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Dynamic Distribution for Inactive Genes in Telephone Model

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Abstract: Gene transcription is the central part of life process and has been a hot topic in life science research for many years. In this work, we discuss the dynamics of inactive genes in two conditions for telegraph model. We obtain the decaying dynamical distribution for the inactive genes. Furthermore, we find that the dynamical distribution is almost horizontal in the beginning region, if the synthesis rate is appropriately large. And we give some simulations to instruct the results.

Keywords: Telegraph model; generating function; inactive gene; distribution

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0 Introduction

All living things in the world, including ourselves, are made of cells. Genes are genetically significant fragments of DNA, which are functional and structural units of genetic materials. In generally, gene expression mainly consists of two processes: transcription and translation. Transcription refers to the process of transferring genetic information from DNA to messenger RNA(mRNA) under the action of RNA polymerase by taking DNA as a template and following the principle of base complementary pairing. mRNA is responsible for the storage and transfer of genetic information. It is translated into the final production proteins.

Almost the functions of all cell work depend on proteins, and the type and quantity of proteins in each cell is mainly determined by gene transcription. Gene transcription is the central part of life process and has been a hot topic in life science research for many years.

Only a few decades ago, scientists were used to observing the reaction processes of multiple cells in a unified way because of the limitations of traditional methods such as Microarray and RNA blotting. These experiments assume implicitly that cells with identical genes have the same cellular function in the same living environment. The experimental data obtained by these means tend to lead people to believe that gene expression is a continuous and definite process. With the development of many advanced detection technologies such as computer image processing and fluorescent protein technology in the early 20th century, researchers could observe the multiple key processes in a single cell in real time. The results of these experiments explained that gene expression is a discontinuous and random process.

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In order to express the randomness of gene transcription, scientists used mathematical models to describe the randomness of gene transcription, and applied modern mathematical models combined with mathematical experimental data to explore the internal dynamics of biological organisms. In the mathematical models, there are a variety of quantitative indexes, such as mean, noise and probability of distribution[1-3]. From the observations of the gene transcription experiments in single cells, biologists can estimate the numbers of the same kind mRNA in a cell accurately. In conjunction with statistical methods, biologists have been able to obtain a lot of data of the distribution about the number of mRNA under different experimental conditions. The theoretical study of these models can not only provide reasonable interpretation of the existing experimental data, but also help us to further understand the mechanism and root cause of the generation and reduction of random phenomena of gene expression. Gene transcription is the first and most important step of gene expression. Therefore, the study of the internal relationship between the number of mRNA production and the random behavior of gene transcription can help us to deeply understand the origin of the randomness of gene expression and further explore the regulation of the overall level of gene expression by the random process in the gene transcription system.

The distribution of mRNA is usually depicted by the probability mass function $P_m(t)$ which determined by the system parameters of the models and it means the probability that there are exactly m mRNA molecules of the gene of our concern at time t in one cell. Researchers usually let it describe the number of mRNA, and it can best describe the randomness of gene expression [4-6]. We express it by the reverse calculation of the generating function $V(z,t)$.

In recent years, the accumulation of more and more experimental data and the innovation of theoretical methods provide new ideas for us to systematically establish and improve the mathematical model of random gene expression. The theoretical study of these patterns can not only provide reasonable interpretation of the existing experimental data, but also help us to further understand the mechanism and root cause of the generation and reduction of random phenomena of gene expression.

