

Realizing OBDA with data dependencies

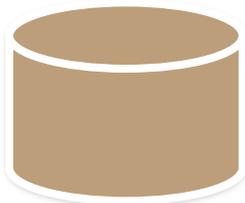
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ABOX CONSTRAINTS

Enforcing dependencies a.k.a completing the data

Enforcing dependencies



Manipulate the data

Inference materialization

Forward chaining (Sesame, OWLim, etc.)

**Not the only way,
often, not the best way**

Man subClass

$\equiv_{\mathcal{A}}$ Human

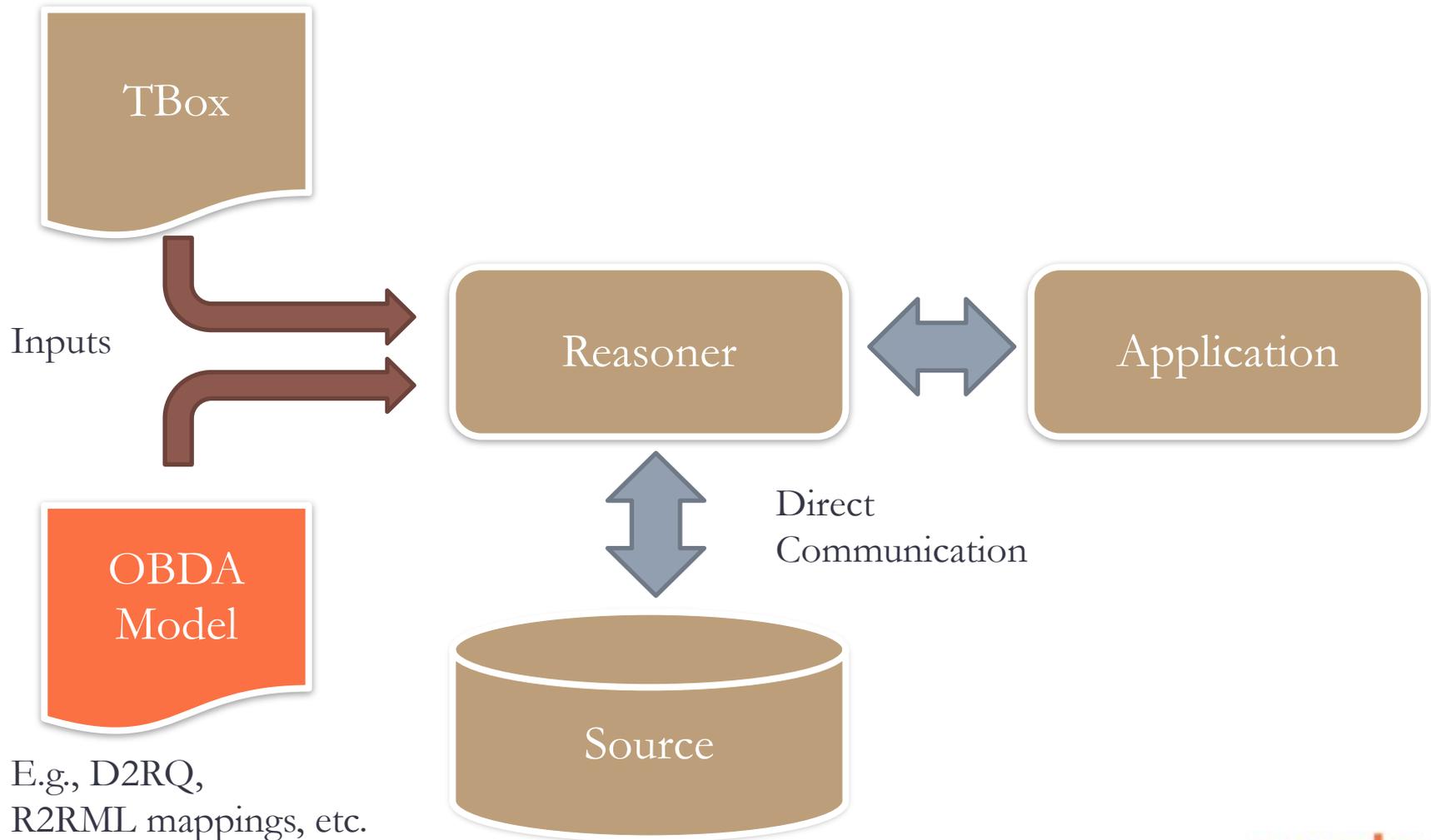
`inverseOf(hasParent, hasChild)`

John hasParent Mary

Mary hasChild John

$hasParent \equiv_{\mathcal{A}} hasChild$

Case I: Virtual RDF Graphs



T-Mappings

- Manipulate the mappings to enforce the semantics of T
- if $\mathcal{T} \models A \sqsubseteq B$ ensure that the mapping(s) for B include the data from the mappings for A

