

Synthetic Biology Open Language



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Berkeley, CA

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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

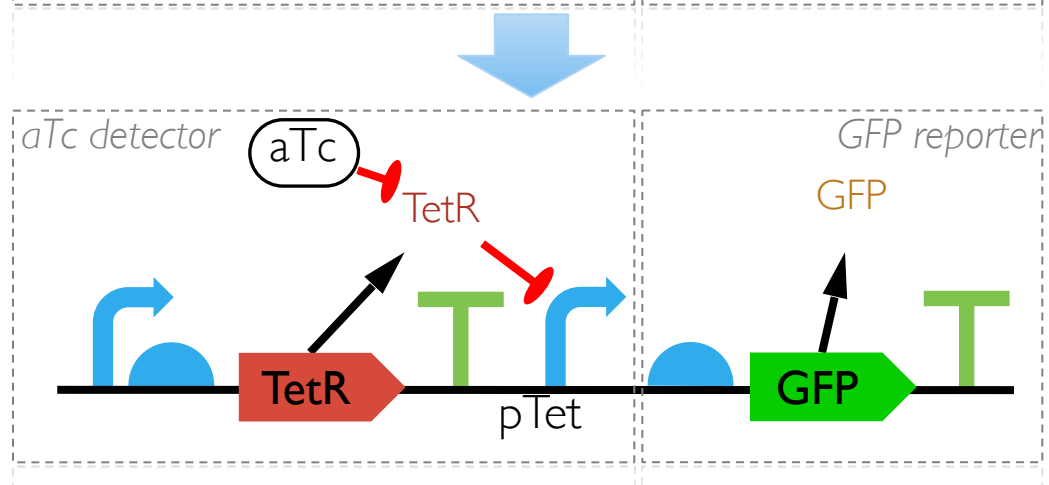
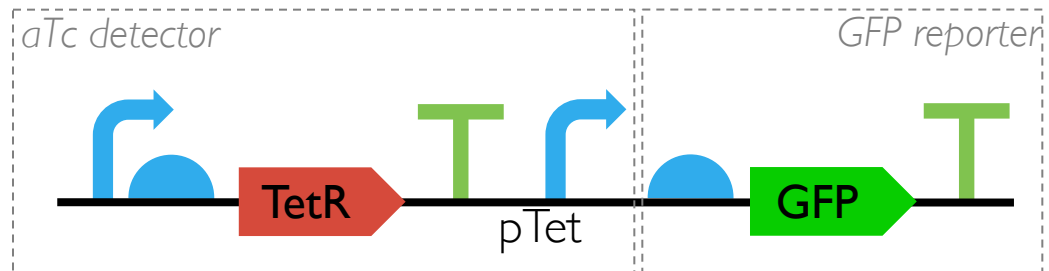
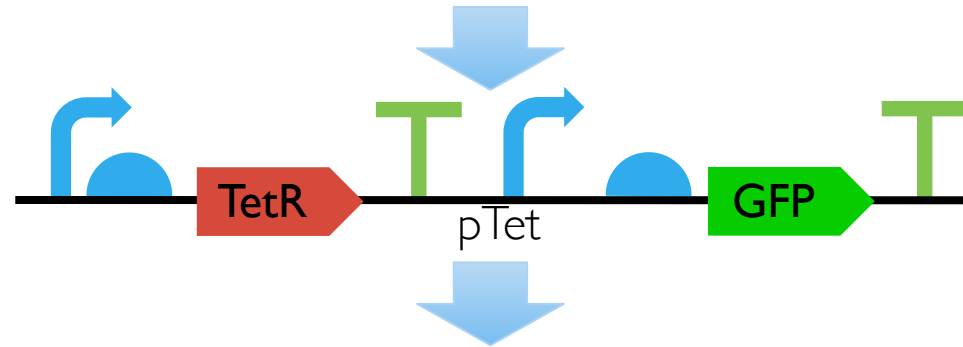
Contains sequence features