It is generally believed that the randomness of the production of gene transcripts comes from the random alternation between the two states of gene on and gene off, and the behavior of the synthesis and the degradation of mRNA at the state of gene on. The telegraph model is one of the classic models, and because of its simplicity and generality, it is considered as the standard model for studying random gene transcription. The diagram is as the following

$$\text{gene off} \underset{k_{\text{off}}}{\overset{k_{\text{on}}}{\rightleftharpoons}} \text{gene on} \xrightarrow{v_{\text{m}}} \text{mRNA} \xrightarrow{k_{\delta}} \emptyset, \tag{1.1}$$

the gene switches randomly between off and on states[7], where k_{on} and k_{off} are the activation and the inactivation rate respectively. The synthesis rate $v_m > 0$ and the degradation rate $k_\delta > 0$ are the birth and the death of mRNAs, respectively. Recently, we obtained lots of data on the histogram of Pm(t)[8-11], and many researchers have studied the distribution profiles of Pm(t)in[4,6,12-14,16]. Theoretical analysis shows that there are only three types of distributions in the telegraph model: decreasing, unimodal and bimodal distribution, and there is a relatively simple correspondence between distribution types and system parameters.

We denote the respective probabilities of m mRNA molecules existing at time t as $P_{m,q}(t)$ at inactive state and $P_{m,e}(t)$ at active state. Let

$$P_m(t) = P_{m,q}(t) + P_{m,e}(t).$$

and we can calculate $P_{m,q}(t)$ and $P_{m,e}(t)$

$$\begin{aligned} P'_{m,q}(t) = {} & k_{\text{off}} P_{m,e}(t) - (mk_{\delta} + k_{\text{on}}) P_{m,q}(t) \\ & + (m+1) k_{\delta} P_{m+1,q}(t), \end{aligned} \tag{1.2}$$

$$P'_{m,e}(t)=k_{\text{on}}P_{m,q}(t)-(v_m+mk_\delta+k_{\text{off}})P_{m,e}(t)+(m+1)k_\delta P_{m+1,e}(t)+v_mP_{m-1,e}(t) \tag{1.3}$$

here $P_{-1,e}(t)=0$. Define

$$P_{0,q}(0)=1,P_{0,e}(0)=P_{m,q}(0)=0 \text{ for } m\geqslant 1 \tag{1.4}$$

Introduce the probability generating functions[15]

$$V_i(z,t)=\sum_{m=0}^{\infty}(z+1)^mP_{m,i}(t),i=1,2,e. \tag{1.5}$$

Then we transform the equations(1.2)、(1.3) as the following

$$\frac{\partial V_q}{\partial t}(z,t)=-k_{\text{on}}V_q(z,t)+k_{\text{off}}V_e(z,t)-k_\delta z\frac{\partial V_q}{\partial z}(z,t), \tag{1.6}$$

$$\frac{\partial V_e}{\partial t}(z,t)=k_{\text{on}}V_q(z,t)-k_{\text{off}}V_e(z,t)+v_mzV_e(z,t)-k_\delta z\frac{\partial V_e}{\partial z}(z,t), \tag{1.7}$$

$$V_q(z,0)=1,V_e(z,0)=0. \tag{1.8}$$

$$V_q(0,t)=\frac{k_{\text{off}}}{k_{\text{off}}+k_{\text{on}}}+\frac{k_{\text{off}}}{k_{\text{off}}+k_{\text{on}}}e^{(k_{\text{off}}+k_{\text{on}})t},$$

$$V_e(0,t)=\frac{k_{\text{on}}}{k_{\text{off}}+k_{\text{on}}}e^{(k_{\text{off}}+k_{\text{on}})t}. \tag{1.9}$$

Solve the equations(1.6)—(1.8), $P_m(t)$ is obtained:

$$P_m(t)=\frac{1}{m!}\left.\frac{\partial^z V(z,t)}{\partial z^m}\right|_{z=-1}, \tag{1.10}$$

where $V(z,t)=V_q(z,t)+V_e(z,t)$ and $m\geqslant 0$. Denote

$$k_1=\frac{k_{\text{off}}}{k_\delta},k_2=\frac{k_{\text{on}}}{k_\delta},\bar{v}_m=\frac{v_m}{k_\delta}. \tag{1.11}$$

