Ontology Alignment

Ontology Alignment

- Ontology alignment
- Ontology alignment strategies
- Evaluation of ontology alignment strategies
- Ontology alignment challenges

Ontologies in biomedical research

- many biomedical ontologies

  e.g. GO, OBO, SNOMED-CT

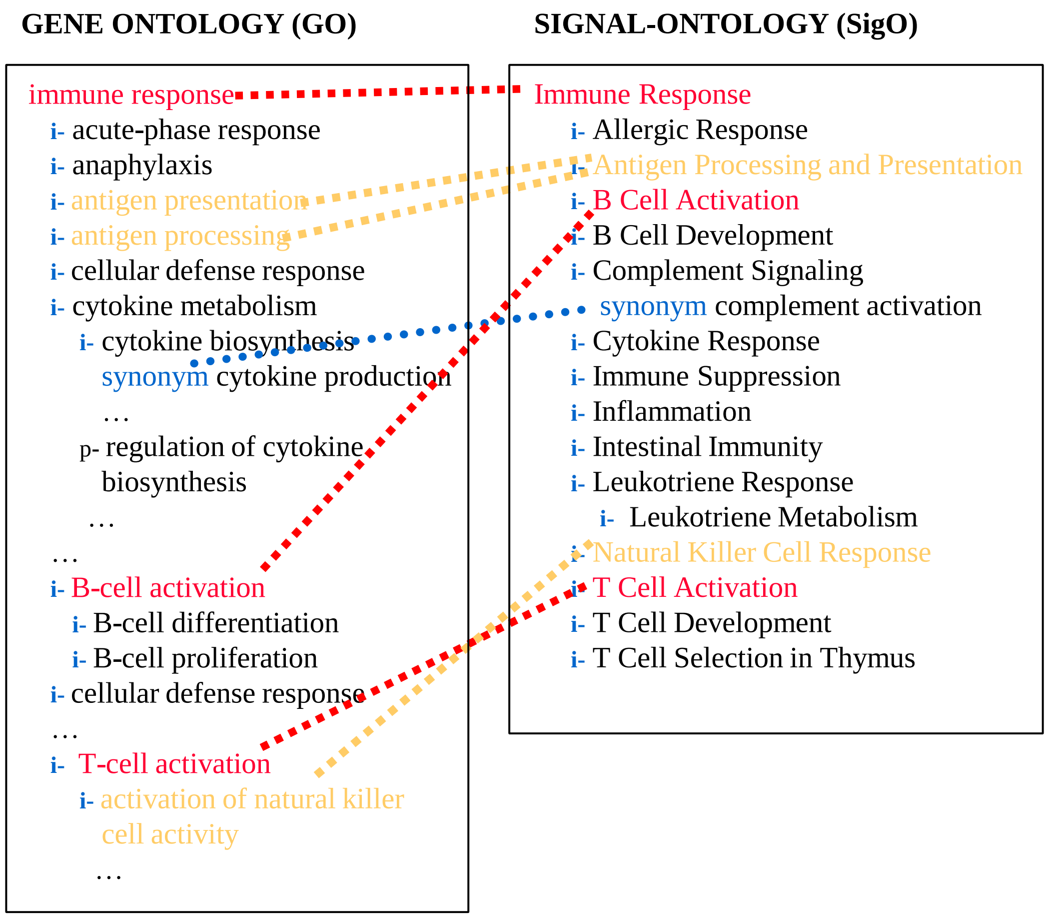
- practical use of biomedical ontologies

  e.g. databases annotated with GO

GENE ONTOLOGY (GO)

immune response
- i- acute-phase response
- i- anaphylaxis
- i- antigen presentation
- i- antigen processing
- i- cellular defense response
- i- cytokine metabolism
  - i- cytokine biosynthesis
    - <u>synonym</u> cytokine production
    - …
  - p- regulation of cytokine biosynthesis
  - …
- …
- i- B-cell activation
  - i- B-cell differentiation
  - i- B-cell proliferation
- i- cellular defense response
- …
- i- T-cell activation
  - i- activation of natural killer cell activity
  - …

Ontologies with overlapping information



Ontologies with overlapping information

- Use of multiple ontologies
  - custom-specific ontology + standard ontology
  - different views over same domain
  - overlapping domains

- Bottom-up creation of ontologies

  experts can focus on their domain of expertise

→ important to know the inter-ontology relationships

GENE ONTOLOGY (GO)

immune response
- i- acute-phase response
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- i- antigen presentation
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- i- cellular defense response
- i- cytokine metabolism
  - i- cytokine biosynthesis
    synonym cytokine production
    …
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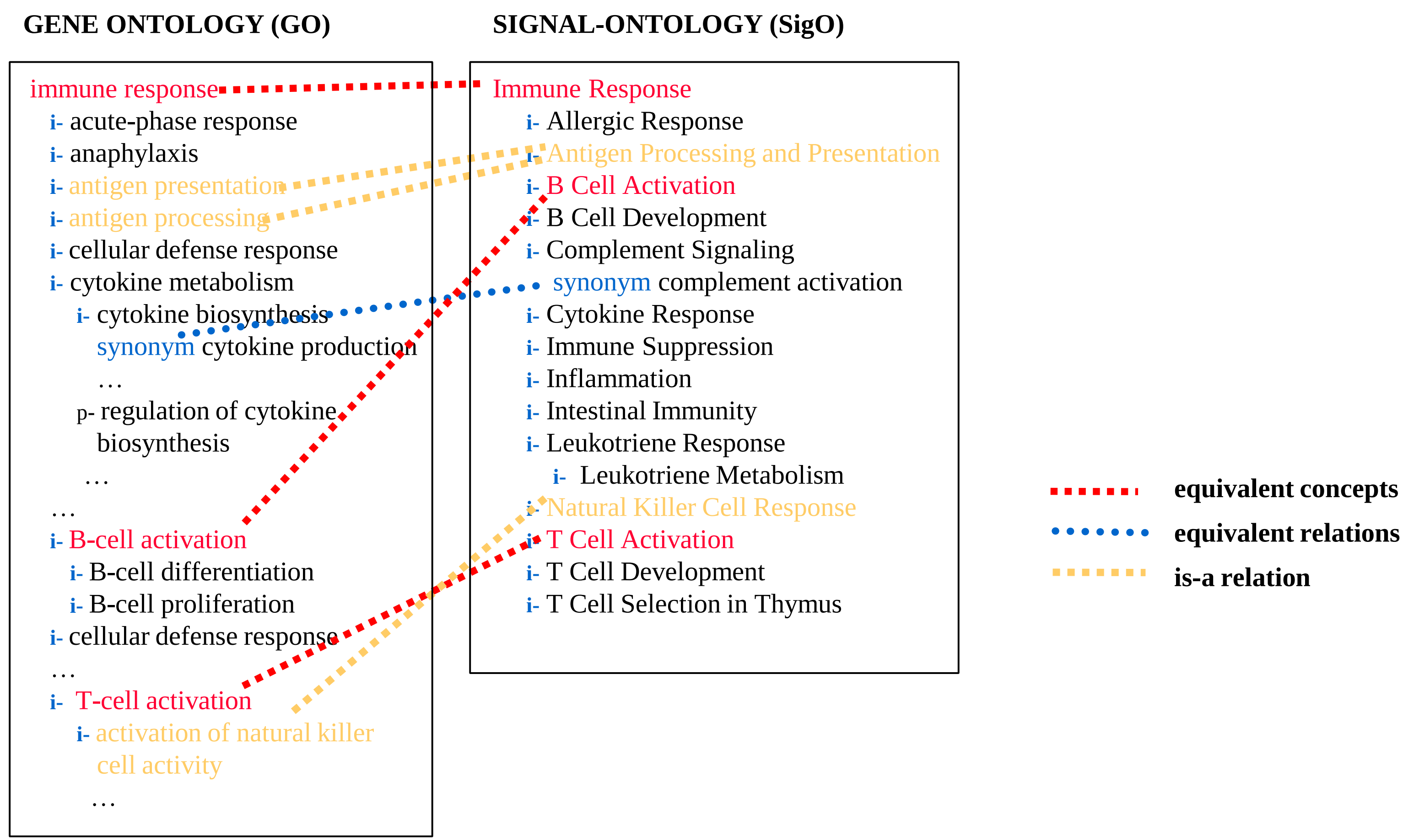
  - i- B-cell differentiation
  - i- B-cell proliferation
- i- cellular defense response
- …
- i- T-cell activation
  - i- activation of natural killer cell activity
  - …

SIGNAL-ONTOLOGY (SigO)

Immune Response
- i- Allergic Response
- i- Antigen Processing and Presentation
- i- B Cell Activation
- i- B Cell Development
- i- Complement Signaling
  synonym complement activation
- i- Cytokine Response
- i- Immune Suppression
- i- Inflammation
- i- Intestinal Immunity
- i- Leukotriene Response
  - i- Leukotriene Metabolism
- i- Natural Killer Cell Response
- i- T Cell Activation
- i- T Cell Development
- i- T Cell Selection in Thymus

Ontology Alignment

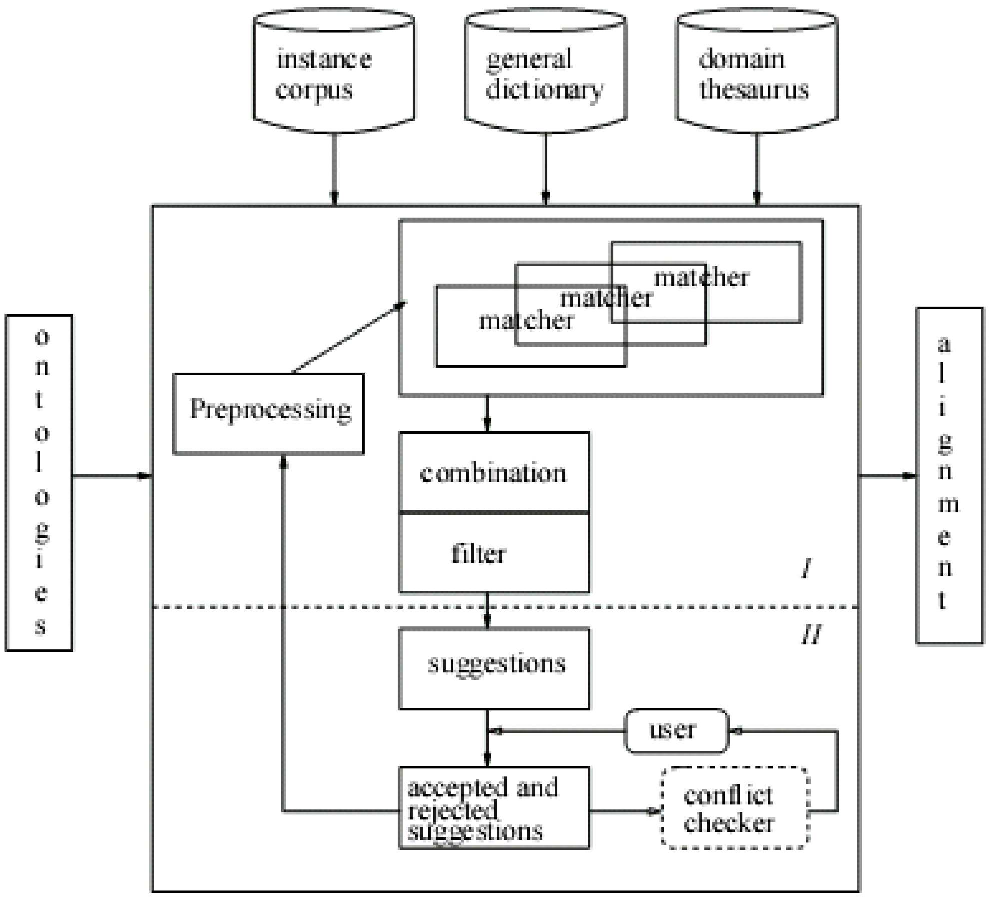


Defining the relations between the terms in different ontologies

Ontology Alignment

- Ontology alignment
- Ontology alignment strategies
- Evaluation of ontology alignment strategies
- Ontology alignment challenges

