

Synthetic Biology Open Language



Presenter: Jacob Beal (BBN Technologies)
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Berkeley, CA

Editors: Angel Goni-Moreno (Newcastle University), Curtis Madsen (Boston University), Umesh P (University of Kerala), Zach Palchick (Zymergen), Nicholas Roehner (BBN Technologies)

Chair: Anil Wipat (Newcastle University)

SBOL Development Group: ~120 members from more than 60 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

Dec, 2017

SBOL Visual 2.0 officially released
SBOL Version 2.2 supports complete design-build-test cycle

Evolution of standards for Bioinformatics

ACTGTGCCGTTAAACGTGATTAAATCCGTACTGATAT...

FASTA

Raw sequence information

GenBank

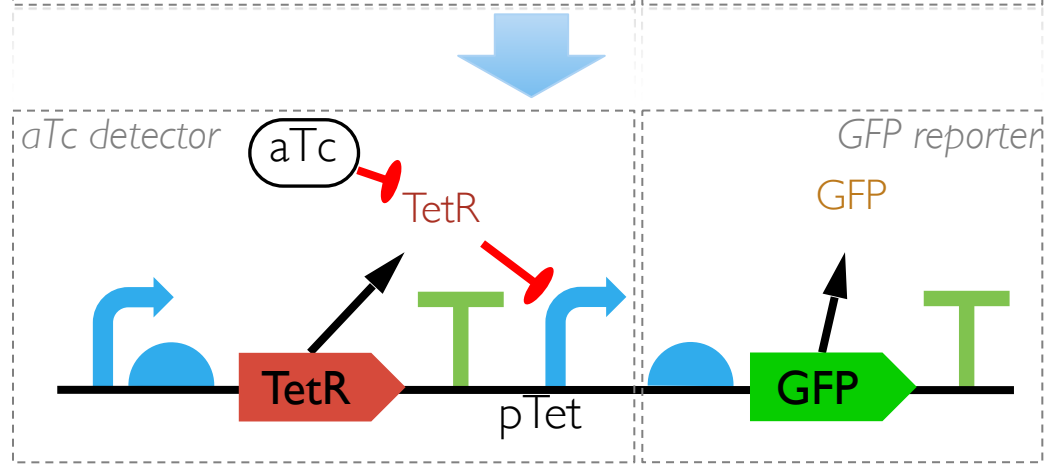
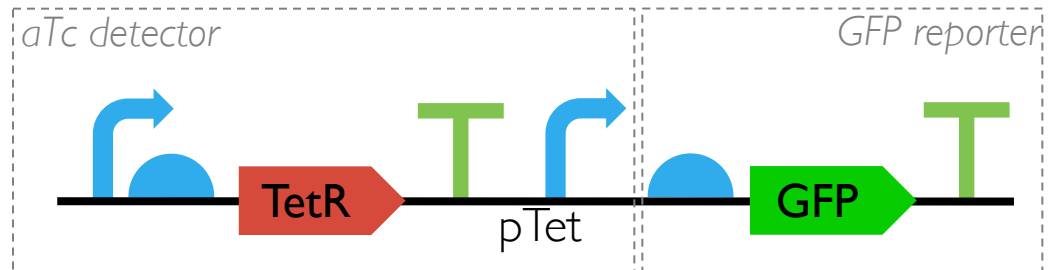
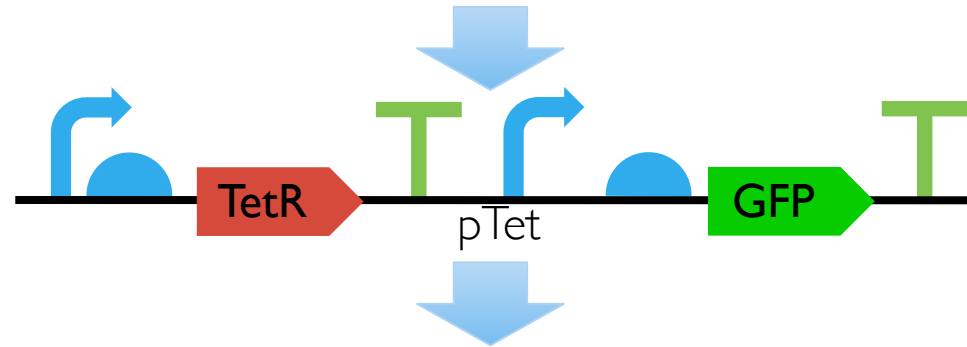
Contains sequence features

SBOL 1

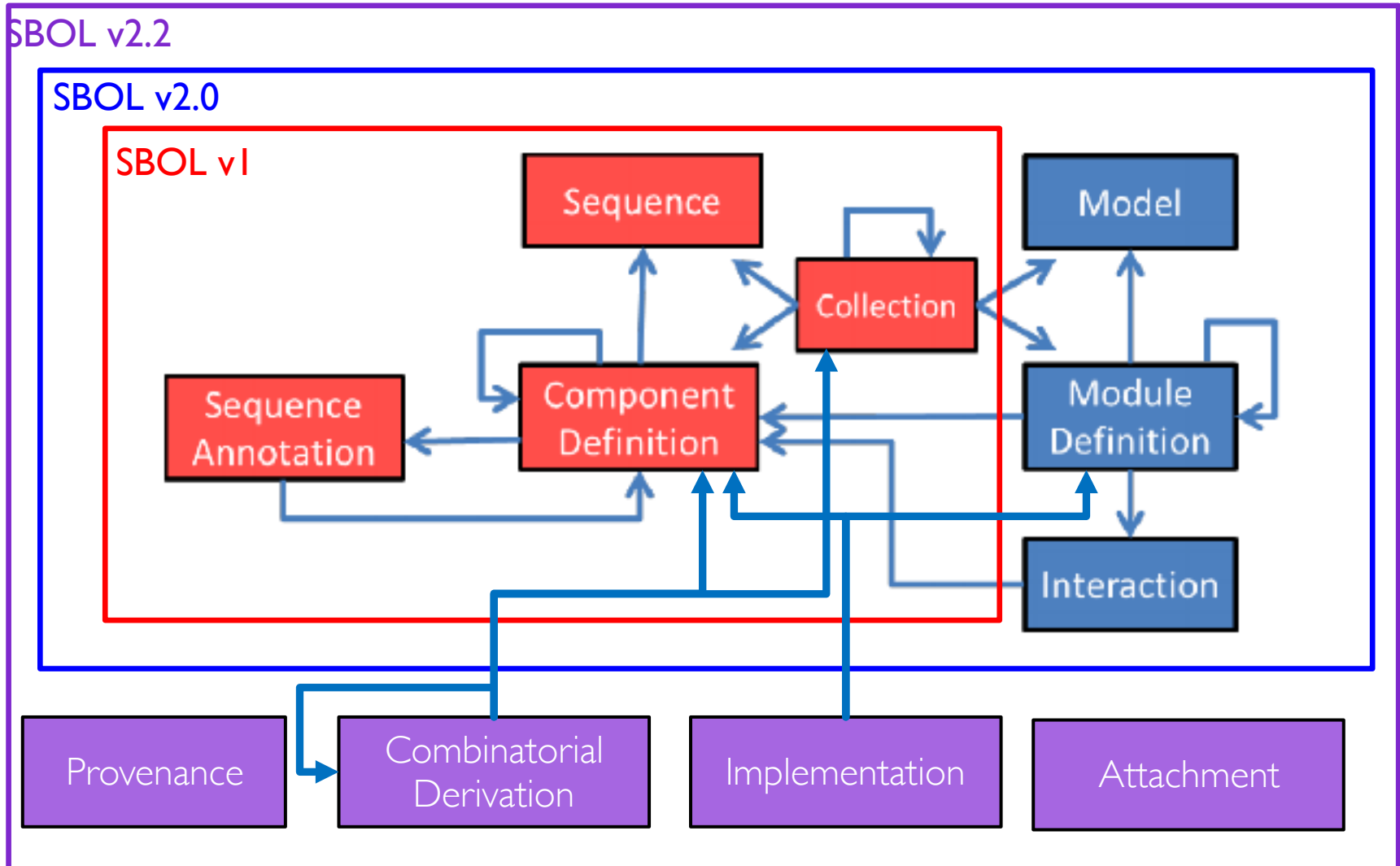
Represents sequence features hierarchically