T-Mappings

- Manipulate the mappings to enforce the semantics of T
- if $\mathcal{T} \models A \sqsubseteq B$ ensure that the mapping(s) for B include the data from the mappings for A

SELECT id FROM t WHERE a = 'a' \rightsquigarrow ?id rdf:type A

SELECT id FROM t WHERE a = 'b' \rightsquigarrow ?id rdf:type B

SELECT id FROM t \rightsquigarrow ?id rdf:type B

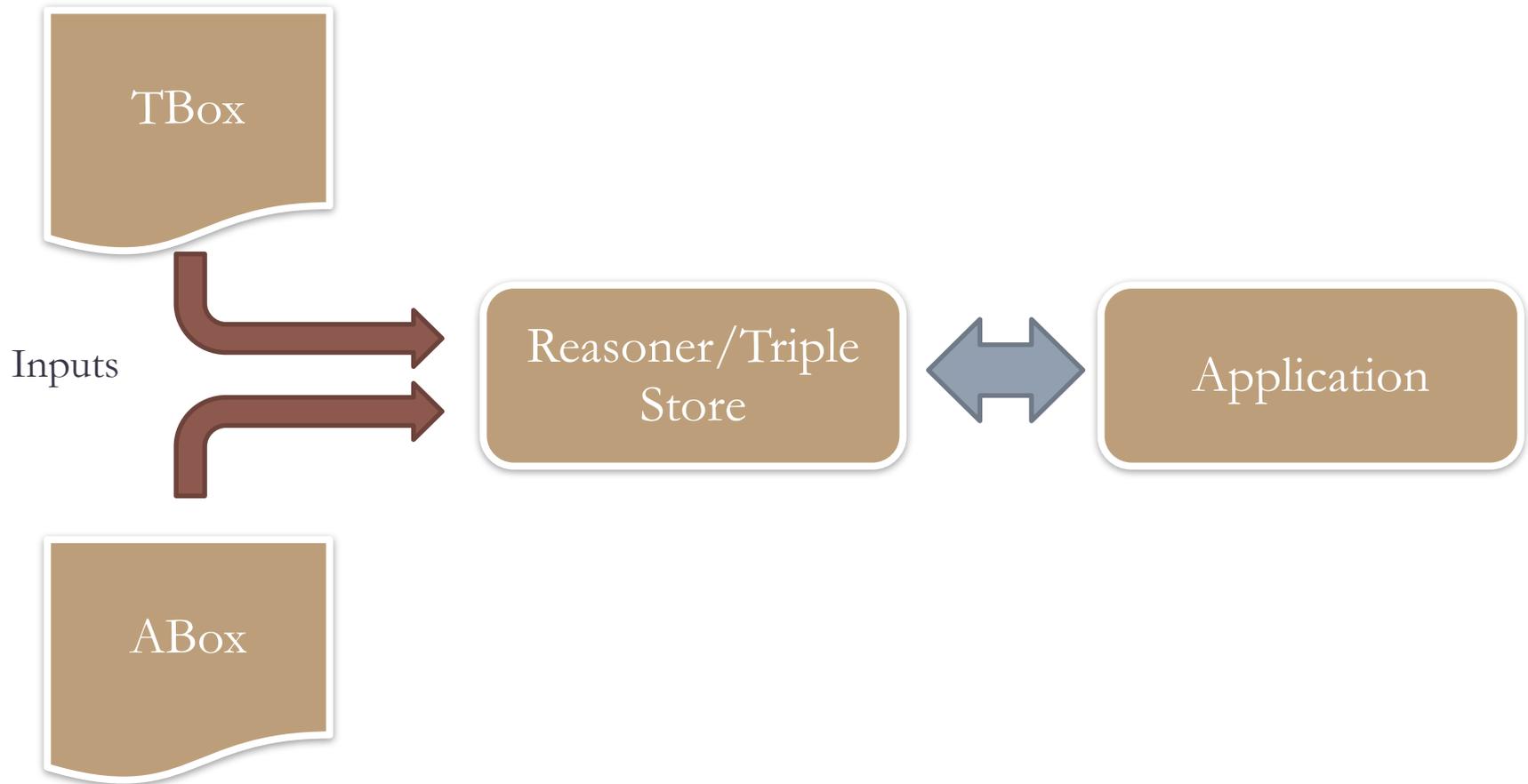
WHERE a = 'b' OR a = 'a'