SBOL 1

Represents sequence features hierarchically

SBOL 2

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

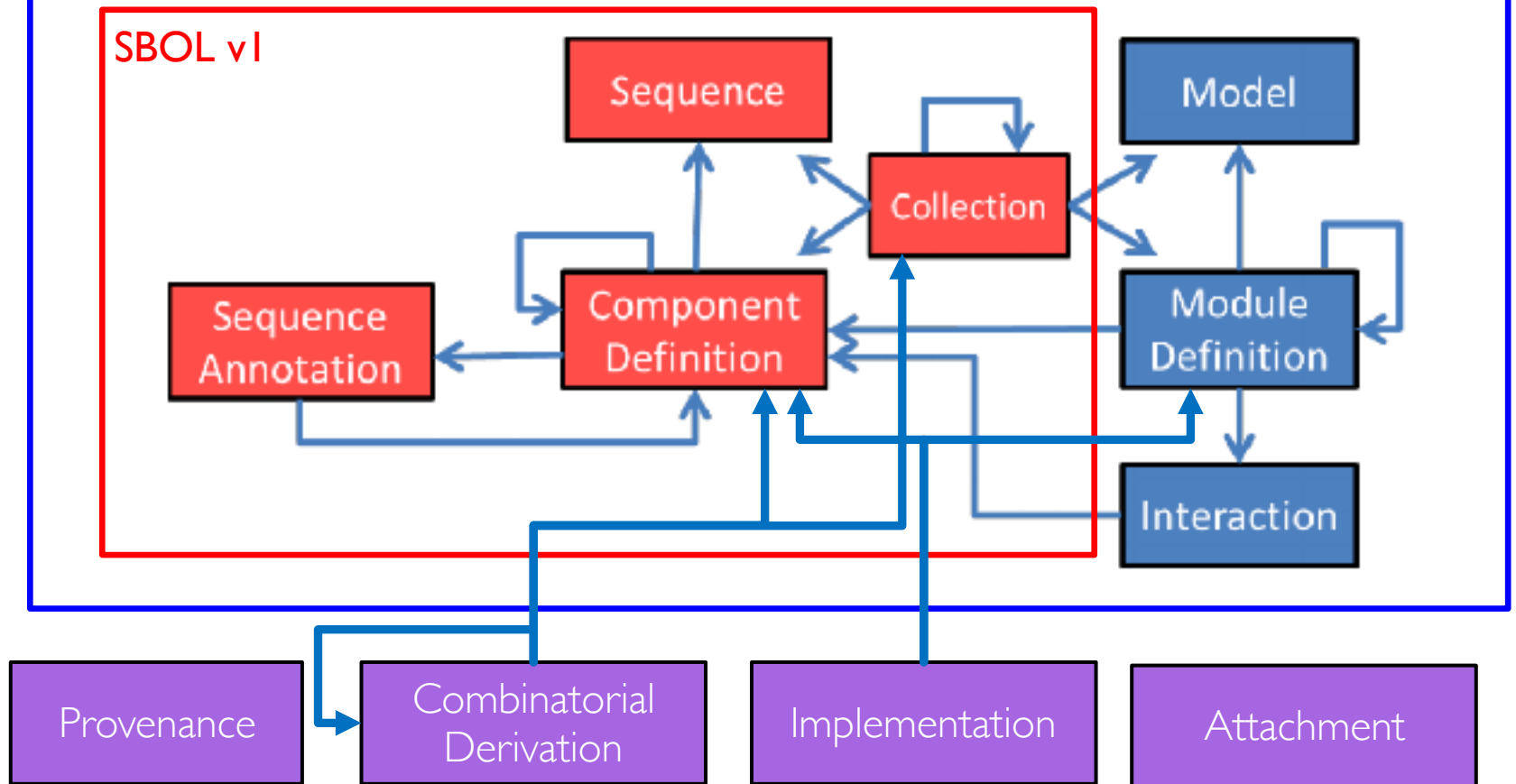


SBOL Data Model

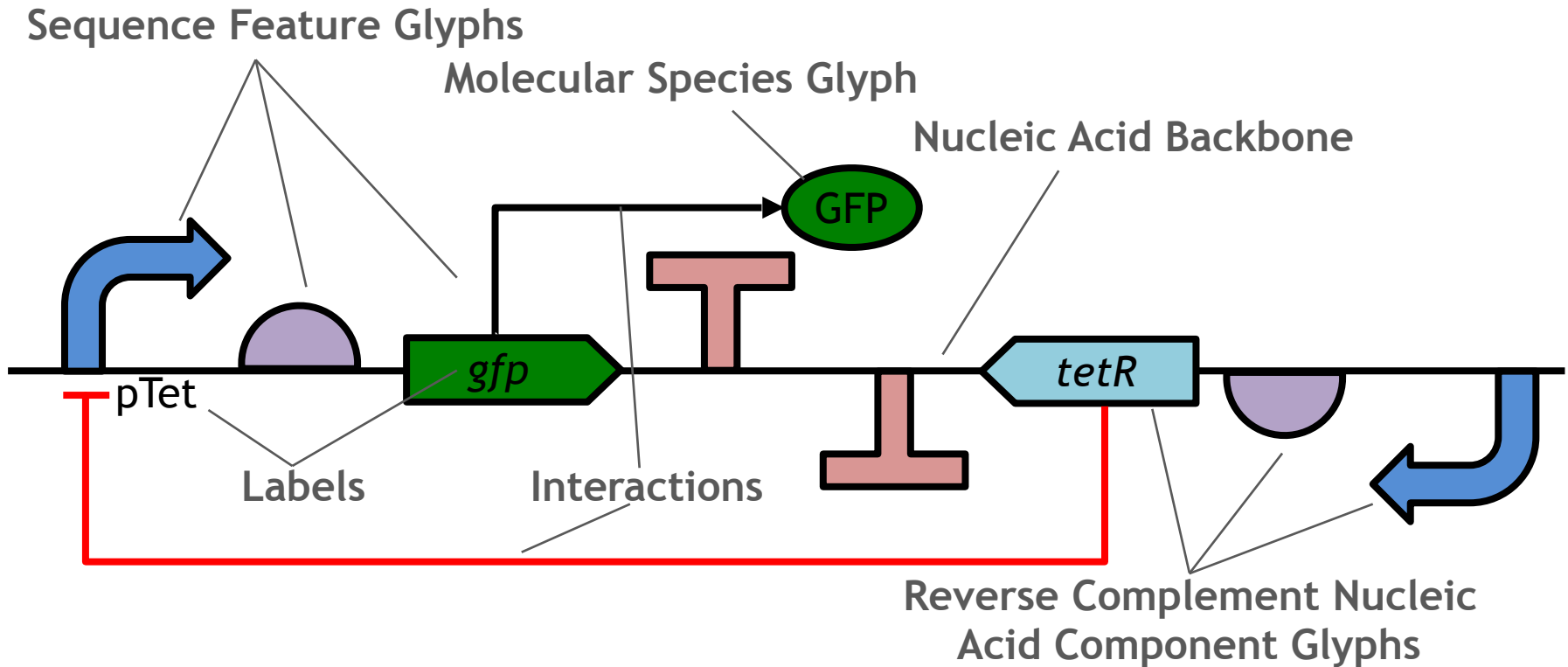
SBOL v2.2

SBOL v2.0

SBOL v1

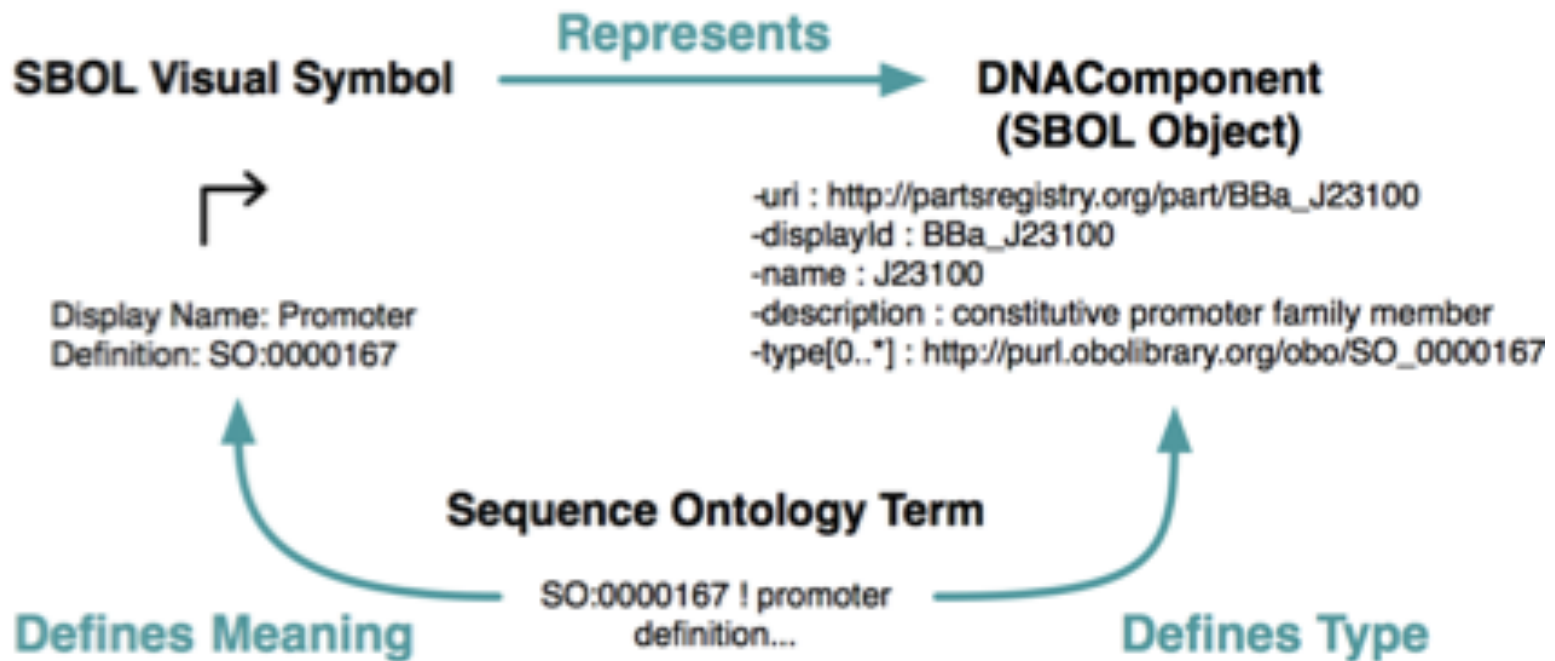


SBOL Visual v2.0

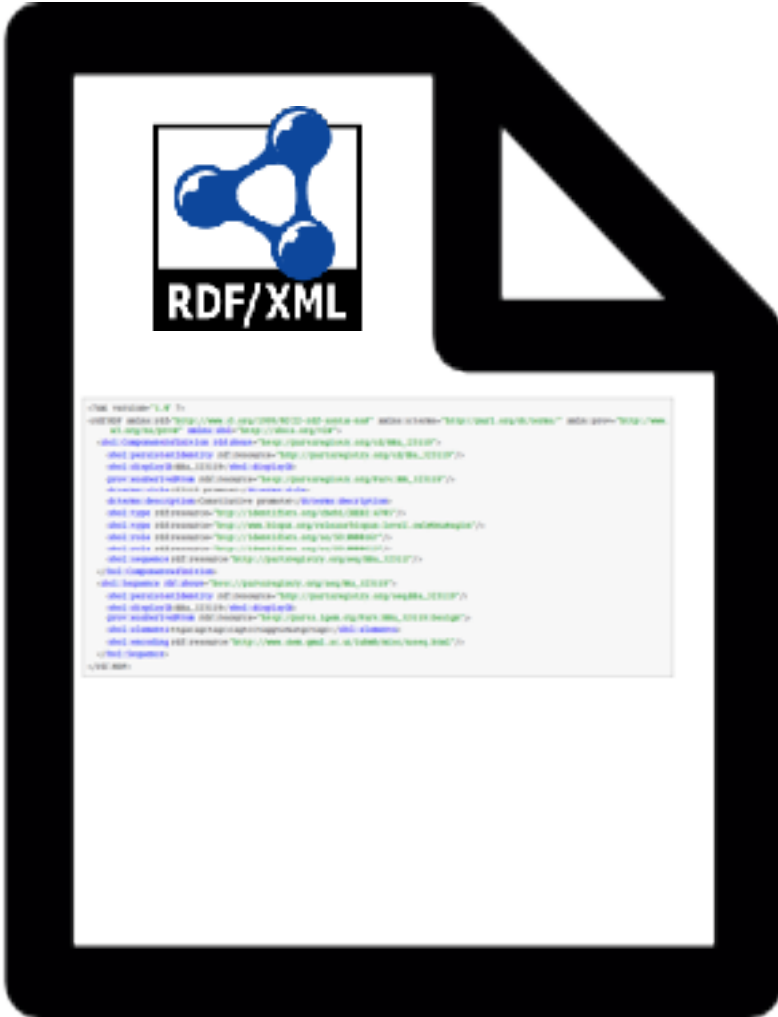


Grey text and lines (including this) are annotations

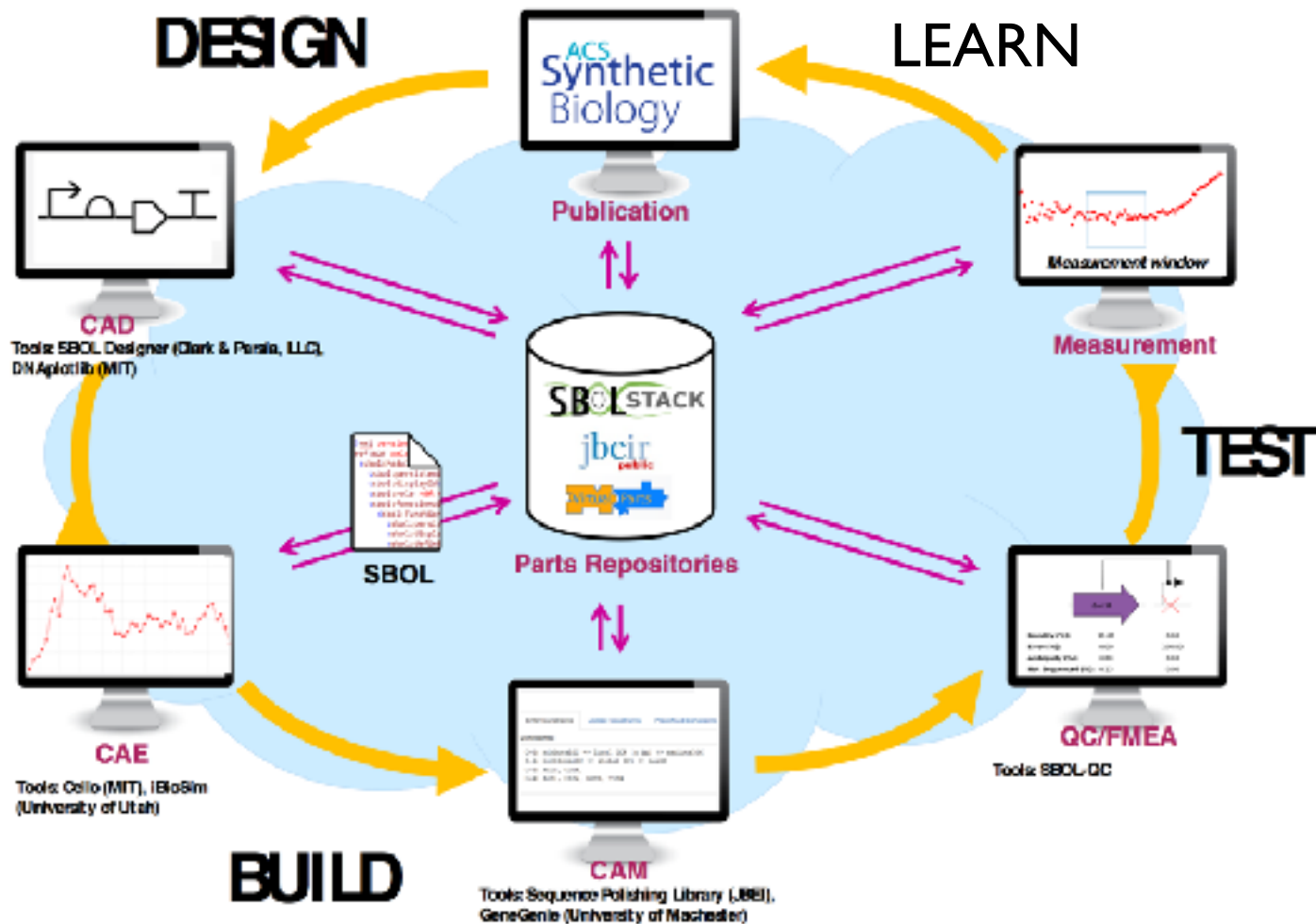
Relation between SBOL Visual and SBOL Data Model



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



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

Data Repositories: SBOLme



جامعة الملك عبد الله
العلوم والتقنية
King Abdullah University of
Science and Technology

COMPUTATIONAL
BIOSCIENCE RESEARCH
CENTER

SBOLme
repository of SBOL parts for metabolic engineering

QueryCatalogInformationAbout

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

With this query, you can search for a compound by its name or its IDs. The acceptable IDs are the KEGG compound IDs and the SBOLme compound IDs.


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



Featured

64

Personal

0

Shared

0





Drafts

0

Pending Approval

1

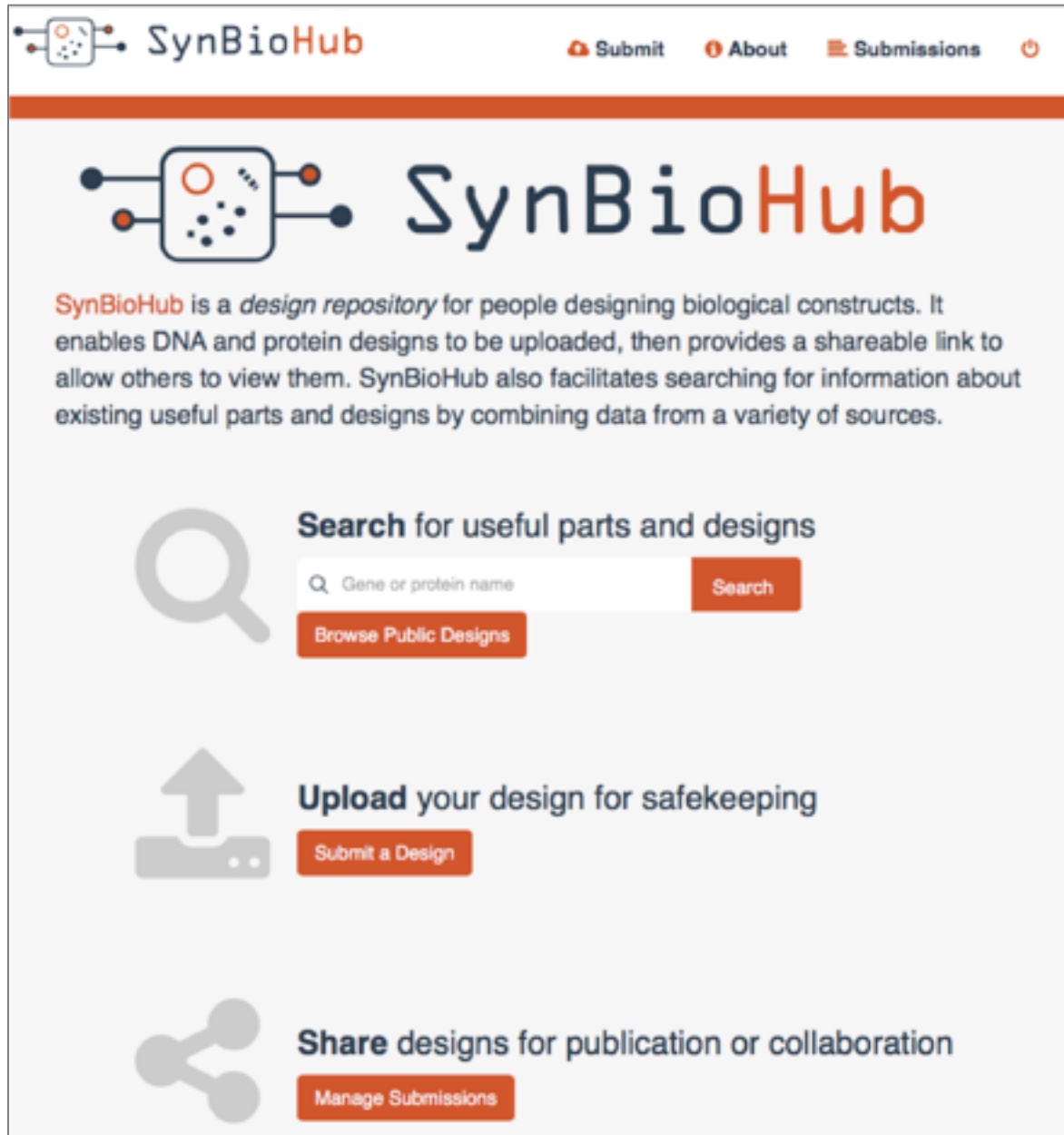
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<input type="checkbox"/>	PLASMID	LCP_000118	pGDP95_pSB1C3-g8Op-minCMV-GFP-RBQpA The 2015 BostonU iGEM team designed a set of mutually orthogonal...		<input type="button" value="Complete"/>		Dec 2, 2015
