

# Software Infrastructure for Synthetic Biology

Zhen Zhang, Tramy Nguyen, Chris Myers
Department of Electrical and Computer Engineering
University of Utah

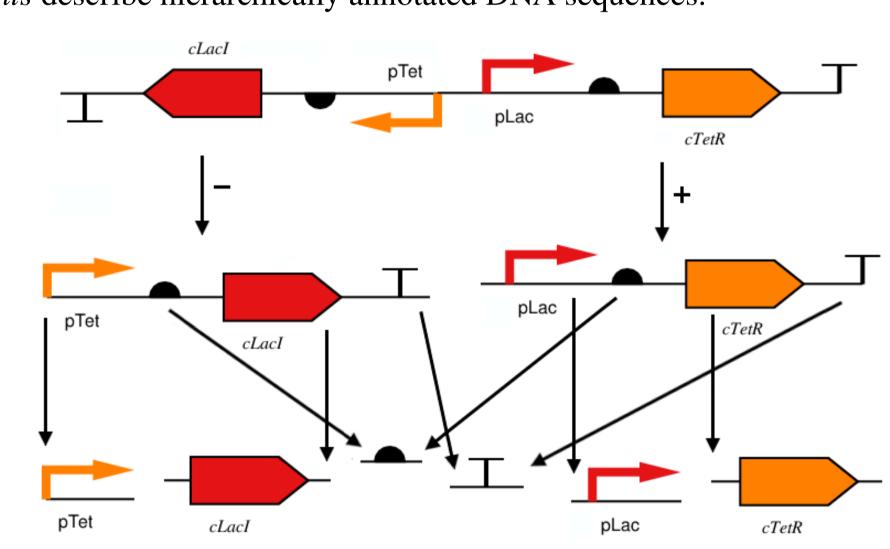


## **Introduction and Motivation**

- Synthetic biology is an engineering discipline where biological components are assembled to form devices or systems with more complex functions [1].
- It includes the following three main aspects:
- Standards define a data representation format for encoding synthetic biology designs.
- Abstraction allows users to focus on high-level designs without worrying about low-level details.
- Decoupling separates the design using software tools from building biological components.
- Missing sequence information in the synthetic biology literature precludes reproducibility and reuse of the published work [3].
- Encoding designs in a restricted standardized format allows different software tools to exchange models and store them for reproducibility and reuse of the past work.
- The infrastructure provided by libSBOLj enables integration of SBOL standards in software tools.

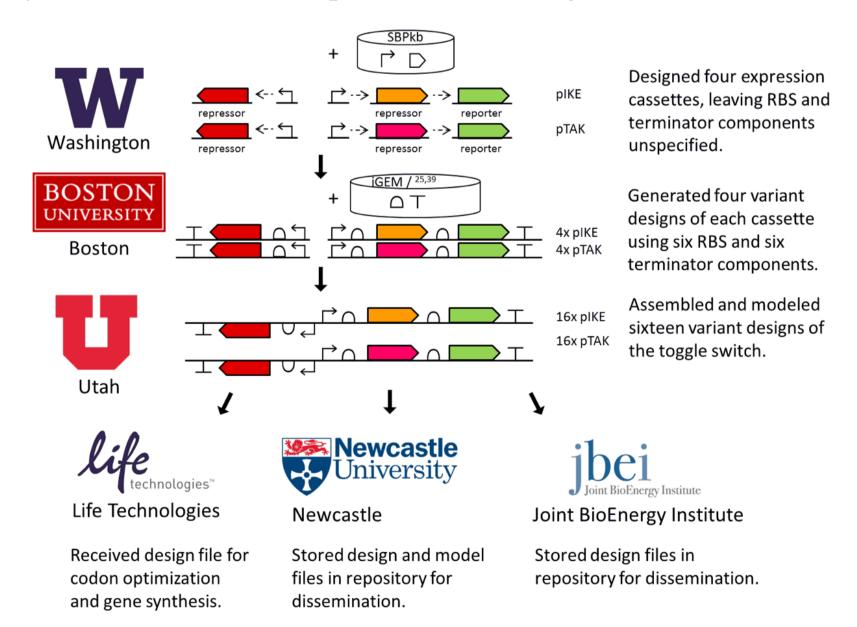
# Synthetic Biology Open Language (SBOL)

- SBOL is a standard electronic data format for exchanging synthetic biology designs.
- Since 2008, SBOL has been developed under an international effort from both experimental and computational synthetic biologists.
- The SBOL 1.1 core data model enables specifications of DNA-level designs [1].
- SBOL 1.1 represents biological building blocks as DNA components.
- DNA components describe hierarchically annotated DNA sequences.