- Use 'completed' mappings for query translation
- Enough for OWL2QL except: $A \sqsubseteq \exists R$

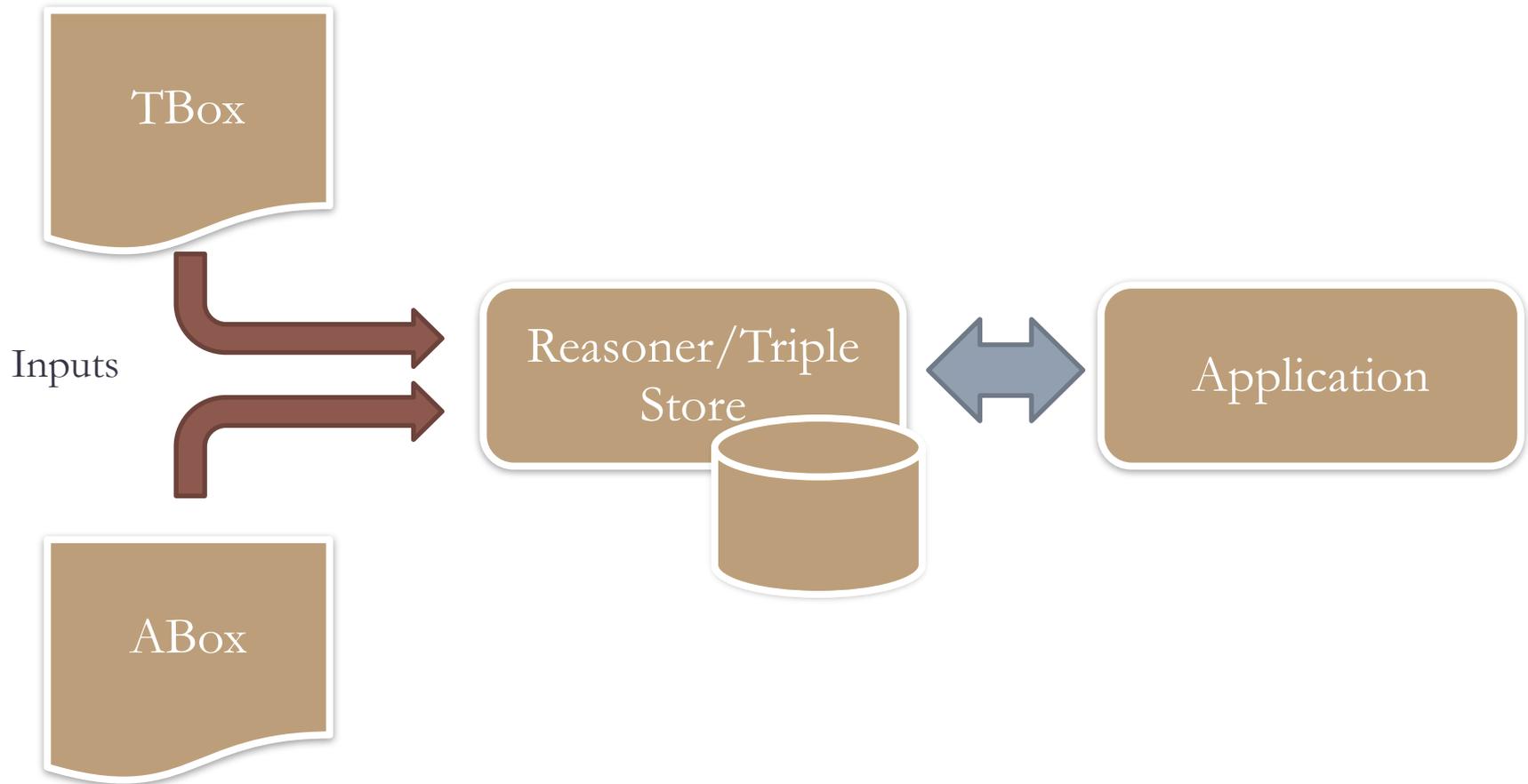
T-Mappings

- Things to care about (for SQL data sources):
 - SQL structure (no sub-queries, no large SQL, 'natural SQL')
 - Redundant JOINS
 - Impedance mismatch: URI's and RDF/OWL datatypes, not SQL types
- Available tools:
 - Partial evaluation
 - Static analysis of SQL (for mappings) and SPARQL (for queries)
- Results in the next slides

