

SBML and Synthetic Biology

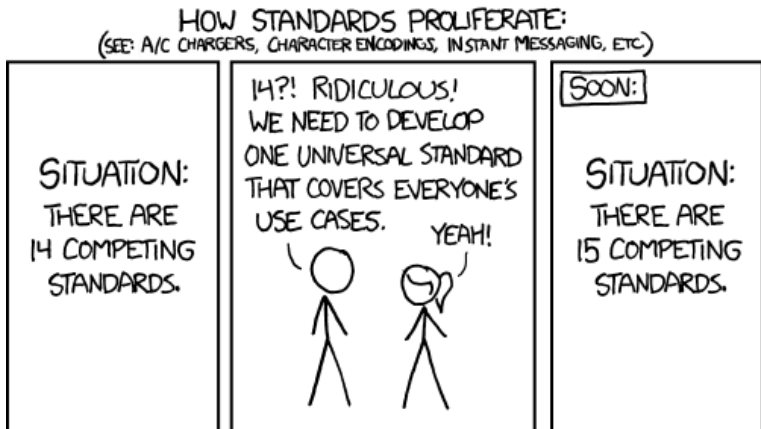
Chris J. Myers

University of Utah

COMBINE 2011

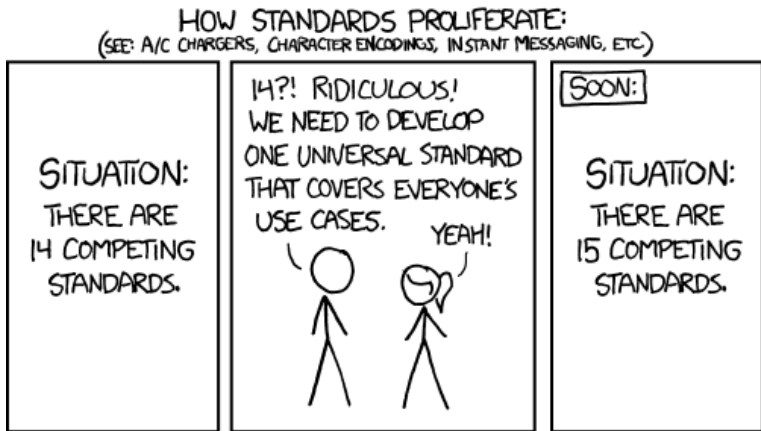
September 5, 2011

Motivation



- Standardized Model Description Language for Multi-Cellular Simulations:
 - Several workshops including one last week at ICSB.
- Synthetic Biology Open Language (SBOL):
 - Emerging standard for synthetic biology.

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Synthetic Biology Open Language (SBOL)



- Developed by the *Synthetic Biology Data Exchange Working Group* (SynBioDEX) including >30 members from academia and industry.
- SBOL meetings:

April 2008	1st SynBioDEX Workshop	University of Washington
July 2009	2nd SynBioDEX Workshop	Stanford University
June 2010	3rd SynBioDEX Workshop	Anaheim, CA
January 2011	4th SynBioDEX Workshop	VirginiaTech
June 2011	5th SynBioDEX Workshop	San Diego, CA
January 2012	6th SynBioDEX Workshop	University of Washington

- At the last meeting, we elected SBOL Editors: Michal Galdzicki (UW), Cesar Rodriguez (BIOFAB), and Mandy Wilson (VBI).
- SBOL webpage: <http://www.sbolstandard.org/>

Recent Announcement

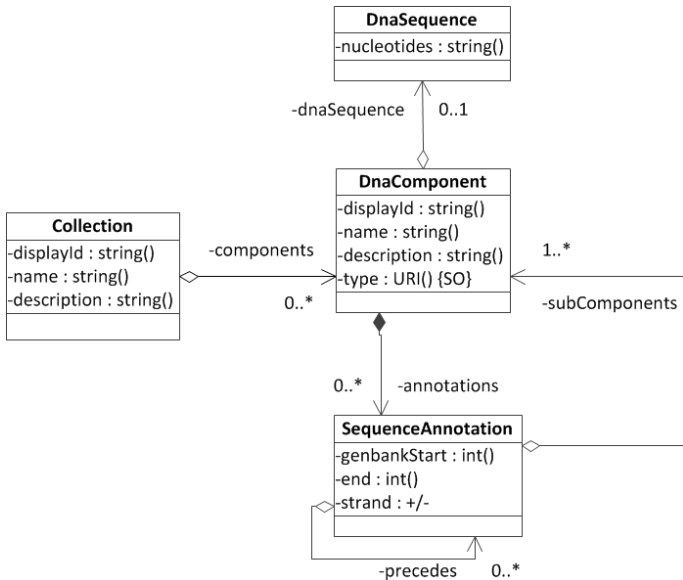
DARPA-BAA-11-60: Living Foundries: Advanced Tools and Capabilities for Generalizable Platforms (ATCG):

To encourage interoperability, all applicable design tools and databases developed under the ATCG program should be compatible with Synthetic Biology Open Language (SBOL) core data model.

