

Welcome to the Synthetic Biology Open Language (SBOL) Developers Workshop

Newcastle University
Newcastle Upon Tyne
August 2016

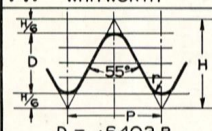
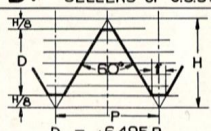
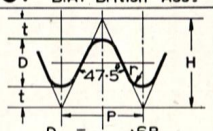

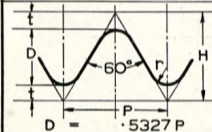
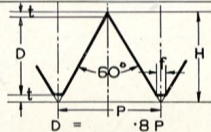
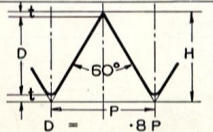
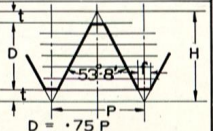
Programme

- 09:00-09:30 Overview of SBOL – Anil Wipat
- 09:30-10:00 SBOL Visual – Jake Beal
- 10:00-11:00 SBOL Data Model – Chris Myers
- 11:00-11:30 Coffee
- 11:30-12:00 SBOL Tools and Resources
 - SBOLStack / SBOL Shorthand / VisBOL – James McLaughlin
 - SBOLDesigner / iBioSim – Michael Zhang
 - SBOL Validator / ICE – Zach Zundel
- 12:00-01:00 Libraries
 - Java library – Chris Myers
 - JavaScript library – James McLaughlin
 - C++ & Python libraries – Bryan Bartley
- 13:00-14:00 Lunch
- 14:00-15:30 SBOL Tutorial (CRISPR/CAS9 example) – Meher Samineni
- 15:30-16:00 Coffee
- 16:00-17:30 User problems – Anil Wipat (moderator)
- 19:00 Dinner









SBOL – promoting data sharing and exchange in Synthetic Biology

Anil Wipat (on behalf of the SBOL community)
ICOS, Computing Science, Centre for Synthetic Biology
and BioEconomy, Newcastle University
UK
(ico2s.org)

Standards

THREAD FORMS.			
A. WHITWORTH  $D = .6403 P$ $H = .9605 P$ $H/8 = .1600 P$ $r = .1373 P$	B. SELLERS or U.S.S.  $D = .6495 P$ $H = .8660 P$ $H/8 = .108 P$ $f = .125 P = P/8$	C. B.A. British Ass'd  $D = .6 P$ $H = .136 P$ $t = .268 P$ $r = .182 P$	D. S.I. Système International.  $D = .6495 P$ $H = .8660 P$ $H/8 = .108 P$ $a = .05 P$ $f = .125 P$ $r = .058 P$
E. C.E.I. Cycle Eng'g Institute.  $D = .5327 P$ $H = .8660 P$ $t = P/6 = .166 P$ $r = P/6 = .166 P$	F. VEE American Sharp Vee.  $D = .8 P$ $H = .8660 P$ $t = .033 P$ $f = .04 P$	G. BRIGGS PIPE.  $D = .8 P$ $H = .8660 P$ $t = .033 P$ Taper = $3/4$ " per foot.	H. LÖWENHERZ.  $D = .75 P$ $H = P$ $t = P/8 = .125 P$ $f = P/8 = .125 P$



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Standards

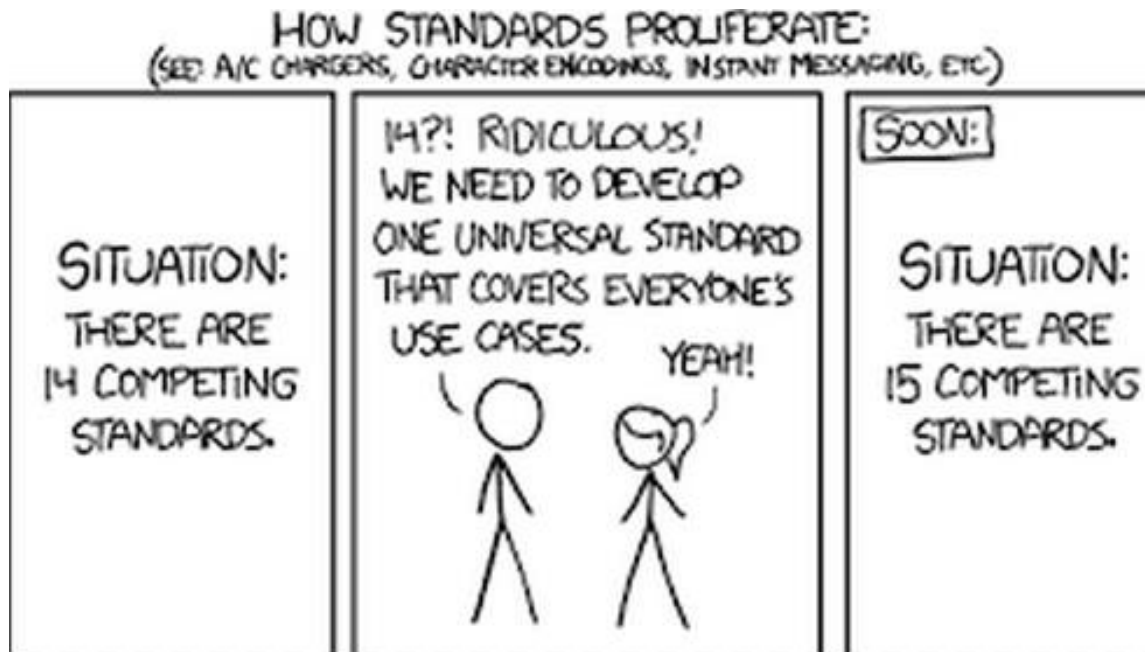


The nice thing about standards is that there are so many of them to choose from.