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<input type="checkbox"/>	STRAIN	LCP_000072	Assembly #1 Recombinase_Level 1 Level 1 for assembly #1.		<input type="button" value="Complete"/>		Nov 15, 2015
<input type="checkbox"/>	STRAIN	LCP_000071	gfp_pich41278_gi NucClo level 0 part.		<input type="button" value="Complete"/>		Nov 15, 2015
<input type="checkbox"/>	STRAIN	LCP_000070	tp4001p-ag-bxb1n-gt-tp401p-to-ag Level 0 part.		<input type="button" value="Complete"/>		Nov 15, 2015
<input type="checkbox"/>	STRAIN	LCP_000069	bfp-pich41258-de NucClo level 0 part.		<input type="button" value="Complete"/>		Nov 15, 2015
<input type="checkbox"/>	STRAIN	LCP_000068	bxb1n-gt_cst NucClo level 0 part.		<input type="button" value="Complete"/>		Nov 15, 2015

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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 section with the SynBioHub logo and a description: '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: 1. 'Search for useful parts and designs' with a magnifying glass icon, a search input field labeled 'Gene or protein name', a 'Search' button, and a 'Browse Public Designs' button. 2. 'Upload your design for safekeeping' with an upload icon, a 'Submit a Design' button. 3. 'Share designs for publication or collaboration' with a share icon and a 'Manage Submissions' button.

SynBioHub

Submit About Submissions

SynBioHub

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.

