

Supplementary Materials for the paper: Dynamical modeling of microRNA action on the protein translation process

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1 Analytical analysis of the case of very inefficient cap structure

We analyze the system of equations

$$\left\{ \begin{array}{l} \frac{d[40S]}{dt} = -k_1[40S][eIF4F] + k_4[80S] \\ \frac{d[eIF4F]}{dt} = -k_1[40S][eIF4F] + k_2[mRNA : 40S] \\ \frac{d[mRNA : 40S]}{dt} = k_1[40S][eIF4F] - k_2[mRNA : 40S] \\ \frac{d[AUG]}{dt} = k_2[mRNA : 40S] - k_3[AUG][60S] \\ \frac{d[60S]}{dt} = -k_3[AUG][60S] + k_4[80S] \\ \frac{d[80S]}{dt} = k_3[AUG][60S] - k_4[80S] \\ Prsynth(t) = k_3[AUG][60S] \end{array} \right. \quad (1)$$

with the following assumptions on the model parameters:

$$k_1 \ll k_4 \ll k_2 \ll k_3; [eIF4F]_0 \ll [40S]_0; [eIF4F]_0 < [60S]_0 < [40S]_0 \quad (2)$$

First of all, notice that, generally speaking, it is not eligible to compare the some parameters k_i : k_1 and k_3 has $\frac{1}{sec \cdot moles}$ dimensionality while k_2 and k_4 are $\frac{1}{sec}$. So instead of comparing k_1 and k_4 , for example, one should rather compare, for example, $k_1[eIF4F]_0$ and k_4 . To facilitate this task, we explicitly consider that $[eIF4F]_0$ is on the order of 10^0 in our model, $[60S]_0$ is at the order of 10^1 and $[40S]_0$ at 10^2 .

1.1 Approximate steady state solution

From the conservation laws

$$[mRNA : 40S] + [40S] + [AUG] + [80S] = [40S]_0, \quad (3)$$

$$[mRNA : 40S] + [eIF4F] = [eIF4F]_0, \quad (4)$$

$$[60S] + [80S] = [60S]_0, \quad (5)$$

and the steady state condition

$$k_2 \cdot [mRNA : 40S]_s = k_3 \cdot [AUG]_s \cdot [60S]_s = k_4 \cdot [80S]_s = k_1 \cdot [40S]_s \cdot [eIF4F]_s, \quad (6)$$

we can derive

$$\begin{aligned} [mRNA : 40S]_s &= \frac{k_4}{k_2} [60S]_0 (1 - x), [AUG]_s = \frac{k_4}{k_3} \left(\frac{1 - x}{x} \right), \\ [eIF4F]_s &= [eIF4F]_0 - \frac{k_4}{k_2} [60S]_0 (1 - x), \\ [60S]_s &= [60S]_0 x, [80S]_s = [60S]_0 (1 - x), \\ [40S]_s &= [40S]_0 - [60S]_0 (1 - x) \left(1 + \frac{k_4}{k_2} \right) - \frac{k_4}{k_3} \left(\frac{1 - x}{x} \right) \end{aligned} \quad (7)$$

where $x = \frac{[60S]_s}{[60S]_0}$ is the fraction of 60S in the free (unbound to mRNA) state.

Using (6) and (7) we obtain an equation on x :

$$\begin{aligned} &x^3 + \\ &+ x^2 \left(\alpha + (\delta - 1) + (\beta - 1) + \frac{[eIF4F]_0}{[60S]_0} \right) \frac{1}{1 + k_4/k_2} + \\ &+ x \left(-\alpha + (\delta - 1)(\beta - 1) + \frac{[eIF4F]_0}{[60S]_0} \left(-1 - 2 \frac{k_4}{k_3[eIF4F]_0} + \frac{k_2}{k_3[60S]_0} + \frac{k_4}{k_2[eIF4F]_0} \right) \right) \frac{1}{1 + k_4/k_2} + \\ &+ \gamma(1 - \beta) = 0, \\ &\alpha = \frac{k_2}{k_1[60S]_0}, \beta = \frac{[eIF4F]_0 k_2}{[60S]_0 k_4}, \gamma = \frac{k_4}{k_3[60S]_0}, \delta = \frac{[40S]_0}{[60S]_0} \end{aligned} \quad (8)$$