Example SBOL Use Cases

- Send a design template for it to be filled in with a DNA sequence.
- Send an annotated DNA sequence for assembly planning.
- Publish a collection of DNA components to be re-used for design of novel DNA circuits.
- Retrieve and send annotated plasmid DNA sequence information between multiple software packages.

SBOL Core Data Model



Software Tools

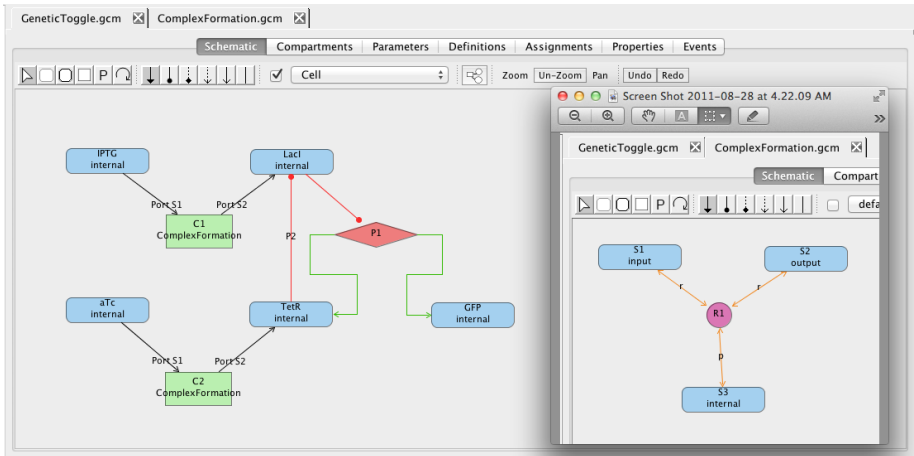
- libSBOLj - java implementation of SBOL core data model, will support serialization in RDF and XML.
- iBioSim - Chris Myers (University of Utah)
- TinkerCell - Herbert Sauro (University of Washington)
- Clotho - Doug Densmore (Boston University)
- GenoCAD - Jean Peccoud (VirginiaTech Bioinformatics Institute)
- gd-ice - Timothy Ham (Joint Bio Energy Institute)
- Electronic Datasheets - Cesar Rodriguez (BioFab)

SBOL in iBioSim

The screenshot shows a web browser window with two tabs: 'lambda.gcm' and 'testFileGamma.rdf'. The main content area is titled 'SBOL Browser' and is divided into two columns: 'Collections:' and 'DNA Components:'. The 'Collections:' list contains 'testFileGamma.rdf/testLibAlpha'. The 'DNA Components:' list contains 'aa', 'lacORF', 'lacOperon', 'lacPromoter', 'lacRBS', 'lacTerminator', 'laciORF', and 'laciPromoter'. The 'lacPromoter' item is selected. Below these lists is a text box containing the following information:

Name: Lac Promoter
Description: This promoter is repressed by LacI.
Type: promoter
DNA Sequence: gattaca

SBOL in iBioSim

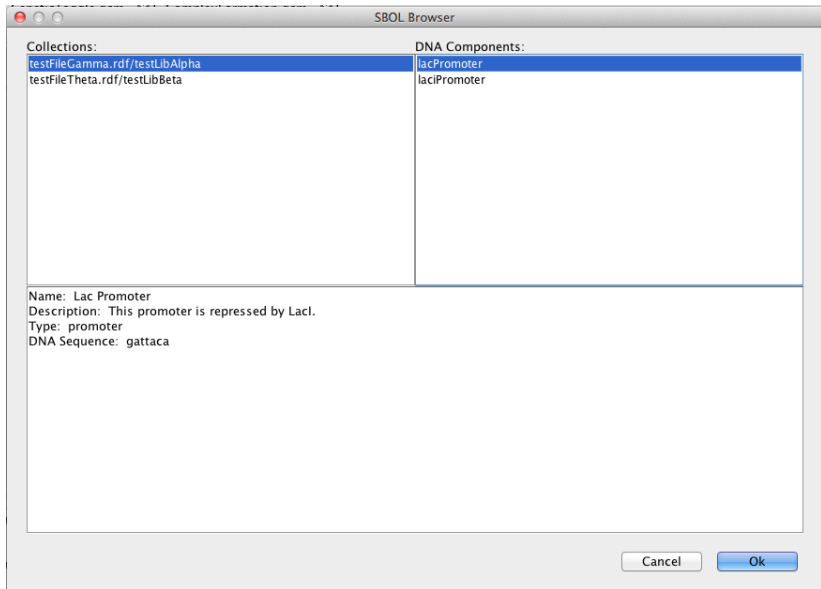


SBOL in iBioSim

Promoter Editor

ID	<input type="text" value="P1"/>
Name	<input type="text"/>
Initial promoter count (ng)	<input type="text" value="default"/> <input type="text" value="2"/>
RNAP binding equilibrium (Ko)	<input type="text" value="default"/> <input type="text" value=".033"/>
Activated RNAP binding equilibrium (Kao)	<input type="text" value="default"/> <input type="text" value="1"/>
Open complex production rate (ko)	<input type="text" value="default"/> <input type="text" value=".05"/>
Stoichiometry of production (np)	<input type="text" value="default"/> <input type="text" value="10"/>
Basal production rate (kb)	<input type="text" value="default"/> <input type="text" value=".0001"/>
Activated production rate (ka)	<input type="text" value="default"/> <input type="text" value=".25"/>
SBOL Promoter	<input type="text" value="Associate SBOL"/> <input type="text"/>
SBOL Terminator	<input type="text" value="Associate SBOL"/> <input type="text"/>