SBOL 2

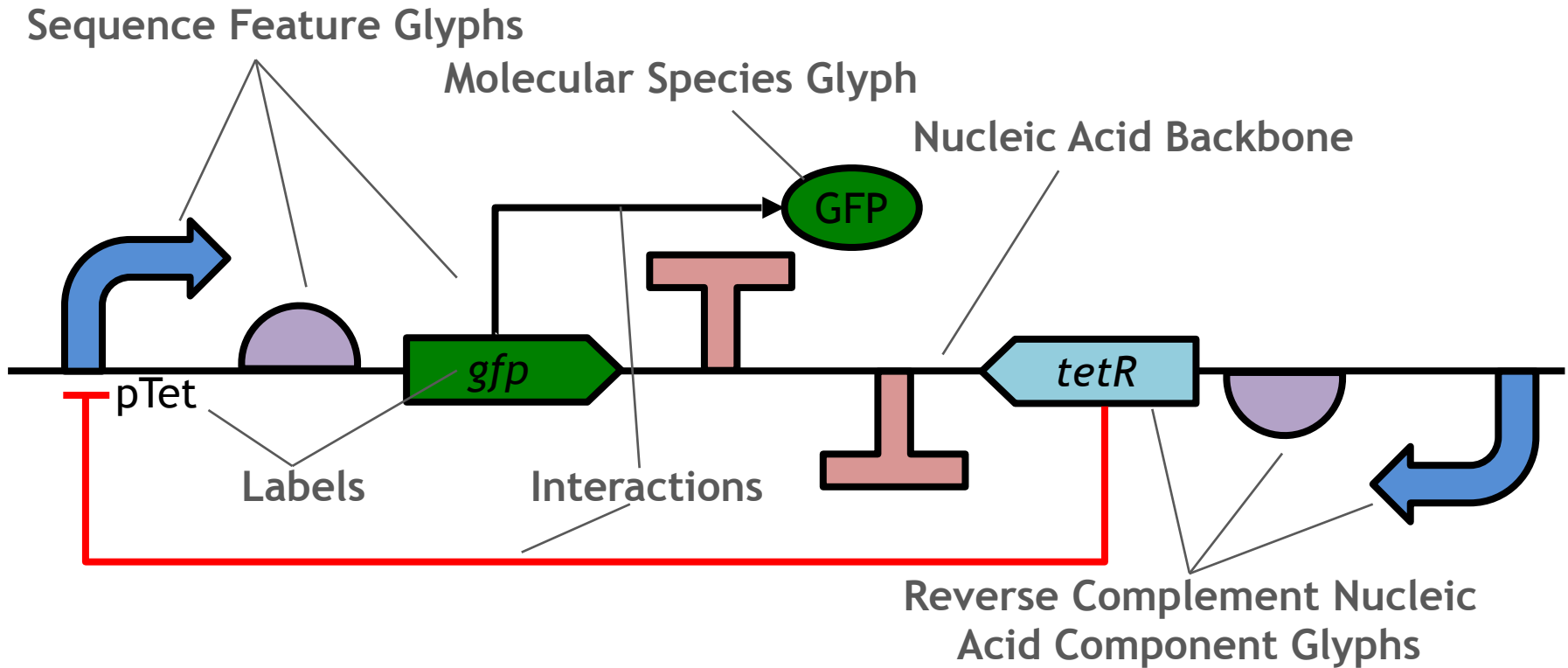
- Represents additional molecule types
- Represents modules with inputs and outputs