Search for useful parts and designs

Gene or protein name Search

Browse Public Designs

Upload your design for safekeeping

Submit a Design

Share designs for publication or collaboration

Manage Submissions

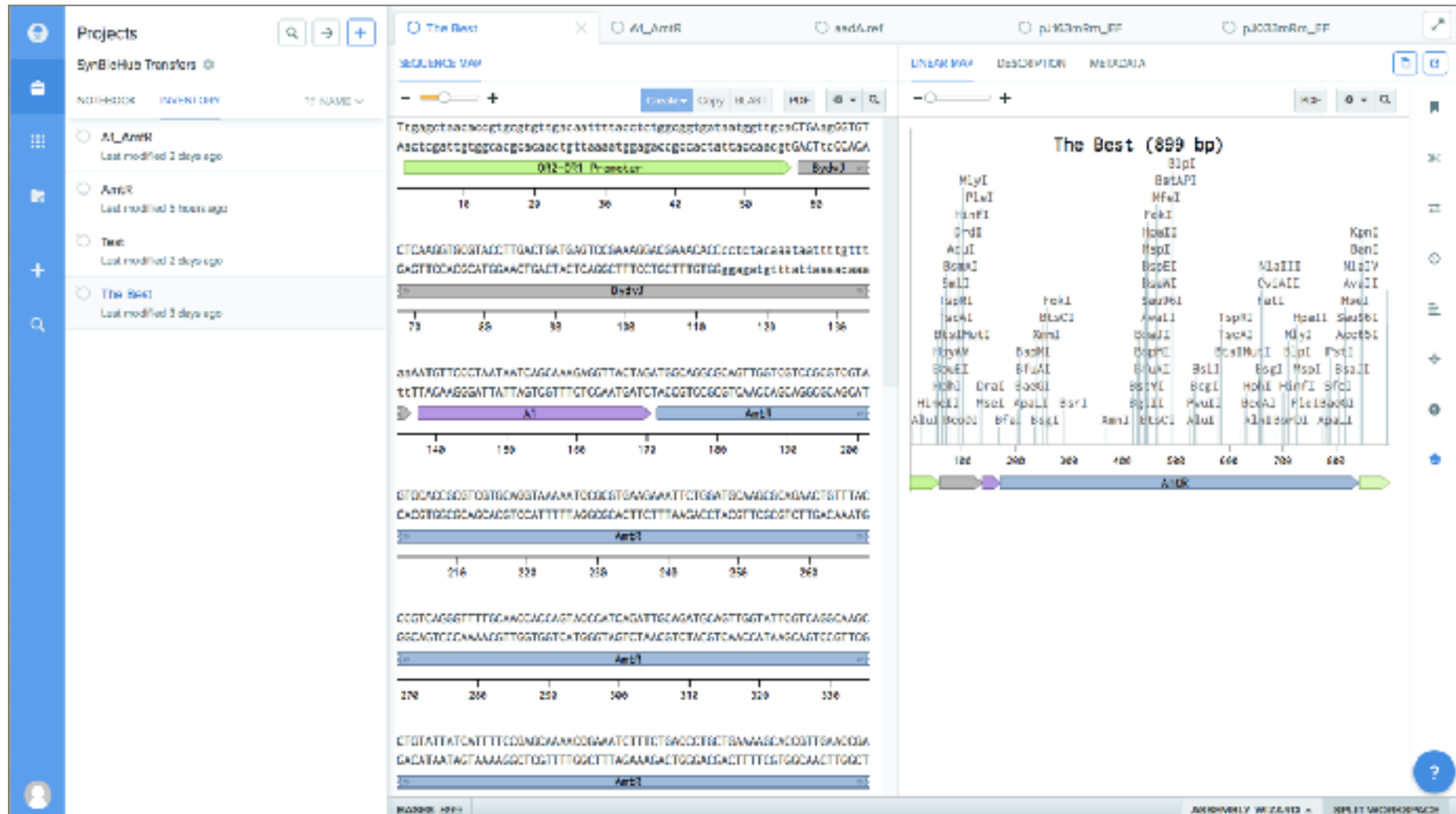


James McLaughlin
Anil Wipat

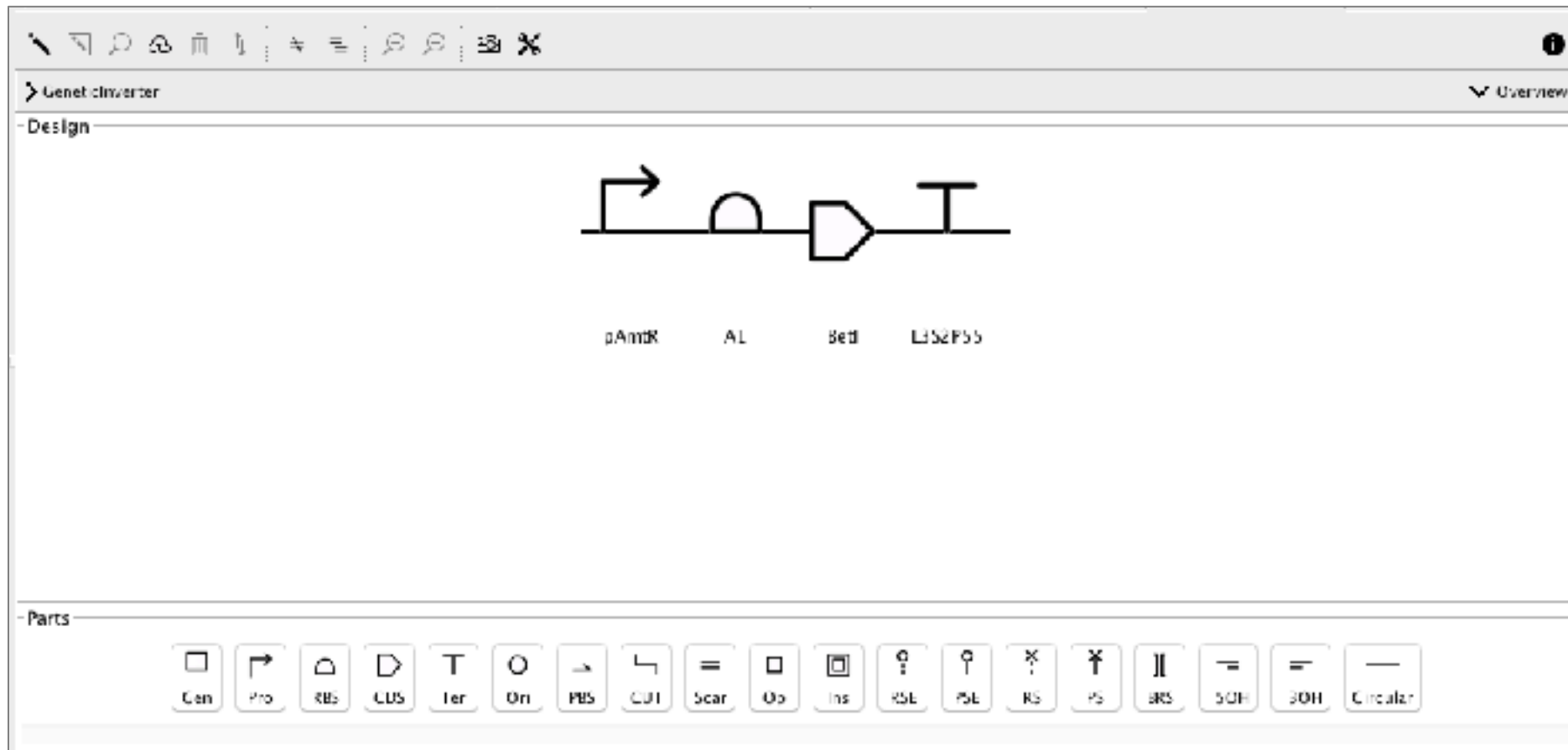


Zach Zundel
Chris Myers

Sequence Editor: Benchling



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

Cello Verilog Options Results About You are logged in as myers Logout

Verilog

choose

```
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
```

design name

Run

Inputs

choose clear

index	name	low RPU	high RPU	DNA sequence
1	pTac	0.0034	2.8	AACGATCGTTGGCTGTGTTGAGAA
2	pTet	0.0018	4.4	TACTCCACCGTTGGCTTTTTCGC

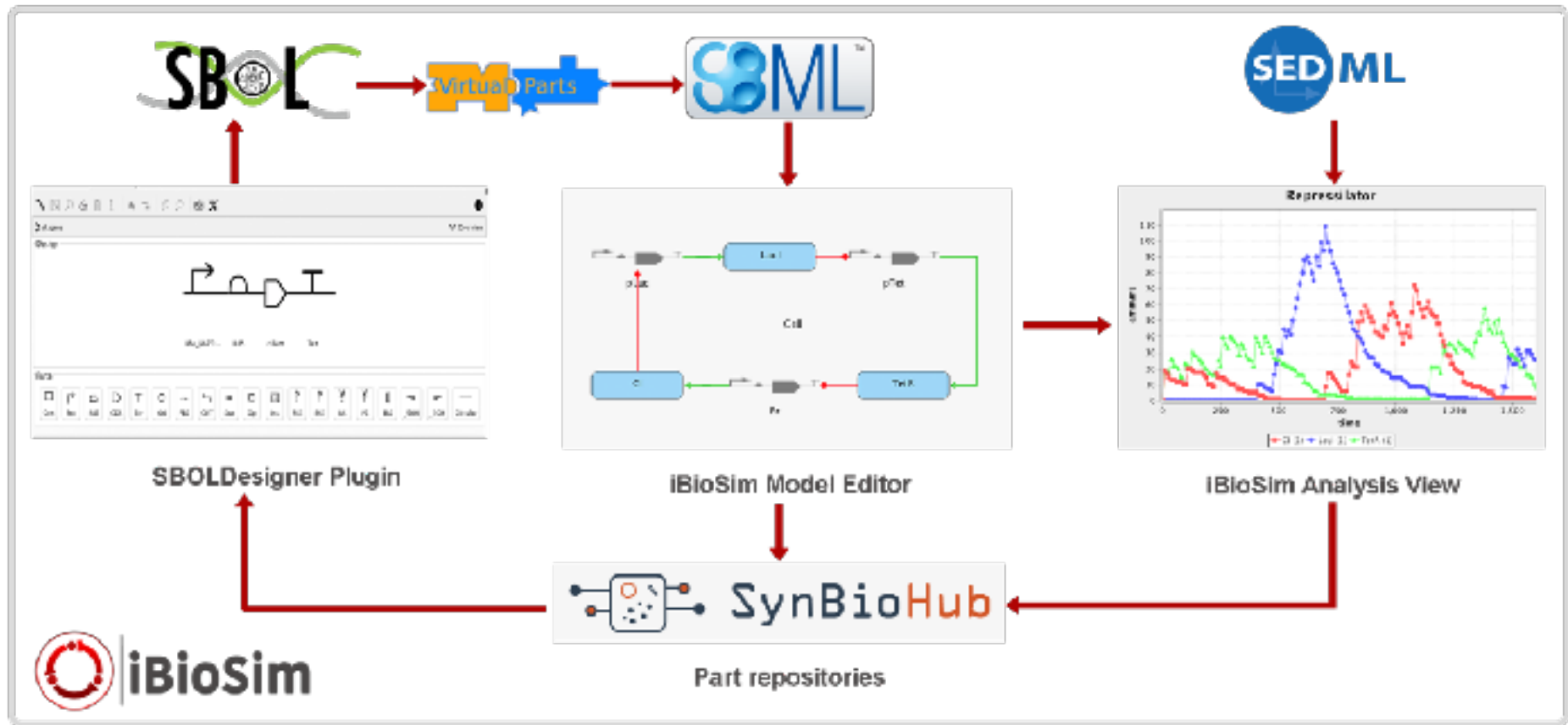
Outputs

choose clear

index	name	DNA sequence
1	YFP	CTGAAGCTGTCAACGGATGTGCTTTCGGTCTGATGAGTCCGT

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.

