IGEM WP Model

Summary

Contents

1 Notations

Here are some conventions about notation.

1. words begin with g represent gene(eg., gSos).
2. words begin with m represent mRNA(eg., mSos).
3. words begin with p represent promoter(eg., pSos).
4. other words represent protein(eg., Sos).
5. α represents transcription term(eg., α_{Sos}).
6. β represents translation term(eg., β_{Sos}).
7. d represents decomposition term(eg., d_{Sos}).

2 2015 KU Model

Since it is a model reproduction work, I am not going to show a lot details about model design. Instead, I am going to point out the key to the model and the problems while I try to reproduce the result. Besides, I'd like to share what I gain in this process.

2.1 Basic Ideas

The basic model to describe the amount of chemical substances is **ODE Model**. If we totally figure out the transformation among chemical substances we concerned about, then we can use some submodels to describe their transformation rate, which is $\frac{\mathrm{d}amount}{\mathrm{d}t}$, the derivative of the amount.

In the following, I will show the basic chemical reactions and the submodels to describe them.

2.2 Transcription and Hill Function

According to central dogma, the first step of build a protein is transcription. If the transcription rate is a const, we can describe the process as $\frac{\mathrm{d}mRNA}{\mathrm{d}t} = r \cdot gRNA$ where r is the transcription rate.

Actually, we always need a transcription factor. Only after the factor is binded to DNA, can they begin to transcribe. Hill Function is used to describe such a situation(cf., Fig.)

$$\theta = \frac{[L]^n}{K_d^n + [L]^n} = \frac{1}{1 + (\frac{K_d}{[L]})^n} \tag{1}$$

θ is the amount of DNA bound by the protein, $[L]$ is the amount of protein, K_d is the dissociation constant and n is the Hill coefficient.

For the repressors, we are interested in how much of the DNA is still unbound and active: $\frac{1}{1+(\frac{[Repressor]}{K_d})^n}$

For the activators, we are interested in how much of the DNA is bound and active: $\frac{1}{1+(\frac{K_d}{[Activator]})^n}$

So the ODE is modified as

$$\frac{\mathrm{d}mRNA}{\mathrm{d}t} = r \cdot (\frac{1}{1 + (\frac{K_d}{[Activator]})^n} gRNA)$$

2.3 Translation

Translation is quite easy. We consider translate rate as a const, so the contribution of translation in derivative term is

$$\frac{\mathrm{d}Protein}{\mathrm{d}t} = r_{Translation} \cdot mRNA$$

2.4 Protein Association and Disassociation

2.5 Ping-Pong Bi-Bi

2.6 Spread

2.7 Reproduction Result and Problems

2.8 What have I gained

3 Our Model

3.1 Baisc View

Our design is a feedback system in which the output protein $RhoA$ can detect the amount of input $TGF - \beta$ and change accordingly through a series of pathways.

The sketch of metabolic pathway is shown as following.