SBOL in iBioSim



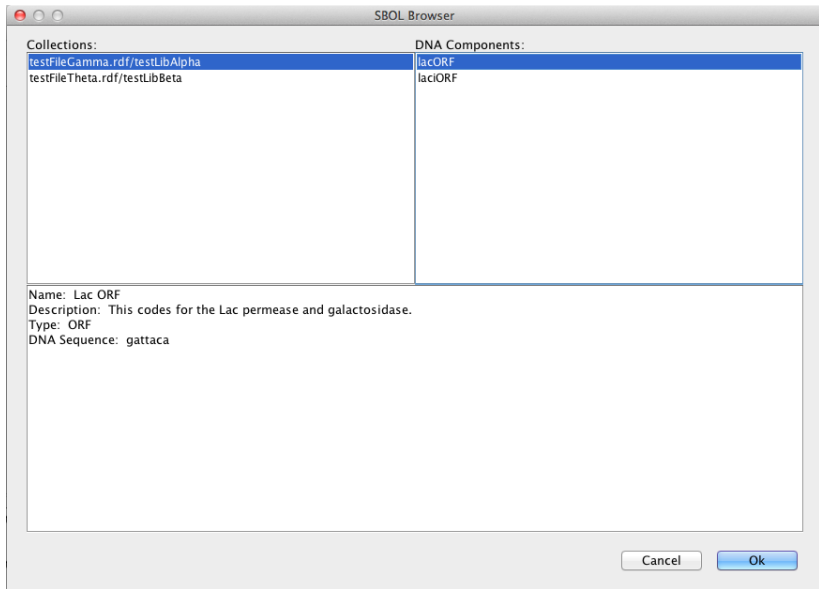
SBOL in iBioSim

Species Editor

ID	LacI	
Name		
Type	internal	
	<input type="checkbox"/> diffusible	<input type="checkbox"/> constitutive
Compartment	default	
Boundary Condition	false	
Constant	false	
Has Only Substance Units	true	
Units	(none)	
Conversion Factor	(none)	
Initial amount/concentration (ns)	default	0
Degradation rate (kd)	default	.0075
Extracellular degradation rate (kecd)	default	.005
Complex formation equilibrium (Kc)	default	0.05
Membrane diffusion rate (fd/rv) (kmdiff)	default	1.0/0.01
Extracellular diffusion rate (kecdiff)	default	1.0
SBOL Ribosome Binding Site	Associate SBOL	
SBOL Open Reading Frame	Associate SBOL	

Cancel Ok

SBOL in iBioSim



SBOL Extensions

- Visualization - appearance of a DNA component.
- Modeling - behavior of a DNA component.
- Experimental - experiments performed on a DNA component.
- Construction - method of assembly for a DNA component.
- Performance - characteristics for a DNA component.
- Host context - environment in which a DNA component can be used.

SBOL Visual Model



Forward Constitutive Promoter



Forward Repressible Promoter



Forward Inducible Promoter



Forward Translation Start Site



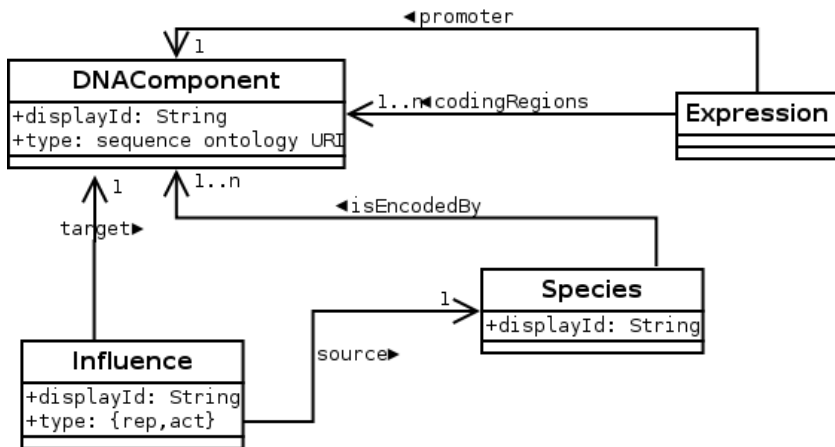
Forward Open Reading Frame



Forward Terminator

etc.

SBOL Modeling Extension (Preliminary)



Discussion

- Should SBOL be an SBML package?
- Should SBOL simply reference an SBML file?
- Should SBOL be invited to Combine/Harmony meetings?