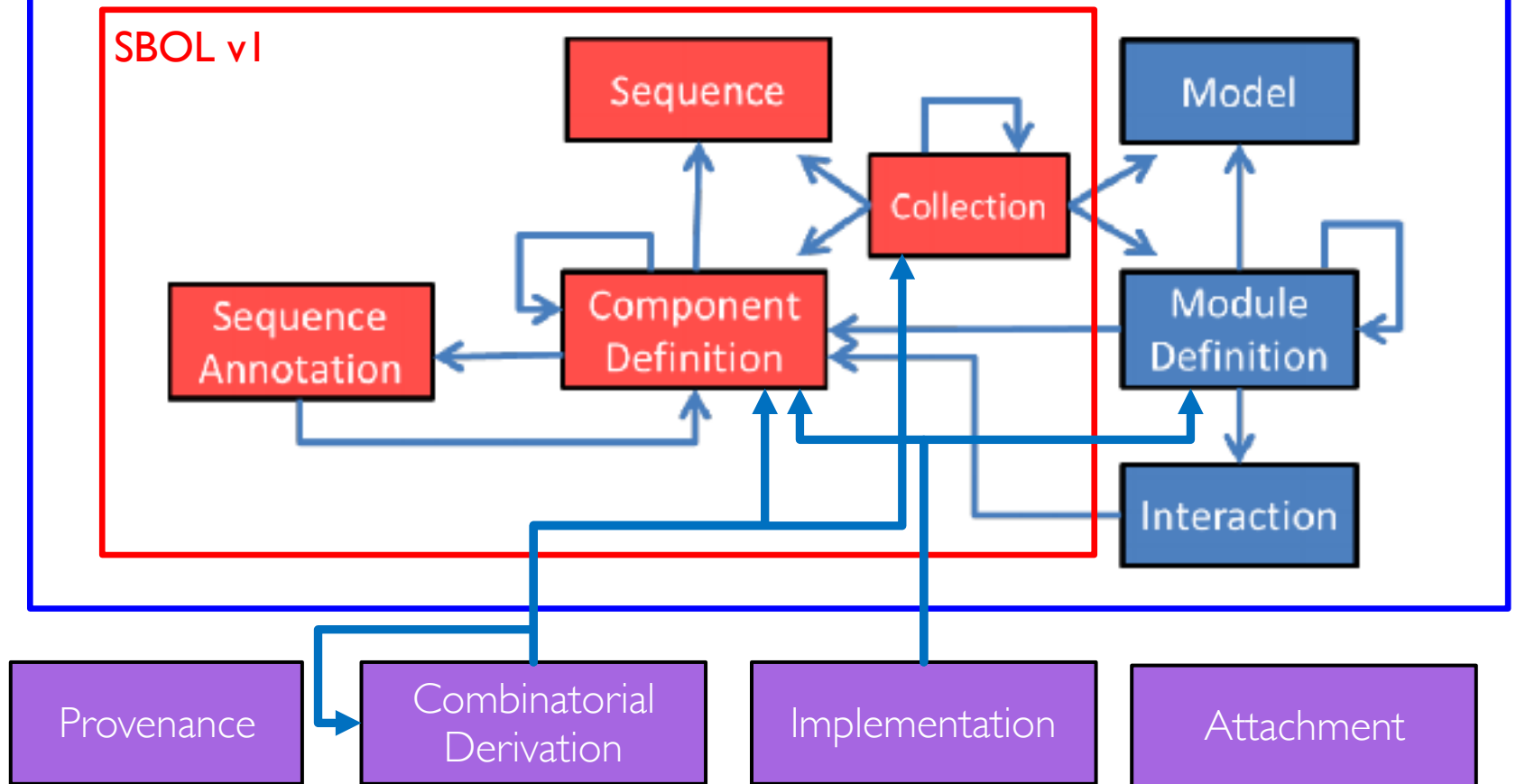
Read all about it in the ACS Synthetic Biology viewpoint article: [Improving Synthetic Biology Communication: Recommended Practices for Visual Depiction and Digital Submission of Genetic Designs](#), or [listen to the interview with Jake Beal and Nathan Hillson](#).

SBOL Data Model

SBOL v2.2

SBOL v2.0

SBOL v1



ComponentDefinition

ComponentDefinition

identity: iGEM#113504

name: "iGEM 2016 interlab reporter"

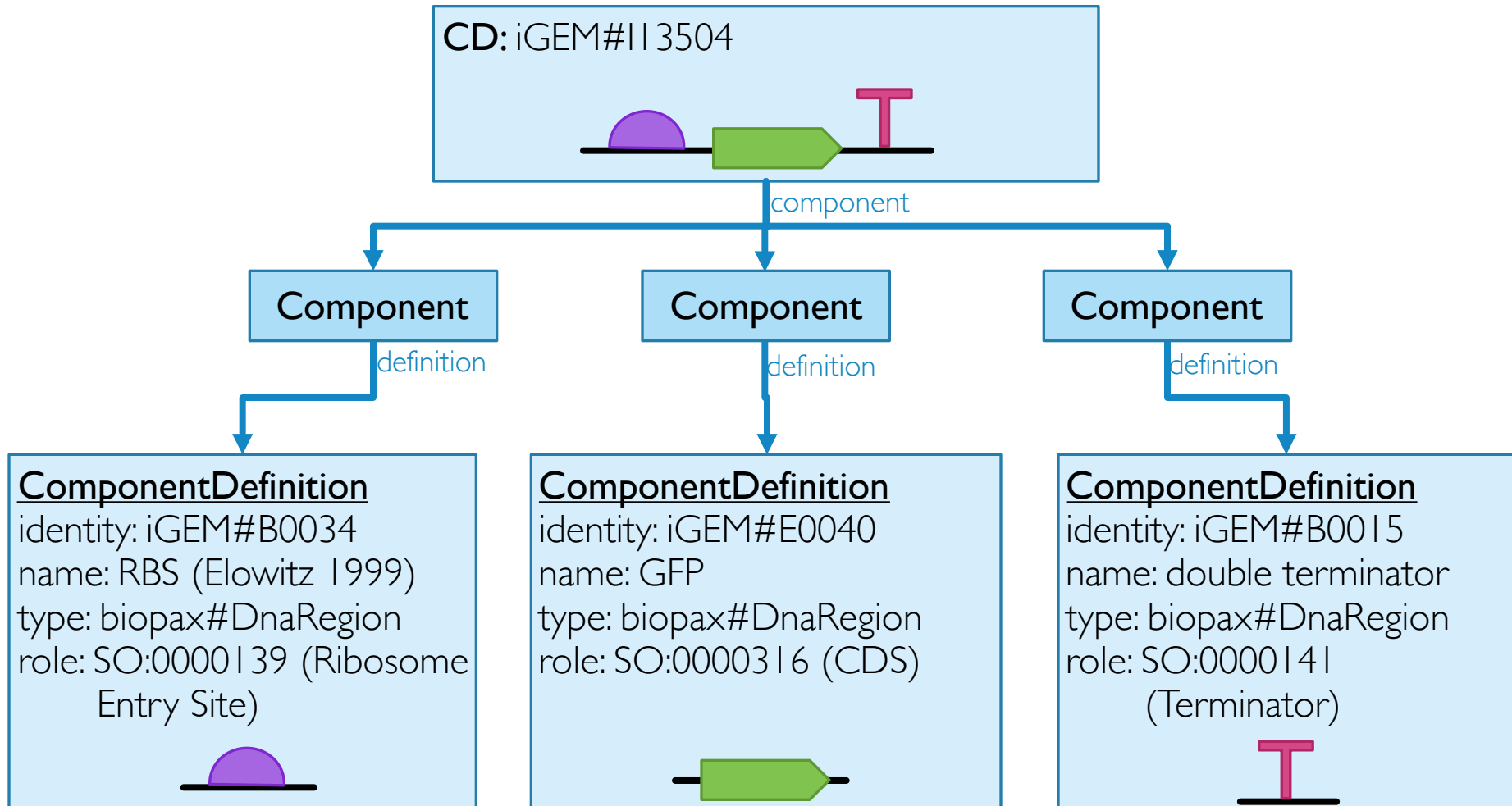
description: "GFP expression cassette
used for 2016 iGEM interlab"