(Andrew S. Tanenbaum)

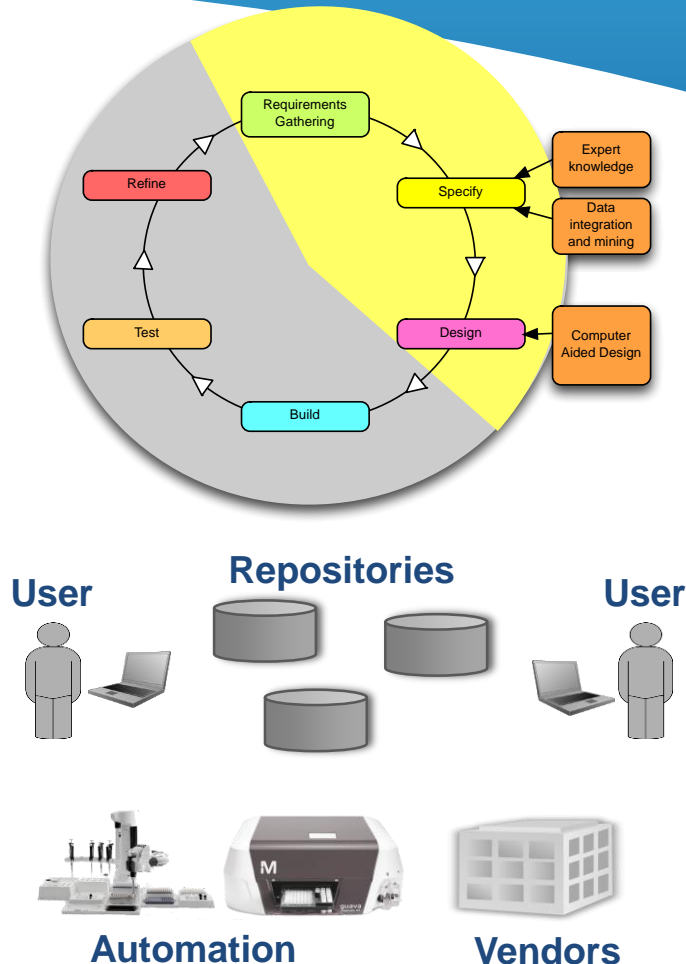
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Standards



What is SBOL – why is it needed?

- * Synthetic Biology is engineering biology
- * Requires movement of data & information
 - * Between people, software & machines
 - * Across geographic and political boundaries
- * Standards needed to ensure interoperability
- * SBOL - a standard way to represent information about synthetic biology designs



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libSBOLjs, libSBOLC, etc.

Essential information for synthetic DNA sequences

To the Editor:

Following a discussion by the workgroup for Data Standards in Synthetic Biology, which met in June 2010 during the Second Workshop on Biodesign Automation in Anaheim, California, we wish to highlight a problem relating to the reproducibility of the synthetic biology literature. In particular, we have noted the very small number of articles reporting synthetic gene networks that disclose the complete sequence of all the constructs they describe.

To our knowledge, there are only a few examples where full sequences have been released. In 2005, a patent application¹ disclosed the sequences of the toggle switches published four years earlier in a paper by Gardner *et al.*². The same year, Basu *et al.*³ deposited their construct sequences for programmed pattern formation into GenBank³. Examples of synthetic DNA sequences derived from standardized parts that have been made available in GenBank include the refactored genome of the bacteriophage

gaps between key components are almost never reported, presumably because they are not considered crucial to the report. Yet, synthetic biology relies on the premise that synthetic DNA can be engineered with base-level precision.

Missing sequence information in papers hurts reproducibility, limits reuse of past work and incorrectly assumes that we know fully which sequence segments are important. For example, many synthetic biologists are currently realizing that translation initiation rates are dependent on more than the Shine-Dalgarno sequence⁴. Sequences upstream of the start codon are crucial for translation rates, yet are underreported. Similarly, it has been demonstrated that intron length can affect the dynamics of genetic oscillators⁵. Many more such examples are likely to emerge.

Because full sequence disclosure is critical, we wonder why the common requirement by many journals to provide GenBank entries for genomes and natural sequences has

and welcome contributions from the greater community.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

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e-mail: peccoud@vt.edu

1. Gardner, T.S. & Collins, J.J. US patent 6,841,376 (2005).
2. Gardner, T.S., Cantor, C.R. & Collins, J.J. *Nature* **403**, 339–342 (2000).
3. Basu, S., Gerchman, Y., Collins, C.H., Arnold, F.H. & Weiss, R. *Nature* **434**, 113–118 (2005).



