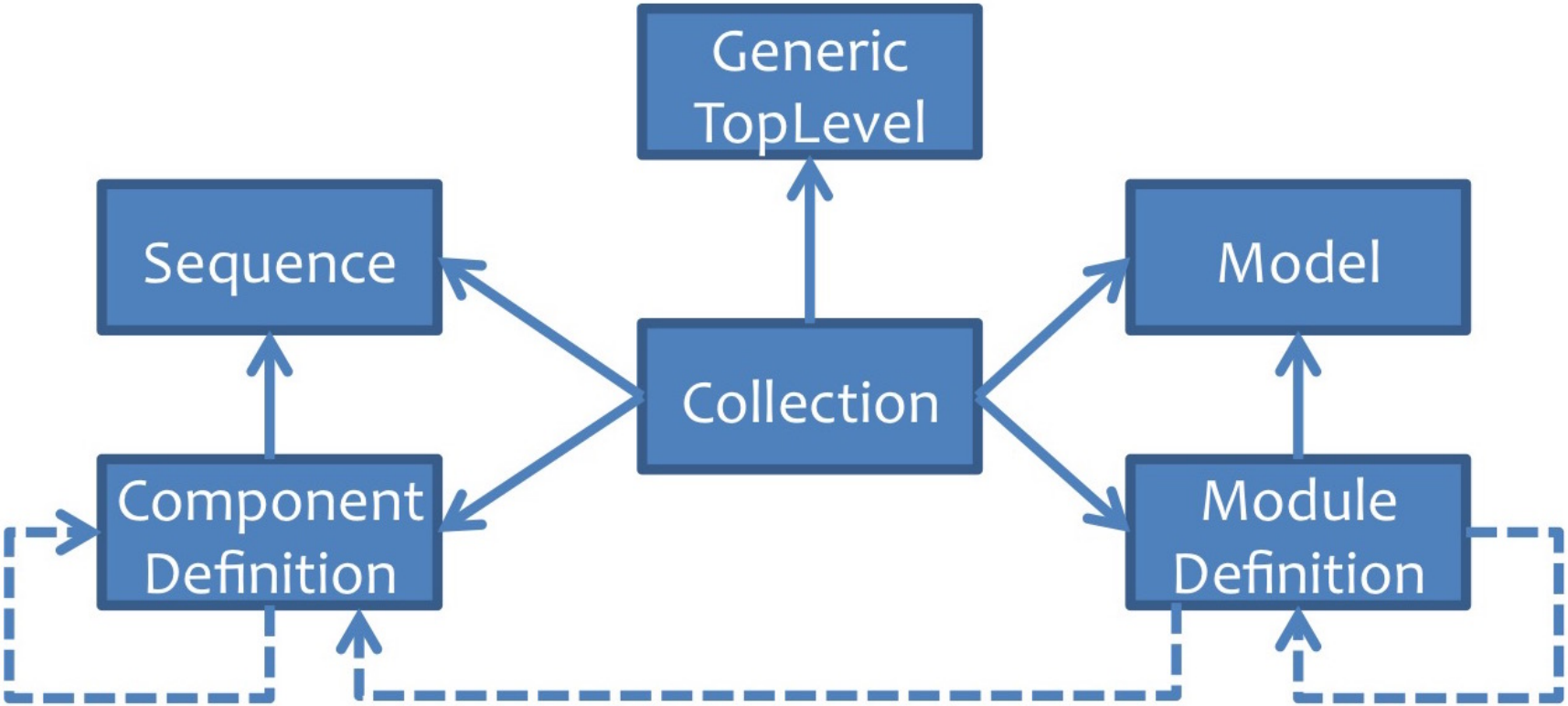
Introduction to the SBOL2 Data Model, the Java Library (libSBOLj), and the Javascript Library (sboljs)

Chris J. Myers

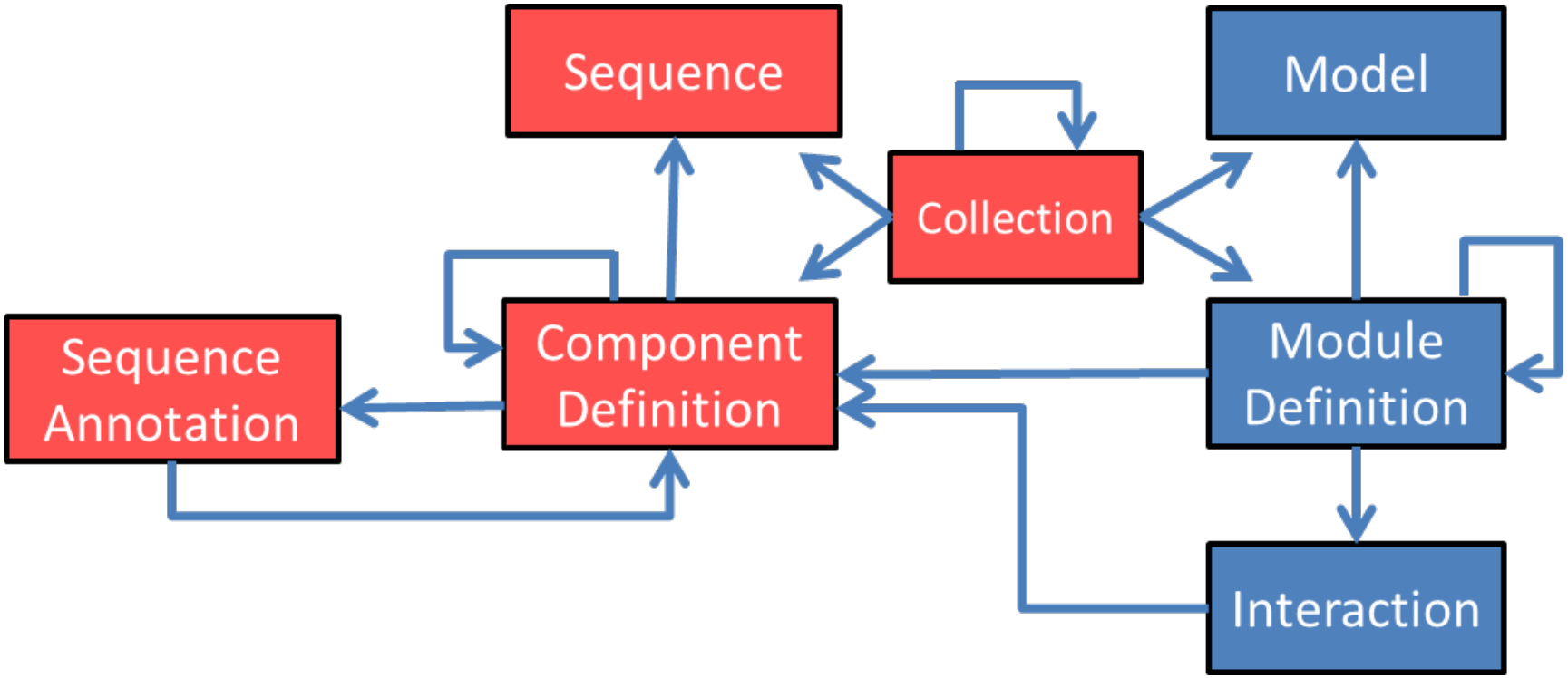
University of Utah

SBOL Workshop
August 1, 2018

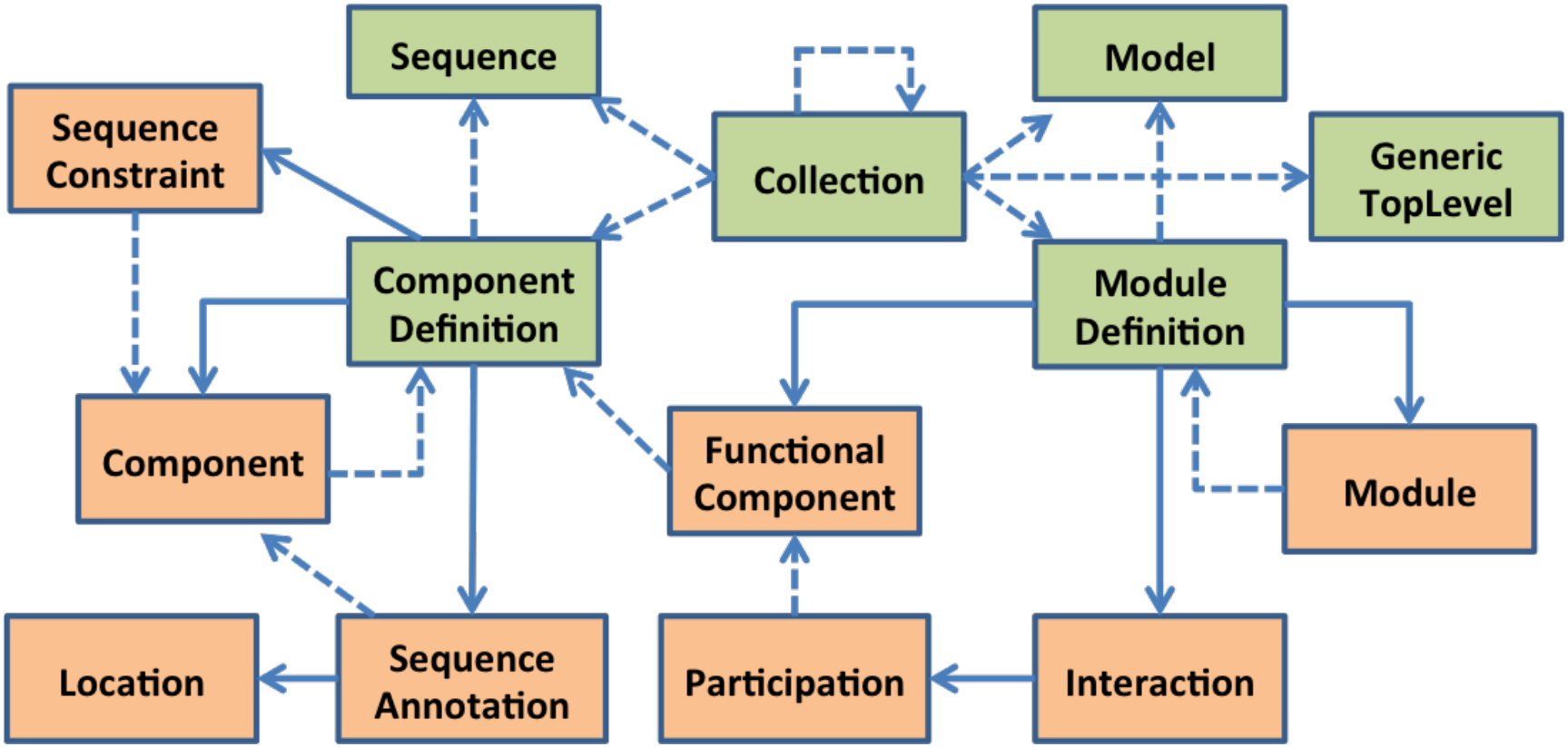
SBOL 2 Data Model



SBOL 2 Data Model



SBOL 2 Data Model



SBOL 2.2 Updates

- Attachment class - serves as a general container for data files.
- Implementation class - represents a physical instance of a synthetic biological construct.
- Provenance ontology (Prov-O):
  - Activity class - something that occurs over a period of time and acts upon or with entities.
  - Agent class - something that bears some form of responsibility for an activity taking place.
  - Plan class - an entity that represents a set of actions or steps intended by one or more agents to achieve some goals.

SBOL Libraries

- Crucial to the success of a standard is software infrastructure to support developers' integration of the standard within their tools.
- There are several library implementations of the SBOL data structure, which provide an *application programmers interface* (API) for tool developers to interact with SBOL data objects.
  - libSBOLj - native Java library
  - sboljs - Javascript library
  - libSBOL - C/C++ library
  - pySBOL - Python library

SBOL Libraries

- Crucial to the success of a standard is software infrastructure to support developers' integration of the standard within their tools.
- There are several library implementations of the SBOL data structure, which provide an *application programmers interface* (API) for tool developers to interact with SBOL data objects.
  - libSBOLj - native Java library
  - sboljs - Javascript library
  - libSBOL - C/C++ library
  - pySBOL - Python library

libSBOLj - native Java SBOL Library

- Library available from Maven central and Sonatype:
  - Group Id - org.sbolstandard
  - Artifact Id - libSBOLj
  - Version - 2.3.1 (latest release)
  - Version - 2.3.2-SNAPSHOT (current version)
- Distribution includes detailed documentation for the class definitions and the methods provided by the API.
- Supports validation/conversion to/from FASTA, GenBank, and SBOL1.
- Includes support to search, fetch, and submit designs to SynBioHub.
- Utilized by an online validator/converter available from the SBOL website, which also provides a webservice to be used by non-java applications.

Example: Converting Cello UCF File to SBOL

- JSON file format including the following sections:
  - Parts - basic DNA parts (promoters, rbs, cds, terminators, etc.)
  - Gate parts - compositions of DNA parts to form complete functions
  - Gates - additional information about these gate parts
  - Other information - response functions, gate toxicity, etc.