Recently, Jiao et al.[17] expressed $P_m(t)$ as simple mathematical functions:

$$P_m(t)=\frac{\bar{v}_m^{\,m}}{m!}\Big[e^{-k_{\text{off}}t}(1-e^{-k_\delta t})^me^{-\bar{v}_m(1-e^{-k_\delta t})}-mk_\delta e^{-k_\delta t}\int_0^t e^{-k_{\text{off}}s}(1-e^{-k_\delta s})^{m-1}e^{\bar{v}_m(e^{-k_\delta s}-1)}\mathrm{d}s+(k_{\text{off}}+\bar{v}_me^{-k_\delta t})\int_0^t e^{-k_{\text{off}}s}(1-e^{-k_\delta s})^m e^{\bar{v}_m(e^{-k_\delta s}-1)}\mathrm{d}s\Big], \tag{1.12}$$

for $k_{\text{on}}=k_\delta$, and

$$P_m(t)=\begin{cases}e^{-k_{\text{on}}t}+k_{\text{on}}e^{\bar{v}_me^{-k_\delta t}}\int_0^t e^{-k_{\text{on}}s}e^{-\bar{v}_me^{-k_\delta s}}\mathrm{d}s, & m=0,\\ \dfrac{k_{\text{on}}\bar{v}_m^{\,m}e^{\bar{v}_m}e^{-k_\delta t}}{m!}\displaystyle\int_0^t e^{-k_{\text{on}}s}(e^{-k_\delta s}-e^{-k_\delta t})^me^{-\bar{v}_me^{-k_\delta s}}\mathrm{d}s, & m=1,2,\cdots\end{cases} \tag{1.13}$$

for $k_{\text{off}}=k_\delta$.

In this paper, we continue to research the transcription in the telephone model and use the mathematics formulas of $P_m(t)$ in[17] to discuss the dynamical distribution of inactive genes in telephone model.

1 Dynamical distribution of inactive genes

If v is appropriately small(e.g. $v_m\leqslant k_\delta$), we can prove that $P_m(t)-P_{m+1}(t)\geqslant 0$, $m=0,1,\cdots$ easily. Therefore, we will focus on the case where the synthesis rate of mRNA is relatively large. The next results show that if genes are easy to be at off state, then they are unlikely to be activated. And we find that no matter how much mRNA is generated, the dynamical distribution is decaying in that condition. The result that the decaying dynamical distribution in the translation system with genes are not be easily activated supports the observation that Raj found in mammalian cells[18].

Theorem 1. Let $k_{\text{off}}=k_\delta$. $\forall t>0$, if $k_{on}\leqslant k_\delta$, then the dynamical distribution is decaying. Furthermore, if $k_{on}=k_{\text{off}}=k_\delta$, and v_m is appropriately large, $P_m(t)$ peaks at $m=0$, and then the dynamic is horizontal for the beginning region at $m\geqslant 1$. In addition, $P_m(t)$ will changes its concavity twice: if $v_m>3k_\delta e^{k_\delta t-3}/2$, the concavity of the curves of $P_m(t)$ is from concave up to concave down; if $v_m>3k_\delta/(1-e^{-k_\delta})$, the concavity is from concave down to concave up at $m=[\bar{v}_m(1-e^{-k_\delta})-1]$. Here $[.]$ repre-

sents the rounding symbol. Especially, if $v_m \geqslant 2k_\delta$, the curves only have one infection point (from concave up to concave down); if $v_m < 2k_\delta$, the curves at steady state are always concave up.