An Alignment Framework



Preprocessing

Preprocessing

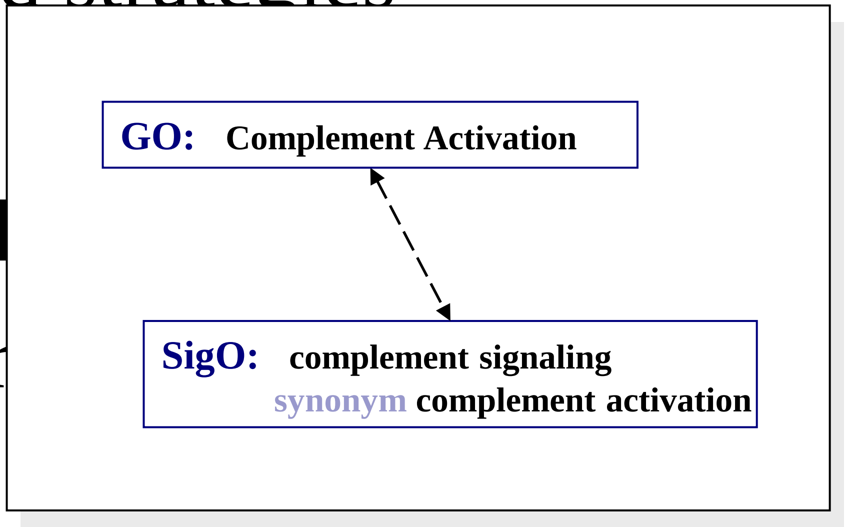
For example,

- Selection of features
- Selection of search space

Matchers

Matcher Strategies

- Strategies based on linguistic matching
- Structure-based strategies
- Constraint-bas
- Instance-based
- Use of auxiliar

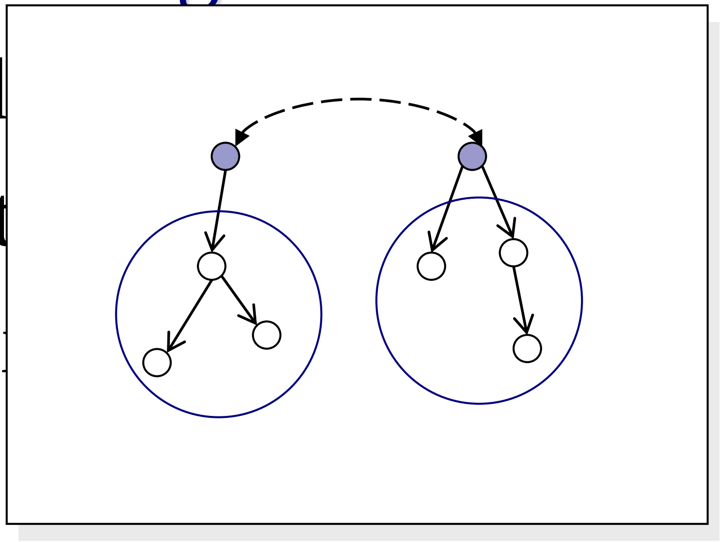


Example matchers

- Edit distance
  - Number of deletions, insertions, substitutions required to transform one string into another
  - aaaa → baab: edit distance 2
- N-gram
  - N-gram : N consecutive characters in a string
  - Similarity based on set comparison of n-grams
  - aaaa : {aa, aa, aa}; baab : {ba, aa, ab}

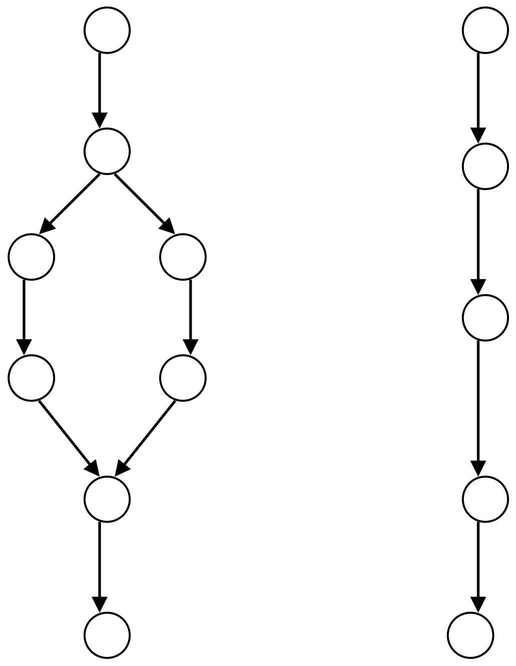
Matcher Strategies

- Strategies based on linguistic matching
- Structure-based strategies
- Constraint-based
- Instance-based st
- Use of auxiliary



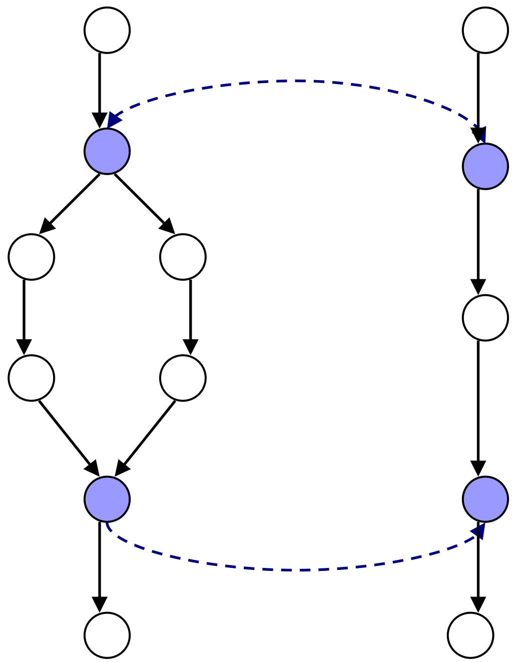
Example matchers

- Propagation of similarity values
- Anchored matching



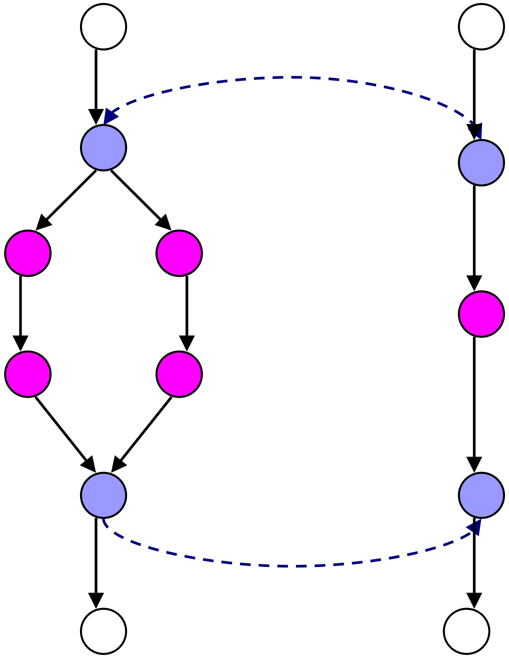
Example matchers

- Propagation of similarity values
- Anchored matching



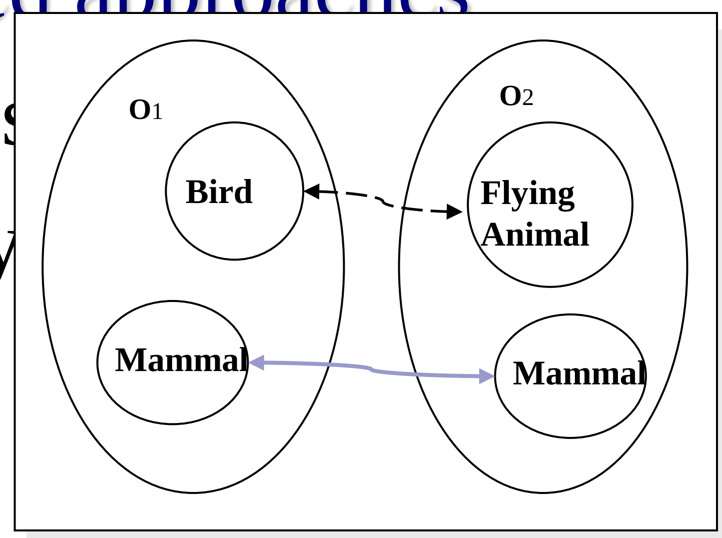
Example matchers

- Propagation of similarity values
- Anchored matching



Matcher Strategies

- Strategies based on linguistic matching
- Structure-based strategies
- Constraint-based approaches
- Instance-based s
- Use of auxiliary



Matcher Strategies

- Strategies based on linguistic matching
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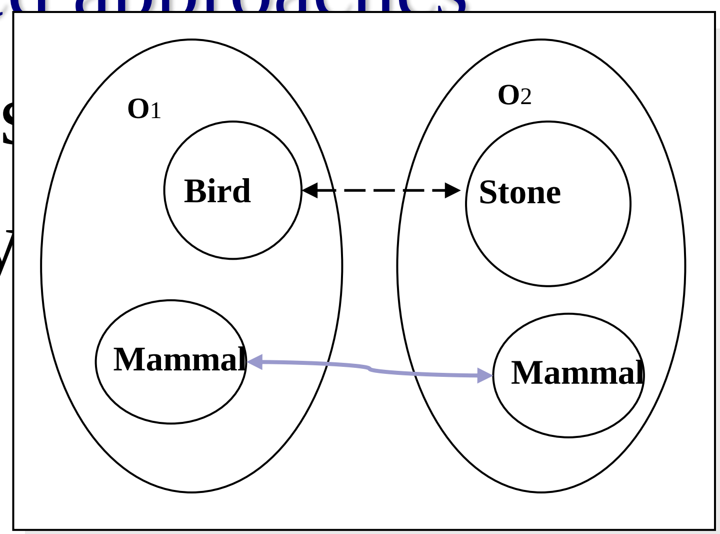
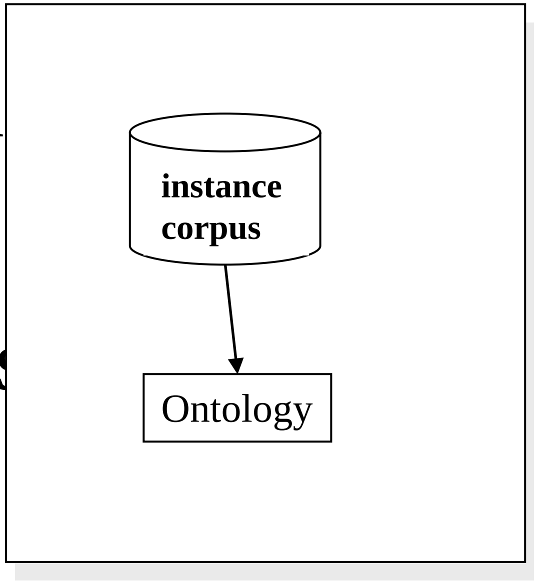


Example matchers

- Similarities between data types
- Similarities based on cardinalities

Matcher Strategies

- Strategies based on linguisti
- Structure-based strategies
- Constraint-based approaches
- Instance-based strategies
- Use of auxiliary information



Example matchers

- Instance-based
- Use life science literature as instances

Learning matchers – instance-based strategies

- Basic intuition

  A similarity measure between concepts can be computed based on the probability that documents about one concept are also about the other concept and vice versa.

Learning matchers - steps

- Generate corpora
  - Use concept as query term in PubMed
  - Retrieve most recent PubMed abstracts
- Generate text classifiers
  - One classifier per ontology / One classifier per concept
- Classification
  - Abstracts related to one ontology are classified by the other ontology’s classifier(s) and vice versa
- Calculate similarities

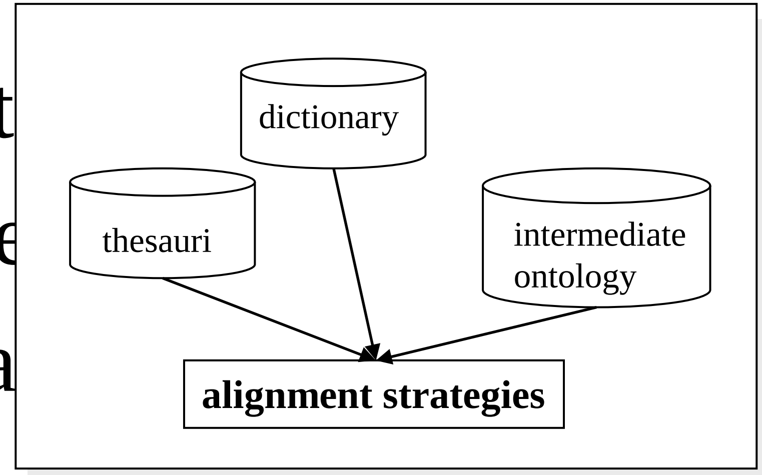
Basic Naïve Bayes matcher

- Generate corpora
- Generate classifiers
  - Naive Bayes classifiers, one per ontology
- Classification
  - Abstracts related to one ontology are classified to the concept in the other ontology with highest posterior probability P(C|d)
- Calculate similarities

$$sim(C_1, C_2) = \frac{n_{NBC2}(C_1, C_2) + n_{NBC1}(C_2, C_1)}{n_D(C_1) + n_D(C_2)}$$

Matcher Strategies

- Strategies based linguist
- Structure-based strategie
- Constraint-based approa
- Instance-based strategies
- Use of auxiliary information



