Text S4  Equivalence with a Previously Proposed Delay Model

Using our non-dimensional scaling the delay model of [23] has the form

\begin{align}
\eta(t) &= \alpha(r_T - r_B) \left( \mu - \int_{t - \tau_I}^t \eta(t') dt' \right), \\
\dot{r}_B &= \eta(t) - \eta(t - \tau_E),
\end{align}

(55a)

(55b)

applicable when the mRNA chains are empty at \( t = 0 \), for which \( \eta(t) \equiv 0 \) for \( t < 0 \). Further, in that work the delays are defined as

\[ \tau_E = \frac{N}{\beta}, \quad \tau_I = \frac{L}{\beta}. \]

(56)

In our PDE-delay model (Text S3), \( r_B \) may be given alternatively through the distribution \( z(s, t) \) as

\[ r_B(t) = \mu \int_0^N z(s, t) ds, \]

(57)

or through the initiation rate \( \eta(t) \) as

\[ r_B(t) = \int_{t\eta(t)}^t \eta(t') dt', \]

(58)

equation S4.4 is obtained from Eq. S4.3 through a change of variables. For the special case of \( \beta_j \) and \( \gamma \) constant and equal to each other, we obtain

\begin{align}
\tau_L(t) &= t - \tau_I, \\
\tau_N(t) &= t - \tau_N,
\end{align}

(59a)

(59b)

and

\[ \dot{r}_B(t) = \eta(t) - \eta(t - \tau_E). \]

(60)

Using Eqs. S4.4 and S4.5a in 18

\[ \eta(t) = \alpha(r_T - r_B) \left( \mu - \int_{t - \tau_I}^t \eta(t') dt' \right). \]

(61)

Eq. S4.7 is identical to S4.1a and Eq. S4.6 to S4.1b. Therefore, the formulations are completely equivalent, for the special case of \( \alpha, r_T, \) and \( c_E \) constant. In our PDE formulation, the delays have a slightly different form than Eq. S4.2, as we take made a mean field approximation to account for the quasi-steady state packing in the ribosome fluxes; this has, in fact, the effect of improving the level of approximation.