

Design Project #1 Part A

Due: September 21, 2012 at 11:59 a.m. on Course website.

NO EXTENSIONS WILL BE GRANTED

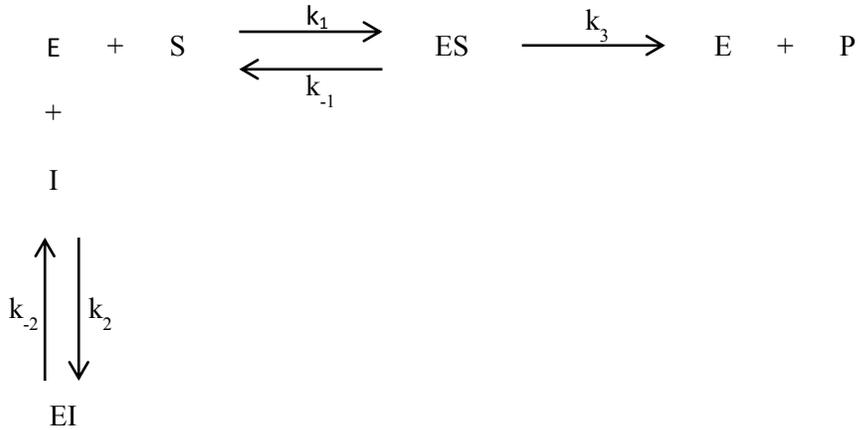
INSTRUCTIONS

This component of the design project is meant to familiarize you with MATLAB. In particular, you will derive various ODEs governing a system's species concentrations and learn how to input them into MATLAB and use ode45 to generate concentration vs. time profiles.

- I. This portion of the design project is due at noon on Friday, September 21. There will be no extensions of deadlines and late submissions will not be accepted.
- II. Please review the information about acceptable forms of collaboration, which is available on the eqwtug'y gdsite and follow the guidelines carefully. NO sharing of code is permitted.
- III. For ease of grading, we've provided a MATLAB skeleton which MUST BE USED. All of your MATLAB code should be contained within this single script and you must rename your MATLAB script as specified below.
- IV. Submit both a MATLAB script and a PDF to Eqwtug'y gdukg under this assignment's heading by the deadline outline above. Information regarding the required contents of the PDF is contained at the end of this document.

Problem 1

Consider a system in which an enzyme E is involved in the conversion of a substrate S into a product P. The enzyme and substrate react reversibly to form a complex ES with forward and reverse rate constants k_1 and k_{-1} respectively. The ES complex reacts to regenerate the original enzyme and the product irreversibly with rate constant k_3 . The system, however, also contains a competitive inhibitor which binds reversibly with the enzyme to form an inactive complex EI. The forward and reverse rate constants governing this binding are k_2 and k_{-2} respectively. A schematic illustrating this reaction system is drawn below:



- Write out 6 differential equations describing how the concentrations of E, S, I, P, ES and EI depend on the aforementioned rate constants and the concentrations of the other species. Do not make any assumptions other than the ones described above.
- Download the MATLAB skeleton code provided on Course website. Rename the function YOURNAMEHERE as LASTNAME_FIRSTNAME and save the file as LASTNAME_FIRSTNAME.m. Using the results from part A, modify the function *diffeq* by specifying the time dependence for each species. Pay special attention to the ordering of the variables *y* and *K* specified at the top of the script.
- In the skeleton, specify the following initial concentrations where indicated:

$$E_0 = 1, S_0 = 1, ES_0 = 0, EI_0 = 0, P_0 = 0, I_0$$

We will ignore units for the simplicity of this assignment. Read the file *parta_data.csv* into the MATLAB environment using the *csvread* command. Where indicated, add code to the skeleton to assign the first column of this data matrix to *t_meas* and the remaining columns of this matrix to *y_meas*. *t_meas* represents the time points at which measurements of each of the species above were made, while *y_meas* represents the time dependent concentrations of each species (the rows corresponds to time points and the columns to species [E], [S], [ES], [EI], [P] and [I] respectively).

Add code to the skeleton to plot *y_meas* vs. *t_meas* using circles for each of the data points. Each species should be plotted in a different color. Add appropriate commands to label the x and y axes and to add a legend to the graph indicating the name of each species.

To copy your figure, you can either save it as a .png file or you can click edit->copy figure and then paste it into a word document.

- d) Specify the command in the *calcfit* function necessary to compute the concentration vs. time profiles of each species in our system. To do so, make use of MATLAB's *ode45* function which performs numerical integration and the function *diffeq* we defined previously. Make sure to use all of the arguments specified as input to *calcfit* and to use the time points contained in *t_points*.

For additional help, type *help ode45* into your console for MATLAB's help information or search online.

- e) The rate constants in our system are all unknown. However, since we have the measured concentration vs. time profiles of each species in our system (from the .csv file) and a function to calculate these profiles given particular rate constants (*calcfit*), we can use numerical optimization to determine good estimates. This part has already been implemented and the optimized values will be assigned to the variable *K_opt*. The simple procedure uses the MATLAB function *lsqcurvefit* to find the set of rate constants that minimizes the squared difference between the computed concentration profiles and the measured profiles.

We want to verify that the estimated rate constants fit the measured profiles well. Using the *calcfit* function and the rate constants in *K_opt*, generate predicted concentration profiles for each species from $t=0$ to $t=1$. Add a command to plot these concentration profiles on the same plot as the original data. Instead of using circles, plot these profiles using solid lines and once again use a different color for each species (the color should match that used previously). The *hold on* command should prevent the plot from resetting.

WHAT TO SUBMIT:

Please submit a PDF named *LASTNAME_FIRSTNAME_WRITEUP.pdf* to Course website under this assignment which contains

- I. 6 differential equations from part A
- II. The plot from part C
- III. The plot from part E, as well as the optimized rate constants contained in *K_opt*

Also submit your completed MATLAB script, which should be named *LASTNAME_FIRSTNAME.m*, to Course website under this assignment's heading

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20.320 Analysis of Biomolecular and Cellular Systems
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