Cello UCF File Example


```
{
  "collection": "parts",
  "type": "cds",
  "name": "AmtR",
  "dnasequence": "ATGGCAGGCGCAGTTGGTCGTCCGCGTCGTAGTGCACCGCGTCGTGCAGGTAAAAATCCGCGTGAAGAAATTC..."
},...
{
  "collection": "gates",
  "regulator": "AmtR",
  "group_name": "AmtR",
  "gate_name": "A1_AmtR",
  "gate_type": "NOR",
  "system": "TetR",
  "color_hexcode": "3BA9E0"
}, ...
{
  "collection": "gate_parts",
  "gate_name": "A1_AmtR",
  "expression_cassettes": [
    {
      "maps_to_variable": "x",
      "cassette_parts": [
        "BydvJ",
        "A1",
        "AmtR",
        "L3S2P55"
      ]
    }
  ],
  "promoter": "pAmtR"
}, ...
```

Parsing Cello JSON File

```
HashMap<String,JSONObject> partsMap = new HashMap<String,JSONObject>();
HashSet<JSONObject> gate_partsArr = new HashSet<JSONObject>();
HashMap<String,JSONObject> gatesMap = new HashMap<String,JSONObject>();
HashMap<String,JSONObject> responseMap = new HashMap<String,JSONObject>();

JSONParser parser = new JSONParser();
JSONArray a = (JSONArray) parser.parse(new FileReader(pathToUCFFile));

for (Object o : a)
{
  JSONObject ucf = (JSONObject) o;

  String collection = (String) ucf.get("collection");

  if (collection.equals("parts")) {
    partsMap.put((String)ucf.get("name"),ucf);
  }
  else if (collection.equals("gate_parts")) {
    gate_partsArr.add(ucf);
  }
  else if (collection.equals("gates")) {
    gatesMap.put((String)ucf.get("gate_name"),ucf);
  }
  else if (collection.equals("response_functions")) {
    responseMap.put((String)ucf.get("gate_name"),ucf);
  }
}
```

SBOL Documents

- libSBOLj organizes all SBOL data within an **SBOLDocument**.
- Example creating an **SBOLDocument**:

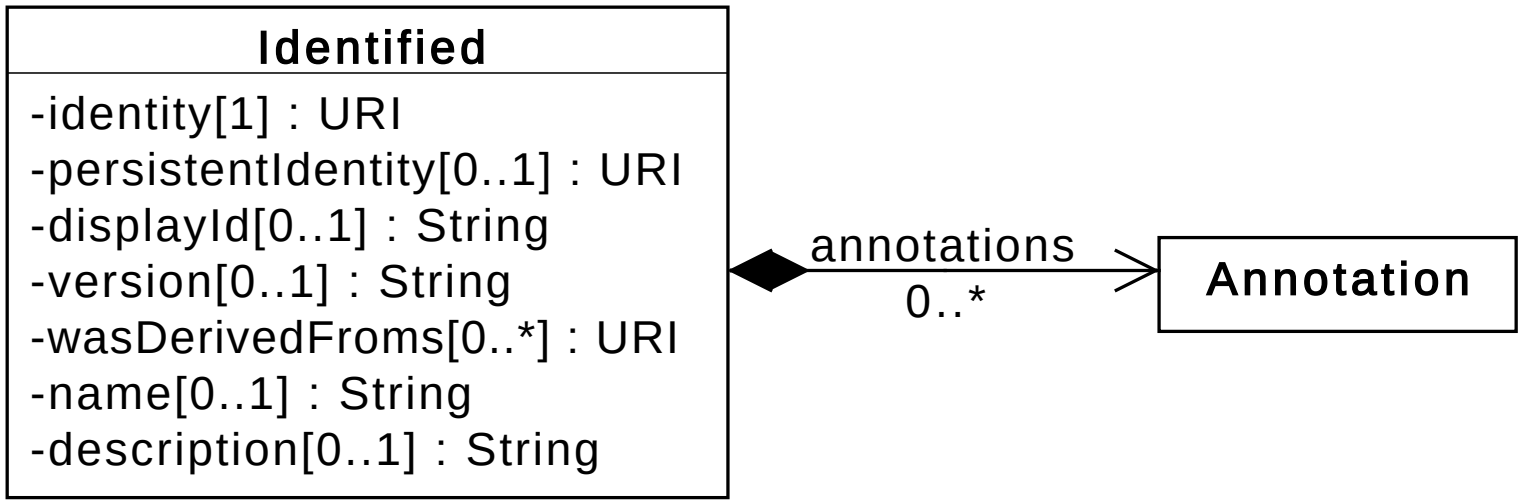
```
String uriPrefix = "http://cellocad.org/";
SBOLDocument document = new SBOLDocument();
document.setDefaultURIprefix(uriPrefix);
document.setComplete(true);
document.setCreateDefaults(true);
```

- Default URI prefix - prefix to use when none provided to create method.
- Complete - ensure that all URI references point to valid SBOL objects.
- Create defaults - implicitly create **ComponentInstances** as needed.

Understanding UML Diagrams

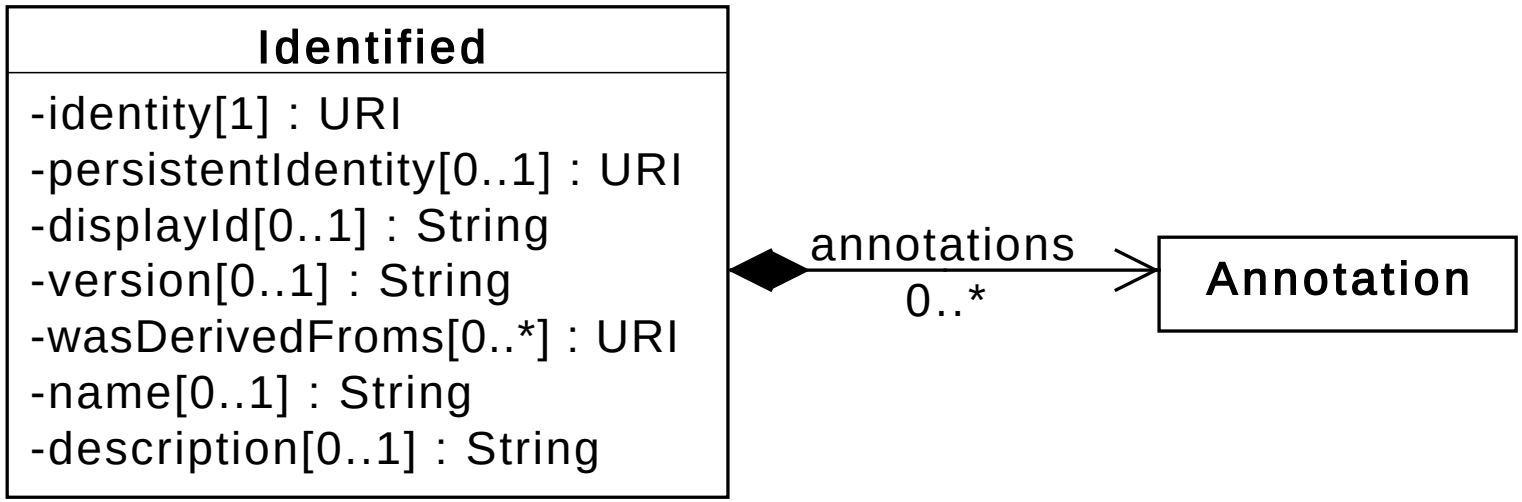
- Classes represented as boxes labeled with their member variables with types and cardinalities.
- Arrows with cardinality indicate associations between classes.
- A hollow diamond at the origin of an arrow represents shared aggregation (i.e., object is referenced and not owned).
- A solid diamond at the origin of an arrow represents composite aggregation (i.e., child object is owned by its parent object).
- Hollow arrows are used to represent inheritance.

Identified (Base Class for All SBOL Objects)



- *identity* - globally unique URI to identify this object (required).
- *persistentIdentity* - identity shared by multiple versions of the same object (optional).
- *displayId* - human-readable id composed of alphanumeric and underscore characters (optional).
- *version* - uses semantic versioning to identify multiple versions of the same object (optional).

Identified (Base Class for All SBOL Objects)



- *wasDerivedFroms* - identities of objects that this is derived from (optional).
- *name* - human-readable String of arbitrary characters (optional).
- *description* - thorough text description of the object (optional).
- *annotations* - additional data about this object (more later).

Compliant Top-Level URIs

$$\langle \textit{URI prefix} \rangle / \langle \textit{displayId} \rangle / \langle \textit{version} \rangle$$

1. The *identity* MUST begin with a *URI prefix* that maps to a domain over which the user has control.
2. The *persistentIdentity* and *displayId* properties are REQUIRED.
3. The *persistentIdentity* MUST end with a delimiter (’/’, ’#’, or ’:’) followed by the *displayId* of the object.
4. If an object is not given a *version*, then its *identity* and *persistentIdentity* properties MUST contain the same *URI*.
5. If an object has a *version*, then its *identity* property MUST contain a *URI* of the form $\langle \textit{persistentIdentity} \rangle / \langle \textit{version} \rangle$".

Compliant Child URIs

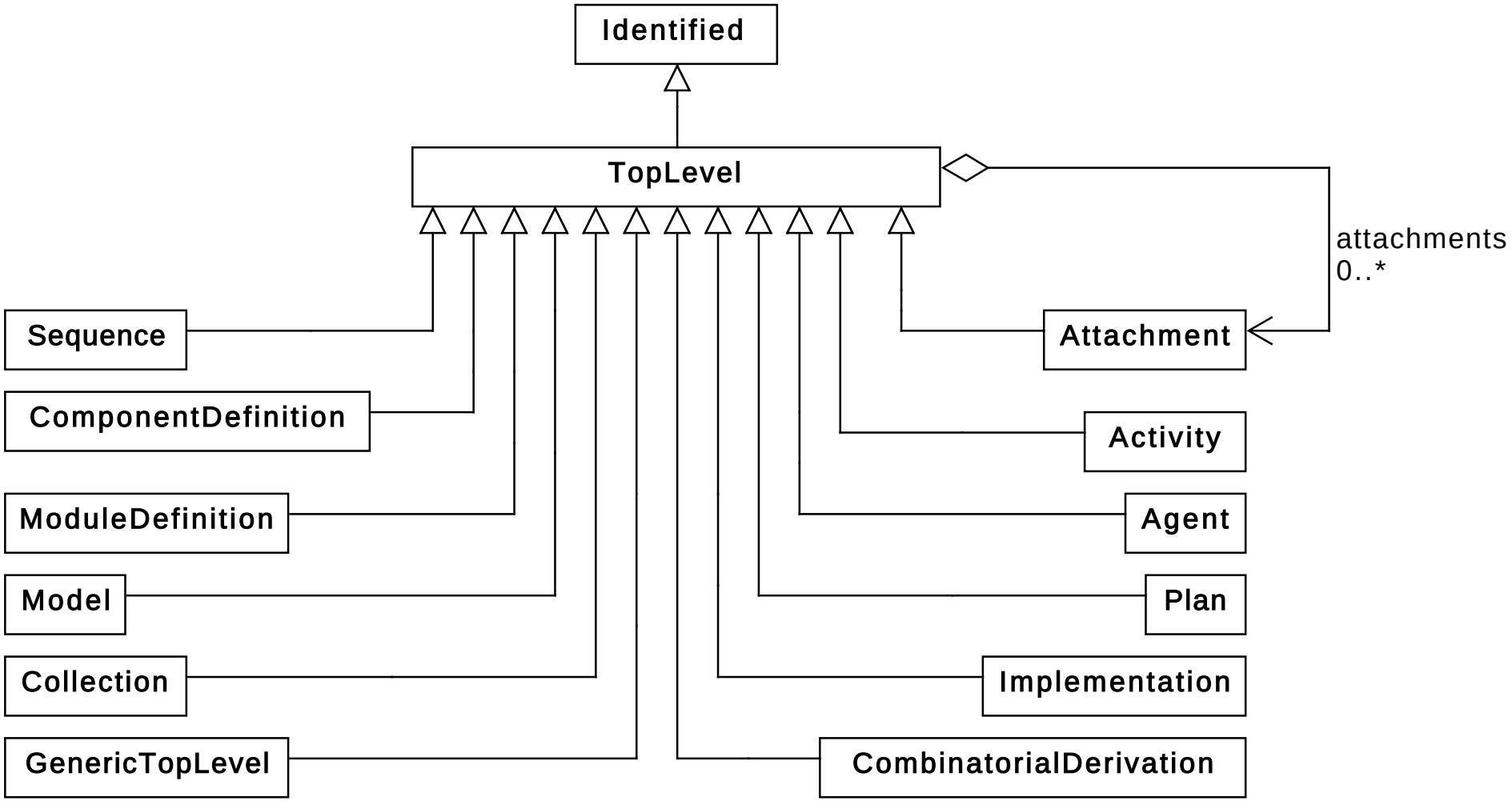
$$\langle \textit{parent persistentIdentity} \rangle / \langle \textit{displayId} \rangle / \langle \textit{parent version} \rangle$$

1. The *persistentIdentity* MUST begin with the *persistentIdentity* of its parent object and be immediately followed by a delimiter (’/’, ’#’, or ’:’) and the *displayId* of the object.
2. The *version* MUST contain the same *String* as the *version* property of the object’s parent object.

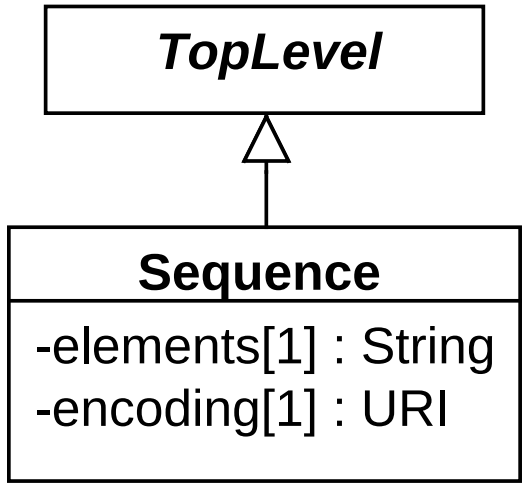
TopLevel Objects

- Each **SBOLDocument** includes a list of each type of **TopLevel** object.
- These lists are organized to allow for easy search by their *unique reference identifiers* (URIs) and validation that they are distinct.
- libSBOLj includes methods for creating, updating, accessing, and removing these data objects, as well as, their child objects.

TopLevel


Identified
TopLevel
attachments
0..*
Sequence
ComponentDefinition
ModuleDefinition
Model
Collection
GenericTopLevel
Attachment
Activity
Agent
Plan
Implementation
CombinatorialDerivation

Sequence



- *elements* - String of characters representing constituents of a biological or chemical molecule.
- *encoding* - URI indicating how elements are to be interpreted.

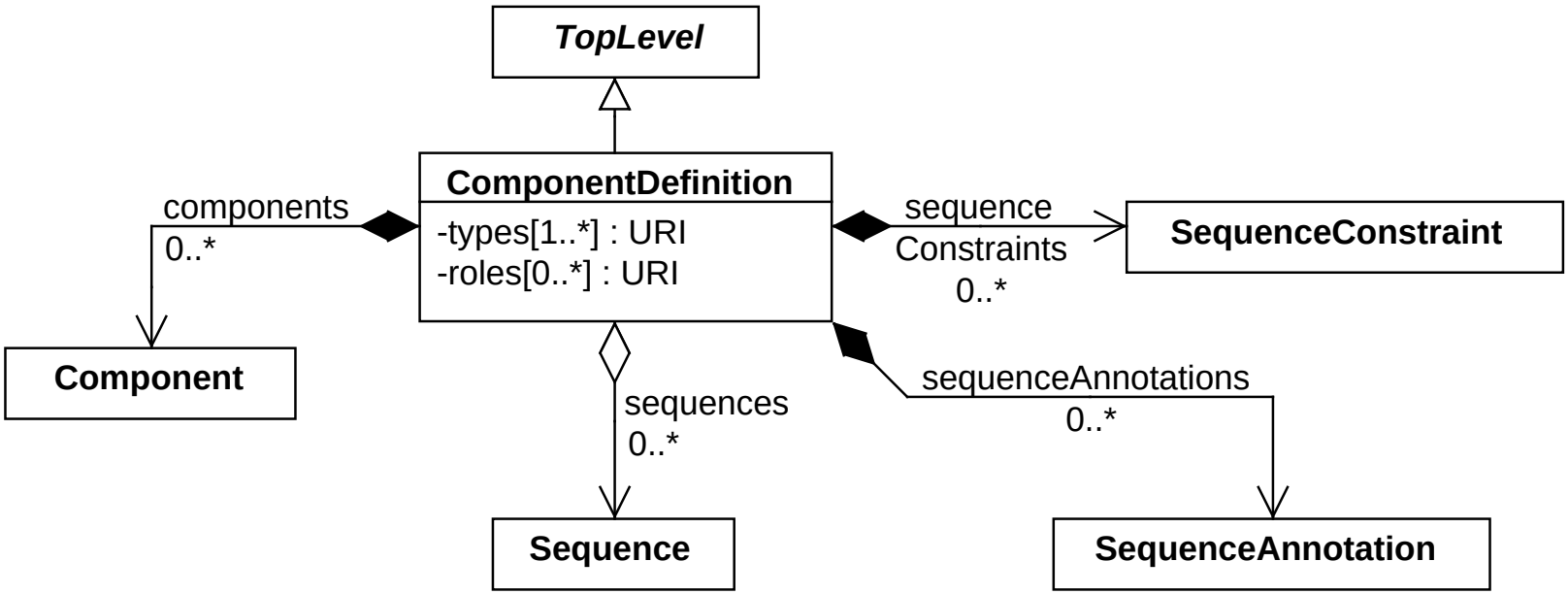
Encoding	**URI**	**CD Type**
IUPAC DNA, RNA	`http://www.chem.qmul.ac.uk/iubmb/misc/naseq.html`	DNA, RNA
IUPAC Protein	`http://www.chem.qmul.ac.uk/iupac/AminoAcid/`	Protein
SMILES	`http://www.opensmiles.org/opensmiles.html`	SmallMolecule