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SBOL v 1



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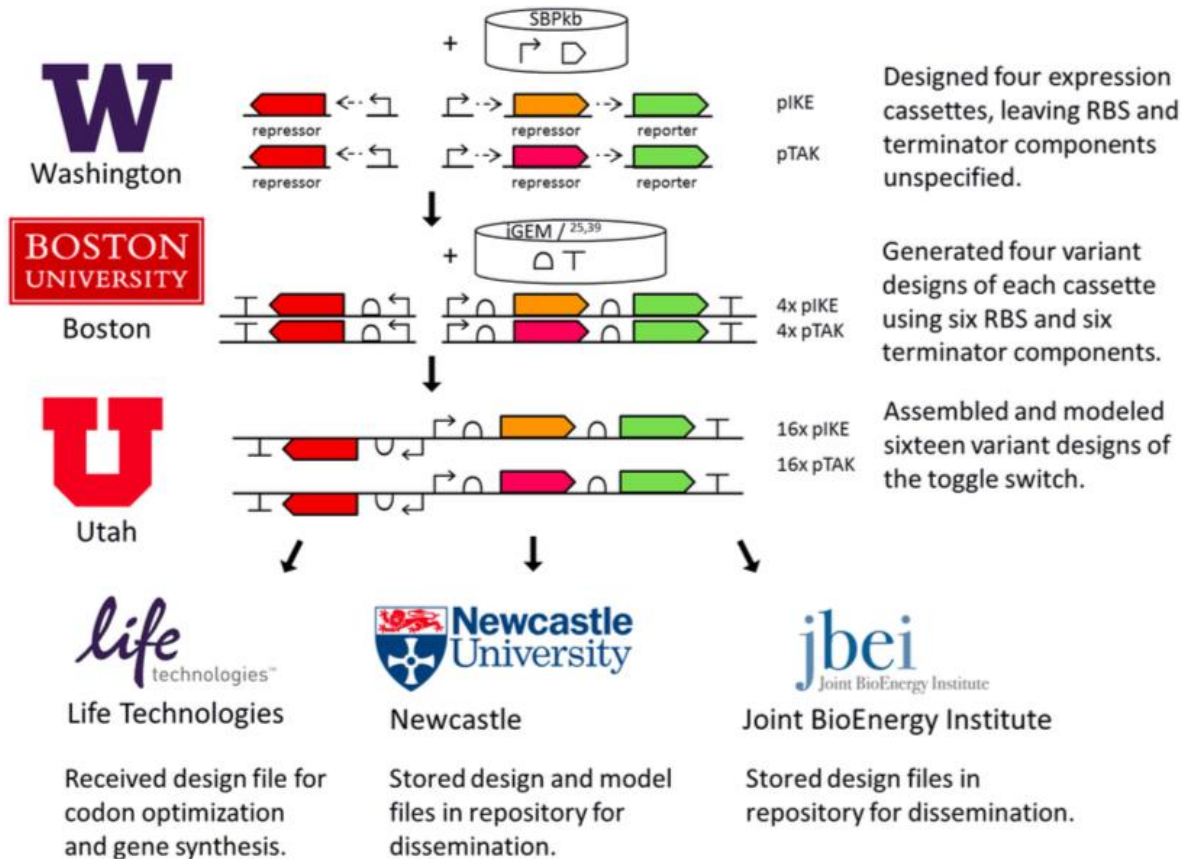
The Synthetic Biology Open Language (SBOL) provides a community standard for communicating designs in synthetic biology

[Michal Galdzicki](#), [Kevin P Clancy](#), [Ernst Oberortner](#), [Matthew Pocock](#), [Jacqueline Y Quinn](#),
[Cesar A Rodriguez](#), [Nicholas Roehner](#), [Mandy L Wilson](#), [Laura Adam](#), [J Christopher](#)
[Anderson](#), [Bryan A Bartley](#), [Jacob Beal](#), [Deepak Chandran](#), [Joanna Chen](#), [Douglas](#)
[Densmore](#), [Drew Endy](#), [Raik Grünberg](#), [Jennifer Hallinan](#), [Nathan J Hillson](#), [Jeffrey D](#)
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✚ *et al.*

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SBOL v 1



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SBOL visual

BBF RFC 93

SBOL Visual






















Synthetic Biology Open Language Visual (SBOL Visual), version 1.0.0

Jacqueline Quinn, Jacob Beal, Swapnil Bhatia, Patrick Cai, Joanna Chen, Kevin Clancy, Nathan Hillson, Michal Galdzicki, Akshay Maheshwari, Umesh P, Matthew Pocock, Cesar Rodriguez, Guy-Bart Stan, Drew Endy

March 21, 2013

SBOL visual

- * Open source graphical notation for SynBio designs
- * SBOL 1 currently, SBOL 2 in progress
- * Spec: DOI [1721.1/78349](https://doi.org/10.17211/78349)

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

Visual Paper

COMMUNITY PAGE

SBOL Visual: A Graphical Language for Genetic Designs

Jacqueline Y. Quinn¹*, Robert Sidney Cox III²*, Aaron Adler³, Jacob Beal³, Swapnil Bhatia⁴, Yizhi Cai⁵, Joanna Chen^{6,7}, Kevin Clancy⁸, Michal Galdzicki⁹, Nathan J. Hillson^{6,7}, Nicolas Le Novère¹⁰, Akshay J. Maheshwari¹¹, James Alastair McLaughlin¹², Chris J. Myers¹³, Umesh P¹⁴, Matthew Pocock^{12,15}, Cesar Rodriguez¹⁶, Larisa Soldatova¹⁷, Guy-Bart V. Stan¹⁸, Neil Swainston¹⁹, Anil Wipat¹², Herbert M. Sauro^{20*}



OPEN ACCESS

Citation: Quinn JY, Cox RS III, Adler A, Beal J, Bhatia S, Cai Y, et al. (2015) SBOL Visual: A Graphical Language for Genetic Designs. *PLoS Biol* 13(12): e1002310. doi:10.1371/journal.pbio.1002310

