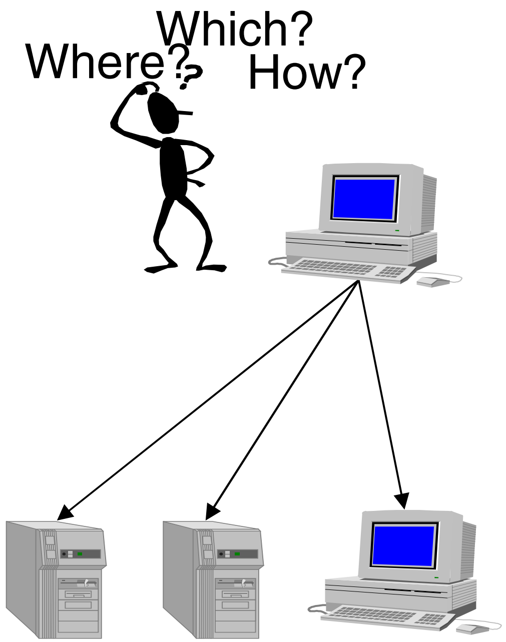
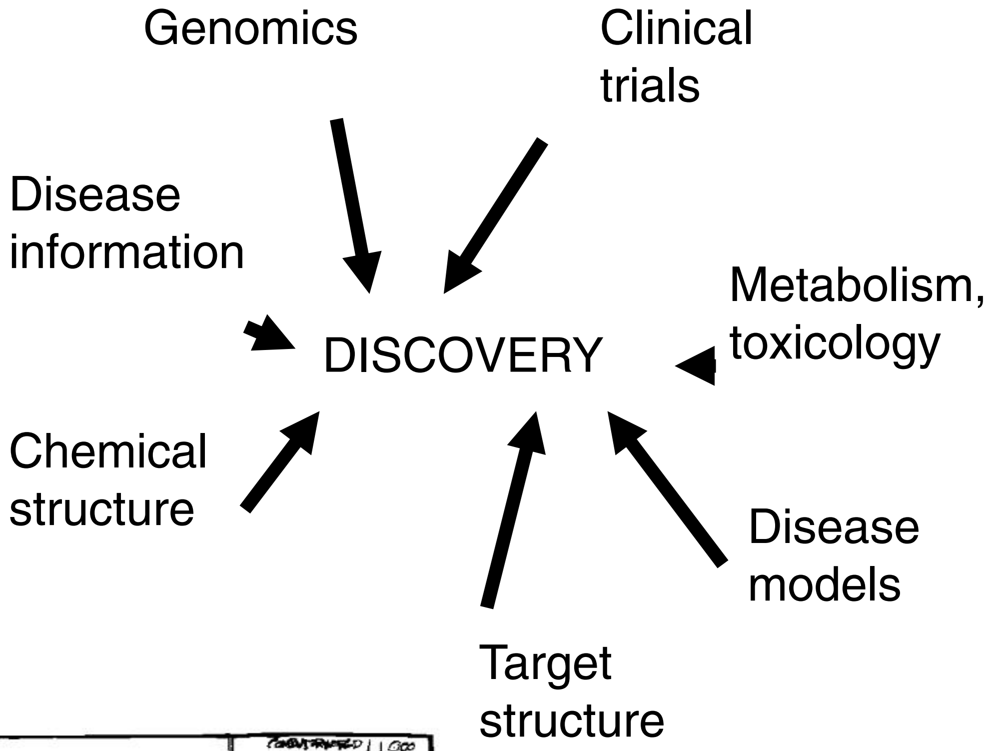
Integration of data sources

Patrick Lambrix
Department of Computer and Information Science
Linköpings universitet

Accessing multiple data sources





Genomics

Clinical trials

Disease information

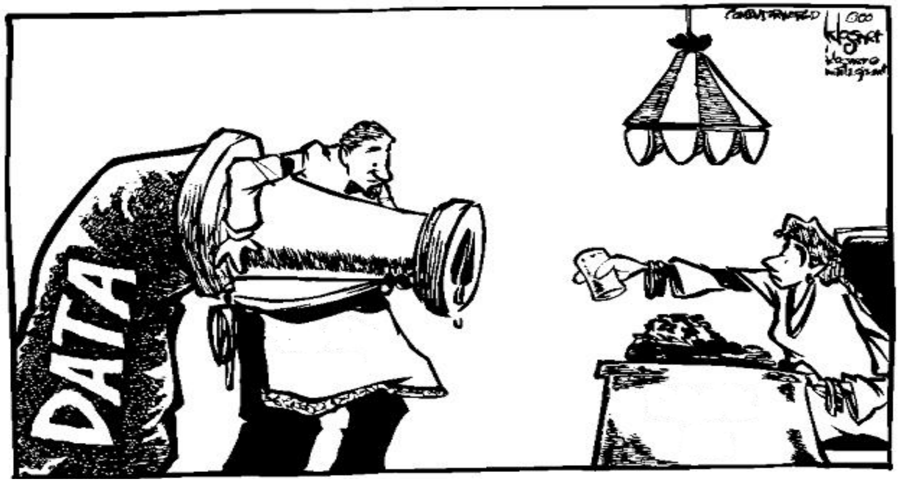
DISCOVERY

Metabolism, toxicology

Chemical structure

Disease models

Target structure

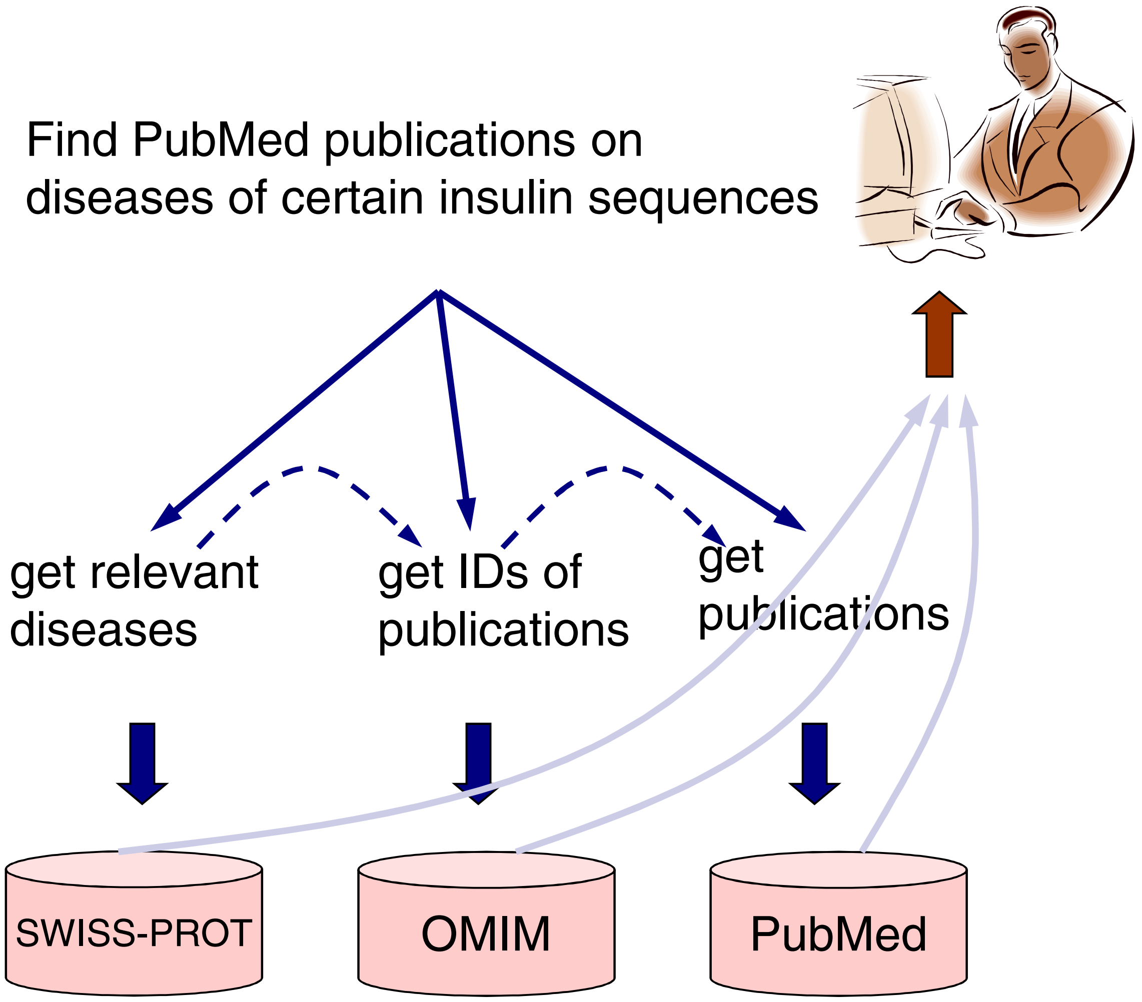


Access to multiple data sources-Problems

- Users need good knowledge on where the required information is stored and how it can be accessed
- Representation of an entity in different data sources can be different.

  Same name in different data sources can refer to different entities.

