

Synthetic Biology Open Language



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NonaTalks, July 17th, 2016

Chicago, IL

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SBOL Development Group: 120 members from more than 50 academic and industrial organizations.

- Three foundational principles of synthetic biology based on engineering practice (Endy 2005):
 - **Standardization**
 - **Abstraction**
 - **Decoupling**
- Synthetic biology was born with the broad goal of engineering or 'wiring' biological circuitry — be it genetic, protein, viral, pathway or genomic — for manifesting logical forms of cellular control. (Collins 2010)
- Biology has long surpassed its mainly descriptive stage, and the questions now asked are increasingly amenable to experimental approaches and theoretical concepts taken from the physical and engineering sciences. (Scwhille 2011)

Standards are a foundational principle of synthetic biology

What is SBOL?

SBOL actually consists of 2 standards:

- **SBOL Data model**
 - a formalized representation of data objects
- **SBOL Visual**
 - a standardized set of schematic symbols for genetic design

To guarantee interoperability between tools and standards, SBOL leverages **ontologies**, such as the Sequence Ontology (SO), Systems Biology Ontology (SBO).

Milestones in the history of SBOL

Apr, 2008

Kick-off at a computational synthetic biology workshop at the University of Washington

Jun, 2011

The **SBOL Developers Group** was officially established with adoption of formal rules of governance and election of editors

Sep, 2011

First version of the **SBOL data model** was released
(BB FRFC 84)

Mar, 2013

First version of the **SBOL Visual** standard was released
(BBF RFC 93)

Jul, 2015

SBOL Version 2.0 was officially released
(BBF RFC 108)

Jun, 2016

ACS Synthetic Biology adopts **SBOL** as publication standard

Evolution of standards for Bioinformatics

FASTA

Raw sequence information

ACTGTGCCGTAAACGTGATTAAATCCGTACTGATAT...