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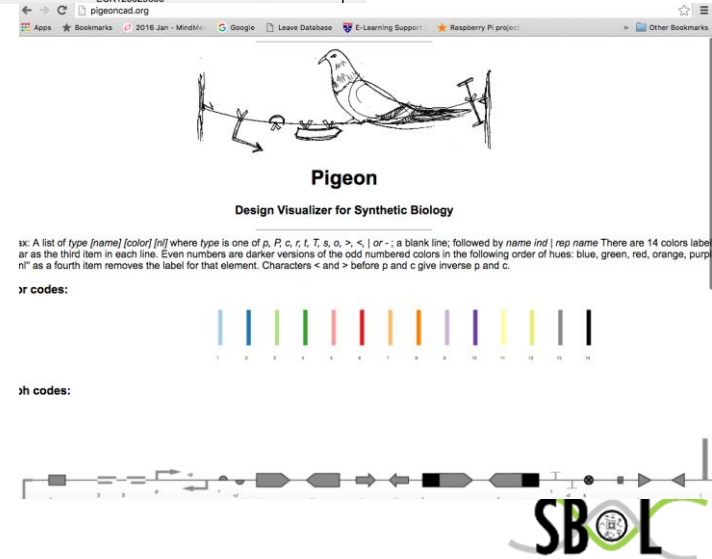
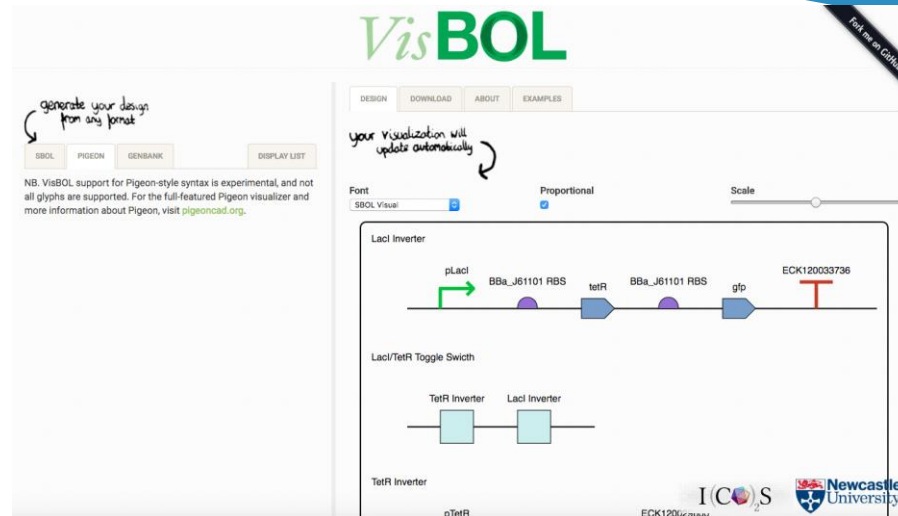
Example tools for the generation of SBOL Visual

- * VisBOL
- * PigeonCAD
- * DNAPlotLib

<http://visbol.org/>

<http://pigeoncad.org/>

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



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SBOL 2 released

libSBOLjs, libSBOLC, etc.

SBOL 2 specification

BBF RFC 108: Synthetic Biology Open Language (SBOL) Version 2.0.0

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Version 2.0.0

SBOL 2 in practise

Sharing Structure and Function in Biological Design with SBOL 2.0

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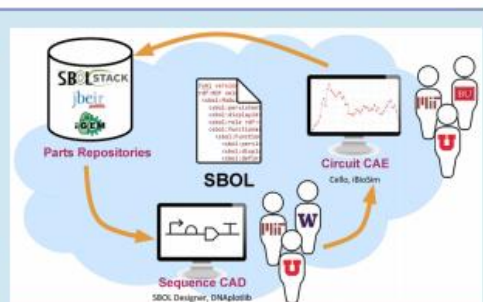
[■]Department of Electrical and Computer Engineering, University of Utah, Salt Lake City, Utah 84112, United States

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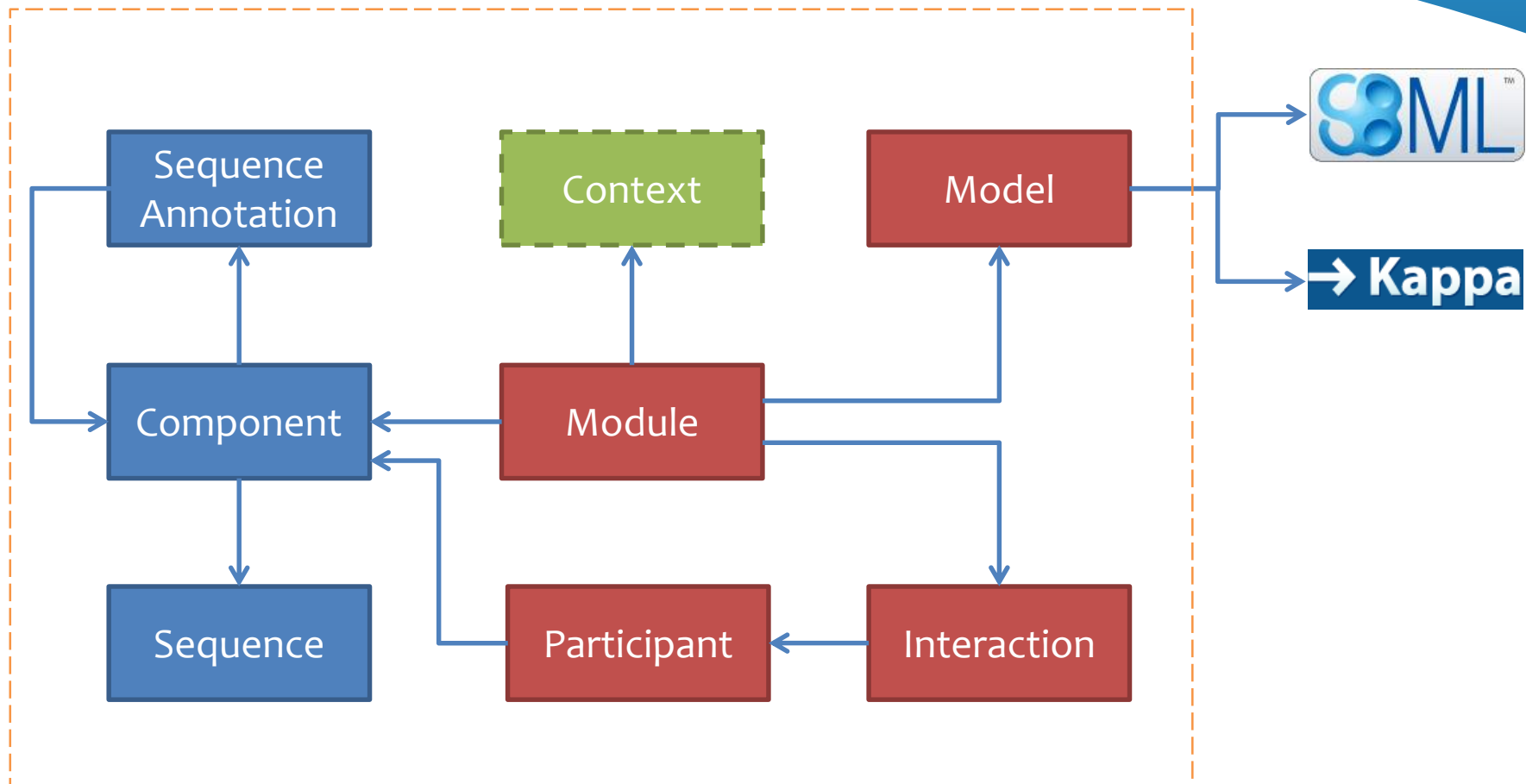
[●]Department of Biomedical Informatics and Medical Education, University of Washington, Seattle, Washington 98195, United States