Creating Sequences for Parts

```
for (JSONObject part : partsMap.values()) {

  String name = (String)part.get("name");
  String dnasequence = (String)part.get("dnasequence");
  Sequence sequence = document.createSequence(name + "_sequence", version, dnasequence,
    Sequence.IUPAC_DNA);
  sequence.setName(name+"_sequence");
  sequence.addWasGeneratedBy(activityURI);
  sequence.createAnnotation(new QName(dcTermsNS,"created","dcTerms"), createdDate);
```

```
<sbol:Sequence rdf:about="http://cellocad.org/AmtR_sequence/1">
  <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR_sequence"/>
  <sbol:displayId> AmtR_sequence </sbol:displayId>
  <sbol:version> 1 </sbol:version>
  <dcterms:title> AmtR_sequence </dcterms:title>
  <prov:wasGeneratedBy rdf:resource="http://cellocad.org/cello2sbol/1"/>
  <dcterms:created> 2017-08-09T13:54Z </dcterms:created>
  <sbol:elements> ATGGCAGGCGCAGTTGGTCGTCCGCGTCGTAGTGCACCGCGTCGTGCAGGTAAAAATCCGCGTGAAGAAATTCTGGATGC
  <sbol:encoding rdf:resource="http://www.chem.qmul.ac.uk/iubmb/misc/naseq.html"/>
</sbol:Sequence>
```

ComponentDefinition



ComponentDefinition (Types/Roles)

CD Type	URI for BioPAX Term
DNA	http://www.biopax.org/release/biopax-level3.owl#DnaRegion
RNA	http://www.biopax.org/release/biopax-level3.owl#RnaRegion
Protein	http://www.biopax.org/release/biopax-level3.owl#Protein
Small Molecule	http://www.biopax.org/release/biopax-level3.owl#SmallMolecule
Complex	http://www.biopax.org/release/biopax-level3.owl#Complex

CD Role	URI for SequenceOntology Term	CD Type
Promoter	http://identifiers.org/so/SO:0000167	DNA
RBS	http://identifiers.org/so/SO:0000139	DNA
CDS	http://identifiers.org/so/SO:0000316	DNA
Terminator	http://identifiers.org/so/SO:0000141	DNA
Gene	http://identifiers.org/so/SO:0000704	DNA
Operator	http://identifiers.org/so/SO:0000057	DNA
Engineered Gene	http://identifiers.org/so/SO:0000280	DNA
mRNA	http://identifiers.org/so/SO:0000234	RNA

Converting Part Type to SBOL ComponentDefinition Role

```
public static URI getRole(String type) {
 String so = "http://identifiers.org/so/";
 if (type.equals("ribozyme")) {
    return URI.create(so + "SO:0000374");
  }
  else if (type.equals("scar")) {
    return URI.create(so + "SO:0001953");
  }
  else if (type.equals("cds")) {
    return URI.create(so + "SO:0000316");
  }
  else if (type.equals("promoter")) {
    return URI.create(so + "SO:0000167");
  }
  else if (type.equals("rbs")) {
    return URI.create(so + "SO:0000139");
  }
  else if (type.equals("terminator")) {
    return URI.create(so + "SO:0000141");
  }
  ...
  else {
    System.err.println("Part Type not found");
    return null;
  }
}
```

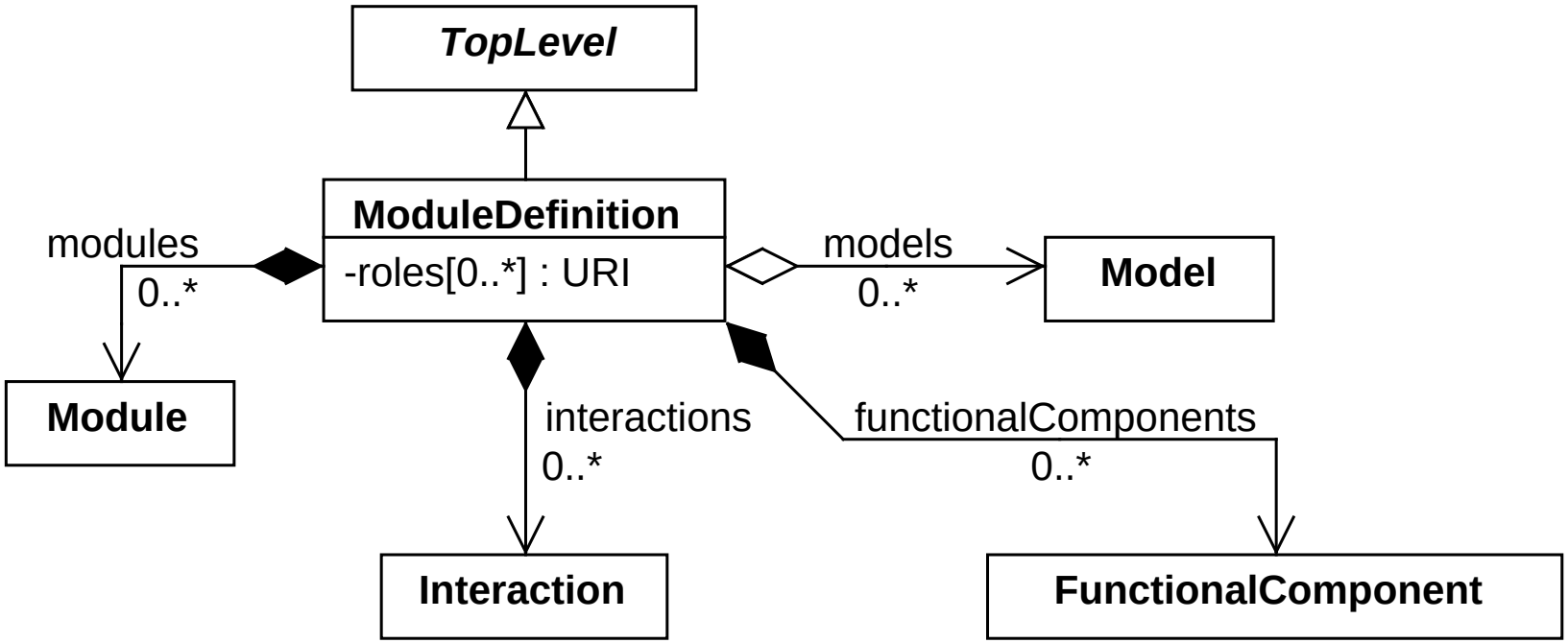
Converting Parts to SBOL ComponentDefinitions

```
ComponentDefinition componentDefinition =
  document.createComponentDefinition(name, version, ComponentDefinition.DNA);
componentDefinition.setName(name);
componentDefinition.addWasGeneratedBy(activityURI);
componentDefinition.createAnnotation(new QName(dcTermsNS,"created","dcTerms"), createdDate);
String partType = (String)part.get("type");
componentDefinition.addRole(getRole(partType));
componentDefinition.addSequence(sequence);

if (partType.equals("cds")) {

  ComponentDefinition proteinComponentDefinition =
    document.createComponentDefinition(name+"_protein", version, ComponentDefinition.PROTEIN);
  proteinComponentDefinition.setName(name+"_protein");
  proteinComponentDefinition.addWasGeneratedBy(activityURI);
  proteinComponentDefinition.createAnnotation(new QName(dcTermsNS,"created","dcTerms"),
    createdDate);
```

Converting Parts to SBOL ComponentDefinitions

```
<sbol:ComponentDefinition rdf:about="http://cellocad.org/AmtR/1">
  <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR"/>
  <sbol:displayId> AmtR </sbol:displayId>
  <sbol:version> 1 </sbol:version>
  <dcterms:title> AmtR </dcterms:title>
  <prov:wasGeneratedBy rdf:resource="http://cellocad.org/cello2sbol/1"/>
  <dcterms:created> 2017-08-09T13:54Z </dcterms:created>
  <sbol:type rdf:resource="http://www.biopax.org/release/biopax-level3.owl#DnaRegion"/>
  <sbol:role rdf:resource="http://identifiers.org/so/SO:0000316"/>
  <sbol:sequence rdf:resource="http://cellocad.org/AmtR_sequence/1"/>
</sbol:ComponentDefinition>

<sbol:ComponentDefinition rdf:about="http://cellocad.org/AmtR_protein/1">
  <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR_protein"/>
  <sbol:displayId> AmtR_protein </sbol:displayId>
  <sbol:version> 1 </sbol:version>
  <dcterms:title> AmtR_protein </dcterms:title>
  <prov:wasGeneratedBy rdf:resource="http://cellocad.org/cello2sbol/1"/>
  <dcterms:created> 2017-08-09T13:54Z </dcterms:created>
  <sbol:type rdf:resource="http://www.biopax.org/release/biopax-level3.owl#Protein"/>
</sbol:ComponentDefinition>
```

ModuleDefinition

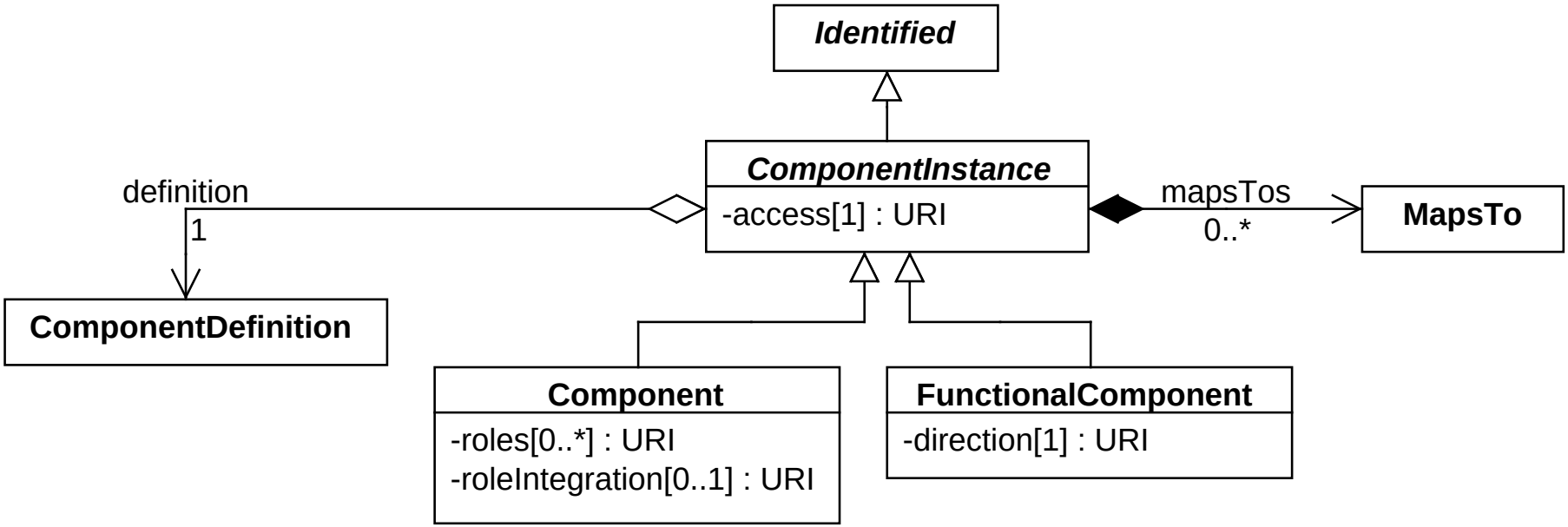


Creating ModuleDefinitions for Genetic Production

```
ModuleDefinition moduleDefinition =
  document.createModuleDefinition(name+"_protein_production", version);
moduleDefinition.setName(name+"_protein_production");
moduleDefinition.addWasGeneratedBy(activityURI);
moduleDefinition.createAnnotation(new QName(dcTermsNS,"created","dcTerms"), createdDate);
```

```
<sbol:ModuleDefinition rdf:about="http://cellocad.org/AmtR_protein_production/1">
  <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR_protein_production"/>
  <sbol:displayId> AmtR_protein_production </sbol:displayId>
  <sbol:version> 1 </sbol:version>
  <dcterms:title> AmtR_protein_production </dcterms:title>
  <prov:wasGeneratedBy rdf:resource="http://cellocad.org/cello2sbol/1"/>
  <dcterms:created>2017-08-09T13:54Z</dcterms:created>
</sbol:ModuleDefinition>
```

FunctionalComponent (Child of ModuleDefinition)



Access URI	**Description**
`http://sbols.org/v2#public`	MAY be referred to by remote **MapsTo** objects.
`http://sbols.org/v2#private`	MUST NOT be referred to by remote **MapsTo** objects.

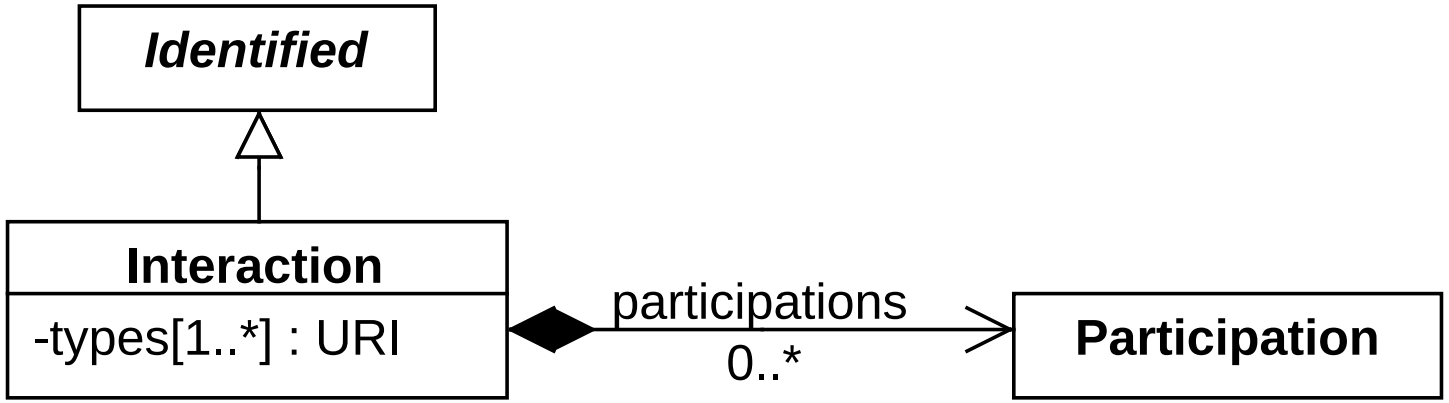
Direction URI	**Description**
`http://sbols.org/v2#in`	Indicates that it is an input.
`http://sbols.org/v2#out`	Indicates that it is an output.
`http://sbols.org/v2#inout`	Indicates that it is both an input and output
`http://sbols.org/v2#none`	Indicates that it is neither an input nor output.