Case II: Reasoners/Triple stores



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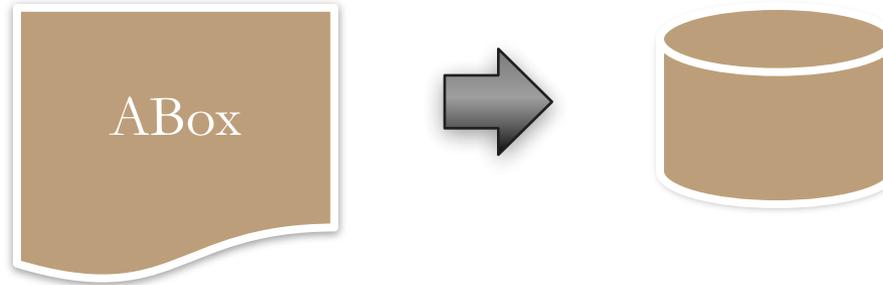
```
SELECT ?x ?z WHERE { ?x foaf ?z }
```

```
SELECT s as x, o as z  
FROM triple WHERE p = 'foaf'
```

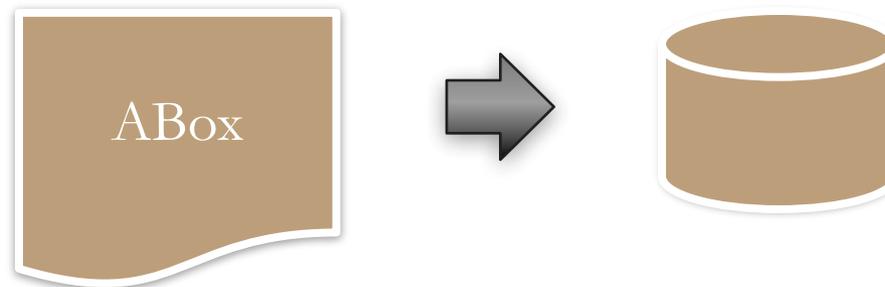
```
SELECT s as x, o as z  
FROM triple WHERE p = 227
```

```
SELECT s as x, o as z  
FROM foaf
```

