Nature-based Information Networking: On Exploring Robustness in TCP Inspired by Cellular Signaling

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ABSTRACT
In this paper we will discuss the similarities found in the dynamics of cellular signal transduction networks in nature and that of communication network protocols. Based on the simplified observations from the signaling processes of the cyclin (*cln*) protein during the cell cycle in yeast, we formulate a generic master equation, which describes the general robustness of the system and can be applied to characterize different variants of the Transmission Control Protocol (TCP) such as FAST, Reno, HSTCP, or STCP. By presenting the generalized controller mechanism for describing the dynamics of *cln* signaling at system level, we infer that any corresponding second order system is similarly controllable. It is our intention that this formulation of a master equation leads to a better quantitative description of the cellular signaling process, as well as to a more robust design of protocols to be applied in new generation network architectures.

Keywords
Cellular signaling, cell cycle, information networks, TCP/RED

1. INTRODUCTION
When we compare the abstract view of the basic dynamics of cellular signaling in nature and that of engineered information networks, we notice that they share a commonality from the viewpoint of informatics. For instance, the robustness found in signal transduction networks in cells is a particular feature, which is also highly desirable in information networks. In this work we specifically consider the signal transduction network of the cell cycle of yeast, which has been a well-studied topic in bioinformatics [1,2]. In previous work the robustness of the cell cycle has been extensively studied and the intention of this paper is to discuss how we can explore hints from nature to improve the design of new protocols in future network architectures. We will begin this paper with a brief outline of signal transduction networks form the viewpoint of information networking and discuss the essential feedback-based dynamics of the cell cycle of yeast, which we refer to as master equation. Based on this equation, we will sketch a controller structure, which incorporates the robustness features and can be used as the basis for a more robust and fair bandwidth sharing in the *Transmission Control Protocol* (TCP).

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2. SIGNAL TRANSDUCTION FROM AN INFORMATION NETWORKING VIEW
The biological functions of signal transduction networks are crucial for the operation of cells. These cellular signal transduction networks take the form of biochemical reactions and we abstractly view the molecules as nodes within an information network and the corresponding biochemical reactions as the links. Thus, signal transduction networks can be represented as graphs with activating or inhibiting unidirectional links [2].

The lifetime of a cell, referred to as the *cell cycle*, is controlled by transitions through various stages of growth leading to *mitosis*, in which the cell splits into two equivalent cells. This feature is one of the most important components of living organisms and it is driven by the periodic dynamics of a family of proteins called *cyclin* (e.g. Cln2). The concentration of cyclin is periodical over time and it roughly resembles the dynamics of the TCP congestion window size in computer networks [3]. Biological models as described in [1] often give a very detailed view of the interactions of the various proteins, but we limit our abstraction to the interaction of two specific quantities, the concentration of the cyclin Cln2 and the mass of the cell. When we transfer this metaphor to information networks, we can find analogies between cyclin as the TCP congestion window size and mass as the bottleneck queue length in an intermediate RED (*Random Early Detection*) router [3].

In general, the dynamics can be formulated by two dynamic equations, one corresponding to the chemical process

$$\frac{d}{dt}\mathrm{Cln2} = \mathrm{f}\left(\mathrm{Cln2},\ \mathrm{mass},\ \mathrm{coefficients}\right)$$

and another to the physical process

$$\mathrm{mass}(t) = g\left(u\left(\mathrm{Cln2}\right),\ v\left(\mathrm{mass}(t-1)\right)\right)$$

where u refers to a positive feedback function from Cln2 and v to a negative feedback function from mass(t-1).

The similarities that can be recognized from the dynamics of cellular signaling and TCP leads to a generalization of the dynamics in terms of mathematical equations. In [4], a generalized equation system is formulated that is suitable to characterize a wide range of TCP variants.

$$\frac{d}{dt} w_i(t) = \kappa_i(t)\left(1 - \frac{q_i(t)}{u_i(t)}\right) \qquad (1)$$

In Eq. (1), $w_i(t)$ refers to the window size of a TCP source i and $q_i(t)$ is the end-to-end packet loss probability. The other functions $\kappa_i(t) = \kappa_i\big(w_i(t), T_i(t)\big)$ and $u_i(t) = u_i\big(w_i(t), T_i(t)\big)$ are used to describe the different flavors of the protocol, i.e., FAST, Reno, HSTCP, STCP, in a single master equation.