Example matchers

- Use of WordNet
  - Use WordNet to find synonyms
  - Use WordNet to find ancestors and descendants in the is-a hierarchy
- Use of Unified Medical Language System (UMLS)
  - Includes many ontologies
  - Includes many alignments (not complete)
  - Use UMLS alignments in the computation of the similarity values

Table 7 Matching Strategies in the participating systems - 1

System	String-based strategies	Structure-based strategies	Constraint-based strategies	Instance-based strategies
AgreementMaker	SubString, Edit-Distance, TF-IDF	✓	✓	✓
ALIN	SimMetrics API[a], WS4J API[b]	✓	-	-
AML	Jaccard, I-Sub	✓	✓	✓
Anchor-Flood	Jaro-Winkler	✓	-	✓
AOAS	Jaro-Winkler	✓	-	-
AOT, AOTL	Edit-Distance, Block-Distance, SLIM-Winkler, Jaro-Winkler, Smith-Winkler, Needleman-Wunsch	-	-	-
AROMA	Jaro-Winkler	✓	✓	-
ASMOV	Edit-Distance	✓	✓	✓
BLOOMS	Jaccard, Exact Match, Lin, Jaro-Winkler	-	-	-
CIDER-CL	Soft TF-IDF, Jaro-Winkler	✓	-	-
CODI	Edit-Distance, Jaro-Winkler, Cosine, Smith-Waterman, Jaccard, Overlap coefficient	✓	✓	✓
COMMAND	UMBC similarity Model	✓	-	-
CroMatcher	N-Gram, TF-IDF	✓	✓	✓
CSA	Edit-Distance, Wu-Palmer, TF-IDF	✓	-	✓
DKP-AOM, DKP-AOM-Lite	SimMetrics API[a]	✓	✓	-
DSSim	Jaccard, Jaro-Winkler	✓	-	-
Eff2Match	Exact Match, TF-IDF	✓	-	-
Falcon-AO	I-Sub, TF-IDF	✓	-	-
FCA-Map	Exact Match	✓	-	-
GeRoMeSuite+SMB	Edit-Distance, Jaro-Winkler, I-Sub, Soft TF-IDF, SecondString Library[c]	✓	-	✓
GMap	Edit-Distance, TF-IDF	✓	-	-
GOMMA, GOMMA-bk	Exact Match, N-gram	✓	-	✓
Hertuda	Damerau-Levenshtein[d]	-	-	-
HotMatch	Damerau-Levenshtein[d]	✓	✓	✓
IAMA	Edit-Distance	-	-	✓

Dragisic Z, Ivanova V, Li H, Lambrix P,
Experiences from the Anatomy track in the Ontology Alignment Evaluation Initiative,
Journal of Biomedical Semantics 8:56, 2017

Table 8 Matching strategies in the participating systems - 2

System	String-based strategies	Structure-based strategies	Constraint-based strategies	Instance-based strategies
JarvisOM	Cosine, WuPalmer, Lin, N-gram	-	-	-
KOSIMap	SimMetrics APP, Degree of commonality coefficient	✓	✓	-
Lily	Edit-Distance	✓	✓	✓
LogMap	I-Sub	✓	-	✓
LPHOM	I-Sub, Mongue-Elkan, 3-Gram, Jaccard, Lin	-	-	-
LYAM++	SOFT TF-IDF, Jaccard	✓	-	-
MaasMatch	Cosine, Edit-Distance, Jaccard, 3-Gram, Longest Common Substring	✓	-	✓
MapSSS	Edit-Distance, Choice based on [10]	✓	✓	-
NBJLM	Set of words-level	✓	-	-
ODGOMS	Longest Common Subsequence, SMOA, TF-IDF	✓	-	-
Optima+	Lin, Smith-Waterman, Needleman-Wunsch Inverse Edit-Distance	✓	-	-
Prior+	Edit-Distance	✓	-	-
RiMOM	Edit-Distance, Cosine	✓	-	✓
RSDLWB	Jaccard, Substring	✓	✓	-
SAMBO, SAMBOdtf	Edit-Distance, 3-Gram	✓	-	✓
ServOMap	Edit-Distance, I-Sub, Q-Gram, TF-IDF, Monge-Elkan, Jaccard	✓	-	-
SOBOM	I-Sub	✓	-	-
StringsAuto	Choice based on [10]	-	-	-
TaxoMap	Lin, 3-gram Degree of commonality coefficient	✓	✓	-
TOAST	✓[b]	✓	-	-
WeSeE	Edit-Distance, TF-IDF	-	-	-
WikiMatch	Jaccard	-	-	-
X-SOM	Edit-Distance, Jaro	✓	-	✓
XMap	Edit distance, Jaro-Winkler, N-gram, Jaccard, Cosine	✓	✓	-
YAM++	Tversky[c], TF-IDF	✓	-	✓

Table 9 Use of auxiliary information by the participating systems

System	Background knowledge						
	UMLS	Uberon	BioPortal	MeSH	FMA	WordNet	Other
AgreementMaker	✓	✓	-	-	-	✓	-
ALIN	-	-	-	-	-	✓	-
AML	✓	✓		✓		✓	-
Anchor-Flood	-	-	-	-	-	✓	-
AOAS	✓	-	-	-	✓	-	-
AOT, **AOTL**	-	-	-	-	-	✓	-
ASMOV	✓	-	-	-	-	✓	-
COMMAND	✓	-	-	-	-	✓	-
CroMatcher	-	✓	-	-	-	✓	-
CSA	-	-	-	-	-	✓	-
DKP-AOM	-	-	-	-	-	✓	-
DSSim	-	-	-	-	-	✓	-
Eff2Match	-	-	-	-	-	✓	-
GOMMA	✓	✓	-	-	✓	-	-
GeRoMeSuite+SMB	-	-	-	-	-	✓	-
Hotmatch	-	-	-	-	-	-	API lanes[a], WikiPedia, Big Huge Thesaurus[b]
JarvisOM	-	-	-	-	-	✓	Apache Lucene[c]
IAMA	-	-	-	-	-	-	Apache Lucene[c]
Lily	-	-	-	-	-	-	Web search (Google)
LogMapBio	-	-	✓	-	-	-	-
LYAM++	-	✓	-	-	-	-	BabelNet[d]
MaasMatch	-	-	-	-	-	✓	-
MapSSS	-	-	-	-	-	-	Google
NBJLM	-	-	-	-	-	✓	-
Optima+	-	-	-	-	-	✓	-
RiMOM	✓	-	-	-	-	✓	Wiki Pages
RSDLWB	-	-	-	-	-	✓	DBpedia[e]
SAMBO	✓	-	-	-	-	✓	-
ServOMap	-	-	-	-	-	✓	Apache Lucene[c]
TaxoMap	-	-	-	-	-	✓	-
TOAST	-	-	-	-	-	✓	-
WeSeE	-	-	-	-	-	-	Microsoft Bing Search JFreeWebSearch[f]
WikiMatch	-	-	-	-	-	-	WikiPedia
XMap	✓		-	-	-	✓	-
X-SOM	-	-	-	-	-	✓	Google
YAM++	-	-	-	-	-	-	Apache Lucene[c]

Combinations

Combination Strategies

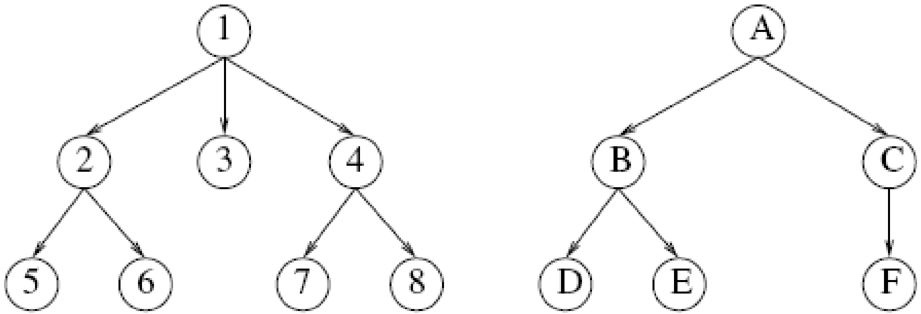
- Usually weighted sum of similarity values of different matchers
- Maximum of similarity values of different matchers

Filtering

Filtering techniques

- Threshold filtering

  Pairs of concepts with similarity higher or equal than threshold are alignment suggestions



sim

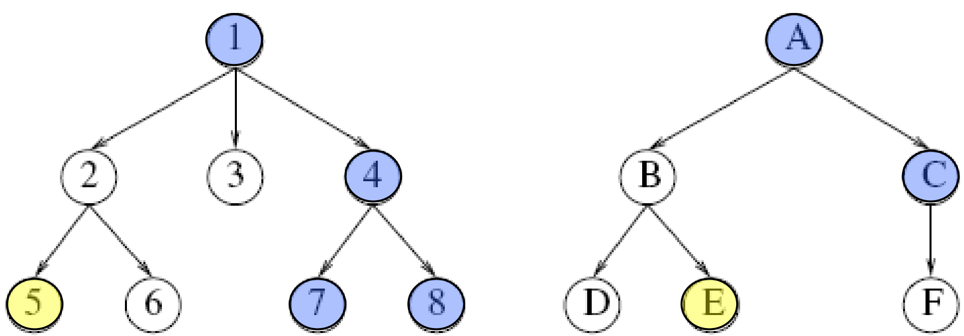
(2, *B*)
(3, *F*) — suggest
(6, *D*)
(4, *C*)
th - - - - - - - - - -
(5, *C*)
(5, *E*) — discard
… …

Filtering techniques

- Double threshold filtering

  (1) Pairs of concepts with similarity higher than or equal to **upper** threshold are alignment suggestions

  (2) Pairs of concepts with similarity between **lower** and **upper** thresholds are alignment suggestions if they make sense with respect to the structure of the ontologies and the suggestions according to (1)



(2, B)

(3, F)

(6, D)

(4, C)

upper-th – – – – – –

(5, C)

(5, E)

lower-th – – – – – –

……

Example alignment system

SAMBO – matchers, combination, filter

Example alignment system SAMBO – suggestion mode

Table 6 Analysis of the components of the participating systems

Systems	Basic processes					
	Preprocessing[D/R]	Matching	Combination	Filtering	Debugging	User interaction*
AgreementMaker	-	✓	✓	✓	-	✓*
ALIN	-	✓	✓	✓	-	✓
AML, AML_bk	D	✓	✓	✓	✓	✓*
Anchor-Flood	D	✓	✓	✓	-	-
AOAS	-	✓	✓	✓	-	-
AOT, AOTL	-	✓	✓	✓	-	-
AROMA	D	✓	✓	✓	-	-
ASMOV	-	✓	✓	✓	✓	✓
BLOOMS	D	✓	✓	✓	-	-
CIDER-CL	D	✓	✓	✓	-	-
CODI	D	✓	✓	✓	✓	-
COMMAND	-	✓	✓	✓	-	-
CroMatcher	D	✓	✓	✓	-	-
CSA	D	✓	✓	✓	-	-
DKP-AOM, DKP-AOM-Lite	D	✓	✓	✓	✓	-
DSSim	R	✓	✓	✓	-	-
Eff2Match	D	✓	✓	✓	-	-
Falcon-AO	R	✓	✓	✓	-	✓*
FCA-Map	D	✓	-	-	✓	-
GeRoMeSuite+SMB	-	✓	✓	✓	✓	✓*
GMap	-	✓	✓	✓	-	-
GOMMA, GOMMAbk	R	✓	✓	✓	✓	✓(*)[1]
Hertuda	D	✓	-	✓	-	✓
HotMatch	D	✓	✓	✓	-	-
IAMA	D	✓	✓	✓	-	-

Dragisic Z, Ivanova V, Li H, Lambrix P,
Experiences from the Anatomy track in the Ontology Alignment Evaluation Initiative,
Journal of Biomedical Semantics 8:56, 2017

JarvisOM	D	✓	✓	✓	-	✓
KOSIMap	D	✓	✓	✓	✓	-
Lily	D	✓	✓	✓	✓	✓*
LogMap, LogMapBio, LogMapC, LogMapLite	D,R	✓	✓	✓	✓	✓*
LPHOM	D	✓	✓	✓	-	-
LYAM++	D	✓	-	✓	-	-
MaasMatch	D	✓	✓	✓	-	-
MapSSS	-	✓	✓	✓	-	-
NBJLM	-	✓	✓	✓	-	-
ODGOMS	D	✓	✓	✓	-	-
Optima+	-	✓	✓	✓	-	-
Prior+	D	✓	✓	✓	-	-
RiMOM	D	✓	✓	✓	-	-
RSDLWB	D	✓	✓	-	-	✓*
SAMBO, SAMBOdtf	-	✓	✓	✓	✓	✓*
ServOMap(L), ServOMBI	D	✓	✓	✓	✓	✓
SOBOM	-	✓	✓	✓	-	-
StringsAuto	-	✓	✓	✓	-	-
TaxoMap	D,R	✓	✓	✓	-	-
TOAST	-	✓	-	-	-	-
WeSeE	D	✓	-	✓	-	✓
WikiMatch	D	✓	-	✓	-	-
X-SOM	-	✓	✓	✓	✓	-
XMap, XMAPGen, XMAPSig	-	✓	✓	✓	-	✓
YAM++	D	✓	✓	✓	✓	-

