Eidgenössische Technische Hochschule Zürich
Swiss Federal Institute of Technology Zurich

Department of Computer Science, ETH Zürich

Synthetic Biology

Assignment #01

Stephanie Fingerhuth, Lorenzo Gatti

Thursday 22nd March, 2012

0.1 The model

The model for a two protein network can be given by the system of equations:

$$\frac{dx}{dt} = f(y) - d_1 x \tag{0.1a}$$
$$\frac{dy}{dt} = g(x) - d_2 y \tag{0.1b}$$

where x and y are the concentration of the two proteins, f and g are "repression functions" and d_1x, d_2y are positive constant describing the protein decay.

$$f(y) = \frac{k_1}{1+[Y]^n}{}^{*} \tag{0.2a}$$
$$g(x) = \frac{k_2}{1+[X]^m}{}^{\dagger} \tag{0.2b}$$

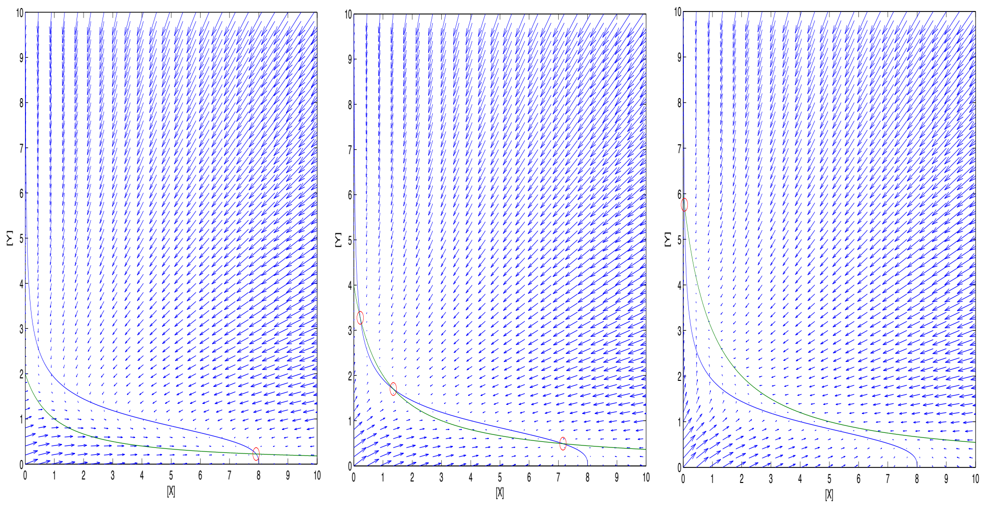
The level of repression of $[X]$ in a "mixed" circuit model is described by a Hill function, which models copperativity of binding between two different molecular species. Using the conditions for a change in the number of steady states derived from nullclines analysis:

$$d_1[X] = \frac{k_1}{1+[Y]^n} * \frac{1}{d_1} = \frac{k_1'}{1+[Y]^n}{}^{\ddagger} \tag{0.3a}$$
$$y_1 = \sqrt[n]{\frac{k_1'}{d_1[X]} - 1} \tag{0.3b}$$
$$d_2[Y] = \frac{k_2}{1+[X]} * \frac{1}{d_2} = \frac{k_2'}{1+[X]^n}{}^{\S} \tag{0.3c}$$
$$y_2 = \frac{k_2'}{1+[X]} \tag{0.3d}$$

The equations 0.3a and 0.3d are solved as functions of $f(x)$ in the form $y = f(x)$.

0.2 Nullcline plots

The analysis performed in graphs 0.1 shows the existence of multiple steady states, which it is the necessary condition to have a switch. The purpose of the switch is to obtain a consisting change in the concentration of a certain protein. The graph 0.1b shows highly transverse nullclines, the system can tolerate more movements of the nullclines without the disappearance of a steady state.



(a) $k_2' = 2$ (b) $k_2' = 4$ (c) $k_2' = 6$

Figure 0.1: Nullclines plots for the parametres $n = 3$, $k_1' = 8$, $k_2' = \{2, 4, 6\}$

Intersection of functions lines are circled in red. These points represent the steady state at different values of the parameter k_2. In the graph 0.1a we can distinguish only one point at high concentration of protein Y as well as in the graph 0.1c where the steady state is reached at high concentration of X. The major difference is visible in the graph 0.1b where we clearly confirm a possible switch, due to the presence of three steady state points.

0.3 Analytic expressions for k_1' and k_2'

According to Matlab *solve* function for the equations:

$$e1 : x = \frac{k_1'}{(1 + y^3)} \tag{0.4a}$$

$$e2 : y = \frac{k2}{(1 + x)} \tag{0.4b}$$

$$e3 : \delta(\frac{k_1}{(1 + y^3)}, y) * \delta(\frac{k_2}{(1 + x)}, x) = 1 \tag{0.4c}$$

we retrieve three solutions:

$$k_1' = \frac{(3 * x^2)}{(2 * x - 1)} \tag{0.5a}$$

$$k_2' = \left(\frac{(x + 1)}{(2 * x - 1)}\right)^{\frac{1}{3}} * (x + 1) \tag{0.5b}$$

$$y = \left(\frac{(x + 1)}{(2 * x - 1)}\right)^{\frac{1}{3}} \tag{0.5c}$$

0.4 Cooperativity plot

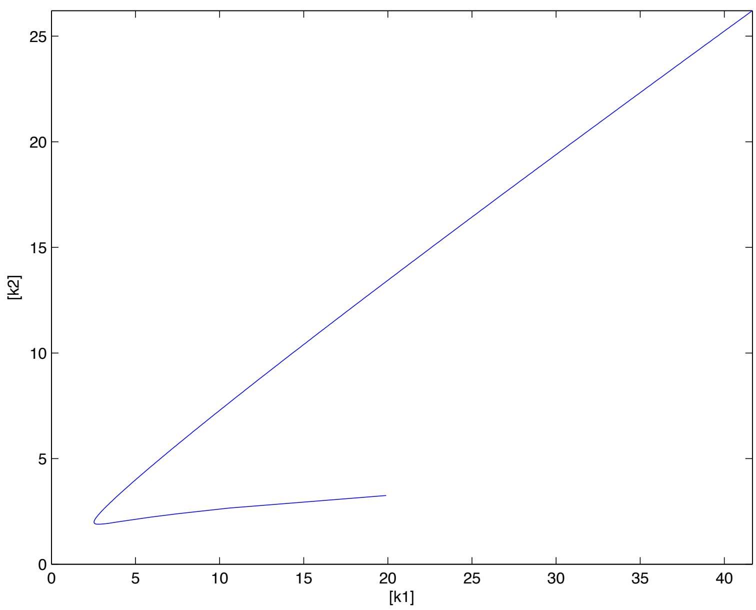


Figure 0.2: Values of the parameter k_1' and k_2' needed for a working switch for particular values of the exponent n in the Hill function ...