SBOL Data Model

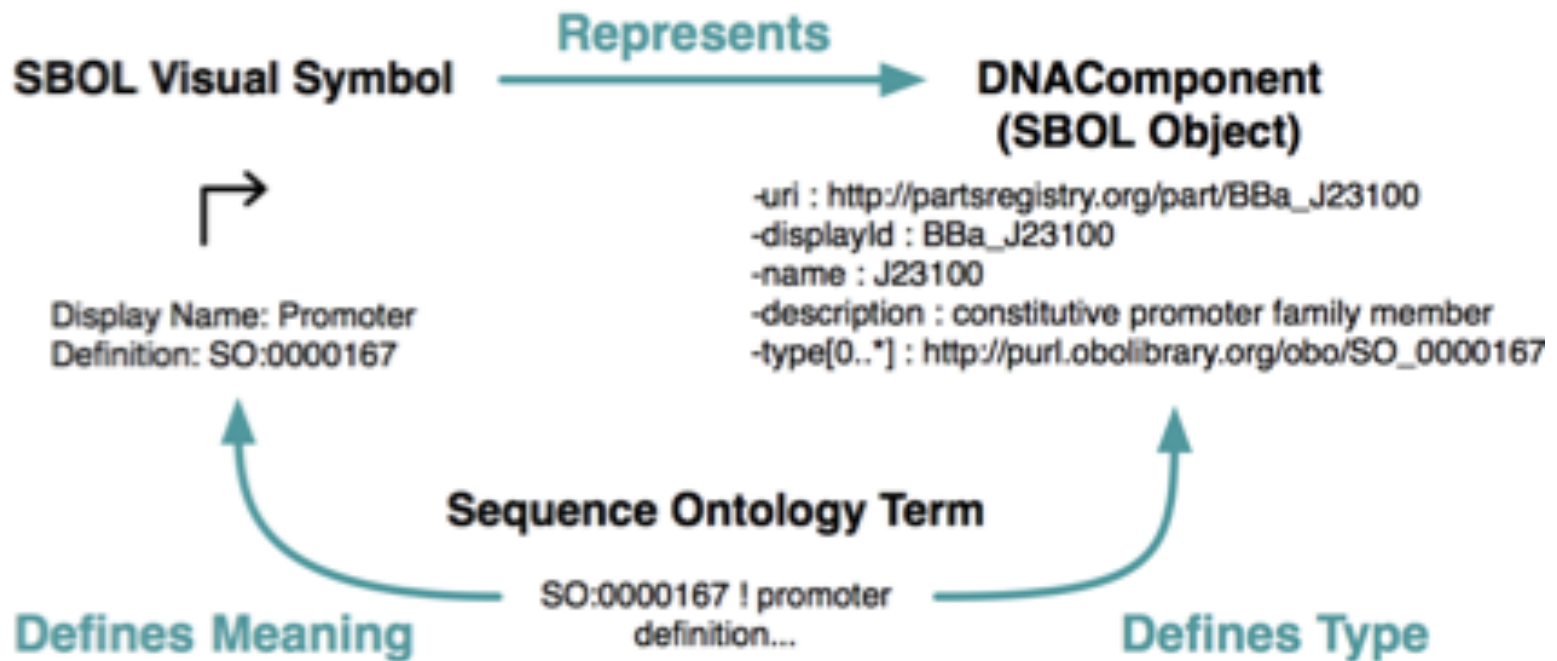


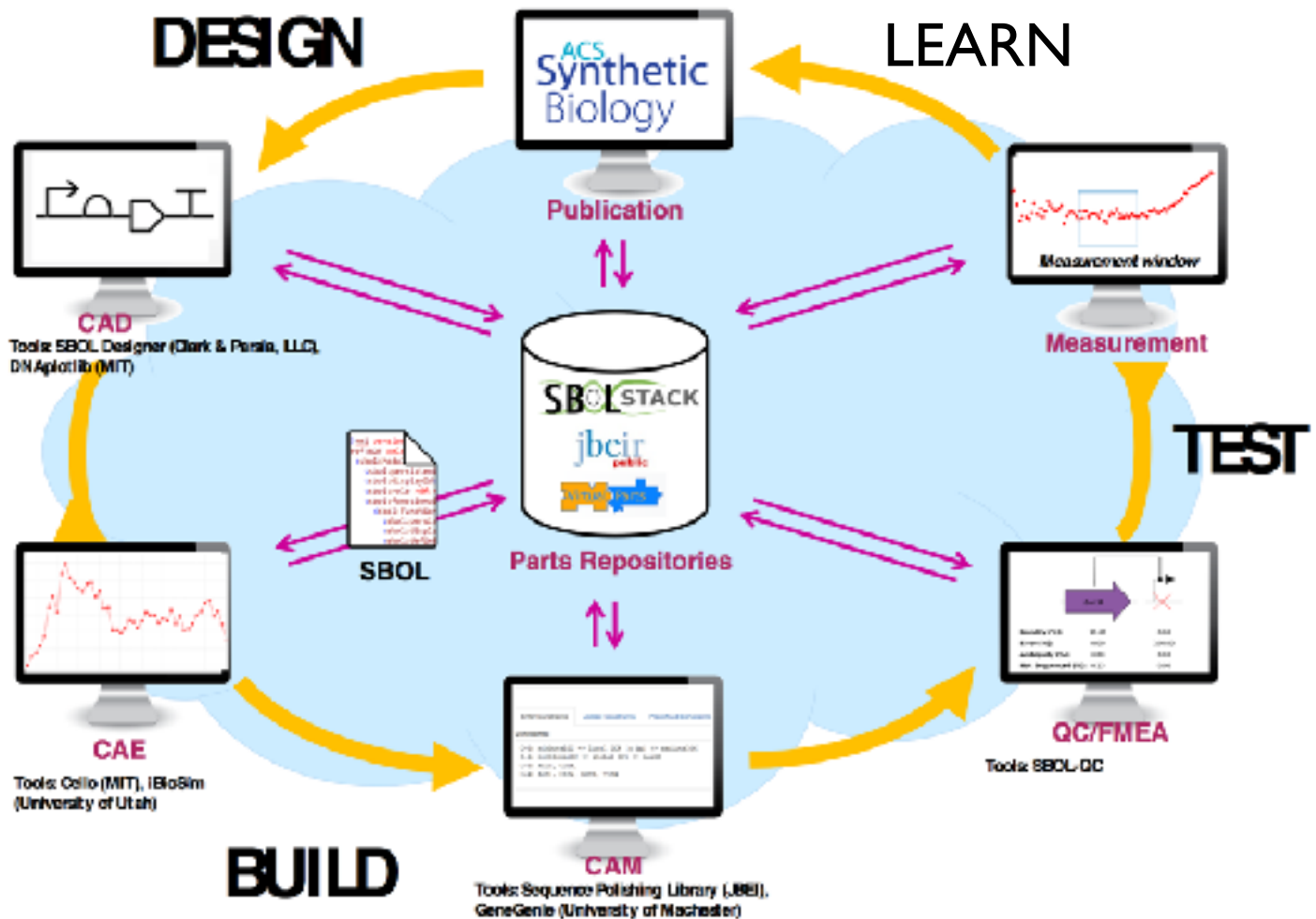
SBOL Visual v2.0



Grey text and lines (including this) are annotations

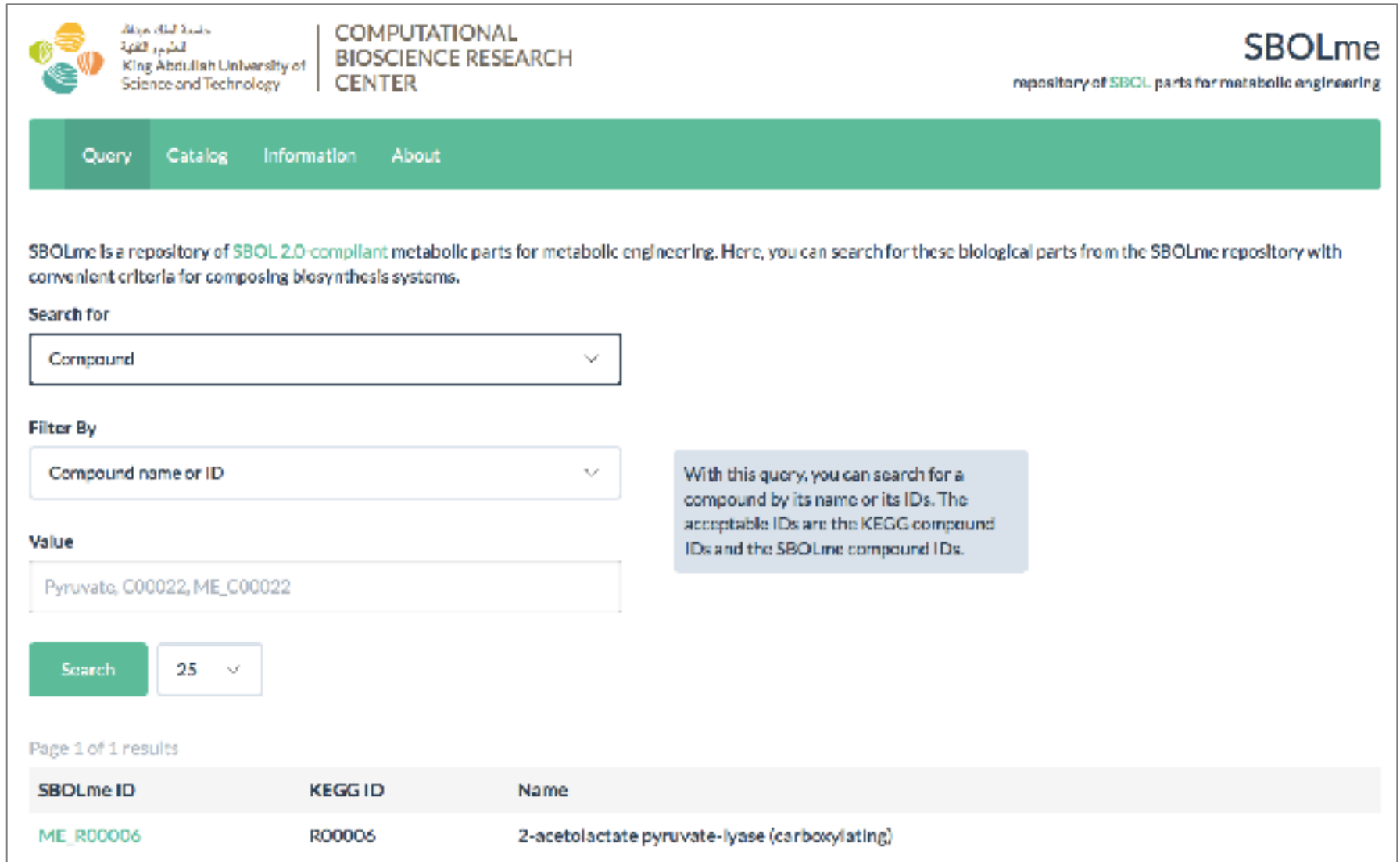
Relation between SBOL Visual and SBOL Data Model





SBOL helps synthetic biologists to collaborate across different stages of (automation-assisted) workflows

Data Repositories: SBOLme



The screenshot shows the SBOLme website interface. At the top left is the logo of King Abdullah University of Science and Technology (KAUST) and the text 'COMPUTATIONAL BIOSCIENCE RESEARCH CENTER'. At the top right is the SBOLme logo and the text 'repository of SBOL parts for metabolic engineering'. Below the header is a green navigation bar with links for 'Query', 'Catalog', 'Information', and 'About'. The main content area features a search form with a 'Search for' dropdown set to 'Compound', a 'Filter By' dropdown set to 'Compound name or ID', and a 'Value' input field containing 'Pyruvate, C00022, ME_C00022'. A green 'Search' button is next to a dropdown showing '25' results. A blue callout box explains that the query can search for a compound by its name or its IDs, including KEGG and SBOLme IDs. Below the search form, it says 'Page 1 of 1 results' and displays a table with one result.

SBOLme is a repository of SBOL 2.0-compliant metabolic parts for metabolic engineering. Here, you can search for these biological parts from the SBOLme repository with convenient criteria for composing biosynthesis systems.

Search for

Compound

Filter By

Compound name or ID

Value

Pyruvate, C00022, ME_C00022

Search 25

Page 1 of 1 results

SBOLme ID	KEGG ID	Name
ME_R00006	R00006	2-acetolactate pyruvate-lyase (carboxylating)

Kuwahara et al., ACS Synthetic Biology (2017)

Includes 28,437 chemical compounds, 6,883 enzyme classes, 9,909 metabolic reactions, and 3,173,238 proteins from 3,908 organisms.

Data Repositories: ICE

The screenshot displays the ICE Registry interface. At the top, there is a search bar and a navigation menu with options like 'ADD TO', 'REMOVE', 'MOVE TO', 'EDIT', 'DELETE', 'SHARE', and 'ACCEPT'. The main content area is a table of genetic parts. The table has columns for checkboxes, part type, ID, description, status, and date. The parts listed include various plasmids and strains, many of which are marked as 'Complete'.

