

Systems Biology Tutorial 2: Chemical kinetics and energetics

Reversible dissociation

Consider the reaction catalysed by mass action kinetics:

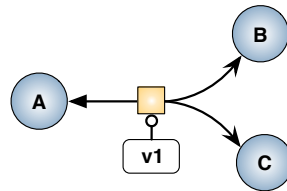
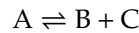


Figure 1: Graphical representation of the reversible dissociation reaction.

The change in the concentration of A is described by the ordinary differential equation (ODE), denoting concentrations by lowercase italics:

$$\frac{da(t)}{dt} = -v_1 \quad (1)$$

$$\text{where} \quad v_1 = k_f \cdot a(t) - k_r \cdot b(t) \cdot c(t) \quad (2)$$

Questions

- (a) What must the units of k_f and k_r be (if time is measured in seconds and concentration in M)?
(b) Write Eq. 2 in the form

$$v_1 = k_f \cdot \left(a - \frac{b \cdot c}{K_{eq}} \right) \quad (3)$$

- (c) Given that $k_f = 23$ and $k_r = 0.5$, what is the unit and value of K_{eq} ?
(d) From the information above, write the ODEs for B and C.
- Solve ODEs with three variable species (a skeleton notebook providing hints is available from the File Downloads section of the course website):
 - For initial values $a(0) = 5$ M, $b(0) = 0$, $c(0) = 0$ and parameters as given, solve the ODEs to calculate how the concentrations of A, B and C evolve over time (up to an end time of 0.5 s). Use PySCeS to do this. A skeleton PySCeS input file (`massaction_skel.psc`) is provided; you will have to edit and complete this before running the simulation.
Hint: You will have to use the PySCeS method `mod.doSim()` and can access the simulation results with `mod.sim`.
 - Plot the concentrations as a function of time using the `mod.SimPlot()` function. You should simulate with sufficient time points to give smooth curves.
 - Using `matplotlib` functions, manually plot the concentrations of all species against time on the same set of axes with different colours. Add axis labels including units.
- Solve ODEs with a one fixed species:
 - For **fixed** $a = 5$ M, initial values $b(0) = 0$ and $c(0) = 0$, and parameters as given, solve the ODEs to calculate how the concentrations of B and C evolve over time.
Hint: Reuse the PySCeS model from the previous question, save it under a new name and make the necessary changes to fix A, i.e. treat the fixed species as a parameter.
 - Plot the mass action ratio as a function of time. To what value does this ratio strive and why?
 - How does the mass action ratio change if you increase the value of k_r ?

4. Use the data set provided (initial rates vs. a in `A.csv`, and initial rates vs. b and c in `BC.csv`) and fit a function of the form given by Eq. 2 to obtain values for k_f and k_r .
- (a) Download the two data files from the File Downloads section of the course website using your browser. You will have to use the following functions to work with the data in Python:
- `pd.read_csv()` for loading the data from file
 - `ax.plot()` for plotting the data
 - `lmfit.Model()` for fitting the data to the function
- (b) First, fit a simplified function to the data for rate vs. a to obtain k_f . The columns of the data set are `[a, rate]`.
- (c) Next, fit a simplified function to the data for rate vs. b and c to obtain k_r . The columns of the data set are `[b, c, rate]`. Plot the fitted simplified rate as a function of B and C in a 3D-plot (refer to plotting hints in the skeleton notebook).
- (d) We can, however, also fit the complete function on all of the data to obtain these parameter values. Combine the datasets into one dataframe which has the following columns: `[a, b, c, rate]`. Fit the full function to obtain values for k_f and k_r .

Hints:

- For any dataframe it is possible to append a new column of zeros (say, this column should be called X): `df['X']=0`
- You can concatenate two dataframes that have the same column labels as follows:
`df3 = pd.concat([df1, df2])`