Creating FunctionalComponents for Genetic Production

```
moduleDefinition.createFunctionalComponent(name, AccessType.PUBLIC,
  componentDefinition.getIdentity(), DirectionType.NONE);

moduleDefinition.createFunctionalComponent(name+"_protein", AccessType.PUBLIC,
  proteinComponentDefinition.getIdentity(), DirectionType.NONE);
```

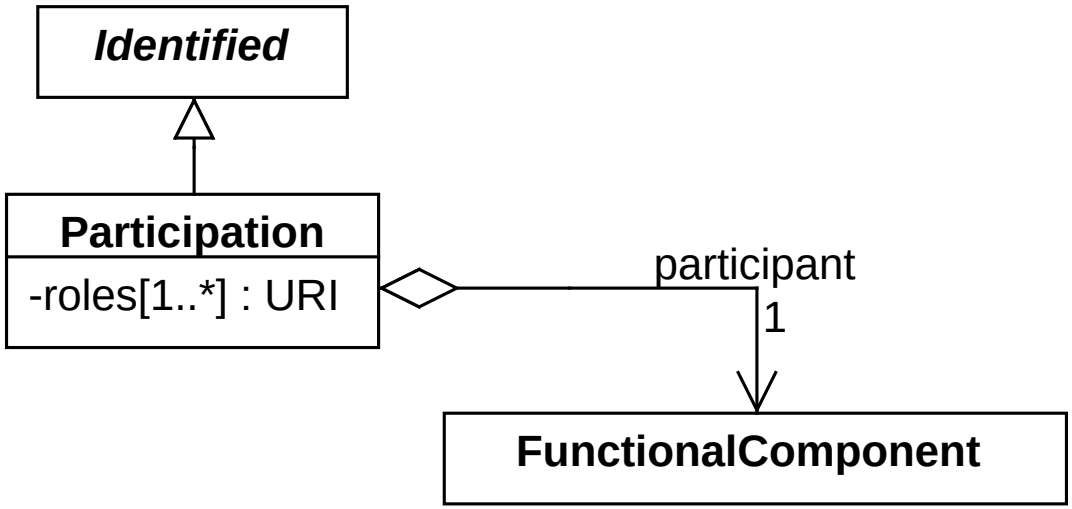
```
<sbol:ModuleDefinition rdf:about="http://cellocad.org/AmtR_protein_production/1">
  ...
  <sbol:functionalComponent>
    <sbol:FunctionalComponent rdf:about="http://cellocad.org/AmtR_protein_production/AmtR/1">
      <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR_protein_production/AmtR"/>
      <sbol:displayId> AmtR </sbol:displayId>
      <sbol:version> 1 </sbol:version>
      <sbol:definition rdf:resource="http://cellocad.org/AmtR/1"/>
      <sbol:access rdf:resource="http://sbols.org/v2#public"/>
      <sbol:direction rdf:resource="http://sbols.org/v2#none"/>
    </sbol:FunctionalComponent>
  </sbol:functionalComponent>
  <sbol:functionalComponent>
    <sbol:FunctionalComponent rdf:about="http://cellocad.org/AmtR_protein_production/AmtR_protein/
      <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR_protein_production/AmtR_prot
      <sbol:displayId> AmtR_protein </sbol:displayId>
      <sbol:version> 1 </sbol:version>
      <sbol:definition rdf:resource="http://cellocad.org/AmtR_protein/1"/>
      <sbol:access rdf:resource="http://sbols.org/v2#public"/>
      <sbol:direction rdf:resource="http://sbols.org/v2#none"/>
    </sbol:FunctionalComponent>
  </sbol:functionalComponent>
</sbol:ModuleDefinition>
```

Interaction (Child of ModuleDefinition)



Interaction Type	**URI for SystemsBiologyOntology Term**
Inhibition	`http://identifiers.org/biomodels.sbo/SBO:0000169`
Stimulation	`http://identifiers.org/biomodels.sbo/SBO:0000170`
Biochemical Reaction	`http://identifiers.org/biomodels.sbo/SBO:0000176`
Non-Covalent Binding	`http://identifiers.org/biomodels.sbo/SBO:0000177`
Degradation	`http://identifiers.org/biomodels.sbo/SBO:0000179`
Genetic Production	`http://identifiers.org/biomodels.sbo/SBO:0000589`
Control	`http://identifiers.org/biomodels.sbo/SBO:0000168`

Participation (Child of Interaction)



Part. Role	URI for SBO Term	Interaction Types
Inhibitor	http://identifiers.org/biomodels.sbo/SBO:0000020	Inhibition
Inhibited	http://identifiers.org/biomodels.sbo/SBO:0000642	Inhibition
Stimulator	http://identifiers.org/biomodels.sbo/SBO:0000459	Stimulation
Stimulated	http://identifiers.org/biomodels.sbo/SBO:0000643	Stimulation
Reactant	http://identifiers.org/biomodels.sbo/SBO:0000010	Non-Covalent Binding, Degradation, Biochemical Reaction
Product	http://identifiers.org/biomodels.sbo/SBO:0000011	Non-Covalent Binding, Genetic Production, Biochemical Reaction
Promoter	http://identifiers.org/biomodels.sbo/SBO:0000598	Inhibition, Stimulation, Genetic Production
Modifier	http://identifiers.org/biomodels.sbo/SBO:0000019	Biochemical Reaction, Control
Modified	http://identifiers.org/biomodels.sbo/SBO:0000644	Biochemical Reaction, Control
Template	http://identifiers.org/biomodels.sbo/SBO:0000645	Genetic Production

Creating Interactions for Genetic Production

```
Interaction interaction = moduleDefinition.createInteraction(name+"_protein_interaction",
  SystemsBiologyOntology.GENETIC_PRODUCTION);
interaction.createParticipation(name, name, SystemsBiologyOntology.TEMPLATE);
interaction.createParticipation(name+"_protein", name+"_protein", SystemsBiologyOntology.PRODUCT);
```

```
  <sbol:interaction>
    <sbol:Interaction rdf:about="http://cellocad.org/AmtR_protein_production/AmtR_protein_interact
      <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR_protein_production/AmtR_prot
      <sbol:displayId> AmtR_protein_interaction </sbol:displayId>
      <sbol:version> 1 </sbol:version>
      <sbol:type rdf:resource="http://identifiers.org/biomodels.sbo/SBO:0000589"/>
      <sbol:participation>
        <sbol:Participation rdf:about="http://cellocad.org/AmtR_protein_production/AmtR_protein_in
          <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR_protein_production/AmtR_
          <sbol:displayId> AmtR </sbol:displayId>
          <sbol:version> 1 </sbol:version>
          <sbol:role rdf:resource="http://identifiers.org/biomodels.sbo/SBO:0000645"/>
          <sbol:participant rdf:resource="http://cellocad.org/AmtR_protein_production/AmtR/1"/>
        </sbol:Participation>
      </sbol:participation>
      <sbol:participation>
        <sbol:Participation rdf:about="http://cellocad.org/AmtR_protein_production/AmtR_protein_in
          <sbol:persistentIdentity rdf:resource="http://cellocad.org/AmtR_protein_production/AmtR_
          <sbol:displayId> AmtR_protein </sbol:displayId>
          <sbol:version> 1 </sbol:version>
          <sbol:role rdf:resource="http://identifiers.org/biomodels.sbo/SBO:0000011"/>
          <sbol:participant rdf:resource="http://cellocad.org/AmtR_protein_production/AmtR_protein
        </sbol:Participation>
      </sbol:participation>
    </sbol:Interaction>
  </sbol:interaction>
</sbol:ModuleDefinition>
```

Cello UCF File Example


```
{
  "collection": "parts",
  "type": "cds",
  "name": "AmtR",
  "dnasequence": "ATGGCAGGCGCAGTTGGTCGTCCGCGTCGTAGTGCACCGCGTCGTGCAGGTAAAAATCCGCGTGAAGAAATTC..."
},...
{
  "collection": "gates",
  "regulator": "AmtR",
  "group_name": "AmtR",
  "gate_name": "A1_AmtR",
  "gate_type": "NOR",
  "system": "TetR",
  "color_hexcode": "3BA9E0"
}, ...
{
  "collection": "gate_parts",
  "gate_name": "A1_AmtR",
  "expression_cassettes": [
    {
      "maps_to_variable": "x",
      "cassette_parts": [
        "BydvJ",
        "A1",
        "AmtR",
        "L3S2P55"
      ]
    }
  ],
  "promoter": "pAmtR"
}, ...
```

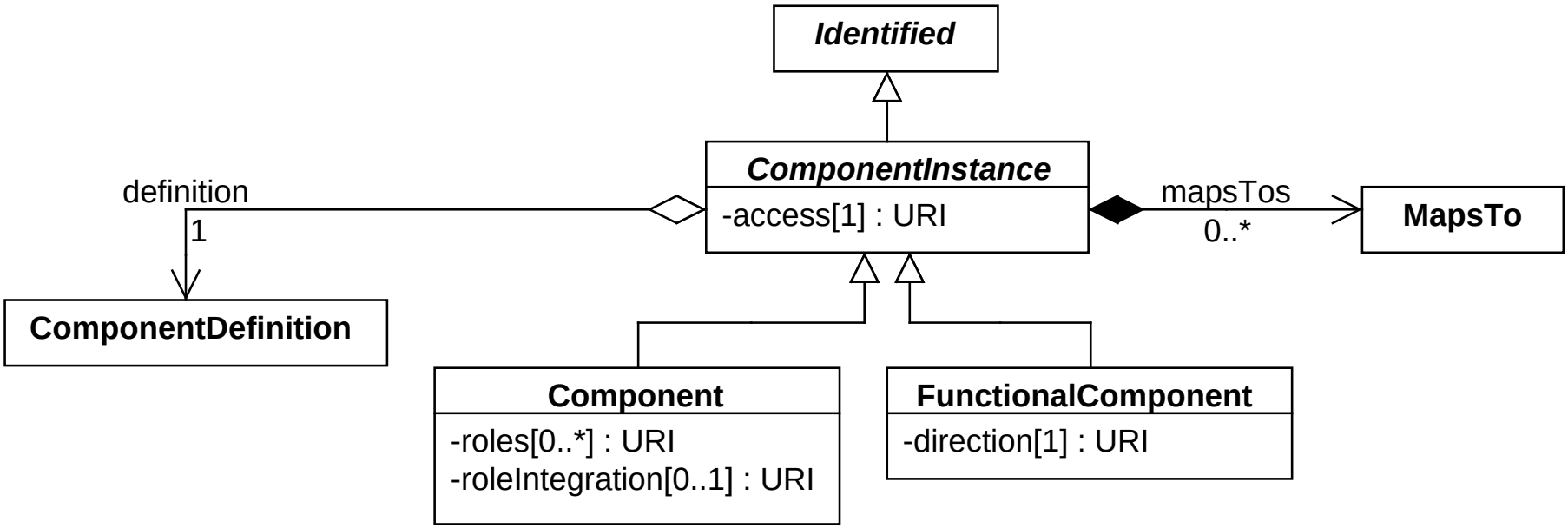
Converting Gate Parts to SBOL ComponentDefinitions

```
for (JSONObject gate : gate_partsArr) {

  String gate_name = (String)gate.get("gate_name");
  ComponentDefinition componentDefinition =
    document.createComponentDefinition(gate_name, version, ComponentDefinition.DNA);
  componentDefinition.setName(gate_name);
  componentDefinition.addRole(SequenceOntology.ENGINEERED_REGION);
  componentDefinition.addWasGeneratedBy(activityURI);

  componentDefinition.createAnnotation(new QName(dcTermsNS,"created","dcTerms"), createdDate);
  componentDefinition.createAnnotation(new QName(celloNS,"family","cello"),
    (String)gatesMap.get(gate_name).get("system"));
  componentDefinition.createAnnotation(new QName(celloNS,"gate_type","cello"),
    (String)gatesMap.get(gate_name).get("gate_type"));
  componentDefinition.createAnnotation(new QName(celloNS,"group_name","cello"),
    (String)gatesMap.get(gate_name).get("group_name"));
  componentDefinition.createAnnotation(new QName(celloNS,"color_hexcode","cello"),
    (String)gatesMap.get(gate_name).get("color_hexcode"));
```

Adding Response Functions to Gate Parts

```
componentDefinition.createAnnotation(new QName(celloNS,"response_function","cello"),
  (String)responseMap.get(gate_name).get("equation"));
JSONArray parameters = (JSONArray)responseMap.get(gate_name).get("parameters");
for (Object obj : parameters) {
  String name = (String)((JSONObject)obj).get("name");
  componentDefinition.createAnnotation(new QName(celloNS,name,"cello"),
    (Double)((JSONObject)obj).get("value"));
}
JSONArray variables = (JSONArray)responseMap.get(gate_name).get("variables");
for (Object obj : variables) {
  String name = (String)((JSONObject)obj).get("name");
  componentDefinition.createAnnotation(new QName(celloNS,name+"_off_threshold","cello"),
    (Double)((JSONObject)obj).get("off_threshold"));
  componentDefinition.createAnnotation(new QName(celloNS,name+"_on_threshold","cello"),
  (Double)((JSONObject)obj).get("on_threshold"));
}
```

Component (Child of ComponentDefinition)