Category	ID	Description	Status	Date
PLASMID	LCP_000117	pGDP95_pSB1C3-g130p-minCMV-GFP-RBQpA The 2015 BostonU iGEM team designed a set of mutually orthogonal...	Complete	Dec 2, 2015
PLASMID	LCP_000118	pGDP95_pSB1C3-g80p-minCMV-GFP-RBQpA The 2015 BostonU iGEM team designed a set of mutually orthogonal...	Complete	Dec 2, 2015
PLASMID	LCP_000116	pGDP95_pSB1C3-g80p-minCMV-GFP-RBQpA The 2015 BostonU iGEM team designed a set of mutually orthogonal...	Complete	Dec 2, 2015
PLASMID	LCP_000079	pGDP110_pSB1C3-g130p_mismatch_1bp_loo10-minCM... The 2015 BostonU iGEM team designed a set of mutually orthogonal...	Complete	Nov 28, 2015
PLASMID	LCP_000078	pGDP90_pSB1C3-g130p_3multi_24bp_minCMV GFP RB... The 2015 BostonU iGEM team designed a set of mutually orthogonal...	Complete	Nov 28, 2015
PLASMID	LCP_000077	pGDP85_pSB1C3_g130p-2-multi-24bp_minCMV GFP_R... The 2015 BostonU iGEM team designed a set of mutually orthogonal...	Complete	Nov 28, 2015
PLASMID	LCP_000076	pGDP23_pSB1C3_g10p_min-CMV_GFP_RGB-A The 2015 BostonU iGEM team designed a set of mutually orthogonal...	Complete	Nov 28, 2015
PLASMID	LCP_000074	pGEX105_pSB1C3_NU6_g8_8P-Cox2-gRNA-scaffold-RB... This part produces a guide RNA that pairs with an operator. This basi...	Complete	Nov 18, 2015
PLASMID	LCP_000073	pGEX105_pSB1C3_NU6_g1_8P-Cox8-gRNA-scaffold-RB... This part produces a guide RNA that pairs with an operator. This basi...	Complete	Nov 18, 2015
STRAIN	LCP_000072	Assembly #1 Recombinase_Level 1 Level 1 for assembly #1.	Complete	Nov 15, 2015
STRAIN	LCP_000071	gfp_pich41278_gi NoClx level 0 part.	Complete	Nov 15, 2015
STRAIN	LCP_000070	tp401p-ag-bxb1p-gt-tp401p-to-ag Level 0 part.	Complete	Nov 15, 2015
STRAIN	LCP_000069	bfp-pich41258-clx NoClx level 0 part.	Complete	Nov 16, 2015
STRAIN	LCP_000058	bxb1b-gt_csd NoClx level 0 part.	Complete	Nov 15, 2015

At the bottom of the page, there are logos for Boston University and MIT, and a footer with the text: © JDSB ICE Registry 2012. All rights reserved. Submit an issue | Help.

