Computational Methods in Biology (Fall 2022)

Enzyme Kinetics

Exercises due October 5

Write an XPP code for enzyme kinetics, including differential equations for substrate (s), enzyme (e), complex (c), and product (p). Use k1p=0.1, k1m=0.05, k2p=0.1, and k2m=0.001, where k1p represents the kinetic rate k_1^+, etc. Assume that, initially, $s = 100$, $e = 10$, and others are zero. Set up your code so that all four variables are plotted (use nplot=4). Include auxiliary variables for the target of the enzyme ($s + c + p$) and for the total enzyme ($e + c$). Also, set the total integration time to 10 time units. Print out the code and include it in your report.

In your answers to the questions below, please include plots.

(1) Run XPP. Open a new window and plot your two auxiliary variables vs. time to ensure conservation of the enzyme and enzyme target concentrations. When you do this, you will need to delete the curves for the other variables that will be included automatically. You can type GD (Graphic stuff – delete) to make this happen.

(2) Now look in the main window. What happens to the distribution of enzyme between free and complexed form? Why did it happen?

(3) What is happening to the substrate and product concentrations? Why? Comment on the transition rate between free and complexed enzyme versus the transition rate between substrate and product.

(4) Next run the simulation until the system equilibrates. About how long does this take? What are the equilibrium levels of the variables (you can look in the Data viewer and click End)? Another way to find the equilibrium state is to type SG (Sing pts – Go).

(5) Create a new XPP program that uses conservation to remove the differential equations for c and p, leaving a planar system of differential equations. Define new parameter R for the initial enzyme concentration (sum of free and bound enzyme), and Q for the initial enzyme target concentration (sum of s, c, and p). These parameters would be used in your algebraic equations for c and p. So that you can plot c and p, add an auxiliary variable for each (e.g., "aux c=c" will work for the complex). Run the code and make sure that the total enzyme and enzyme target concentrations are conserved. Turn in the code.

(6) Run this new code out to equilibrium. Is it the same as it was for the last code? (it should be!) How does the equilibrium change if you remove the complex–to–product back-reaction? Why does all the substrate ultimately get converted to product in this case?

(7) Create a final XPP program that assumes Michaelis-Menten kinetics. Define a new expression V_{max} and Michaelis-Menten coefficient K_D, as discussed in class. Run this out to equilibrium. Are there any major differences between this equilibrium state and that of the planar system?