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SEPIO: An Ontology-Based Modeling Framework for Evidence and Provenance Information

Session S27: Open, Expert-curated, Harmonized, and Standardized Precision Oncology Knowledge, Ontologies and APIs

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The SEPIO Modeling Framework

The Scientific Evidence and Provenance Information Ontology

- **SEPIO** is the foundation of an **ontology-based modeling framework** for computable representation of **scientific assertions** and the **evidence** and **provenance** supporting them.

- The core SEPIO model is **domain-agnostic** but **extensible** with domain-specific content, and capable of representing any type of assertion and evidence.

- The broader **modeling framework** enables creation of **custom schema** for specific applications called **SEPIO Profiles**.

- **Ontology-based data models** use terms from ontologies to structure data:
  - Mappings from data model **types** and **attributes** to ontology **classes** and **properties**
  - Ontology terms used to build **value sets** for data collection

Benefits of Ontology-Based Models

1. **Promote understanding and communication** of the domain and the data by providing a unifying conceptual model and terminology
2. **Improve searchability** of data by leveraging relationships in ontology for semantic search and query expansion
3. **Allow algorithmic derivation of new knowledge** based on information encoded in the ontology
   a. Description logic reasoners use computable semantics of ontology to draw novel inferences and perform consistency checks
   b. Semantic similarity algorithms can operate on graphical relationships between ontology terms to infer similarity of entities annotated with them
4. **Facilitate data integration**, **discovery**, and **analysis** by exploiting modern semantic web standards and tools (linked data, RDF, JSON-LD)

SEPIO Supports Diverse Assertions Across the Basic Science, Translational, and Clinical Spectrum

Established

Monarch Initiative: genotype-phenotype associations from human and model organism knowledgebases

ClinGen: clinical interpretations of genes and variants

Developing

GA4GH: variant annotations and phenotype associations

CIViC/VICC: somatic variant interpretations

Exploratory

HL7 Clinical Genomics: patient level genomic data

GloBI/iDigBio: biodiversity, insect life history assertions

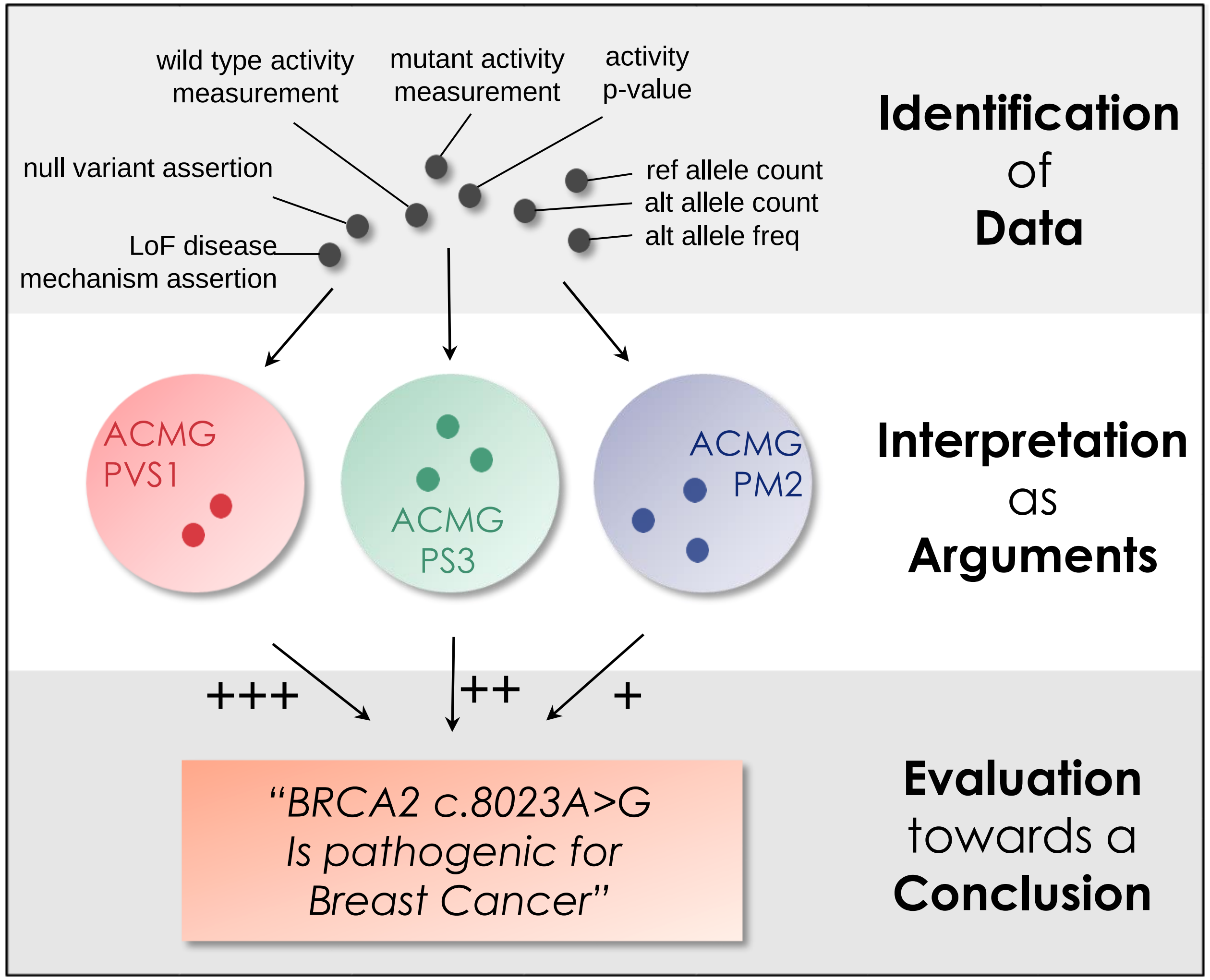
The SEPIO Worldview

We view the act of making an evidence-based assertion as involving **three universal tasks:**

1. The **identification** of **data** that might be used as evidence for a proposition

2. The **interpretation** of this data as independent **arguments** for or against this proposition

3. The **evaluation** of all arguments towards a final **conclusion** about the truth of the proposition


wild type activity measurement
mutant activity measurement
activity p-value
null variant assertion
ref allele count
alt allele count
alt allele freq
LoF disease mechanism assertion
Identification of Data
ACMG PVS1
ACMG PS3
ACMG PM2
Interpretation as Arguments
+++
++
+
"BRCA2 c.8023A>G Is pathogenic for Breast Cancer"
Evaluation towards a Conclusion

The SEPIO Core Model

A central axis of three core classes represent the outputs of each universal task.

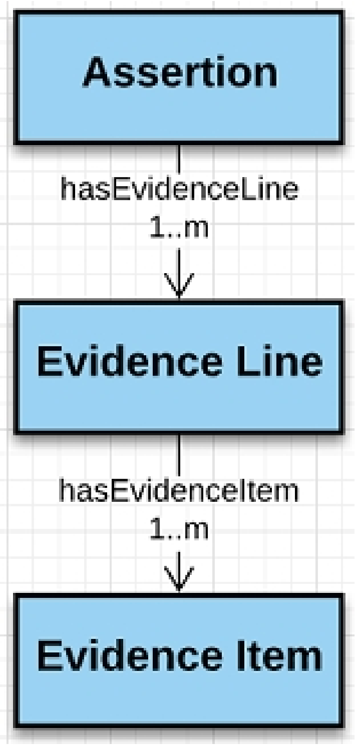
Universal Task

3 **Evaluation** towards a **Conclusion** produces

2 **Interpretation** as **Arguments** produces

1 **Identification** of **Data** produces

SEPIO Central Axis



Assertion

hasEvidenceLine 1..m

Evidence Line

hasEvidenceItem 1..m

Evidence Item

Example

Counsyl Genetics' 2015 claim that "BRCA2 c.8023A>G Is pathogenic for Breast Cancer"

The argument made by the raw counts and calculated frequency of BRCA2 c.8023A>G, as providing moderate supporting argument for its pathogenicity (ACMG criteria PM2)

The 0.0021% population frequency of the BRCA2 c.8023A>G variant in ExAC.

Alignment of the model with this universal paradigm is key to its broad applicability.