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Evaluation measures

- Precision:

$$\frac{\text{\# correct mapping suggestions}}{\text{\# mapping suggestions}}$$

- Recall:

$$\frac{\text{\# correct mapping suggestions}}{\text{\# correct mappings}}$$

- F-measure: combination of precision and recall

Ontology Alignment Evaluation Initiative

http://oaei.ontologymatching.org/

OAEI

- Since 2004, Evaluation of *systems*
- Different tracks (2022)
  - Ontologies
    - Anatomy, conference, ,Bio-ML, biodiversity and ecology, food nutrition , materials science,
    - Multilingual: multifarm (9 languages)
    - Complex
    - Interactive
  - Instance matching and link discovery
  - Data schema
  - Knowledge graphs

OAEI

- Evaluation measures
  - Precision/recall/f-measure
  - recall of non-trivial mappings

  - full / partial golden standard

OAEI 2020

- Anatomy:
  - 10 systems
  - best system for f: f=0.941, p=0.984, r=0.93, r+=0.817, 37 seconds
  - 2 systems produce coherent mappings

OAEI Anatomy Track 2007-2016*

- Components
  - Almost all systems implement preprocessing, matchers, combination, filtering components
  - Debugging component and GUI rarely implemented
- Matching strategies
  - Variety of string-based strategies
  - Most often string and structured-based strategies
- Use of background knowledge
  - Almost all systems use sources of background knowledge

* Dragisic Z, Ivanova V, Li H, Lambrix P, Experiences from the Anatomy track in the Ontology Alignment Evaluation Initiative, *Journal of Biomedical Semantics* 8:56, 2017.

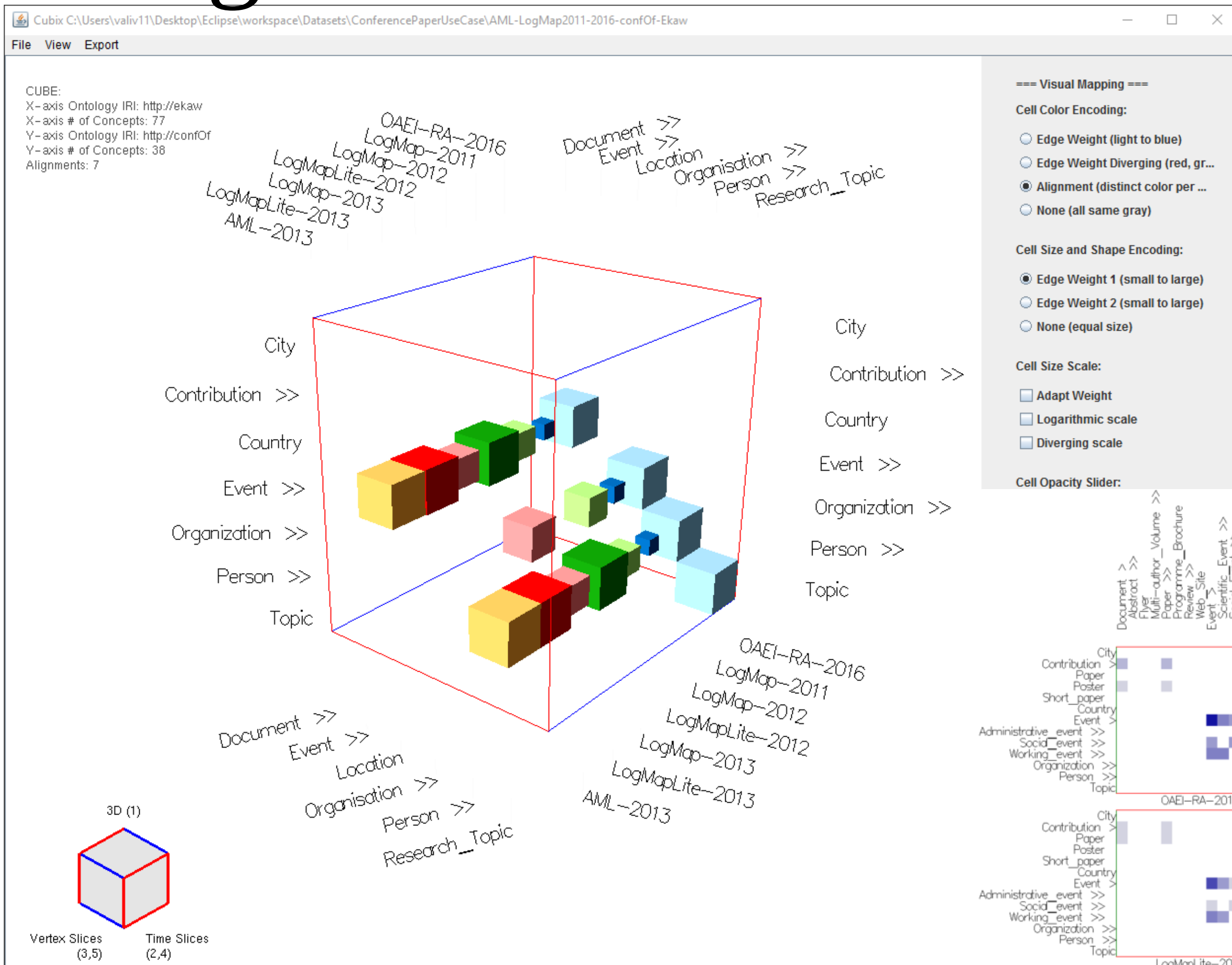
Complementary evaluation

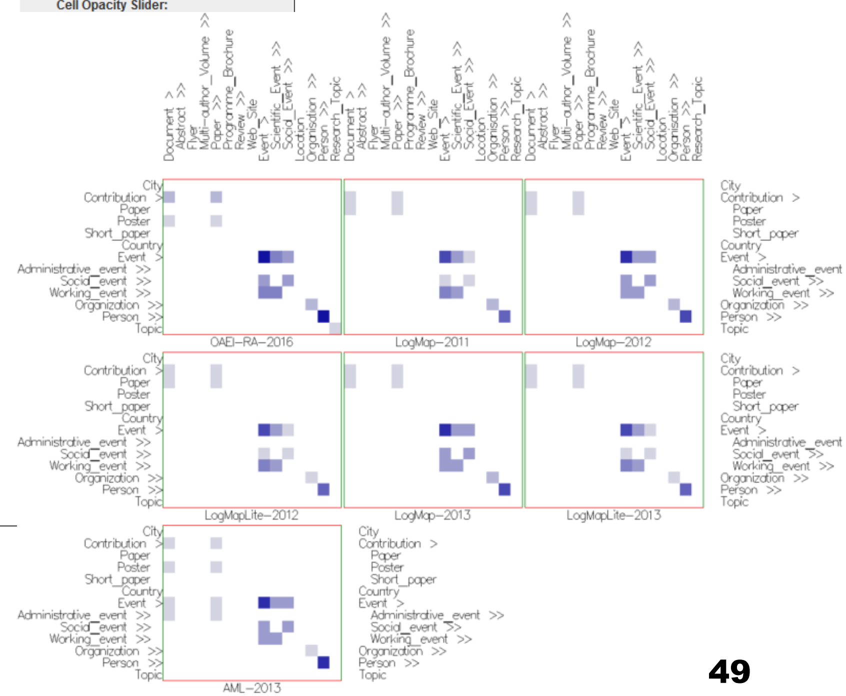
Alignment cubes

- Interactive visualization of alignments
- Region-level, mapping level
- Missing mappings
- Often found mappings

- http://www.ida.liu.se/~patla00/research/AlignmentCubes/

Alignment cubes





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- Evaluation of ontology alignment strategies
- Ontology alignment challenges

Challenges

- Large-scale matching evaluation
- Efficiency of matching techniques
  - parallellization
  - distribution of computation
  - approximation of matching results (not complete)
  - modularization of ontologies
  - optimization of matching methods

Challenges

- Matching with background knowledge
  - partial alignments
  - reuse of previous matches
  - use of domain-specific corpora
  - use of domain-specific ontologies

- Matcher selection, combination and tuning
  - recommendation of algorithms and settings

Challenges

- User involvement
  - visualization
  - user feedback
- Explanation of matching results
- Social and collaborative matching
- Alignment management: infrastructure and support

Further reading

Starting points for further studies

Further reading ontology alignment

- http://www.ontologymatching.org
(plenty of references to articles and systems)

- Ontology alignment evaluation initiative: http://oaei.ontologymatching.org
(home page of the initiative)

- Euzenat, Shvaiko, *Ontology Matching*, Springer, 2007.

- Shvaiko, Euzenat, Ontology Matching: state of the art and future challenges, *IEEE Transactions on Knowledge and Data Engineering* 25(1):158-176, 2013.

- Dragisic Z, Ivanova V, Li H, Lambrix P, Experiences from the Anatomy track in the Ontology Alignment Evaluation Initiative, *Journal of Biomedical Semantics* 8:56, 2017.

Further reading ontology alignment

Systems at LiU / IDA / ADIT

- Lambrix, Tan, SAMBO – a system for aligning and merging biomedical ontologies, *Journal of Web Semantics*, 4(3):196-206, 2006.

(description of the SAMBO tool and overview of evaluations of different matchers)

- Lambrix, Tan, A tool for evaluating ontology alignment strategies, *Journal on Data Semantics*, VIII:182-202, 2007.

(description of the KitAMO tool for evaluating matchers)

- Lambrix P, Kaliyaperumal R, A Session-based Ontology Alignment Approach enabling User Involvement, *Semantic Web Journal* 8(2):225-251, 2017.

- Ivanova V, Bach B, Pietriga E, Lambrix P, Alignment Cubes: Towards Interactive Visual Exploration and Evaluation of Multiple Ontology Alignments, 16th International Semantic Web Conference, 400-417, 2017.

Further reading ontology alignment

- Chen, Tan, Lambrix, Structure-based filtering for ontology alignment,*IEEE WETICE workshop on semantic technologies in collaborative applications*, 364-369, 2006.

(double threshold filtering technique)

- Tan, Lambrix, A method for recommending ontology alignment strategies, *International Semantic Web Conference*, 494-507, 2007.

  Ehrig, Staab, Sure, Bootstrapping ontology alignment methods with APFEL, *International Semantic Web Conference*, 186-200, 2005.

  Mochol, Jentzsch, Euzenat, Applying an analytic method for matching approach selection, *International Workshop on Ontology Matching*, 2006.

(recommendation of alignment strategies)

- Lambrix, Liu, Using partial reference alignments to align ontologies, *European Semantic Web Conference*, 188-202, 2009.

(use of partial alignments in ontology alignment)

Further reading ontology alignment

User Involvement

- Li H, Dragisic Z, Faria D, Ivanova V, Jimenez-Ruiz E, Lambrix P, Pesquita C, User validation in ontology alignment: functional assessment and impact, *The Knowledge Engineering Review*, 2019.

- Ivanova V, Lambrix P, Åberg J, Requirements for and Evaluation of User Support for Large-Scale Ontology Alignment, *12th Extended Semantic Web Conference - ESWC 2015*, LNCS 9088, 3-20, 2015.

Ontology Completion and Debugging

Defects in ontologies

- Syntactic defects
  - E.g. wrong tags or incorrect format
- Semantic defects
  - E.g. unsatisfiable concepts, incoherent and inconsistent ontologies
- Modeling defects
  - E.g. wrong or missing relations

Example - incoherent ontology

- Example: DICE ontology
  - Brain ⊑ CentralNervousSystem ⊓ BodyPart ⊓ ∃systempart.NervousSystem ⊓ ∃ region.HeadAndNeck ⊓ ∀region.HeadAndNeck

    A brain is a central nervous system and a body part which has a system part that is a nervous system and that is in the head and neck region.

  - CentralNervousSystem ⊑ NervousSystem

    A central nervous system is a nervous system.

  - BodyPart ⊑¬NervousSystem

    Nothing can be at the same time a body part and a nervous system.