type: biopax#DnaRegion

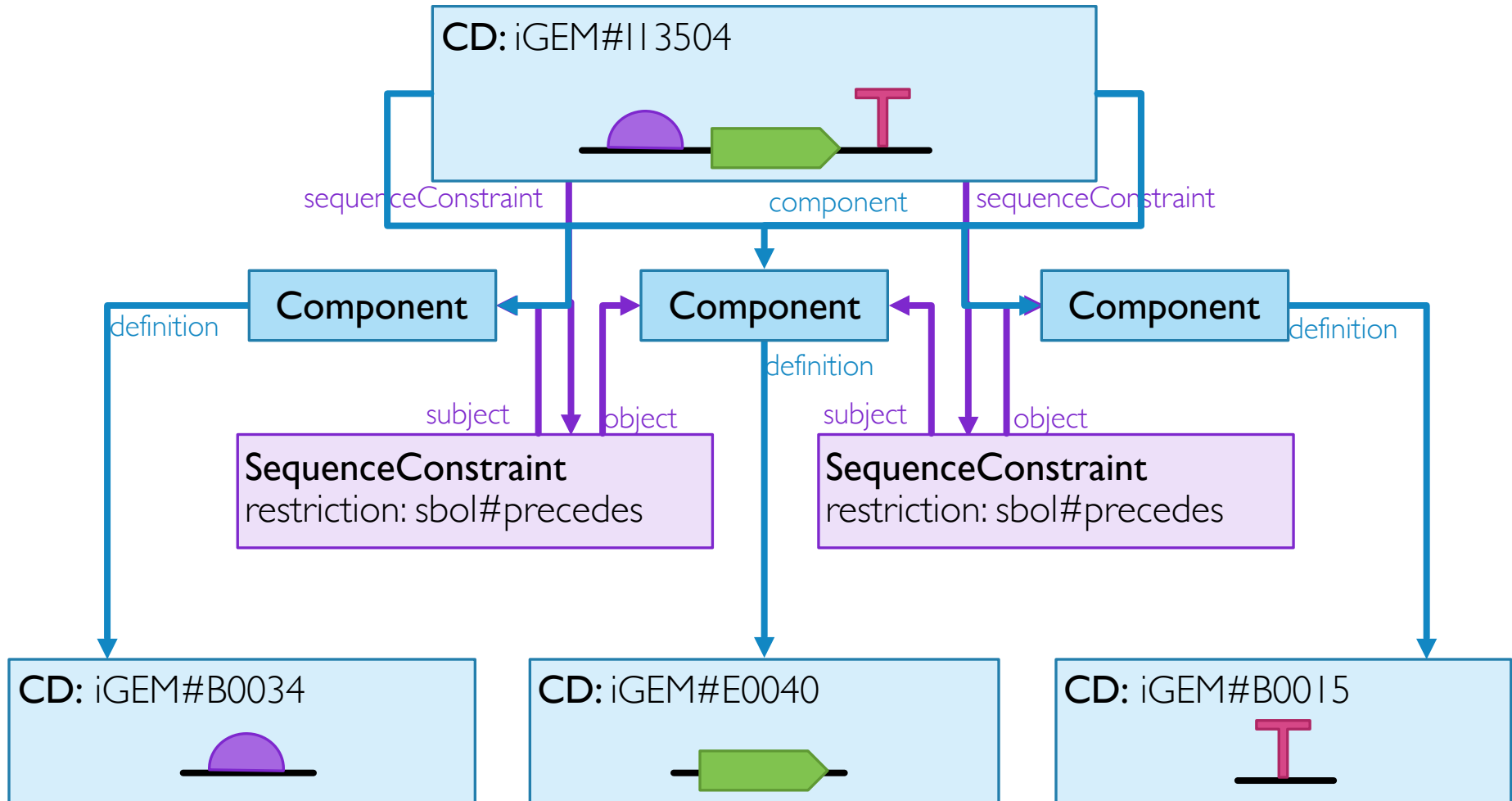
role: SO:0000804 (Engineered Region)