Hierarchical composition of the DNA component for a genetic toggle switch in SBOL Version 1.1.

• Encoding a genetic toggle switch [2] in SBOL 1.1 allows the design to be assembled, optimized, tested, and stored by software tools developed at different organizations.

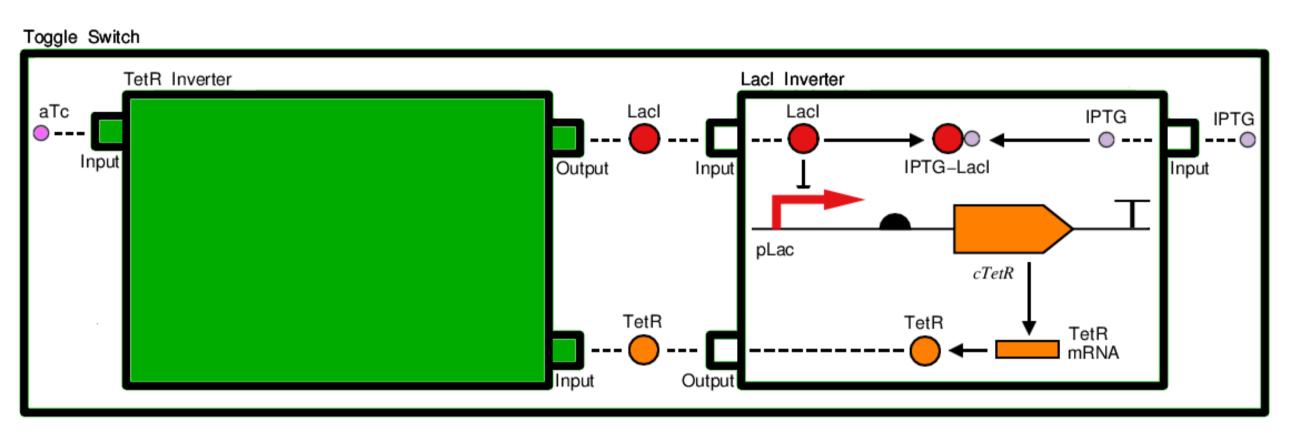


Demonstration of a collaboration to design a genetic toggle switch.

• It demonstrates the potential for collaborative work on complex synthetic biology designs.

## **SBOL 2.0**

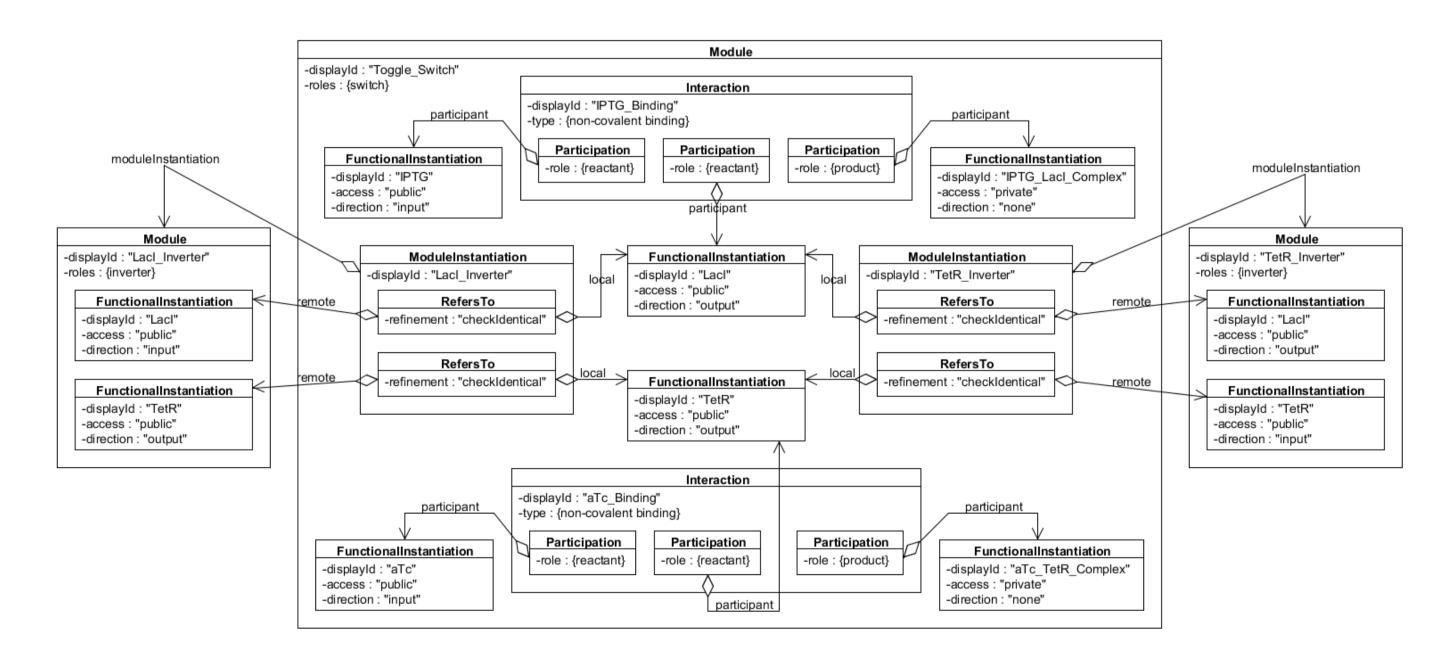
- The SBOL 2.0 proposal [4] allows specifications of more types of *components*, such as DNA, RNA, proteins, small molecules, etc.
- Interactions represent relationships between components, such as activation, repression, complex formation, etc.
- A module groups several interactions to represent a useful functional block.
- A module can be connected to an informative external behavioral *model* represented in a different language (i.e., SBML, CellML, Matlab, etc.).
- SBOL 2.0 includes constructs to hierarchical module definitions.



