Parallel stochastic simulation using graphics processing units for the Systems Biology Toolbox for MATLAB

Supplemental material

Example reaction systems

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This document presents the six chemical reaction systems used to compare the performance of the fat and thin threading approaches.

1 Oregonator

The Oregonator is a model simulating the oscillating Belousov-Zhabotinskii reaction, which was discovered in 1951, developed by Field, Körös and Noyes [2, 5]. The reaction system of the Oregonator describing the general kinetic scheme of the Belousov-Zhabotinskii reaction is given by:

\[
\begin{align*}
R_1 : & \quad \bar{X}_1 + Y_2 \xrightarrow{c_1} Y_1 \\
R_2 : & \quad Y_1 + Y_2 \xrightarrow{c_2} Z_1 \\
R_3 : & \quad \bar{X}_2 + Y_1 \xrightarrow{c_3} 2 Y_1 + Y_3 \\
R_4 : & \quad 2Y_1 \xrightarrow{c_4} Z_2 \\
R_5 : & \quad \bar{X}_3 + Y_3 \xrightarrow{c_5} Y_2.
\end{align*}
\]

The species marked with a bar are assumed to be in excess and therefore taken as constant. The reaction rates are \( c_1 = 10.0 \text{ h}^{-1}, \ c_2 = 0.5 \text{ h}^{-1}, \ c_3 = 104.0 \text{ h}^{-1}, \ c_4 = 0.016 \text{ h}^{-1}, \ c_5 = 1.04 \text{ h}^{-1} \) and the initial conditions at \( t = 0 \text{ h} \) for the molecular populations are \( Y_1 = 500, \ Y_2 = 1000, \ Y_3 = 2000, \ Z_1 = 2000, \ Z_2 = 50000 \) [3].
The circadian rhythm is an approximately 24-hour cycle in biochemical or behavioural processes of many living entities, including plants, animals, and bacteria, to keep internal sense of daily time and regulate behavior accordingly. The model used is the simplified circadian cycle model by Vilar et al. [6] based on the model of Barkai and Leibler [1].

The biochemical network of the circadian oscillator model is given in Figure 1. The core of the network is intracellular transcription regulation of the two genes involved, an activator gene $D_A$ and a repressor gene $D_R$. Oscillations arise since the activator binds to the promoters of both genes simultaneously. Thus, with the activator $A$ the repressor $R$ is expressed. The repressor $R$, in turn, inactivates $A$ forming the complex $C$. Taken with permission from Vilar et al. [6].

2 Circadian cycle

The circadian rhythm is an approximately 24-hour cycle in biochemical or behavioural processes of many living entities, including plants, animals, and bacteria, to keep internal sense of daily time and regulate behavior accordingly. The model used is the simplified circadian cycle model by Vilar et al. [6] based on the model of Barkai and Leibler [1].

The biochemical network of the circadian oscillator model is given in Figure 1. The core of the network is intracellular transcription regulation of the two genes involved, an activator gene $D_A$ and a repressor gene $D_R$. Both are transcribed into mRNA $M_A$ and $M_R$, respectively, and subsequently translated into the activator protein $A$ and repressor protein $R$. The activator $A$ binds to the $A$ and $R$ promoters simultaneously, increasing their transcription. $A$ acts as the positive element in transcription, whereas $R$ acts as the negative element by repressing the activator. The cycle is completed by repressor degradation and re-expression of the activator [6].

The molecular species of the circadian cycle model are:

- activator DNA $D_A$
• activator mRNA $M_A$
• activator protein $A$
• activator DNA-promoter complex $D'_A$
• repressor DNA $D_R$
• repressor mRNA $M_R$
• repressor protein $R$
• repressor DNA-promoter complex $D'_R$
• inactivated activator-repressor complex $C$

The reactions of the circadian cycle model are:

$R_1$: \[A + D_A \xrightarrow{\gamma_A} D'_A\]

$R_2$: \[D'_A \xrightarrow{\Theta_A} D_A + A\]

$R_3$: \[A + D_R \xrightarrow{\gamma_R} D'_R\]

$R_4$: \[D'_R \xrightarrow{\Theta_R} D_R + A\]

$R_5$: \[D_A \xrightarrow{\alpha_A} M_A\]

$R_6$: \[D'_A \xrightarrow{\alpha'_A} M_A\]

$R_7$: \[D_R \xrightarrow{\alpha_R} M_R\]

$R_8$: \[D'_R \xrightarrow{\alpha'_R} M_R\]

$R_9$: \[M_A \xrightarrow{\delta_{M_A}} \emptyset\]

$R_{10}$: \[M_A \xrightarrow{\beta_A} A\]

