1 seen as in the constant environment, i.e. the closed system at mean field. The dimer which can be cancelled out connect the binding between two single population. On the other hand, one numeric method is applied to solve the problem, making compare with the stochastic process[7] on approximation equation of the mean switching time(MST) with the transform between two status (we studied the switching time with four situations, both multiplicative and asymptotic of single population and the binding and degradation between two population.) Again, this method is also calculated based on the Hamiltonians. We give out the MST with respect to N/N_c denoting N as the population number of interest and N_c as the threshold of certain status(either of that population or the other population). Since our study only based on data in the process of transforming in the constant environment, extinction is not considered in this paper. To study both intrinsic and extrinsic noise with the exciting and inhibiting bursts is the potential topic in the future. In the following contents, the first chapter is the proposition of the model, based on least action with LDT and MTS approximation with one stochastic differential equation (SDE) [8]separately; And the second chapter gives numeric experiments based on Hamilton Markov Chain computation of the expression data of hax1 and $HS - 1$; In the last chapter, the results is analysed with both hamiltonian, realization size, convergence, the rewards computation taking the continuous markov chain as Poisson process[9] and etc. In the appendix, there also includes the complete proof of model with action S based on hamilton not only based on the explicit equation in this paper. Some descriptive Statistics and pre-computation based on the data can be accessed through link in availability. As the process related to motor coordination and function, the Hax's function in regulation, B cell's signal transduction can be further studied with more data considering its excitability and metastability functions with stimulation of drugs for instance in the future as well.

2 Proposed Model

Molecular interactions are studied on phenotypic data of the mRNA