Hierarchical toggle switch module in SBOL 2.0.

# libSBOLj 2.0

- libSBOLj 2.0 is a native Java implementation of SBOL 2.0 data structure.
- It provides an API for tool developers to interact with SBOL data objects.
- Serialization of libSBOLj 2.0 has also been implemented.
- Users are able to read/write SBOL 2.0 files.
- SBOL 1.1 can be converted to SBOL 2.0 files.
- Serialization can support RDF/XML, Turtle, and JSON formats.
- Methods are available for data operations (i.e., creating, storing, accessing, nesting, etc.).
- It includes detailed documentation for class definitions and methods in the API.
- The goal for the library development is to ease the adoption of SBOL 2.0 by tool developers.



Hierarchical UML model of a toggle switch in SBOL 2.0.

```
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  </sbol:Collection>
  <sbol:ModuleDefinition rdf:about="http://www.async.ece.utah.edu/LacI_Inv/1/0">
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    </sbol:interaction>
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```

#### **Discussion**

<?xml version="1.0" ?>

- Standards are important in the synthetic biology field.
- SBOL 1.1 is limited to only describing components constructed from DNA.
- SBOL 2.0 introduces more generalized components, the interactions between them, and hierarchical module that group components implementing a desired function.
- A java based library of SBOL 2.0 has been implemented (libSBOLj 2.0).
- Additional functions and error checking routines continue to be added to ease adoption of SBOL 2.0.
- Please see: http://www.sbolstandard.org/

### References

- [1] M. Galdzicki, K. P. Clancy, E. Oberortner, M. Pocock, J. Y. Quinn, C. A. Rodriguez, N. Roehner, M. L. Wilson, L. Adam, J. C. Anderson, B. A. Bartley, J. Beal, D. Chandran, J. Chen, D. Densmore, D. Endy, R. Gruenberg, J. Hallinan, N. J. Hillson, J. D. Johnson, A. Kuchinsky, M. Lux, G. Misirli, J. Peccoud, H. A. Plahar, E. Sirin, G-B. Stan, A. Villalobos, A. Wipat, J. H. Gennari, C. J. Myers, and H. M. Sauro. The synthetic biology open language (sbol) provides a community standard for communicating designs in synthetic biology. *NATURE BIOTECHNOLOGY*, 32:545–550, 2014.
- [2] T. S. Gardner, C. R. Cantor, and J. J. Collins. Construction of a genetic toggle switch in *escherichia coli*. *Nature*, 403:339–342, 2000.
- [3] J. Peccoud, J. C. Anderson, D. Chandran, D. Densmore, M. Galdzicki, M. W. Lux, C. A. Rodriguez, G-B. Stan, and H. M. Sauro. Essential information for synthetic DNA sequences. *Nature Biotechnology*, 29(1):22–22, Jan 2011.
- [4] N. Roehner, E. Oberortner, M. Pocock, J. Beal, K. Clancy, C. Madsen, G. Misirli, A. Wipat, H. Sauro, and C. J. Myers. Proposed data model for the next version of the synthetic biology open language. *ACS Synthetic Biology*, 4(1):57–71, 2015. PMID: 24896221.