$R_{11}$: \[M_R \xrightarrow{\delta_{M_R}} \emptyset\]

$R_{12}$: \[M_R \xrightarrow{\beta_R} R\]

$R_{13}$: \[A + R \xrightarrow{\gamma_C} C\]

$R_{14}$: \[A \xrightarrow{\delta_A} \emptyset\]

$R_{15}$: \[R \xrightarrow{\delta_R} \emptyset\]

$R_{16}$: \[C \xrightarrow{\delta_A} R\]

with the reaction rates $\alpha_A = 50 \text{ h}^{-1}$, $\alpha'_A = 500 \text{ h}^{-1}$, $\alpha_R = 0.01 \text{ h}^{-1}$, $\alpha'_R = 50 \text{ h}^{-1}$, $\beta_A = 50 \text{ h}^{-1}$, $\beta_A = 5 \text{ h}^{-1}$, $\delta_{M_A} = 10 \text{ h}^{-1}$, $\delta_{M_R} = 0.5 \text{ h}^{-1}$, $\delta_A = 1 \text{ h}^{-1}$, $\delta_R = 0.2 \text{ h}^{-1}$, $\gamma_A = 1 \text{ h}^{-1}$, $\gamma_R = 1 \text{ h}^{-1}$, $\gamma_C = 2 \text{ h}^{-1}$, $\Theta_A = 100 \text{ h}^{-1}$. The initial number of molecules at $t = 0 \text{ h}$ are $D_A = D_R = 1$, $D'_A = D'_R = M_A = M_R = A = R = C = 0$. Since the model assumes the complex $C$ turns into $R$ by degradation of $A$, the rate $\delta_A$ appears twice [6].
3 lac-operon

This simplified model of the lac-operon is taken from Wilkinson Wilkinson [7]. The lac-operon consists of three genes and is required for the transport and metabolism of lactose in some bacteria, e.g. *Escherichia coli*. It is regulated by several factors including the availability of glucose and of lactose. The lac-operon is one of the foremost examples of prokaryotic gene regulation.

It is composed of a promoter $P$, the operator $Op$ and three genes $lacZ$, $lacY$, and $lacA$. Of these three genes, only $lacZ$ expressing $\beta$-galactosidase is part of the model. $\beta$-galactosidase is an intracellular enzyme cleaving the disaccharide lactose into glucose and galactose. The inhibitor $I$ binds either to lactose $L$ or the operator $Op$. If the inhibitor is bound to the operon, its transcription is prevented. Thus in the presence of lactose fewer inhibitor molecules bind to the operon and the operon’s expression level increases [4].

The molecular species of the lac-operon model are:

- inhibitor gene $I_{DNA}$
- inhibitor transcript $I_{RNA}$
- Inhibitor protein $I$
- operon $Op$
- RNA polymerase $RNAP$
- RNA polymerase bound to operon $RNAP-Op$
- operon transcript $RNA$
- $\beta$-galactosidase $Z$
- lactose $L$
- lactose bound to inhibitor $I-L$
The reactions of the lac-operon model are:

\[
\begin{align*}
R_1: & \quad I_{DNA} & \overset{c_1}{\rightarrow} & \quad I_{DNA} + I_{RNA} \\
R_2: & \quad I_{RNA} & \overset{c_2}{\rightarrow} & \quad I_{RNA} + I \\
R_3: & \quad I + L & \overset{c_3}{\rightarrow} & \quad I - L \\
R_4: & \quad I - L & \overset{c_4}{\rightarrow} & \quad I + L \\
R_5: & \quad I + Op & \overset{c_5}{\rightarrow} & \quad I - Op \\
R_6: & \quad I - Op & \overset{c_6}{\rightarrow} & \quad I + Op \\
R_7: & \quad Op + RNAp & \overset{c_7}{\rightarrow} & \quad RNAp - Op \\
R_8: & \quad RNAp - Op & \overset{c_8}{\rightarrow} & \quad Op + RNAp \\
R_9: & \quad RNAp - Op & \overset{c_9}{\rightarrow} & \quad Op + RNAp + RNA \\
R_{10}: & \quad RNA & \overset{c_{10}}{\rightarrow} & \quad RNA + Z \\
R_{11}: & \quad L + Z & \overset{c_{11}}{\rightarrow} & \quad Z \\
R_{12}: & \quad I_{RNA} & \overset{c_{12}}{\rightarrow} & \quad \emptyset \\
R_{13}: & \quad I & \overset{c_{13}}{\rightarrow} & \quad \emptyset \\
R_{14}: & \quad I - L & \overset{c_{14}}{\rightarrow} & \quad L \\
R_{15}: & \quad RNA & \overset{c_{15}}{\rightarrow} & \quad \emptyset \\
R_{16}: & \quad Z & \overset{c_{16}}{\rightarrow} & \quad \emptyset .
\end{align*}
\]