Supporting Information

ABSTRACT: The Synthetic Biology Open Language (SBOL) is a standard that enables collaborative engineering of biological systems across different institutions and tools. SBOL is developed through careful consideration of recent synthetic biology trends, real use cases, and consensus among leading researchers in the field and members of commercial biotechnology enterprises. We demonstrate and discuss how a set of SBOL-enabled software tools can form an integrated, cross-organizational workflow to recapitulate the design of one of the largest published genetic circuits to date, a 4-input AND sensor. This design encompasses the structural components of the system, such as its DNA, RNA, small molecules, and proteins, as well as the interactions between these components that determine the system's behavior/function. The demonstrated workflow and resulting circuit design illustrate



SBOL 2.0



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SBOL Community



SBOL Developers Group includes 116 members from more than 30 organizations.

SBOL Community

- * **SBOL Chair** – Anil Wipat (Newcastle) formerly Herbert Sauro (U. of Washington)
- * **SBOL Steering Committee** – Jake Beal, Kevin Clancy, Doug Densmore, John Genari, Nathan Hilson, Chris Myers, Herbert Sauro
- * **SBOL Editors** – Tramy Nguyen (Utah), Jacob Beal (BBN Technologies), Robert Sidney Cox (Kobe), Raik Grunberg (Montreal) and James McLaughlin (Newcastle).
- * **Past SBOL Editors** - Michal Galdzicki (U. of Washington), Ernst Oberortner (JGI/BU), Matthew Pocock (Newcastle), Jacqueline Quinn (Google), Cesar Rodriguez (Autodesk), Nick Roehner (BU) and Mandy Wilson (VBI), Bryan Bartley (U. of Washington), Goksel Misirli (Newcastle).

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Infrastructure & tools

Libraries (libSBOL)

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

All libraries are under active development. The latest release of the Java, and Javascript libraries now support SBOL 2.0. In addition a beta release of the C/C++ libraries supporting SBOL 2.0 are now available. Python bindings for SBOL 1.1 and SBOL 2.0 are currently available.

SBOL and SBML

- * SBOL to SBML and back

- * Misirli et al., (2011)
- * Roehner et al., ACS Synthetic Biology (2013)
- * Roehner et al., ACS Synthetic Biology (2014)
- * Nguyen/Myers, IWBD (2015)



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Research Article

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Generating Systems Biology Markup Language Models from the Synthetic Biology Open Language

Nicholas Roehner,^{*,†} Zhen Zhang,[‡] Tramy Nguyen,[‡] and Chris J. Myers[‡]

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Lacl Inverter

A Converter from the Systems Biology Markup Language to the Synthetic Biology Open Language

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Infrastructure - applications

Software	Type	Visual	Data Model
ICE	Repository	Yes	Yes
SBOL Hub	Repository	No	Yes
GenBank Converter	Helper	No	Yes
MoSeC	Helper	No	Yes
DNAplotlib	Visualization	Yes	Yes
Pigeon	Visualization	Yes	No
VisBOL	Visualization	Yes	Yes
Benchling	DNA Design	No	Yes
DeviceEditor	DNA Design	Yes	Yes
Eugene	DNA Design	Yes	Yes
GeneGenie	DNA Design	No	Yes
GenoCAD	DNA Design	Yes	Yes
SynBad	DNA Design	Yes	Yes
TeselaGen	DNA Design	Yes	Yes
VectorEditor	DNA Design	No	Yes
Cello	Circuit Design	Yes	Yes
iBioSim	Circuit Design	No	Yes
RetroPath	Circuit Design	No	Yes
SBROME	Circuit Design	No	Yes
TinkerCell	Circuit Design	Yes	Yes
BioCompiler	Circuit Design	Yes	Yes
Clotho 3.0	Assembly	Yes	Yes
Raven	Assembly	Yes	No



