Research Coordination Network for Systems and Synthetic Biology Standards

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Research Coordination Network

- In June, we submitted a proposal to NSF to establish a *research coordination network* (RCN) for systems and synthetic biology standards.
- The goal of this RCN is to facilitate the synthetic biology community in joining the system biology's COMBINE organization.
- RCN steering committee:
  - Chris Myers (Utah), Chair
  - Gary Bader (Toronto)
  - Douglas Densmore (Boston)
  - Mike Hucka (Caltech)
  - Nicolas Le Novère (Babraham)
  - Jacqueline Quinn (Google)
  - Herbert Sauro (Washington)
  - Falk Schreiber (Monash)
  - Dagmar Waltemath (Rostock)
  - Anil Wipat (Newcastle)

Focus of Research Coordination

- Specification infrastructure
- Metadata and annotations
- COMBINE archive
- SBOL Visual/SBGN
- SBOL/SBML/SED-ML
- SBOL/BioPAX
- Repositories
- Journals
- Compliance testing

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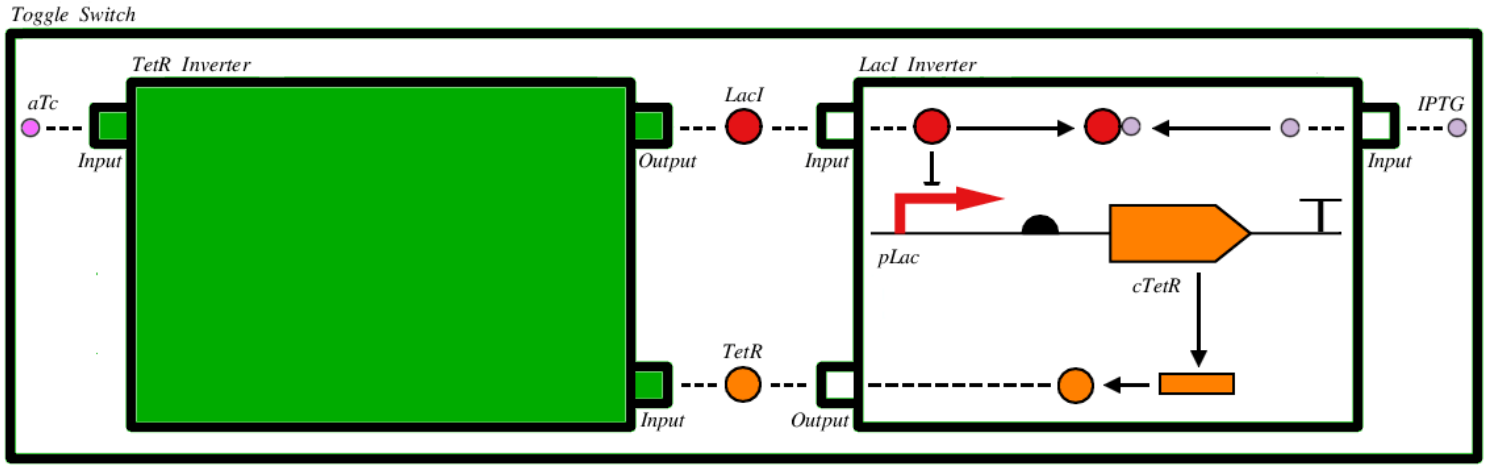
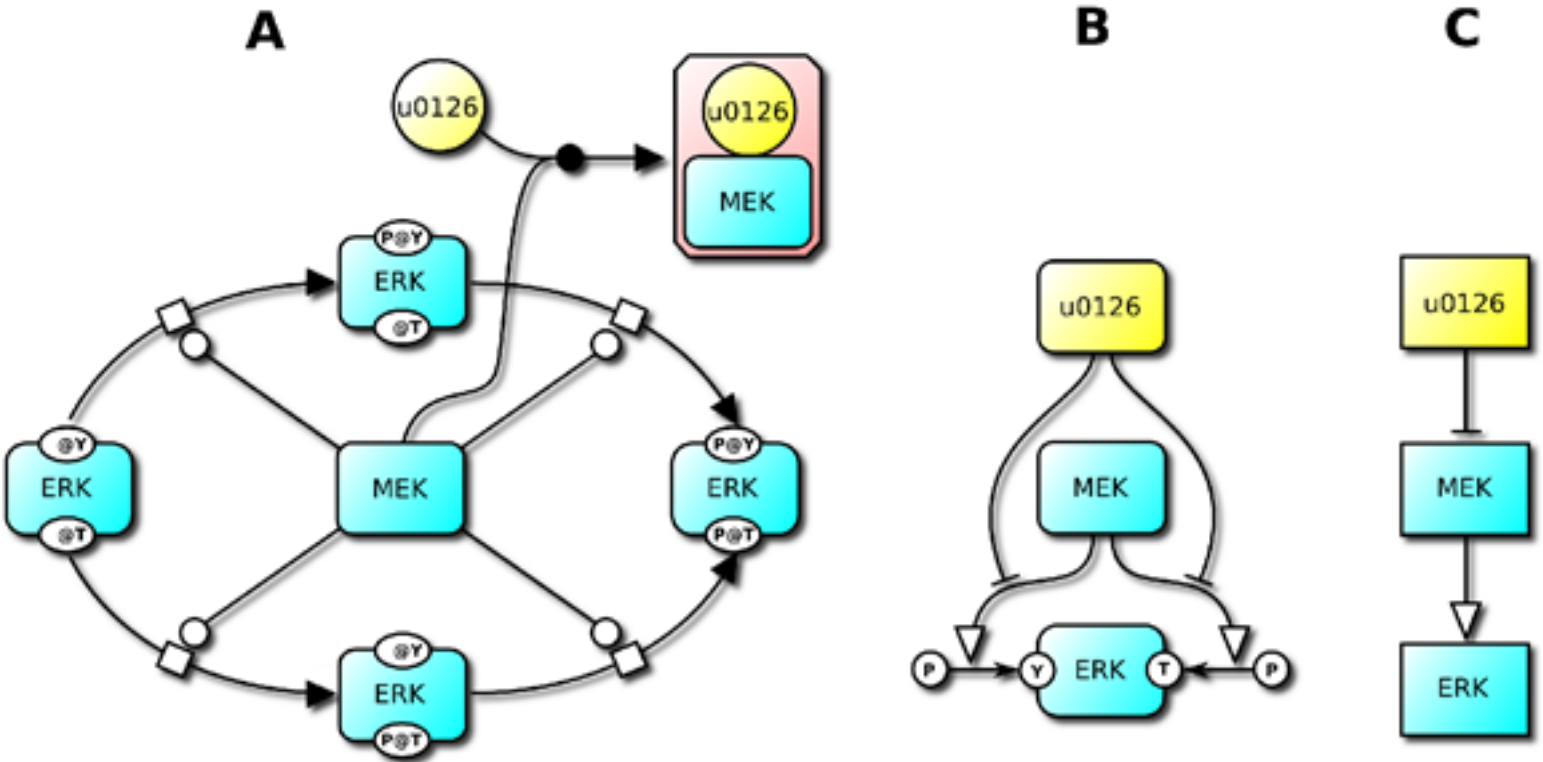
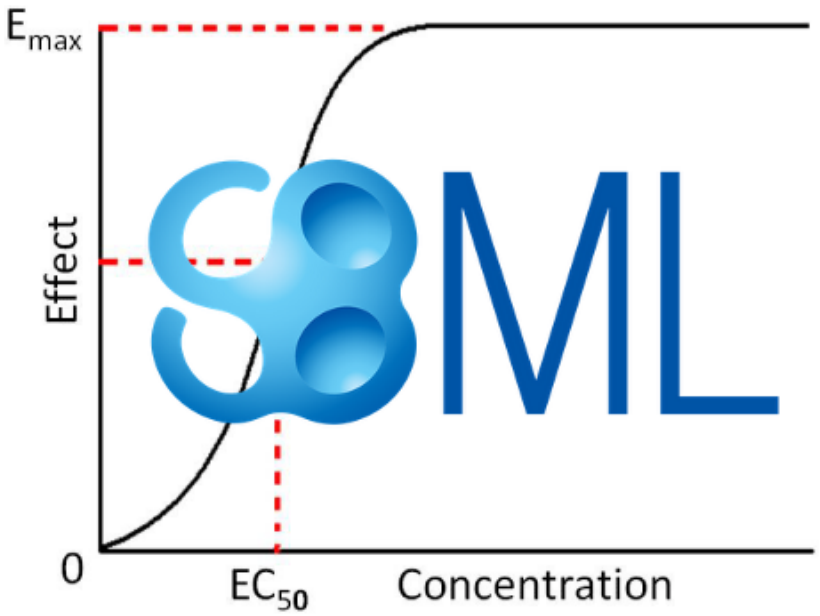
SBOL Visual/SBGN