Queries over multiple data sources



Find PubMed publications on
diseases of certain insulin sequences

get relevant
diseases

get IDs of
publications

get
publications

SWISS-PROT

OMIM

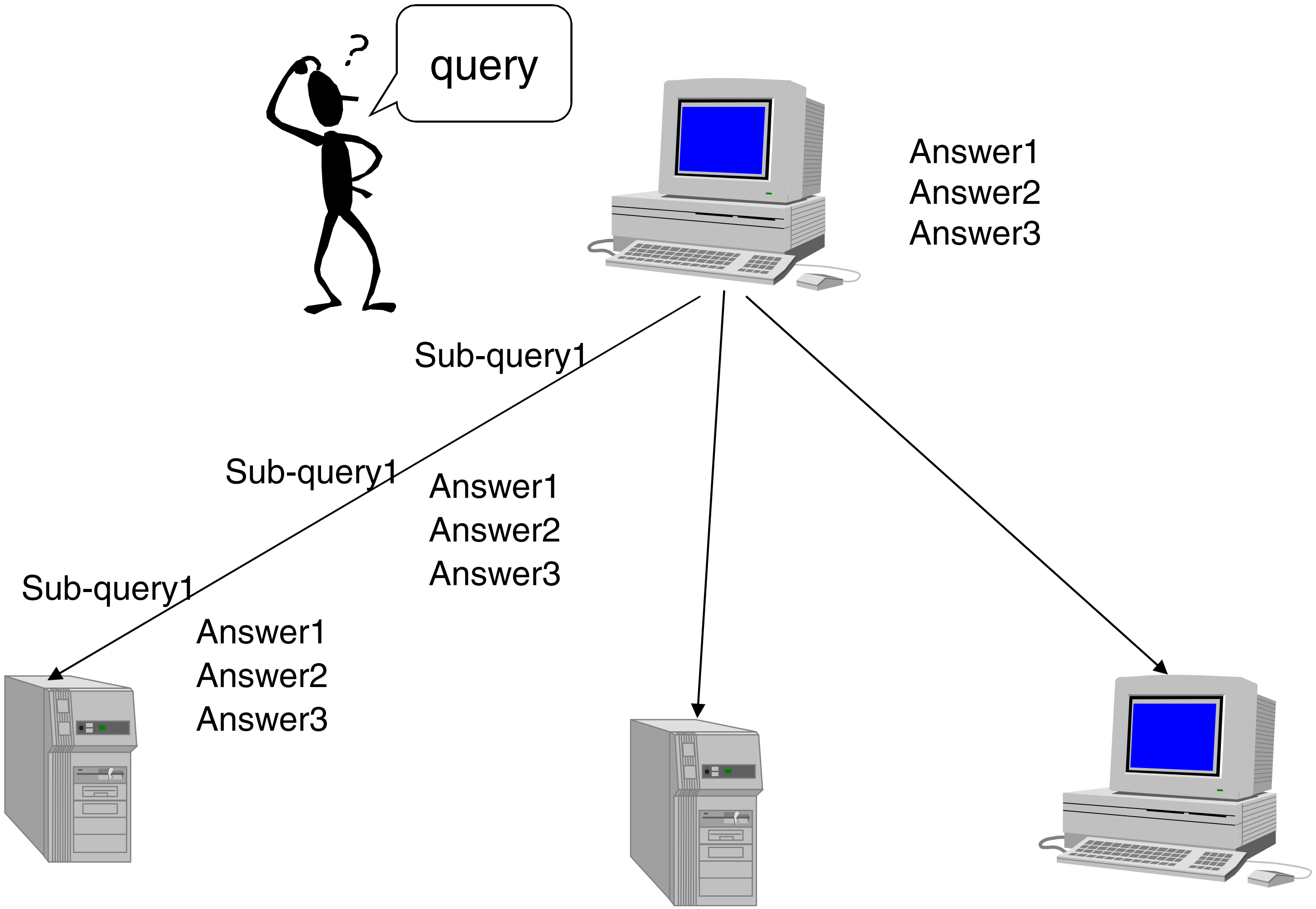
PubMed

- Find
- Divide & order
- Execute
- Combine

Access to multiple data sources - steps

- Decide which data sources should be used
- Divide query into sub-queries to the data sources
- Decide in which order to send sub-queries to the data sources
- Send sub-queries to the data sources - use the terminology of the data sources
- Merge results from the data sources to an answer for the original query

→ mistake in any step can lead to inefficient processing of the query or failure to get a result