Ham et al., Nucleic Acid Research (2012)

Data Repositories: SynBioHub



The screenshot shows the SynBioHub website. At the top, there is a navigation bar with the SynBioHub logo on the left and links for 'Submit', 'About', and 'Submissions' on the right. Below the navigation bar is a large header area with the SynBioHub logo and the text: 'SynBioHub is a *design repository* for people designing biological constructs. It enables DNA and protein designs to be uploaded, then provides a shareable link to allow others to view them. SynBioHub also facilitates searching for information about existing useful parts and designs by combining data from a variety of sources.'

Below the header, there are three main sections:

- Search for useful parts and designs:** This section features a magnifying glass icon, a search input field with the placeholder text 'Gene or protein name', and a 'Search' button. Below the search field is a 'Browse Public Designs' button.
- Upload your design for safekeeping:** This section features an upload icon (a square with an upward arrow) and a 'Submit a Design' button.
- Share designs for publication or collaboration:** This section features a share icon (three circles connected by lines) and a 'Manage Submissions' button.

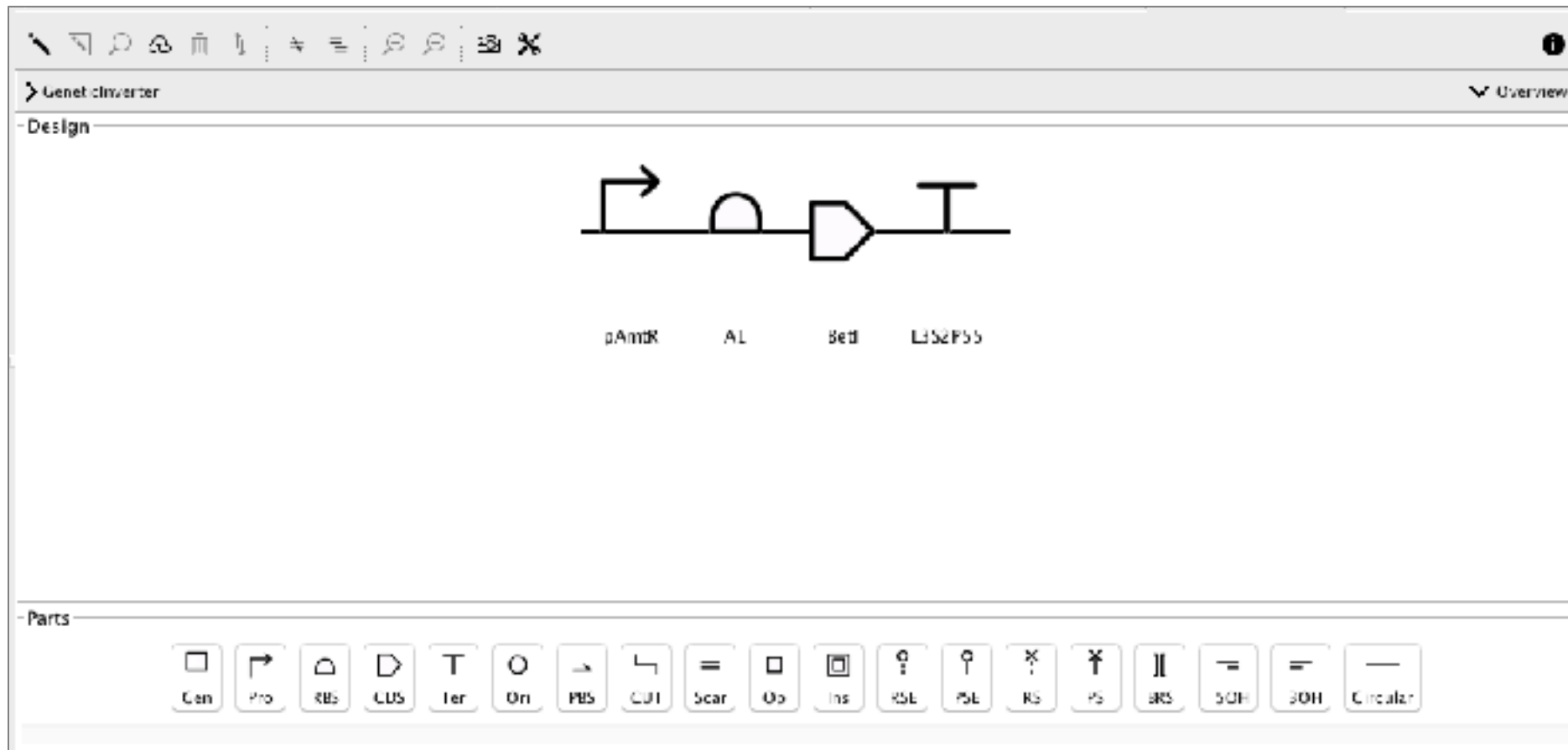


James McLaughlin
Anil Wipat



Zach Zundel
Chris Myers

Sequence Editor: SBOL Designer



Zhang et al., ACS Synthetic Biology (2017)

Other sequence editors that support SBOL: **DeviceEditor**, **J5**, **VectorEditor** (JBEI), **DNAPlotLib** (MIT/UW/Bristol), **Eugene** (Boston), **GenoCAD** (VBI), **BOOST** (JGI), etc.

Circuit Design Tools: Cello

The screenshot displays the Cello web interface. At the top, there are navigation tabs: Cello, Verilog, Options, Results, and About. On the right, it says "You are logged in as myers" with a Logout button.

The main interface is divided into two main sections:

- Verilog:** A text editor showing a Verilog module definition. A dropdown menu above the editor is set to "choose". The code is as follows:

```
1 module A(output out1, input in1, in2);
2   always@(in1, in2)
3   begin
4     case({in1, in2})
5       2'b00: {out1} = 1'b0;
6       2'b01: {out1} = 1'b0;
7       2'b10: {out1} = 1'b0;
8       2'b11: {out1} = 1'b1;
9     endcase
10  end
11 endmodule
12
```
- Inputs:** A section with a dropdown menu set to "choose" and a "clear" button. Below it is a table with the following data:

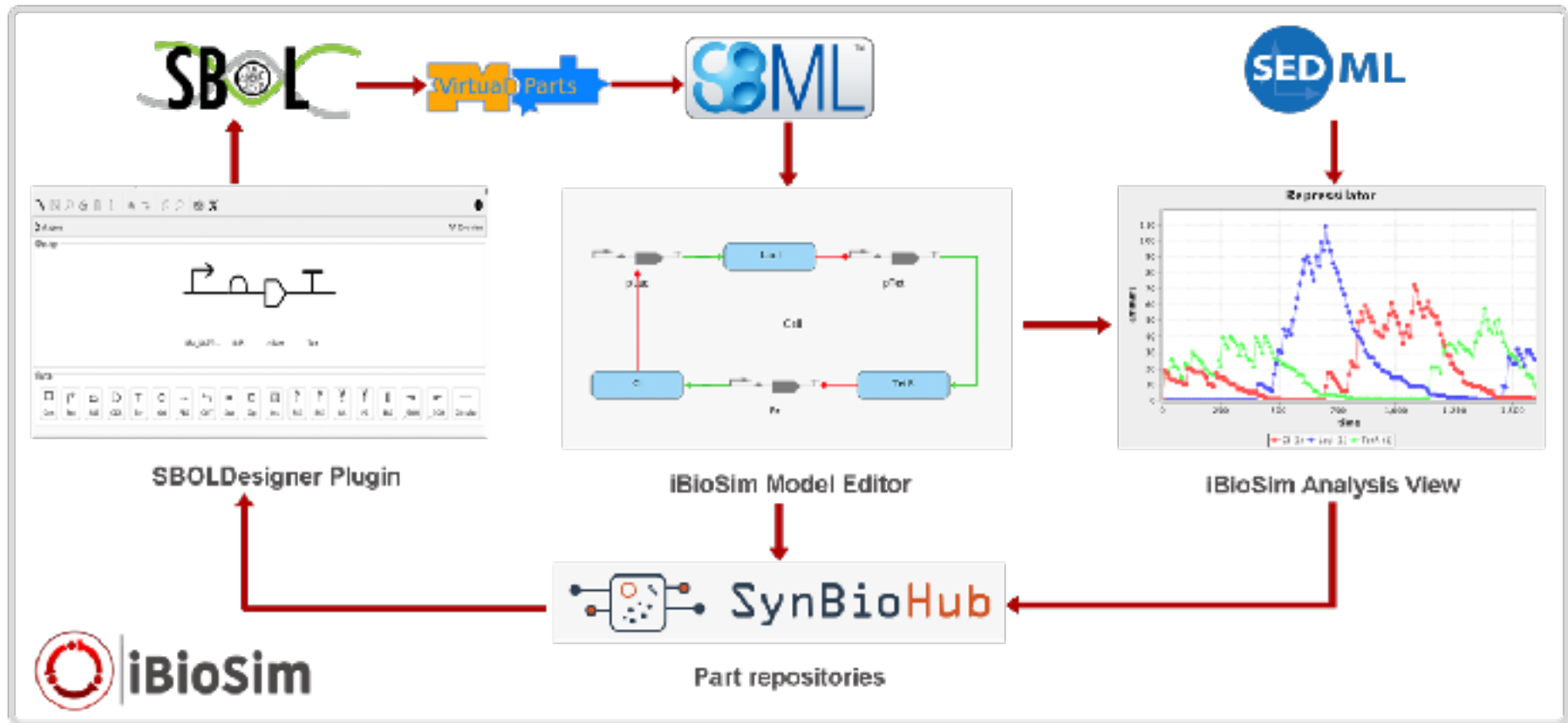
index	name	low RPU	high RPU	DNA sequence
1	pTac	0.0034	2.8	AACGATCGTTGGCTGTGTTGAGAA
2	pTet	0.0018	4.4	TACTCCACCGTTGCGCTTTTTCOC'
- Outputs:** A section with a dropdown menu set to "choose" and a "clear" button. Below it is a table with the following data:

index	name	DNA sequence
1	YFP	CTGAAGCTGTCAOCGGATGTGCTTTCOCGGTCTGATGAGTCCGT

At the bottom of the Verilog section, there is a text input field labeled "design name" and a green "Run" button.

