Large deviation properties of population averages: An indicator of gene expression dynamics in a single cell

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Population of genetically identical cells are heterogenous in their phenotypes. We investigate the stochasticity in simple gene expression networks to elucidate how it works at a single cell level and its impact on the total output signal contributed by multiple cells. Consider a model of gene expression network where activated genes produce mRNA and protein in a sequential manner with and without feedback. While searching for signatures of such networks from the output data of a collection of cells, we observe that the mean signal provides only partial information. To overcome this, we introduce the idea of sample mean where the the sample size can be controlled. When we calculate the sample mean for a set of sub-population of cells, we obtain a distribution whose variance and large deviation properties are characterised by the underlying gene expression network. We obtain the probability generating function for chemical master equations for three simple regulatory networks without feedback and exactly calculate the first and second moments in the steady state. We also report the (i) mean, (ii) standard deviation and (iii) assymptotic properties of the sample mean distribution of outputs generated by a collection of independent networks active in each cell. The sample mean can be observed in experiments and its distribution can be used to infer about the underlying gene expression network resulting in cell heterogeneity.