query

Sub-query1

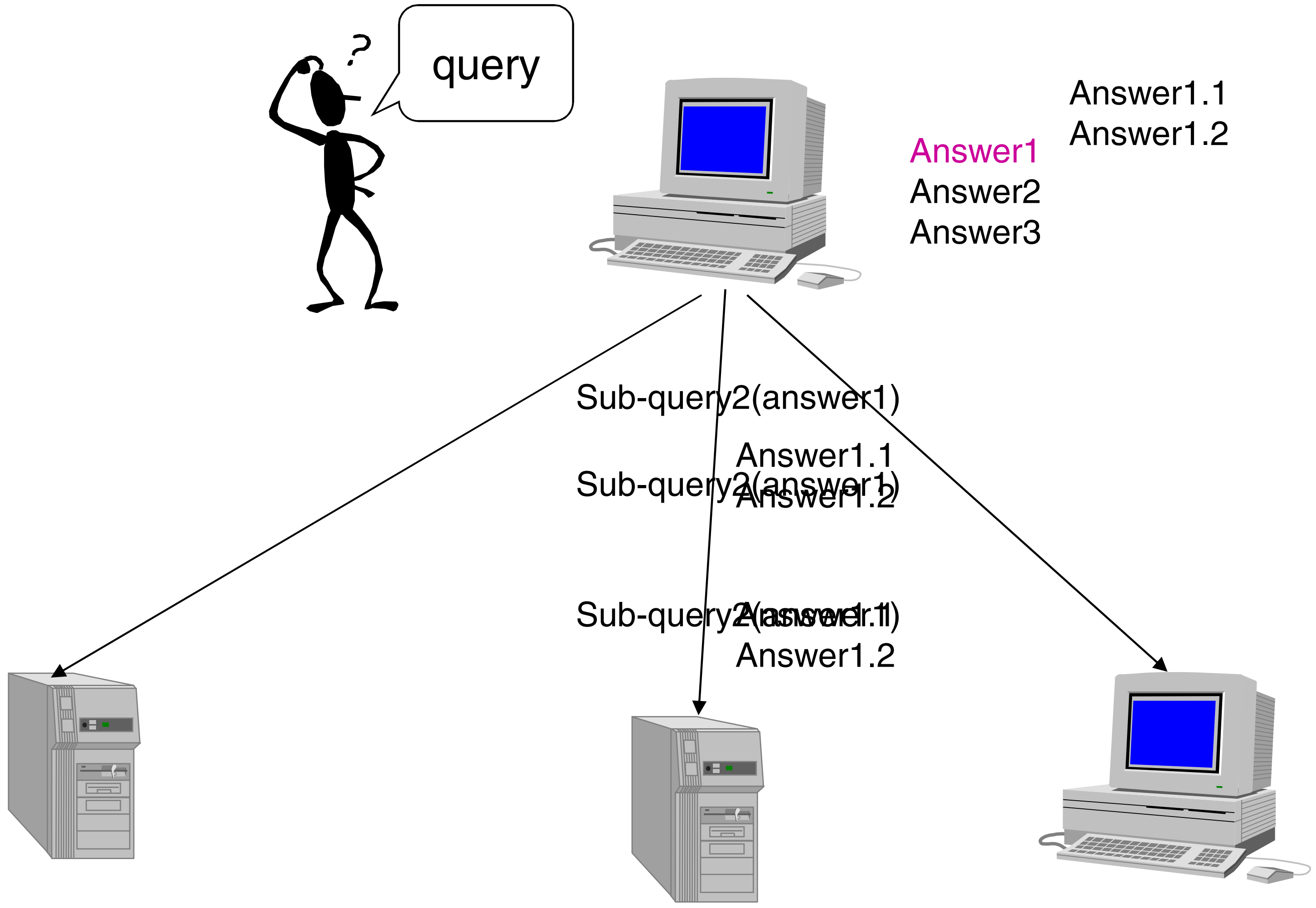
Sub-query1

Sub-query1

Answer1
Answer2
Answer3

Answer1
Answer2
Answer3

Answer1
Answer2
Answer3



Answer1
Answer2
Answer3

Answer1.1
Answer1.2

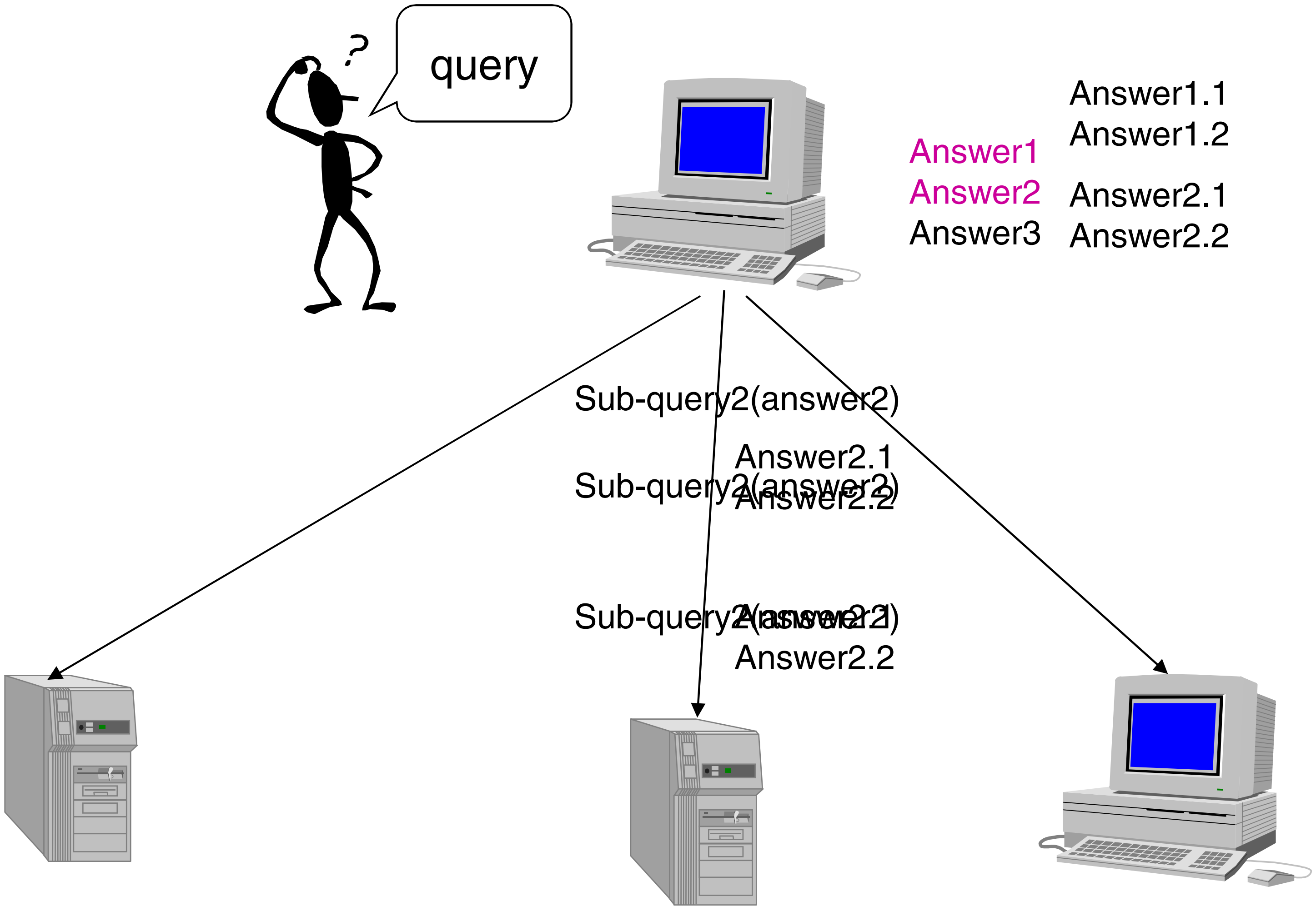
Sub-query2(answer1)

Answer1.1
Answer1.2

Sub-query2(answer1)

Sub-query2(answer1)

Answer1.1
Answer1.2



query

Answer1
Answer2
Answer3

Answer1.1
Answer1.2
Answer2.1
Answer2.2

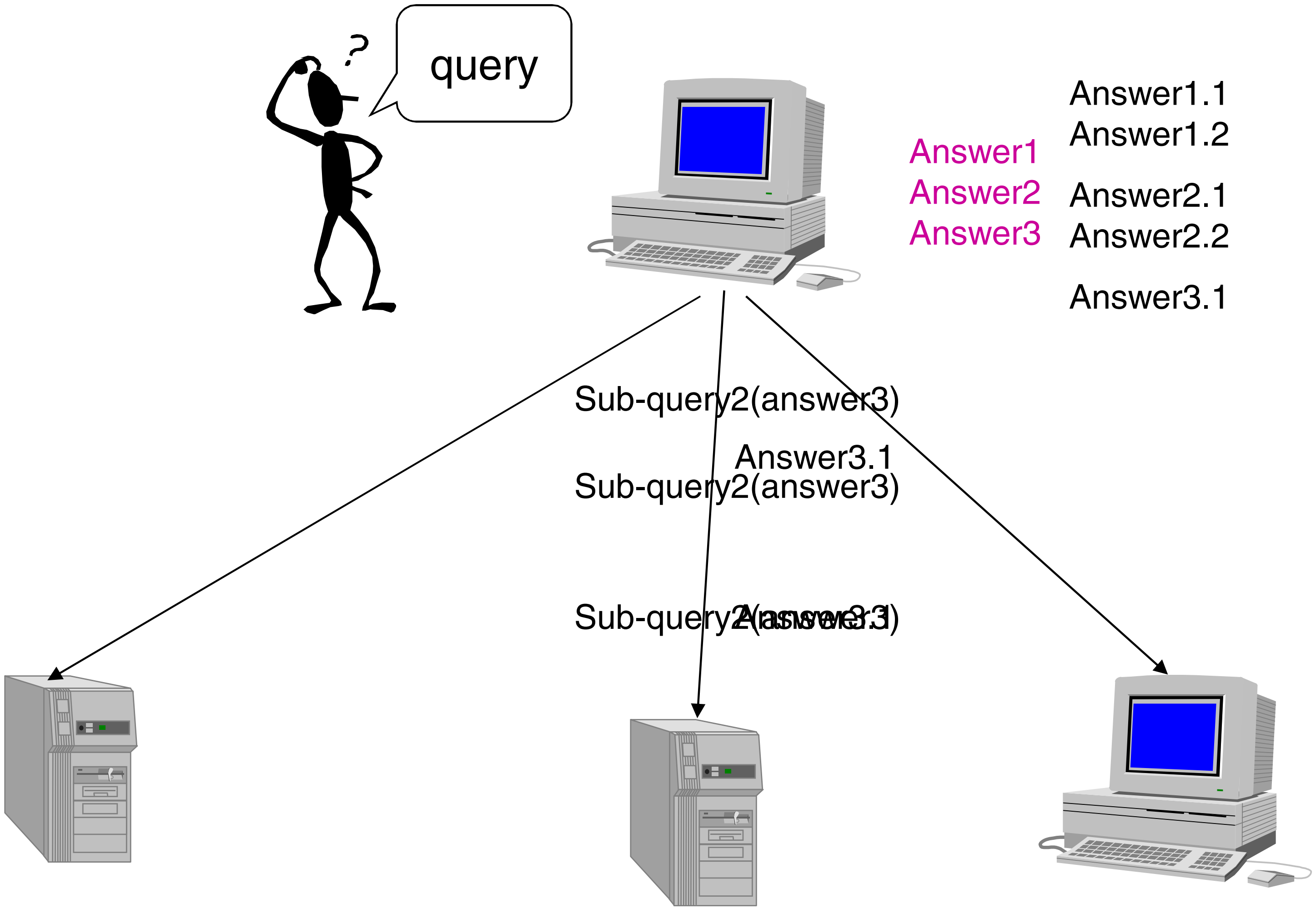
Sub-query2(answer2)

Answer2.1
Answer2.2

Sub-query2(answer2)

Sub-query2(answer1)