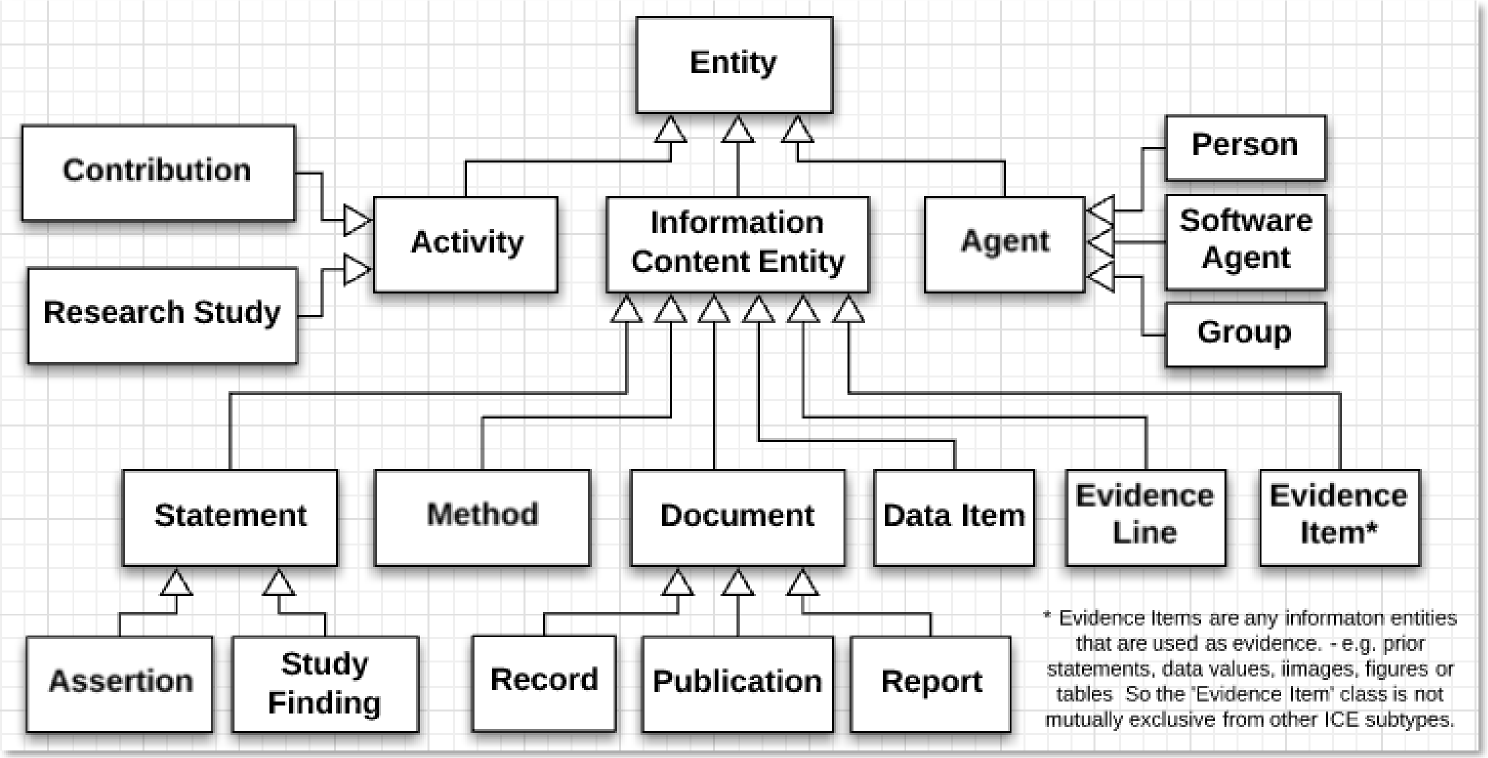
The SEPIO Modeling Framework

The modeling framework is comprised of four components that enable creation of ontology-based schema for specific domains and applications

1. **SEPIO Core Ontology:** defines the foundational, domain-agnostic model
2. **SEPIO Information Model:** provides a view of the ontology specifying how the terms and design patterns it defines can be used to structure data
3. **SEPIO Profiles:** a mechanism to create custom data models by extending the core model and ontology to provide schema for particular applications
4. **SEPIO Value Sets:** a model to create ontology-based collections of terms to constrain specific aspects of data collection

1. The SEPIO Core Ontology

- Defines a generic conceptual model on which specific data models are built
- OWL2 ontology, adheres to OBO Foundry Principles
- Reuses terms from community ontologies where possible
- Enables comprehensive mapping of data model **types** and **attributes** to ontology **classes** and **properties**

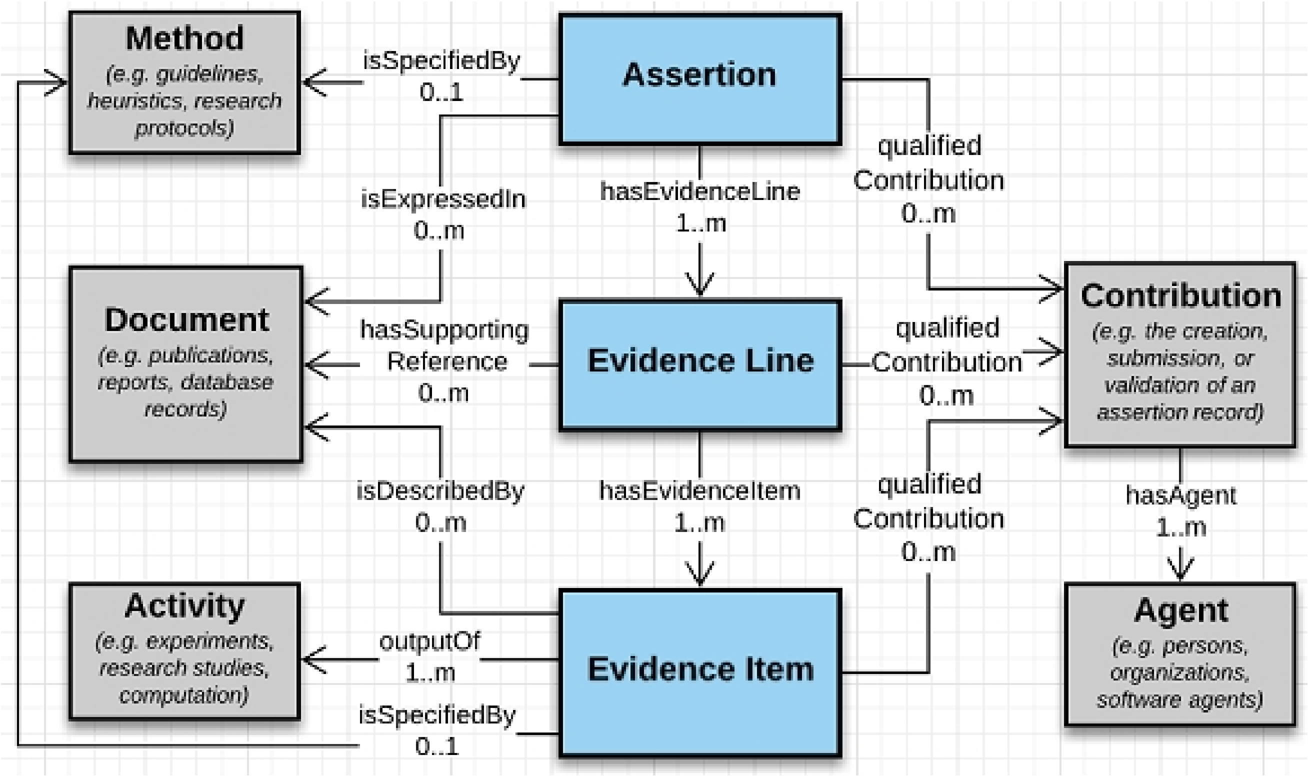


* Evidence Items are any informaton entities that are used as evidence. - e.g. prior statements, data values, iimages, figures or tables So the 'Evidence Item' class is not mutually exclusive from other ICE subtypes.

Hierarchical relationships between the high-level classes/types in the SEPIO core ontology and model

1. The SEPIO Core Ontology

- Defines a generic conceptual model on which specific data models are built
- OWL2 ontology, adheres to OBO Foundry Principles
- Reuses terms from community ontologies where possible
- Enables comprehensive mapping of data model **types** and **attributes** to ontology **classes** and **properties**



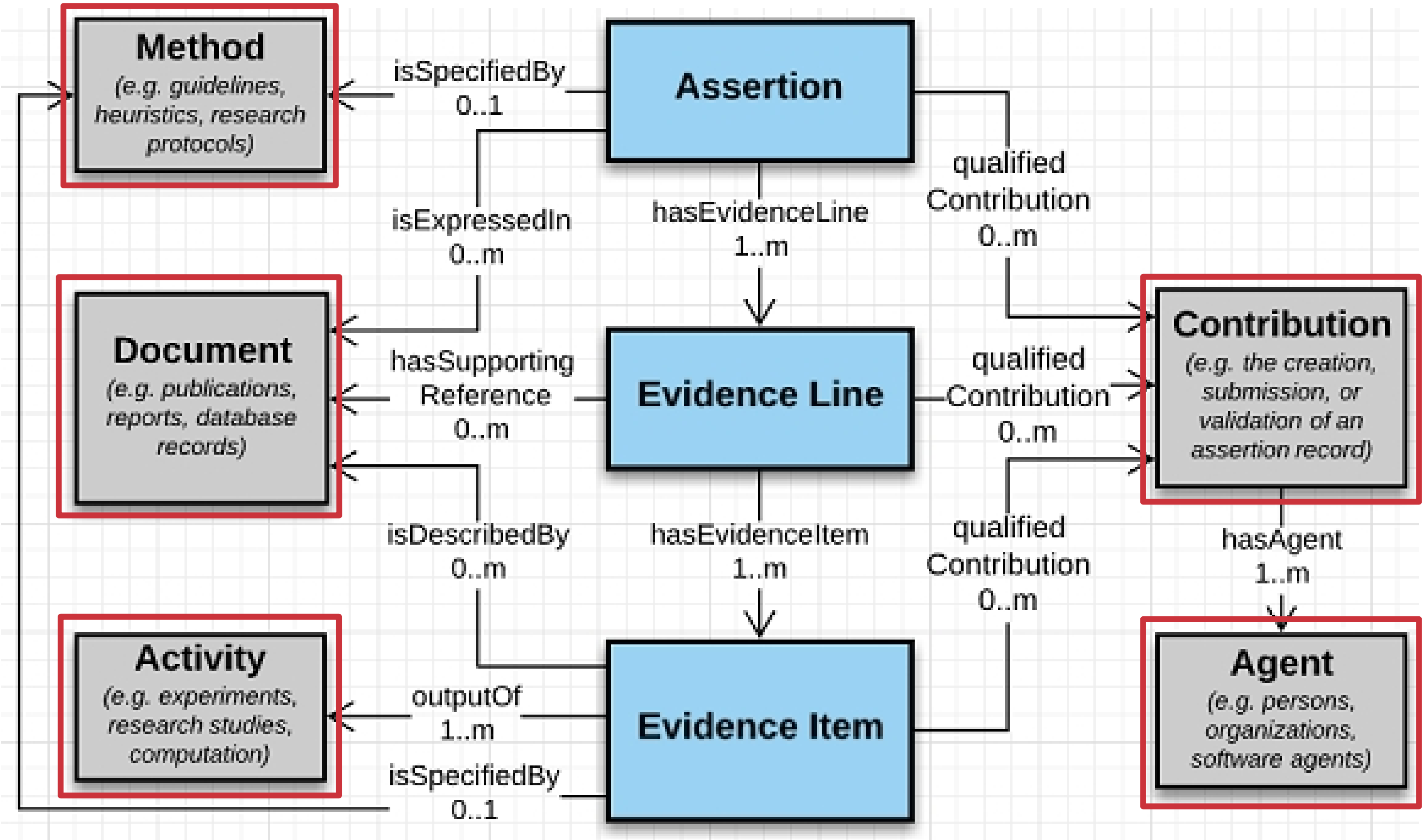
Relationships between high-level concepts in the core model

1. The SEPIO Ontology: Provenance

Provenance

Surrounding the core axis are concepts that let us describe how, when and by whom these core artifacts were created:

- **Contributions** made by **Agents**
- **Activities** they perform to do so, and any **resources** used
- **Methods** that specify activities
- **Documents** that describe them.