Slide from G. Qi

Example - inconsistent ontology

- **Example from Foaf:**
  - **Person(timbl)**
  - **Homepage(timbl, http://w3.org/)**
  - **Homepage(w3c, http://w3.org/)**
  - **Organization(w3c)**
  - **InverseFunctionalProperty(Homepage)**
  - **DisjointWith(Organization, Person)**
- **Example from OpenCyc:**
  - **ArtifactualFeatureType(PopulatedPlace)**
  - **ExistingStuffType(PopulatedPlace)**
  - **DisjointWith(ExistingObjectType,ExistingStuffType)**
  - **ArtifactualFeatureType $\sqsubseteq$ ExistingObjectType**

Slide from G. Qi

Example - missing is-a relations

- In 2008 Ontology Alignment Evaluation Initiative (OAEI) Anatomy track, task 4
  - Ontology MA : Adult Mouse Anatomy Dictionary (2744 concepts)
  - Ontology NCI-A : NCI Thesaurus - anatomy (3304 concepts)
  - 988 mappings between MA and NCI-A
    - 121 missing is-a relations in MA
    - 83 missing is-a relations in NCI-A

Influence of missing structure

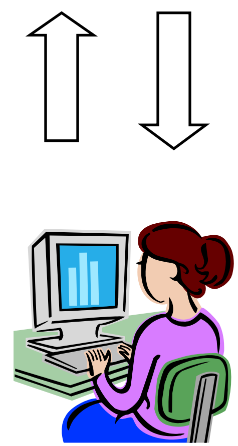
- Ontology-based querying.

Medical Subject Headings (MeSH)

All MeSH Categories

- **Diseases Category**
  - **Eye Diseases**
    - **Scleral Diseases**
      - **Scleritis**

...



return 1617 articles

Influence of missing structure

- Incomplete results from ontology-based queries

Medical Subject Headings (MeSH)

All MeSH Categories

- Diseases Category
  - Eye Diseases
    - Scleral Diseases
      - ~~Scleritis~~

...

return 1617 articles

return 695 articles

57% results are missed !

Defects in ontologies and ontology networks

- Ontologies and ontology networks with defects, although often useful, also lead to problems when used in semantically-enabled applications.

→ Wrong conclusions may be derived or valid conclusions may be missed.

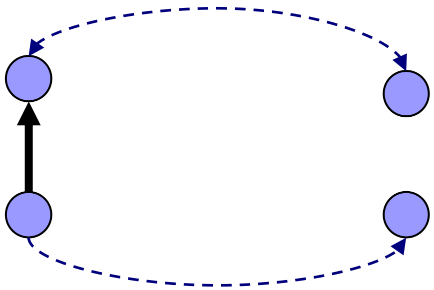
Completion and debugging process

- Detection (find candidate defects)
- Validation (real defects)
- Repair (remove wrong, add correct)

Detection

Many approaches

- inspection
- ontology learning or evolution
- using linguistic and logical patterns
  - animals *such as* dogs and cats
- by using knowledge intrinsic to an ontology network



- by using machine learning and statistical methods

Repairing

Definition 1. (Repair)[15]

Let $\mathcal{T}$ be a TBox. Let M and W be finite sets of TBox axioms. Let Or be an oracle that, given a TBox axiom, returns true or false. A repair for Complete-Debug-Problem CDP$(\mathcal{T}, Or, M, W)$ is any pair of finite sets of TBox axioms (A, D) such that

(i) $\forall\ \psi_a \in A$: $Or(\psi_a) =$ true;

(ii) $\forall\ \psi_d \in D$: $Or(\psi_d) =$ false;

(iii) $(\mathcal{T} \cup A) \setminus D$ is consistent;

(iv) $\forall\ \psi_m \in M$: $(\mathcal{T} \cup A) \setminus D \models \psi_m$;

(v) $\forall\ \psi_w \in W$: $(\mathcal{T} \cup A) \setminus D \not\models \psi_w$.

Current work usually focuses on debugging or completion, but not both.
Most work on debugging.

Ontology Debugging

Example : an Incoherent Ontology

Consider the following TBox $\mathcal{T}^*$, where A, B and C are primitive and $A_1, \ldots, A_7$ defined concept names:

$ax_1: A_1 \dot{\sqsubseteq} \neg A \sqcap A_2 \sqcap A_3$	$ax_2: A_2 \dot{\sqsubseteq} A \sqcap A_4$
$ax_3: A_3 \dot{\sqsubseteq} A_4 \sqcap A_5$	$ax_4: A_4 \dot{\sqsubseteq} \forall s.B \sqcap C$
$ax_5: A_5 \dot{\sqsubseteq} \exists s.\neg B$	$ax_6: A_6 \dot{\sqsubseteq} A_1 \sqcup \exists r.(A_3 \sqcap \neg C \sqcap A_4)$
$ax_7: A_7 \dot{\sqsubseteq} A_4 \sqcap \exists s.\neg B$	

DL Reasoner

The ontology is incoherent!
The set of unsatisfiable concepts are : $\{A_1, A_3, A_6, A_7\}$.

What are the root causes of these defects?

Explain the Semantic Defects

- We need to identify the sets of axioms which are necessary for causing the logic contradictions.

$ax_1 : A_1 \dot{\sqsubseteq} \neg A \sqcap A_2 \sqcap A_3$	$ax_2 : A_2 \dot{\sqsubseteq} A \sqcap A_4$
$ax_3 : A_3 \dot{\sqsubseteq} A_4 \sqcap A_5$	$ax_4 : A_4 \dot{\sqsubseteq} \forall s.B \sqcap C$
$ax_5 : A_5 \dot{\sqsubseteq} \exists s.\neg B$	$ax_6 : A_6 \dot{\sqsubseteq} A_1 \sqcup \exists r.(A_3 \sqcap \neg C \sqcap A_4)$
$ax_7 : A_7 \dot{\sqsubseteq} A_4 \sqcap \exists s.\neg B$	

  - For example, for the unsatisfiable concept "A_1", there are two sets of axioms.

$$ax_1 : A_1 \dot{\sqsubseteq} \underline{\neg A} \sqcap A_2 \sqcap A_3$$
$$ax_2 : A_2 \dot{\sqsubseteq} \underline{A} \sqcap A_4$$

$$ax_1 : A_1 \dot{\sqsubseteq} \neg A \sqcap A_2 \sqcap \underline{A_3}$$
$$ax_3 : A_3 \dot{\sqsubseteq} \underline{A_4 \sqcap A_5}$$
$$ax_4 : A_4 \dot{\sqsubseteq} \underline{\forall s.B} \sqcap C$$
$$ax_5 : A_5 \dot{\sqsubseteq} \underline{\exists s.\neg B}$$

Minimal Unsatisfiability Preserving Sub-TBoxes (MUPS)

Definition 1 Let A be a concept which is unsatisfiable in a TBox $\mathcal{T}$. A set $\mathcal{T}' \subseteq \mathcal{T}$ is a *minimal unsatisfiability-preserving sub-TBox (MUPS)* of $\mathcal{T}$ if

- A is unsatisfiable in $\mathcal{T}'$, and
- A is satisfiable in every sub-TBox $\mathcal{T}'' \subset \mathcal{T}'$.

We will abbreviate the set of MUPS of $\mathcal{T}$ and A by $mups(\mathcal{T}, A)$.

$$mups(\mathcal{T}^*, A_1) = \{\{ax_1, ax_2\}, \{ax_1, ax_3, ax_4, ax_5\}\}$$

- The MUPS of an unsatisfiable concept imply the solutions for repairing.

  → Remove at least one axiom from each axiom set in the MUPS

Example

$$mups(\mathcal{T}^*, A_1) = \{\{\cancel{ax_1}, ax_2\}, \{\cancel{ax_1}, \cancel{ax_3}, \cancel{ax_4}, ax_5\}\}$$
$$mups(\mathcal{T}^*, A_3) = \{\{\cancel{ax_3}, \cancel{ax_4}, ax_5\}\}$$
$$mups(\mathcal{T}^*, A_6) = \{\{\cancel{ax_1}, ax_2, \cancel{ax_4}, ax_6\}, \{\cancel{ax_1}, \cancel{ax_3}, \cancel{ax_4}, ax_5, ax_6\}\}$$
$$mups(\mathcal{T}^*, A_7) = \{\{\cancel{ax_4}, ax_7\}\}$$

- Possible ways of repairing all the unsatisfiable concepts in the ontology:

$$\{ax_1, ax_3, ax_4\}$$

How to represent all these possibilities?

Minimal Incoherence Preserving Sub-TBox (MIPS)

Definition 2 Let $\mathcal{T}$ be an incoherent TBox. A TBox $\mathcal{T}' \subseteq \mathcal{T}$ is a *minimal incoherence-preserving sub-TBox (MIPS) of* $\mathcal{T}$ if

- $\mathcal{T}'$ is incoherent, and
- every sub-TBox $\mathcal{T}'' \subset \mathcal{T}'$ is coherent.

$$mups(\mathcal{T}^*, A_1) = \{\{ax_1, ax_2\}, \{ax_1, ax_3, ax_4, ax_5\}\}$$
$$mups(\mathcal{T}^*, A_3) = \{\{ax_3, ax_4, ax_5\}\}$$
$$mups(\mathcal{T}^*, A_6) = \{\{ax_1, ax_2, ax_4, ax_6\}, \{ax_1, ax_3, ax_4, ax_5, ax_6\}\}$$
$$mups(\mathcal{T}^*, A_7) = \{\{ax_4, ax_7\}\}$$

We will abbreviate the set of MIPS of $\mathcal{T}$ by $mips(\mathcal{T})$. For $\mathcal{T}^*$ we get three MIPS:

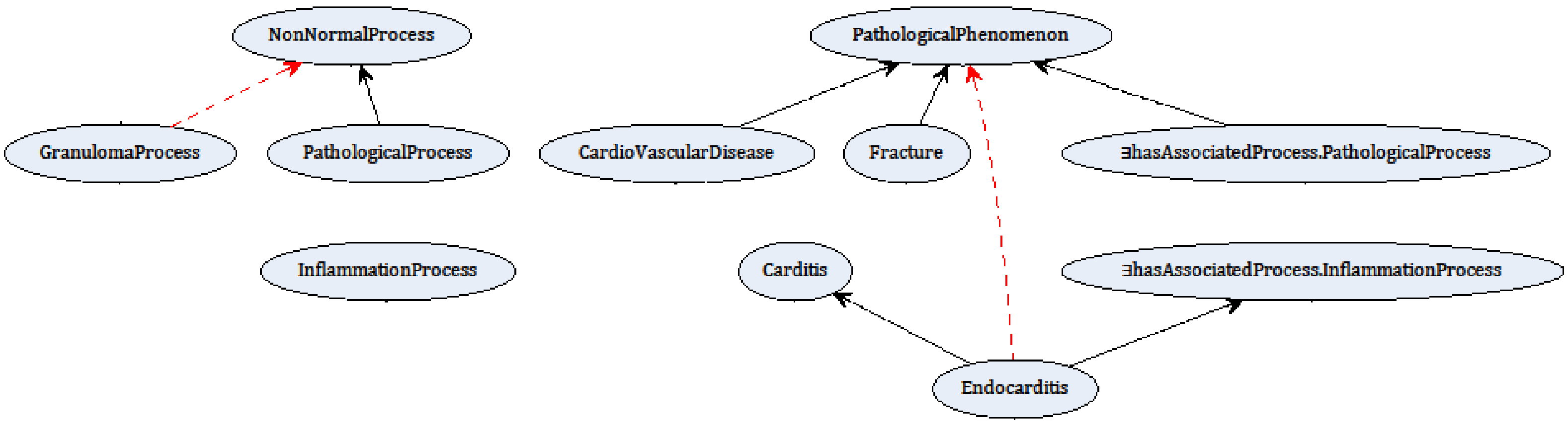
$$mips(\mathcal{T}^*) = \{\{ax_1, ax_2\}, \{ax_3, ax_4, ax_5\}, \{ax_4, ax_7\}\}$$

A possible repairing is $\{ax_i\} \cup \{ax_j\} \cup \{ax_k\}$, where

- $ax_i \in \{ax_1, ax_2\}$
- $ax_j \in \{ax_3, ax_4, ax_5\}$
- $ax_k \in \{ax_4, ax_7\}$

Completing the is-a structure of ontologies

Example



Repairing actions:

$\{$Endocarditis $\dot{\sqsubseteq}$ PathologicalPhenomenon, GranulomaProcess $\dot{\sqsubseteq}$ NonNormalProcess$\}$

$\{$Carditis $\dot{\sqsubseteq}$ CardioVascularDisease, GranulomaProcess $\dot{\sqsubseteq}$ PathologicalProcess$\}$

$\{$Carditis $\dot{\sqsubseteq}$ Fracture, GranulomaProcess $\dot{\sqsubseteq}$ NonNormalProcess$\}$