Nielsen et al., Science (2016)

Circuit Design Tools: iBioSim



Madsen et al., IEEE Design & Test (2012)

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>)

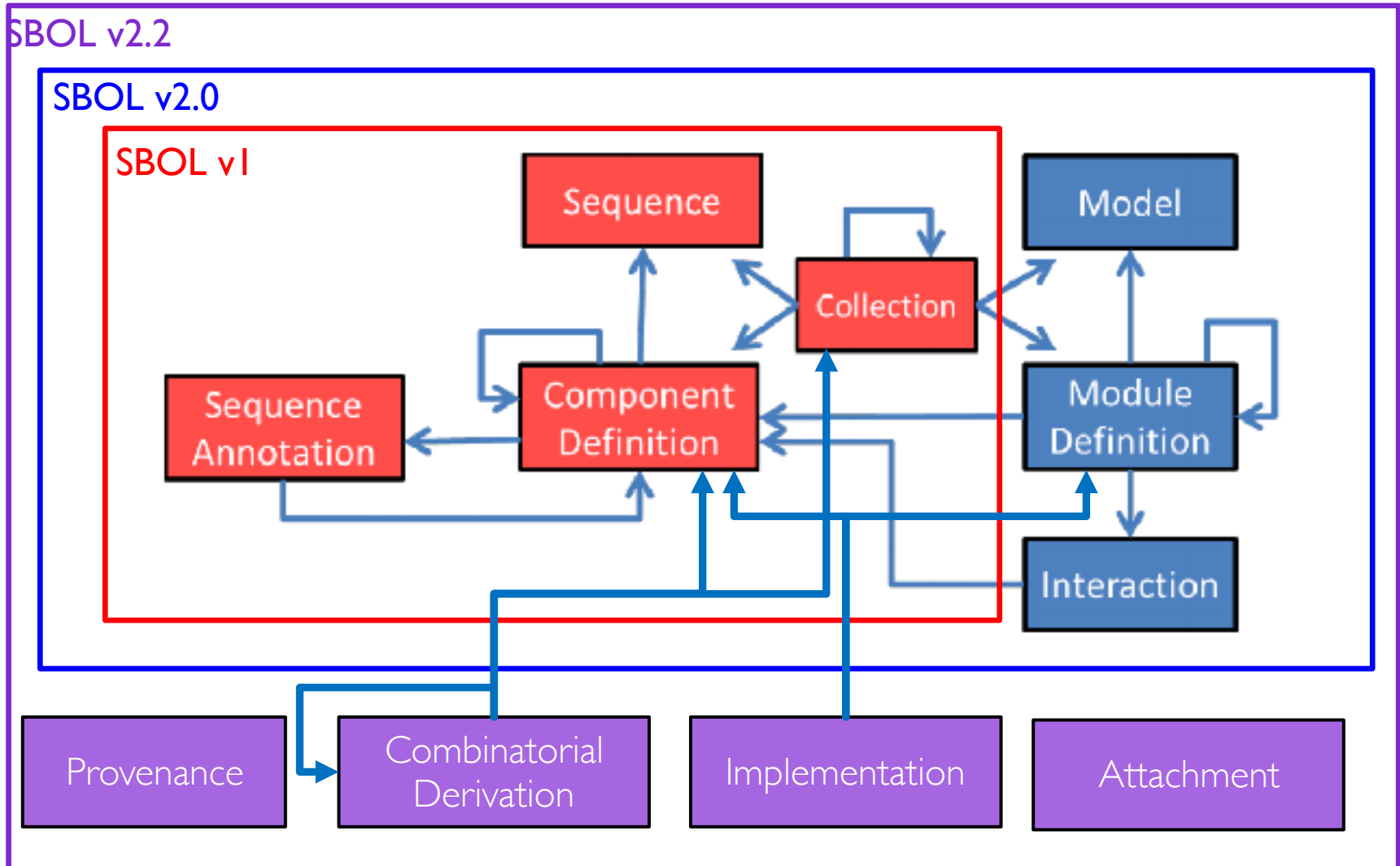
- Online documentation
- Getting started tutorials
- Sample projects
- Code examples

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 the initial repository.

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](#).

SBOL Data Model



ComponentDefinition

ComponentDefinition

identity: iGEM#113504

name: "iGEM 2016 interlab reporter"

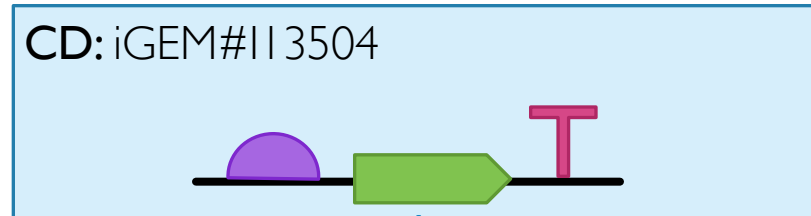
description: "GFP expression cassette
used for 2016 iGEM interlab"

type: biopax#DnaRegion

role: SO:0000804 (Engineered Region)