Answer2.1
Answer2.2



query

Answer1
Answer2
Answer3

Answer1.1
Answer1.2

Answer2.1
Answer2.2

Answer3.1

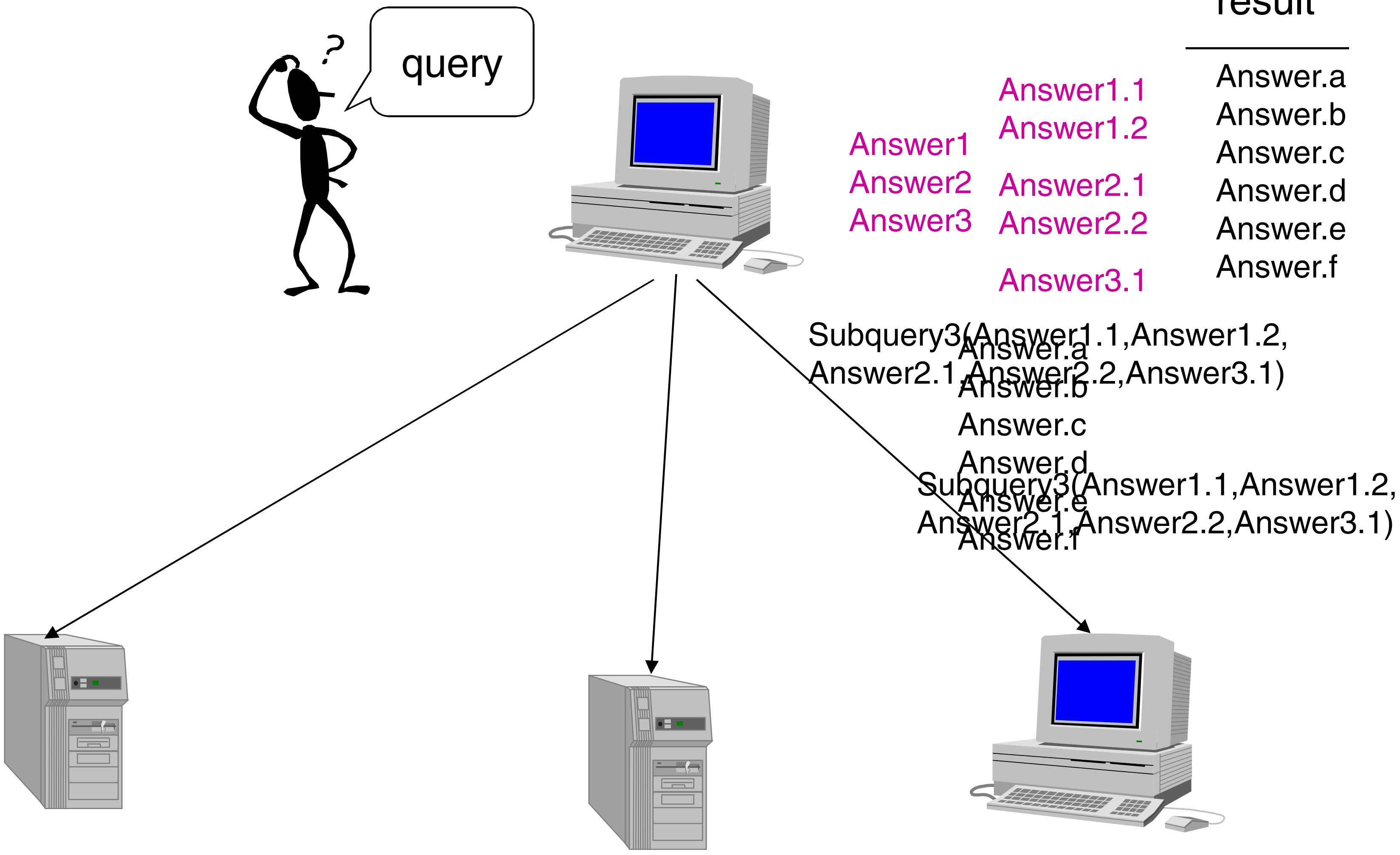
Sub-query2(answer3)

Answer3.1

Sub-query2(answer3)

Sub-query2(answer3)

Answer3.1



result

Answer.a
Answer.b
Answer.c
Answer.d
Answer.e
Answer.f

Answer1.1
Answer1.2
Answer2.1
Answer2.2
Answer3.1

Answer1
Answer2
Answer3

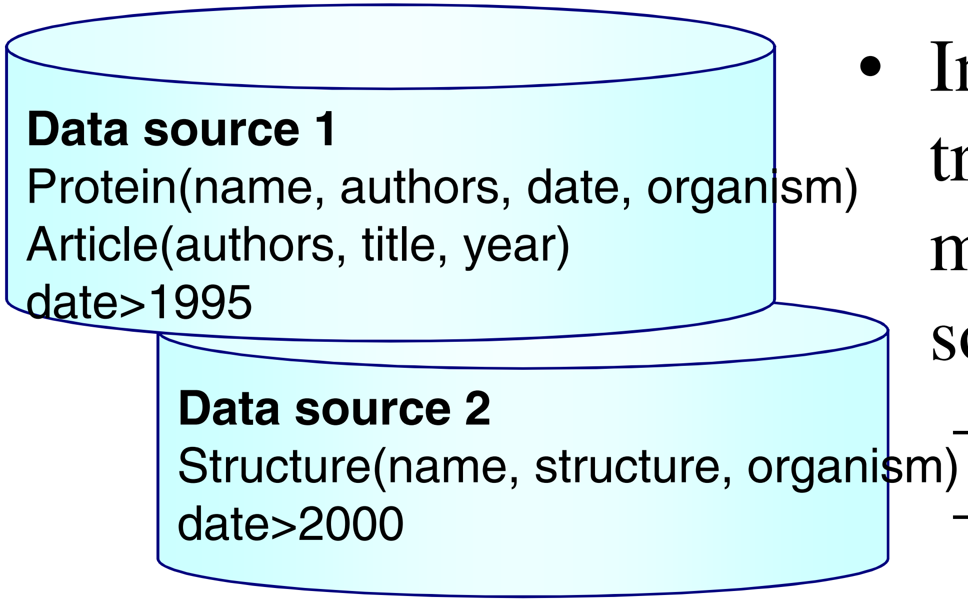
Subquery3(Answer1.1,Answer1.2,
Answer2.1,Answer2.2,Answer3.1)

Answer.a
Answer.b
Answer.c
Answer.d
Answer.e
Answer.f

Subquery3(Answer1.1,Answer1.2,
Answer2.1,Answer2.2,Answer3.1)

Problem formulation

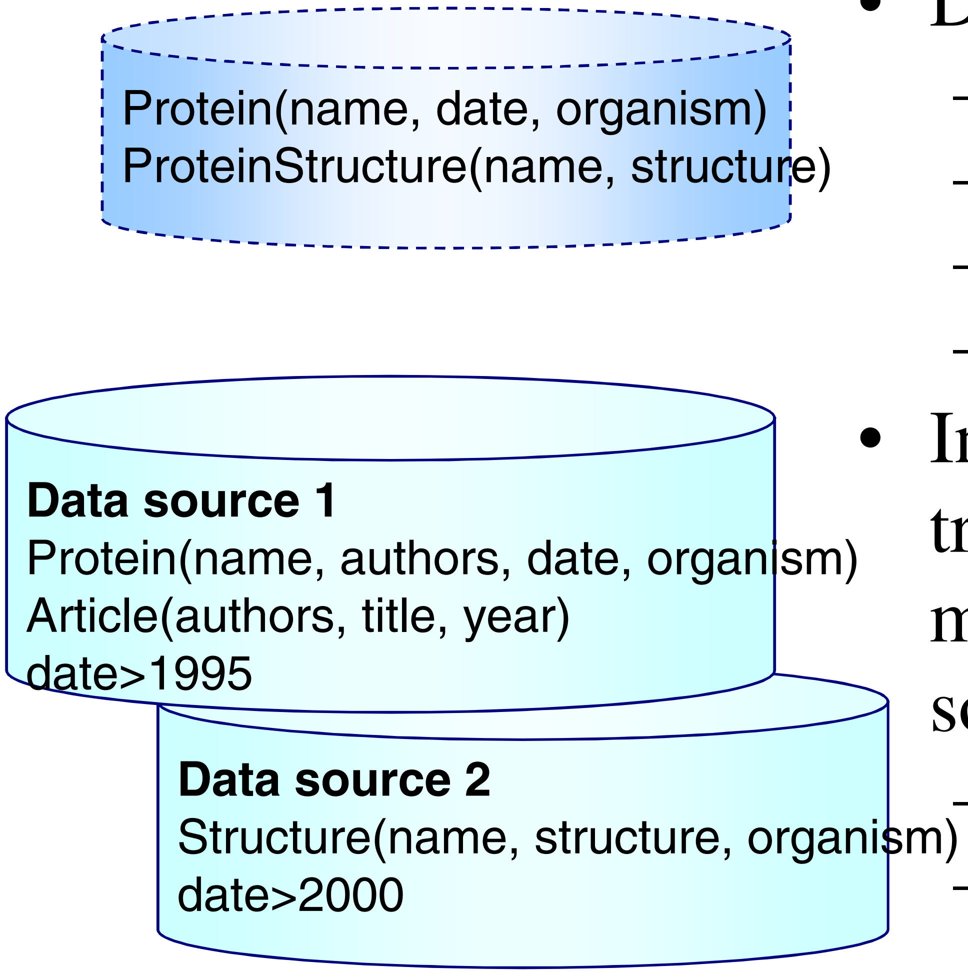
- Data source properties
  - Autonomous data sources
  - Different data models
  - Differences in terminology
  - Overlapping, redundant data
- Integration aims to provide transparent access to multiple heterogenous data sources
  - uniform query language
  - uniform representation of results



Data source 1
Protein(name, authors, date, organism)
Article(authors, title, year)
date>1995

Data source 2
Structure(name, structure, organism)
date>2000

Problem formulation



Protein(name, date, organism)
ProteinStructure(name, structure)

Data source 1
Protein(name, authors, date, organism)
Article(authors, title, year)
date>1995

Data source 2
Structure(name, structure, organism)
date>2000

- Data source properties
  - Autonomous data sources
  - Different data models
  - Differences in terminology
  - Overlapping, redundant data
- Integration aims to provide transparent access to multiple heterogenous data sources
  - uniform query language
  - uniform representation of results