This core model lets us separately track the provenance behind how data is generated, interpreted as evidence, and collectively evaluated to make a final assertion.

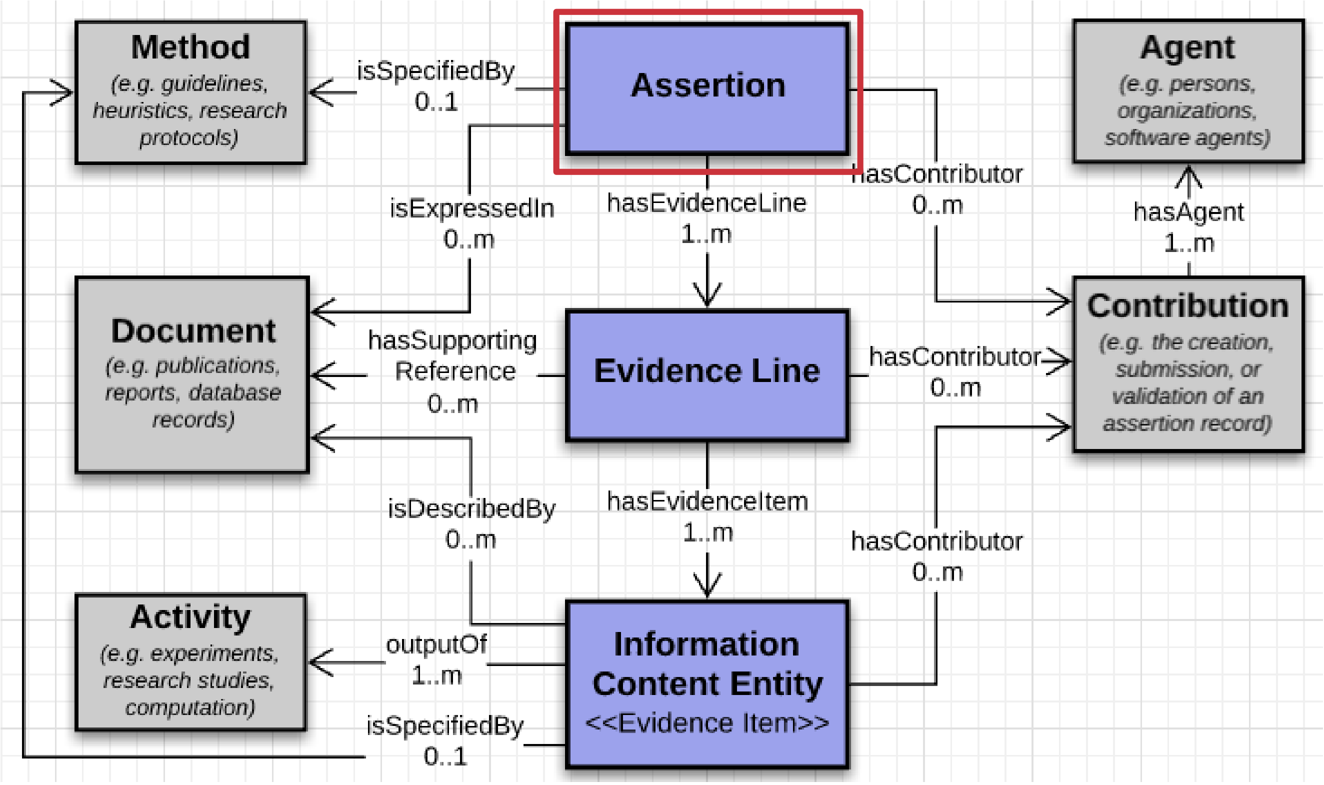
1. The SEPIO Core Ontology

Assertion

Definition: an evidence-based statement of purported truth, as made by a particular agent on particular occasion.

Example: Counsyl Genetics' 2015 Assertion that the BRCA2 variant c.8023A>G is pathogenic for Breast Cancer.

Comments: Assertions put forth a particular 'Proposition' as true. More than one Assertion, made by different agents on different occasions, can put forth the same Proposition.



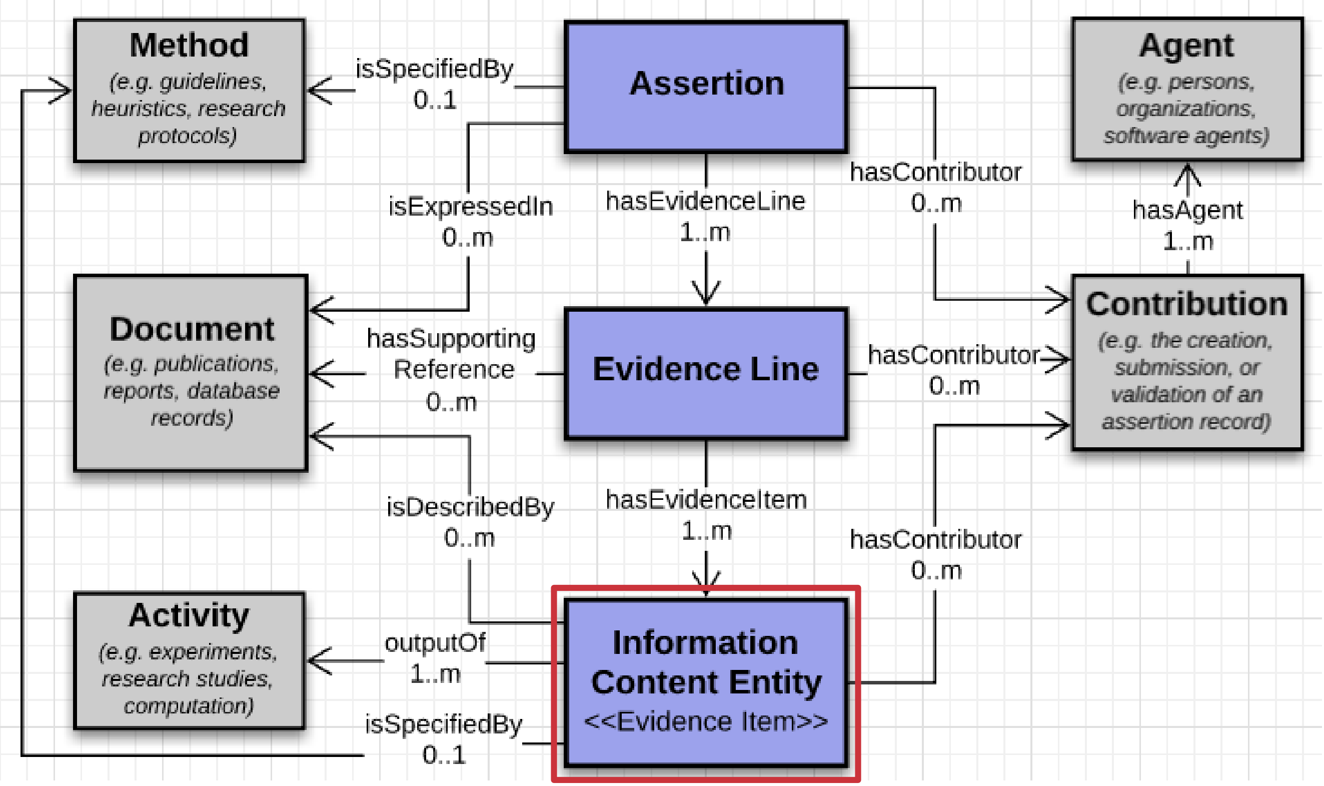
1. The SEPIO Core Ontology

Evidence Item

Definition: an individual piece of information that is interpreted to build an argument for or against an Assertion

Example: the 0.0021% population frequency of the BRCA2 variant c.8023A>G in healthy NFE individuals in ExAC.

Comments: Evidence Items can be primary data, derived statistical calculations, tables/figures depicting these data, statements summarizing the results of a particular study, or prior assertions based on their own lines of evidence.



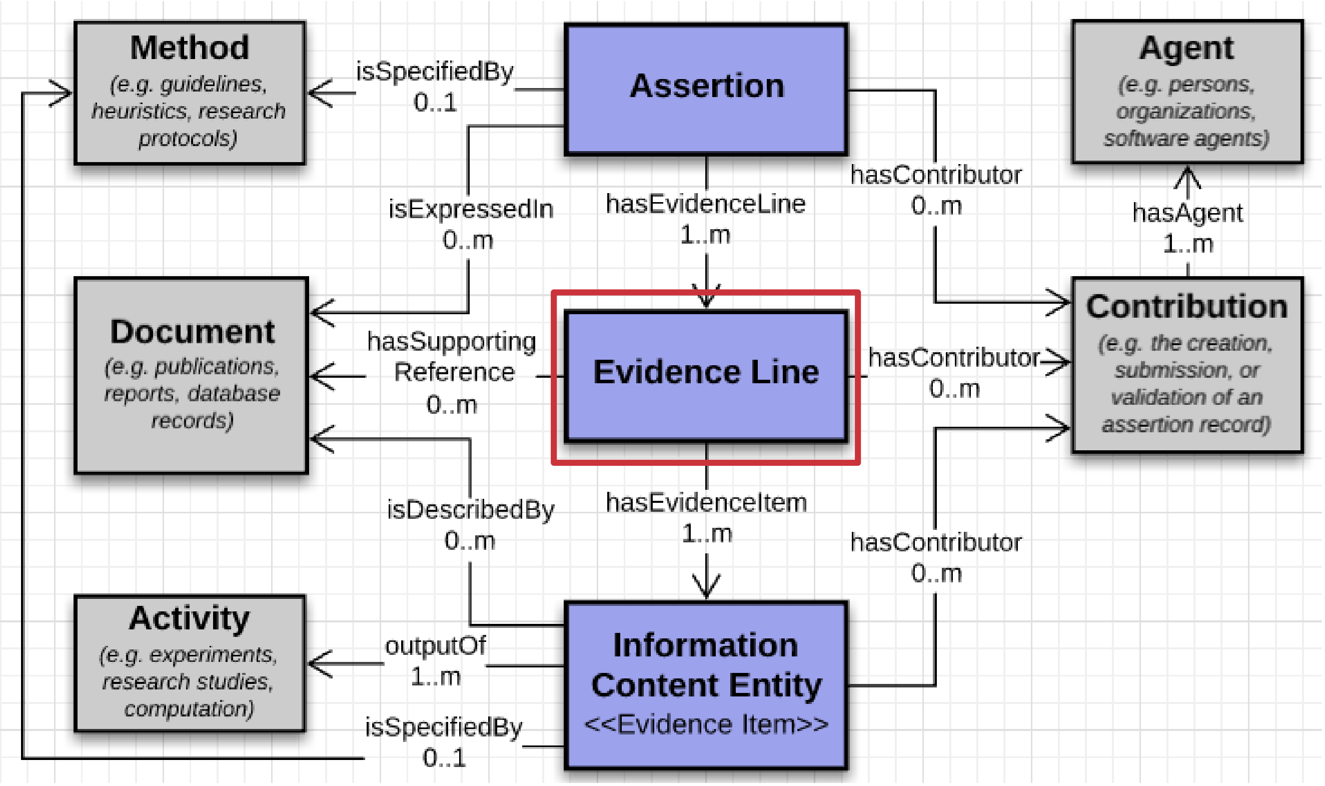
1. The SEPIO Core Ontology

Evidence Line

Definition: independent, meaningful arguments relevant to the validity of an Assertion, that are supported by one or more Evidence Items

Example: the argument made for the BRCA2 variant's pathogenicity based on its observed absence in healthy populations.

