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VAE-CME

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1 Birth Death Model

Consider a simple non-Markovian system where molecules are produced at a rate ρ and are removed from the system (degraded) after a fixed time delay τ :

$$\emptyset \xrightarrow{\rho} N, N \xrightarrow{\tau} \emptyset \tag{1}$$

The training set is the distribution from 1×10^4 samples using the SSA.In the experiment, we assume $\rho = 20$, $\tau = 10$ and truncation N = 271.

Both encoder and decoder are multilayer perceptron with one hidden layer. The objective function is chosen as the sum of mean-squared-error and KL divergence. For the training we used the standard adaptive moment estimation algorithm (ADAM). The weight of mean-squared-error needs to be increased, and the learning rate needs to be decreased from approximately 0.25 to 0.01 during the training process.

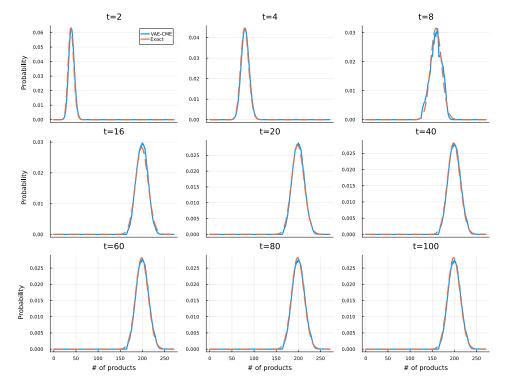


Figure 1: Birth Death Model Fitting

2 On Off Model

3 Bursty Model

We consider Bursty Model, which is the same as Birth Death Model, except that the binding of RNAPs to the promoter occurs in bursts whose size i is distributed according to the geometric distribution $b^i/(1+b)^{i+1}$; this

can be described by the reaction scheme:

$$\emptyset \xrightarrow{\alpha\beta^{i}} iN, i = 1, 2, 3, ...$$

$$N \stackrel{\tau}{\Rightarrow} \emptyset$$
(2)

To achieve the best fitting performance, the analytical solution of the Bursty model's probability distribution (See SI in [1]) is used as the training set. In the experiment, we assume $\alpha=0.0282$, $\beta=3.46$, $\tau=120$ and truncation N=64.

The same as before, we choose the sum of mean-squared-error and KL divergenc as the objective function, ADAM as the optimizer. And the weight of mean-squared-error needs to be increased, the learning rate needs to be decreased

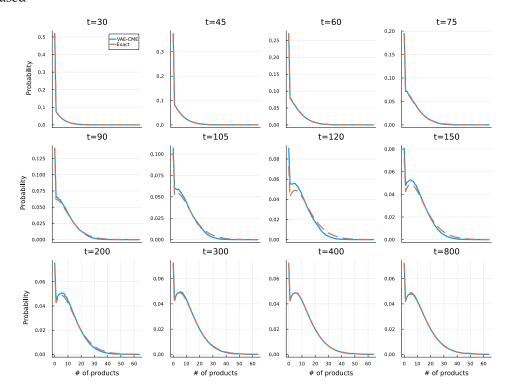


Figure 2: Bursty Model Fitting

- 3.1 Control Mean of time delay τ
- 3.2 Control Variance of time delay τ
- 4 Oscillation Model
- 4.1 Reducing sample size
- 5 Exact solution for variable time delay τ

References

[1] Qingchao Jiang, Xiaoming Fu, Shifu Yan, Runlai Li, Wenli Du, Zhixing Cao, Feng Qian, and Ramon Grima. Neural network aided approximation and parameter inference of non-markovian models of gene expression. Nature communications, 12(1):2618, 2021.