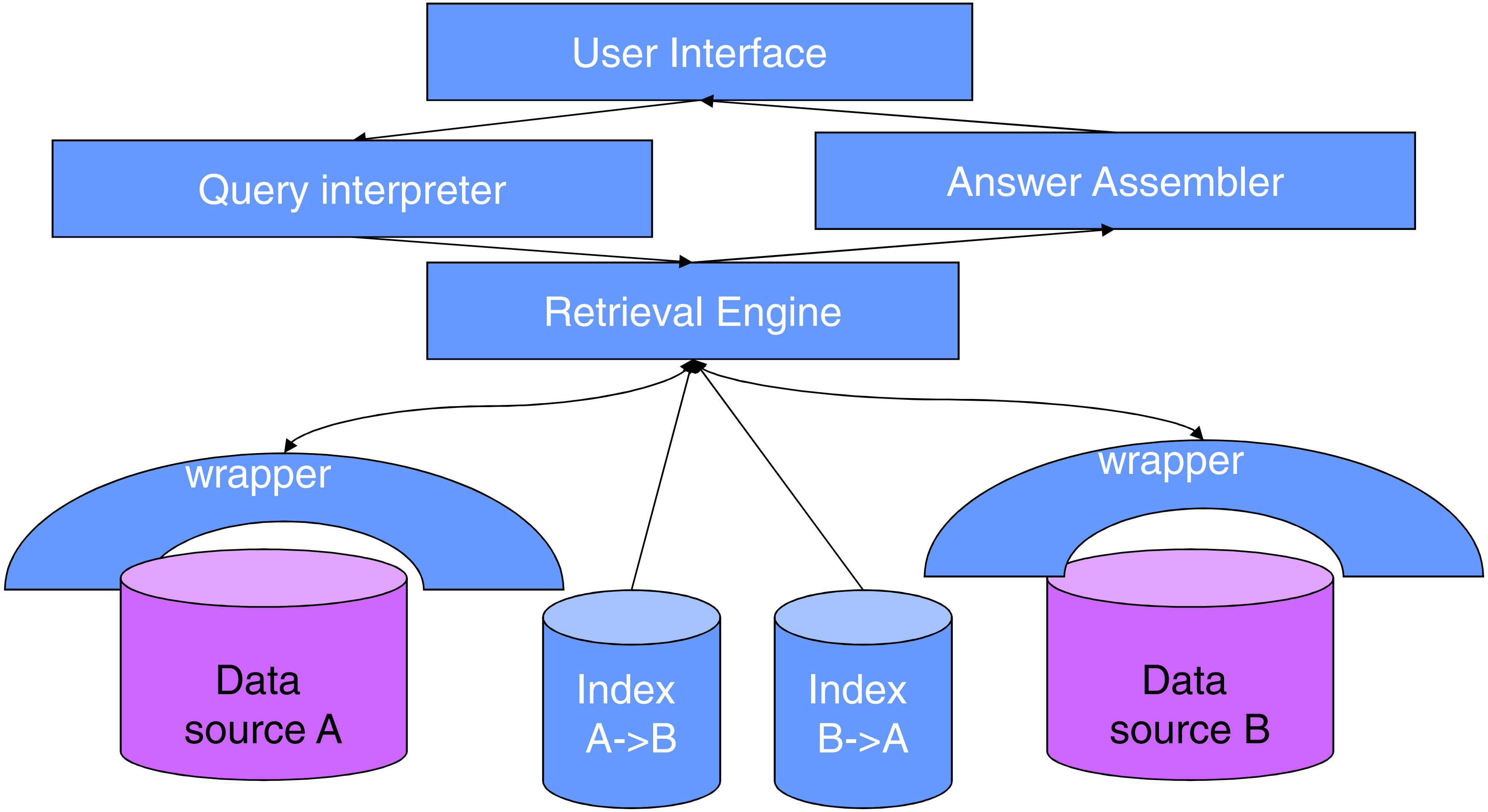
Methods for integration

- Link driven federations
  - Explicit links between data sources.
- Warehousing
  - Data is downloaded, filtered, integrated and stored in a warehouse. Answers to queries are taken from the warehouse.
- Mediation or View integration
  - A global schema is defined over all data sources.

Link driven federations

- Creates explicit links between data sources
- query: get interesting results and use web links to reach related data in other data sources

Link driven federations



User Interface

Query interpreter

Answer Assembler

Retrieval Engine

wrapper

Data
source A

Index
A->B

Index
B->A

wrapper

Data
source B

SRS

- Integrates more than 300 resources
- Possible to add own resources
- interface: SRSWWW, getz
- http://srs.ebi.ac.uk/

SRS – query language

- text search

[swissprot-des:kinase]

documents in swissprot that contain 'kinase' in the 'description'-field

[swissprot-des:kin*]

documents in swissprot that contain a word that starts with 'kin' in the 'description'-field

SRS – query language

- boolean operators:

  and (&), or (|), andnot (!)

[swissprot-des:(adrenergic & receptor) ! (alpha1A)]

documents in swissprot that contain ’adrenergic’ and ’receptor’ in the ’description’-field, but not ’alpha1A’

SRS – query language

- boolean operators:

  and (&), or (|), andnot (!)

[swissprot-des:kinase] & [swissprot-org:human]

documents in swissprot that contain ’kinase’ in the ’description’-field and ’human’ in the ’organism’-field

SRS – query language

- links

[swissprot-des:kinase] > PDB

documents in PDB that are referred to from documents in swissprot that contain ’kinase’ in the ’description’-field

SRS – query language

- links

[swissprot-id: acha_human] > prosite > swissprot

documents in swissprot that are referred to from documents in prosite that are referred to from documents in swissprot that contain ’acha_human’ in the ’id’- field

SRS – query language

- links

[swissprot-org:human] >
    [swissprot-features:transmem]

documents in swissprot that contain ’transmem’ in the ’features’-field and that are referred to from documents in swissprot that contain ’human’ in the ’organism’-field

SRS – query language

- multiple sources

```
[{swissprot sptremb}-des:kinase]

[dbs={swissprot sptremb}-des:kinase]
  &  [dbs-org:human]
```

Link driven federations

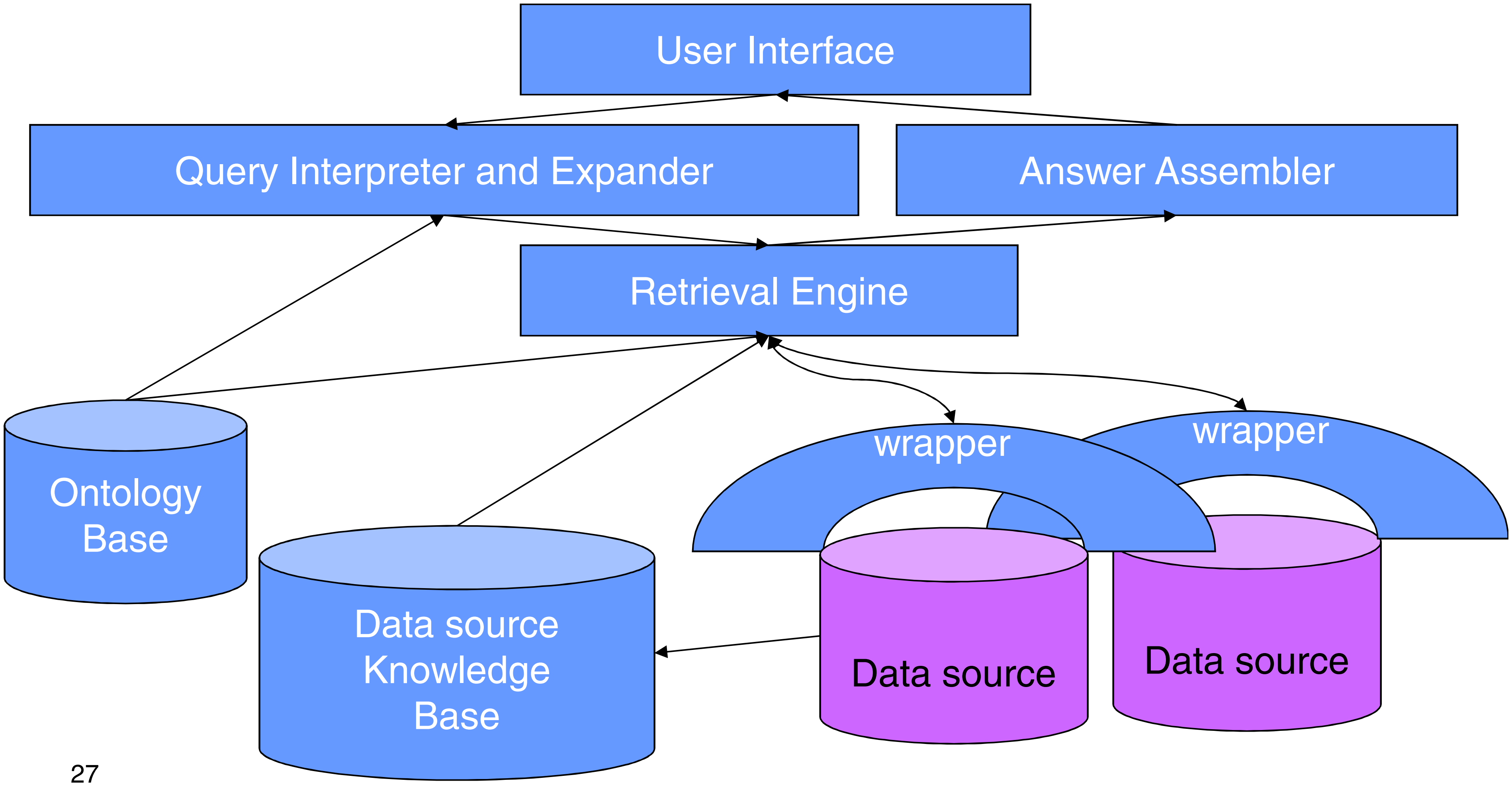
- Advantages
  - complex queries
  - fast
- Disadvantages
  - require good knowledge
  - syntax based
  - terminology problem not solved