Comments: Representing Evidence Items separately from the 'arguments' they make is an important feature that lets us describe properties of information emerging only through its interpretation as evidence.



1. The SEPIO Core Ontology

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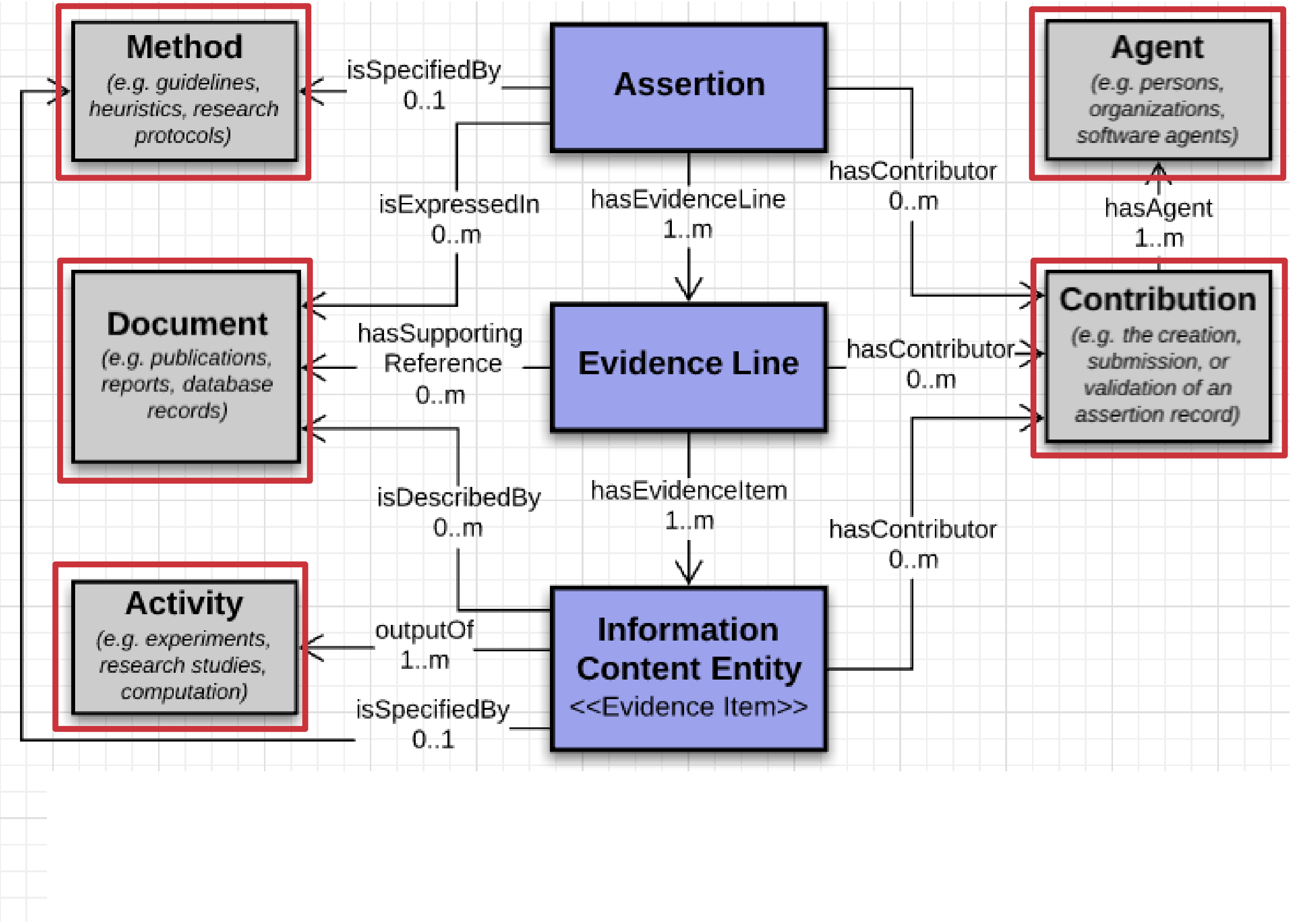
Provenance

Surrounding the core axis are familiar concepts that let us describe in rich detail who, how, and when these core informational objects were created:

- **Contributions** made to them by **Agents**
- **Activities** they perform to do so
- **Methods** that specify these activities
- **Documents** created to describe them.



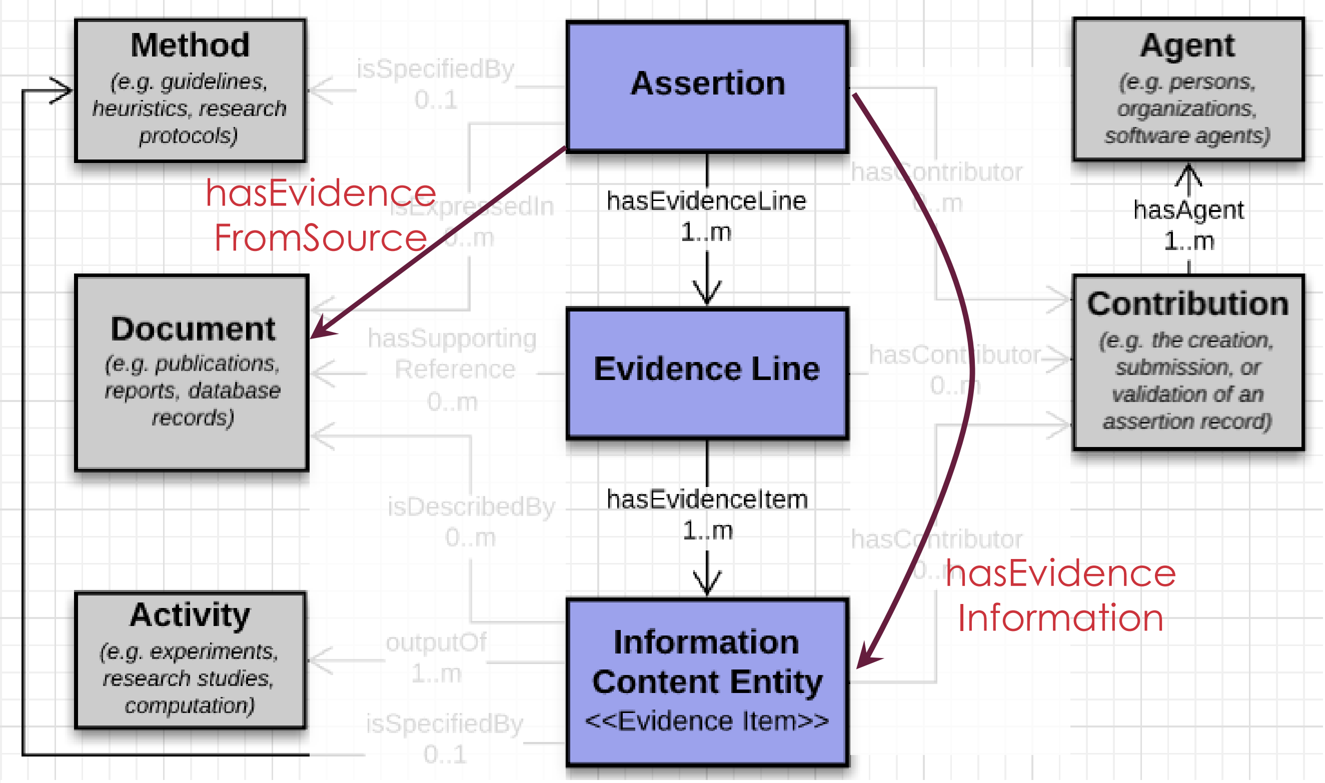
1. The SEPIO Core Ontology

Shortcut Relations

SEPIO provides relationships that can directly link objects normally connected via multiple edges in a fully normalized model, to support concise representation of data with sparser evidence and provenance metadata.