Proof. When $k_{\text{off}} = k_\delta$, according (1.13), when $m \geqslant 1$, we can calculate directly that

$$P_{m+1}(t) - P_m(t) = \frac{k_{\text{on}} \bar{v}_m^{m+1} e^{\bar{v}_m e^{-k_\delta t}}}{(m+1)!} \int_0^t \frac{(e^{-k_\delta s} - e^{-k_\delta t})^m}{e^{k_{\text{on}} s + v_m e^{-k_\delta s}}} \left[(e^{-k_\delta s} - e^{-k_\delta t}) - \frac{m+1}{\bar{v}_m} \right] \mathrm{d}s. \tag{2.1}$$

In addition, we can also estimate $P_{m+1}(t) - P_m(t)$ in another way. By using integration by parts, we reformulate $P_m(t), m \geqslant 1$

$$\begin{aligned} P_m(t) = & -\frac{k_1 \bar{v}_m^m e^{\bar{v}_m e^{-k_\delta t}}}{(m+1)!} \int_0^t e^{(k_\delta - k_{\text{on}})s} e^{-\bar{v}_m e^{-k_\delta s}} \mathrm{d}(e^{-k_\delta s} - e^{-k_\delta t})^{m+1} \\ = & \frac{k_1 \bar{v}_m{}^m e^{-v_m(1-e^{-k_\delta t})}}{(m+1)!} (1 - e^{-k_\delta t})^{m+1} \\ & - \frac{(k_{\text{on}} - k_\delta) \overline{k_{\text{on}}} \bar{v}_m{}^m e^{\bar{v}_m e^{-k_\delta t}}}{(m+1)!} \int_0^t e^{-(k_{\text{on}} - k_\delta)s} (e^{-k_\delta s} - e^{-k_\delta t})^{m+1} e^{-\bar{v}_m e^{-k_\delta s}} \mathrm{d}s \\ & + \frac{k_{\text{on}} \bar{v}_m{}^{m+1} e^{\bar{v}_m e^{-k_\delta t}}}{(m+1)!} \int_0^t e^{-k_{\text{on}} s} (e^{-k_\delta s} - e^{-k_\delta t})^{m+1} e^{-\bar{v}_m e^{-k_\delta s}} \mathrm{d}s. \end{aligned}$$

Because the last part of the above equation is $P_{m+1}(t)$. By introducing the new variable

$$Q_m(t, \bar{v_m}) = \int_0^t e^{-(k_{\text{on}} - k_\delta)s} e^{\bar{v_m}(1 - e^{-k_\delta t})} \left(\frac{e^{-k_\delta s} - e^{-k_\delta t}}{1 - e^{-k_\delta t}} \right)^{m+1} \mathrm{d}s, \tag{2.2}$$

We can get a useful expression

$$P_{m+1}(t) - P_m(t) = \frac{k_1 (k_{\text{on}} - k_\delta) \bar{v}_m{}^m}{(m+1)!} \frac{(1 - e^{-k_\delta t})^{m+1}}{e^{v_m(1 - e^{-k_\delta t})}} \left(Q_m(t, \bar{v}_m) - \frac{1}{k_{\text{on}} - k_\delta} \right). \tag{2.3}$$

According (1.13) and (2.3), we have

$$P_0(t) - P_1(t) = e^{-k_{\text{on}} t} + \bar{k}_{\text{on}} (1 - e^{-k_\delta t}) e^{-v_m(1 - e^{-k_\delta t})} + \frac{(1 - k_1) e^{k_\delta t}}{\bar{v}_m} P_1(t), \tag{2.4}$$

and when $m = 1, 2, \cdots$, we obtain

$$P_m(t) - P_{m+1}(t) = \frac{k_1 \bar{v}_m e^{-v_m(1 - e^{-k_\delta t})}}{(m+1)!} (1 - e^{-k_\delta t})^{m+1} + \frac{(1 - k_1) e^{k_\delta t}}{\bar{v}_m} P_{m+1}(t). \tag{2.5}$$

When $k_{\text{on}} \leqslant k_d$, according (2.4) and (2.5), we have $P_{m+1}(t) < P_m(t)$. This means we can obtain the decaying distribution of mRNA at any time.