Description logic EL

- Concepts

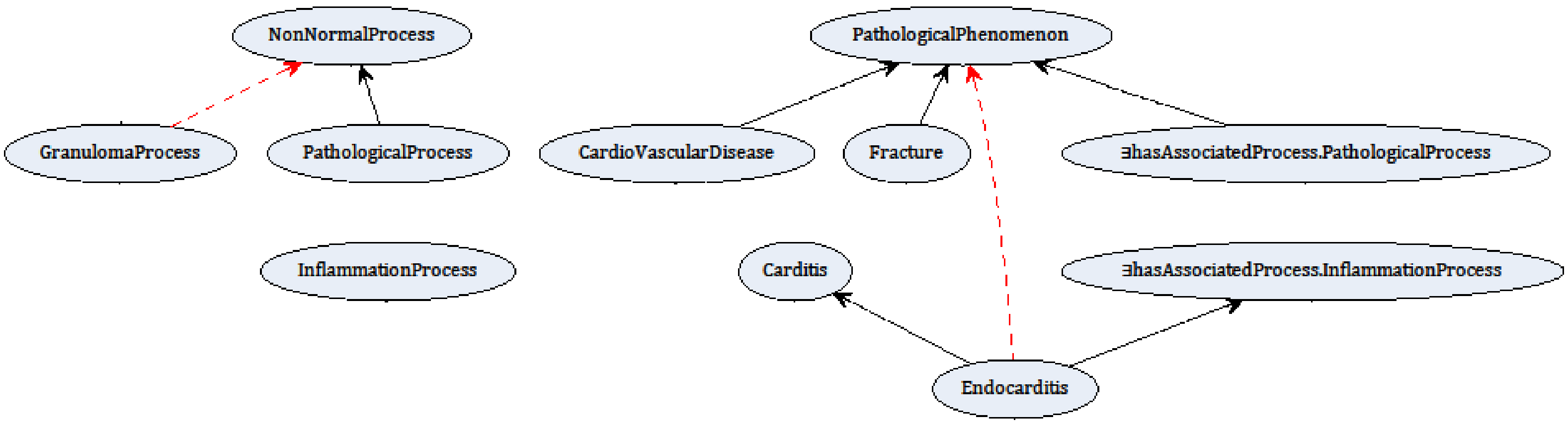
Atomic concept	A
Universal concept	$\top$
Intersection of concepts	$C \sqcap D$
Existential restriction	$\exists r.C$

- Terminological axioms: equivalence and subsumption

Generalized Tbox Abduction Problem – GTAP(**T**,**C**,Or,M)

- Given
  - **T**- a Tbox in EL
  - **C**- a set of atomic concepts in **T**
  - M = $\{A_i \subseteq B_i\}_{i=1..n}$ and $\forall$ i:1..n: A_i, $B_i \in$ **C**
  - Or: $\{C_i \subseteq D_i \mid C_i, D_i \in$ **C**$\}$ → {true, false}
- Find
  - S = $\{E_i \subseteq F_i\}_{i=1..k}$ such that
    $\forall$ i:1..k: E_i, $F_i \in$ **C** and Or($E_i \subseteq F_i$) = true
    and T U S is consistent and T U S |= M

GTAP - example



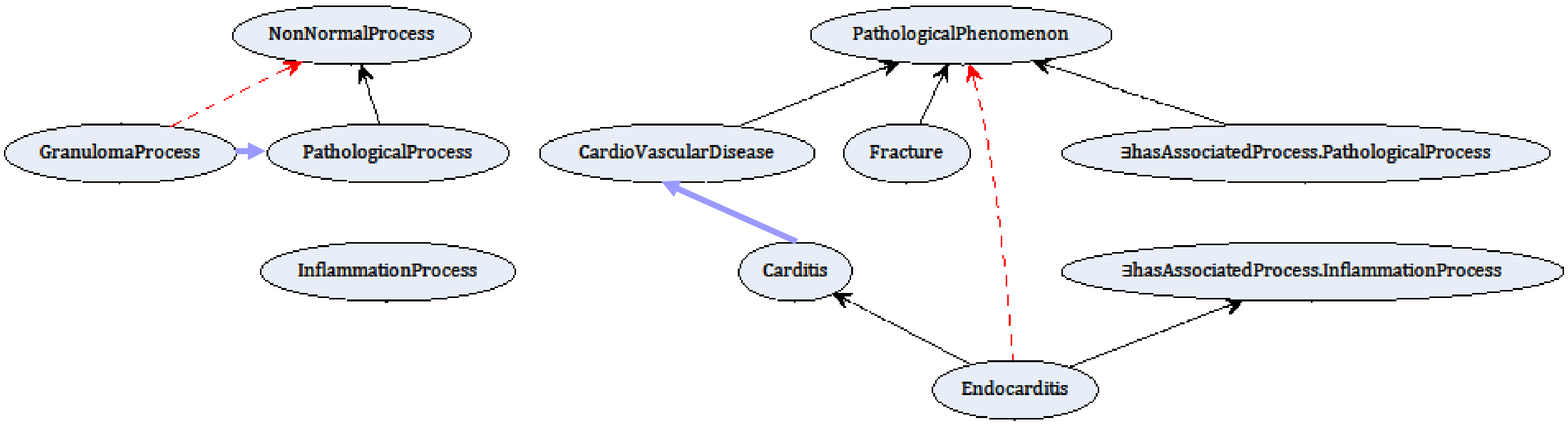
C = { GranulomaProcess, CardioVascularDisease, PathologicalPhenomenon, Fracture, Endocarditis, Carditis, InflammationProcess, PathologicalProcess, NonNormalProcess}

T = { GranulomaProcess $\dot{\sqsubseteq} \top$, hasAssociatedProcess $\dot{\sqsubseteq} \top \times \top$,
CardioVascularDisease $\dot{\sqsubseteq}$ PathologicalPhenomenon, Fracture $\dot{\sqsubseteq}$ PathologicalPhenomenon,
$\exists$hasAssociatedProcess.PathologicalProcess $\dot{\sqsubseteq}$ PathologicalPhenomenon,
Endocarditis $\dot{\sqsubseteq}$ Carditis, Endocarditis $\dot{\sqsubseteq}$ $\exists$hasAssociatedProcess.InflammationProcess,
PathologicalProcess $\dot{\sqsubseteq}$ NonNormalProcess }

M = { Endocarditis $\dot{\sqsubseteq}$ PathologicalPhenomenon, GranulomaProcess $\dot{\sqsubseteq}$ NonNormalProcess }

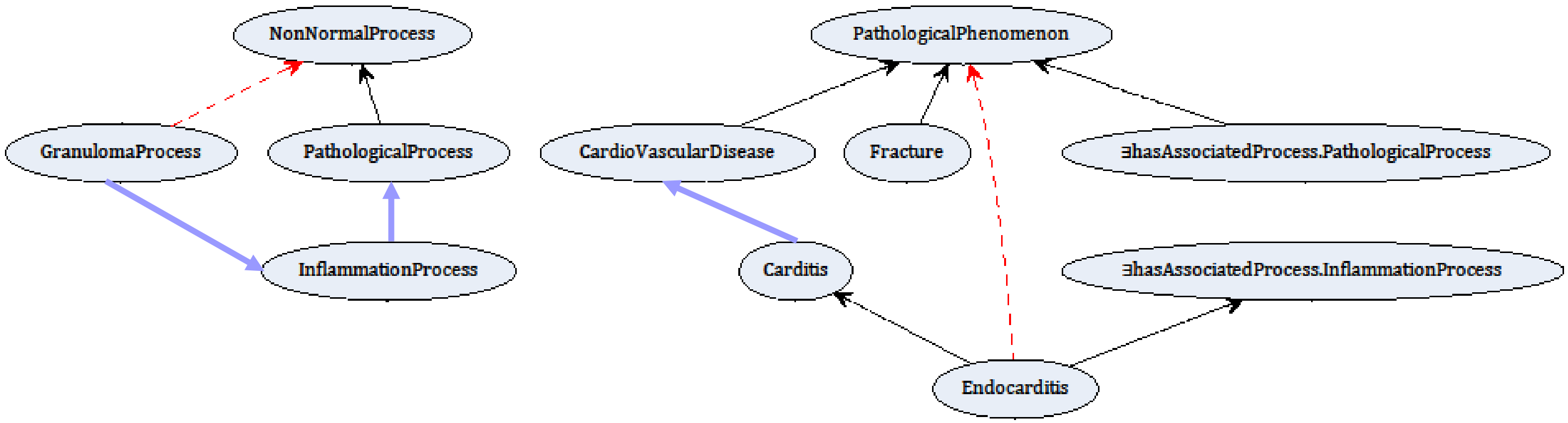
Preference criteria

- There can be many solutions for GTAP



Preference criteria

- There can be many solutions for GTAP



Not all are equally interesting.

More informative

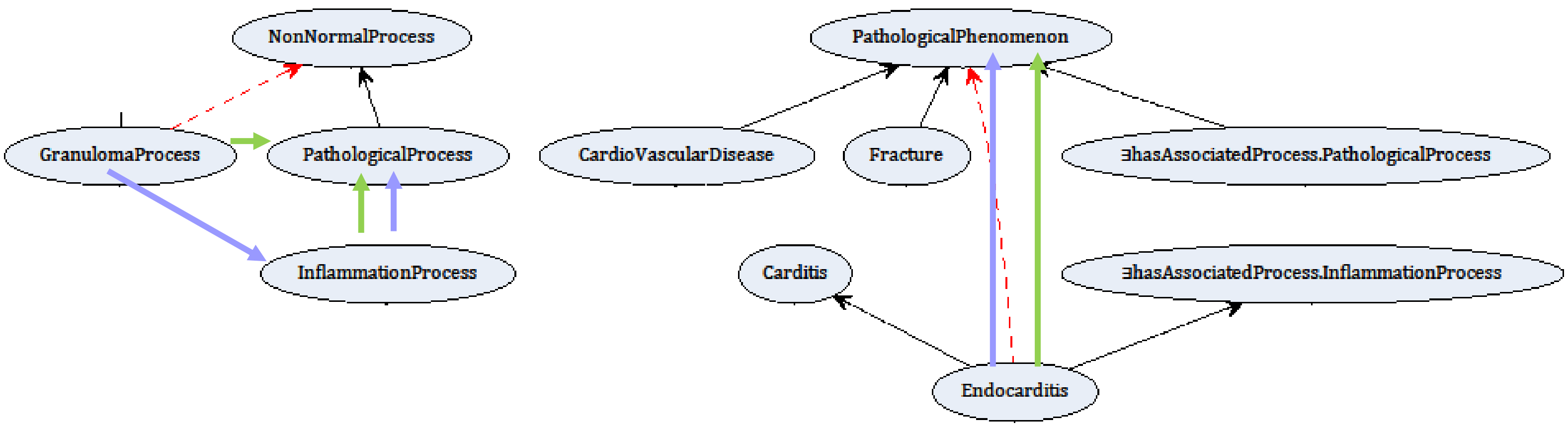
- Let *S* and *S'* be two solutions to GTAP(**T**,**C**,Or,M). Then,

 - *S* is more informative than *S'*
iff **T** U *S* |= *S'* but not **T** U *S'* |= *S*

 - *S* is equally informative as *S'*
iff **T** U *S* |= *S'* and **T** U *S'* |= *S*