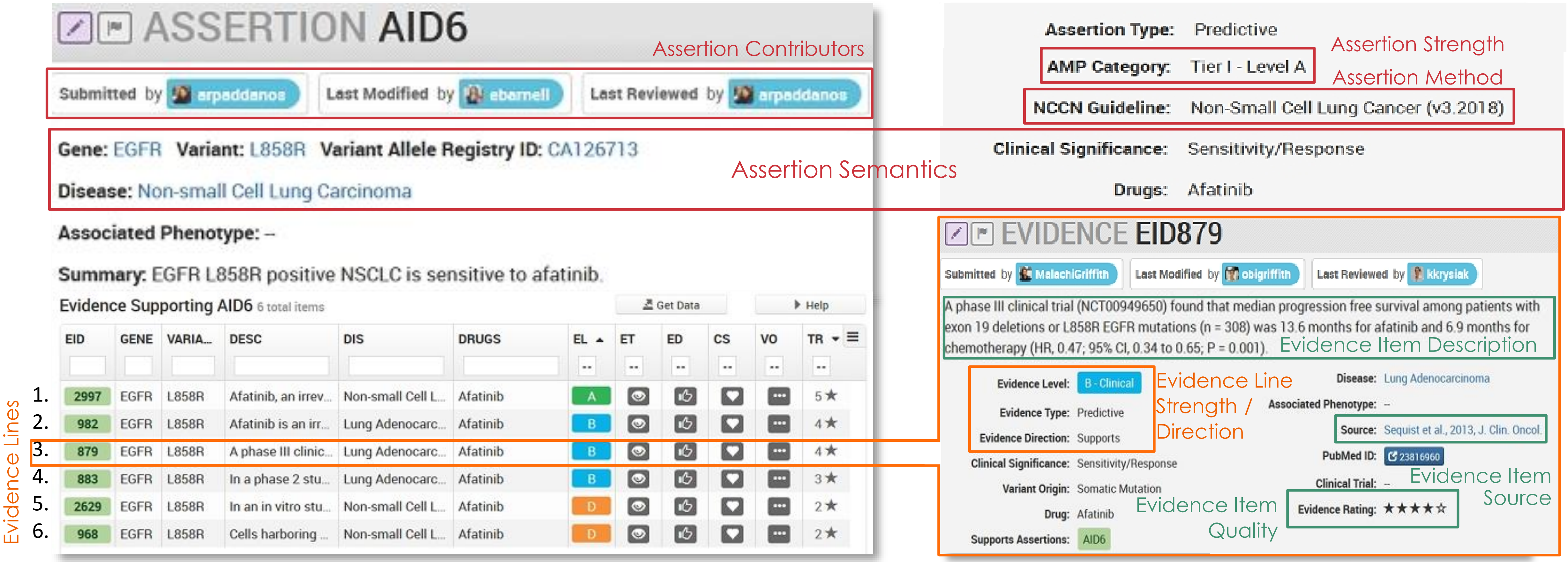
hasEvidenceFromSource: connects an Assertion directly to a document that contains info interpreted as evidence to support it

hasEvideneInformation: connects an Assertion directly to an Evidence Item



A CIViC ‘Predictive’ Variant Interpretation

Assertion: “*EGFR L858R* *positive* *NSCLC* *is sensitive to* *Afatinib*”



ASSERTION AID6

Assertion Contributors

Submitted by arpaddanos | Last Modified by ebarnell | Last Reviewed by arpaddanos

Assertion Semantics

Gene: EGFR **Variant:** L858R **Variant Allele Registry ID:** CA126713

Disease: Non-small Cell Lung Carcinoma

Associated Phenotype: –

Summary: EGFR L858R positive NSCLC is sensitive to afatinib.

Evidence Supporting AID6 6 total items

Get Data | Help

Evidence Lines

	EID	GENE	VARIA...	DESC	DIS	DRUGS	EL ▲	ET	ED	CS	VO	TR ▼
							--	--	--	--	--	--
1.	2997	EGFR	L858R	Afatinib, an irrev...	Non-small Cell L...	Afatinib	A	👁	👍	♥	⋯	5★
2.	982	EGFR	L858R	Afatinib is an irr...	Lung Adenocarc...	Afatinib	B	👁	👍	♥	⋯	4★
3.	879	EGFR	L858R	A phase III clinic...	Lung Adenocarc...	Afatinib	B	👁	👍	♥	⋯	4★
4.	883	EGFR	L858R	In a phase 2 stu...	Lung Adenocarc...	Afatinib	B	👁	👍	♥	⋯	3★
5.	2629	EGFR	L858R	In an in vitro stu...	Non-small Cell L...	Afatinib	D	👁	👍	♥	⋯	2★
6.	968	EGFR	L858R	Cells harboring ...	Non-small Cell L...	Afatinib	D	👁	👍	♥	⋯	2★

Assertion Type: Predictive

Assertion Strength

AMP Category: Tier I - Level A

Assertion Method

NCCN Guideline: Non-Small Cell Lung Cancer (v3.2018)

Clinical Significance: Sensitivity/Response

Drugs: Afatinib

EVIDENCE EID879

Submitted by MalachiGriffith | Last Modified by obigriffith | Last Reviewed by kkrysiak

A phase III clinical trial (NCT00949650) found that median progression free survival among patients with exon 19 deletions or L858R EGFR mutations (n = 308) was 13.6 months for afatinib and 6.9 months for chemotherapy (HR, 0.47; 95% CI, 0.34 to 0.65; P = 0.001).

Evidence Item Description

Evidence Level: B - Clinical

Evidence Type: Predictive

Evidence Direction: Supports

Evidence Line Strength / Direction

Clinical Significance: Sensitivity/Response

Variant Origin: Somatic Mutation

Drug: Afatinib

Supports Assertions: AID6

Disease: Lung Adenocarcinoma

Associated Phenotype: –

Source: Sequist et al., 2013, J. Clin. Oncol.