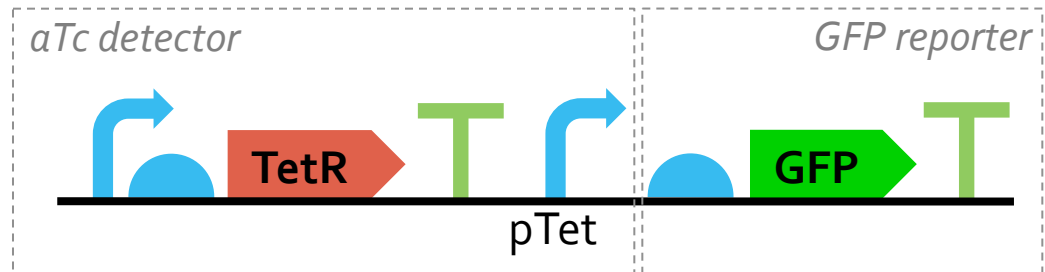
GenBank

Contains sequence features



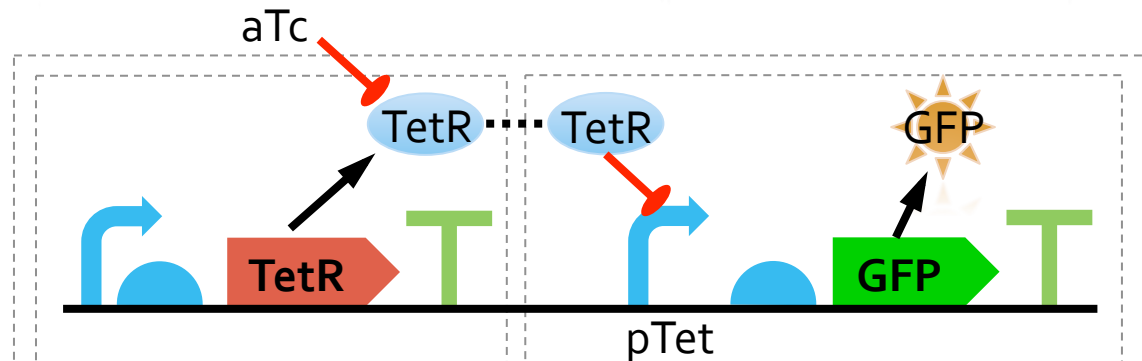
SBOL 1.1

Represents sequence features hierarchically



SBOL 2.0

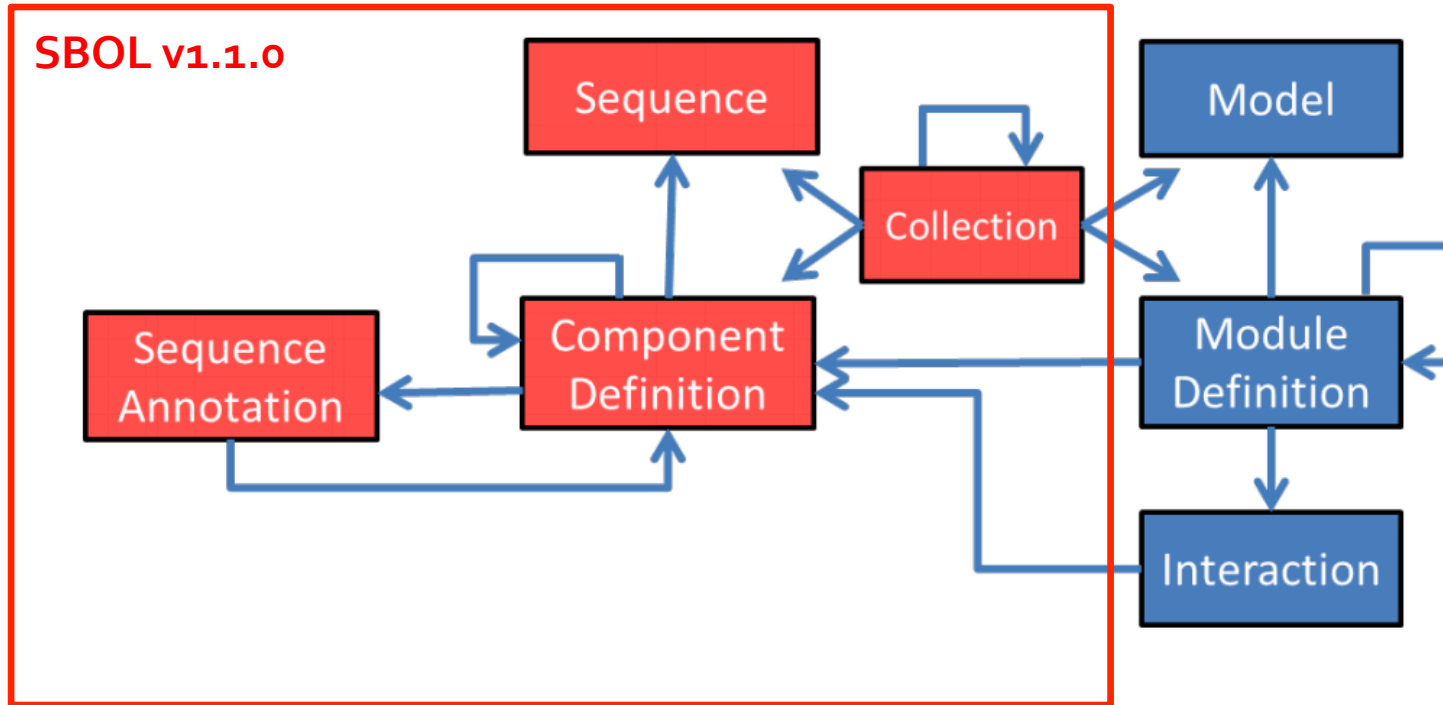
- Represents additional molecule types
- Represents modules with inputs and outputs






















