

Computational Systems Biology

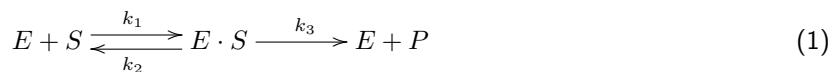
636-0007-00 U, Autumn 2025

Assignment 11

(Issue: 05-Dec-2025)

1 Stochastic Simulation of a Biochemical System

We want to consider the following simple reaction sequence of an irreversible enzymatic reaction that converts a substrate S into a product P:



For this system, please perform the following tasks:

- a) Implement Gillespie's Direct Method in MATLAB or Python and simulate the temporal evolution of the system until $t = 1000s$ for the initial conditions and parameter values given in table 1. Calculate the propensities a_j according to:

$$a_j = k_j \cdot \prod_{i=1}^N n_i^{\max(-v_{ij}, 0)} \quad (2)$$

where N represents the total number of species in the system and the v_{ij} denote the stoichiometric coefficients (negative by default for reactants!). Plot the resulting trajectories of all species into a single plot using the `stairs` command (MATLAB) or `matplotlib.pyplot.stairs` (Python).

- b) For the initial conditions and parameter values given above, perform a series of 50 simulations and plot the resulting time courses. Calculate the mean and the standard deviation (relative to the mean value) at the last time point (about) $t = 1000s$ for each species by averaging over all simulation runs. How do these values change when you repeat the simulations using $n_S(t = 0) = 1000$?
- c) [optional] Compare the results from (b) with those of a deterministic description of the equivalent system to equation (1)



where r is given by Michaelis-Menten kinetics of the form

$$r = r^{max} \cdot \frac{c_S}{K_m + c_S} \quad (4)$$

The conversion between absolute molecule numbers and concentrations as well as for the associated constants is as follows:¹

$$r^{max} = \tilde{k}_3 \cdot c_{E,tot} \quad (5)$$

$$K_m = \frac{\tilde{k}_2 + \tilde{k}_3}{\tilde{k}_1} \quad (6)$$

$$\tilde{k}_j = k_j \cdot (N_A \cdot V)^{-1 - \sum_i v_{ij}} \quad (7)$$

$$c_i = \frac{n_i}{N_A \cdot V} \quad (8)$$

¹Note that formula (7) only applies to reactions without multimerization of identical reactant molecules (Gillespie 1977), which is the case here.

Here, $N_A = 6.022 \cdot 10^{23}$ molecules/mol denotes Avogadro's number and $-\sum_i v_{ij}$ represents the *molecularity* of the reaction (i.e., the negative sum of reactant reaction orders considering negative stoichiometric coefficients for reactants) involved in reaction channel j . For example, for an irreversible reaction



with $r_j = k_j \cdot n_A \cdot n_B^2$ we obtain $-\sum_i v_{ij} = -(-1 - 2) = 3$. k_j stands for the kinetic reaction constant referring to absolute molecule numbers, whereas \tilde{k}_j is the equivalent constant in terms of a molar representation.

Simulate the deterministic system employing the ODE solver `ode45` (MATLAB) or `scipy.integrate.solve_ivp` (Python). Compare the resulting species numbers calculated from the corresponding concentrations at the end of the simulation to the mean and standard deviation obtained in simulation runs of part (b). Do they appear to converge to the same mean?

References:

Gillespie, D.T. (1977). Exact Stochastic Simulation of Coupled Chemical-Reactions. *J. Phys. Chem.* 81(25): 2340-2361.

Some useful MATLAB commands and help entries for this exercise:

`cumsum`, `rand`, `stairs`, `ode45`, `std`, `mean`

Some useful Python commands and help entries for this exercise:

`numpy.cumsum`, `numpy.random`, `matplotlib.pyplot.stairs`, `scipy.integrate.solve_ivp`, `numpy.std`, `numpy.me`

Submission:

Please address any questions to

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Table 1: Parameter values and initial conditions of the enzymatic reaction.

Parameter	Parameter Value	Unit
cell volumne V	10^{-13}	l
k_1	10^{-3}	$molecules^{-1} \cdot s^{-1}$
k_2	10^3	s^{-1}
k_3	200	s^{-1}

Initial Condition	Molecule Number	Unit
n_S	100	–
n_E	20	–
$n_{E \cdot S}$	0	–
n_P	0	–