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CS 6760 Project Proposal

Rule Based Models

The combinatorial complexity of some biological circuits can become intractable. One method that has been presented to solve this synthetic biology problem is rule-based modeling. A rule based model defines a set of rules for the molecules within the biological system. For example, a molecule X could have two different binding sites with rules defining how and when it is able to bind with other molecules. The rule will define what conditions are necessary for a molecule to bind with X and at what rate the reaction happens. For example, X might bind with Y if phosphorous is present but will bind with Z when phosphorous is not present. In this way a rule-based model defines rules for how each molecule in a system interacts with other molecules. In this framework it is possible to keep track of the state of the molecule.

The ultimate goal of my project is to create software to analyze and simulate a rule-based biological model. This is an ambitious project so some time will be necessary to understanding the SBML of rule-based models and learning the Libsbml python package in addition to the coding of the model simulation. I will use the following steps to guide me:

Step 1 – Try to create a simple rule-based model using current software such as BioNetGen or Kappa. Use the softwre to simulate the biological circuit to understand how it works.

Step 2 – Export the SBML file and import it into python using the libsbml python library.

Step 3 – Become familiar with the internal libsbml methods and how to use them. One example of this is to iterate through the rules and molecules of the model and print them out.

Step 4 – This step is to implement the necessary algorithms for analysis and simulation of the model. Ideally there will be graphs produced to visualize the circuit and the activity of the molecules, similar to what we have done before. This step will become more defined as I learn more about libsbml and the sbml for rule-based models.