EXPASY
LOGIN
LOGOUT
Eric Langevin / 1995

Mediation

- Define a global schema over the data sources
- high level query language

Mediation



User Interface

Query Interpreter and Expander

Answer Assembler

Retrieval Engine

Ontology Base

Data source Knowledge Base

wrapper

wrapper

Data source

Data source

Mediation

- Advantages
  - complex queries
  - requires less knowledge
  - solution for terminology problem
  - semantics based

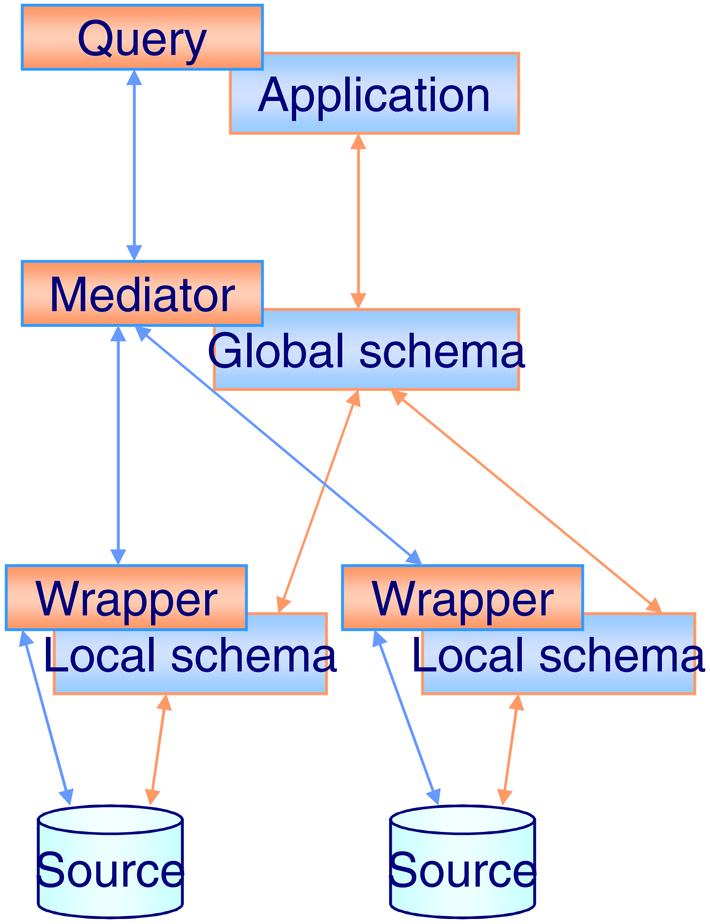
Mediation

- Disadvantages

  - more computation

  - view maintenance

Mediation



- Query problem

  How to answer queries expressed using the global schema.

- Modeling problem

  How to model the global schema, data sources and mappings.

Queries

- Queries use the global schema
- Conjunctive queries
  - ☐ select-project-join queries

head if body/subgoals

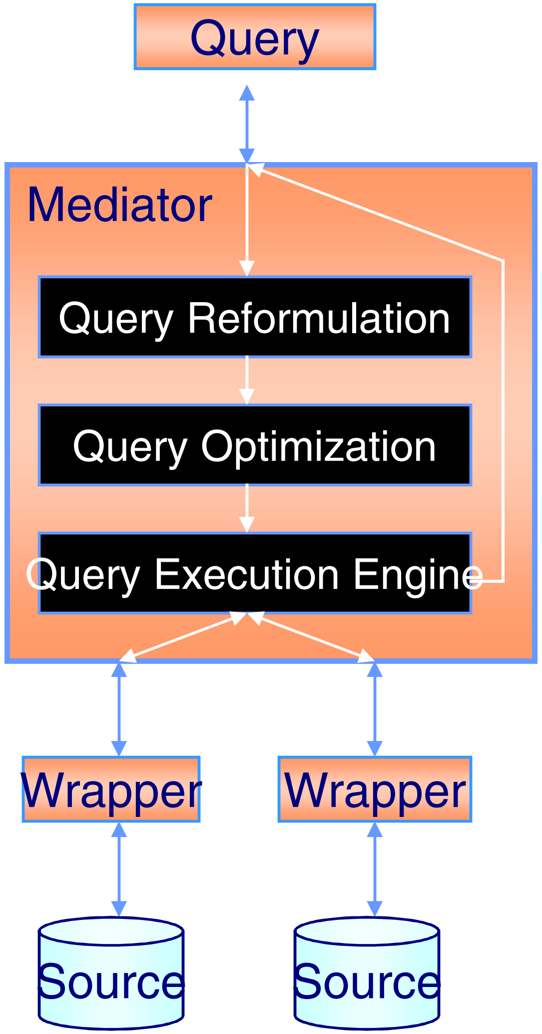
p(X,Z) :- a(X,Y), b(Y,Z)

q(name, structure) :- Protein(name, 2001, ‘human’),
ProteinStructure(name, structure)

- Mediator reformulates queries in terms of a set of queries that use the local schemas. Equivalence and containment of queries needs to be preserved.

  - Q1 is contained in Q2
  if the result of Q1 is a subset of the result of Q2.

Mediator

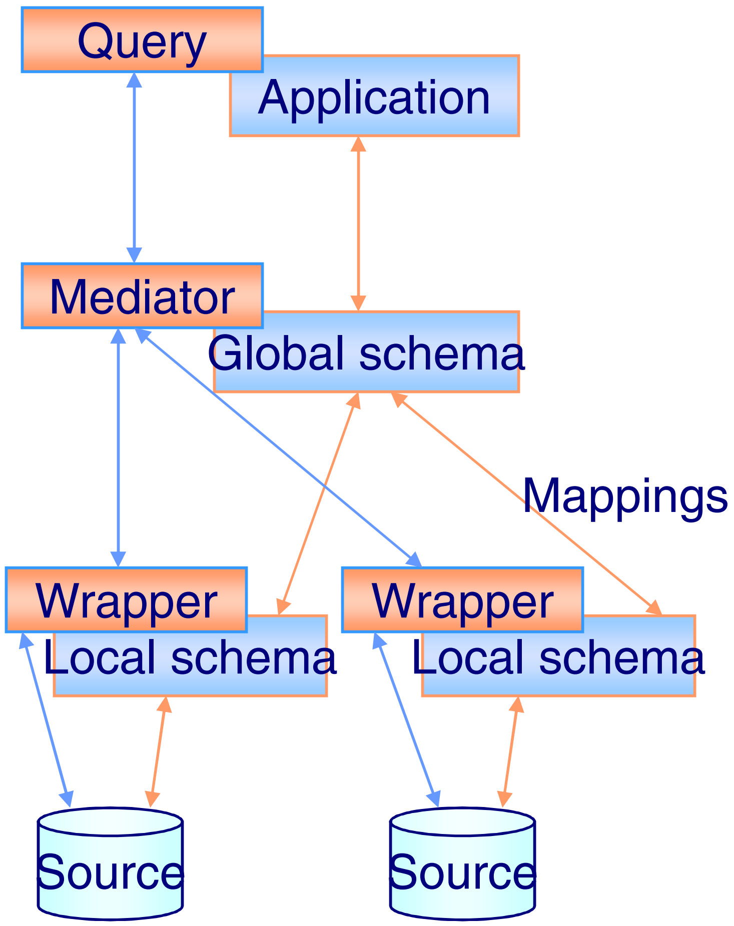


- Mediator is responsible for query processing
  - reformulation of queries, decide query plan
  - query optimization
  - execution of query plan, assemble results into final answer

Issues:

- Semantically correct reformulation
- Access only relevant data sources

Knowledge



- Description of data source content
  - global schema (domain model/ontology)
  - local schema (data source model)
- Information for integration
  - mapping
- Capabilities
  - attributes and constraints
  - processing capabilities
  - completeness
  - cost of query answering
  - reliability
- Used for
  - selection of relevant data sources
  - query plan formulation
  - query plan optimization

Mapping

- Relation between domain and data source content

Global schema:	Data source local schema:
Protein(name, date, organism)	DS1(name, authors, date, organism)
ProteinStructure(name, structure)	DS2(name, structure, organism)

  - ☐ Global as view
    The global schema is defined in terms of source terminology

Protein(name, date, organism) :- DS1(name, authors, date, organism)

ProteinStructure(name, structure) :- DS2(name, structure, organism)

Mapping

- Relation between domain and data source content

Global schema:
Protein(name, date, organism)
ProteinStructure(name, structure)

Data source local schema:
DS1(name, authors, date, organism)
DS2(name, structure, organism)

  - ☐ Local as view
    The sources are defined in terms of the global schema.