Access URI

`http://sbols.org/v2#public`

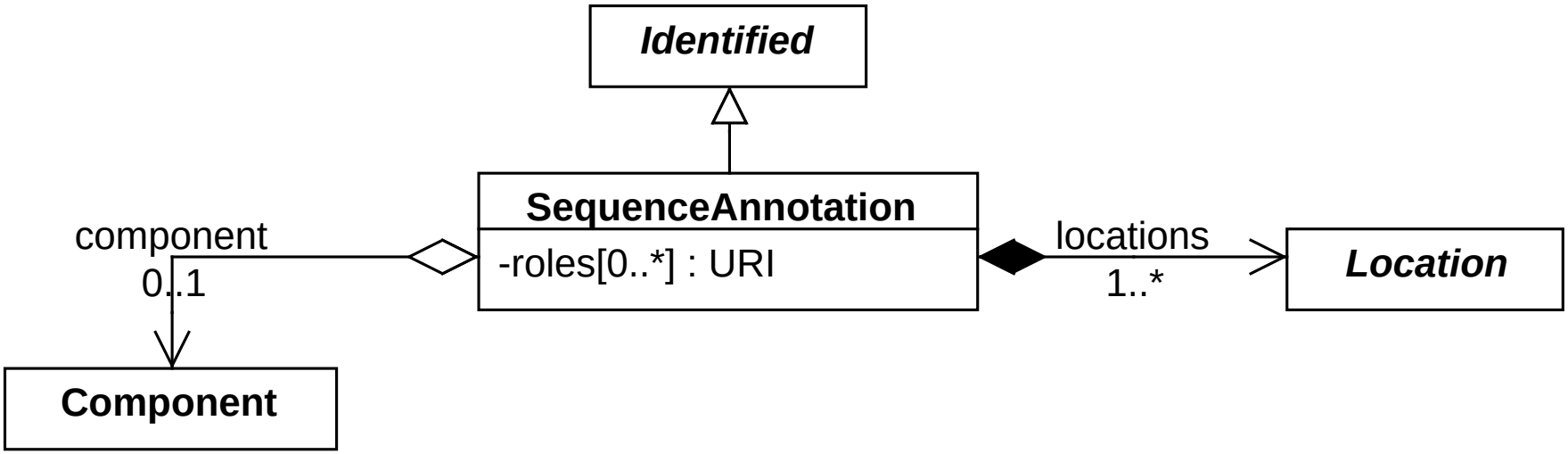
`http://sbols.org/v2#private`

Description

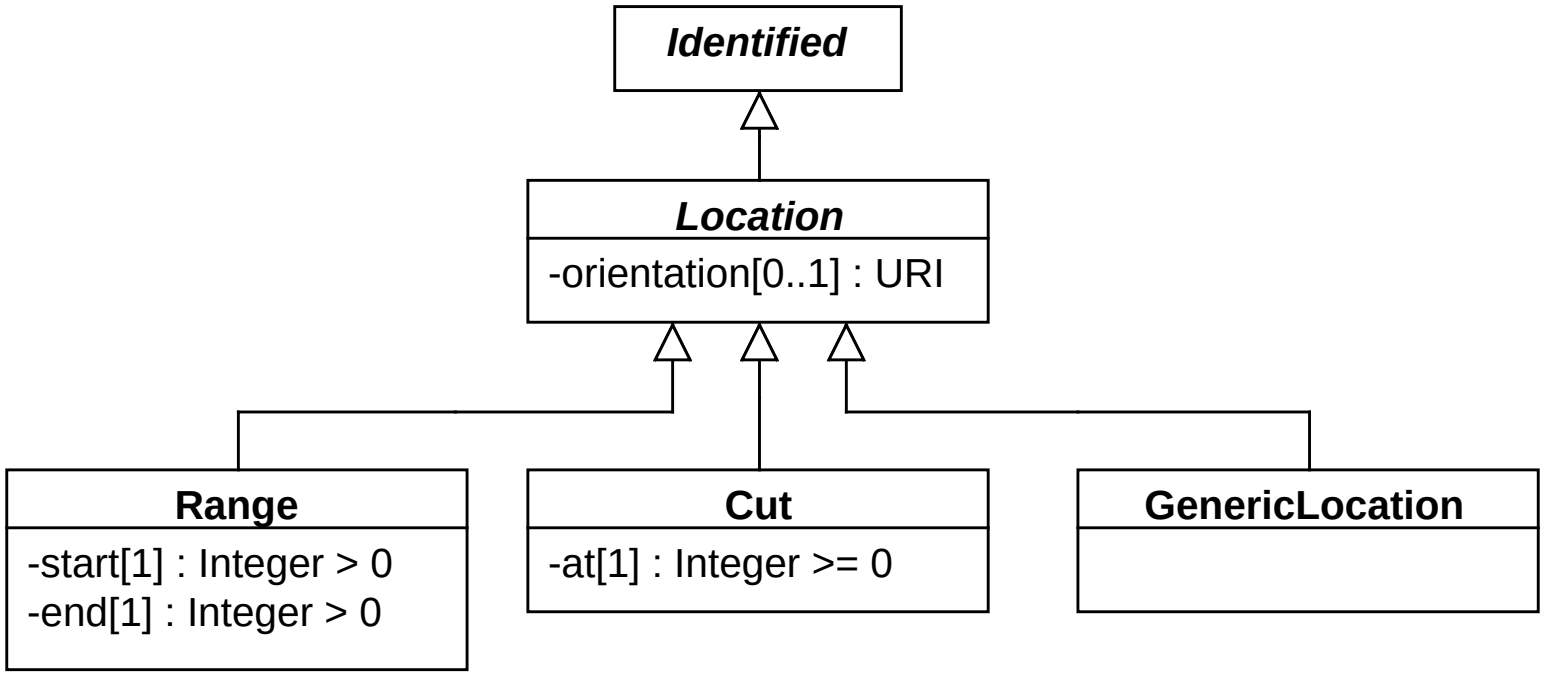
MAY be referred to by remote **MapsTo** objects.

MUST NOT be referred to by remote **MapsTo** objects.

SequenceAnnotation (Child of ComponentDefinition)



Location (Child of SequenceAnnotation)



Orientation URI

`http://sbols.org/v2#inline`

`http://sbols.org/v2#reverseComplement`

Description

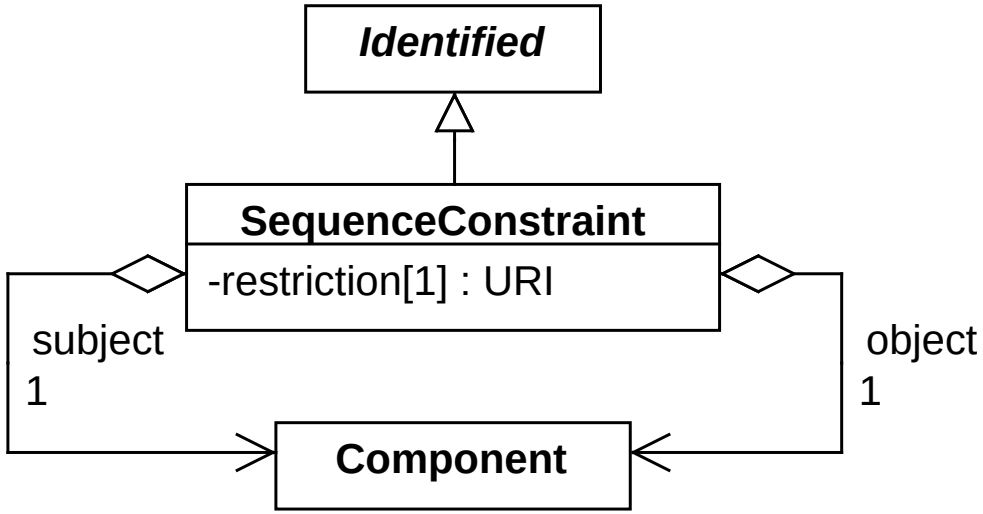
The region is inline with the sequence.

The region is on the reverse-complement translation.

Creating Composite Gates Using SequenceAnnotations

```
JSONArray expression_cassettes = (JSONArray) gate.get("expression_cassettes");
String seq = "";

for (Object obj : expression_cassettes) {

  int annotationCount = 0;
  int start = 1;

  JSONObject expression_cassette = (JSONObject) obj;
  JSONArray cassette_parts = (JSONArray)expression_cassette.get("cassette_parts");

  for (Object obj2 : cassette_parts) {

    String partId = (String)obj2;
    ComponentDefinition partComponentDefinition =
      document.getComponentDefinition(partId, version);
    String cass_seq = document.getSequence(partId+"_sequence",version).getElements();
    seq += cass_seq;

    componentDefinition.createComponent(partId, AccessType.PUBLIC, partId, version);

    SequenceAnnotation sa =
      componentDefinition.createSequenceAnnotation("annotation"+annotationCount,
      "range", start, start + cass_seq.length() - 1, OrientationType.INLINE);

    sa.setComponent(partId);
    start += cass_seq.length();
    annotationCount++;
```

SequenceConstraint (Child of ComponentDefinition)



Restriction URI

`http://sbols.org/v2#precedes`
`http://sbols.org/v2#sameOrientationAs`
`http://sbols.org/v2#oppositeOrientationAs`

Description

subject MUST precede *object* **Component**.
subject & *object* MUST have same orientation.
subject & *object* MUST have opposite orientations.

Creating Composite Gates Using SequenceConstraints

```
JSONArray expression_cassettes = (JSONArray) gate.get("expression_cassettes");
for (Object obj : expression_cassettes) {

  int constraintCount = 0;
  Component previousComponent = null;
  Component currentComponent = null;

  JSONObject expression_cassette = (JSONObject) obj;
  JSONArray cassette_parts = (JSONArray)expression_cassette.get("cassette_parts");

  for (Object obj2 : cassette_parts) {

    String partId = (String)obj2;
    ComponentDefinition partComponentDefinition =
      document.getComponentDefinition(partId, version);
    currentComponent = componentDefinition.createComponent(partId, AccessType.PUBLIC,
      partId, version);

    if (previousComponent != null) {
      componentDefinition.createSequenceConstraint("constraint"+constraintCount,
        RestrictionType.PRECEDES,
        previousComponent.getIdentity(), currentComponent.getIdentity());
      constraintCount++;
    }

    previousComponent = currentComponent;
```

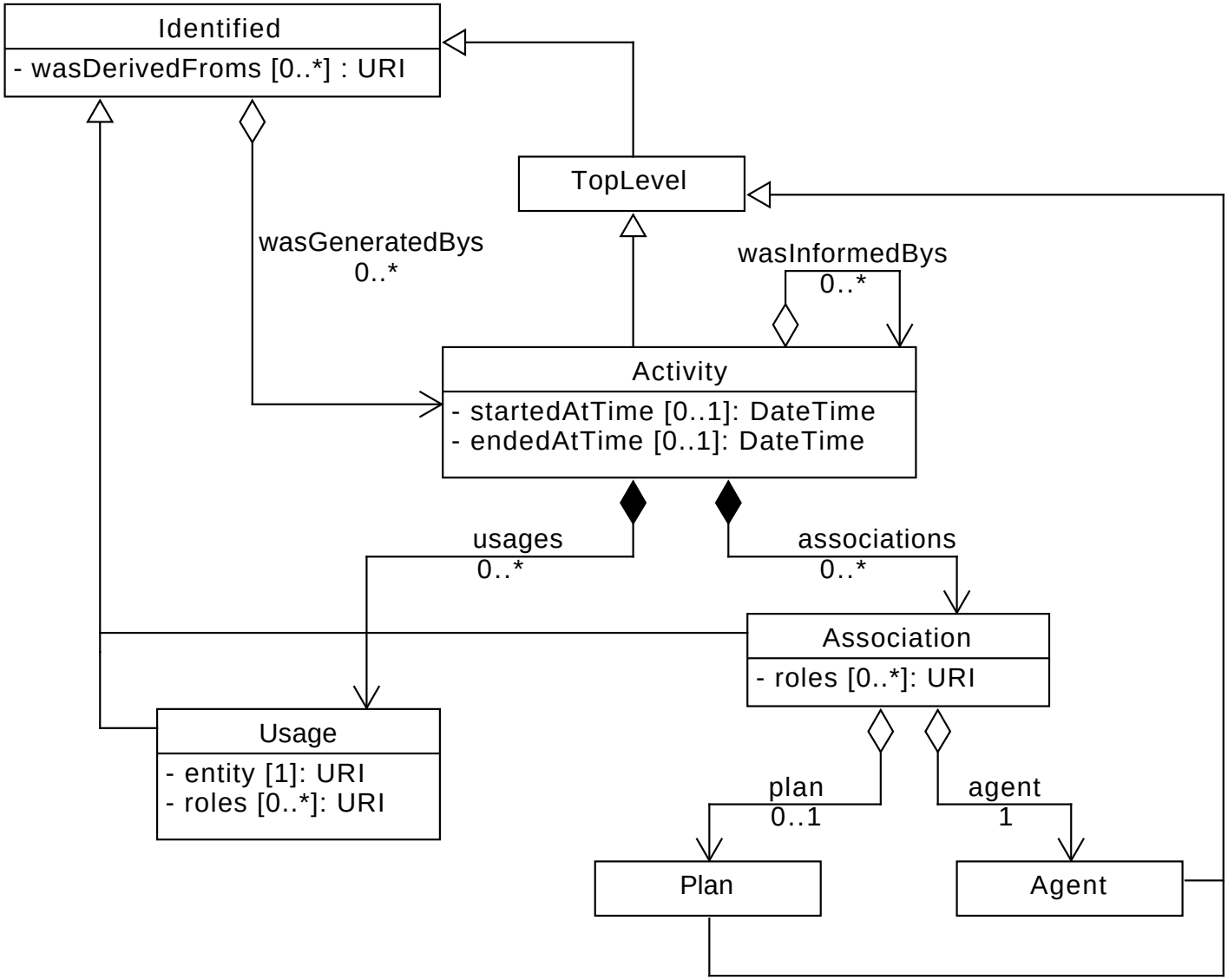
Creating ModuleDefinitions for Inhibition

```
if (partComponentDefinition.getRoles().contains(SequenceOntology.CDS)) {

  String promoter = (String)gate.get("promoter");

  if (document.getModuleDefinition(partId+"_"+promoter+"_repression", version)==null) {

    ModuleDefinition moduleDefinition =
      document.createModuleDefinition(partId+"_"+promoter+"_repression", version);
    moduleDefinition.addWasGeneratedBy(activityURI);
    moduleDefinition.createAnnotation(new QName(dcTermsNS,"created","dcTerms"), createdDate);

    Interaction interaction =
      moduleDefinition.createInteraction(partId+"_"+promoter+"_repression",
      SystemsBiologyOntology.INHIBITION);
    interaction.createParticipation(partId+"_protein_participation", partId+"_protein",
      SystemsBiologyOntology.INHIBITOR);
    interaction.createParticipation(promoter+"_promoter_participation", promoter,
      SystemsBiologyOntology.INHIBITED);
  }
}
```

Creating the Composite Sequence

```
Sequence sequence = document.createSequence(gate_name+"_sequence", version, seq,
  Sequence.IUPAC_DNA);
sequence.setName(gate_name+"_sequence");
sequence.addWasDerivedFrom(derivedFrom);
sequence.addWasGeneratedBy(activityURI);
sequence.createAnnotation(new QName(dcTermsNS,"created","dcTerms"), createdDate);
componentDefinition.addSequence(sequence);
```

Provenance Ontology Classes

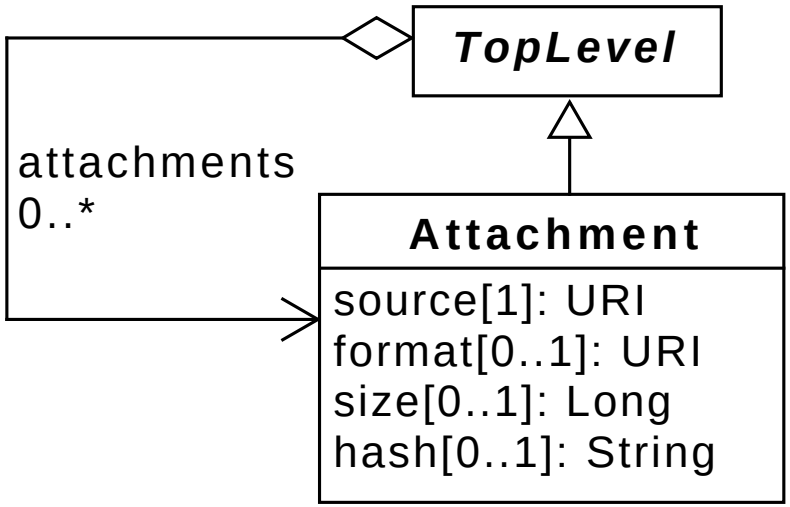


Creating the CelloUCF2SBOL Agent

```
Agent agent = document.createAgent("CelloUCF2SBOL", version);
agent.setName("Cello UCF to SBOL");
agent.setDescription("A script to convert Cello UCF parts and metadata to SBOL 2 documents.");
agent.createAnnotation(new QName(dcNS,"source","dc"), URI.create("https://github.com/MyersResearch
agent.createAnnotation(new QName(dcNS,"creator","dc"), "Prashant Vaidyanathan");
agent.createAnnotation(new QName(dcNS,"creator","dc"), "Chris J. Myers");
```

```
<prov:Agent rdf:about="http://cellocad.org/CelloUCF2SBOL/1">
  <sbol:persistentIdentity rdf:resource="http://cellocad.org/CelloUCF2SBOL"/>
  <sbol:displayId>CelloUCF2SBOL</sbol:displayId>
  <sbol:version>1</sbol:version>
  <dcterms:title> Cello UCF to SBOL</dcterms:title>
  <dcterms:description> A script to convert Cello UCF parts and metadata to SBOL 2 documents.</dct
  <dc:source rdf:resource="https://github.com/MyersResearchGroup/UCF2SBOL"/>
  <dc:creator> Prashant Vaidyanathan</dc:creator>
  <dc:creator> Chris J. Myers</dc:creator>
</prov:Agent>
```