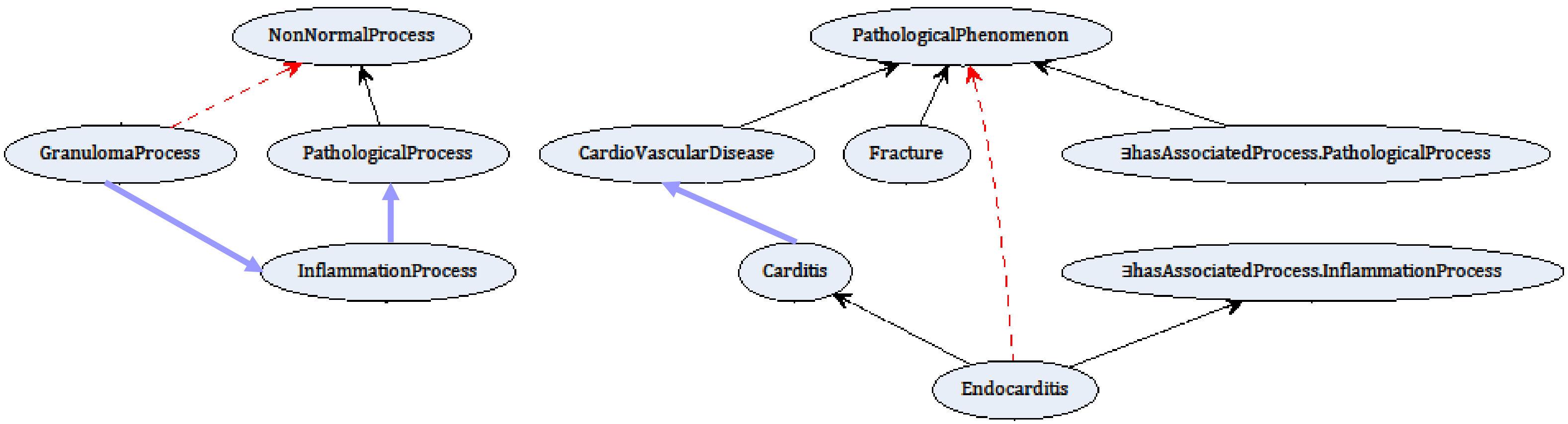
More informative

- 'Blue' solution is more informative than 'green' solution



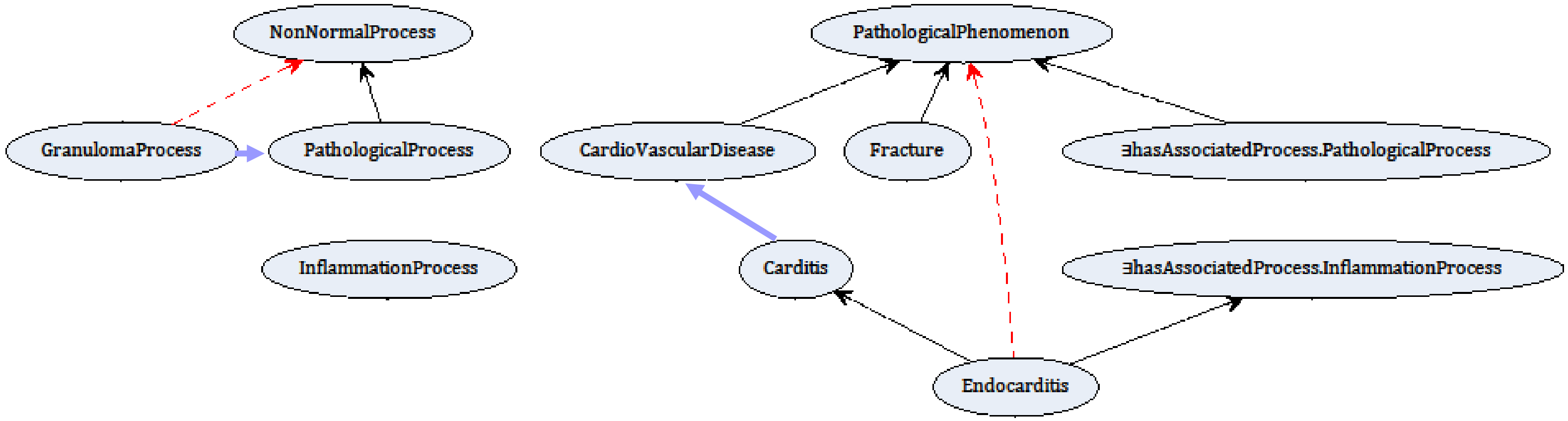
Semantic maximality

- A solution *S* to GTAP(**T**,**C**,Or,M) is semantically maximal iff there is no solution *S*' which is more informative than *S*.



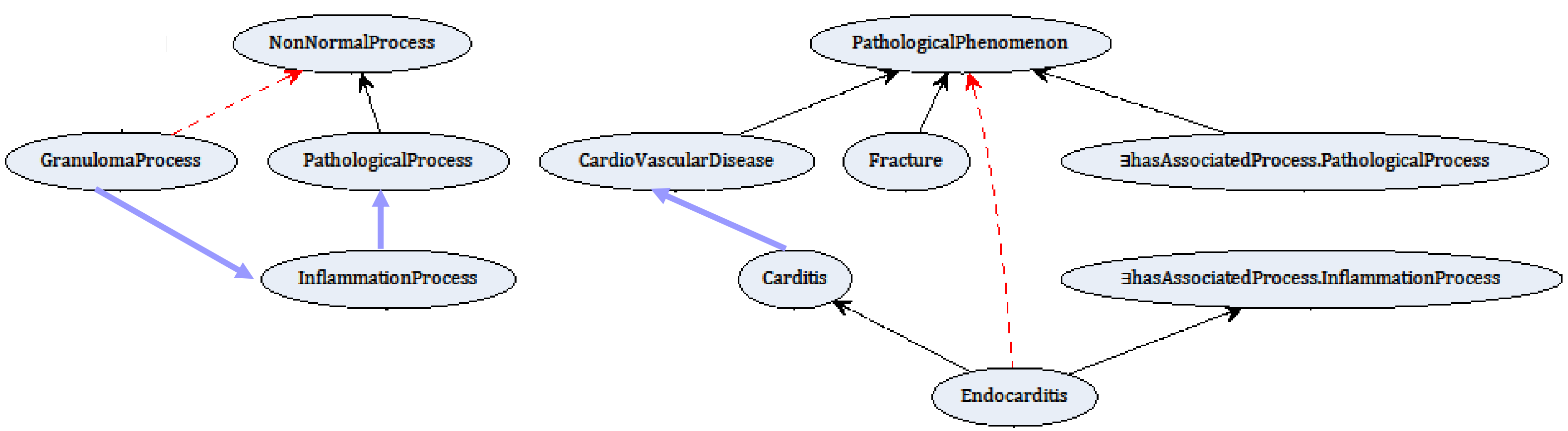
Subset minimality

- A solution *S* to GTAP(**T**,**C**,Or,M) is subset minimal iff there is no proper subset *S*' of *S* that is a solution.



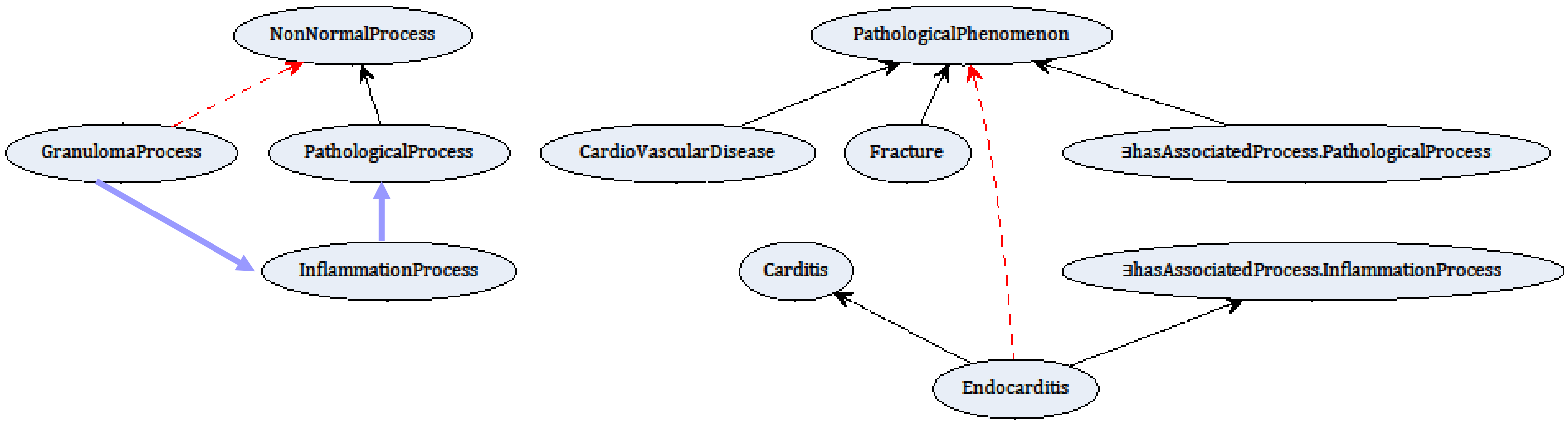
Combining with priority for semantic maximality

- A solution *S* to GTAP(**T**,**C**,Or,M) is maxmin optimal iff *S* is semantically maximal and there is no other semantically maximal solution that is a proper subset of *S*.



Combining with priority for subset minimality

- A solution *S* to GTAP(**T**,**C**,Or,M) is minmax optimal iff *S* is subset minimal and there is no other subset minimal solution that is more informative than *S*.



Combining with equal preferences

- A solution *S* to GTAP(**T**,**C**,Or,M) is skyline optimal iff there is no other solution that is a proper subset of *S* and that is equally informative than *S*.
  - All subset minimal, minmax optimal and maxmin optimal solutions are also skyline optimal solutions.
  - Semantically maximal solutions may or may not be skyline optimal.

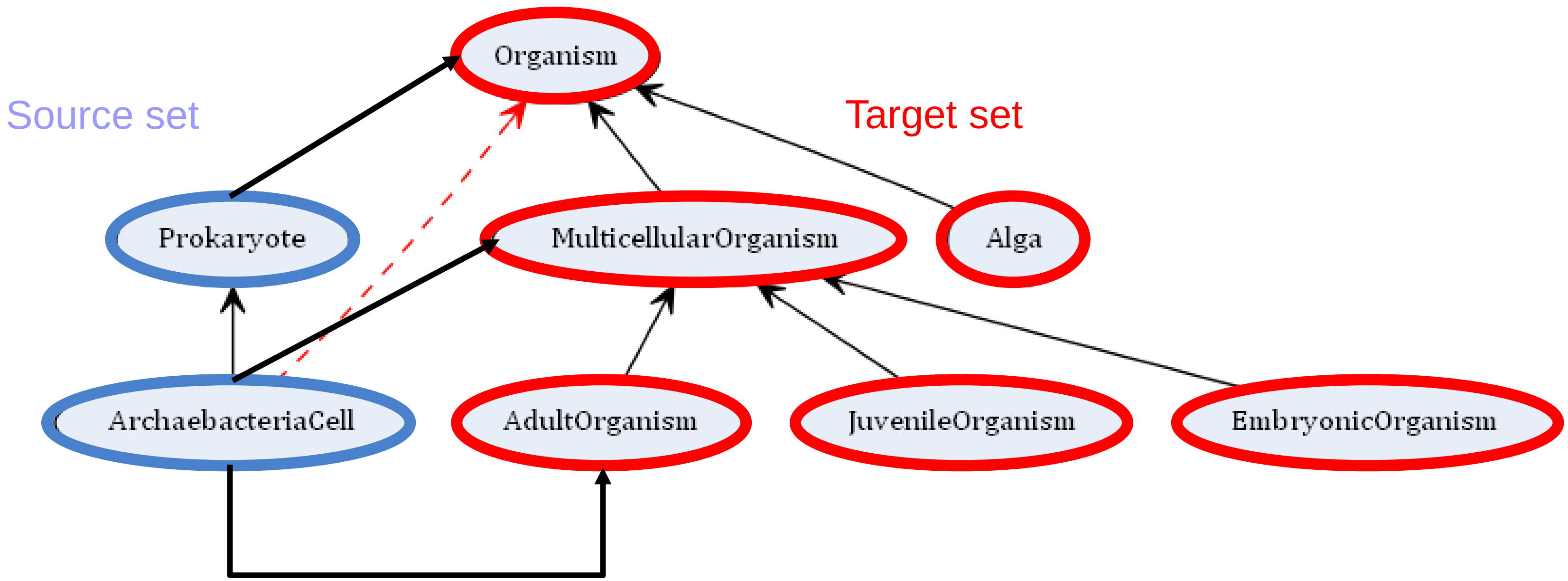
Preference criteria - conclusions

- In practice it is not clear how to generate maxmin or semantically maximal solutions (the preferred solutions)
- Skyline optimal solutions are the next best thing and are easy to generate