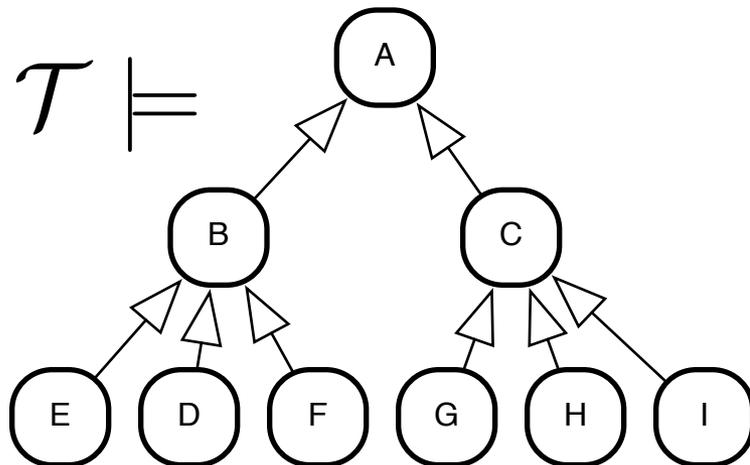
Creating semantic triple storage



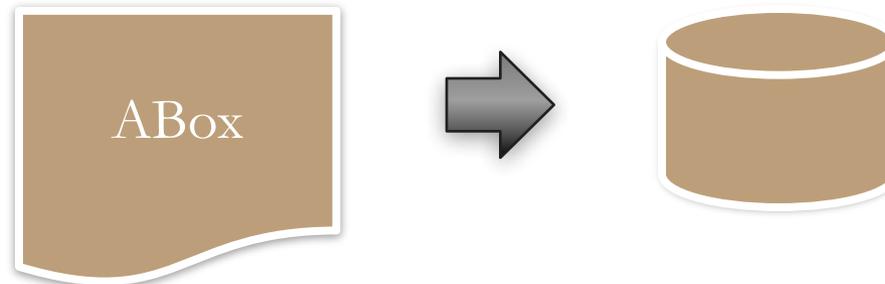
Creating semantic triple storage



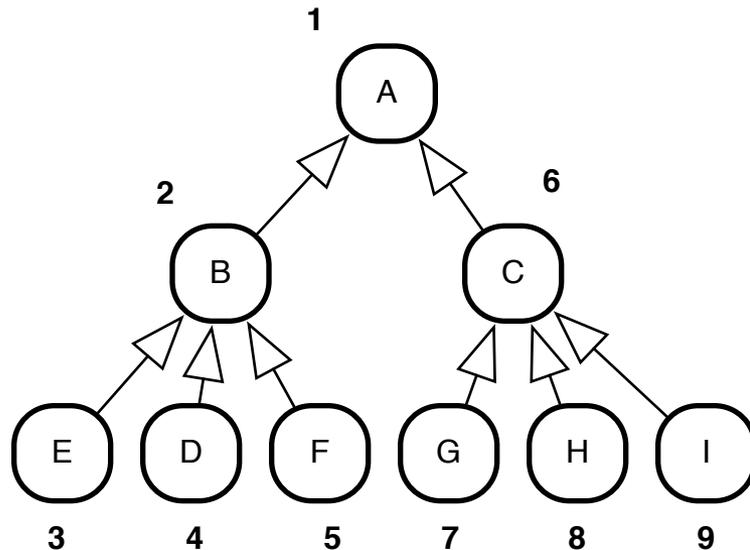
1. Encode the hierarchies of \mathcal{T} in indexes



Creating semantic triple storage



1. Encode the hierarchies of T in **indexes**



ABox:

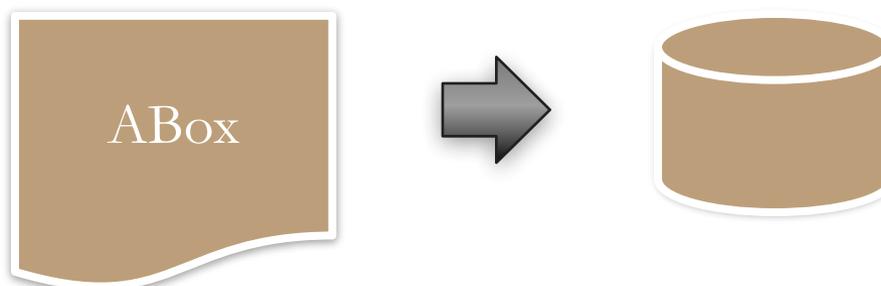
d **rdf:type** **D**

h **rdf:type** **H**

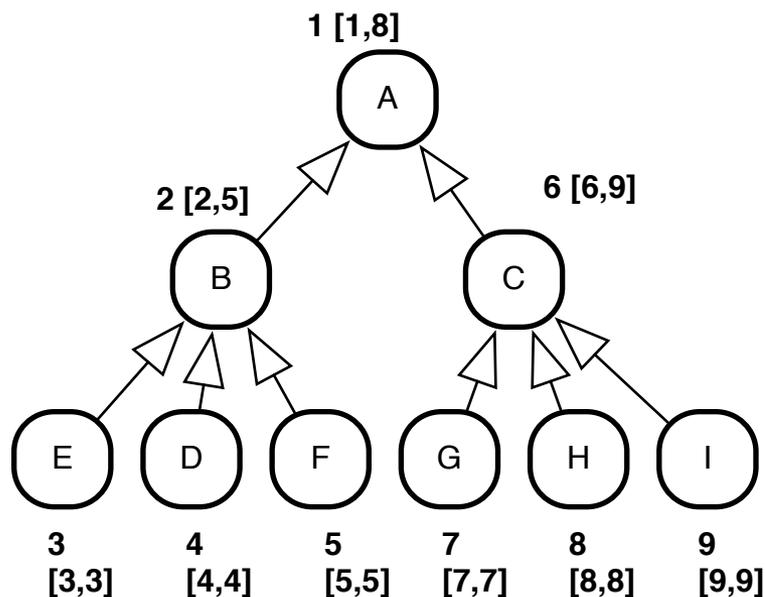
Insert into your data structure using those indexes

s	p	o
d	rdf:type	4
h	rdf:type	8

Creating semantic triple storage



3. Define **intervals** to retrieve your data



4. Create mappings using those intervals



```
?s rdf:type A
SELECT s FROM t WHERE IDX >= 1 AND
                        IDX <= 8
```