Attachment


TopLevel
attachments
0..*
Attachment
source[1]: URI
format[0..1]: URI
size[0..1]: Long
hash[0..1]: String

Creating the UCF File Attachment

```
Attachment attachment = document.createAttachment("Eco1C1G1T1_UCF", version,
  URI.create("https://github.com/MyersResearchGroup/UCF2SBOL/blob/master/" +
    "UCF2SBOL/src/main/resources/Eco1C1G1T1.UCF.json"));
```

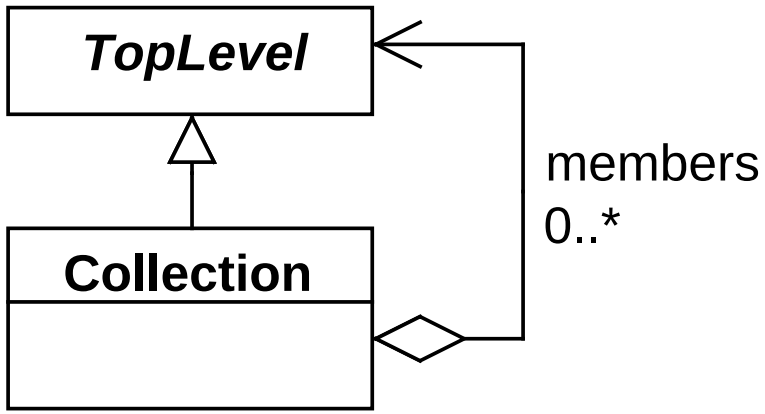
```
<sbol:Attachment rdf:about="http://cellocad.org/Eco1C1G1T1_UCF/1">
  <sbol:persistentIdentity rdf:resource="http://cellocad.org/Eco1C1G1T1_UCF"/>
  <sbol:displayId>Eco1C1G1T1_UCF</sbol:displayId>
  <sbol:version>1</sbol:version>
  <sbol:source rdf:resource="https://github.com/MyersResearchGroup/UCF2SBOL/blob/master/UCF2SBOL/s
</sbol:Attachment>
```

Creating the CelloUCF2SBOL Actvity

```
Activity activity = document.createActivity("CelloUCF2sbol_Activity", version);
activity.setName("Cello␣UCF␣to␣SBOL␣conversion");
activity.setDescription("Conversion␣of␣the␣Cello␣UCF␣parts␣and␣metadata␣to␣SBOL␣2␣documents.");
activity.setEndedAtTime(DateTime.now());
activityURI = activity.getIdentity();
activity.createAssociation("association", agent.getIdentity());
activity.createUsage("UCF_file", attachment.getIdentity());
```

```
<prov:Activity rdf:about="http://cellocad.org/CelloUCF2sbol_Activity/1">
  <sbol:persistentIdentity rdf:resource="http://cellocad.org/CelloUCF2sbol_Activity"/>
  <sbol:displayId>CelloUCF2sbol_Activity</sbol:displayId>
  <sbol:version>1</sbol:version>
  <dcterms:title> Cello UCF to SBOL conversion</dcterms:title>
  <dcterms:description> Conversion of the Cello UCF parts and metadata to SBOL 2 documents.</dcter
  <prov:endedAtTime>2018-07-29T16:39:14.613-06:00</prov:endedAtTime>
  <prov:qualifiedAssociation>
    <prov:Association rdf:about="http://cellocad.org/CelloUCF2sbol_Activity/association/1">
      <sbol:persistentIdentity rdf:resource="http://cellocad.org/CelloUCF2sbol_Activity/associatio
      <sbol:displayId>association</sbol:displayId>
      <sbol:version>1</sbol:version>
      <prov:agent rdf:resource="http://cellocad.org/CelloUCF2SBOL/1"/>
    </prov:Association>
    </prov:qualifiedAssociation>
    <prov:qualifiedUsage>
      <prov:Usage rdf:about="http://cellocad.org/CelloUCF2sbol_Activity/UCF_File/1">
        <sbol:persistentIdentity rdf:resource="http://cellocad.org/CelloUCF2sbol_Activity/UCF_File
        <sbol:displayId>UCF_File</sbol:displayId>
        <sbol:version>1</sbol:version>
        <prov:entity rdf:resource="http://cellocad.org/Eco1C1G1T1_UCF/1"/>
      </prov:Usage>
    </prov:qualifiedUsage>
</prov:Activity>
```

Collection

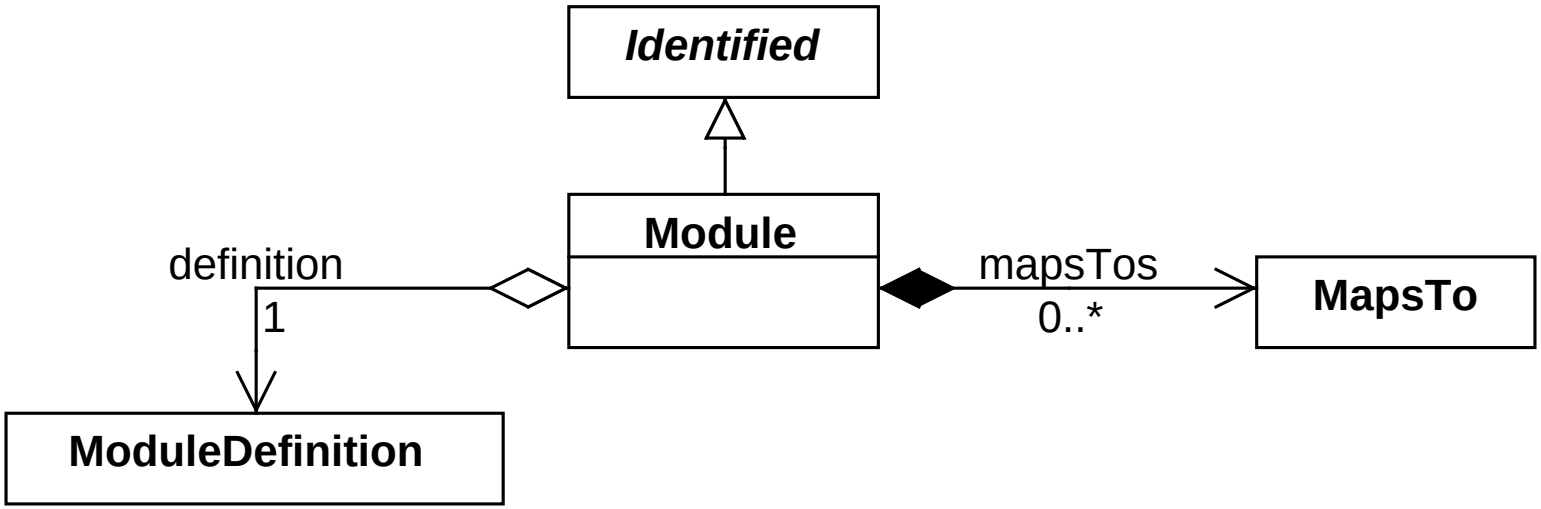


Creating CDS Part Collection

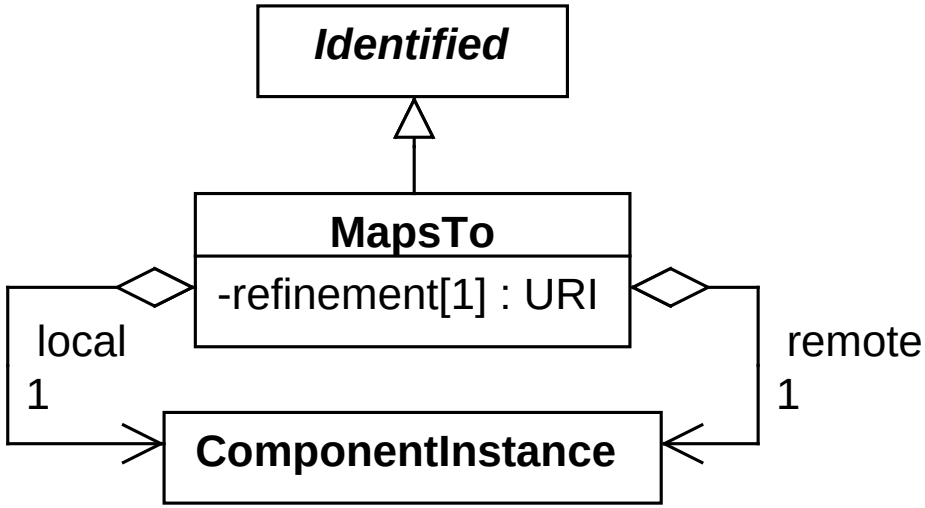
```
Collection cdsCollection = document.createCollection("cdsCollection", version);
for (ComponentDefinition cd : document.getComponentDefinitions()) {
  if (cd.containsRole(SequenceOntology.CDS)) {
    cdsCollection.addMember(cd.getIdentity());
  }
}
```

```
<sbol:Collection rdf:about="http://cellocad.org/cdsCollection/1">
  <sbol:persistentIdentity rdf:resource="http://cellocad.org/cdsCollection"/>
  <sbol:displayId> cdsCollection </sbol:displayId>
  <sbol:version> 1 </sbol:version>
  <sbol:member rdf:resource="http://cellocad.org/SrpR/1"/>
  <sbol:member rdf:resource="http://cellocad.org/AmeR/1"/>
  <sbol:member rdf:resource="http://cellocad.org/HlyIIR/1"/>
  <sbol:member rdf:resource="http://cellocad.org/AmtR/1"/>
  <sbol:member rdf:resource="http://cellocad.org/PhlF/1"/>
  <sbol:member rdf:resource="http://cellocad.org/BM3R1/1"/>
  <sbol:member rdf:resource="http://cellocad.org/BetI/1"/>
</sbol:Collection>
```

Module (Child of ModuleDefinition)



MapsTo (Child of ComponentInstance)



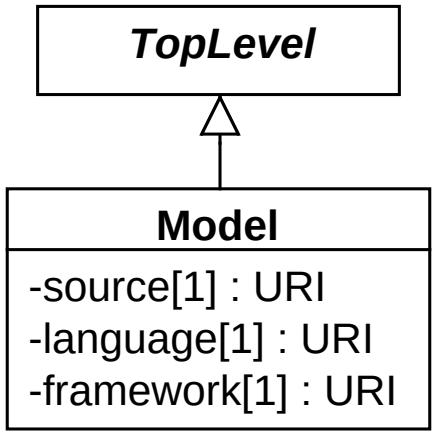
Refinement URI

`http://sbols.org/v2#useRemote`
`http://sbols.org/v2#useLocal`
`http://sbols.org/v2#verifyIdentical`
`http://sbols.org/v2#merge`

Description

All references MUST dereference to the *remote* **CI**.
All references MUST dereference to the *local* **CI**.
The *definition* of the *local* and *remote* MUST be same **CD**.
All references MUST dereference to both objects.

Model



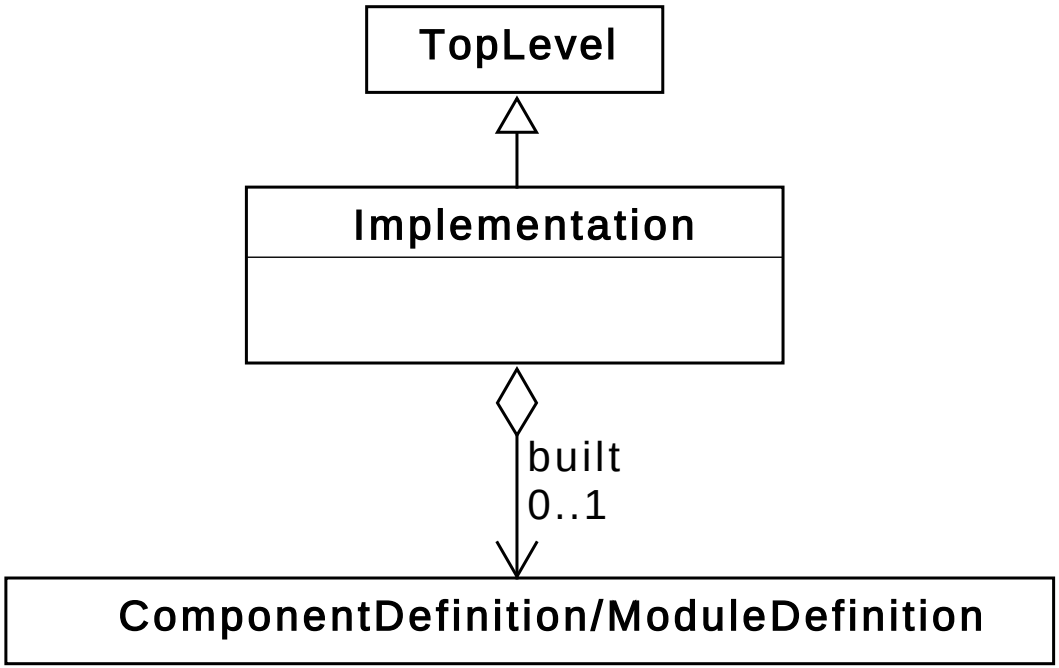
- *source* - URI reference to the source file for the model.
- *language* - URI that species language in which the model is implemented.