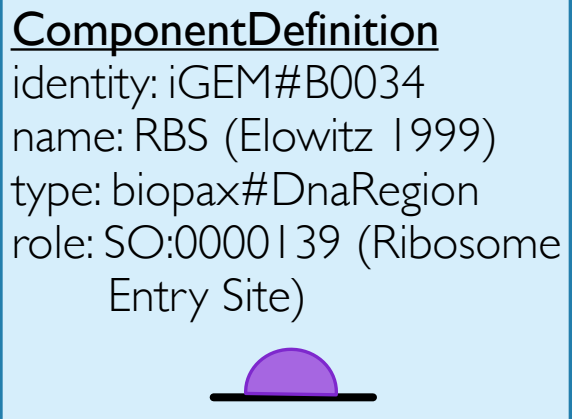
Component



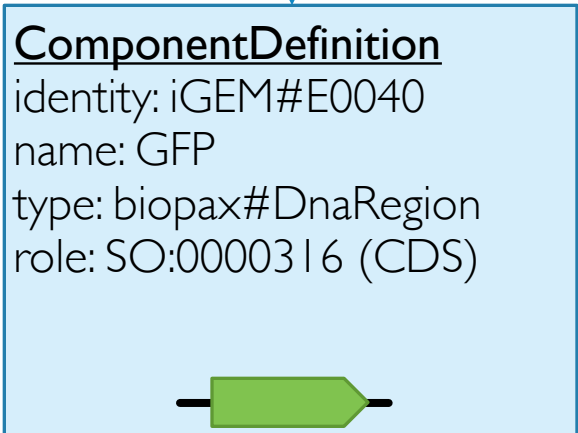
component



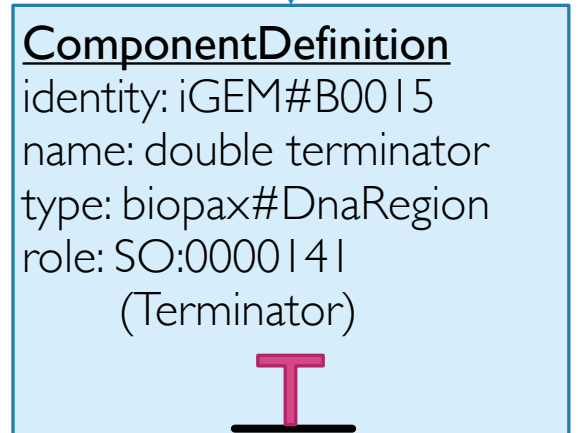
definition



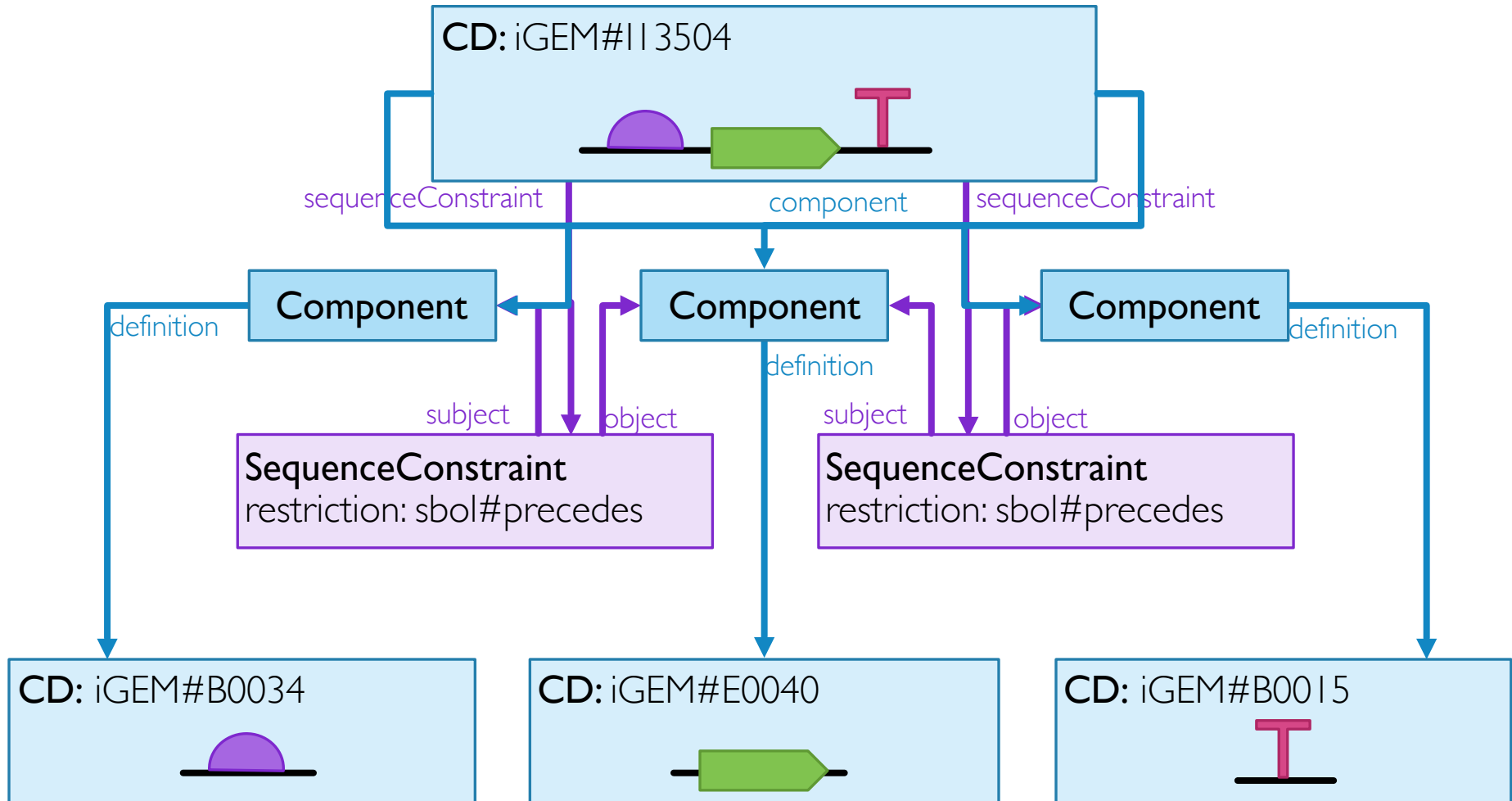
definition



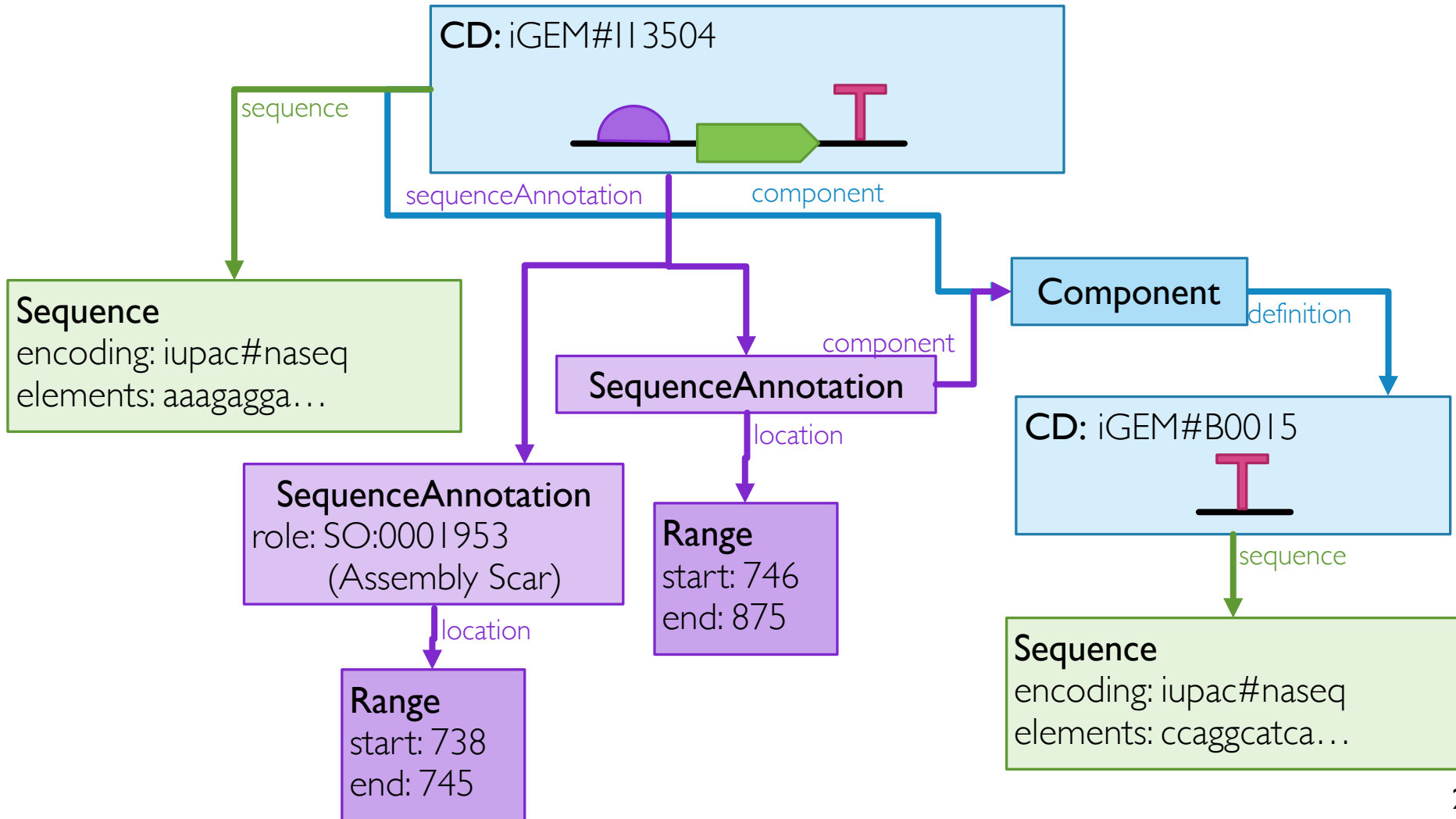
definition



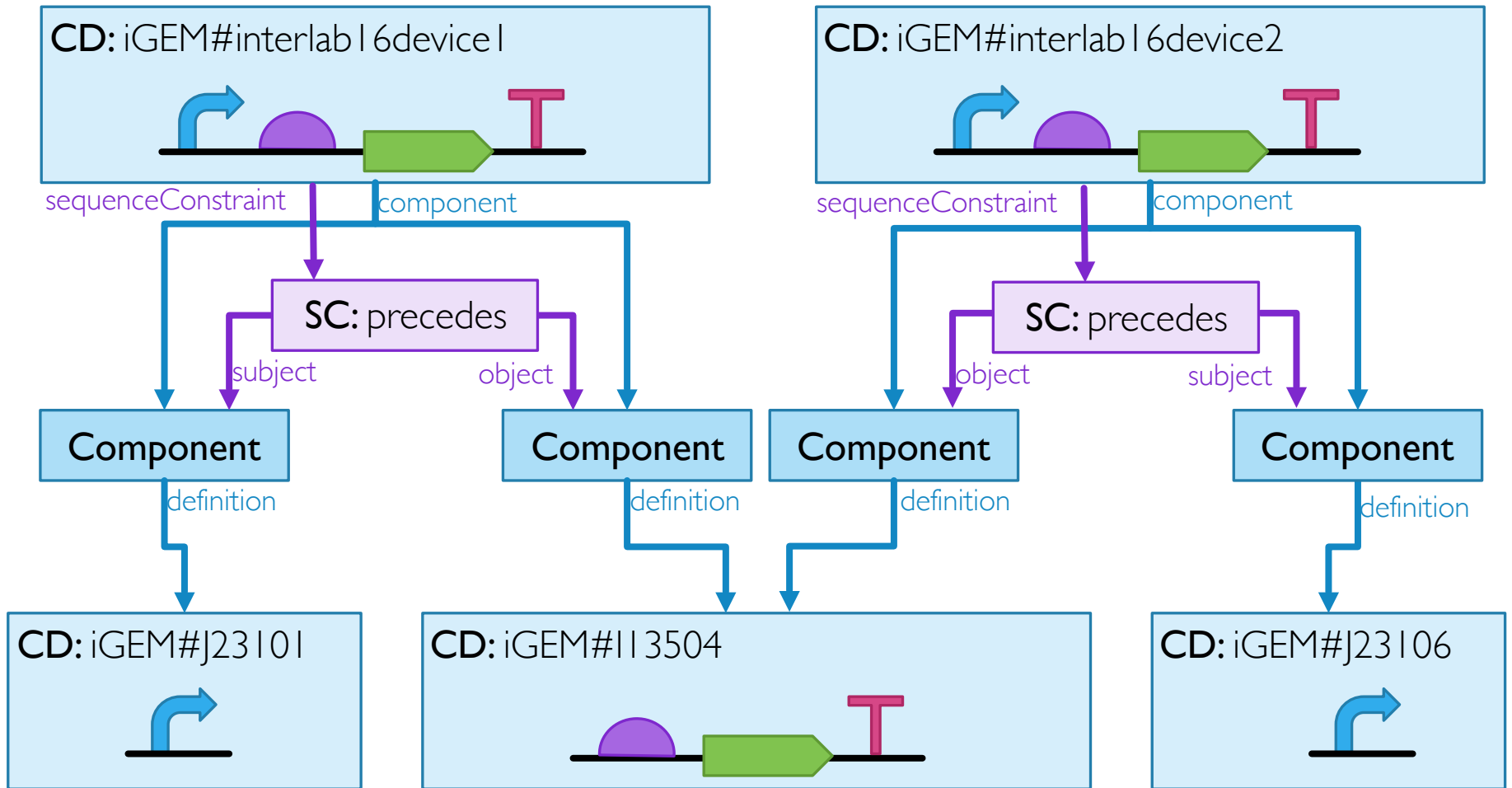
SequenceConstraint



Sequence, SequenceAnnotation



Reusing Components



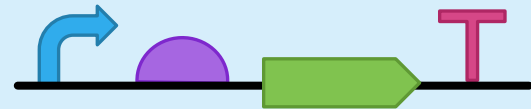
Collection

Collection:

identity: iGEM#interlab16
name: "iGEM 2016 interlab parts"
description: "Collection of parts used for 2016 iGEM interlab"