SBOL Data Model

SBOL v2.0.0

SBOL v1.1.0

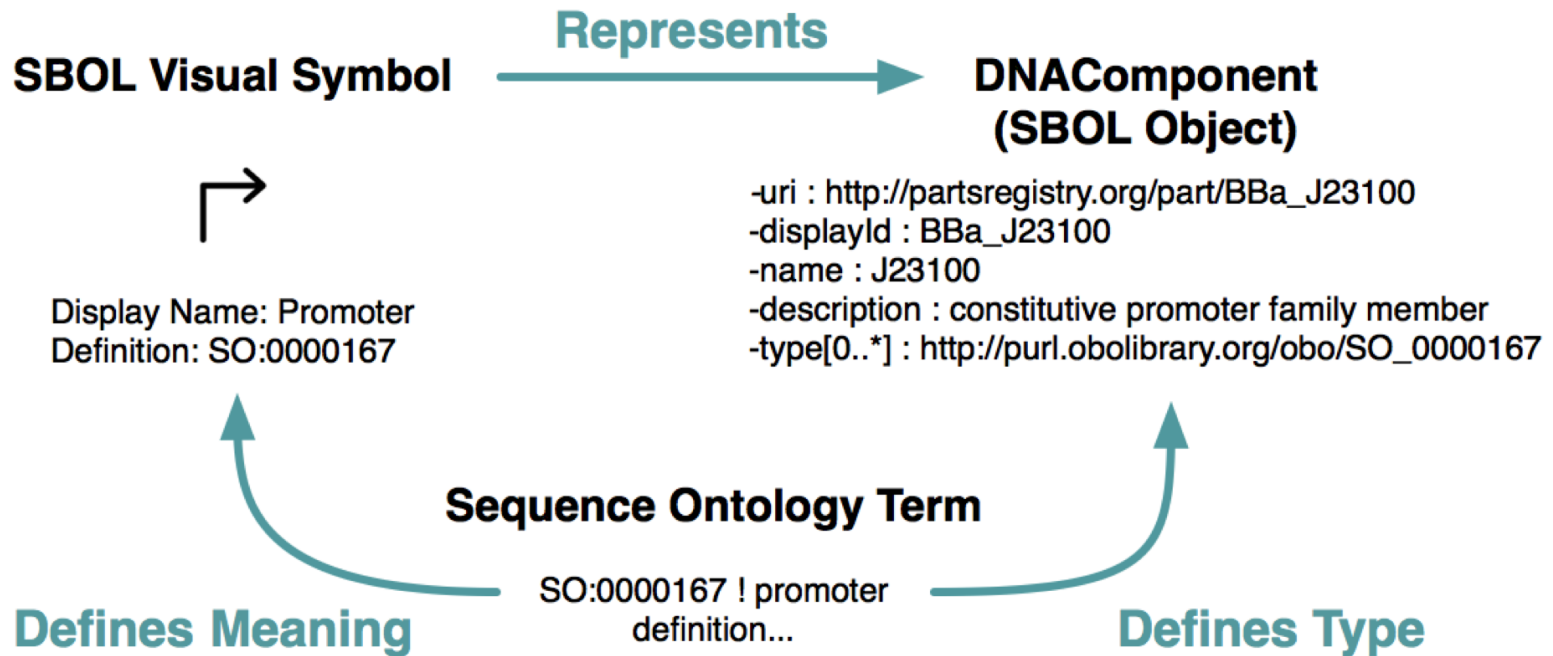


SBOL Visual v1.0.0

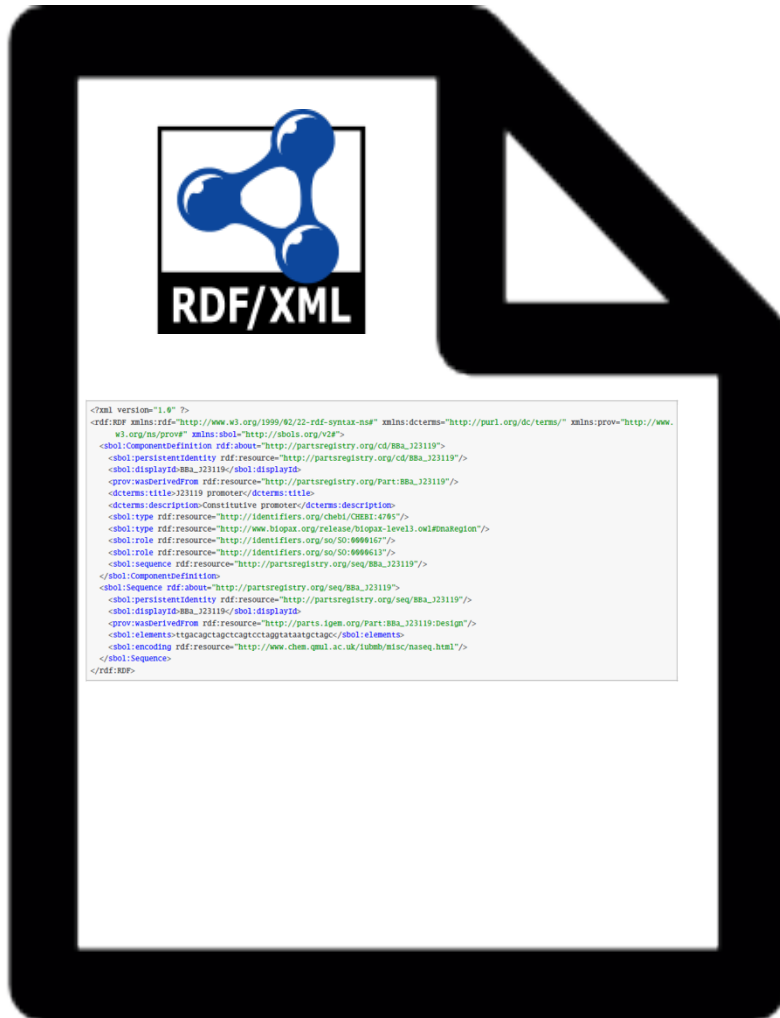
| | |
|---|---|
|  promoter |  origin of replication |
|  cds |  primer binding site |
|  ribosome entry site |  blunt restriction site |
|  terminator |  sticky restriction site |
|  operator |  5' overhang |
|  insulator |  3' overhang |
|  ribonuclease site |  assembly scar |
|  rna stability element |  signature |
|  protease site |  user defined |
|  protein stability element | |