Moreover, if $k_{\text{on}} = k_\delta$, then (2.4) and (2.5) can be reduced respectively as

$$P_0(t) - P_1(t) = e^{-k_\delta t} + (1 - e^{-k_\delta t}) e^{-v_m(1 - e^{-k_\delta t})} \tag{2.6}$$

and

$$P_m(t) - P_{m+1}(t) = \frac{\bar{v}_m^m e^{-v_m(1 - e^{-k_\delta t})}}{(m+1)!} (1 - e^{-k_\delta t})^{m+1}, \quad m = 1, 2, \cdots. \tag{2.7}$$

Note that when v_m is large enough and in the finite region of m, we have

$$P_0(t) - P_1(t) \sim e^{-k_\delta t} \text{ and}$$
$$P_m(t) \sim P_{m+1}(t), \text{ for } m \geqslant 1$$

This means if v_m is appropriately large, we can always see the decaying distribution and then the dynamic is almost horizontal for the beginning region at $m \geqslant 1$.

In addition, (2.6) and (2.7) mean that

$$P_2(t) - 2P_1(t) + P_0(t) = \frac{(1 - e^{-k_\delta t}) e^{-v_m(1 - e^{-k_\delta t})}}{2} (2 - \bar{v}_m (1 - e^{-k_\delta t})) + e^{-k_\delta t} \tag{2.8}$$

and when $m = 2, 3, \cdots$,

$$P_{m+1}(t) - 2P_m(t) + P_{m-1}(t) = \frac{\bar{v_m}^{m-1} (1 - e^{-k_\delta t})^m e^{-\bar{v_m}(1 - e^{-k_\delta t})}}{(m+1)!} (m + 1 - \bar{v_m}(1 - e^{-k_\delta t})). \tag{2.9}$$

We first analysis the concavity of the curves in the

region about $m=1,2,3$. Take the derivative of(2.8) with respect to v, we get the unique minimum point of the equation(2.8) $v_m=3/(1-e^{-k_\delta t})$. Substitute this minimum point into(2.8)and note that $v>3k_\delta e^{k_\delta t-3}/2$,we have $P_2(t)-2P_1(t)+P_0(t)>0$. This means the concavity of the distribution curves is concave up.

When $m\geqslant 1$ and $v_m>3k_\delta/(1-e^{-k_\delta t})$, according(2.9), it is easy to verify that the sign of $P_{m+1}(t)-2P_m(t)+P_{m-1}(t)$ is changed at $m=[\bar{v}_m(1-e^{-k_\delta t})-1]$. Therefore,the distribution only has one infection point $m=[\bar{v}_m(1-e^{-k_\delta t})-1]$ when $m=1,2,\cdots$.

In particular,(2.8)are(2.9)reduced as the following at the steady state ($t\to\infty$)

$$P^*_{m+1}-2P^*_m+P^*_{m-1}=\frac{\bar{v}_m{}^{m-1}e^{-\bar{v}_m}}{(m+1)!}(m+1-\bar{v}_m),\quad m=1,2,\cdots.$$

this shows if $v_m\geqslant 2k_\delta$,the distribution curves are from concave down to concave up at the unique inflection point $m=[\bar{v}_m-1]$ at the steady state, while when $v_m<2k_\delta$,the distribution curves always keep concave down.

Theorem 2. Suppose $k_{on}=k_\delta$. $\forall\, t>0$,if $k_{on}\geqslant k_\delta$, then $P_m(t)$ decays monotonically about m.

Proof. When $k_{on}=k_\delta$,we rewrite $P_m(t)$ as the following forms by applying(1.12)

$$\begin{aligned}P_m(t)=&\frac{\bar{v}_m{}^m e^{-k_{on}t}}{m!}(1-e^{-k_\delta t})^m e^{-\bar{v}_m(1-e^{-k_\delta t})}\\&+\frac{\bar{v}_m{}^m}{m!}(k_{on}+v_m e^{-k_\delta t})\int_0^t e^{-k_{on}s}(1-e^{-k_\delta s})^m e^{\bar{v}_m(e^{-k_\delta s}-1)}\mathrm{d}s\\&-\frac{mk_d\bar{v}_m{}^m e^{-k_\delta t}}{m!}\int_0^t e^{-k_{on}s}(1-e^{-k_\delta s})^{m-1}e^{\bar{v}_m(e^{-k_\delta s}-1)}\mathrm{d}s.\end{aligned}\tag{2.10}$$