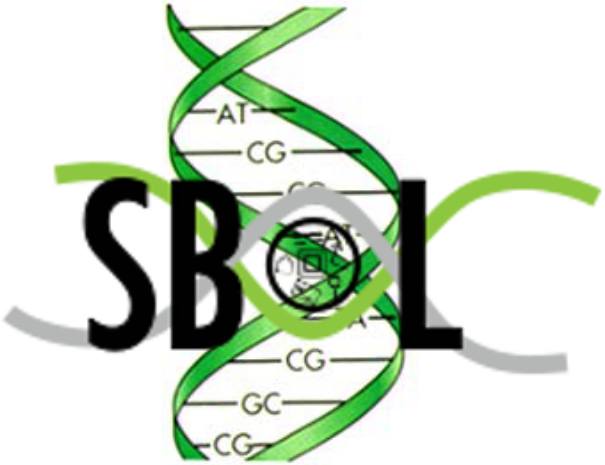


Connecting SBML to SBOL



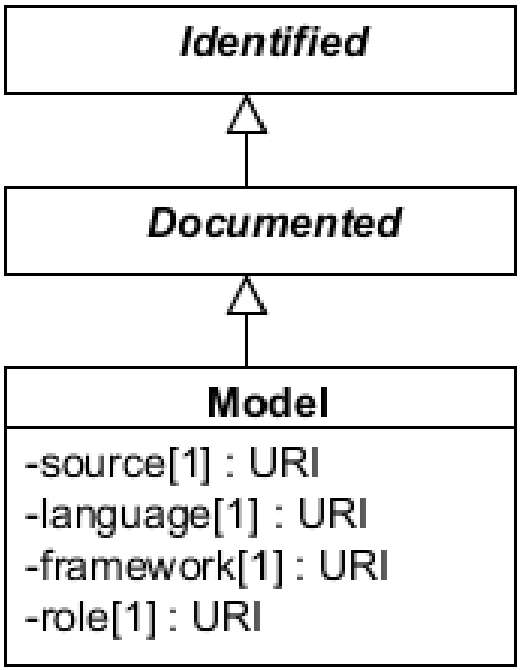
SBML

RDF/XML
Annotation



Roehner et al., ACS Synthetic Biology (2013).