5. Complement with **T-mappings** to cover domain, range and inverse inferences

EXPERIMENTS-BENCHS

Query rewriting with Semantic Indexes

Experiments - LUBM

- LUBM3X-Lite - Larger LUBM in OWL 2 QL fragment
- 14 original LUBM queries
- Consumer hardware (Macbook Pro)
- 50 Universities
 - 6,863,227 data triples (ABox assertions)
- Systems tested:
 - Quest - (Over PostgreSQL)
 - Sesame
 - Requiem
 - OwlGres
 - Presto
- Measures: Rewriting size/complexity, Loading time, Execution

Experiments - LUBM - Rewriting

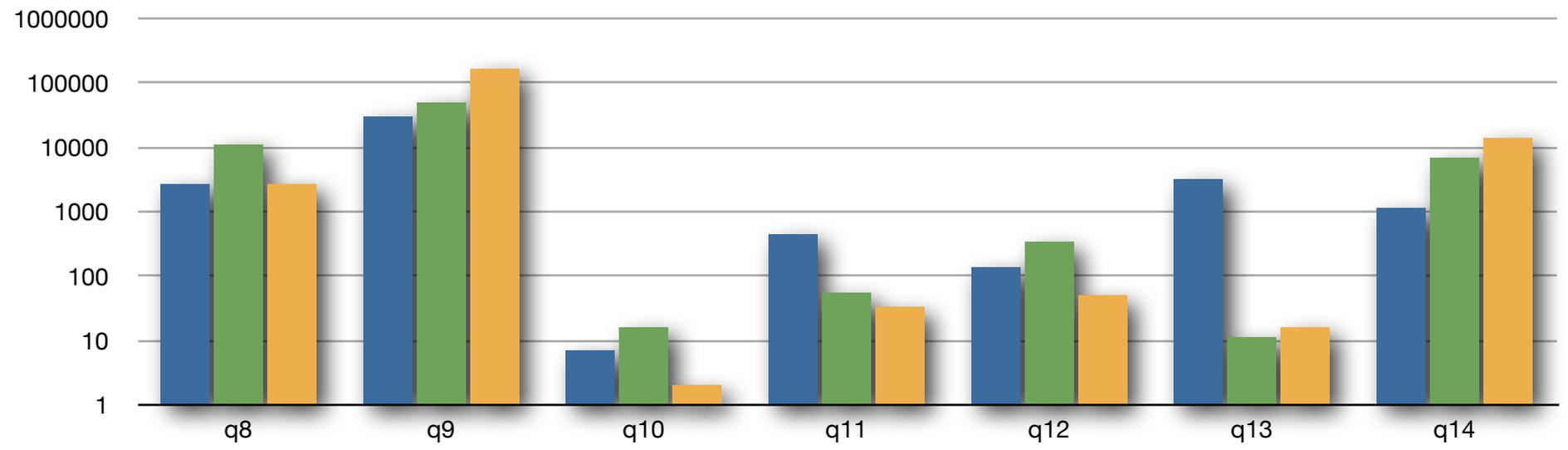
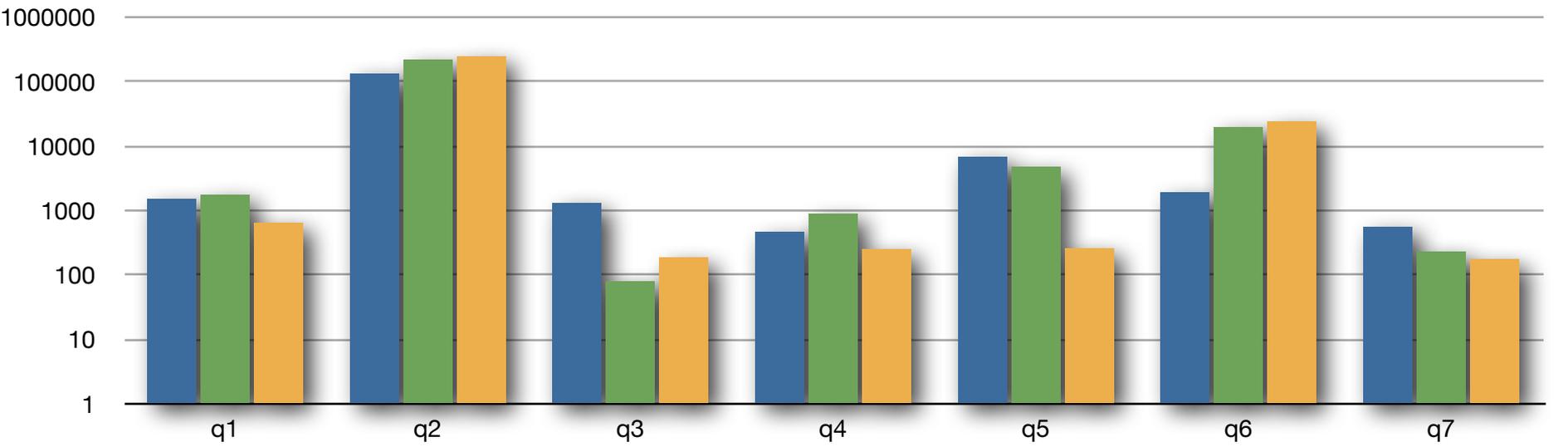
Q	Qs(b)	Qs(f)	Rq(n)	Rq(g)	Pr(d)	Pr(c)
1	9	1	42	3	4	3
2	17496	1	17496	972	22	729
3	153	1	150	3	4	3
4	162	1	1356	27	28	27
5	1476	1	5322	69	67	66
6	12	1	12	12	13	12
7	1620	1	1512	108	19	108
8	3888	1	1296	1296	31	2916
9	-	1	-	-	22	324
10	36	1	111	12	13	12
11	18	1	18	18	10	18
12	162	1	162	162	16	162
13	1845	1	1560	15	16	15
14	3	1	3	3	4	3