Take partial integration to (2.10),we have

$$\begin{aligned}P_m(t)=&\frac{\bar{v}_m{}^m e^{-k_{on}t}}{m!}(1-e^{-k_\delta t})^m e^{-\bar{v}_m(1-e^{-k_\delta t})}\\&+\frac{\bar{v}_m{}^m}{k_\delta(m+1)!}(k_{on}+v_m e^{-k_\delta t})\int_0^t e^{(k_\delta-k_{on})s}e^{\bar{v}_m(e^{-k_\delta s}-1)}\mathrm{d}(1-e^{-k_\delta s})^{m+1}\\&-\frac{\bar{v}_m{}^m e^{-k_\delta t}}{m!}\int_0^t e^{(k_\delta-k_{on})s}e^{\bar{v}_m(e^{-k_\delta s}-1)}d(1-e^{-k_\delta s})^m\\=&\frac{\bar{v}_m{}^m e^{-k_{on}t}}{m!}(1-e^{-k_\delta t})^m e^{-\bar{v}_m(1-e^{-k_\delta t})}\\&+\frac{\bar{v}_m{}^m}{k_\delta(m+1)!}(k_{on}+v_m e^{-k_\delta t})e^{(k_\delta-k_{on})t}(1-e^{-k_\delta t})^{m+1}e^{\bar{v}_m(e^{-k_\delta t}-1)}\\&-\frac{\bar{v}_m{}^m(k_\delta-k_{on})}{k_\delta(m+1)!}(k_{on}+v_m e^{-k_\delta t})\int_0^t e^{(k_\delta-k_{on})s}e^{\bar{v}_m(e^{-k_\delta s}-1)}(1-e^{-k_\delta s})^{m+1}\mathrm{d}s\\&+\frac{\bar{v}_m{}^{m+1}}{(m+1)!}(k_{on}+v_m e^{-k_\delta t})\int_0^t e^{-k_{on}s}e^{v_m(e^{-k_\delta s}-1)}(1-e^{-k_\delta s})^{m+1}\mathrm{d}s\\&-\frac{\bar{v}_m{}^m e^{-k_\delta t}}{m!}e^{(k_\delta-k_{on})t}(1-e^{-k_\delta t})^m e^{\bar{v}_m(e^{-k_\delta t}-1)}\\&-\frac{k_\delta\bar{v}_m{}^{m+1}e^{-k_\delta t}}{m!}\int_0^t e^{-k_{on}s}e^{\bar{v}_m(e^{-k_\delta s}-1)}(1-e^{-k_\delta s})^m\mathrm{d}s\\&+\frac{\bar{v}_m{}^m(k_\delta-k_{on})e^{-k_\delta t}}{m!}\int_0^t e^{(k_\delta-k_{on})s}e^{\bar{v}_m(e^{-k_\delta s}-1)}(1-e^{-k_\delta s})^m\mathrm{d}s.\end{aligned}$$

Note the expression of $P_m(t)$ in(1.12), we can further simplify the above equation as

$$P_m(t)=P_{m+1}(t)+\frac{k_2\bar{v}_m{}^m e^{(k_\delta-k_{\text{on}})t}e^{-\bar{v}_m(1-e^{-k_\delta t})}}{(m+1)!}(1-e^{-k_\delta t})^{m+1}-\frac{\bar{v}^m(k_\delta-k_{\text{on}})}{m!}\times\int_0^t\frac{e^{\bar{v}_m(e^{-k_\delta s}-1)}}{e^{(k_{\text{on}}-k_\delta)s}}(1-e^{-k_d s})^m\left[(1-e^{-k_\delta s})\frac{k_2+\bar{v}_m e^{-k_\delta t}}{m+1}-e^{-k_\delta t}\right]\mathrm{d}s. \tag{2.11}$$