PubMed ID: 23816960

Clinical Trial: –

Evidence Rating: ★★★★☆

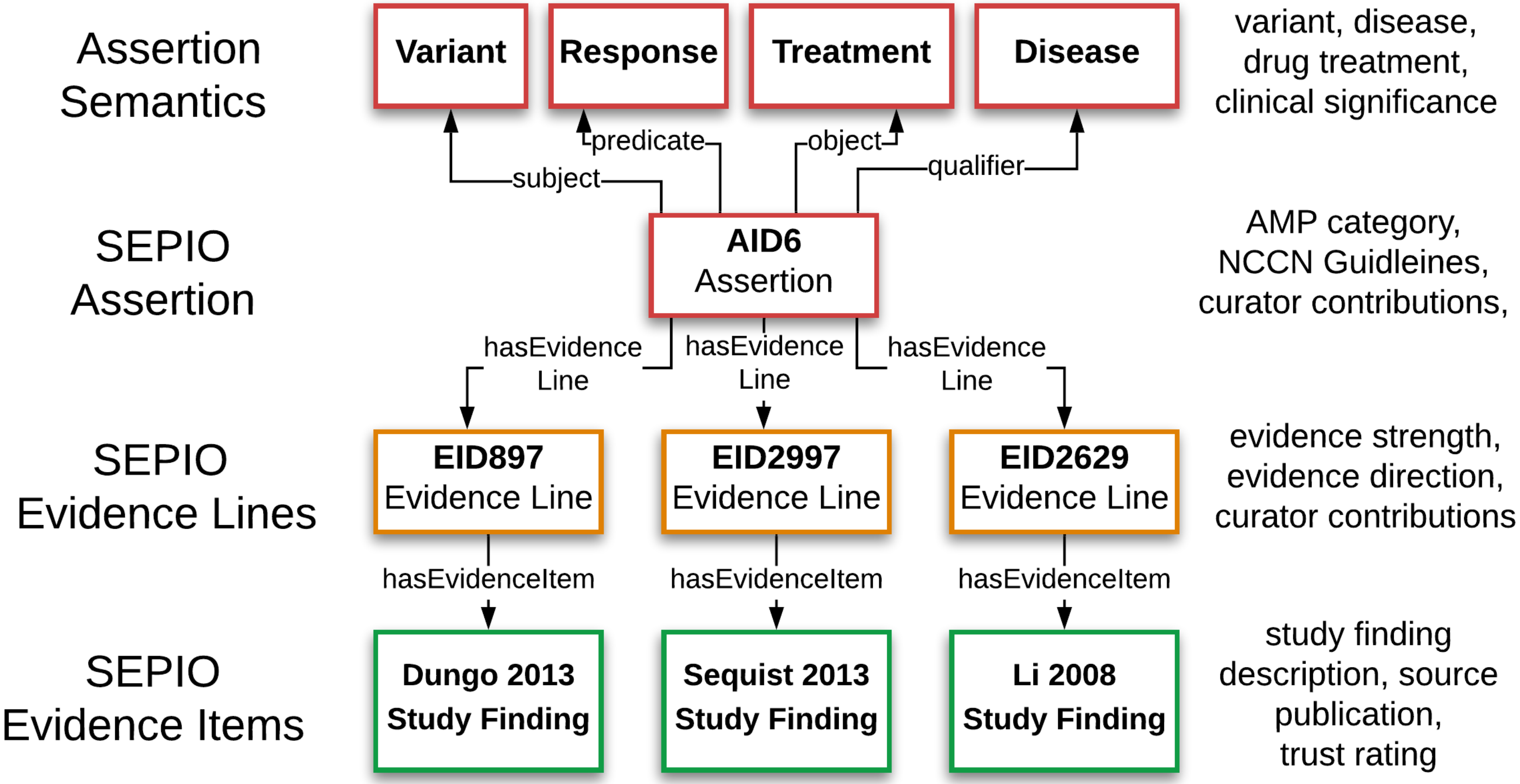
Evidence Item Quality

Evidence Item Source

https://civicdb.org/events/assertions/6/summary

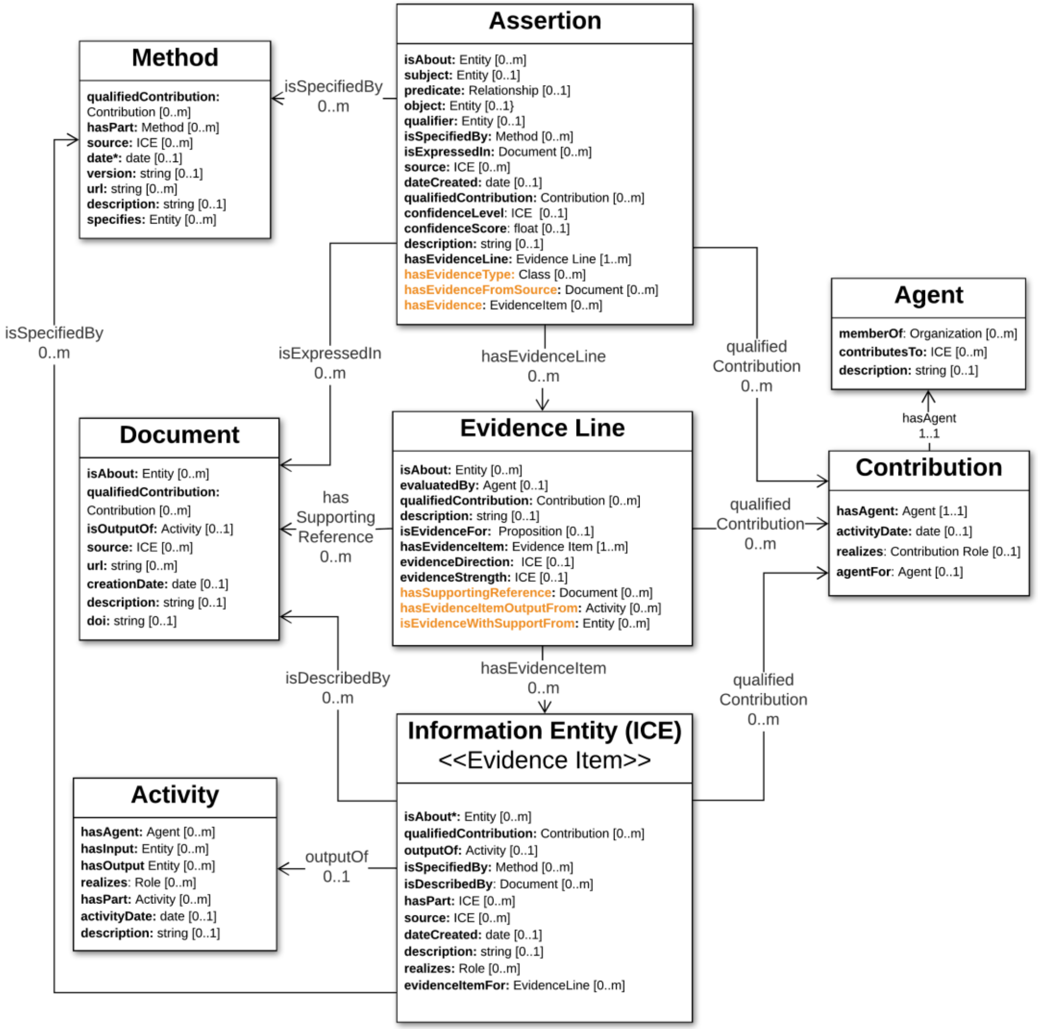
A CIViC ‘Predictive’ Variant Interpretation

Assertion: *“EGFR L858R positive NSCLC is sensitive to Afatinib”*



2. The SEPIO Information Model

- Provides a view of the ontology as a data model
- Specifies all the ways the terms/ design patterns in the ontology can be used to structure data
- Provides a starting point from which to derive a custom schema for a particular application (SEPIO Profiles)



Method

qualifiedContribution: Contribution [0..m]
hasPart: Method [0..m]
source: ICE [0..m]
date*: date [0..1]
version: string [0..1]
url: string [0..m]
description: string [0..1]
specifies: Entity [0..m]

Assertion

isAbout: Entity [0..m]
subject: Entity [0..1]
predicate: Relationship [0..1]
object: Entity [0..1}
qualifier: Entity [0..1]
isSpecifiedBy: Method [0..m]
isExpressedIn: Document [0..m]
source: ICE [0..m]
dateCreated: date [0..1]
qualifiedContribution: Contribution [0..m]
confidenceLevel: ICE [0..1]
confidenceScore: float [0..1]
description: string [0..1]
hasEvidenceLine: Evidence Line [1..m]
hasEvidenceType: Class [0..m]
hasEvidenceFromSource: Document [0..m]
hasEvidence: EvidenceItem [0..m]

Agent

memberOf: Organization [0..m]
contributesTo: ICE [0..m]
description: string [0..1]

Document

isAbout: Entity [0..m]
qualifiedContribution: Contribution [0..m]
isOutputOf: Activity [0..1]
source: ICE [0..m]
url: string [0..m]
creationDate: date [0..1]
description: string [0..1]
doi: string [0..1]

Evidence Line

isAbout: Entity [0..m]
evaluatedBy: Agent [0..1]
qualifiedContribution: Contribution [0..m]
description: string [0..1]
isEvidenceFor: Proposition [0..1]
hasEvidenceItem: Evidence Item [1..m]
evidenceDirection: ICE [0..1]
evidenceStrength: ICE [0..1]
hasSupportingReference: Document [0..m]
hasEvidenceItemOutputFrom: Activity [0..m]
isEvidenceWithSupportFrom: Entity [0..m]

Contribution

hasAgent: Agent [1..1]
activityDate: date [0..1]
realizes: Contribution Role [0..1]
agentFor: Agent [0..1]

Activity

hasAgent: Agent [0..m]
hasInput: Entity [0..m]
hasOutput Entity [0..m]
realizes: Role [0..m]
hasPart: Activity [0..m]
activityDate: date [0..1]
description: string [0..1]

Information Entity (ICE)
<<Evidence Item>>

isAbout*: Entity [0..m]
qualifiedContribution: Contribution [0..m]
outputOf: Activity [0..1]
isSpecifiedBy: Method [0..m]
isDescribedBy: Document [0..m]
hasPart: ICE [0..m]
source: ICE [0..m]
dateCreated: date [0..1]
description: string [0..1]
realizes: Role [0..m]
evidenceItemFor: EvidenceLine [0..m]

3. SEPIO Profiles

Profiles extend/refine the core ontology and information model to generate schema customized for a particular application

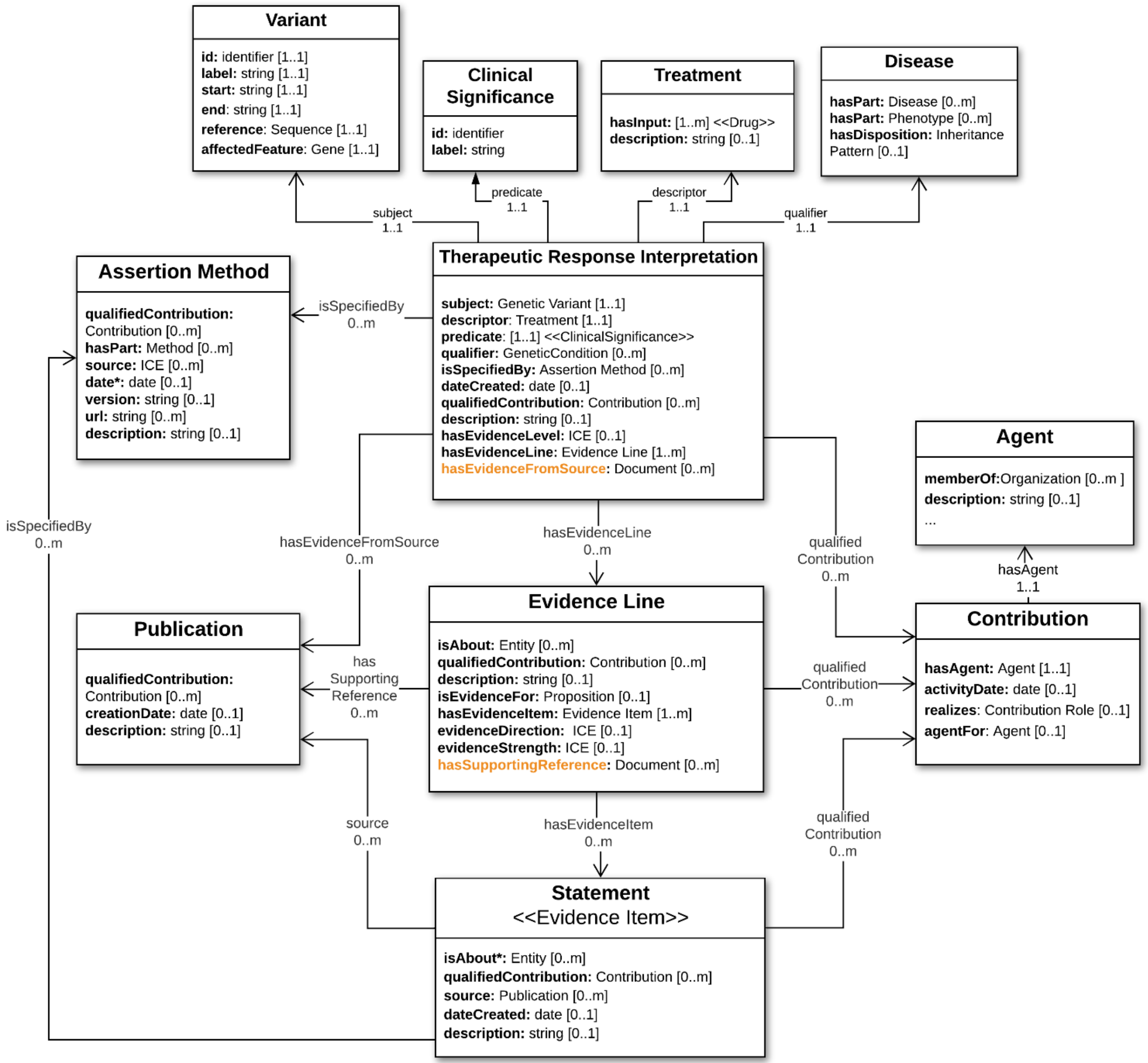
Schema typically use formats like JSON-LD that have native support for ontology mapping.