Quinn et al., PLoS Biology (2015)

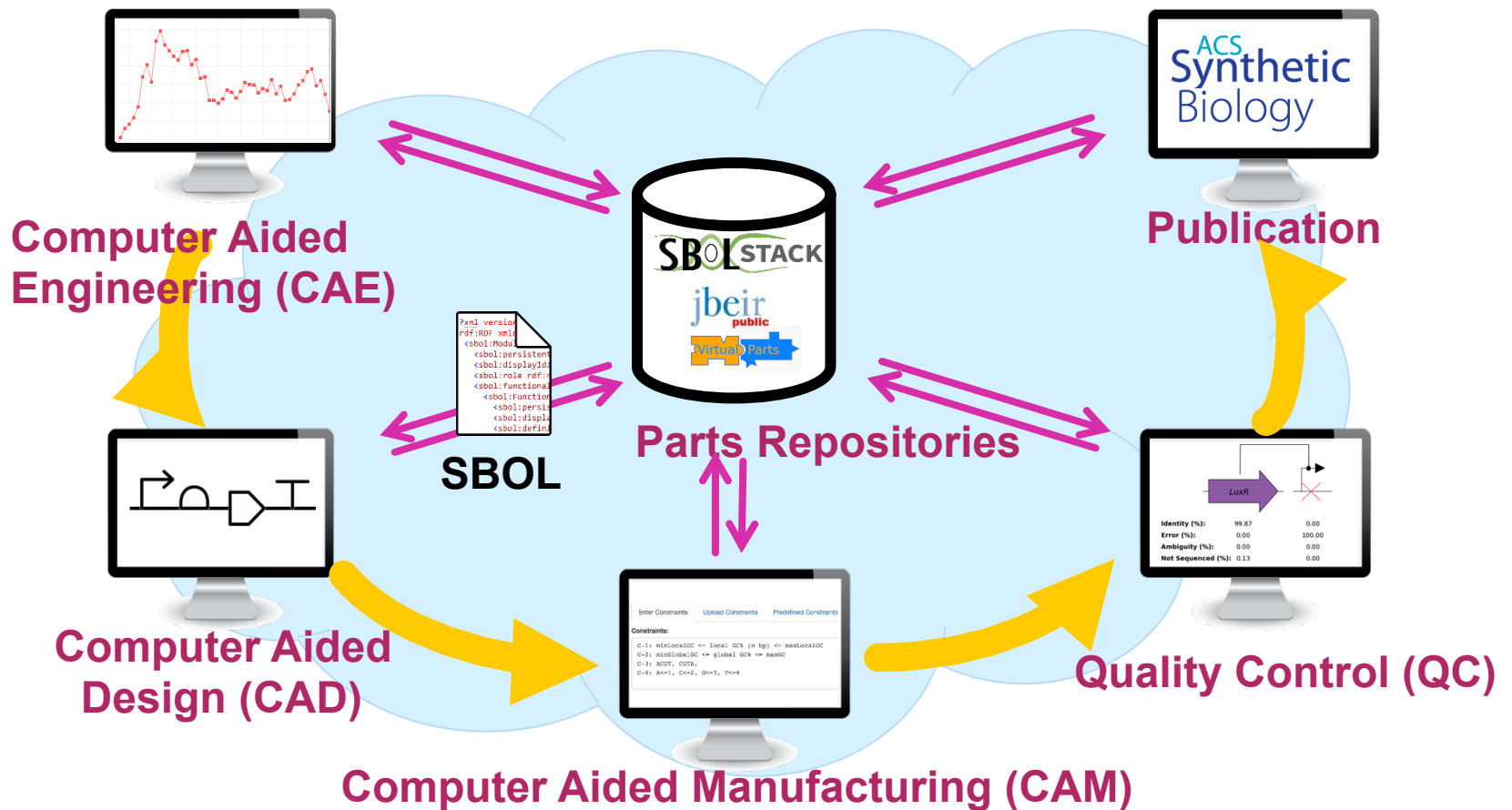
Relation between SBOL Visual and SBOL Data Model



