Excercise "Introduction to Systems Biology"

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Exercise 1: Chemotaxis

Implement the most simple chemotaxis model:

• The probability of a methylated receptor to be active is given by

$$p = 1 - \frac{L}{L + K_L},$$

with ligand concentration L and Michaelis-Menten constant K_L .

• The concentration of activated receptors T_a is given by

$$T_a = p T_m$$

with T_m the concentration of methylated receptors.

• The dynamic of the concentration of methylated receptors is given by

$$\dot{T}_m = k_R R - k_B B \frac{T_a}{K_B + T_a}.$$

Thus, the methylating enzyme R acts in the saturated region of the kinetics and the demethylating enzyme B can only influence active receptors. Please note the difference as well as the relationship between T_a and T_m .

• Dynamic of phosphorylated $CheA_p$:

$$\dot{A}_p = k_A (A_{tot} - A_p) T_a - k_Y A_p (Y_{tot} - Y_p)$$

• Dynamic of phosphorylated $CheY_p$:

$$\dot{Y}_p = k_Y A_p (Y_{tot} - Y_p) - \gamma_Y Y_p$$

Simulate the system

- with the parameters $K_L = 1$, $k_R = 1$, $k_B = 10$, $K_B = 1$, $k_A = 10$, $k_Y = 1$, $\gamma_Y = 1$, R = 0.01, R = 1, R = 10, R
- ullet and a ligand concentration L of

$$L = \left\{ \begin{array}{ll} 0.1 & \text{for } 0 \leq t < 50s \\ 0.3 & \text{for } 50 \leq t < 100s \\ 0.5 & \text{for } 100 \leq t < 150s \\ 0.3 & \text{for } 150 \leq t < 200s. \end{array} \right.$$

Analyze the (well scaled) time course of the ligand concentration as well as of the individual components, and understand the underlying mechanism.