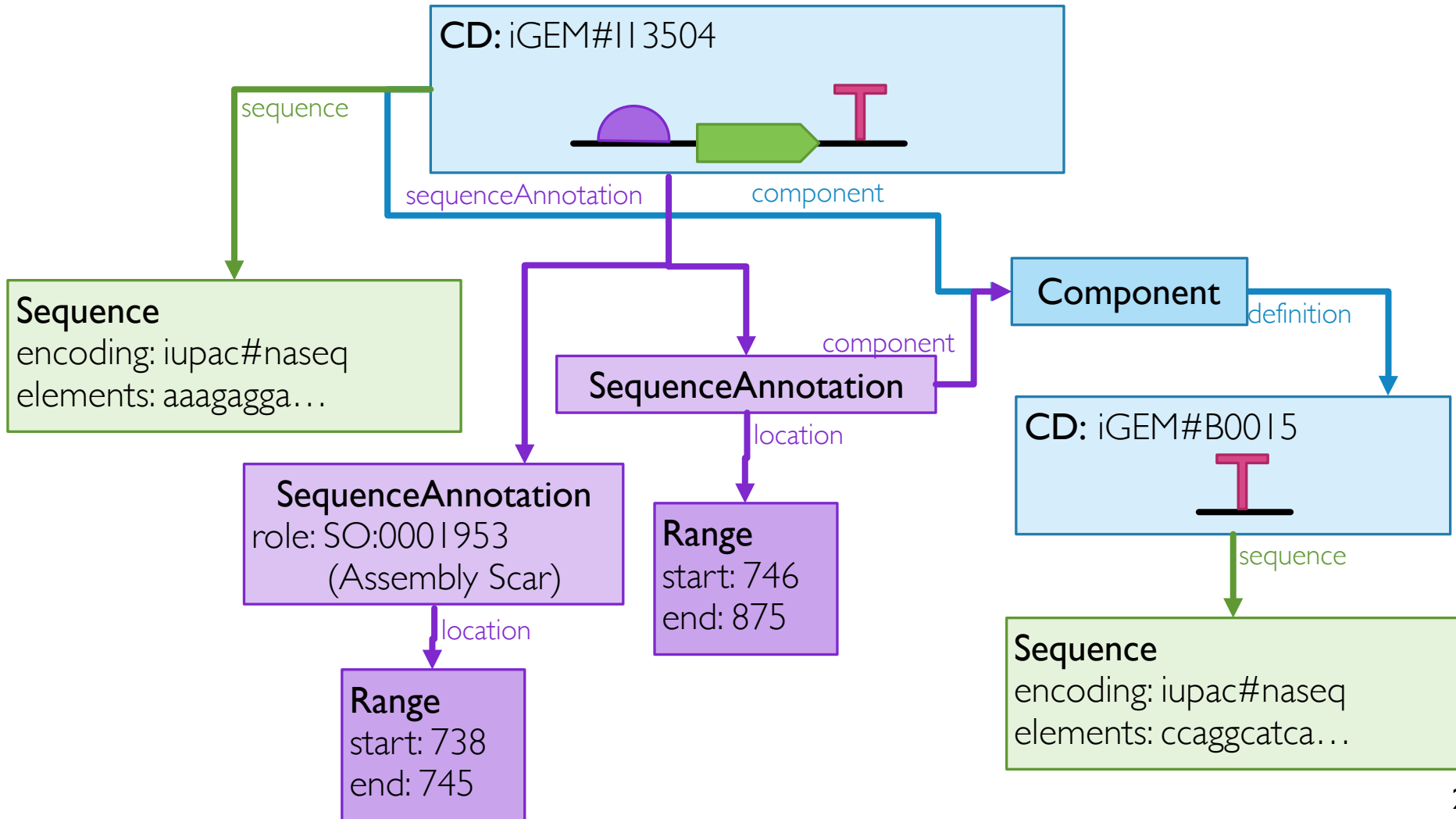
Component



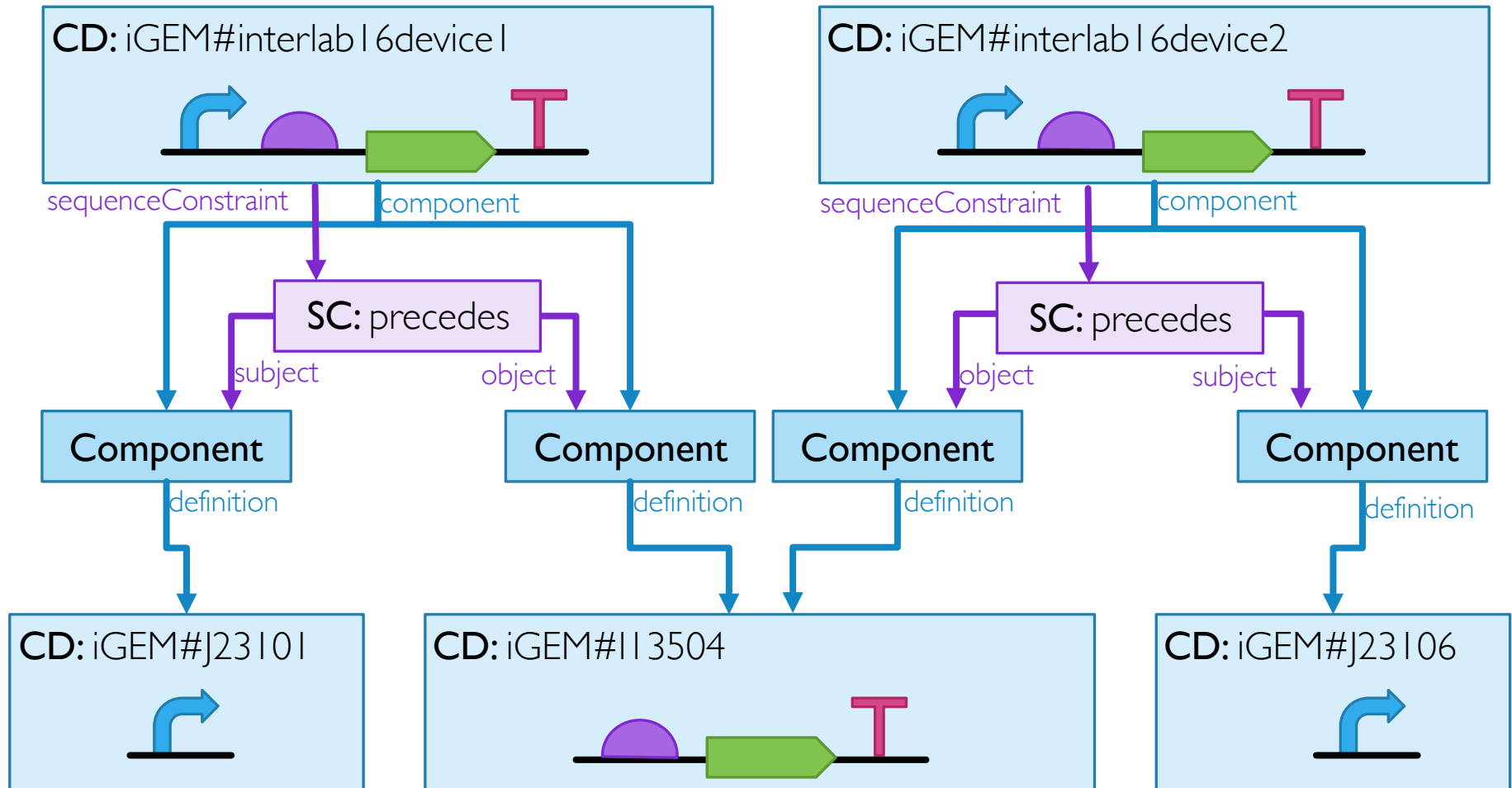
SequenceConstraint



Sequence, SequenceAnnotation



Reusing Components



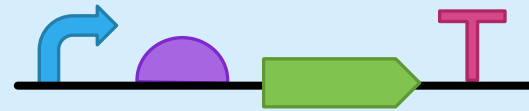
Collection

Collection:

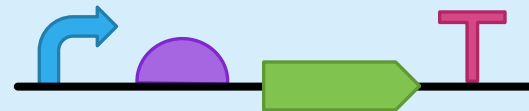
identity: iGEM#interlab16
name: "iGEM 2016 interlab parts"
description: "Collection of parts used for
2016 iGEM interlab"

member

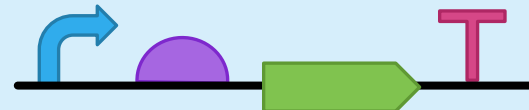
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CD: iGEM#interlab16device2



CD: iGEM#interlab16device3



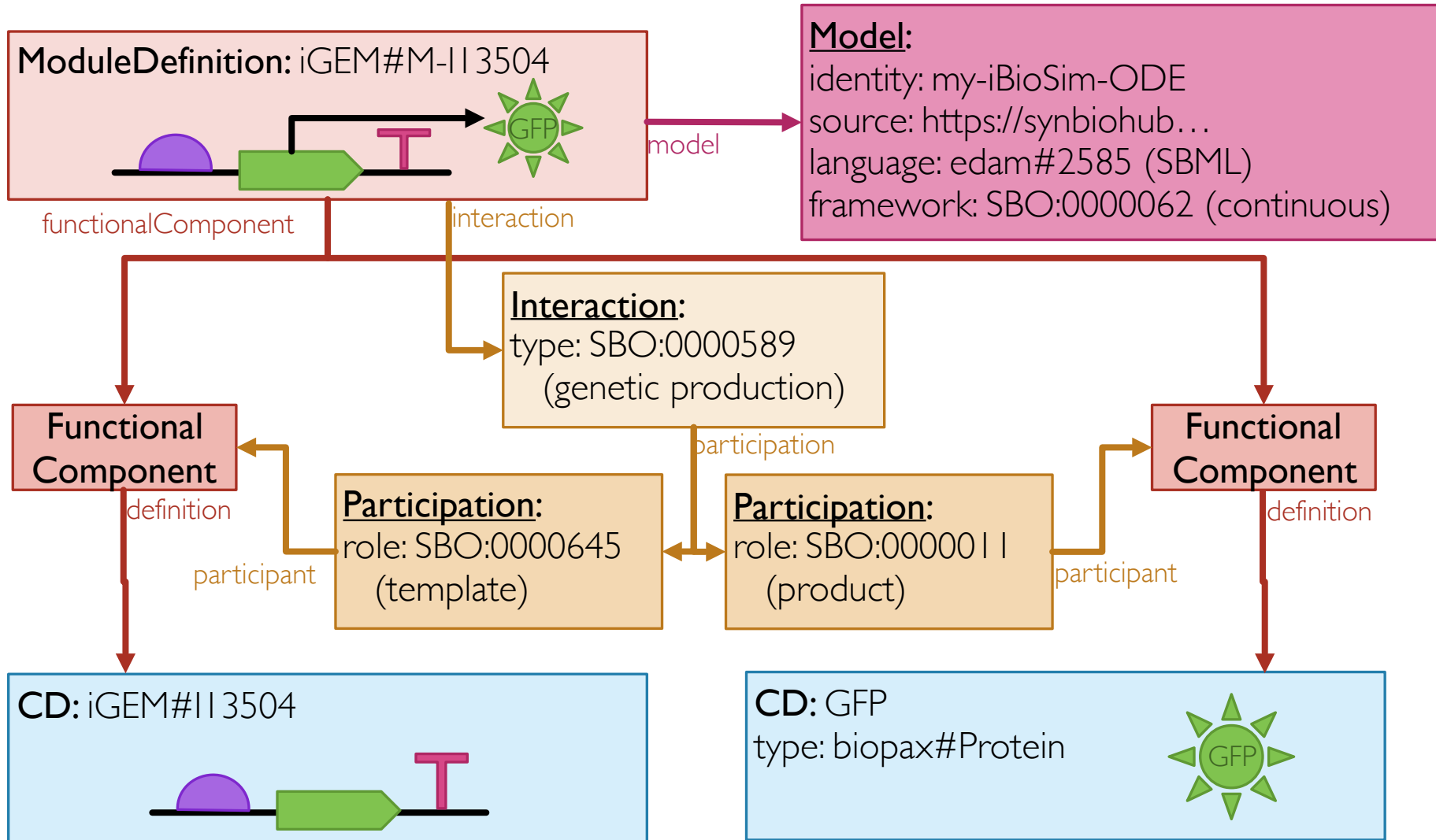
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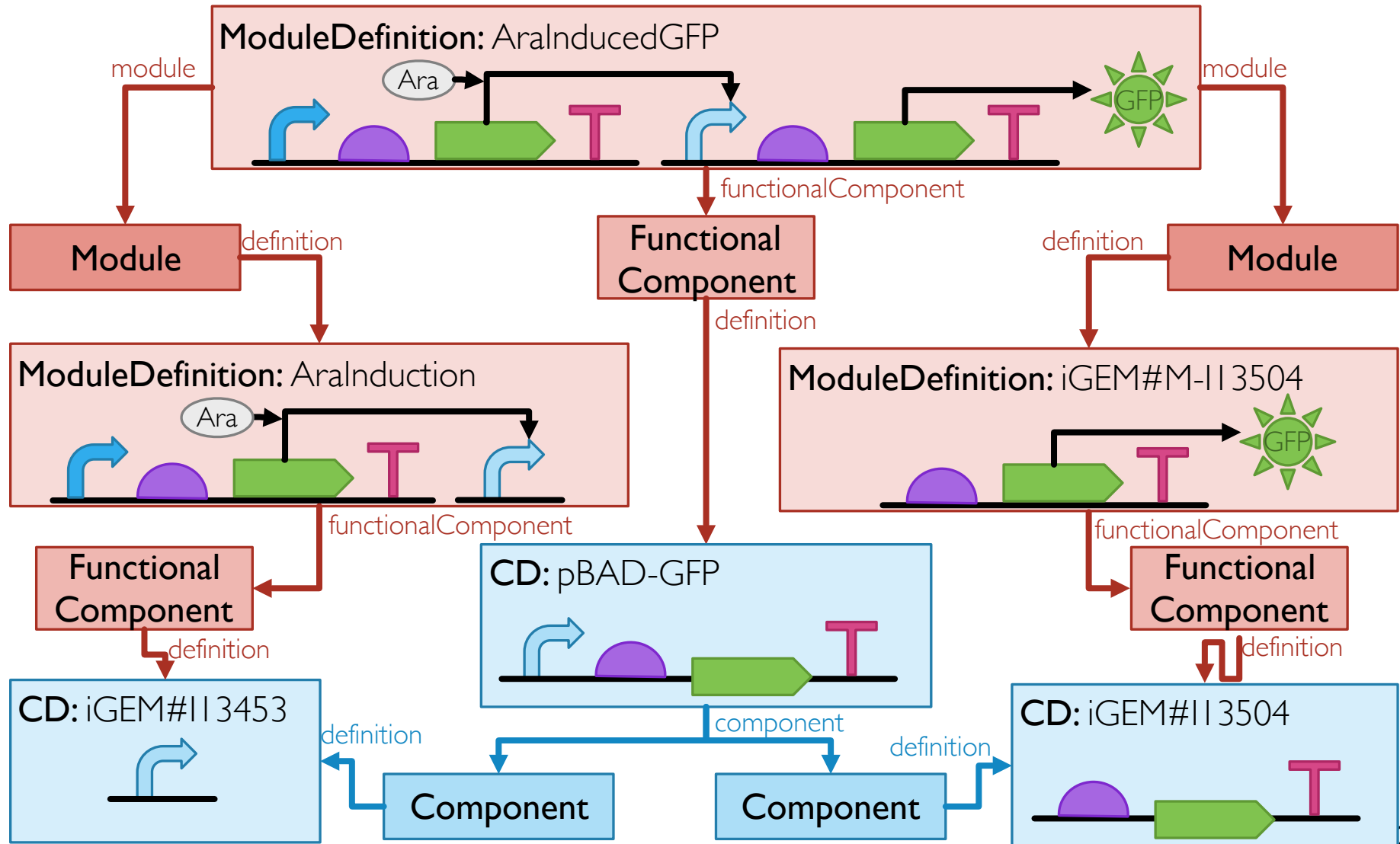
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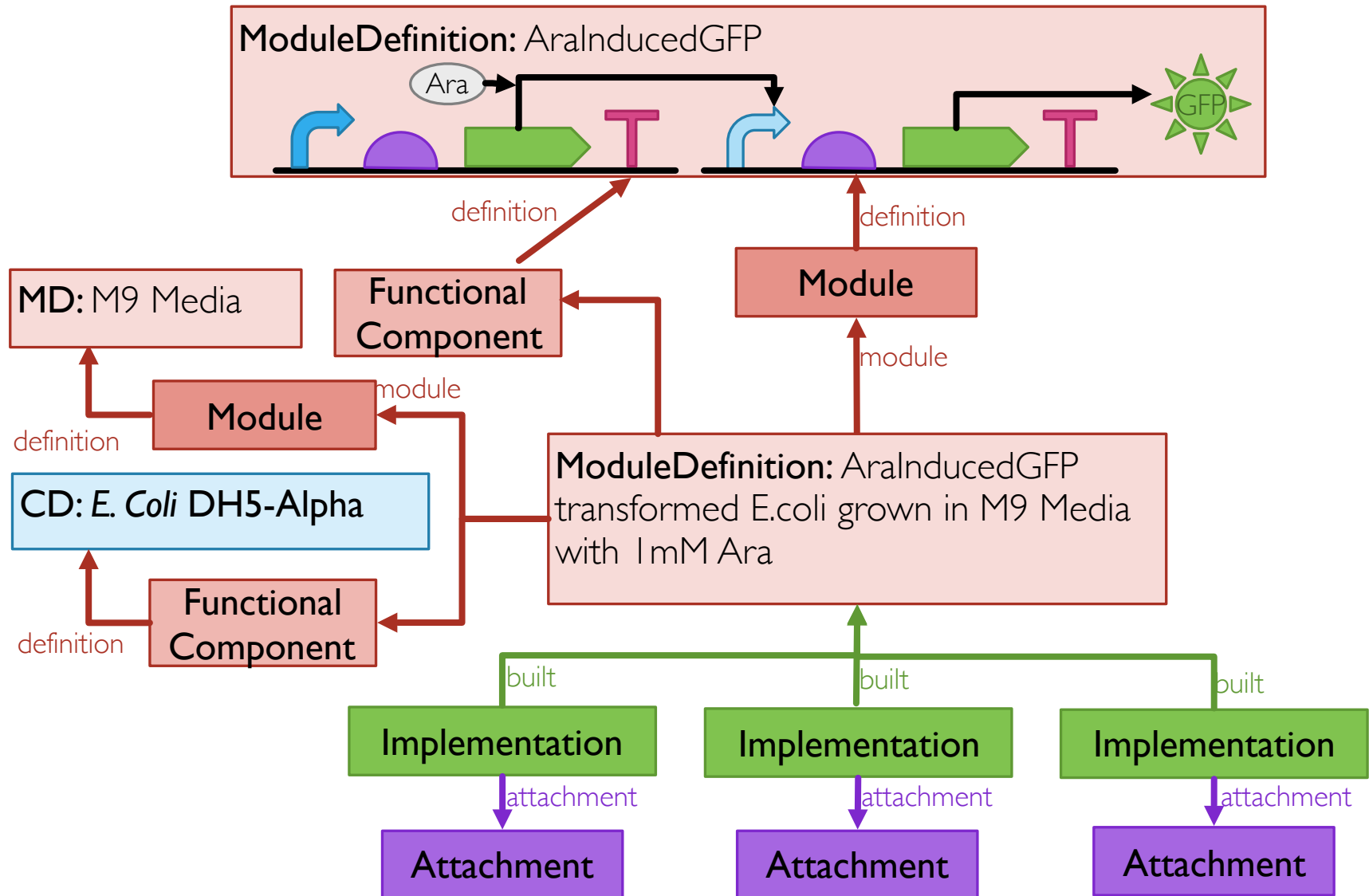
ModuleDefinition



