

Component Specification

1. **Software components.** High level description of the software components such as: *data manager*, which provides a simplified interface to your data and provides application specific features (e.g., querying data subsets); and *visualization manager*, which displays data frames as a plot. Describe at least 3 components specifying: what it does, inputs it requires, and outputs it provides.
 - a. Tellurium is a systems biology and kinetics package for python. Since I will be using Tellurium to use Michaelis Mentin kinetics for my Cas12a enzyme, I will only input the concentrations of the Cas complex and that the reaction is occurring at steady state. There will be no outputs.
 - b. Matplotlib.pyplot is a plotting package in python that will help me make graphics. The inputs will be what type of graphic I will be creating with the model. The output will be various graphics, such as fluorescence intensity versus drug concentration.
 - c. Numpy is a mathematical package in python that helps with computation. There will not be any inputs or outputs, but it will be used throughout the model for calculating equations.
2. **Interactions to accomplish use cases.** Describe how the above software components interact to accomplish at least one of your use cases.

The user will first enter their data, which includes the DNA sequence, nucleotide concentration, and drug of interest. Then, I will use the numpy package to calculate how long it will take for the DNA to be synthesized to the Cas12a activation region. Once the DNA is synthesized, I will use Tellurium to model the kinetics. Finally, I will use matplotlib.pyplot to show the graphs with the real-time curves.

3. **Preliminary plan.** A list of tasks in priority order.
 - (1) I first need to convert the inputs the user gave me, specifically the DNA sequence, into a readable data frame.
 - (2) I will add a section that adds the known parts of the DNA template into variables.
 - (3) I will then model the reverse transcriptase kinetics to find out how fast the nucleotides are added to the template given a specific template.
 - (4) I then will work on converting Cas12a kinetics to fluorescence
 - (5) Then I will incorporate various drug concentrations once the model is working
 - (6) I will then plot all of the components
 - (7) I will need to figure out how to do a pop up box for the inputs.