Connecting SBOL to SBML

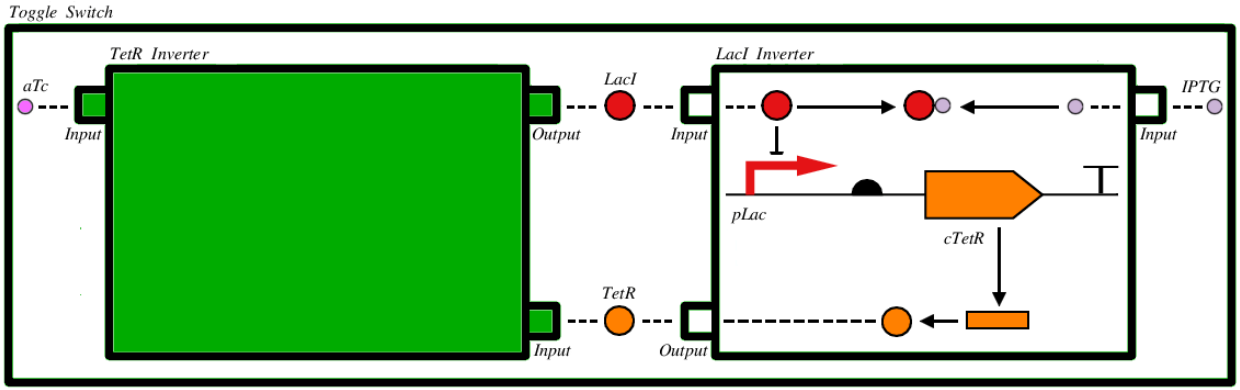


- *Source* is pointer to model file location.
- *Language* may be SBML, CellML, Matlab, etc.
- *Framework* is modeling formalism (ODE, stochastic, Boolean, etc.).
- *Role* is the purpose of the model.

SBOL/SBML/SED-ML: Discussion

- Are we happy with the methods proposed for connecting SBOL and SBML models?
- Where do we draw the line between SBOL functional information and SBML models?
- Should we be translating SBOL's functional information into SBML models or vice versa?

SBOL/BioPAX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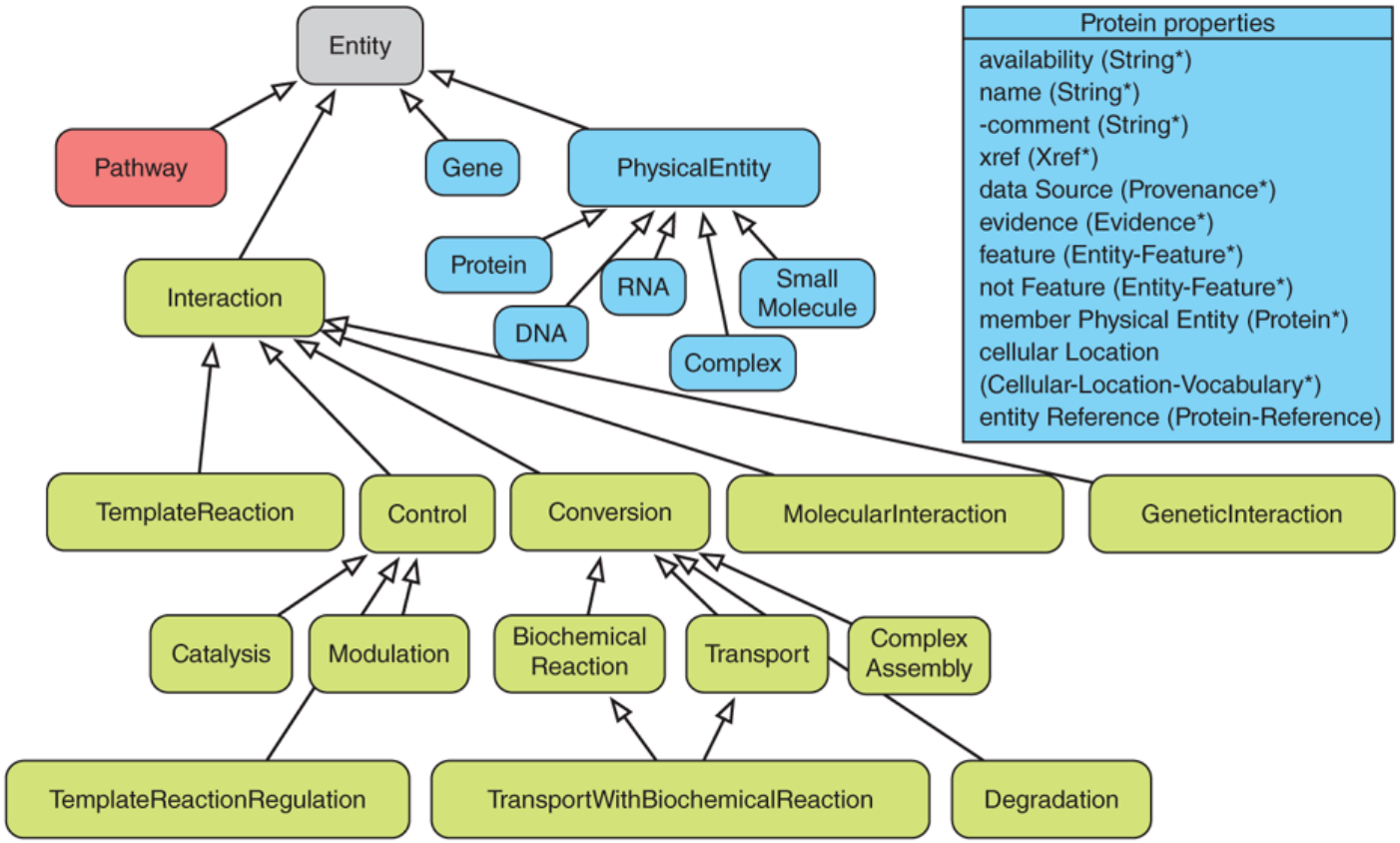
LacI Inverter
aTc
Input
Output
LacI
IPTG
pLac
cTetR
TetR


