BDAthlon Problem #2
Title: A SBOL/BioPax Converter
Area: Standards and Exchange

Problem Description:

The Synthetic Biology Open Language (SBOL) is a standard for describing genetic designs. BioPax is a standard for describing biological pathways. Although BioPax's focus has been on naturally occurring pathways, there is no reason that it could not be used to describe artificial pathways. Furthermore, synthetic pathways typically leverage existing pathways to perform new functions, so the data stored in BioPax may be useful to the synthetic biology domain. Therefore, converters between SBOL and BioPax formats would be extremely useful.

In this problem, you are to develop either a basic SBOL to BioPax converter, or a basic BioPax to SBOL converter, or time permitting, both. The converter should implement the following mappings:

1. SBOL ComponentDefinitions ←→ BioPax PhysicalEntities.
2. SBOL ModuleDefinitions ←→ BioPax Pathways
3. SBOL Interactions ←→ BioPax Interactions

Objectives:

1. Objective one – create a basic SBOL to BioPax converter
2. Objective two – create a basic BioPax to SBOL converter

Coding requirements:

Develop your converter(s) as an Eclipse Maven Project. You should use libSBOLj 2.1.0 for processing SBOL data objects and Paxtools v5.0.0 for processing BioPax data objects.

Evaluation Criteria:

We will provide you one test case for a Genetic Toggle Switch in both SBOL and BioPax formats. We will evaluate your converter(s) using this and similar test files. You are welcome to use any example SBOL/BioPax files that you can find to test your converter. Please provide the tests that you use with your code.

Resources:

- SBOL Standard (http://sbolstandard.org)
- libSBOLj (http://sbolstandard.org/software/libSBOL/java/)
- BioPax Standard (http://www.biopax.org)
- Paxtools (https://biopax.github.io/Paxtools/)