Table 2: Reformulation size (# CQs/Rules), smallest in bold

Experiments - LUBM - Loading

- Time required to load and process all triples
 - Jena: 5 hrs timeout
 - Sesame: 2 hrs 20 m
 - Owlgres: 1 hr 25 m
 - Quest: 104 s

Execution Time (ms)



■ Quest ■ Owlgres ■ Sesame



Experiments - Resource Index

- Experimentation using Stanford's “**Resource Index**”
- **Semantic search** over **annotated documents**
- 200 ontologies from Bio-portal (only hierarchies 200k concepts, millions of subClassOf)



A screenshot of the Stanford Resource Index search interface. At the top, there is a search bar with a 'View Demo' link to its right. Below the search bar is a 'Search' button and a 'Clear' button. A light blue box contains instructions: 'To begin, type in text and select a matching term. Examples: melanoma, lupus, breast cancer, ... Click search and select a repository.' Below this is the 'Ontology filters' section, which displays a grid of 20 different biological resources. Each resource is represented by a small icon, a numerical count, and the resource name. The resources are arranged in two columns. The first column includes ARKS GoldMiner (1155), ArrayExpress (28343), ClinicalTrials.gov (122591), Database of Genotypes and Phenotypes (269), Gene Expression Omnibus DataSets (31483), Online Mendelian Inheritance in Man (22186), PharmGKB [Disease] (837), PharmGKB [Gene] (1242), PubMed (1158025), ResearchCrossroads (1033651), UniProt KB (533515), and caNameLab (894). The second column includes Adverse Event Reporting System Data (1172883), BioStemmaps (2434), Conserved Domain Database (CDD) (46346), DrugBank (4774), HGAD (823), Pathway Commons (2323), PharmGKB [Drug] (1643), PubChem (121349), Reactome (208093), Stanford Microarray Database (18838), and WikiPathways (1721).

Experiments - Resource Index

- Current system uses **forward chaining**
 - Naive chase: 7 days
 - Optimized chase: 40 mins
 - Cost 16 GB + 70 GB chase data
 - Split second responses
- **Pure query rewriting** approaches

- **Semantic index**-based rewriting
 - DAG computation and indexing 5 mins
 - Cost: 16 GB
 - Single queries, split second responses

```
SELECT ?x WHERE {  
  ?x a DNA_Repair_Gene.  
  ?x a Antigen_Gene.  
  ?x a Cancer_Gene  
}
```

- Materialized, 3s execution time)
- Pure query rewriting: not-feasible (467k UCQs or 250 datalog rules)
- Semantic Index based rewriting, 3 s

```
SELECT DISTINCT r0.element_id as element_id  
FROM RI.CT_ANN r0  
  JOIN RI.CT_ANN r1 ON r0.element_id = r1.element_id  
  JOIN RI.CT_ANN r2 ON r1.element_id = r2.element_id  
WHERE  
  ((r0.idx >= 1783559 AND r0.idx <= 1783657)) AND  
  ((r1.idx >= 1782996 AND r1.idx <= 1783029)) AND  
  ((r2.idx >= 1783115 AND r2.idx <= 1783253));
```