The reaction rates are \( c_1 = 0.02 \text{h}^{-1}, c_2 = 0.1 \text{h}^{-1}, c_3 = 0.005 \text{h}^{-1}, c_4 = 0.1 \text{h}^{-1}, c_5 = 1 \text{h}^{-1}, c_6 = 0.01 \text{h}^{-1}, c_7 = 0.1 \text{h}^{-1}, c_8 = 0.01 \text{h}^{-1}, c_9 = 0.03 \text{h}^{-1}, c_{10} = 0.1 \text{h}^{-1}, c_{11} = 1e - 5 \text{h}^{-1}, c_{12} = 0.01 \text{h}^{-1}, c_{13} = 0.002 \text{h}^{-1}, c_{14} = 0.002 \text{h}^{-1}, c_{15} = 0.01 \text{h}^{-1}, c_{16} = 0.001 \text{h}^{-1}. \) The chosen initial molecular populations at \( t = 0 \) are \( I_{DNA} = 10, I_{RNA} = 0, I = 50, Op = 10, RNAp = 1000, RNA = 0, Z = 0, L = 1640000, I - L = 0, I - Op = 0, RNAp - Op = 0. \) The number of RNA polymerases RNAp is kept constant [7].

### 4 Fully connected reaction network

The fully connected reaction network consists of 6 chemical species \( X_1 \) to \( X_6 \) which can be reversibly converted into each other at a reaction rate of \( c = 1 \text{h}^{-1}. \) Initially all molecules are of species \( X_1. \) The fully connected reaction network consists of 6 species and 30 reactions:

\[
\begin{align*}
R_1: & \quad X_1 & \overset{c}{\rightarrow} & \quad X_2 \\
R_3: & \quad X_1 & \overset{c}{\rightarrow} & \quad X_4 \\
R_5: & \quad X_1 & \overset{c}{\rightarrow} & \quad X_5 \\
R_7: & \quad X_1 & \overset{c}{\rightarrow} & \quad X_3 \\
R_2: & \quad X_2 & \overset{c}{\rightarrow} & \quad X_1 \\
R_4: & \quad X_4 & \overset{c}{\rightarrow} & \quad X_1 \\
R_6: & \quad X_5 & \overset{c}{\rightarrow} & \quad X_1 \\
R_8: & \quad X_3 & \overset{c}{\rightarrow} & \quad X_1
\end{align*}
\]
\[ R_9 : X_1 \stackrel{c}{\rightarrow} X_6, \quad R_{10} : X_6 \stackrel{c}{\rightarrow} X_1 \]
\[ R_{11} : X_2 \stackrel{c}{\rightarrow} X_3, \quad R_{12} : X_3 \stackrel{c}{\rightarrow} X_2 \]
\[ R_{13} : X_2 \stackrel{c}{\rightarrow} X_4, \quad R_{14} : X_4 \stackrel{c}{\rightarrow} X_2 \]
\[ R_{15} : X_2 \stackrel{c}{\rightarrow} X_5, \quad R_{16} : X_5 \stackrel{c}{\rightarrow} X_2 \]
\[ R_{17} : X_2 \stackrel{c}{\rightarrow} X_6, \quad R_{18} : X_6 \stackrel{c}{\rightarrow} X_2 \]
\[ R_{19} : X_3 \stackrel{c}{\rightarrow} X_4, \quad R_{20} : X_2 \stackrel{c}{\rightarrow} X_3 \]
\[ R_{21} : X_3 \stackrel{c}{\rightarrow} X_5, \quad R_{22} : X_5 \stackrel{c}{\rightarrow} X_3 \]
\[ R_{23} : X_3 \stackrel{c}{\rightarrow} X_6, \quad R_{24} : X_6 \stackrel{c}{\rightarrow} X_3 \]
\[ R_{25} : X_4 \stackrel{c}{\rightarrow} X_5, \quad R_{26} : X_5 \stackrel{c}{\rightarrow} X_4 \]
\[ R_{27} : X_4 \stackrel{c}{\rightarrow} X_6, \quad R_{28} : X_6 \stackrel{c}{\rightarrow} X_4 \]
\[ R_{29} : X_5 \stackrel{c}{\rightarrow} X_6, \quad R_{30} : X_6 \stackrel{c}{\rightarrow} X_5. \]

The initial molecular populations at time \( t = 0 \) h are \( X_1 = 1000000, X_2 = X_3 = X_4 = X_5 = X_6 = 0 \).

References