Apply mean value theorem of integrals and combine the expression of $P_m(t)$ in(1.12), we can use $P_{m+1}(t)$ to express the last term of the above equation

$$\frac{\bar{v}_m{}^m(k_\delta-k_{\text{on}})}{m!}\int_0^t e^{(k_\delta-k_{\text{on}})s}e^{\bar{v}_m(e^{-k_\delta s}-1)}(1-e^{-k_\delta s})^m\left((1-e^{-k_\delta s})\frac{k_2+\bar{v}_m e^{-k_\delta t}}{m+1}-e^{-k_\delta t}\right)\mathrm{d}s$$
$$=\frac{(1-k_2)e^{k_\delta\sigma}}{\bar{v}_m}\left(P_{m+1}(t)-\frac{\bar{v}_m{}^{m+1}e^{-k_2 t}}{(m+1)!}(1-e^{-k_\delta t})^{m+1}e^{-\bar{v}_m(1-e^{-k_\delta t})}\right), \tag{2.12}$$

where $\sigma\in(0,t)$, which is depended on k_{on}, v_m and k_δ. Therefore, we substitute(2.12) into(2.11) and finally get

$$P_m(t)-P_{m+1}(t)=\frac{(k_2-1)e^{k_\delta\sigma}}{\bar{v}_m}P_{m+1}(t)+\frac{\bar{v}^m(1-e^{-k_\delta t})^{m+1}}{e^{k_{\text{on}}t}e^{\bar{v}_m(1-e^{-k_\delta t})}(m+1)!}\left[e^{k_\delta\sigma}+k_{\text{on}}^-(e^{k_\delta t}-e^{k_\delta\sigma})\right], \tag{2.13}$$

where $\sigma\in(0,t)$. It is obviously if $k_{\text{on}}\geqslant k_\delta$, the right-hand side of(2.13) is greater than 0. This shows $P_m(t)-P_{m+1}(t)\geqslant 0, m=0,1,\cdots$. The theorem 2 is prove.

2 Numerical simulations

We use numerical simulations to demonstrate the above theorems.

Example 3.1 Assume $k_{\text{on}}=k_\delta=0.05\,\text{min}^{-1}$, $v_m=2\text{min}^{-1}$ and $k_{\text{off}}=0.15\text{min}^{-1}$. We see decaying distributions at $t=12,22$min and steady state in figure 1. This supports the result in Theorem 2.1.

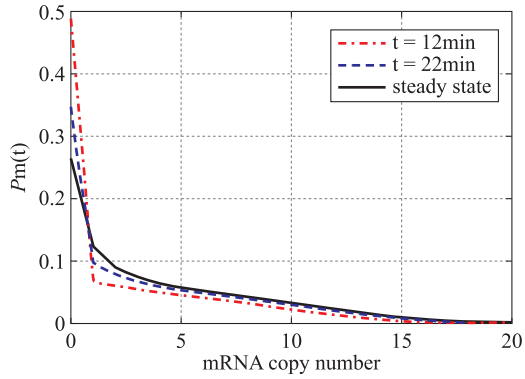

Fig. 1 For genes that are not easily activated, we describe the change of the profile of Pm(t) about the number of mRNA m at different time according(1.13) at the condition $k_{\text{on}}=k_\delta=0.05\text{min}^{-1}$. Define $v_m=2\text{min}^{-1}$, $k_{\text{off}}=0.15\text{min}^{-1}$. As shown in the figure, we see decaying distributions at $t=12$, 22 min and steady state.

Example 3.2 Assume $k_{\text{on}}=k_{\text{off}}=k_\delta=0.15\text{min}^{-1}$ and $v_m=2\text{min}^{-1}$. In figure 2, we see decaying distributions and almost horizontal distribution curves for the beginning region at $t=12,22$min and steady state. This also supports the result in Theorem 2.1.