SBOL is serialized in RDF/XML Format

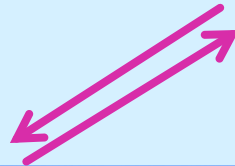


- XML allows data to be structured in hierarchical trees, is well-supported and well-understood by software developers
- RDF makes data integration across networks easier

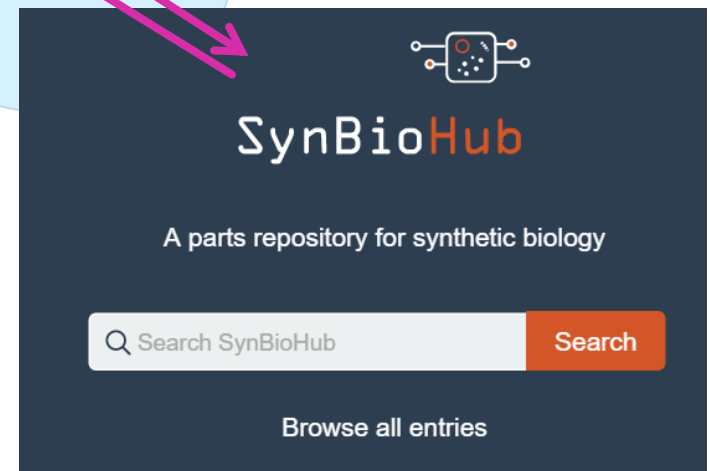
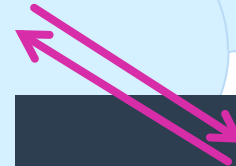


Share and re-use biological parts with repositories

- Search for parts through a web interface or programmatically
- Journal integration for "one-click" private review
- Import SBOL/FASTA/GenBank, Export SBOL



```
StackFrontend frontend = new StackFrontend(stackURI);  
ComponentDefinition def = frontend.fetchComponent(componentURI);
```



The SBOL Stack: A Platform for Storing, Publishing, and Sharing Synthetic Biology Designs

Curtis Madsen, James Alastair McLaughlin, Göksel Mısırlı, Matthew Pocock, Keith Flanagan, Jennifer Hallinan, and Anil Wipat
ACS Synthetic Biology **2016** 5 (6), 487-497
DOI: 10.1021/acssynbio.5b00210

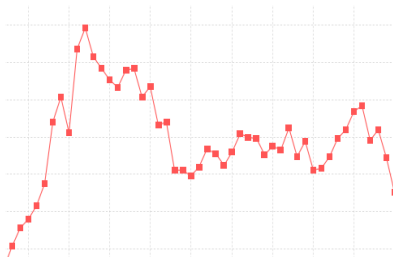
Computer Aided Engineering (CAE)