DS1(name, authors, date, organism) -:
Protein(name, date, organism), date >1995
DS2(name, structure, organism) -: Protein(name, date, organism),
ProteinStructure(name, structure), date >2000

Query processing in GAV

Query: give name and structure for human proteins with date ‘2001’.
q(name, structure) :- Protein(name, 2001, ‘human’),
ProteinStructure(name, structure)

GAV: Protein(name, date, organism) :- DS1(name, authors, date, organism)
ProteinStructure(name, structure) :- DS2(name, structure, organism)

- No explicit representation of data source content
- Mapping gives direct information about which data satisfies the global schema.
- Query is processed by expanding the query atoms according to their definitions.

New query: q(name, structure) :-
DS1(name, authors, 2001, ’human’), DS2(name, structure, organism)

Query processing in LAV

Query: give name and structure for human proteins with date ‘2001’.
q(name, structure) :- Protein(name, 2001, ‘human’),
ProteinStructure(name, structure)

LAV: DS1(name, authors, date, organism) -:
Protein(name, date, organism), date >1995
DS2(name, structure, organism) -: Protein(name, date, organism),
ProteinStructure(name, structure), date >2000

- Mapping does not give direct information about which data satisfies the global schema.
- To answer the query it needs to be inferred how the mappings should be used.

Query processing in LAV

Query: give name and structure for human proteins with date ‘2001’.
q(name, structure) :- Protein(name, 2001, ‘human’),
ProteinStructure(name, structure)

LAV: DS1(name, authors, date, organism) -:
Protein(name, date, organism), date >1995
DS2(name, structure, organism) -: Protein(name, date, organism),
ProteinStructure(name, structure), date >2000

- Bucket algoritm (Information Manifold)
  - ☐ For each sub-goal in query create bucket of relevant views.
  - ☐ Define rewritings of query. Each rewriting consists of one conjunct from every bucket. Check whether the resulting conjunction is contained in the query.
  - ☐ The result is the union of the rewritings.

New query: q(name, structure) :-
DS1(name, authors, 2001, ’human’), DS2(name, structure, organism)

Comparison GAV - LAV

- Global as view
  - Clear how data sources interact
  - When a data source is added, the global schema can change
  - Query processing is easy

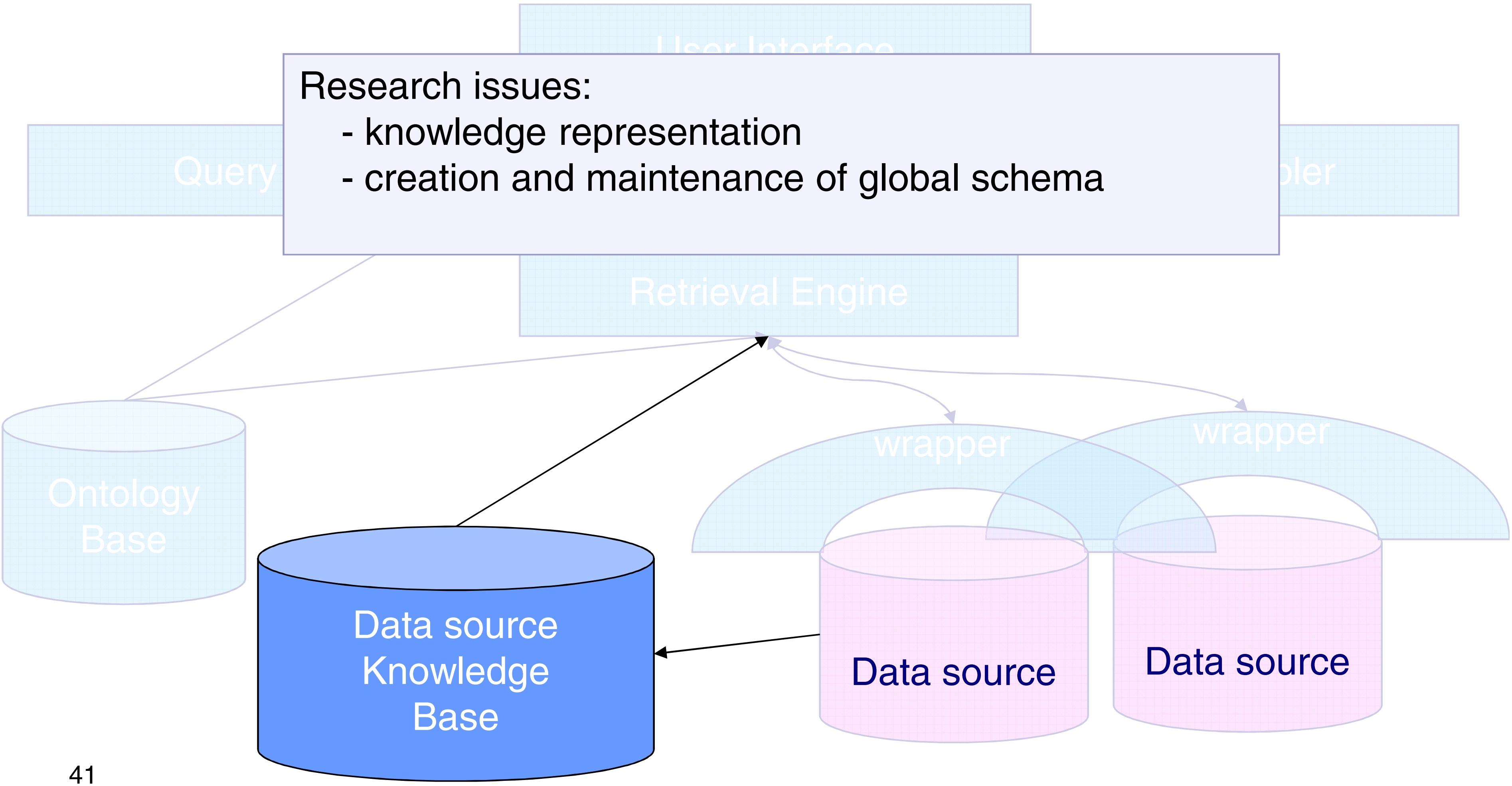
- Local as view
  - Each data source is specified in isolation
  - Easy to add data sources
  - Easier to specify constraints on the contents of sources
  - Query processing requires reasoning

Capabilities

- Most common capabilities describe attributes
  - ☐ f - free, attribute can be specified or not
  - ☐ b - bound, a value must be specified for the attribute, all values are permitted
  - ☐ u - unspecified, not permitted to specify a value for the attribute
  - ☐ c[S] - value should be one of the values in finite set S
  - ☐ o[S] - value is not specified or one of the values in finite set S

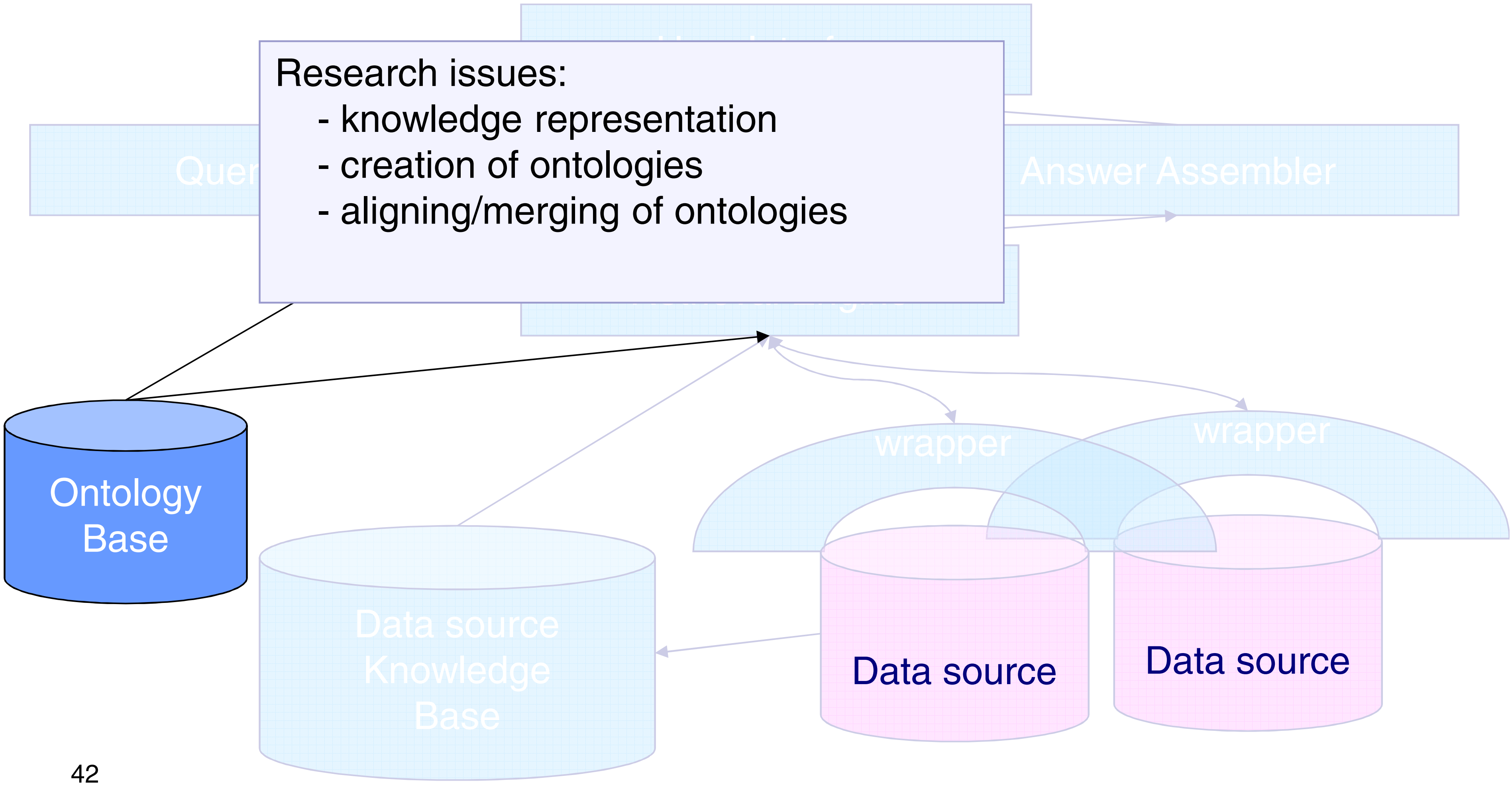
DS1: (name, authors, date, organism) f f b c[human mouse]