Entity
Pathway
Gene
PhysicalEntity
Protein
RNA
Small Molecule
DNA
Complex
Interaction
TemplateReaction
Control
Conversion
MolecularInteraction
GeneticInteraction
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Biochemical Reaction
Transport
Complex Assembly
TemplateReactionRegulation
TransportWithBiochemicalReaction
Degradation
Protein properties
availability (String*)
name (String*)
-comment (String*)
xref (Xref*)
data Source (Provenance*)
evidence (Evidence*)
feature (Entity-Feature*)
not Feature (Entity-Feature*)
member Physical Entity (Protein*)
cellular Location
(Cellular-Location-Vocabulary*)
entity Reference (Protein-Reference)

SBOL/BioPAX: Discussion

- Can translators be developed to extract interactions from BioPAX?
- Can interactions in SBOL be converted into BioPAX?
- Should SBOL refer to BioPAX records for the information eliminating the need for these interactions to be stored within the SBOL file at all?

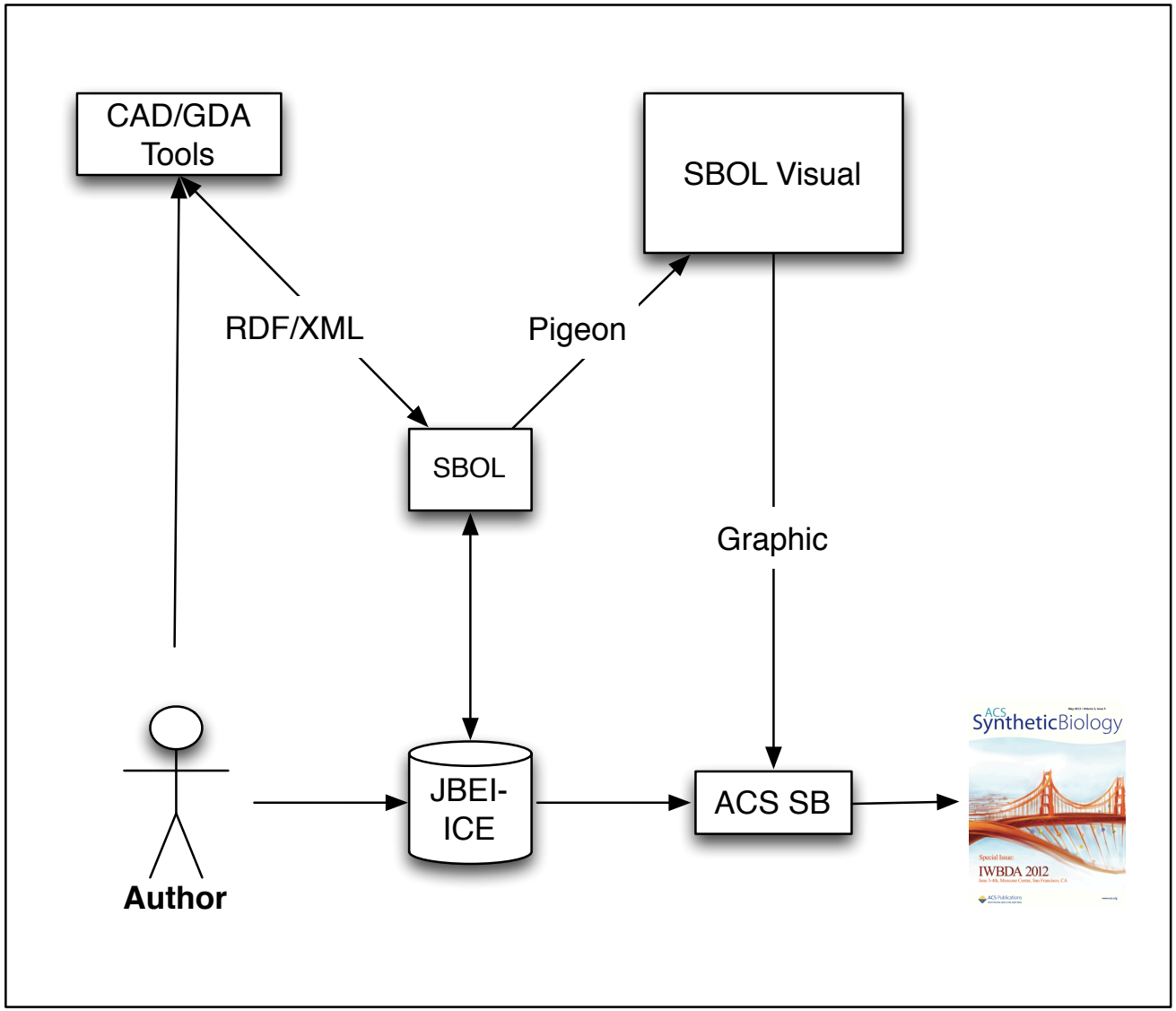
Repositories: Discussion

- Many repositories for separate standards:
  - Pathway Commons (BioPAX)
  - BioModels (SBML)
  - iGEM Registry, JBEI-ICE, SBOL-Stack (SBOL)
  - Virtual Parts (SBOL/SBML)
- It would be desirable to have a single interface enabling a user to obtain all the necessary data from one information portal.
- How might this work?

Journals

- The use of standards for DNA sequence data became commonplace when journals began to require them for publication.
- While there are journals that encourage the use of standards, such as SBML, for modeling, there are currently no journals that require it.
- In order to encourage journals to require these standard data representations, the impact on the authors must be minimized.
- We should have a user friendly portal to their repositories that enables authors to easily deposit their models and designs.
- These interfaces should allow authors to provide their information in an intuitive way while storing their information using an appropriate standard.
- This task is perhaps the one that has the potential to have the largest overall impact on the community.

SBOL and ACS Synthetic Biology



Journals: Discussion

- How do we convince journals to encourage (and ideally require) the use of standards?
- How can we make it easier for authors to use standards in their journal publications?
- What infrastructure is needed to support this effort?

Compliance Testing

- The challenge:
  - A standard should be broad enough to support users needs.
  - A standard should not be so broad that no tools support the standard.
- If a standard is too light, users complain they cannot encode their data.
- If a standard is too heavy, users complain that tools do not interoperate.
- In both cases, the standard is blamed, but this is really a tool problem.
- A possible solution is *compliance testing*.

Compliance Testing: Discussion

- What does it mean for a tool to support a standard?
- How do we encourage tool developers to fully support a standard?
- How do we collect data on the degree of standard support by tools?
- How do we advertise this information?
- Should COMBINE sanction workflows known to work?

Final Question

- Are there other areas where systems and synthetic biology can coordinate their efforts?