Forward-engineering Biological Systems

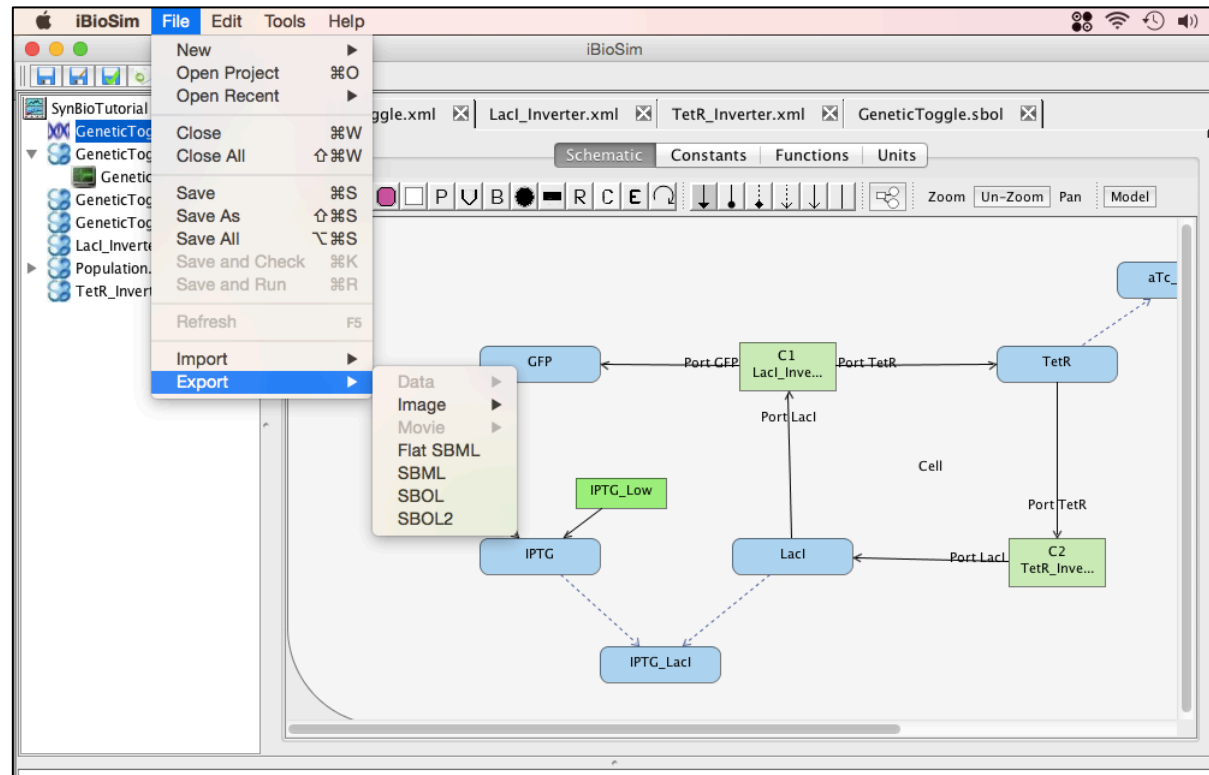
iBioSim

www.async.ece.utah.edu/ibiosim/

- Graphical design of reaction networks
- Simulate ordinary differential equations (ODEs), SSA (Stochastic Simulation Algorithm)