Gene

iBio

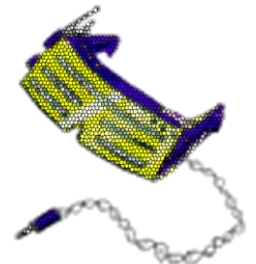


SBOL
STACK



Pigeon

Design Visualizer for Synthetic Biology



DeviceEditor

I(C₂)S

SBOL Design

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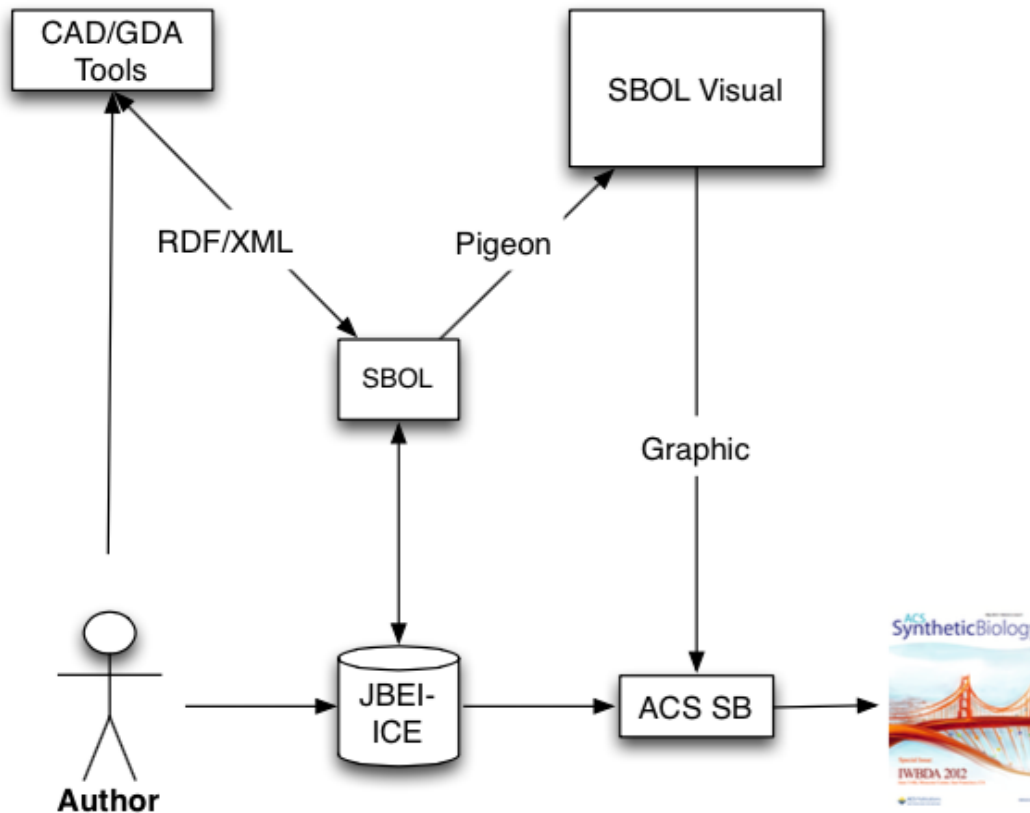
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Publishing



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Viewpoint

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Improving Synthetic Biology Communication: Recommended Practices for Visual Depiction and Digital Submission of Genetic Designs

Nathan J. Hillson,^{*,†,‡,§,||} Hector A. Plahar,^{†,‡,||} Jacob Beal,^{*,⊥} and Ranjini Prithviraj[#]

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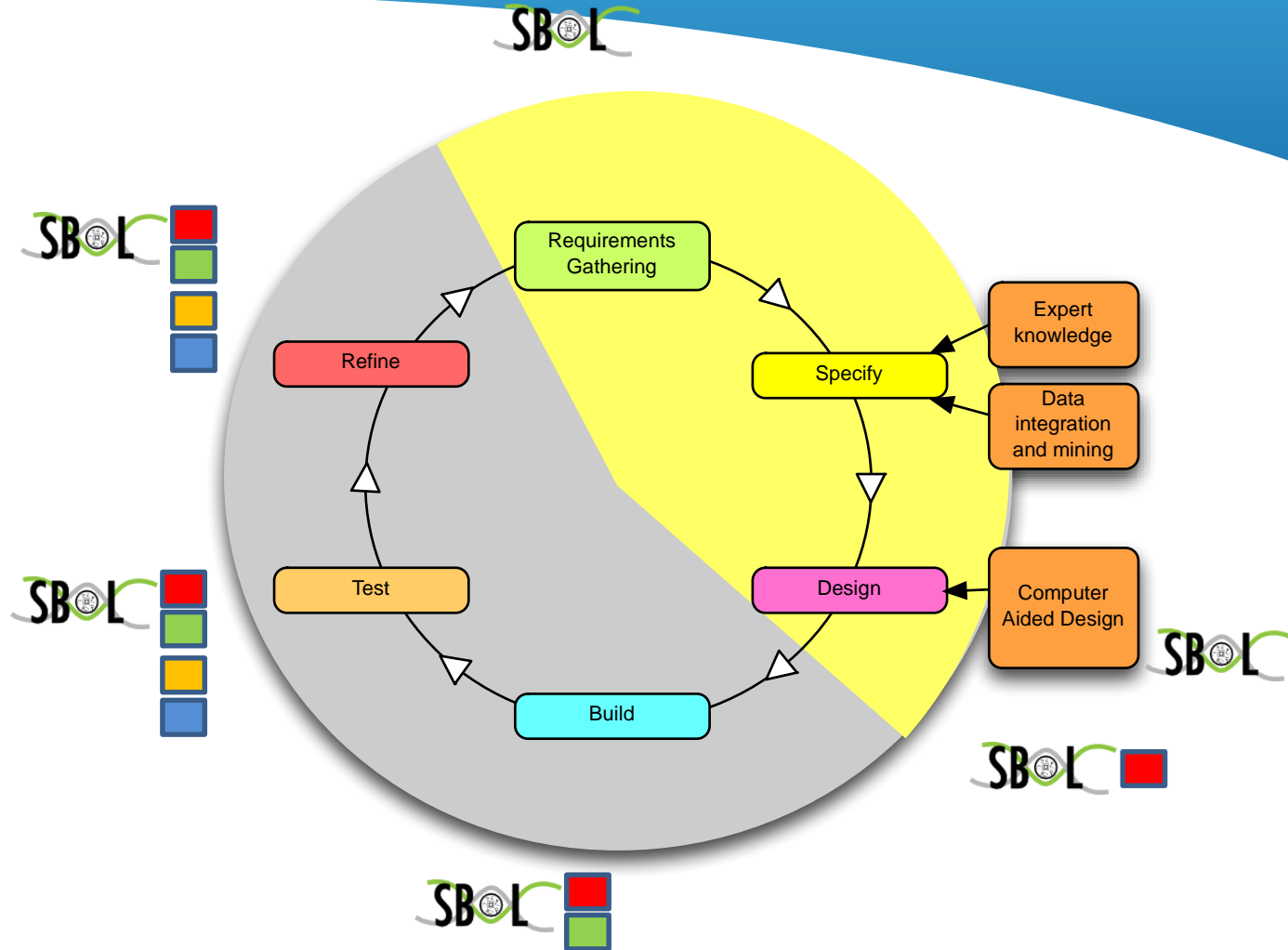
[#]ACS Synthetic Biology, American Chemical Society, Washington, D.C. 20036, United States