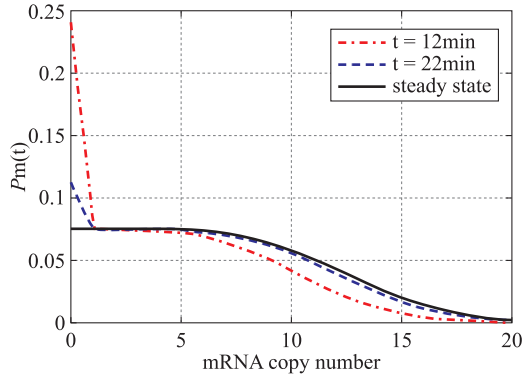

Fig. 2 We describe the change of the profile of Pm(t) about the number of mRNA m at different time according(1.13) at the condition $k_{\text{on}}=k_{\text{off}}=k_\delta=0.15\text{min}^{-1}$. Define $v_m=2\text{min}^{-1}$. As shown in the figure, we see decaying distributions and almost horizontal distribution curves for the beginning region at $t=12,22$min and steady state.

Example 3.3 Assume $k_{on}=k_{\delta}=0.05\,\mathrm{min}^{-1}$, $v_m=2\mathrm{min}^{-1}$ and $k_{off}=0.07\,\mathrm{min}^{-1}$. We see decaying distributions at $t=12,22$min and steady state in figure 3 . This supports the result in Theorem 2.2.

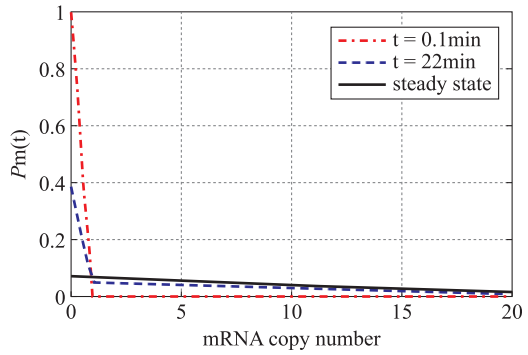

Fig. 3 When genes are easy at off state, we describe the change of the profile of Pm(t) about the number of mRNA m at different time according(1.12). We let $k_{on}=k_{\delta}=0.05\mathrm{min}^{-1}$, $v_m=2\mathrm{min}^{-1}$. Define $k_{off}=0.07\mathrm{min}^{-1}$, that means genes are easy to get back off state. As shown in the figure, we see decaying distributions at $t=0.1,22$ min and steady state.

3 Conclusion

In this work, we research the dynamics of inactive genes in two conditions for telegraph model. We prove that the dynamical distribution is always decaying for the inactive genes. Furthermore, if $k_{on}=k_{off?}=k_{\delta}$, and v_m is appropriately large, $P_m(t)$ peaks at $m=0$, and then the dynamic is horizontal for the beginning region at $m\geqslant 1$.

If genes are not easy to be activate($k_{on}\leqslant k_{\delta}$ and $k_{off}\geqslant k_{\delta}$), theorem 1 and theorem 2 show that the decaying distribution in the telephone model is usually not determined by the numbers of mRNA, but often determined by the average durations at off state. In fact, for the transcriptional systems of most higher organisms, genes are more likely to be at off state. Therefore, our theoretical results reflect the changes in the ability of its transcriptional mechanism to regulate the mRNA distribution in some extent about the process of the evolution of organisms. This decaying distribution during the process of transcriptional of inactive genes also supports the experimental results in mammalian cells[18]. In the reference[18], they found that the distribution of the number of the transcripts is decaying with a longer tail. A longer tail means that a larger number of mRNA molecules are generated during transcription, but because genes in mammalian cells are not easily activated, so it results a decreasing distribution of mRNA numbers.

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