Model Language	URI for EDAM Term
SBML	http://identifiers.org/edam/format_2585
CellML	http://identifiers.org/edam/format_3240
BioPAX	http://identifiers.org/edam/format_3156

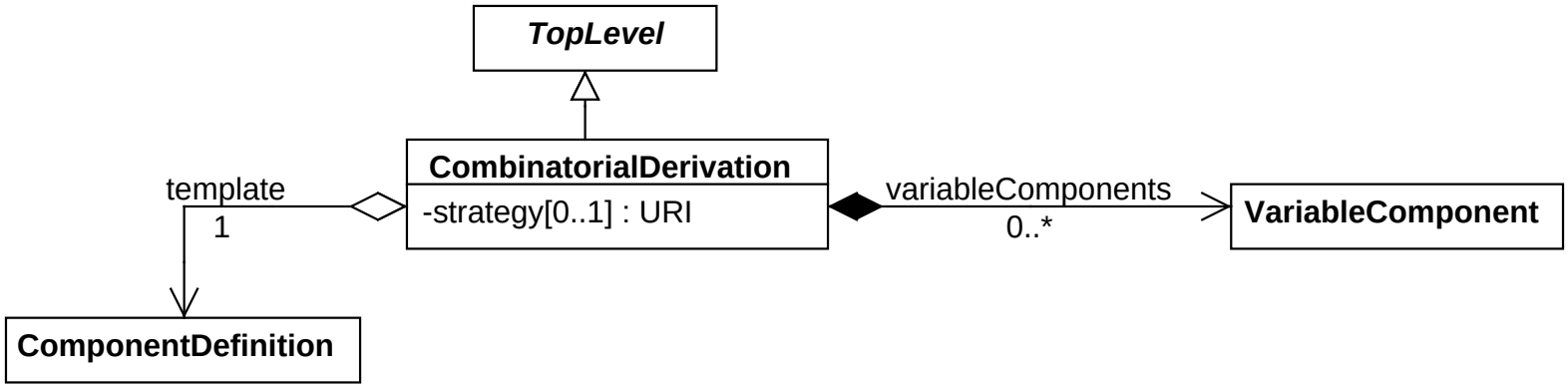
- *framework* - URI that species modeling framework used.

Framework	URI for SBO Term
Continuous	http://identifiers.org/biomodels.sbo/SBO:0000062
Discrete	http://identifiers.org/biomodels.sbo/SBO:0000063

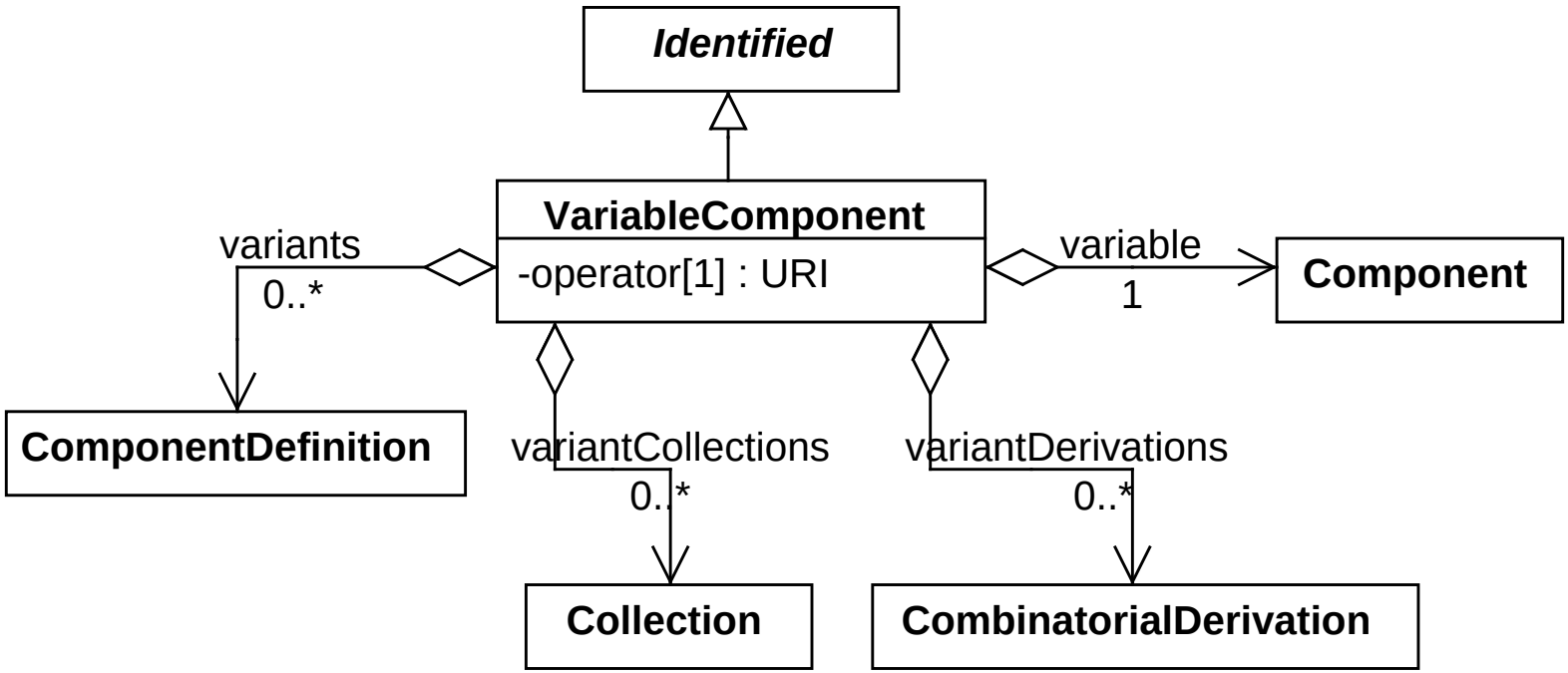
Implementation



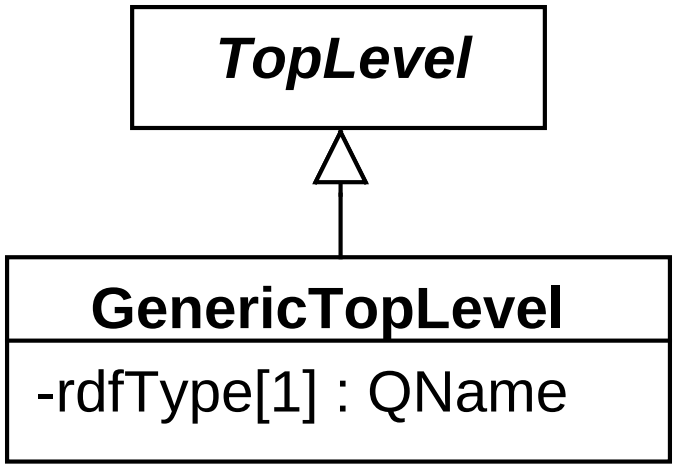
CombinatorialDerivation



VariableComponent



GenericTopLevel



GenericTopLevel Objects and Annotations

- Software tools that need to store data that is not encoded within SBOL can do so using **GenericTopLevel** objects and custom **Annotations**.
- When the library reader encounters a tag for a **TopLevel** object that it does not recognize, this data is stored within a **GenericTopLevel** object.
- Within **TopLevel** objects, when a tag is not recognized the data is stored within a custom **Annotation** object.
- Tools using our library that do not recognize this data will round-trip it unmodified when writing an SBOL file.
- Tools that would like to make use of this data can interpret and manipulate the raw data, which is stored in a tree-like data structure.

Serialization Methods

- SBOLWriter class:

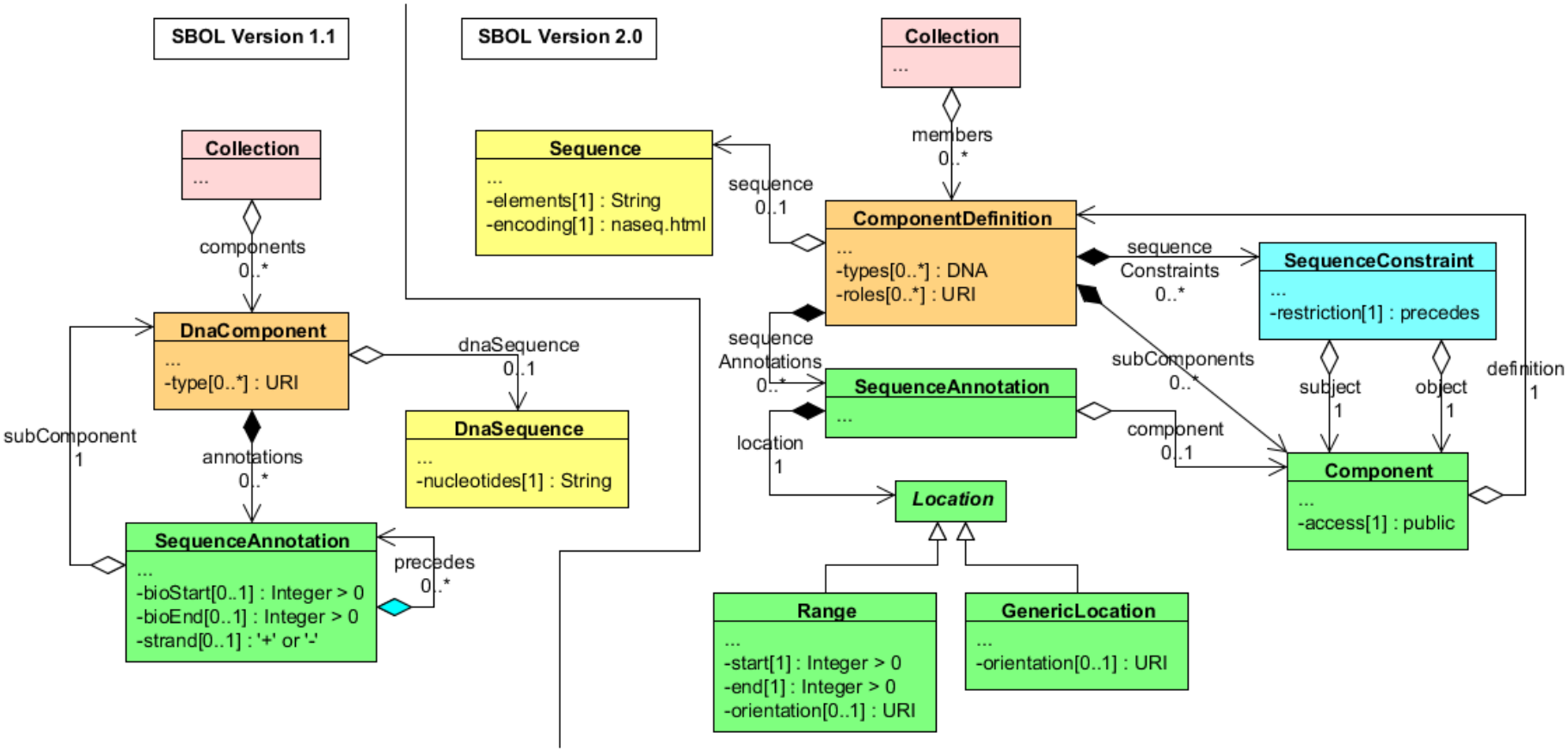
```
SBOLWriter.setKeepGoing(true);

SBOLWriter.write(document, String OR File OR OutputStream);
SBOLWriter.write(document, String OR File OR OutputStream, fileType);
fileType = SBOLDocument.RDF, RDFV1, GENBANK, FASTAformat
document.write(String OR File OR OutputStream, fileType);

SBOLWriter.clearErrors();
SBOLWriter.getNumErrors();
SBOLWriter.getErrors();
```

- SBOLReader class:

```
SBOLReader.setURIPrefix("http://cellocad.org/");
SBOLReader.setVersion("1");
SBOLReader.setKeepGoing(true);

SBOLReader.getSBOLVersion(String OR File OR InputStream);
SBOLDocument document = SBOLReader.read(String OR File OR InputStream);
document.read(String OR File OR InputStream);

SBOLReader.clearErrors();
SBOLReader.getNumErrors();
SBOLReader.getErrors();
```

Conversion

- Supports conversion to/from GenBank and FASTA formats.
- Reads/Writes SBOL 1.1 data files.



Validation

- Many validation rules checked when documents are read.

```
SBOLReader.setKeepGoing(true);
SBOLDocument document = SBOLReader.read(file);
if (SBOLReader.getNumErrors() > 0) {
    for(String error : SBOLReader.getErrors()) {
        System.out.println(error);
    }
}
```

- Remaining validation rules checked by validateSBOL method.

```
boolean complete = true;      // Check that all referenced objects are included
boolean compliant = true;     // Check that all URIs are compliant
boolean bestPractice = true; // Check best practice validation rules
SBOLValidate.validateSBOL(document,complete,compliant,bestPractice);
if (SBOLValidate.getNumErrors() > 0) {
    for(String error : SBOLValidate.getErrors()) {
        System.out.println(error);
    }
}
```

- Method to compare to SBOLDocuments.

```
SBOLValidate.compareDocuments(file,document,file2,document2);
```

SynBioHub Repository Support

- Uploading SBOL to SynBioHub:

```
SynBioHubFrontend sbh = new SynBioHubFrontend(databaseURL,databasePrefix);
sbh.login(loginEmail, password);
sbh.createCollection(collectionId, collectionVersion, collectionName,
  collectionDescription,collectionPubMedId, true);
sbh.attachFile(URI.create(databasePrefix + "/user/" + loginUser + "/" + collectionId + "/"
  + collectionId + "_collection/" + collectionVersion), pathToUCFFile);
SBOLDocument doc = sbh.getSBOL(URI.create(databasePrefix + "/user/" + loginUser + "/"
  + collectionId + "/" + collectionId + "_collection/" + collectionVersion));
for (Attachment attachment : doc.getAttachments()) {
  activity.createUsage("UCF_file", attachment.getIdentity());
}
sbh.addToCollection(URI.create(databasePrefix + "/user/" + loginUser + "/" +
  collectionId + "/" + collectionId + "_collection/" + collectionVersion), false, document);
```

- Other SynBioHub functions:

```
public String getAttachment(URI attachmentURI, String path)
public String getAttachment(URI attachmentURI, OutputStream outputStream)
public int getCount(String objectType)
public ArrayList<IdentifiedMetadata> getRootCollectionMetadata()
public ArrayList<IdentifiedMetadata> getSubCollectionMetadata(URI parentCollectionUri)
public ArrayList<IdentifiedMetadata> getMatchingComponentDefinitionMetadata(String name,
  Set<URI> roles, Set<URI> types, Set<URI> collections, Integer offset, Integer limit)
public ArrayList<IdentifiedMetadata> search(SearchQuery query)
public String sparqlQuery(String query)
```

More Information

- `libSBOLj` is open source under the Apache 2.0 License.
- More information: `http://sbolstandard.org/libsbol/`.
  - Current snapshot (2.3.2-SNAPSHOT) on GitHub and Sonatype.
  - Latest release (Version 2.3.1) on GitHub and Maven.
  - Issue tracker for reporting bugs and feature requests.
  - JavaDocs for all public methods.
  - A brief getting started tutorial.
  - A detailed code example and sample project for a CRISPR circuit.
  - Several example code files.

sboljs - Javascript SBOL library

- Developed by James McLaughlin at Newcastle University and myself.
- Prerequisites: node.js and npm.
- Install: npm install sboljs

Creating an SBOL Document

```
var SBOLDocument = require('sboljs');
...
var sbol = new SBOLDocument();
```