ABSTRACT: Research is communicated more effectively and reproducibly when articles depict genetic designs consistently and fully disclose the complete sequences of all reported constructs. *ACS Synthetic Biology* is now providing authors with updated guidance and piloting a new tool and publication workflow that facilitate compliance with these recommended practices and standards for visual representation and data exchange.



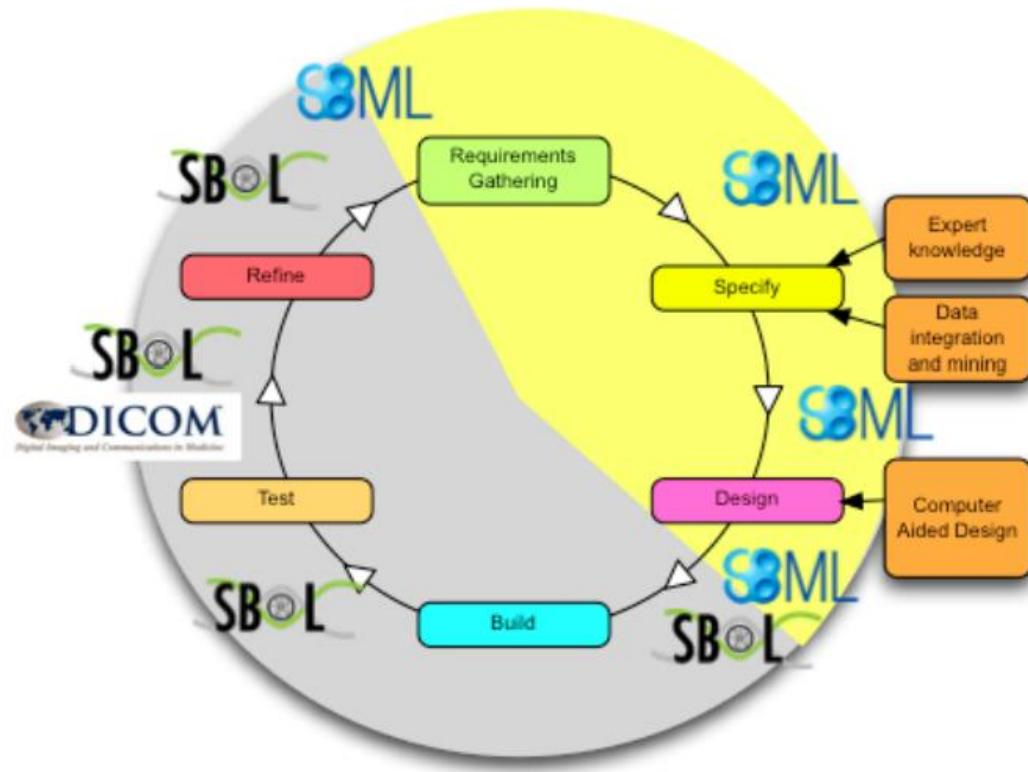
SBOL is not just about design

- * An SBOL design specified
- * SBOL data should be able to travel around the SB cycle
- * Capturing data as it goes



