

Description of Codes for Chapter 2: Transport and Reaction of Solutes in Biological Systems

Section 2.2.2: Volume Changes in Isolated Glomeruli

The main script to run the simulations described in this section is 'glomeruls.m'. This script calls the function 'dXdT_glomer', which is used by the ODE integrator to estimate the solution to Equations (2.25) and generate Figures 2.5 and 2.6.

Section 2.3.1: Xylose Fermentation by Yeast

The script 'Bioreactor1.m' is used to generate Figures 2.7 and 2.8 for the fermentation model. This script calls the ODE file 'dXdT_reactor1.m' to compute Equations (2.39).

The script 'Bioreactor2.m' is used to generate Figure 2.9 for the mixed bioreactor with flow. This script calls the ODE file 'dXdT_reactor2.m' to compute Equations (2.42).

Section 2.4.1: One-Dimensional Distributed Reaction System

The script 'Bioreactor3.m' is used to generate Figure 2.13. This script calls the ODE file 'dXdT_reactor1.m' to integrate the kinetic equations.

Section 2.4.2: Fluorescence Recovery after Photobleaching

The script 'FRAP1.m' is used to generate the simulations described in Section 2.4.2. This script also plots the data that are stored in the files 'normalized_CCIIS_FRAPdata_1micron.mat' and 'normalized_CCIIS_FRAPdata_halfmicron.mat'. The method used here is detailed in Section 9.6.1 of the appendix.

(Note Exercise 2.8 asks the reader to modify these codes to simulate for diffusion and exchange to generate Figure 2.18.)