Approach

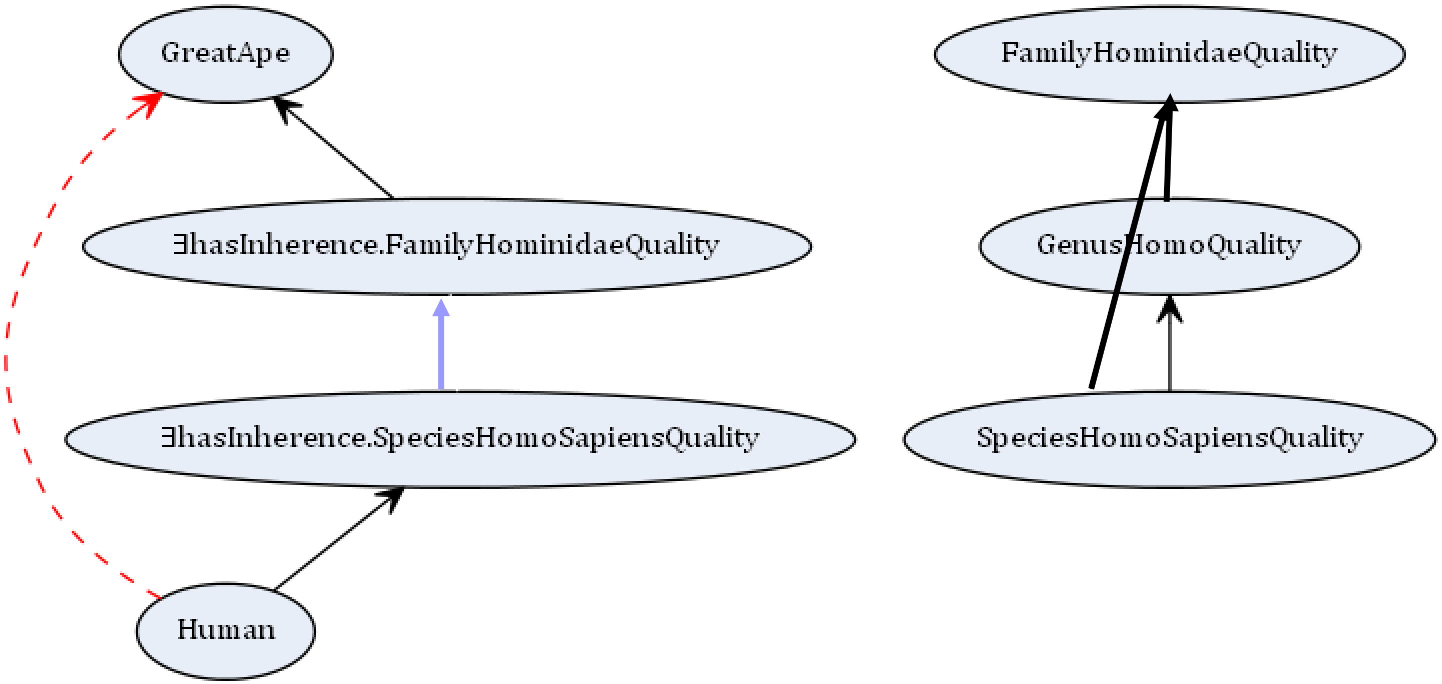
- Input
  - Normalized EL - TBox
  - Set of missing is-a relations (correct according to the domain)
- Output – a skyline-optimal solution to GTAP
- Iteration of three main steps:
  - Creating solutions for individual missing is-a relations
  - Combining individual solutions
  - Trying to improve the result by finding a solution which introduces additional new knowledge (more informative)

Intuition 1

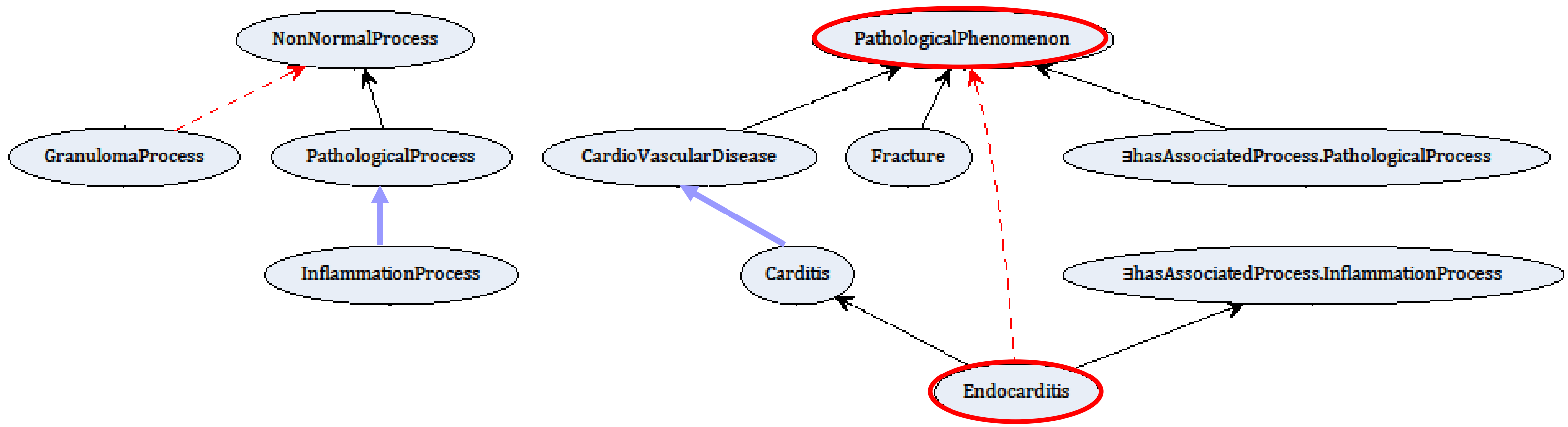


Source set
Target set
Organism
Prokaryote
MulticellularOrganism
Alga
ArchaebacteriaCell
AdultOrganism
JuvenileOrganism
EmbryonicOrganism

Intuitions 2/3



Example – repairing single is–a relation



~~Endocarditis $\dot\sqsubseteq$ PathologicalPhenomenon~~

~~Endocarditis $\dot\sqsubseteq$ Fracture~~ false

~~Endocarditis $\dot\sqsubseteq$ CardioVascularDisease~~

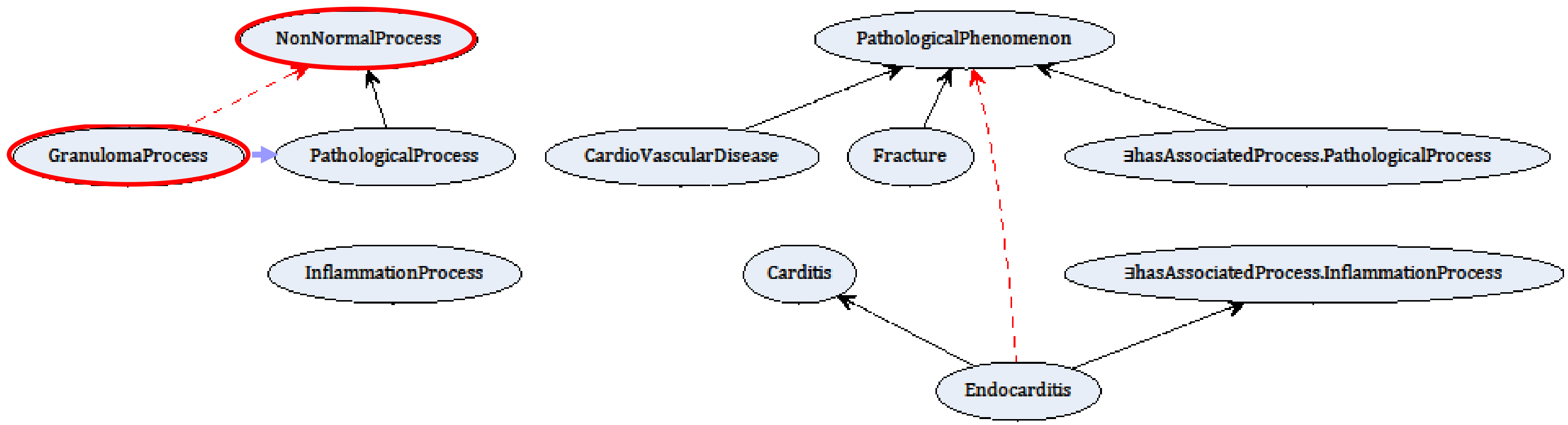
~~Carditis $\dot\sqsubseteq$ PathologicalPhenomenon~~

~~Carditis $\dot\sqsubseteq$ Fracture~~ false

Carditis $\dot\sqsubseteq$ CardioVascularDisease

InflammationProcess $\dot\sqsubseteq$ PathologicalProcess

Example – repairing single is–a relation



~~$\text{GranulomaProcess} \;\dot{\sqsubseteq}\; \text{NonNormalProcess}$~~

$\text{GranulomaProcess} \;\dot{\sqsubseteq}\; \text{PathologicalProcess}$

Algorithm - Repairing multiple is-a relations

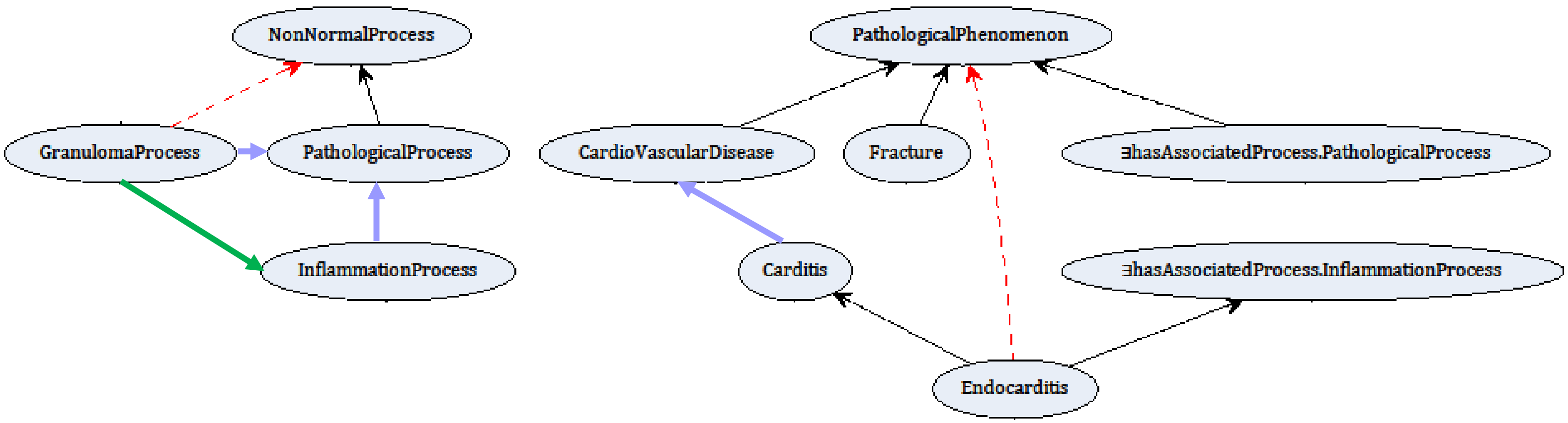
- Combine solutions for individual missing is-a relations
- Remove redundant relations while keeping the same level of informativness
- Resulting solution is a skyline optimal solution

$$\{\text{InflammationProcess} \mathrel{\dot\sqsubseteq} \text{PathologicalProcess},\\ \text{Carditis} \mathrel{\dot\sqsubseteq} \text{CardioVascularDisease},\\ \text{GranulomaProcess} \mathrel{\dot\sqsubseteq} \text{PathologicalProcess}\}$$

Algorithm – improving solution

- Solution S from previous step may contain relations which are not derivable from the ontology.
- These can be seen as new missing is-a relations.
- We can solve a new GTAP problem: GTAP(**T** U *S*, **C**, Or, *S*)

Example – improving solutions



$$\text{GranulomaProcess} \dot{\sqsubseteq} \text{InflammationProcess}$$

$$\{\text{InflammationProcess} \dot{\sqsubseteq} \text{PathologicalProcess},$$
$$\text{Carditis} \dot{\sqsubseteq} \text{CardioVascularDisease},$$
$$\text{GranulomaProcess} \dot{\sqsubseteq} \text{InflammationProcess}\}$$

Algorithm properties

- Sound
- Skyline optimal solutions

Experiments

Two use-cases

- Case 1: given missing is-a relations
  AMA and a fragment of NCI-A ontology – OAEI 2013
  - AMA (2744 concepts) – 94 missing is-a relations
    → 3 iterations, 101 in repairing (47 additional new knowledge)
  - NCI-A (3304 concepts) – 58 missing is-a relations
    → 3 iterations, 54 in repairing (10 additional new knowledge)

- Case 2: no given missing is-a relations
  Modified BioTop ontology
  - Biotop (280 concepts, 42 object properties)
    randomly choose is-a relations and remove them: 47 'missing'
    → 4 iterations, 41 in repairing (40 additional new knowledge)

Further reading

Starting points for further studies

Further reading ontology debugging

Debugging and Completing Ontologies

- Lambrix P, Completing and Debugging Ontologies: state of the art and challenges in repairing ontologies, 2019. *Journal of Data and Information Quality*, 2023.

Debugging Ontologies

- Schlobach S, Cornet R. Non-Standard Reasoning Services for the Debugging of Description Logic Terminologies. *18th International Joint Conference on Artificial Intelligence - IJCAI03*, 355-362, 2003.
- Schlobach S. Debugging and Semantic Clarification by Pinpointing. *2nd European Semantic Web Conference - ESWC05*, LNCS 3532, 226-240, 2005.

Further reading ontology debugging

Completing ontologies

- Fang Wei-Kleiner, Zlatan Dragisic, Patrick Lambrix. Abduction Framework for Repairing Incomplete EL Ontologies: Complexity Results and Algorithms. 28th AAAI Conference on Artificial Intelligence - AAAI 2014, 1120-1127, 2014.

- Lambrix P, Ivanova V, A unified approach for debugging is-a structure and mappings in networked taxonomies, *Journal of Biomedical Semantics* 4:10, 2013.

- Lambrix P, Liu Q, Debugging the missing is-a structure within taxonomies networked by partial reference alignments, *Data & Knowledge Engineering* 86:179-205, 2013.