- Import or export both SBML and SBOL 2.0



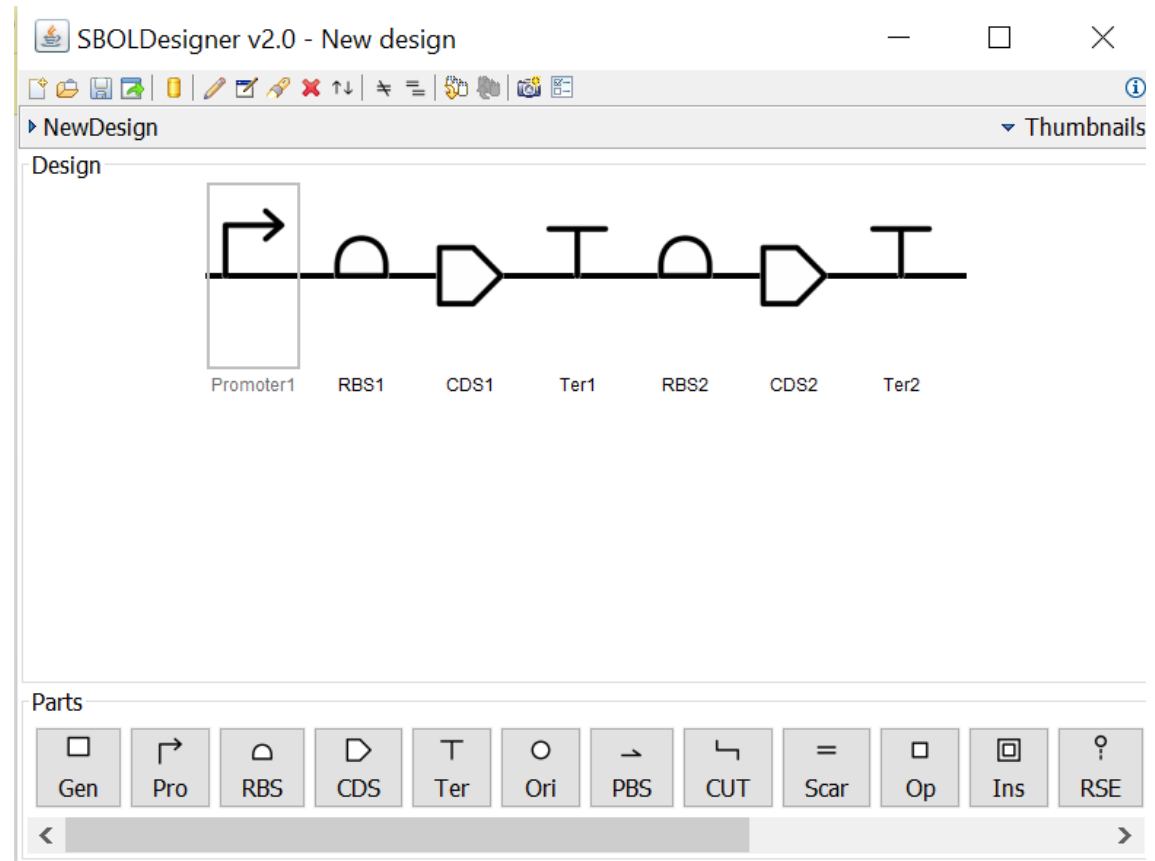
Computer Aided Design (CAD)

Sequence assembly without cutting and pasting

SBOLDesigner

www.async.ece.utah.edu/SBOLDesigner/

- Connect to parts repositories in the cloud
- Design hierarchical sequences
- Switch between nucleotide and schematic representations



Computer Aided Manufacturing (CAM)

Design sequences for DNA synthesis

<https://boost.jgi.doe.gov>

Build-Optimization Software Tools (BOOST)

- Scans a sequence against DNA synthesis constraints (eg, repeats, %GC content, hairpins)
- Makes necessary corrections (if desired)
- Partitions sequences into synthesizable building blocks
- Import/Export as FASTA, GenBank, or SBOL



Select Task:

☐ Detect

☒ Polish

Sequences

Enter Sequence(s)

Upload Sequence(s)

Select a file:

Choose File sequences.sbol

Accepted Formats:

- FASTA
- GenBank
- SBOL
- CSV

SBOL

Synthesis Constraints

Predefined Vendors:

DOE Joint Genome Institute

[Disclaimer](#)

Output Sequences

Original

Modified

Logs

Downloads

- [Download original sequences](#)
- [Download modified sequences](#)
- [Download log of modifications file](#)

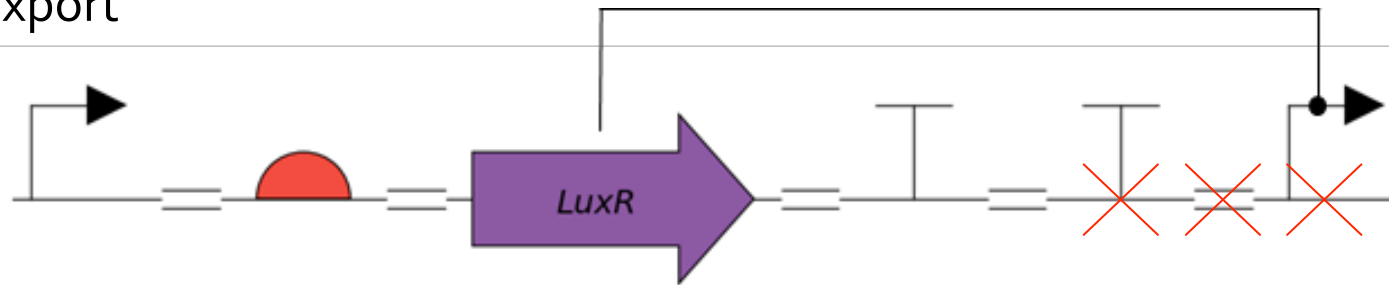
Quality Control (QC)