The profiling mechanism allows implementers to:

- Specialize core types for their domain (e.g. Assertion -> Variant Interpretation)
- Apply application-specific cardinalities, data type constraints, and value sets

SEPIO can support simple or complex profiles, depending on the richness of target data

A CIViC ‘Somatic Interpretation’ Profile



Variant
id: identifier [1..1]
label: string [1..1]
start: string [1..1]
end: string [1..1]
reference: Sequence [1..1]
affectedFeature: Gene [1..1]

Clinical Significance
id: identifier
label: string

Treatment
hasInput: [1..m] <<Drug>>
description: string [0..1]

Disease
hasPart: Disease [0..m]
hasPart: Phenotype [0..m]
hasDisposition: Inheritance Pattern [0..1]

subject 1..1
predicate 1..1
descriptor 1..1
qualifier 1..1

Therapeutic Response Interpretation
subject: Genetic Variant [1..1]
descriptor: Treatment [1..1]
predicate: [1..1] <<ClinicalSignificance>>
qualifier: GeneticCondition [0..m]
isSpecifiedBy: Assertion Method [0..m]
dateCreated: date [0..1]
qualifiedContribution: Contribution [0..m]
description: string [0..1]
hasEvidenceLevel: ICE [0..1]
hasEvidenceLine: Evidence Line [1..m]
hasEvidenceFromSource: Document [0..m]

Assertion Method
qualifiedContribution: Contribution [0..m]
hasPart: Method [0..m]
source: ICE [0..m]
date*: date [0..1]
version: string [0..1]
url: string [0..m]
description: string [0..1]

isSpecifiedBy 0..m
isSpecifiedBy 0..m
hasEvidenceFromSource 0..m
hasEvidenceLine 0..m
qualified Contribution 0..m

Agent
memberOf: Organization [0..m]
description: string [0..1]
...

hasAgent 1..1

Evidence Line
isAbout: Entity [0..m]
qualifiedContribution: Contribution [0..m]
description: string [0..1]
isEvidenceFor: Proposition [0..1]
hasEvidenceItem: Evidence Item [1..m]
evidenceDirection: ICE [0..1]
evidenceStrength: ICE [0..1]
hasSupportingReference: Document [0..m]

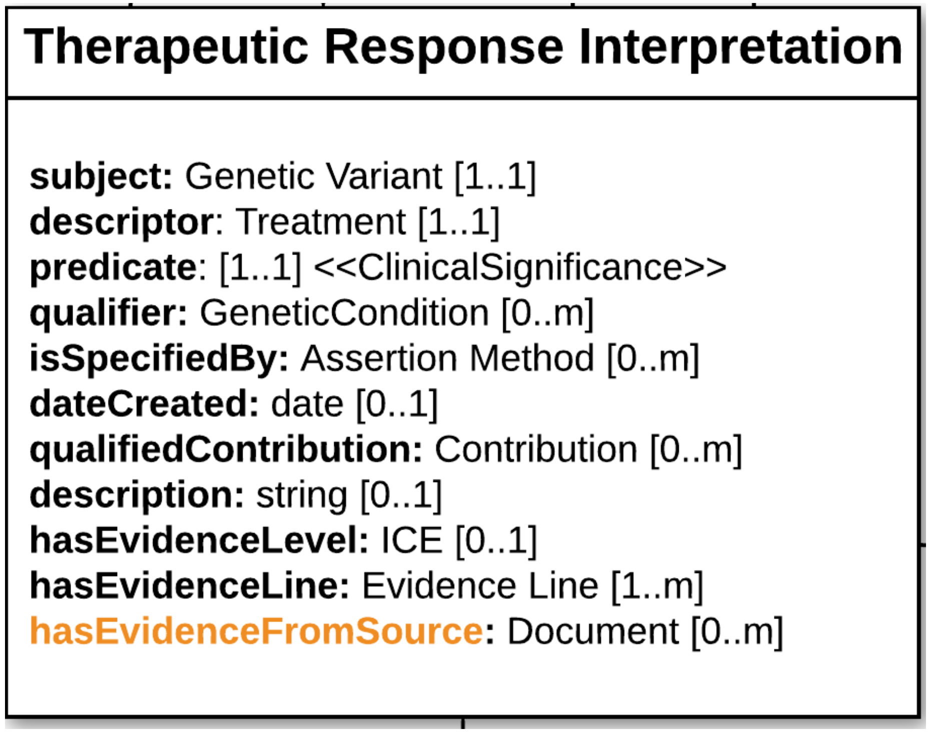
Publication
qualifiedContribution: Contribution [0..m]
creationDate: date [0..1]
description: string [0..1]

has Supporting Reference 0..m
qualified Contribution 0..m

Contribution
hasAgent: Agent [1..1]
activityDate: date [0..1]
realizes: Contribution Role [0..1]
agentFor: Agent [0..1]

source 0..m
hasEvidenceItem 0..m
qualified Contribution 0..m

Statement
<<Evidence Item>>
isAbout*: Entity [0..m]
qualifiedContribution: Contribution [0..m]
source: Publication [0..m]
dateCreated: date [0..1]
description: string [0..1]



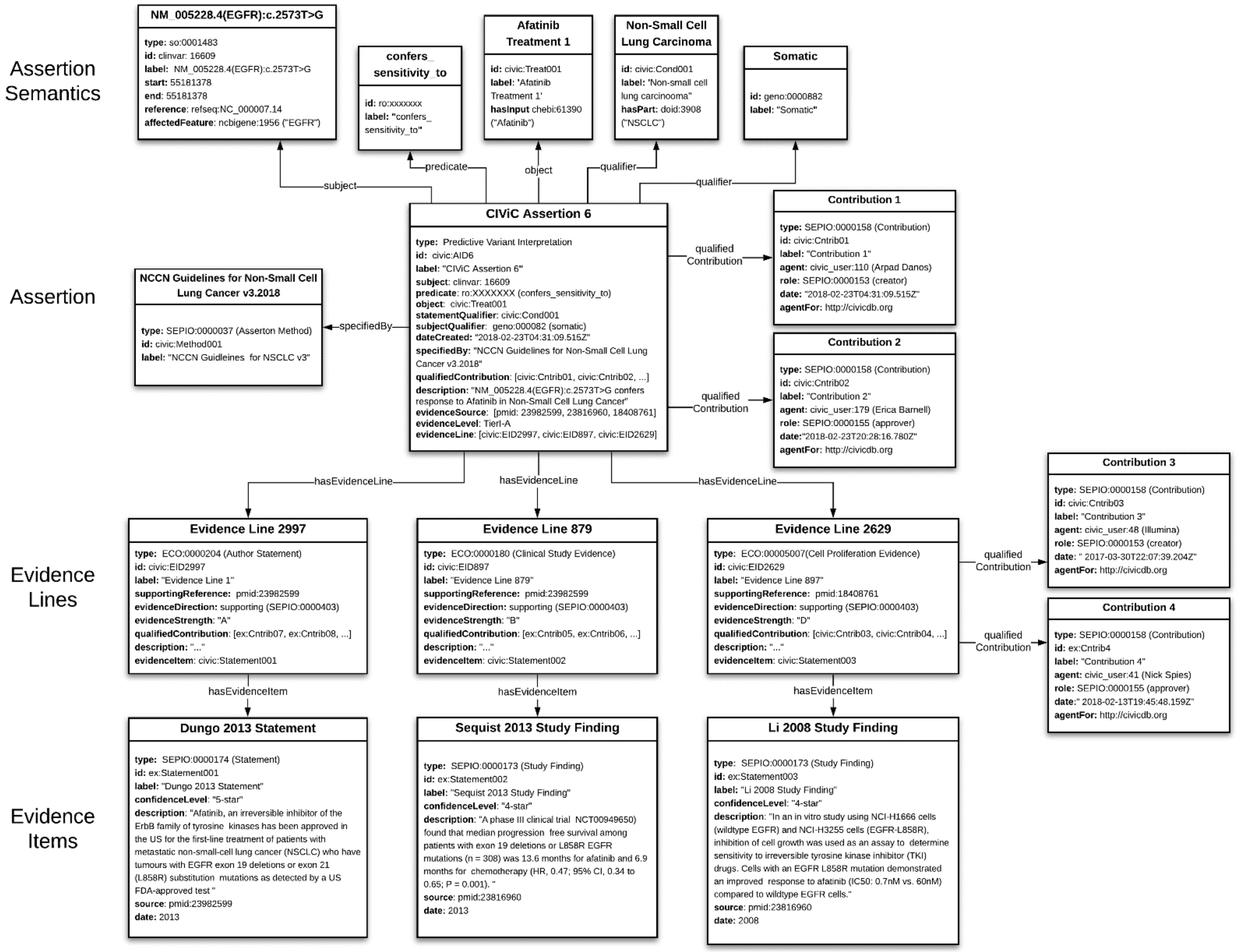
Therapeutic Response Interpretation

subject: Genetic Variant [1..1]
descriptor: Treatment [1..1]
predicate: [1..1] <<ClinicalSignificance>>
qualifier: GeneticCondition [0..m]
isSpecifiedBy: Assertion Method [0..m]
dateCreated: date [0..1]
qualifiedContribution: Contribution [0..m]
description: string [0..1]
hasEvidenceLevel: ICE [0..1]
hasEvidenceLine: Evidence Line [1..m]
hasEvidenceFromSource: Document [0..m]

- Assertion semantics
- Assertion strength
- Evidence Line direction and strength
- Evidence Item descriptions, source, quality
- curator contributions to assertions, evidence lines, and evidence items

A Somatic Interpretation Data Example

Assertion: *"EGFR L858R positive NSCLC is sensitive to Afatinib"*



NM_005228.4(EGFR):c.2573T>G

type: so:0001483
id: clinvar: 16609
label: NM_005228.4(EGFR):c.2573T>G
start: 55181378
end: 55181378
reference: refseq:NC_000007.14
affectedFeature: ncbigene:1956 ("EGFR")

confers_ sensitivity_to

id: ro:xxxxxxx
label: "confers_ sensitivity_to**"**

Afatinib Treatment 1

id: civic:Treat001
label: 'Afatinib Treatment 1'
hasInput chebi:61390 ("Afatinib")

Non-Small Cell Lung Carcinoma

id: civic:Cond001
label: 'Non-small cell lung carcinooma"
hasPart: doid:3908 ("NSCLC")

Somatic

id: geno:0000882
label: "Somatic**"**

CIViC Assertion 6

type: Predictive Variant Interpretation
id: civic:AID6
label: "CIViC Assertion 6"
subject: clinvar: 16609
predicate: ro:XXXXXXX (confers_sensitivity_to)
object: civic:Treat001
statementQualifier: civic:Cond001
subjectQualifier: geno:000082 (somatic)
dateCreated: "2018-02-23T04:31:09.515Z"
specifiedBy: "NCCN Guidelines for Non-Small Cell Lung Cancer v3.2018"
qualifiedContribution: [civic:Cntrib01, civic:Cntrib02, ...]
description: "NM_005228.4(EGFR):c.2573T>G confers response to Afatinib in Non-Small Cell Lung Cancer"
evidenceSource: [pmid: 23982599, 23816960, 18408761]
evidenceLevel: TierI-A
evidenceLine: [civic:EID2997, civic:EID897, civic:EID2629]

NCCN Guidelines for Non-Small Cell Lung Cancer v3.2018

type: SEPIO:0000037 (Asserton Method)
id: civic:Method001
label: "NCCN Guidleines for NSCLC v3"

