

Goal: enable mathematical analysis of SBOL

Suggestions:

- leverage SBML standard, i.e. SBML package
 - if we go this route, what is required in this package
 - connect with SBML/COMBINE
- allow black-box models that are based on data
 - SBML assignment rules can do this
-

Challenges:

- There are different “realizations” of the same design
 - each realization represents a different “tweak” or other minor change
 - each realization *may* require a different SBML model
- What is the representation that unites all the realizations
- Changes in sequence are related to changes in model
 - changes in model can be reactions, parameters, molecular species, etc

Possible solution:

- Connect a DNA component to a fragment of the complete SBML model
 - “fragment” is implemented using hierarchical extension
 - OR “fragments” can be connected together by merging uuid
- Have a very high-level description of a design
 - very difficult to represent explicitly