Automated screening and failure analysis of DNA constructs

SBOL-QC

- Python package for creating automated quality control reports
- SBOL import/export

<https://github.com/SynBioDex/SBOL-QC>



| | | | | | | | | | | | |
|---------------------------|--------|--------|--------|--------|-------|--------|-------|--------|-------|--------|--------|
| Identity (%): | 100.00 | 100.00 | 100.00 | 100.00 | 99.87 | 100.00 | 91.25 | 100.00 | 12.20 | 0.00 | 0.00 |
| Error (%): | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 85.37 | 100.00 | 100.00 |
| Ambiguity (%): | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Not Sequenced (%): | 0.00 | 0.00 | 0.00 | 0.00 | 0.13 | 0.00 | 8.75 | 0.00 | 2.44 | 0.00 | 0.00 |

<https://github.com/SynBioDex/dnaplotlib>

Open Source Libraries

Software libraries which import and export SBOL files are freely available at the [Synthetic Biology Data Exchange](#) on GitHub under the Apache 2.0 license. Libraries are implemented in:

- [Java](#)
- [Javascript](#)
- [C/C++](#)
- [Python](#)

Developer support includes (see <http://sbolstandard.org/software/libsbol>)

- Online documentation
- Getting started tutorials
- Sample projects
- Code examples

ACS Synthetic Biology has officially adopted SBOL as publication standard

- **SBOL Visual** is the recommended graphical notation for depicting genetic constructs
- **SBOL 2.0 Data Model** is the preferred format for nucleic acid sequences.
- Manuscript submission, review, and production process is linked to SBOL-enabled repositories
- **Joint Bioenergy Institute (JBEI)** has set up an initial repository to be integrated.

Read all about it in the ACS Synthetic Biology viewpoint article:
[Improving Synthetic Biology Communication: Recommended Practices for Visual Depiction and Digital Submission of Genetic Designs](#), or
[listen to the interview with Jake Beal and Nathan Hillson](#).

Read more about SBOL (feel free to contact authors for an unedited manuscript)

"Improving Synthetic Biology: Recommended Practices for Visual Depiction and Digital Submission of Genetic Designs", *ACS Synthetic Biology*, vol. 5, no. 6, pp. 449-451, Jun. 2016. [doi: 10.1021/acssynbio.6b00146](https://doi.org/10.1021/acssynbio.6b00146)

"Sharing structure and function in biological design with SBOL 2.0," *ACS Synthetic Biology*, vol. 5, no. 6, pp. 498-506, Apr. 2016. [doi: 10.1021/acssynbio.5b00215](https://doi.org/10.1021/acssynbio.5b00215)

"libSBOLj 2.0: A Java Library to Support SBOL 2.0," *IEEE Life Sciences Letters*, vol. 1, no. 4, pp. 34-37, Mar. 2016. doi:[10.1109/LLS.2016.2546546](https://doi.org/10.1109/LLS.2016.2546546)

"SBOL Visual: A Graphical Language for Genetic Designs," *PLoS Biol*, vol. 13, no. 12, Dec. 2015. [doi:10.1371/journal.pbio.1002310](https://doi.org/10.1371/journal.pbio.1002310)

Visit us at
sbolstandard.org

Join SBOL!

To join our group contact the editors at:
sbol-editors@googlegroups.com

There will be a one-day workshop to introduce software developers to SBOL on August 15th, 2016. The workshop will be held immediately before the [International Workshop for Bio-design Automation](#) (IWBDa) at Newcastle University, Newcastle-upon-Tyne, UK.

The next official SBOL workshop will be held concurrent with the COMBINE workshop in Newcastle-upon-Tyne, UK in September 19 -23, 2016.
http://co.mbine.org/events/COMBINE_2016

Acknowledgments



SBOL Stack



SBOL-QC

DNAPlotlib



iBioSim



BOOST



SBOLDesigner