Based on this description and the similarities of the cellular signaling process and TCP, we extend (1) to include a feedback component in a *generalized master equation* [5] as in Eq. (2)

$$\frac{d}{dt} w_i(t) = \kappa_i(t)\left(1 - \frac{q_i(t)}{u_i(t)}\right) + \varphi_i(t) \qquad (2)$$

where we now consider $\kappa_i(t) = k_G \exp(\mu\, t)$ inspired by the exponential growth of the cell mass and the additional functions as follows.

$$u_i(t) = \frac{k_1}{\sum_{l_1} k_{01} w_i(t)^{l_1} + \sum_{l_2} k_{02} q_i(t)^{l2} + \sum_{l_3} k_{03} T_i(t)^{l3}}$$

$$\varphi_i(t) = \frac{k_2\; k_G\; \exp(\mu\, t)\; \zeta_i(t)}{\sum_{m_1} k_{21} w_i(t)^{m_1} + \sum_{m_2} k_{22} q_i(t)^{m2} + \sum_{m_3} k_{23} T_i(t)^{m3}}$$

where

$$\zeta_i(t) = \left(\frac{k_3}{\sum_{z_1} k_{31} w_i(t)^{m_1} + \sum_{z_2} k_{32} q_i(t)^{m2} + \sum_{z_3} k_{33} T_i(t)^{m3}} \right)^{-1}.$$

All indices $l_i, m_i, z_i \in (-\infty, +\infty), i = 1,2,3$ are integer values.

3. PROPOSAL OF ROBUST SYSTEM CONTROLLER STRUCTURE

Based on the dynamics of the signal transduction network of the cell cycle [2,5,6], we propose a robust controller structure as illustrated in Fig. 1, where Cln2 and Cln3 are cyclin and $k_i, i = 1,2,3$ are the coefficients for the feedback to the controller.

Let us consider a second order system to describe the state transitions of the above controller

$$X(t+1) = A\; X(t) + B\; U(t)$$

where $X(t)$ is the state vector and $U(t)$ is the input signal. Matrices A and B control the influence of the input signal and the previous state and can be given as

$$A = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \qquad B = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}$$

where $A_{1,1} = B_{1,2} = 1$ provide the control and $A_{2,2} = B_{2,1} = 1$ are used for communication. The matrix $B : AB$ has a rank of 2, which states that the system is controllable where ":" refers to *merge* operator for matrices as defined in automatic control theory.

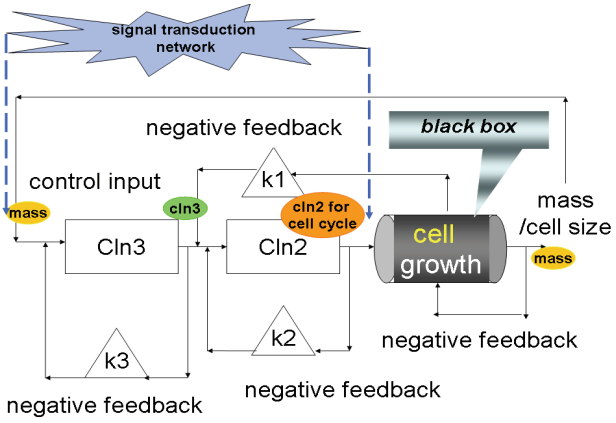

Figure 1: The controller structure for the signal transduction network that consists of Cln2 and Cln3 with feedbacks

4. CONCLUSION

In this paper we briefly discussed the analogies between the signaling processes of the biological cell cycle and TCP and generalizing their dynamics by a master equation, inspired by analytical models for TCP/RED and the dynamics of cyclin. Based on its robustness features [6], we propose a generic controller structure for a biologically inspired scheme for robust information network control.

5. REFERENCES

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