cell doubling time: 28 min

cell volumn: 10^{-15} L

G_tot: 17 copies, 28.2nM

Ptot: 40 nM

U: molecular weight is 426 g/mol, and in simulation the concentration is in ng/ml, you can use the molecular weight to convert concentration between ng/ml and nM. Typical working concentration of U: 0 - 100 ng/ml

Assume the protein is relatively stable, it's half response time is just 28min

$$\frac{\ln 2}{\delta_P} = 28\text{min} \implies \delta_P = 0.02475525645\text{min}^{-1}$$

RNA degradation rate δ_M : 10 times protein so: 0.25 min-1

*biological reasonable α_M : 1 min-1, we need to choose a value about this much

*biological reasonable α_P: 1min-1 (2 times the value in the paper because we explicitly model dimerization)

$k_1 = 0.42\text{nM}^{-1}\text{min}^{-1}$

$k_{-1} = 4.2 \times 10^{-4}\text{min}^{-1}$

$k_2 = 5.8\text{nM}^{-1}\text{min}^{-1}$

$k_{-2} = 5.8 \times 10^{-2}\text{min}^{-1}$

*Dimerization: p + p = pp, Ku = p^2/pp

gas constant R = 8.314 J/(K*mol)

temperature T = 37 degrees celsius = 310.15K

From ref 21: $\Delta G_U^0 = -RL \ln K_U$, and the range of delta G in three conditions: is 78 ± 3.8kJ/mol 71 ± 4.3kJ/mol, 76 ± 4.6kJ/mol, so we might want to try a delta G in range 66.7 - 81.8 kJ/mol, corresponding to K_U of 5.9×10^{-12} to 1.7×10^{-14} (what

is the unit????)

Half time is 50s, so K_U:

We need to select above marked parameters so that they match the following:

parameter selection Criteria:

(1) In fig3: full saturation needs to be achieved at U = 25 ng/ml (also in ref 20 fig3)

In [ ]:

In [ ]: