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Linking and Building Ontologies of Linked Data

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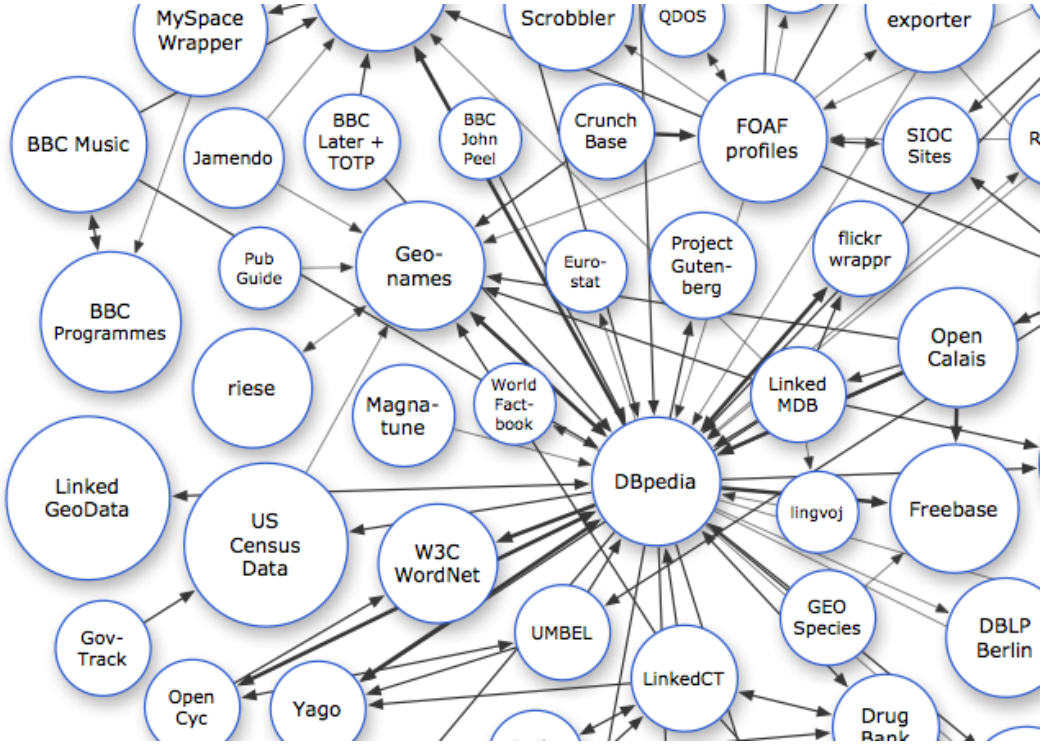
Web of Linked Data

- Vast collection of interlinked information
- Different sources with different schemas



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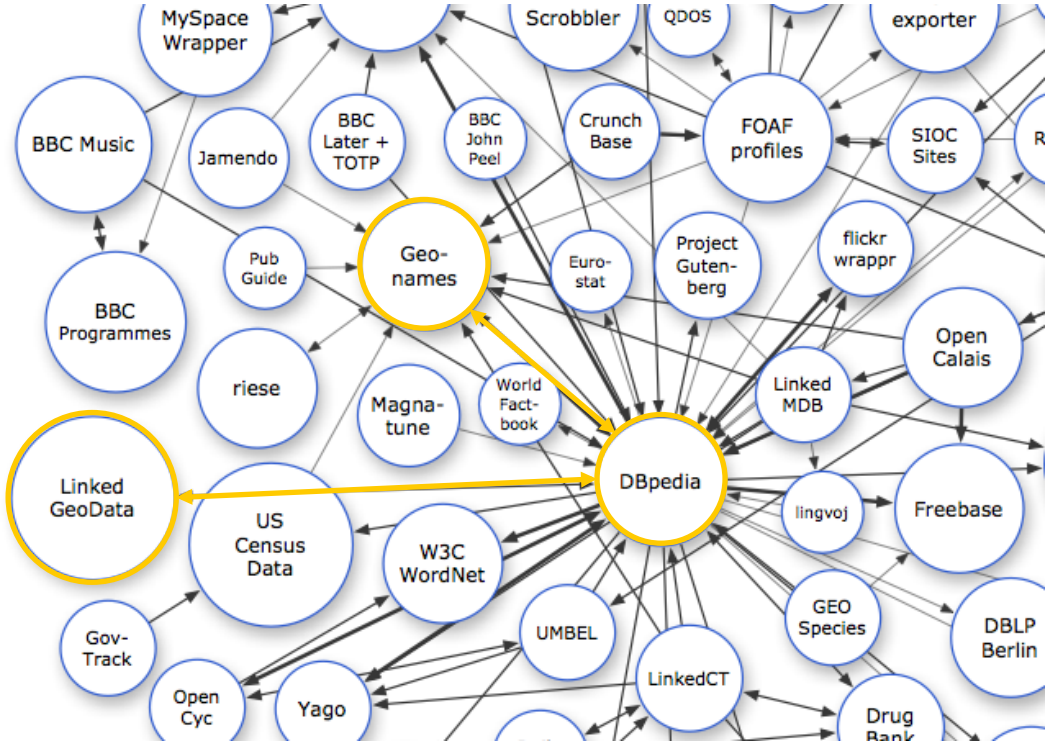
Web of Linked Data

- Interlinked instances in the various domains
- Equivalent instances linked with *owl:sameAs*

Geospatial Domain



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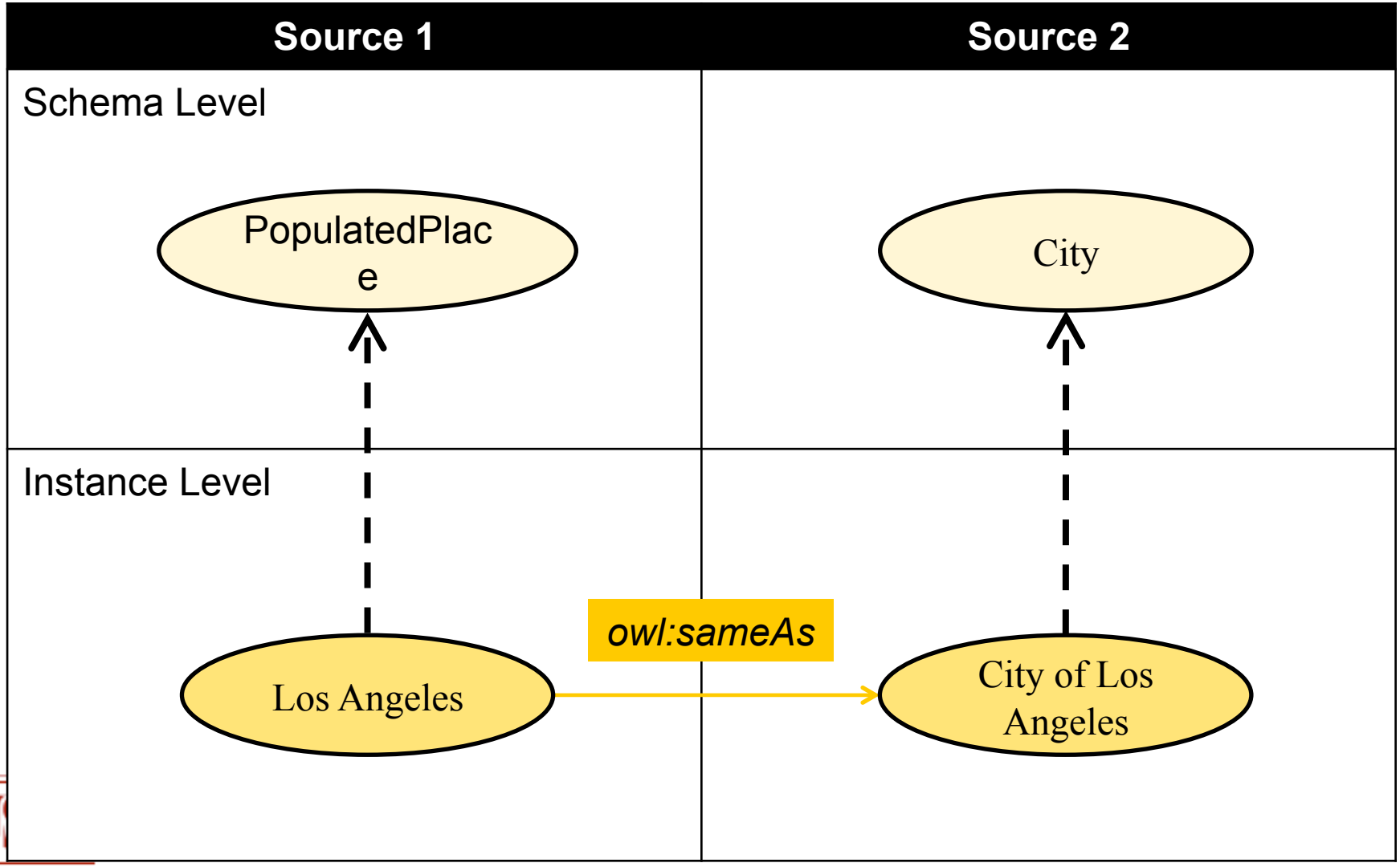
Interlinked Instances



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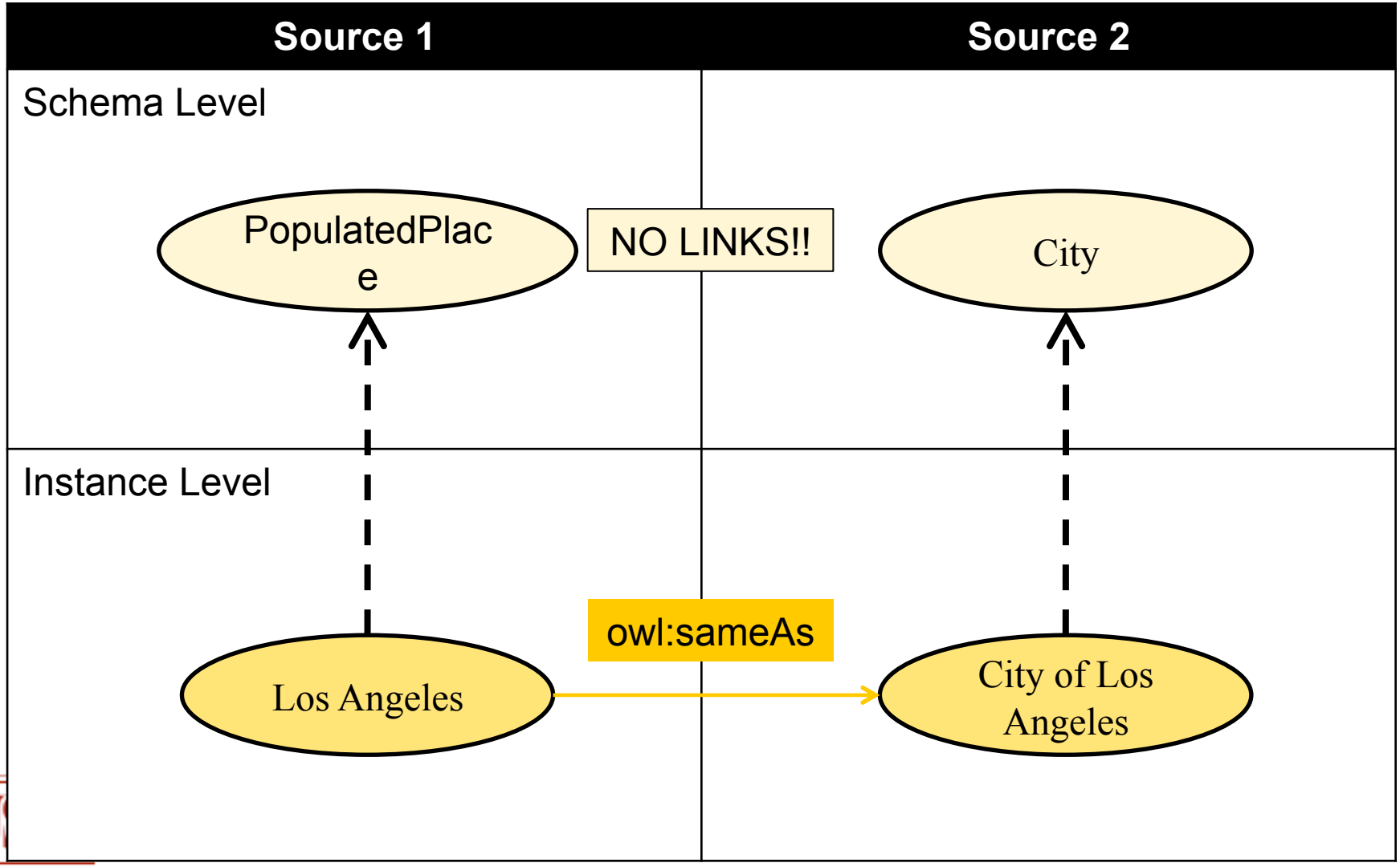
Disjoint Schemas



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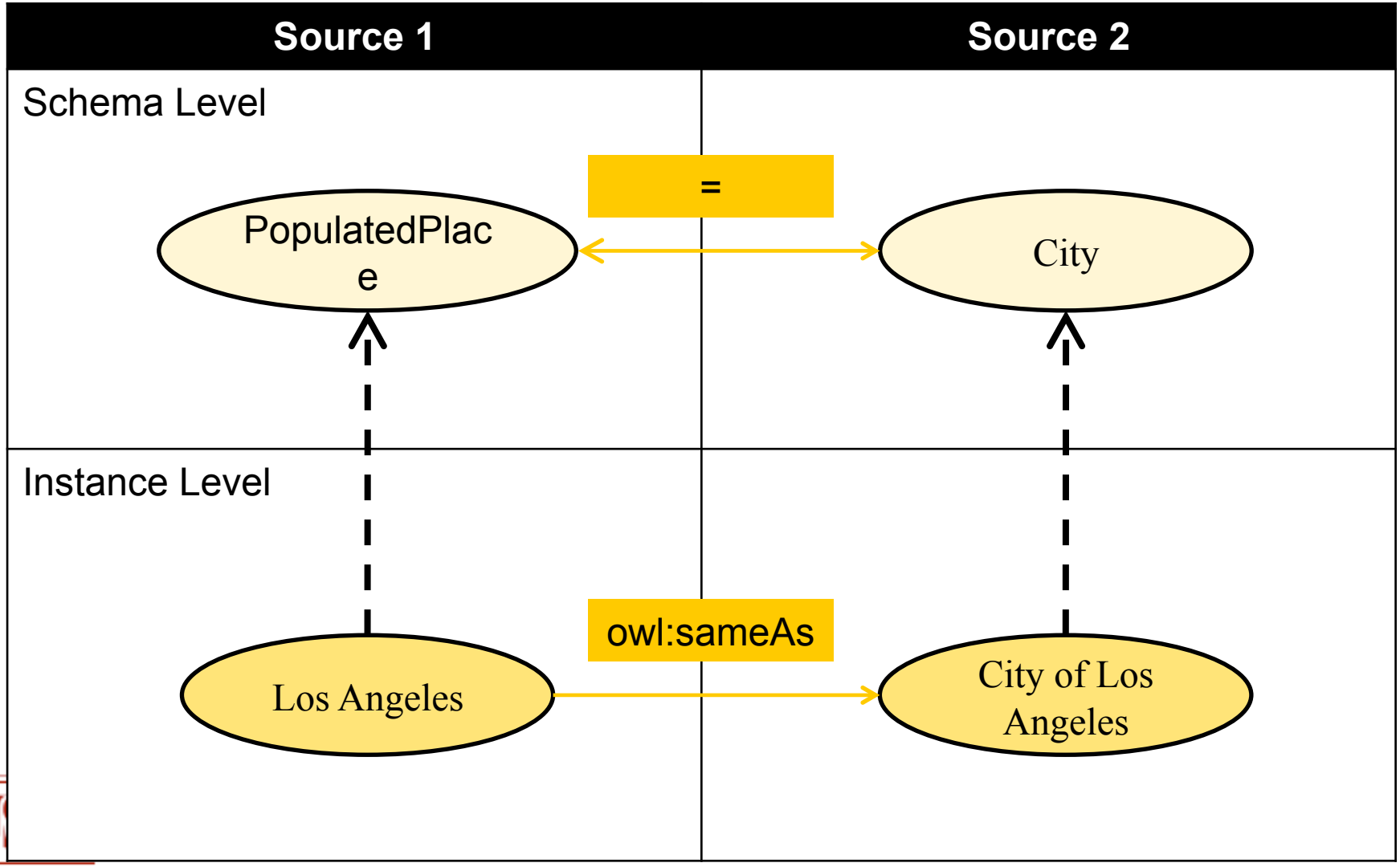
Objective 1: Find Schema Alignments



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Ontologies of Linked Data

- Ontologies can be highly specialized
  - e.g. DBpedia has classes for *Educational Institutions, Bridges, Airports, etc.*
- But some can be rudimentary
  - e.g. in Geonames all instances only belong to a single class – 'Feature'
  - Derived from RDBMS schemas from which Linked Data was generated

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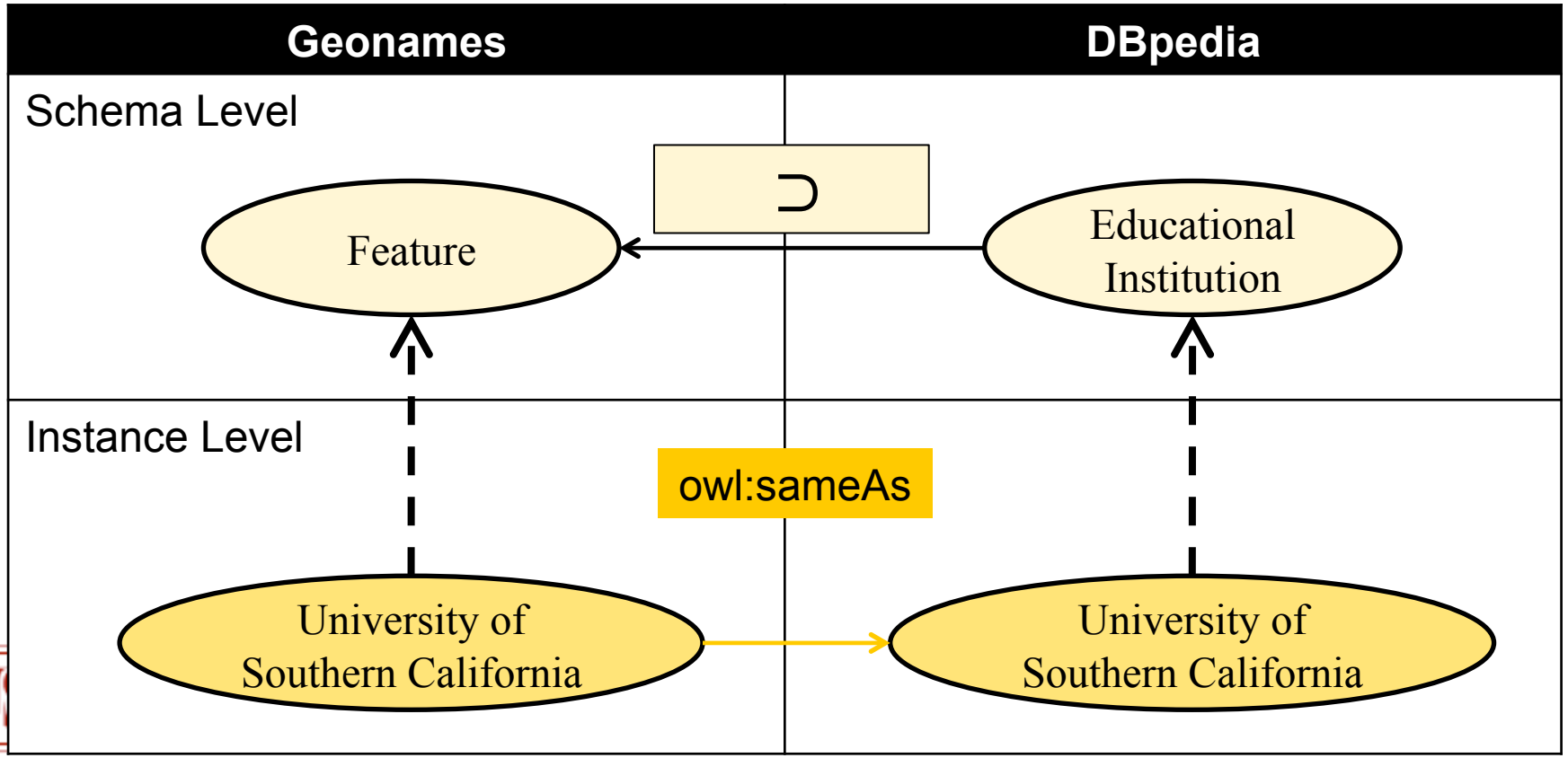
Traditional Alignments

- There might not exist exact equivalences between classes in two sources
- Only subset relations possible



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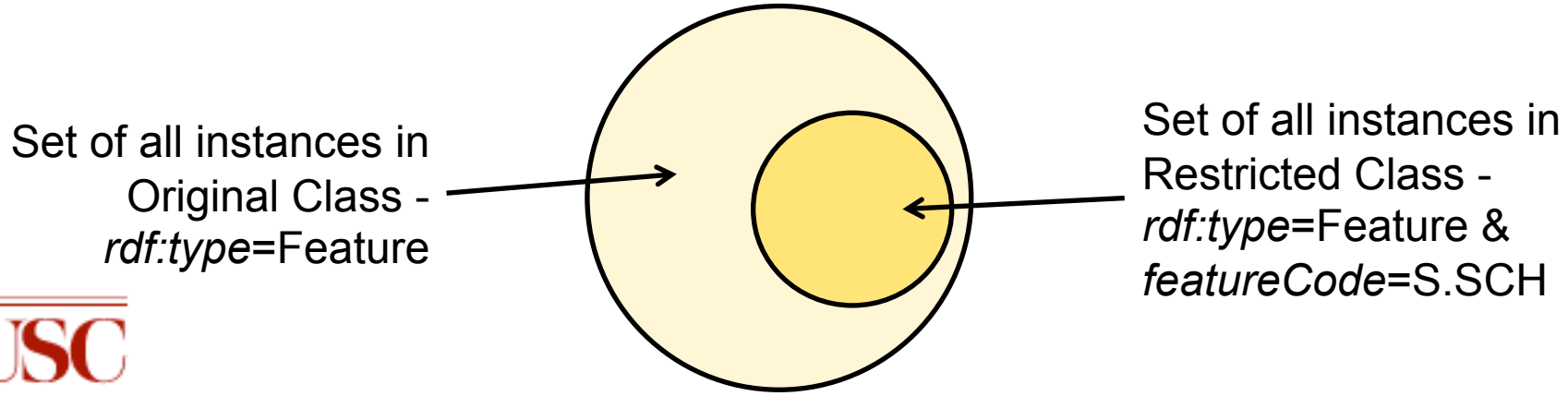
Restriction Classes

- A specialized class can be created by restricting the value of one or more properties
- The following Venn diagram explains a restriction class in Geonames with a restriction on the value of the *featureCode* property as 'S.SCH'



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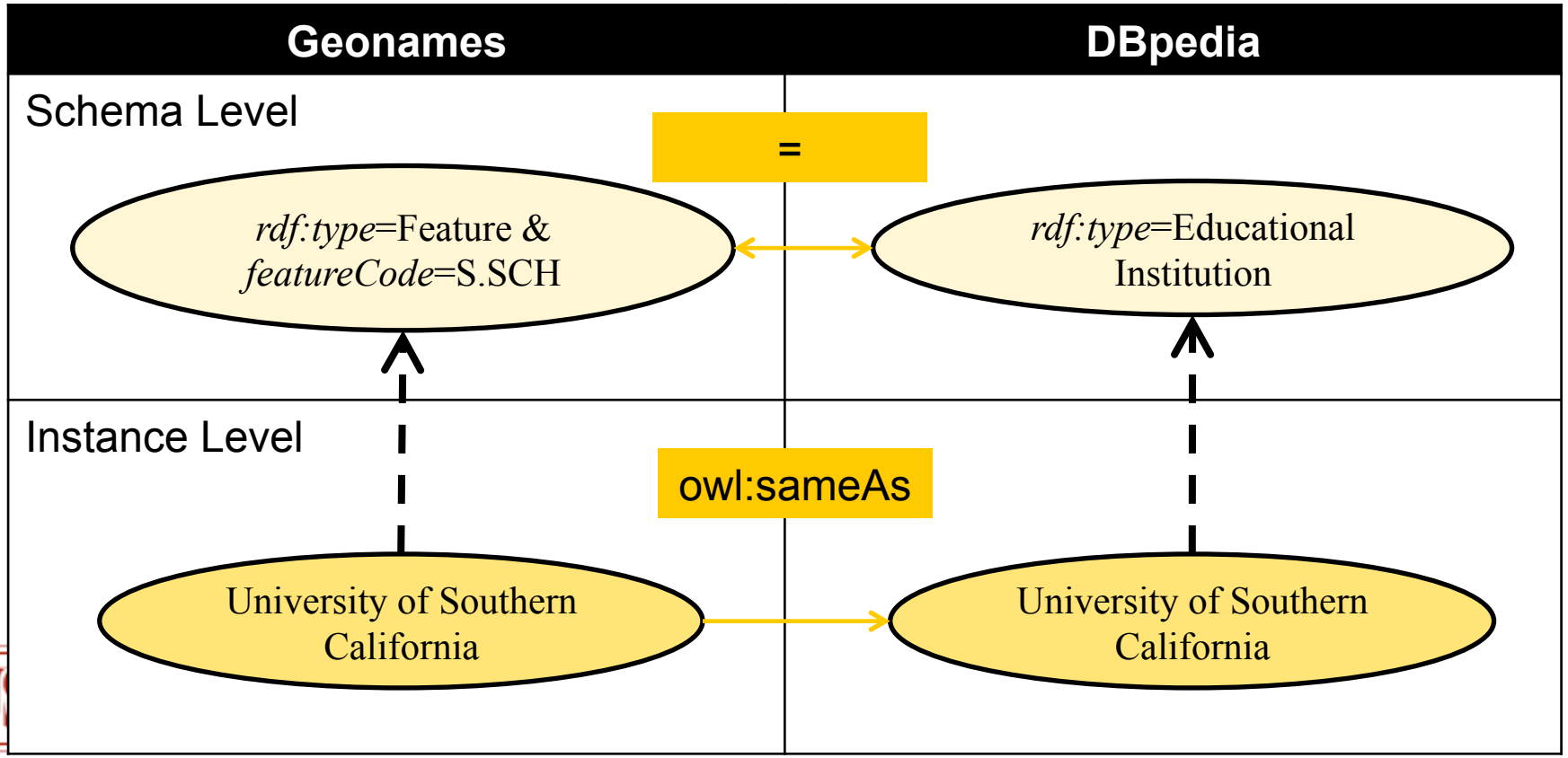
Objective 2: Find Alignments Between Restriction Classes

- Find and model specialized descriptions of classes



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Domains

- Geospatial
  - Dbpedia
  - LinkedGeoData
  - Geonames
- Zoology
  - Geospecies
  - Dbpedia
- Genetics (Bio2RDF)
  - GeneID
  - MGI

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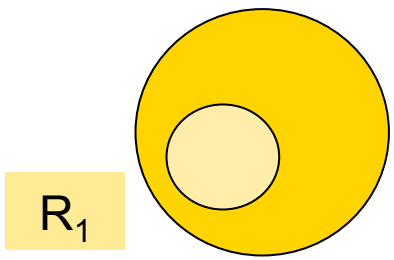
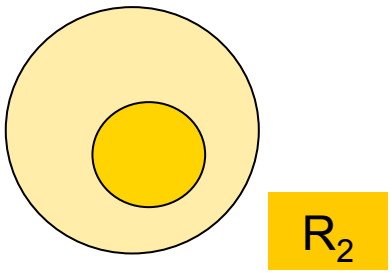
Approach

- Aligning Restriction Classes





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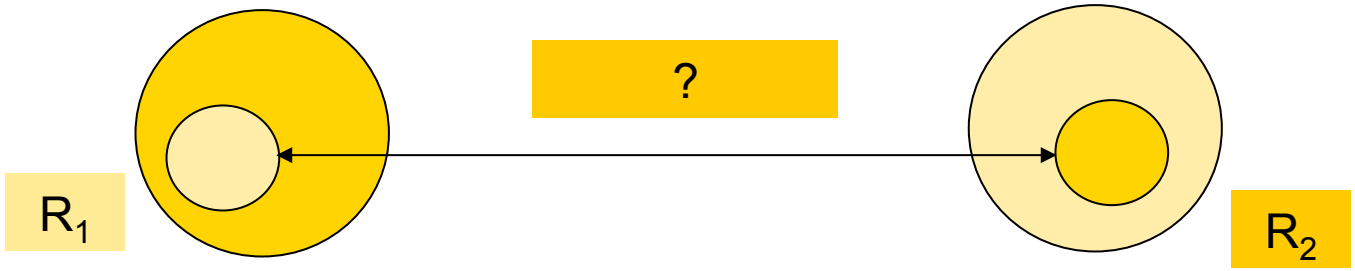
Approach

- Aligning Restriction Classes



- Find relation between the two restriction classes
  - Equivalent
  - Subset

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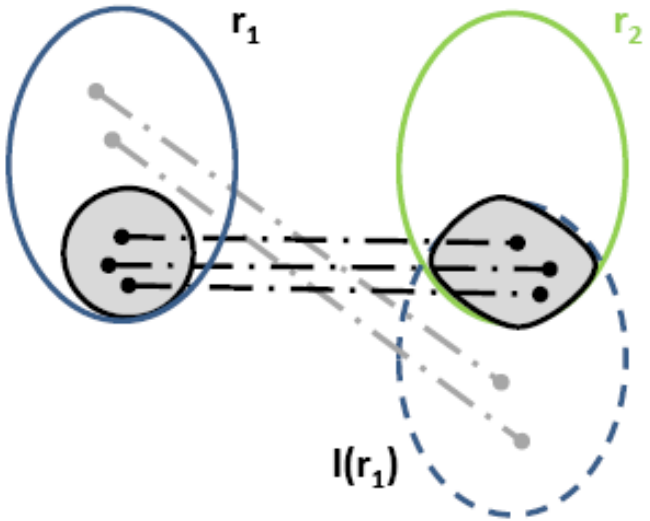
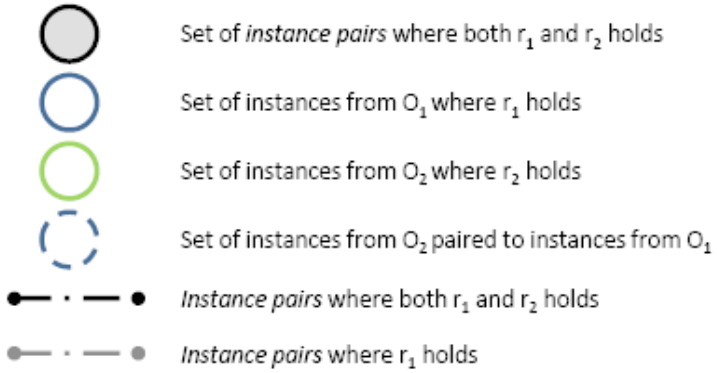
Extensional Approach to Ontology Alignment



Set Representation	Relation
	Disjoint
	$r_1 \subset r_2$
	$r_2 \subset r_1$
	$r_1 = r_2$
	Not enough support

Key:



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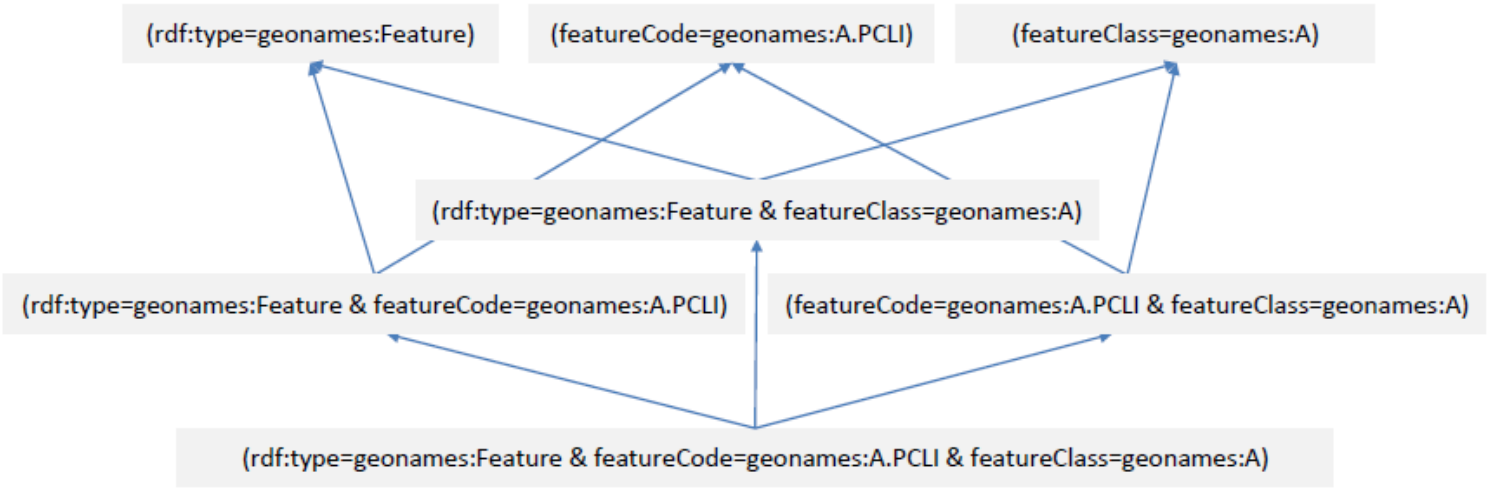
Lattice of Restriction Classes

- Instances belonging to a restriction class also belong to parent restriction class
  - e.g. restrictions from Geonames below



- This also results in a hierarchy in the alignments, which our algorithm exploits

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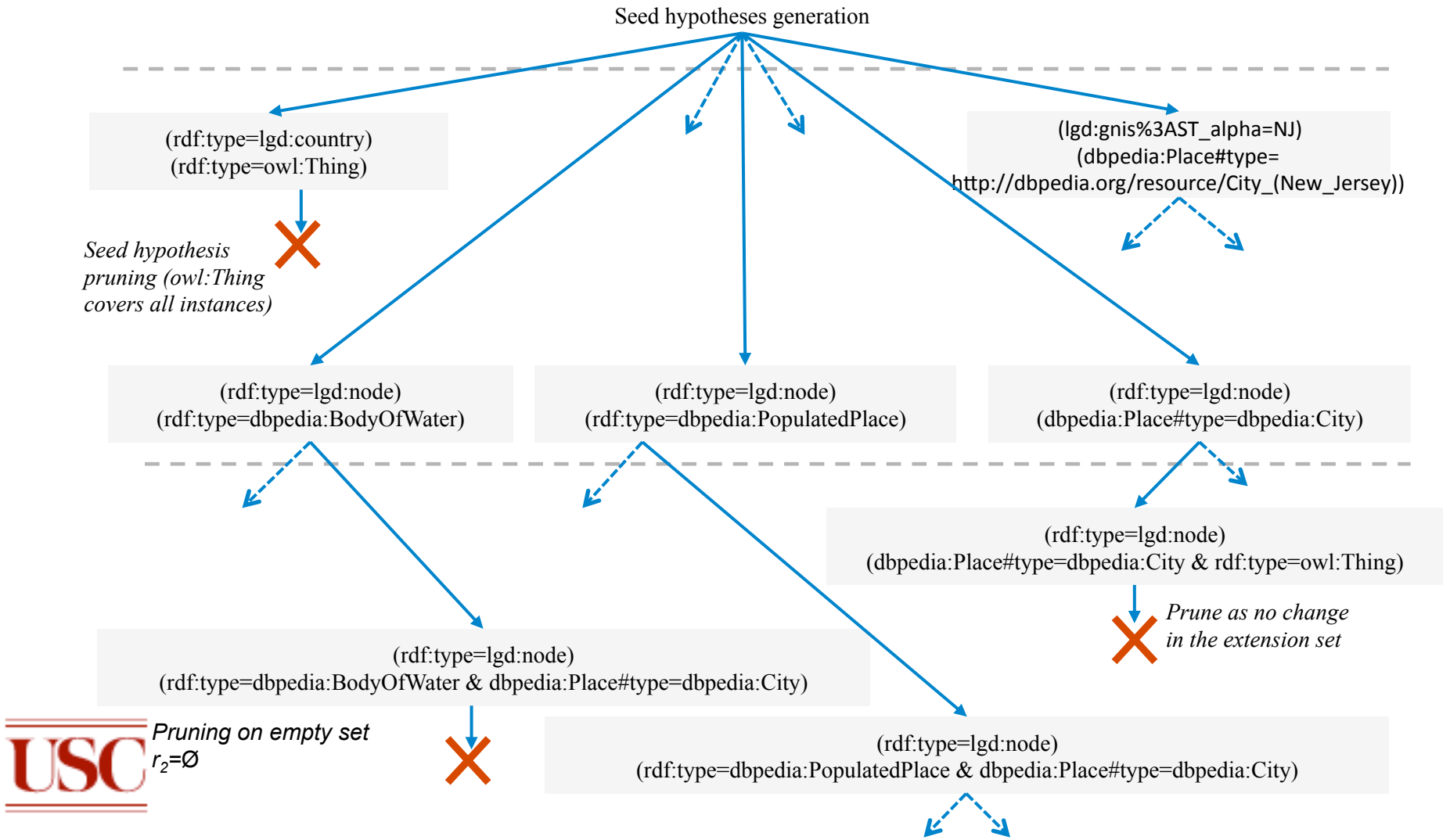
Exploration of Hypotheses Search Space (LinkedGeoData with DBpedia)



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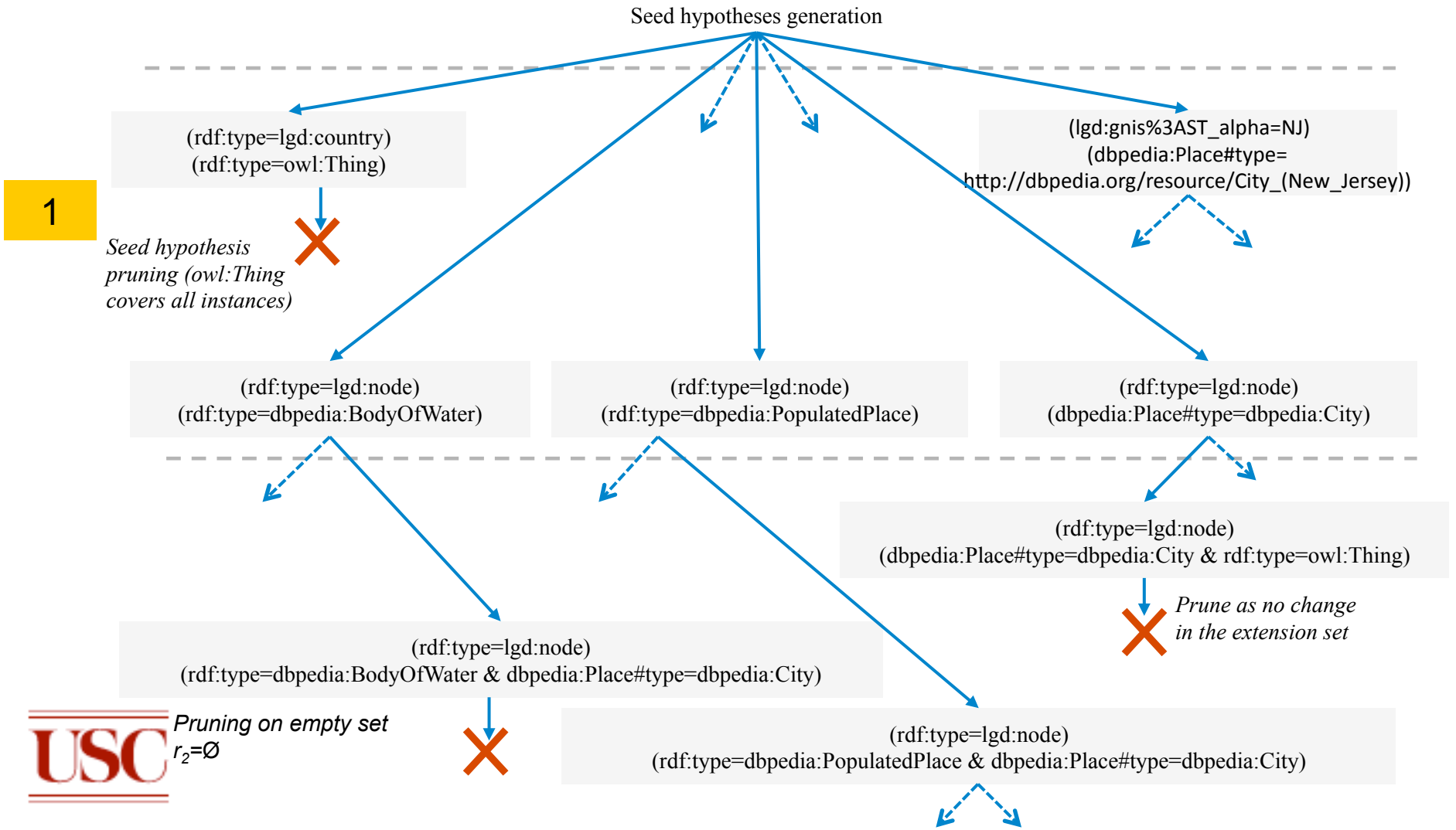
1. Prune seed hypothesis if either restriction covers all instances in that source



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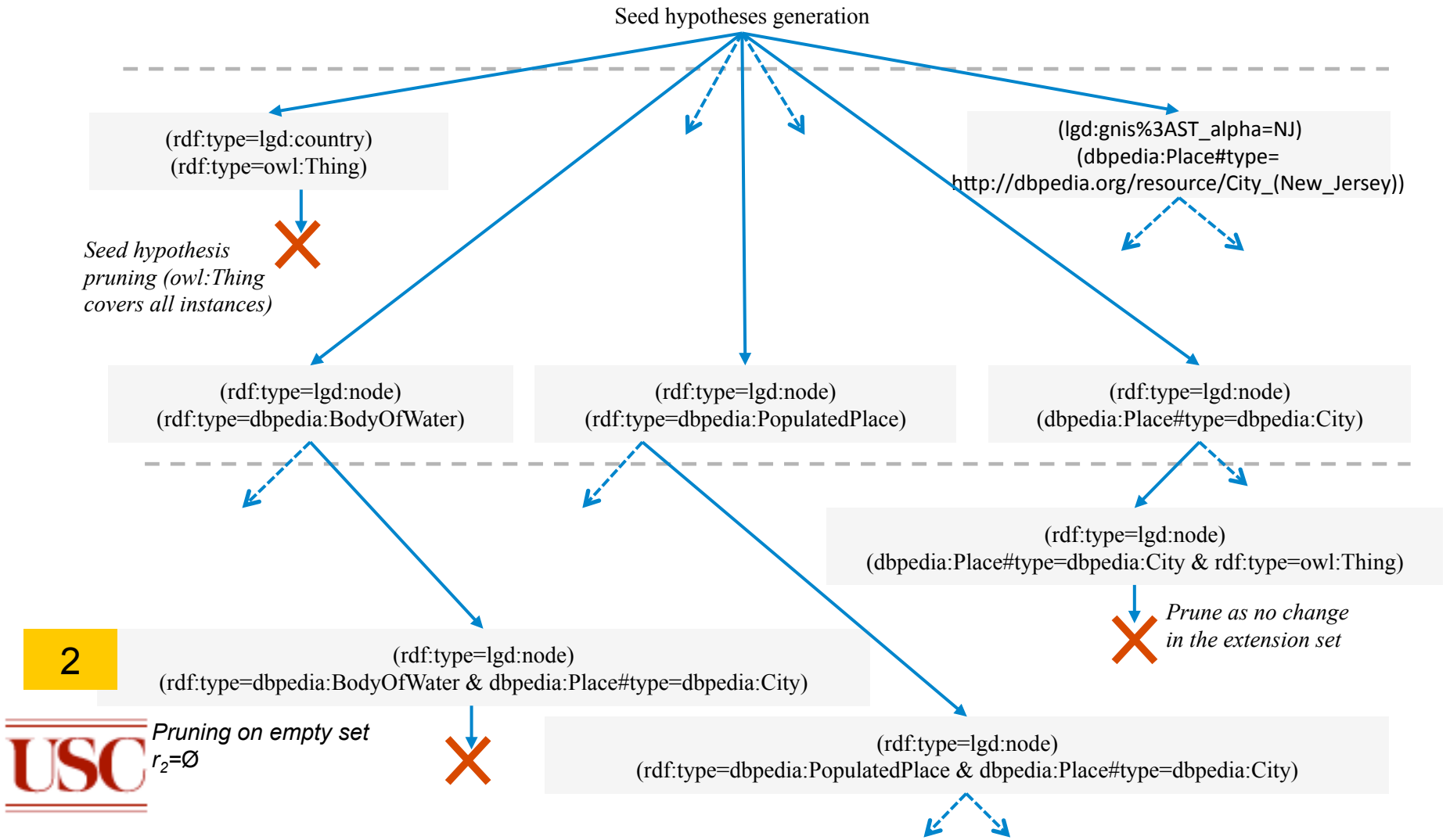
2. Number of instance pairs supporting hypothesis must be above a threshold



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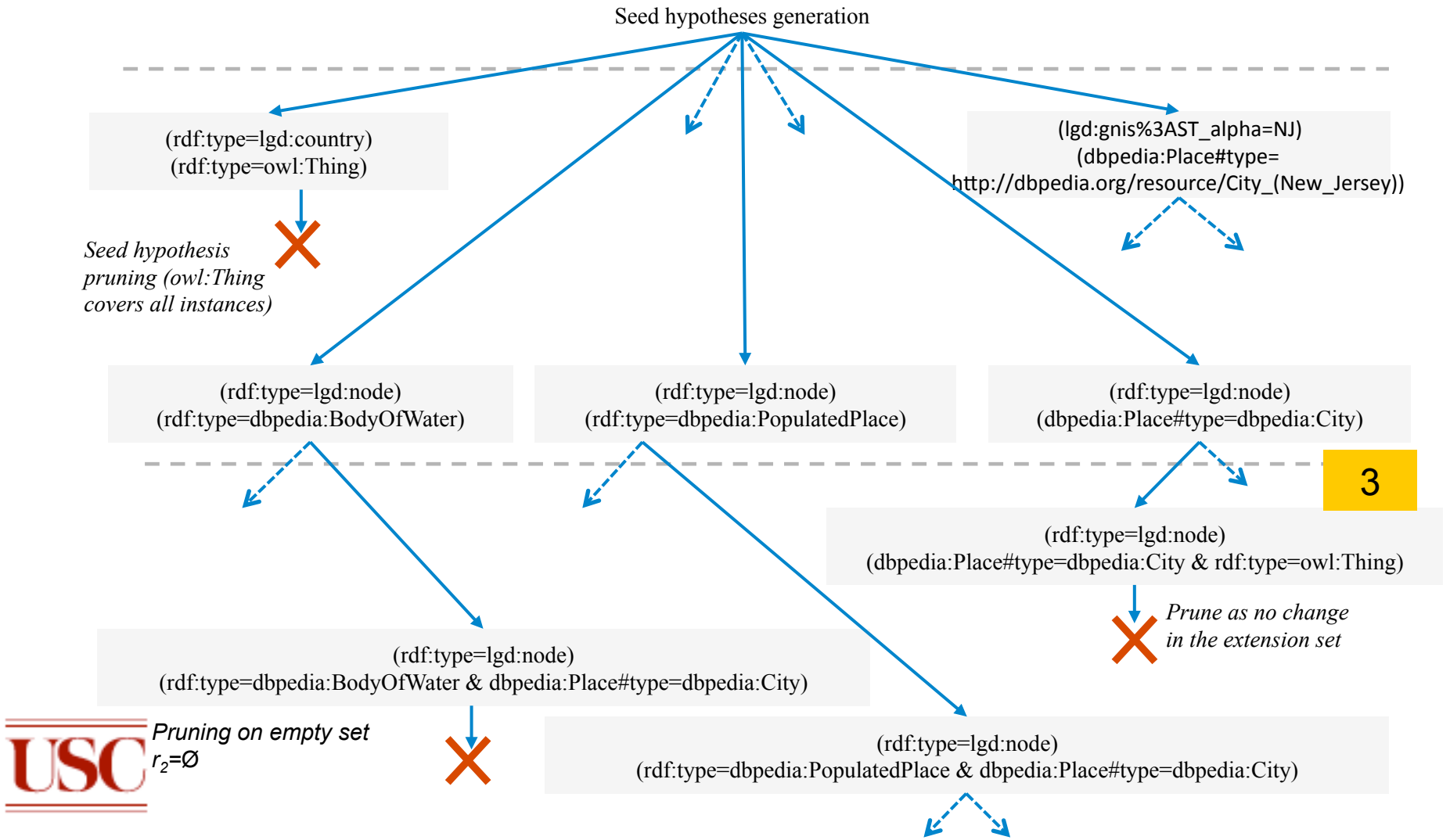
3. Prune if the added constraint does not change the extension



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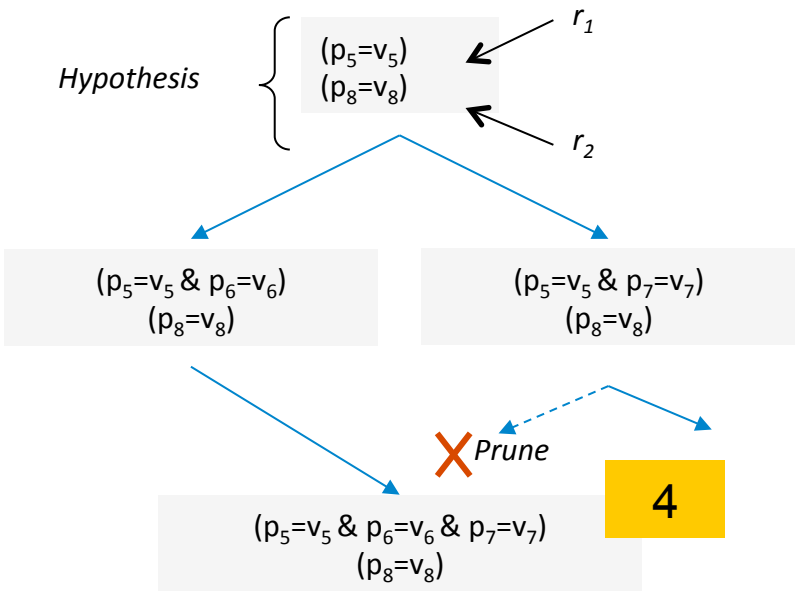
4. Lexicographic ordering

Lexicographic ordering provides a systematic search by pruning hypotheses with reverse order



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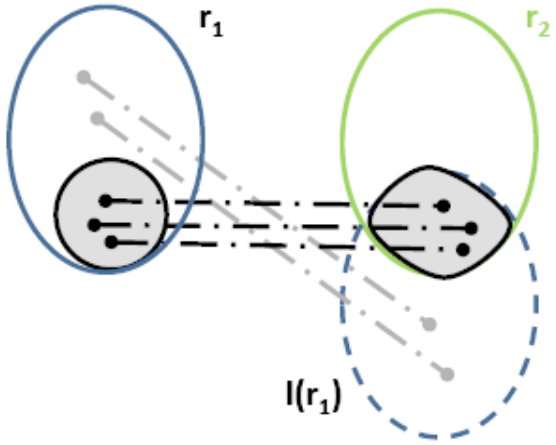
Relaxed Scoring



Set Representation	Relation	$P = \frac{\lvert I(r_1) \cap r_2 \rvert}{\lvert r_2 \rvert}$	$R = \frac{\lvert I(r_1) \cap r_2 \rvert}{\lvert r_1 \rvert}$	P′	R′
	Disjoint	= 0	= 0	≤ 0.01	≤ 0.01
	$r_1 \subset r_2$	< 1	= 1	> 0.01	≥ 0.90
	$r_2 \subset r_1$	= 1	< 1	≥ 0.90	> 0.01
	$r_1 = r_2$	= 1	= 1	≥ 0.90	≥ 0.90
	Not enough support	0 < P < 1	0 < R < 1	0.01 < P′ < 0.90	0.01 < R′ < 0.90

- Compensates for missing, inconsistent in the data

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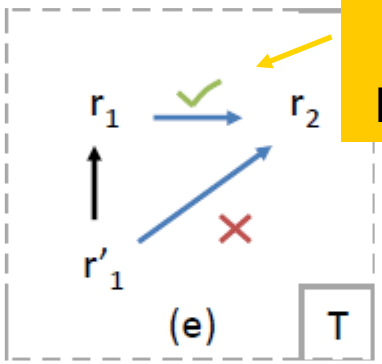
Post-processing: Removing Implied Alignments

GEONAMES *restriction*	DBPEDIA *restriction*
geonames:featureCode=geonames:S.SCH	rdf:type=dbpedia:EducationalInstitution
geonames:featureCode=geonames:S.SCH & geonames:inCountry=geonames:US	rdf:type=dbpedia:EducationalInstitution



Keep the simpler definition
&
Remove the implied definition

Key:
$r_i \rightarrow r_j$: Subset relations ($r_i \subset r_j$) found by the algorithm.
$r_i \dashrightarrow r_j$: Implied subset relations.
$r'_i \rightarrow r_j$: Subset relation by construction.
T: Transitivity in subset relations. One relation can be eliminated.
C: Cycle in subset relations. Hence, all classes are equivalent.
✕ : Relation eliminated by the rule.
✓ : Relation retained by the rule.

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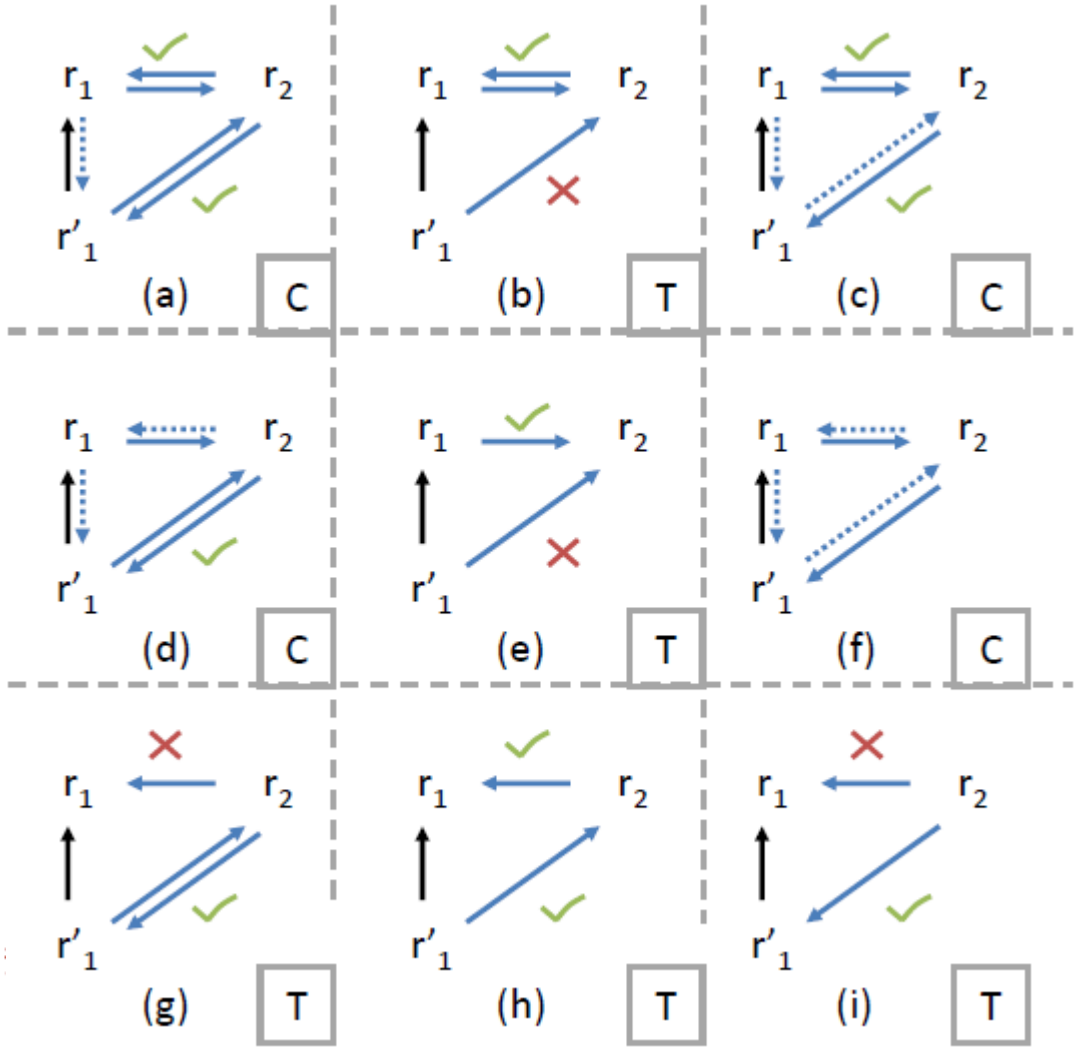
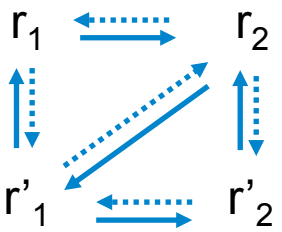
Removing Implied Alignments





Cascading

Key:

$r_i \longrightarrow r_j$: Subset relations ($r_i \subset r_j$) found by the algorithm.

$r_i \dashrightarrow r_j$: Implied subset relations.

$r'_i \longrightarrow r_j$: Subset relation by construction.

T: Transitivity in subset relations. One relation can be eliminated.

C: Cycle in subset relations. Hence, all classes are equivalent.

✗ : Relation eliminated by the rule.

✓ : Relation retained by the rule.

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Results: Geospatial Domain

#	LinkedGeoData *restriction*	DBpedia *restriction*	Relation
1	rdf:type=lgd:node	rdf:type=owl:Thing	$r_1 = r_2$
2	rdf:type=lgd:aerodrome	rdf:type=dbpedia:Airport	$r_1 = r_2$
3	rdf:type=lgd:island	rdf:type=dbpedia:Island	$r_1 = r_2$
4	lgd:gnis_%3AST_alpha=NJ	dbpedia:Place#type= http://dbpedia.org/resource/City_(New_Jersey)	$r_1 = r_2$
5	rdf:type=lgd:village	rdf:type=dbpedia:PopulatedPlace	$r_1 \subset r_2$
#	Geonames *restriction*	DBpedia *restriction*	Relation
6	geonames:featureClass=geonames:P	rdf:type=dbpedia:PpopulatedPlace	$r_1 = r_2$
7	geonames:featureClass=geonames:H	rdf:type=dbpedia:BodyOfWater	$r_1 = r_2$
8	geonames:parentFeature=http://sws.geonames.org/3174618/	dbpedia:City_region=http://dbpedia.org/resource/Lombardy	$r_1 = r_2$
9	geonames:featureCode=geonames:S.SCH	rdf:type=dbpedia:EducationalInstitution	$r_1 = r_2$
10	geonames:featureCode=geonames:S.SCH & geonames:inCountry=geonames:US	rdf:type=dbpedia:EducationalInstitution	$r_1 = r_2$
11	geonames:featureCode=geonames:T.MT	rdf:type=dbpedia:Mountain	$r_1 \subset r_2$

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Results: Zoology Domain

#	GEOSPECIES *restriction*	DBPEDIA *restriction*	Relation
12	geospecies:inKingdom=http://lod.geospecies.org/kingdoms/Aa	rdf:type=dbpedia:Animal	$r_1 = r_2$
13	geospecies:hasOrderName=Lepidoptera	dbpedia:order=http://dbpedia.org/resource/Lepidoptera	$r_1 = r_2$
14	geospecies:hasOrderName=Lepidoptera	dbpedia:kingdom=http://dbpedia.org/resource/Animal & dbpedia:order=http://dbpedia.org/resource/Lepidoptera	$r_1 = r_2$
15	geospecies:hasGenusName=Falco	dbpedia:genus=http://dbpedia.org/resource/Falcon	$r_1 = r_2$
16	geospecies:hasOrderName=Primates	dbpedia:order=http://dbpedia.org/resource/Primates	$r_2 \subset r_1$

#	GEOSPECIES *restriction*	GEOSPECIES *restriction*	Relation
20	geospecies:hasKingdomName=Animalia	geospecies:inKingdom=http://lod.geospecies.org/kingdoms/Aa	$r_1 = r_2$
21	geospecies:hasClassName=Insecta	geospecies:inClass= http://lod.geospecies.org/bioclasses/aQado	$r_1 \subset r_2$
22	geospecies:inFamily= http://lod.geospecies.org/families/amTJ9	geospecies:hasSubfamilyName=Sigmodontinae	$r_2 \subset r_1$

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Results: Genetics Domain

#	MGI *restriction*	GENEID *restriction*	Relation
17	bio2rdf:subType=Pseudogene	bio2rdf:subType=pseudo	$r_1 = r_2$
18	bio2rdf:subType=Pseudogene & mgi:genomeStart=17	geneid:chromosome=17 & bio2rdf:subType=pseudo	$r_1 = r_2$
19	bio2rdf:chromosomePosition=-1.00 & mgi:genomeStart=4	geneid:chromosome=4 & bio2rdf:subType=pseudo	$r_2 \subset r_1$

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Results: Alignments Found

- Equivalences, Subset alignments before and after removing implied alignments

Source 1 (O_1)	Source 2 (O_2)	$\#(r_1 = r_2)$ total	$\#(r_1 = r_2)$ best matches	$\#(r_1 \subset r_2)$ before	$\#(r_1 \subset r_2)$ after	$\#(r_2 \subset r_1)$ before	$\#(r_2 \subset r_1)$ after
LinkedGeoData	DBpedia	158	152	2528	1837	1804	1627
Geonames	DBpedia	31	19	809	400	1384	1247
Geospecies	DBpedia	509	420	9112	2294	6098	4455
MGI	GeneID	10	9	2031	1869	3594	2070
Geospecies	Geospecies	94	88	1550	1201	-	-

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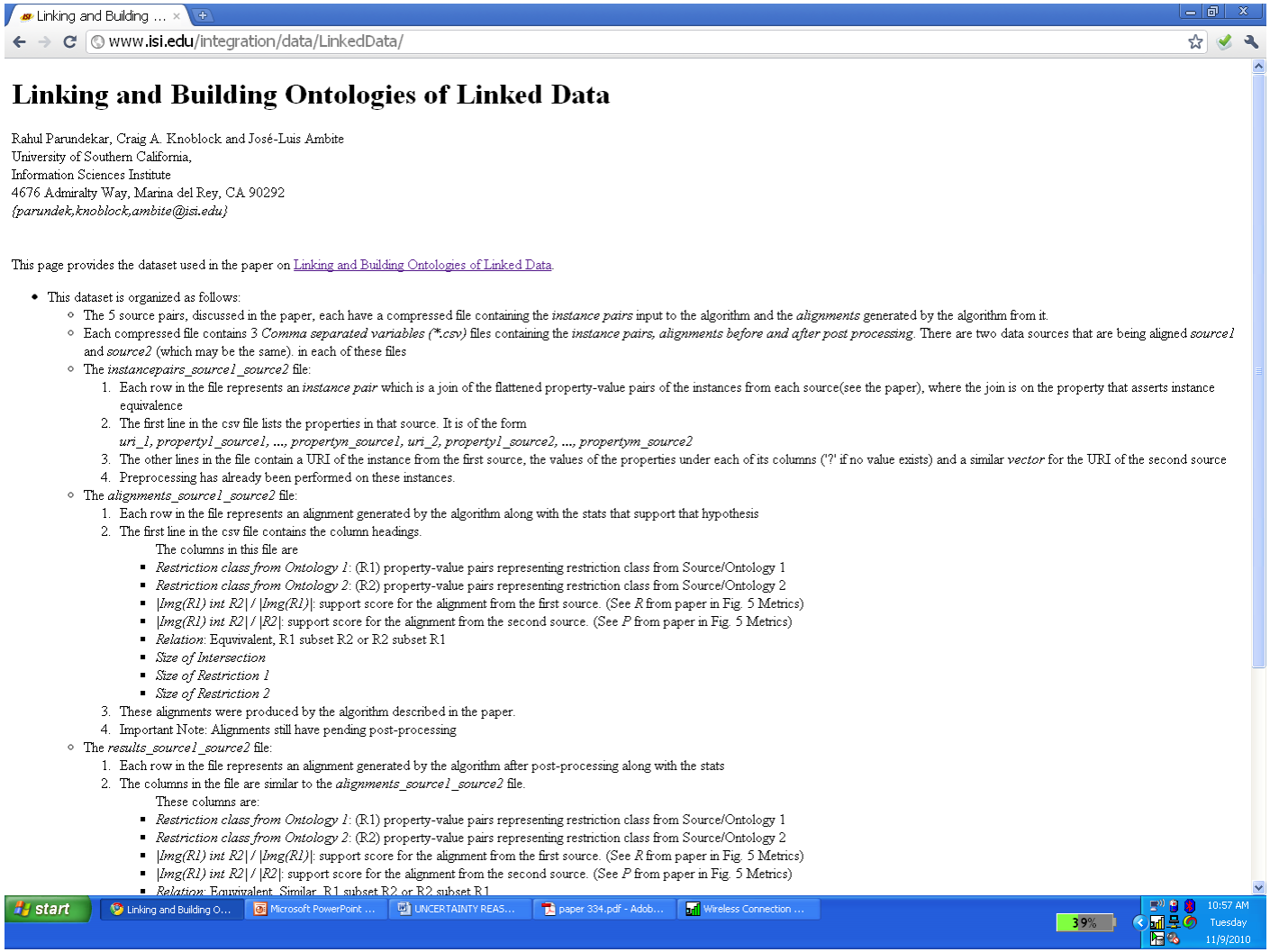
Datasets: http://www.isi.edu/integration/data/LinkedData



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Related Work

- Euzenat et al. – Ontology Matching
  - Terminological
  - Structural
  - Semantic
- FCA-Merge, Duckham et al.
  - Use extensional techniques
- GLUE
  - Uses an extensional technique after performing machine learning operations

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Conclusion

- Our algorithm generates alignments, consisting of conjunctions of restriction classes
  - Extensional approach on Linked Data
  - Use of restriction classes
- Alignments based on the actual data
  - We determine the relationships based on the data
  - Schemas of linked sources can be readily modeled and used
- Algorithm also able to
  - Specialize ontologies where original were rudimentary
  - Find complimentary hierarchy across an ontology

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Future Work

- How to actually understand these alignments

#	MGI *restriction*	GENEID *restriction*	Relation
17	bio2rdf:subType=Pseudogene	bio2rdf:subType=pseudo	$r_1 = r_2$
18	bio2rdf:subType=Pseudogene & mgi:genomeStart=17	geneid:chromosome=17 & bio2rdf:subType=pseudo	$r_1 = r_2$
19	bio2rdf:chromosomePosition=-1.00 & mgi:genomeStart=4	geneid:chromosome=4 & bio2rdf:subType=pseudo	$r_2 \subset r_1$

- Scalability
  - Pre-procesing of the sources
  - Faster alignment processing

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