BDAthlon Problem #3
Title: A common representation of multicellular genetic circuits using the Synthetic Biology Open Language
Area: Standards and Exchange

Background:

Data standards are an important aspect of biological design automation. Using data standards, designs can be exchanged unambiguously between different tools without the loss of information. The Synthetic Biology Open Language (SBOL) has been developed as a community standard to computationally capture information about genetic circuit designs, constituent components and their order. SBOL 2.0 allows specifying not only DNA-based components but also proteins and small molecules using `ComponentDefinition` entities. SBOL's `ModuleDefinition` can then be used to represent different biological relationships using `Interactions`. An `Interaction` entity provides a common semantics to list all of the participants and their roles in a particular biological interaction. SBOL is RDF/XML based and has a flexible data model. These entities can be associated with custom metadata, or annotations, such as when a design is created and so on. Moreover, custom and application specific data entities can be defined using SBOL's `TopLevelEntity`. In addition to this RDF/XML based language, the visualization of different genetic components is also standardized. SBOL Visual provides a set of defined glyphs in order to increase the human understanding of genetic circuits.

Problem Description:

SBOL is ideal to exchange information about the structure of genetic circuits and interactions between different genetic components. However, this language is currently not suitable to represent multicellular genetic circuits. As multicellular behavior can emerge due to different phenotypes of cells having identical DNA sequences, different organisms can also be involved to implement a desired function. Moreover, using SBOL, it is not clear how a genetic circuit is included in engineered cells, whether circuits are incorporated directly into the chromosome or are included as parts of plasmids. These details should be ambiguously documented in order to increase the reproducibility of designs across different labs and to electronically exchange designs between different tools.

Objectives:

1. Develop an SBOL extension to represent multicellular genetic circuits using SBOL2.0
2. Develop, or modify, an SBOL library of your choice to read and write SBOL documents according to your extension.
3. Develop, or modify, a tool to simulate or to visualize SBOL documents produced for multicellular genetic circuits.

Coding requirements:

An SBOL library of your choice.

Evaluation Criteria:

Demonstrate that SBOL documents produced according to the extension developed are read and written without the loss of information. Submit your library code as required by the competition as detailed at the start of the competition. Please provide both the source code and the reusable APIs (such as jar files in Java) or executables. Provide screenshots of the tool developed as well.

Resources:

- SBOL 2.0 Standard:
  http://dx.doi.org/10.2390/biecoll-jib-2015-272
- SBOL APIs: https://github.com/SynBioDex
- SBOL Visual: http://dx.doi.org/10.1371/journal.pbio.1002310