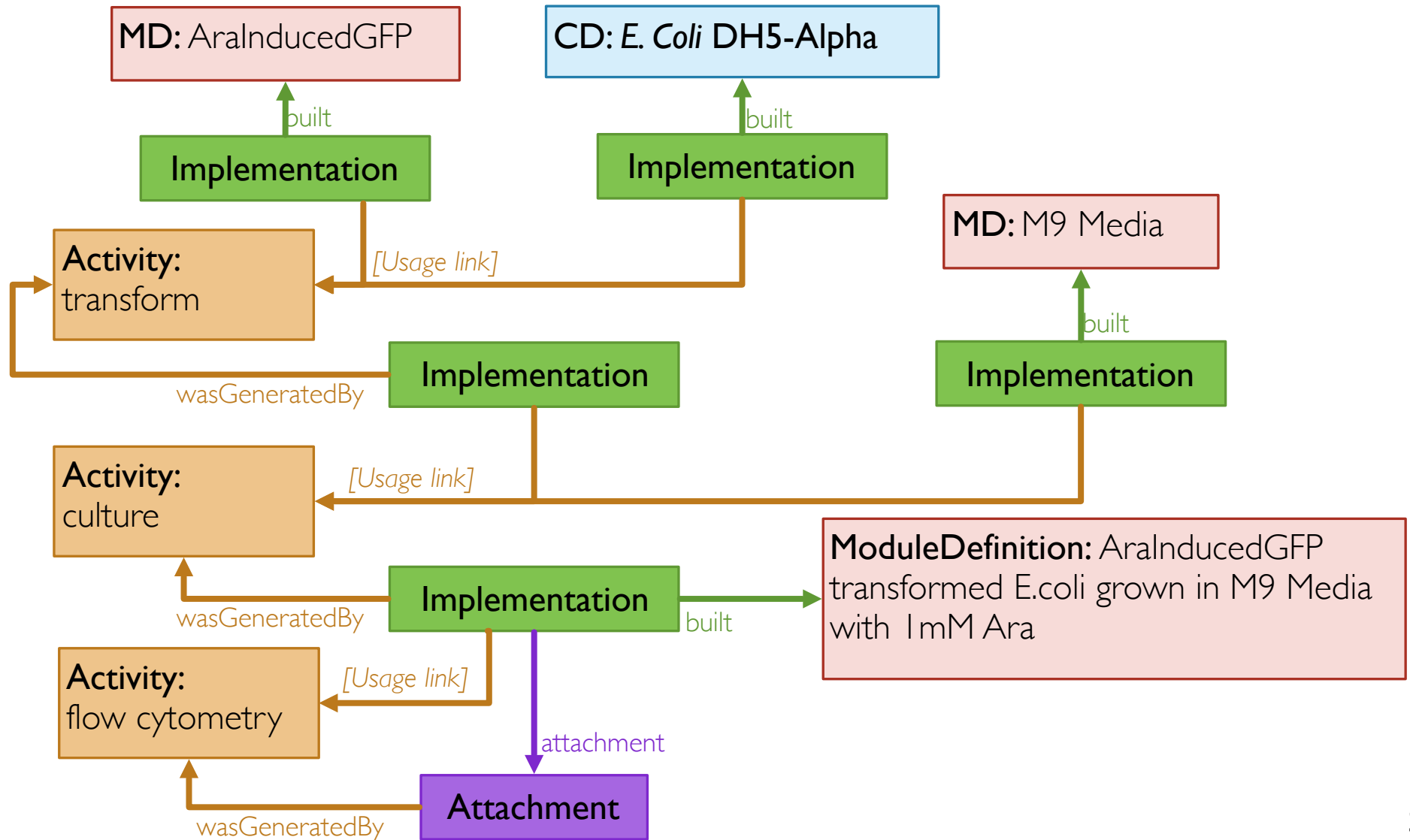
Composing Modules



Linking Designs, Protocols, and Data



Linking Designs, Protocols, and Data



Next up:

libraries & hands-on experience

Acknowledgments