Having in mind $k_4 \ll k_2$ and assuming that $[eIF4F]_0/[60S]_0$ is sufficiently small, we simplify it to

$$x^3 + x^2(\alpha + (\delta - 1) + (\beta - 1)) + x(-\alpha + (\delta - 1)(\beta - 1)) + \gamma(1 - \beta) = 0, \quad (9)$$

From the inequalities on the parameters of the model, we have $\delta > 1$, $\gamma \ll 1$, the constant term $\gamma(1 - \beta)$ of the equation (9) should be much smaller than the other polynomial coefficients, and the equation (9) should have one solution close to zero and two others:

$$\begin{aligned} x_0 &\approx \frac{\gamma(\beta - 1)}{-\alpha + (\beta - 1)(\delta - 1)} \\ x_1 &= \frac{1}{2} \left(-(\alpha + \beta + \delta) + 2 + \sqrt{(\alpha + \beta + \delta)^2 - 4\beta\delta} \right) \\ x_2 &= \frac{1}{2} \left(-(\alpha + \beta + \delta) + 2 - \sqrt{(\alpha + \beta + \delta)^2 - 4\beta\delta} \right) \end{aligned} \quad (10)$$

If $k_1 \gg k_4/[eIF4F]_0$ then we have a situation already solved in the main body of the paper. Let us consider the opposite situation, when $k_1 \ll k_4/[eIF4F]_0$. In this case $\alpha \gg \beta + \delta$ and

$$\begin{aligned} x_0 &\approx \frac{\gamma(\beta - 1)}{-\alpha} = \frac{k_1 k_4}{k_3 k_2} - \frac{k_1 [eIF4F]_0}{k_3 [60S]_0} \\ x_1 &\approx 1 - \frac{\beta \delta}{\alpha} = 1 - \frac{k_1 [eIF4F]_0 [40S]_0}{k_4 [60S]_0} \\ x_2 &\approx -\alpha < 0 \end{aligned} \quad (11)$$

If $\alpha \gg \beta + \delta$ then the solution of the model can be approximated by the dominant system from Fig. 5 of the main body of the paper, Stage 1:

$$\begin{aligned} &\begin{bmatrix} [eIF4F](t) \\ [mRNA : 40S](t) \\ [AUG](t) \\ [80S] \end{bmatrix} \\ &= \frac{[eIF4F]_0}{\frac{1}{k'_1} + \frac{1}{k_2}} \left(\begin{bmatrix} 1/k'_1 \\ 1/k_2 \\ 1/k'_3 \\ 1/k_4 \end{bmatrix} + \frac{1}{k_2} \begin{bmatrix} 1 \\ -1 \\ 0 \\ \frac{k_2}{k'_1 + k_2} \end{bmatrix} e^{-(k'_1 + k_2)t} - \left(\frac{1}{k_4} + \frac{1}{k'_1 + k_2} \right) \begin{bmatrix} 0 \\ 0 \\ 0 \\ 1 \end{bmatrix} e^{-k_4 t} \right) \end{aligned} \quad (12)$$

and $[60S] = [60S]_0$, $[40S] = [40S]_0$. This solution is valid on the interval $[0; t']$, $t' = \frac{1}{k'_1 + k_2} + \frac{[60S]_0}{10[eIF4F]_0} \left(\frac{1}{k'_1} + \frac{1}{k_2} \right)$. Following the recipe from the main body of the paper, after this moment it can be prolonged with quasiequilibrium approximation:

$$\begin{aligned} A &= \frac{[eIF4F]_0}{k_4 \left(\frac{1}{k'_1} + \frac{1}{k_2} \right)} \\ [80S](t) &= \frac{[60S]_0}{10} + A \left(1 - e^{-k_4(t-t')} \right), [40S](t) = \frac{[40S]_0 - [80S](t)}{1 + \frac{k'_1}{k_2} [eIF4F]_0}, [60S](t) = [60S]_0 - [80S](t), \\ [eIF4F](t) &= \frac{k_2 \cdot [eIF4F]_0}{k_1 [40S](t)}, [mRNA : 40S](t) = \frac{k_1 [40S](t) [eIF4F]_0}{k_2}, \\ [AUG](t) &= \frac{[eIF4F]_0}{\left(\frac{1}{k'_1} + \frac{1}{k_2} \right) k_3 ([60S]_0 - [80S](t))} \end{aligned} \quad (13)$$