EXPERIMENTS-BENCHS

Virtual RDF graphs with SPARQL

Experiments - Fish Deli (virtual graph)

- By Parsia et. al [SSWS12]
- FishBase: Fish species database, currently deployed. ETL based.
- FishMark:
 - FishBank data set 20,186,775 triples
 - 22 queries (based on queries from user logs, building a use scenario)
- Systems involved:
 - Virtuoso
 - MySQL 5.5
 - Quest 1.7 alpha (July 12)
- Measure: Queries per second (each query 100 times)
- Machine: Consumer PC (Mac mini, 2.6 GHz + 16 GB Ram)

ID	Query name	Virtuoso	Quest	MySQL
1	CommonName	132	850	1262
2	SpeciesPage	1	552	840
3	Genus	167	753	1025
4	Species	192	870	1249
5	FamilyInformation	17	572	840
6	FamilyAllfish	141	704	1113
7	FamilyNominalSpecies	161	773	1060
8	FamilyListOfPictures	50	578	742
9	CollaboratorPage	27		824
10	PicturePage	68	711	1166
11	CAAllFish	24	316	629
12	CSpeciesInformation	7	598	1009
13	CFreshwater	6	201	212
14	CIntroduced	9	303	479
15	CEndemic	13	656	985
16	CReefAssociated	4	266	378
17	CPelagic	7	337	532
18	CGameFish	9	580	845
19	CCommercial	12	556	748
20	CUsedForAquaculture	12	779	1229
21	CPotentialAquaculture	34	694	957
22	CAquariumTrade	66	815	1251

Table 4. Query results of the 22 queries in qps (queries per second)

```
SELECT * WHERE {  
    $x a :Species .  
    $x :genus "Alosa"^^xsd:string .  
    $x :species "alosa"^^xsd:string .  
    $x :isFoundInCountry ?id .  
    $countryID :countryName "algeria"^^xsd:string .  
    $countryID :factbook ?Factbook .  
    $countryID :refersToCountry ?id .  
    $id :status ?occurence .  
    $id :inFreshwater ?freshwater .  
    $id :inBrackish ?brackish .  
    $id :inSaltwater ?marine .  
    $id :importance ?importance .  
    $id :abundance ?abundance .  
    $id :abundanceRef ?abundanceRef .  
    $id :regulations ?regulations .  
    $id :regulationsRef ?regulationsRef .  
    $id :importanceRef ?importanceRef .  
    $id :comments ?comments .  
}
```

```

SELECT
  4 AS "freshwaterQuestType", " AS "freshwaterLang", QVIEW1.`Freshwater` AS `freshwater`,
  4 AS "marineQuestType", " AS "marineLang", QVIEW1.`Saltwater` AS `marine`,
  4 AS "brackishQuestType", " AS "brackishLang", QVIEW1.`Brackish` AS `brackish`,
  ...
  3 AS "commentsQuestType", " AS "commentsLang", QVIEW1.`Comments` AS `comments`
FROM
  `species` QVIEW0,
  `country` QVIEW1,
  `countref` QVIEW2
WHERE
  (QVIEW1.`C_Code` = QVIEW2.`C_Code`)
  AND (QVIEW0.`SpecCode` = QVIEW1.`SpecCode`)
  AND (QVIEW0.`Genus` = 'Alosa')
  AND (QVIEW0.`Species` = 'alosa')
  AND (QVIEW2.`PAESE` = 'algeria')

```

CONCLUSIONS

Conclusions

- Introduced **ABox dependencies** to describe the structure of data
- Showed how to **optimize TBoxes w.r.t. dependencies**,
- Introduced “**Semantic Index**” repositories
- Introduced “**T-Mappings**” for mapping processing
- Not detailed:
 - How to translate from SPARQL-SQL for query rewriting
 - How to generate efficient SQL (partial evaluation)
 - How to optimize efficiently with static analysis
 - How to deal with impedance mismatch

Conclusions

- Query answering by query rewriting can be done efficiently
- Current prototypes outperform well established commercial systems
 - See **-ontop-** and **Quest**
 - <http://obda.inf.unibz.it/protege-plugin/>

- Further developments in:

Optique™



THANK YOU