member

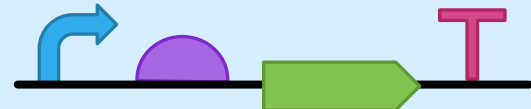
CD: iGEM#interlab16device1



CD: iGEM#interlab16device2



CD: iGEM#interlab16device3



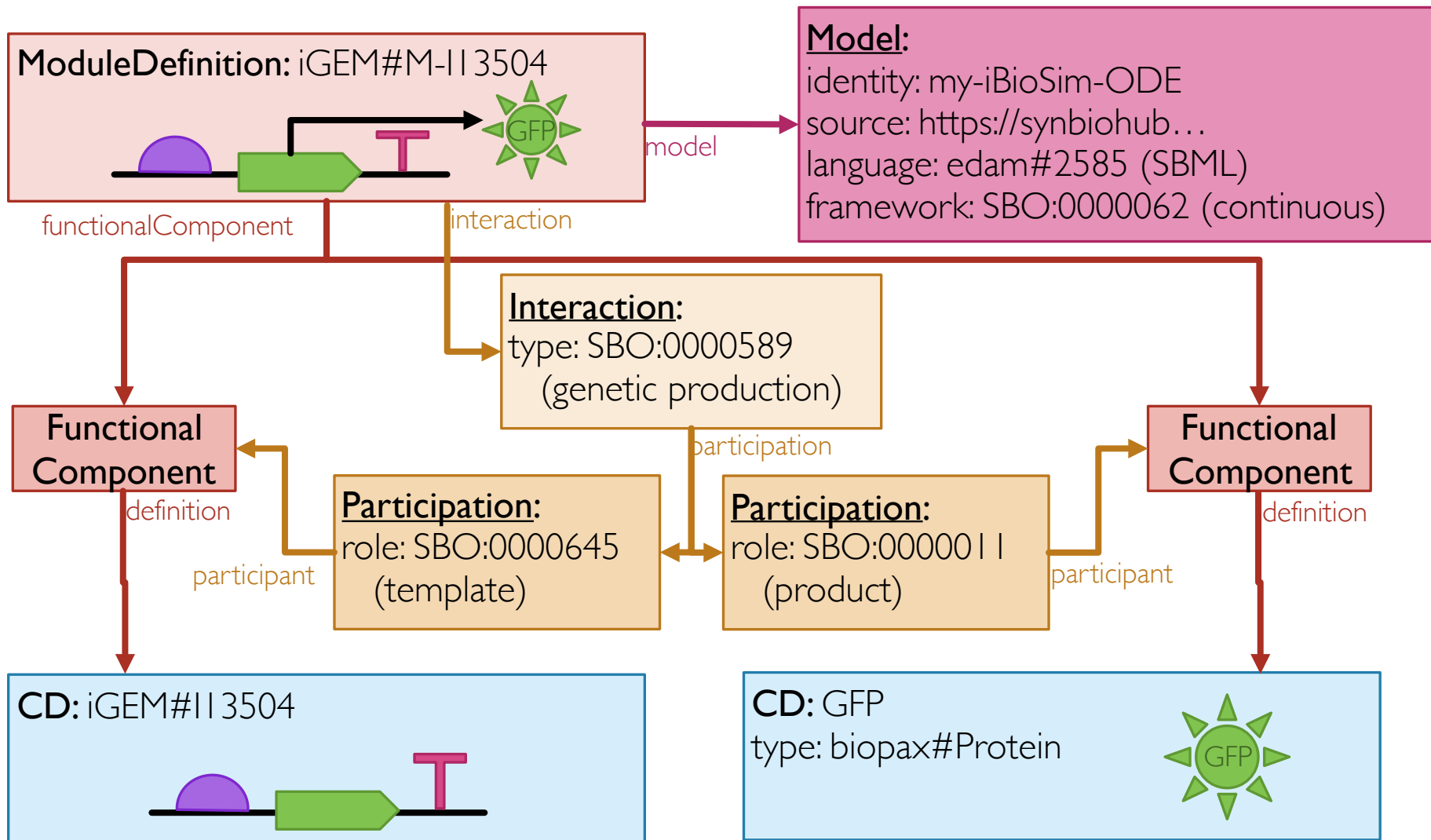
CD: iGEM#interlab16positiveControl



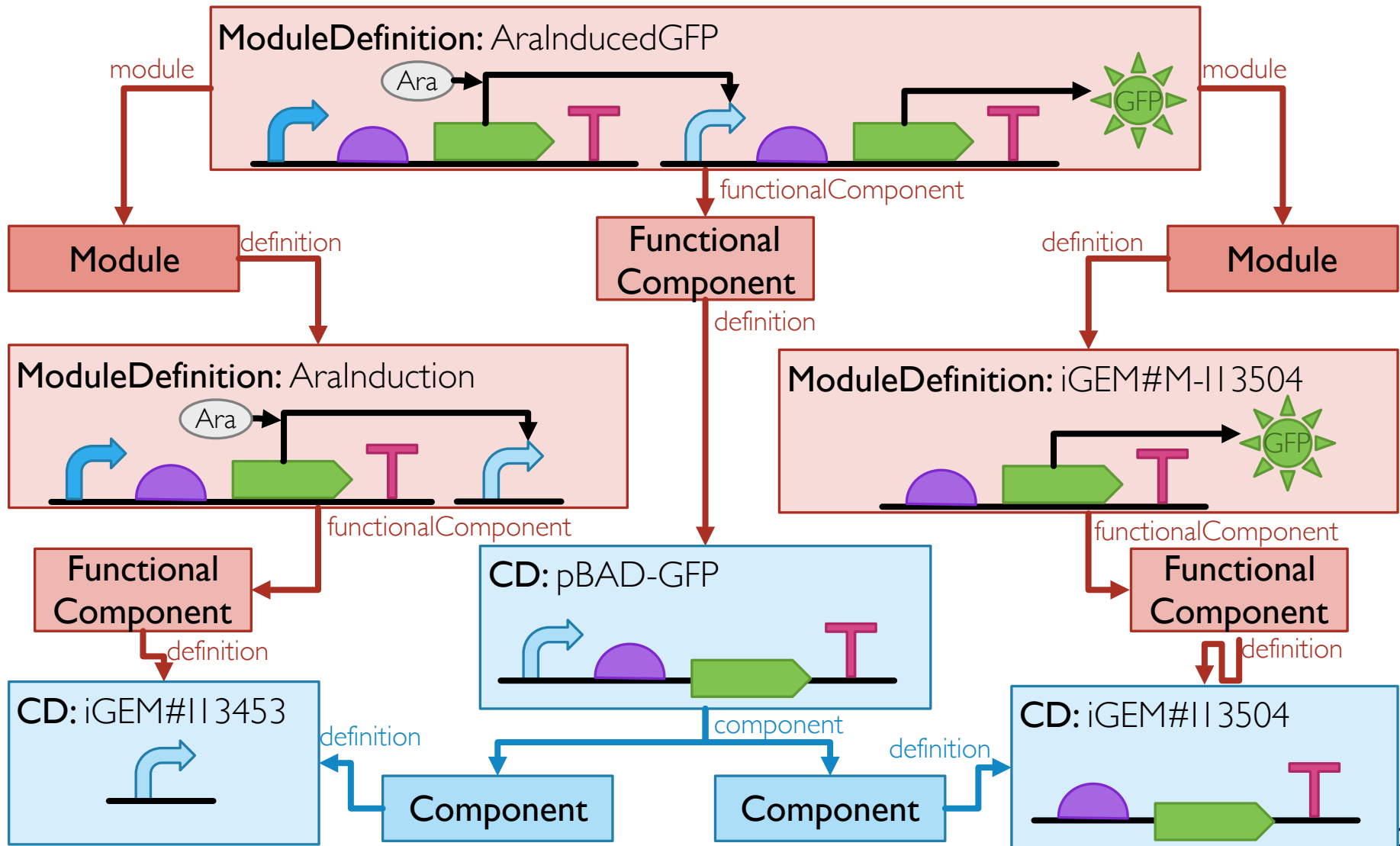
CD: iGEM#interlab16negativeControl



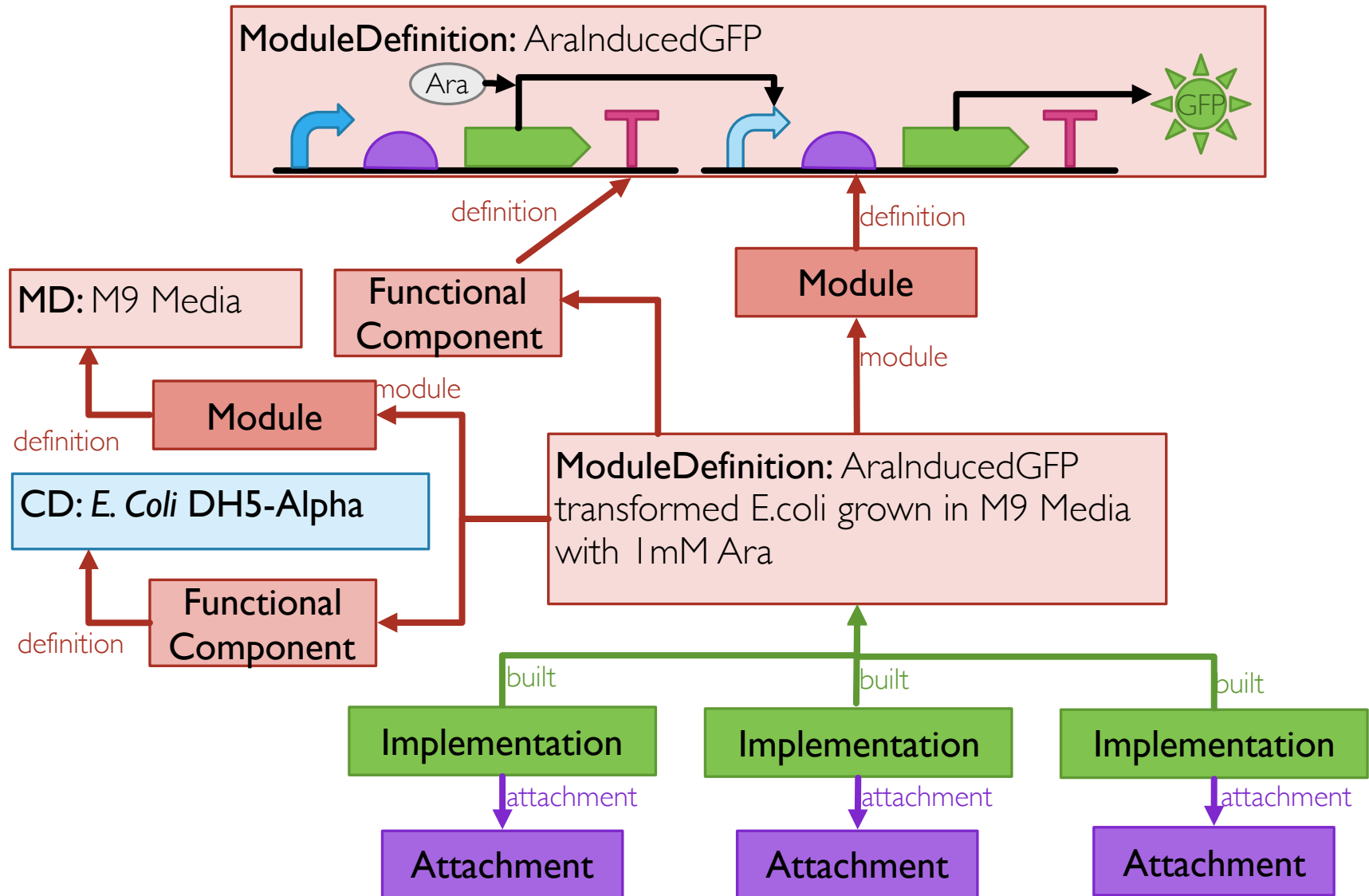
ModuleDefinition



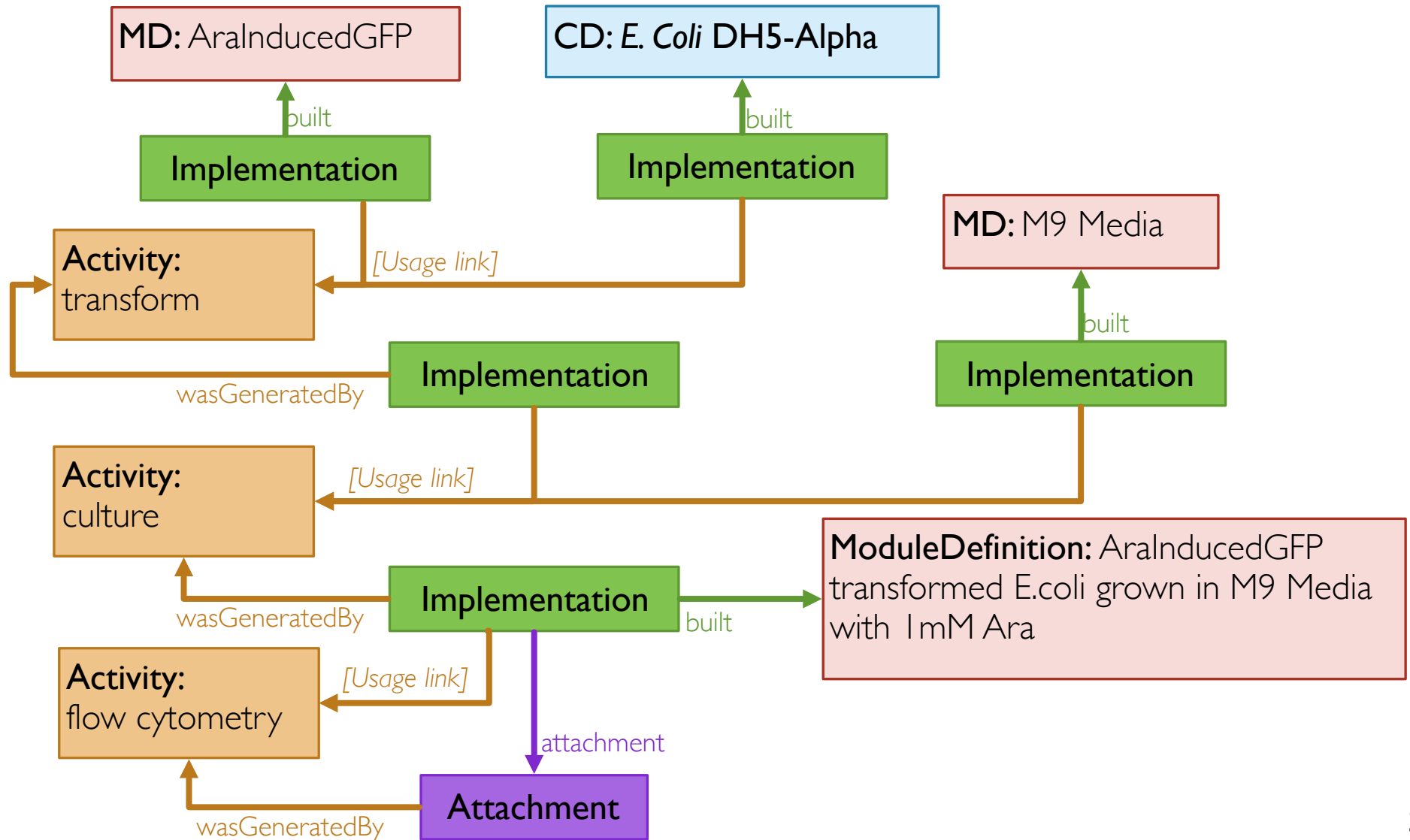
Composing Modules



Linking Designs, Protocols, and Data



Linking Designs, Protocols, and Data



Next up:

libraries & hands-on experience

Acknowledgments



EPSRC

Engineering and Physical Sciences
Research Council