Contribution 1

type: SEPIO:0000158 (Contribution)
id: civic:Cntrib01
label: "Contribution 1"
agent: civic_user:110 (Arpad Danos)
role: SEPIO:0000153 (creator)
date: "2018-02-23T04:31:09.515Z"
agentFor: http://civicdb.org

Contribution 2

type: SEPIO:0000158 (Contribution)
id: civic:Cntrib02
label: "Contribution 2"
agent: civic_user:179 (Erica Barnell)
role: SEPIO:0000155 (approver)
date:"2018-02-23T20:28:16.780Z"
agentFor: http://civicdb.org

Evidence Line 2997

type: ECO:0000204 (Author Statement)
id: civic:EID2997
label: "Evidence Line 1"
supportingReference: pmid:23982599
evidenceDirection: supporting (SEPIO:0000403)
evidenceStrength: "A"
qualifiedContribution: [ex:Cntrib07, ex:Cntrib08, ...]
description: "..."
evidenceItem: civic:Statement001

Evidence Line 879

type: ECO:0000180 (Clinical Study Evidence)
id: civic:EID897
label: "Evidence Line 879"
supportingReference: pmid:23982599
evidenceDirection: supporting (SEPIO:0000403)
evidenceStrength: "B"
qualifiedContribution: [ex:Cntrib05, ex:Cntrib06, ...]
description: "..."
evidenceItem: civic:Statement002

Evidence Line 2629

type: ECO:00005007(Cell Proliferation Evidence)
id: civic:EID2629
label: "Evidence Line 897"
supportingReference: pmid:18408761
evidenceDirection: supporting (SEPIO:0000403)
evidenceStrength: "D"
qualifiedContribution: [civic:Cntrib03, civic:Cntrib04, ...]
description: "..."
evidenceItem: civic:Statement003

Contribution 3

type: SEPIO:0000158 (Contribution)
id: civic:Cntrib03
label: "Contribution 3"
agent: civic_user:48 (Illumina)
role: SEPIO:0000153 (creator)
date: " 2017-03-30T22:07:39.204Z"
agentFor: http://civicdb.org

Contribution 4

type: SEPIO:0000158 (Contribution)
id: ex:Cntrib4
label: "Contribution 4"
agent: civic_user:41 (Nick Spies)
role: SEPIO:0000155 (approver)
date:" 2018-02-13T19:45:48.159Z"
agentFor: http://civicdb.org

Dungo 2013 Statement

type: SEPIO:0000174 (Statement)
id: ex:Statement001
label: "Dungo 2013 Statement"
confidenceLevel: "5-star"
description: "Afatinib, an irreversible inhibitor of the ErbB family of tyrosine kinases has been approved in the US for the first-line treatment of patients with metastatic non-small-cell lung cancer (NSCLC) who have tumours with EGFR exon 19 deletions or exon 21 (L858R) substitution mutations as detected by a US FDA-approved test "
source: pmid:23982599
date: 2013

Sequist 2013 Study Finding

type: SEPIO:0000173 (Study Finding)
id: ex:Statement002
label: "Sequist 2013 Study Finding"
confidenceLevel: "4-star"
description: "A phase III clinical trial NCT00949650) found that median progression free survival among patients with exon 19 deletions or L858R EGFR mutations (n = 308) was 13.6 months for afatinib and 6.9 months for chemotherapy (HR, 0.47; 95% CI, 0.34 to 0.65; P = 0.001). "
source: pmid:23816960
date: 2013

Li 2008 Study Finding

type: SEPIO:0000173 (Study Finding)
id: ex:Statement003
label: "Li 2008 Study Finding"
confidenceLevel: "4-star"
description: "In an in vitro study using NCI-H1666 cells (wildtype EGFR) and NCI-H3255 cells (EGFR-L858R), inhibition of cell growth was used as an assay to determine sensitivity to irreversible tyrosine kinase inhibitor (TKI) drugs. Cells with an EGFR L858R mutation demonstrated an improved response to afatinib (IC50: 0.7nM vs. 60nM) compared to wildtype EGFR cells."
source: pmid:23816960
date: 2008

CIViC Assertion 6

type: Theraapeutic Response Interpretation
id: civic:AID6
label: "CIViC Assertion 6**"**
description: "NM_005228.4(EGFR):c.2573T>G confers response to Afatinib in Non-Small Cell Lung Cancer"

Generic Metadata

subject: clinvar: 16609
predicate: confers_sensitivity_to
object: pubchem:10184653 (afatinib)
statementQualifier: doid:3908 (NSCLC)
subjectQualifier: geno:000082 (somatic)

Assertion Semantics

dateCreated: "2018-02-23T04:31:09.515Z"
specifiedBy: "NCCN NSCLC Guidelines v3.2018"
qualifiedContribution: [civic:Cntrib01, civic:Cntrib02, ...]

Assertion Provenance

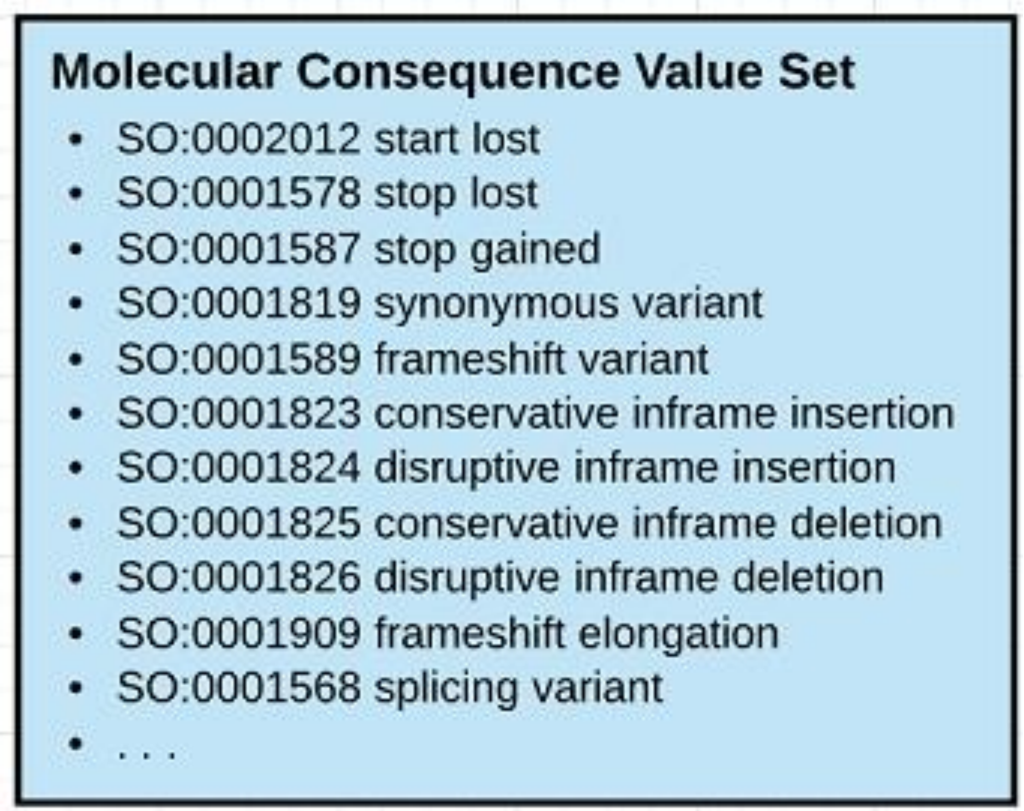
evidenceSource: [pmid: 23982599, 23816960, 18408761]
evidenceLevel: TierI-A
evidenceLine: [civic:EID2997, civic:EID897, civic:EID2629]

Assertion Quality / Evidence

4. SEPIO Value Sets

- SEPIO provides **a meta-model** for creating **ontology-based value sets** for particular profiles

- Allow tools to leverage knowledge encoded in ontologies for **improved search and analysis**, and can **make connections to other datasets** using the same ontologies.



Molecular Consequence Value Set

- SO:0002012 start lost
- SO:0001578 stop lost
- SO:0001587 stop gained
- SO:0001819 synonymous variant
- SO:0001589 frameshift variant
- SO:0001823 conservative inframe insertion
- SO:0001824 disruptive inframe insertion
- SO:0001825 conservative inframe deletion
- SO:0001826 disruptive inframe deletion
- SO:0001909 frameshift elongation
- SO:0001568 splicing variant
- . . .

Status and Future Plans for SEPIO

Short Term:

- Collect feedback from pilot adopters to improve the model and framework
- Prepare an initial ontology release (~3 mo.)

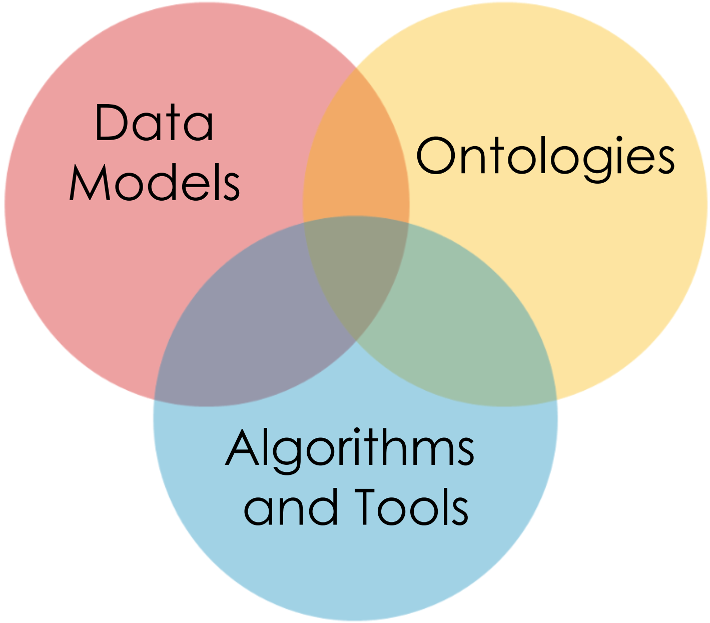
Medium Term:

- Create implementation guide and improved documentation for adopters (3 mo.)
- Develop reference implementation and code to support developers (6 mo.)

Long Term:

- Build out a broader infrastructure of supporting ontologies, algorithms, and tools

A synergy between data models, ontologies, and algorithms/tools that will realize the full potential of the Framework.



Interested adopters - contact us and present your use case. We’d love to work with you!