

Markov Property and Scale-free Organization of Gene Expression

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Keywords: gene expression, Markov property, scale-free, stochastic process

1 Introduction

Evolutional gene expression organization has recently been studied by measuring the *mRNA* abundance (gene expression) for tens of thousands of genes in parallel (GeneChips arrays) [3]. These experiments on *mRNA* abundance have revealed that gene expression exhibits a scale-free organization, which is highly conserved in all the major five kingdoms of life, from *Bacteria* to *Human* [3]. Therefore, the gene expression distribution $p(k)$ (probability that a gene has an amount of expression k) decays as a power-law $k^{-\gamma}$ [1].

In order to uncover the origin of this scale-free organization, we consider a stochastic process with Markov property (i.e., the future is governed by the present and does not depend on the past). This assumption is very natural for biology since all biological systems obey the physical laws, which also manifest this property. Surprisingly, scale-free organization spontaneously emerges from Markov property in the following construction (Fig. 1). (See [2] for more details.)

2 Method and Results

A stochastic process is said to have Markov property if the conditional probability density function $p(k_n, t_n | k_{n-1}, t_{n-1}; \dots; k_0, t_0)$ satisfies

$$p(k_n, t_n | k_{n-1}, t_{n-1}; \dots; k_0, t_0) = p(k_n, t_n | k_{n-1}, t_{n-1}), \quad (1)$$

for arbitrary $t_n > \dots > t_0$, where k_i denotes the expression level at time t_i ($i = 1, \dots, n$).

If the system exhibits the Markov property, then it must obey Master equation [4], which describes how the system changes over time. Our approach uses experimental data of instantaneous transition probability from [3]. If we insert this information into Master equation, it is reduced to a specific Kolmogorov equation. Interestingly, it is equivalent to one of the most well known model in financial engineering: Black-Scholes model (B-S). By using stochastic theory [4], we solve (B-S) model and we obtain the probability that a gene has an amount of expression k at time t :

$$p(k, t) = \frac{1}{\sqrt{2\pi(\sigma k)^2(t-t_0)}} \exp\left[-\frac{(\log(k/k_0) - (\mu - \frac{1}{2}\sigma^2)(t-t_0))^2}{2\sigma^2(t-t_0)}\right], \quad (2)$$

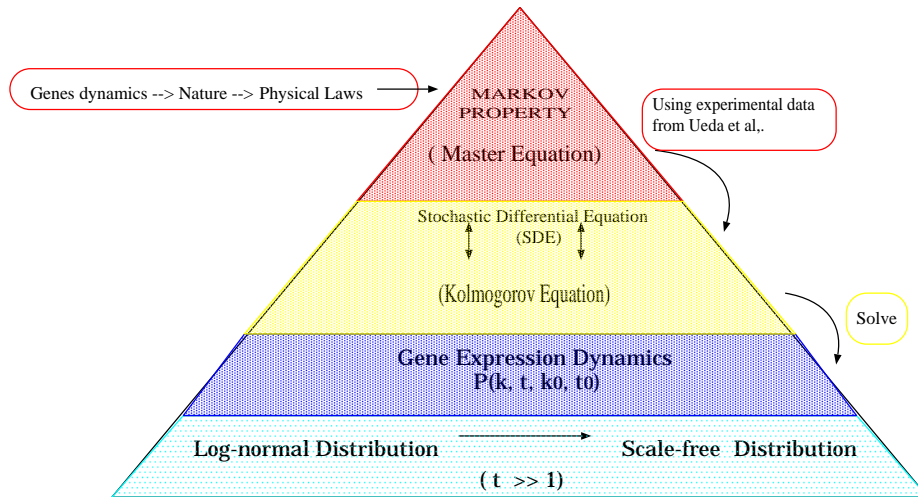


Figure 1: Scheme of the fundamental levels of our construction. From Markov property (or equivalently Master Equation) to scale-free distribution.

where k_0 denotes initial expression level at time t_0 , μ is the average of gene expression changes and σ is the square root of the diffusion of gene expression. When the system evolves for large time, the gene expression is organized as scale-free distribution

$$p(k) \propto k^{\frac{2\mu/\sigma^2-5}{4}}, \quad (3)$$

where $p(k)$ denotes $p(k, t)$ when $t \rightarrow \infty$. By knowing μ and σ from experimental data, it is straightforward to obtain the exponent of the scale-free distribution for each organism. For example, we have obtained $\gamma = 1.81$ for the organism *S. Cerevisiae* in good agreement with experimental results in [3], by using $\mu = -0.07$ and $\sigma = 0.25$. The same procedure can be applied for obtaining γ values for different organisms. Furthermore, Eq. (2) predicts small corrections at low and high expression levels reflecting the log-normal distribution, and elucidates robustness (stability) of gene expression systems.

This gene expression mechanics may provide a better understanding of cell dynamics. As a future work, this approach may be extended for studying multi-gene correlation dynamics, in order to extract information about gene functionality.

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