Creating a GenericTopLevel

```
var actVersion = 1;
var actDisplayId = 'cello2sbol';
var actPersistantIdentity = urlprefix + actDisplayId;
var activityURI = actPersistantIdentity + '/' + actVersion;

const activity = sbol.genericTopLevel(activityURI, provNS + 'Activity');
activity.version = actVersion;
activity.displayId = actDisplayId;
activity.name = 'Cello UCF to SBOL conversion';
activity.description = 'Conversion of the Cello UCF parts and metadata to SBOL2';
activity.addStringAnnotation(dcNS + 'creator', 'Prashant Vaidyanathan');
activity.addStringAnnotation(dcNS + 'creator', 'Chris J. Myers');
// TODO: Need to change to PROV endedAtTime
activity.addStringAnnotation('http://purl.org/dc/terms/created', today.toISOString() + '');
activity.persistentIdentity = actPersistantIdentity;
activity.uri = activityURI;
```

Parsing Cello UCF JSON File

```
var ucf = JSON.parse(fs.readFileSync(ucfFilepath) + '');

var gate_partsArr = [];
var partsMap = {};
var partsSBOL = {}
var gatesMap = {};
...

//Go through the UCF file to store collections in local data structures (arrays and maps)
ucf.forEach(function (collection) {

    switch (collection.collection) {
        case 'parts':
            //partsArr.push(collection);
            partsMap[collection.name] = collection;
            break;
        case 'gate_parts':
            gate_partsArr.push(collection);
            break;
       case 'gates':
            gatesMap[collection.gate_name] = collection;
            break;
        ...
    }

}, this);
```

Converting Parts to SBOL (1)

```
Object.keys(partsMap).forEach(function (partkey) {
    var part = partsMap[partkey];
    var partName = part.name;

    if (!(partName in partsSBOL)) {
        const componentDefinition = sbol.componentDefinition()
        componentDefinition.version = version;
        componentDefinition.displayId = part.name;
        componentDefinition.name = part.name;
        componentDefinition.persistentIdentity = urlprefix + componentDefinition.displayId;
        componentDefinition.uri = componentDefinition.persistentIdentity + '/' +
          componentDefinition.version;
        componentDefinition.wasDerivedFrom = derivedFrom;
        componentDefinition.addUriAnnotation(provNS + 'wasGeneratedBy', activityURI);
        componentDefinition.addRole(getPartType(part.type));
        componentDefinition.addType(SBOLDocument.terms.dnaRegion);

        const sequence = sbol.sequence()
        sequence.displayId = part.name + '_sequence';
        sequence.name = part.name + '_sequence';
        sequence.version = version;
        sequence.elements = part.dnasequence;
        sequence.persistentIdentity = urlprefix + sequence.displayId;
        sequence.uri = sequence.persistentIdentity + '/' + sequence.version;
        sequence.wasDerivedFrom = derivedFrom;
        sequence.encoding = SBOLDocument.terms.dnaSequence;
        sequence.addUriAnnotation(provNS + 'wasGeneratedBy', activityURI);
        componentDefinition.addSequence(sequence)
```

Converting Parts to SBOL (2)

```
// Create a Protein
if (part.type === 'cds') {
  const proteinComponentDefinition = sbol.componentDefinition();
  proteinComponentDefinition.version = version;
  proteinComponentDefinition.displayId = componentDefinition.displayId + '_protein';
  proteinComponentDefinition.name = componentDefinition.displayId + '_protein';
  proteinComponentDefinition.persistentIdentity = urlprefix +
    proteinComponentDefinition.displayId;
  proteinComponentDefinition.uri = proteinComponentDefinition.persistentIdentity + '/' +
    proteinComponentDefinition.version;
  proteinComponentDefinition.addType(SBOLDocument.terms.protein);
  proteinComponentDefinition.addUriAnnotation(provNS + 'wasGeneratedBy', activityURI);
  partsSBOL[partName + '_protein'] = proteinComponentDefinition.uri;

  const moduleDefinition = sbol.moduleDefinition();
  moduleDefinition.name = proteinComponentDefinition.displayId + '_production';
  moduleDefinition.version = version;
  moduleDefinition.displayId = proteinComponentDefinition.displayId + '_production';
  moduleDefinition.persistentIdentity = urlprefix + moduleDefinition.displayId;
  moduleDefinition.uri = moduleDefinition.persistentIdentity + '/' + moduleDefinition.version;
  moduleDefinition.addUriAnnotation(provNS + 'wasGeneratedBy', activityURI);
```

Converting Parts to SBOL (4)

```
//Functional Component for Coding sequence
const functionalComponentCDS = sbol.functionalComponent();
functionalComponentCDS.version = version;
functionalComponentCDS.displayId = componentDefinition.displayId + '_functionalComponent';
functionalComponentCDS.name = componentDefinition.name + '_functionalComponent';
functionalComponentCDS.persistentIdentity = moduleDefinition.persistentIdentity + '/' +
  functionalComponentCDS.displayId;
functionalComponentCDS.uri = functionalComponentCDS.persistentIdentity + '/' +
  functionalComponentCDS.version;
functionalComponentCDS.definition = componentDefinition;

//Functional Component for Protein
const functionalComponentProt = sbol.functionalComponent();
functionalComponentProt.version = version;
functionalComponentProt.displayId = proteinComponentDefinition.displayId + '_functionalComponent';
functionalComponentProt.name = proteinComponentDefinition.name + '_functionalComponent';
functionalComponentProt.persistentIdentity = moduleDefinition.persistentIdentity + '/' +
  functionalComponentProt.displayId;
functionalComponentProt.uri = functionalComponentProt.persistentIdentity + '/' +
  functionalComponentProt.version;
functionalComponentProt.definition = proteinComponentDefinition;
```

Converting Parts to SBOL (5)

```
//CDS to Protein interaction
const interaction = sbol.interaction();
interaction.displayId = proteinComponentDefinition.displayId + '_interaction';
interaction.name = interaction.displayId;
interaction.version = version;
interaction.persistentIdentity = moduleDefinition.persistentIdentity + '/' +
  interaction.displayId;
interaction.uri = interaction.persistentIdentity + '/' + interaction.version;
interaction.addType(productionSBO);

const participationCDS = sbol.participation();
participationCDS.version = version;
participationCDS.name = componentDefinition.displayId + '_participation';
participationCDS.displayId = componentDefinition.displayId + '_participation';
participationCDS.persistentIdentity = interaction.persistentIdentity + '/' +
  participationCDS.displayId;
participationCDS.uri = participationCDS.persistentIdentity + '/' + participationCDS.version;
participationCDS.addRole(templateSBO);
participationCDS.participant = functionalComponentCDS;

const participationProt = sbol.participation();
participationProt.version = version;
participationProt.name = proteinComponentDefinition.displayId + '_participation';
participationProt.displayId = proteinComponentDefinition.displayId + '_participation';
participationProt.persistentIdentity = interaction.persistentIdentity + '/' +
  participationProt.displayId;
participationProt.uri = participationProt.persistentIdentity + '/' + participationProt.version;
participationProt.addRole(productSBO);
participationProt.participant = functionalComponentProt;

interaction.addParticipation(participationCDS);
interaction.addParticipation(participationProt);
```

Converting Parts to SBOL (6)

```
      moduleDefinition.addFunctionalComponent(functionalComponentCDS);
      moduleDefinition.addFunctionalComponent(functionalComponentProt);
      moduleDefinition.addInteraction(interaction);
    }
    componentDefinition.addStringAnnotation('http://purl.org/dc/terms/created',
      datecreated.toISOString() + '');
    var uriVal = componentDefinition.uri;
    partsSBOL[partName] = uriVal;
  }
}, this);
```

Converting Gate Parts to SBOL (1)

```
gate_partsArr.forEach(function (gpart) {
  var gpartName = gpart.gate_name;
  const componentDefinition = sbol.componentDefinition();
  componentDefinition.version = version;
  componentDefinition.displayId = gpartName;
  componentDefinition.name = gpartName;
  componentDefinition.persistentIdentity = urlprefix + componentDefinition.displayId;
  componentDefinition.uri = componentDefinition.persistentIdentity + '/' +
    componentDefinition.version;
  componentDefinition.wasDerivedFrom = derivedFrom;
  componentDefinition.addUriAnnotation(provNS + 'wasGeneratedBy', activityURI);
  componentDefinition.addUriAnnotation(tetR_family, gatesMap[gpartName].system);
  componentDefinition.addUriAnnotation(group_name, gatesMap[gpartName].group_name);
  componentDefinition.addUriAnnotation(gate_type, gatesMap[gpartName].gate_type );
  componentDefinition.addUriAnnotation(color_hexcode, gatesMap[gpartName].color_hexcode);
```

Converting Gate Parts to SBOL (2)

```
gpart.expression_cassettes.forEach(function (expression_cassettesArr) {

  var seq = "";
  var annotationCount = 0;
  var start = 1;

  expression_cassettesArr.cassette_parts.forEach(function (cassette) {

    const component = sbol.component();
    component.version = version;
    component.displayId = cassette;
    component.name = cassette;
    component.persistentIdentity = componentDefinition.persistentIdentity + '/' +
      component.displayId;
    component.uri = component.persistentIdentity + '/' + component.version;
    component.definition = sbol.lookupURI(partsSBOL[cassette]);
    componentDefinition.addComponent(component);
```

Converting Gate Parts to SBOL (3)

```
var cass_seq = partsMap[cassette].dnasequence;
  seq += cass_seq;

  const sa = sbol.sequenceAnnotation();
  sa.displayId = 'annotation' + annotationCount;
  annotationCount++;
  sa.name = cassette;
  sa.version = version;
  sa.persistentIdentity = componentDefinition.persistentIdentity + '/' + sa.displayId;
  sa.uri = sa.persistentIdentity + '/' + sa.version;
  sa.component = component;
  sa.description = partsMap[cassette].type;

  const range = sbol.range();
  range.displayId = 'range';
  range.persistentIdentity = sa.persistentIdentity + '/' + range.displayId;
  range.version = version;
  range.uri = range.persistentIdentity + '/' + range.version;
  range.start = start;
  var end = start + cass_seq.length - 1;
  range.end = end;
  range.orientation = 'http://sbols.org/v2#inline';

  sa.addLocation(range);
  componentDefinition.addSequenceAnnotation(sa);
```

Converting Gate Parts to SBOL (4)

```
//Create Protein - Promoter repression Module definition
if (partsMap[cassette].type === 'cds') {
  if (!(cassette in moduleDefnMap)) {
     const moduleDefinition = sbol.moduleDefinition();
      moduleDefinition.version = version;
      moduleDefinition.name = cassette + '_' + gpart.promoter + '_repression';
      moduleDefinition.displayId = cassette + '_' + gpart.promoter + '_repression';
      moduleDefinition.persistentIdentity = urlprefix + moduleDefinition.displayId;
      moduleDefinition.uri = moduleDefinition.persistentIdentity + '/' +
        moduleDefinition.version;
      moduleDefinition.addUriAnnotation(provNS + 'wasGeneratedBy', activityURI);

      const functionalComponentCDS = sbol.functionalComponent();
      functionalComponentCDS.version = version;
      functionalComponentCDS.name = cassette + '_protein_functionalComponent';
      functionalComponentCDS.displayId = cassette + '_protein_functionalComponent';
      functionalComponentCDS.persistentIdentity = moduleDefinition.persistentIdentity + '/' +
        functionalComponentCDS.displayId;
      functionalComponentCDS.uri = functionalComponentCDS.persistentIdentity + '/' +
        functionalComponentCDS.version;
      functionalComponentCDS.definition = sbol.lookupURI(partsSBOL[cassette + '_protein']);

      const functionalComponentProm = sbol.functionalComponent();
      functionalComponentProm.version = version;
      functionalComponentProm.name = gpart.promoter + '_functionalComponent';
      functionalComponentProm.displayId = gpart.promoter + '_functionalComponent';
      functionalComponentProm.persistentIdentity = moduleDefinition.persistentIdentity + '/' +
        functionalComponentProm.displayId;
      functionalComponentProm.uri = functionalComponentProm.persistentIdentity + '/' +
        functionalComponentProm.version;
      functionalComponentProm.definition = sbol.lookupURI(partsSBOL[gpart.promoter]);
```

Converting Gate Parts to SBOL (5)

```
//Protein - Promoter Interaction
const interaction = sbol.interaction();
interaction.version = version;
interaction.name = cassette + '_' + gpart.promoter + '_interaction';
interaction.displayId = cassette + '_' + gpart.promoter + '_interaction';
interaction.persistentIdentity = moduleDefinition.persistentIdentity + '/' +
  interaction.displayId;
interaction.uri = interaction.persistentIdentity + '/' + interaction.version;
interaction.addType(inhibitionSO);

//Protein participation
const participantProt = sbol.participation();
participantProt.version = version;
participantProt.name = cassette + '_protein_participation';
participantProt.displayId = cassette + '_protein_participation';
participantProt.persistentIdentity = interaction.persistentIdentity + '/' +
  participantProt.displayId;
participantProt.uri = participantProt.persistentIdentity + '/' + participantProt.version;
participantProt.addRole(inhibitorSO);
participantProt.participant = functionalComponentCDS;

//Promoter participation
const participantProm = sbol.participation();
participantProm.version = version;
participantProm.name = gpart.promoter + '_participation';
participantProm.displayId = gpart.promoter + '_participation';
participantProm.persistentIdentity = interaction.persistentIdentity + '/' +
  participantProm.displayId;
participantProm.uri = participantProm.persistentIdentity + '/' + participantProm.version;
participantProm.addRole(inhibitedSO);
participantProm.participant = functionalComponentProm;
```

Converting Gate Parts to SBOL (6)

```
      interaction.addParticipation(participantProt);
      interaction.addParticipation(participantProm);

      moduleDefinition.addFunctionalComponent(functionalComponentCDS);
      moduleDefinition.addFunctionalComponent(functionalComponentProm);
      moduleDefinition.addInteraction(interaction);

      moduleDefnMap[cassette] = gpart.promoter;
    }
  }

  start += cass_seq.length;

});
```

Converting Gate Parts to SBOL (7)

```
    const sequence = sbol.sequence()
    sequence.displayId = gpartName + '_sequence';
    sequence.name = gpartName + '_sequence';
    sequence.version = version;
    sequence.elements = seq;
    sequence.persistentIdentity = urlprefix + sequence.displayId;
    sequence.uri = sequence.persistentIdentity + '/' + sequence.version;
    sequence.wasDerivedFrom = derivedFrom;
    sequence.encoding = SBOLDocument.terms.dnaSequence;
    sequence.addUriAnnotation(provNS + 'wasGeneratedBy', activityURI);
    componentDefinition.addSequence(sequence);

  }, this);

  componentDefinition.addType(SBOLDocument.terms.dnaRegion);
  componentDefinition.addRole(gate_parts_so);
  componentDefinition.addStringAnnotation('http://purl.org/dc/terms/created', datecreated.toISOStr
}, this);
```

Writing the SBOL File

```
var fs = require('fs');

fs.writeFile(resultSBOL, sbol.serializeXML(), function (err) {
    if (err) {
        return console.log(err);
    }

    console.log("Cello SBOL file created!");
});
```

Conclusion (SBOL Compliant Software)

- Can either support all classes or only a subset.
- Can support import of SBOL, export of SBOL, or both (lossy/lossless).
- SBOL Test Suite is currently under development here:
  `https://github.com/SynBioDex/SBOLTestSuite`
- Validate SBOL files generated using the SBOL Validator found here:
  `http://www.async.ece.utah.edu/sbol-validator/`
- Report SBOL-compliant software by filling out the survey found here:
  `http://sbolstandard.org/applications/`