SBOL is not just about design

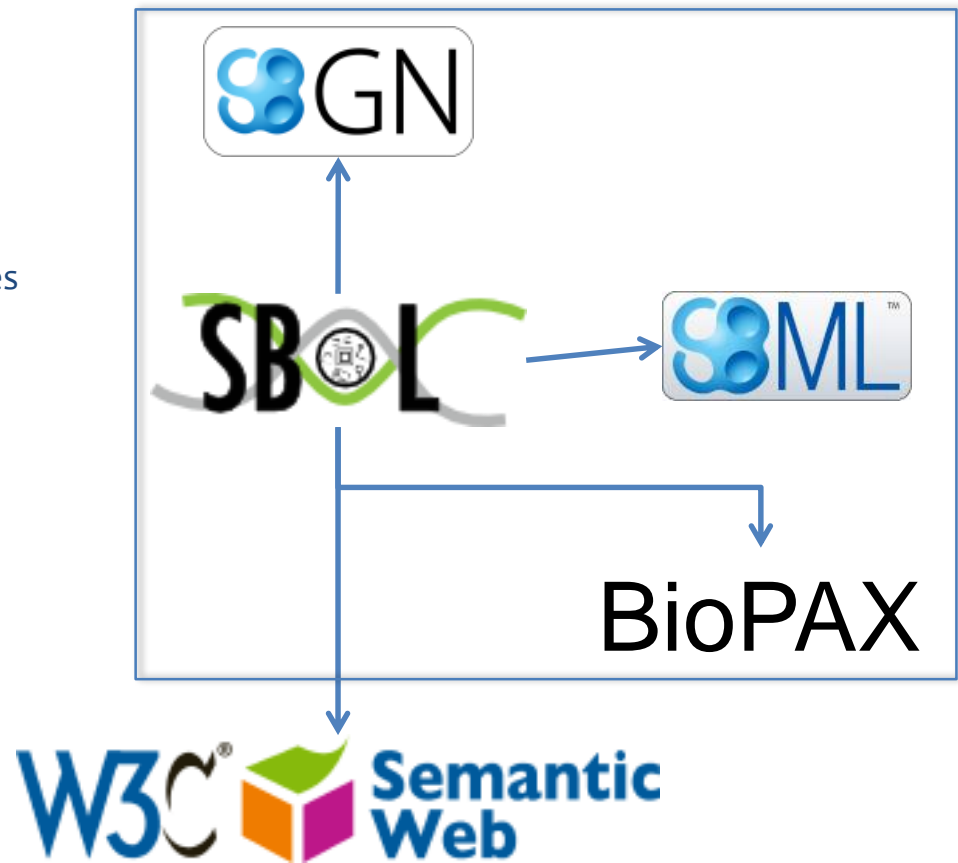
- * AND
- * Work with other standards



SBOL & COMBINE



- * **SBOL is part of something bigger**
- * **COMBINE** an initiative to coordinate systems biology standards
- * Enables interaction with communities developing other standards
 - * SBOL Visual/SBGN
 - * SBOL/SBML/SED-ML
 - * SBOL/BioPAX
- * Provides
 - * Specification infrastructure
 - * Metadata and annotations
 - * COMBINE archive
 - * Repositories
 - * Compliance testing



SBOL & COMBINE



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COMBINE 2016

Dates: **September 19-24, 2016**

Location: **Newcastle upon Tyne, UK**

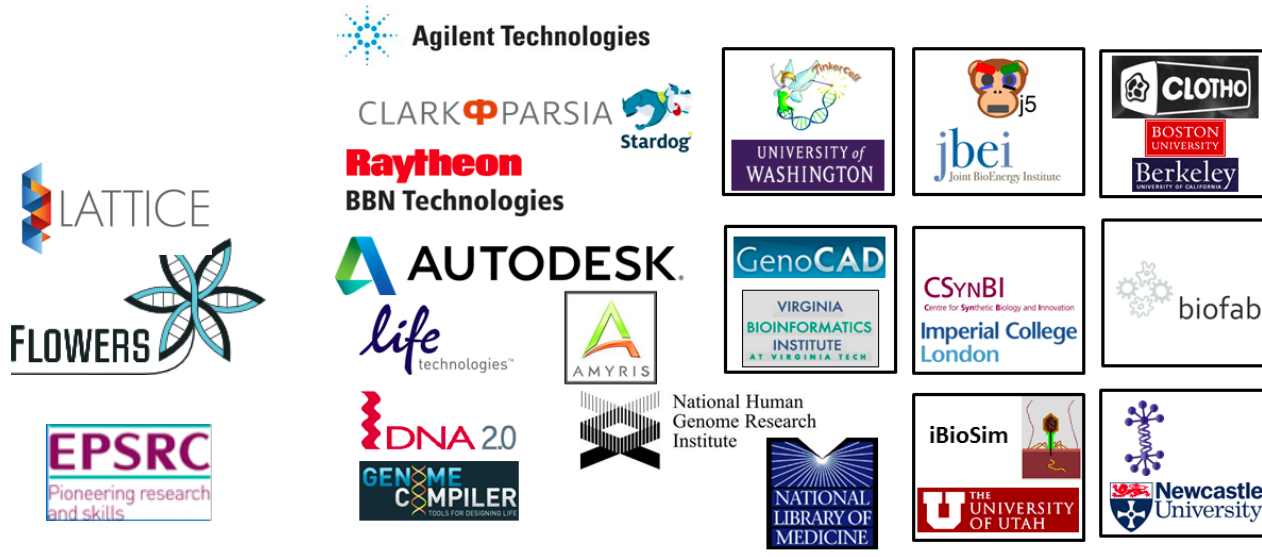
Hosted by: [Newcastle University](#)

The "Computational Modeling in Biology" Network (COMBINE) is an initiative to coordinate the development of the various community standards and formats in systems biology and related fields.

COMBINE is a workshop-style event with oral presentation, posters, and breakout sessions. The five meeting days will include talks about the [COMBINE standards and associated or related standardization efforts](#), as well as presentations of tools using these standards. Oral presentations will be selected from the submitted abstracts. In addition to oral presentations, poster sessions will allow people to inform each other about their software and other projects in a setting that fosters interaction and in-depth discussion.

The 2016 COMBINE meeting will be held in Newcastle upon Tyne, UK from September 19 to 24, 2016: the main Workshop will run 19-23 September and an SBGN Workshop will be held on September 24.

Acknowledgements



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