Formulas (12-13) completely describes the dynamics of the system in the case $k_1 \ll k_4/[eIF4F]_0$. However, if $\alpha \approx \beta + \delta$ (i.e., when $k_1 \approx k_4/[eIF4F]_0$) then an other dominant system approximates the last stage of relaxation, when $[60S](t)$ becomes much smaller than $[AUG](t)$. Here the same quasi steady-state asymptotic as in the main body of the paper (Stage 2) is valid (see formula (42-44) of the main text). This completes the analysis of the system behaviour in the case when k_1 is relatively small with respect to other parameters. On the Fig. 1 one can see the comparison of these solutions with numerical simulations.

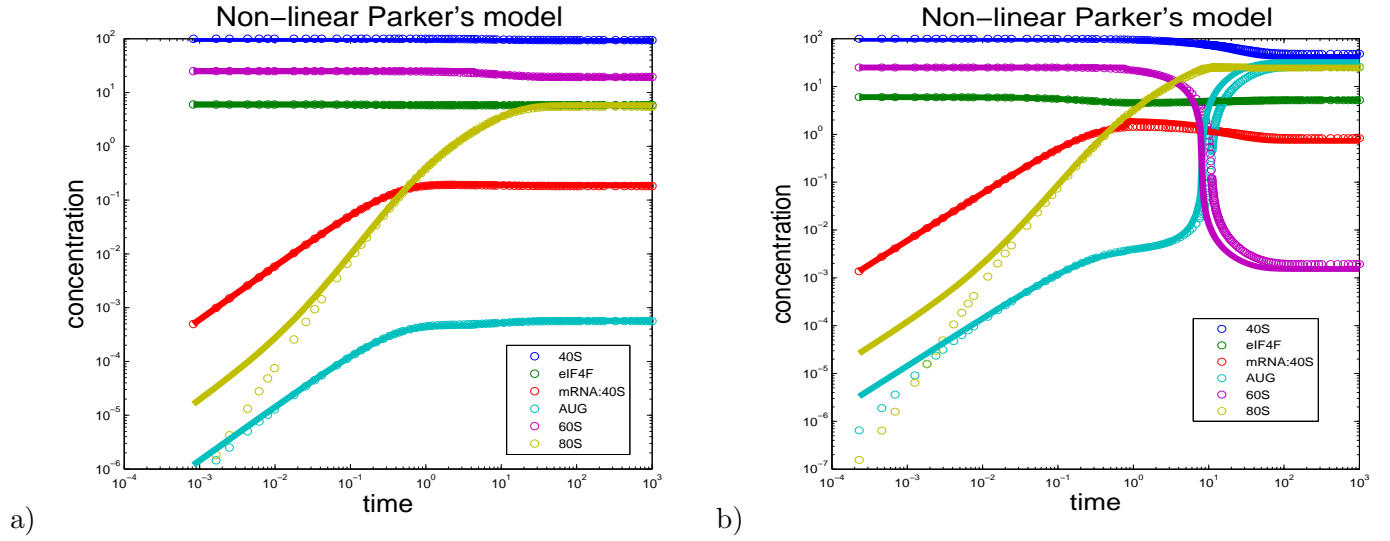


Figure 1: a) Simulation of the non-linear protein translation model with parameters $k_1 = 0.001$, $k_2 = 3$, $k_3 = 50$, $k_4 = 0.1$, $[40S]_0 = 100$, $[60S]_0 = 25$, $[eIF4F]_0 = 6$. b) Same as a) but $k_1 = 0.01$. Circles represent the numerical simulation while solid lines gives the analytical solution.