Mediation



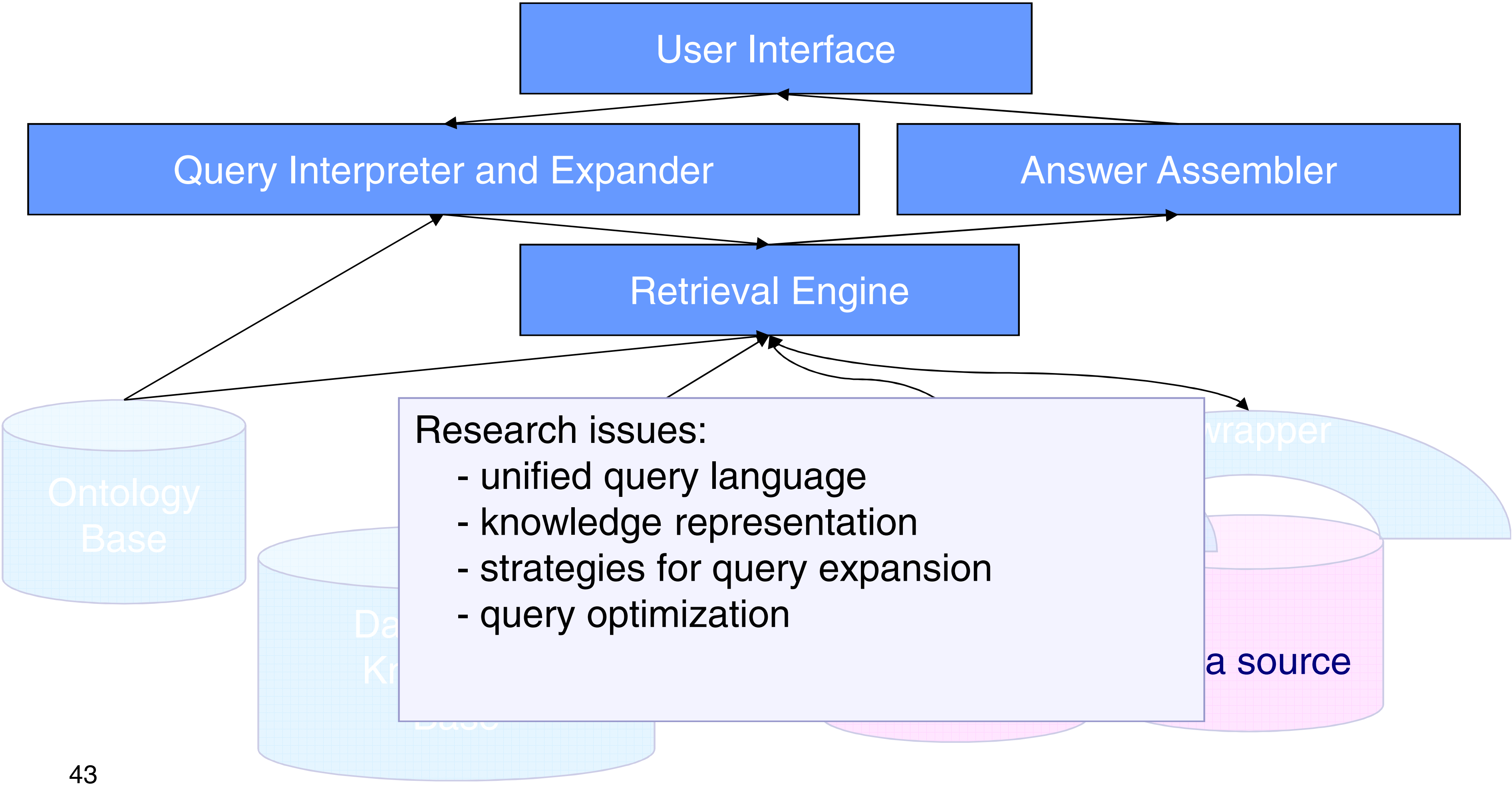
Research issues:
- knowledge representation
- creation and maintenance of global schema

Mediation



Research issues:
- knowledge representation
- creation of ontologies
- aligning/merging of ontologies

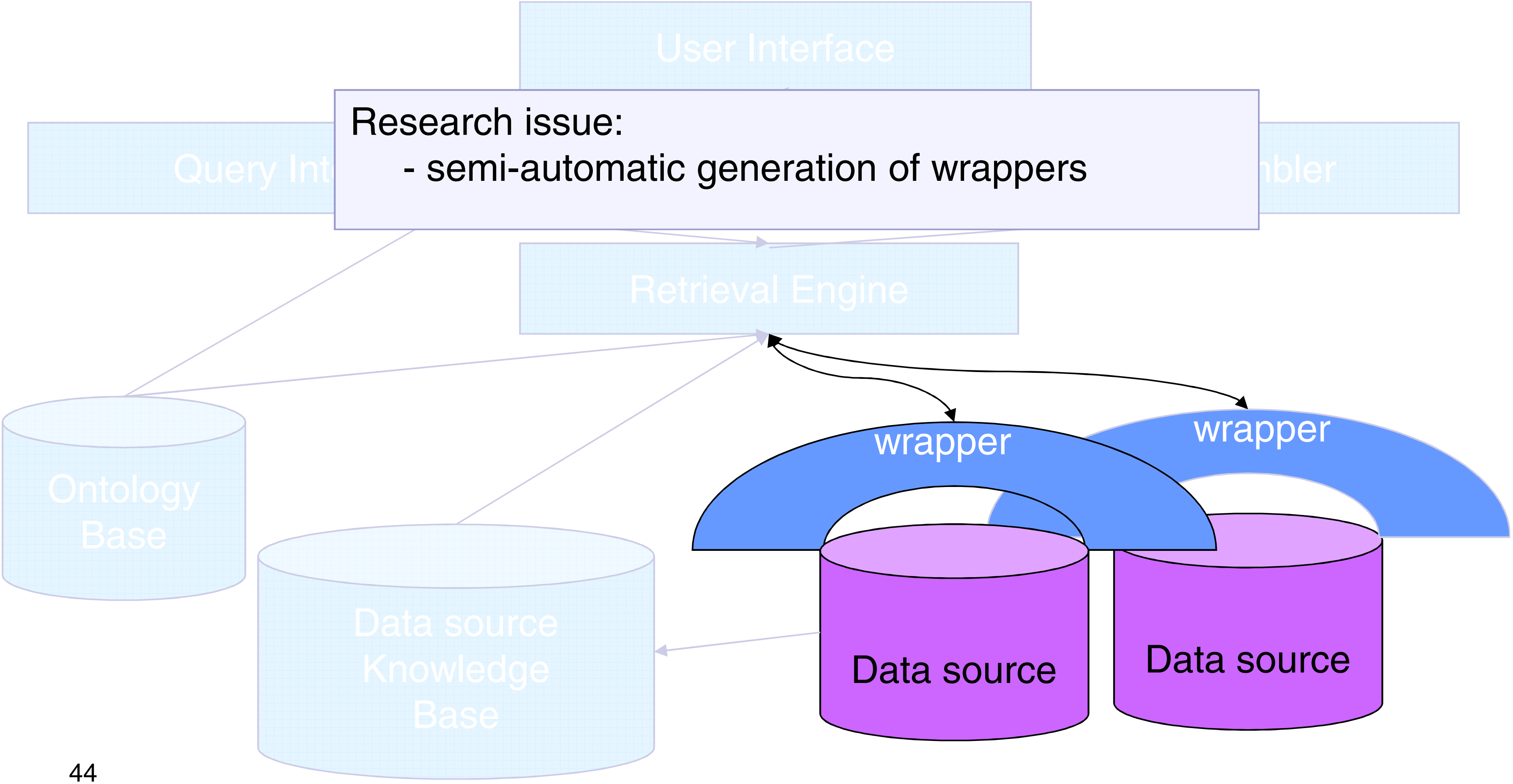
Mediation



Research issues:

- unified query language
- knowledge representation
- strategies for query expansion
- query optimization

Mediation



Research issue:
- semi-automatic generation of wrappers