# Dataspaces: The Tutorial

Day 2

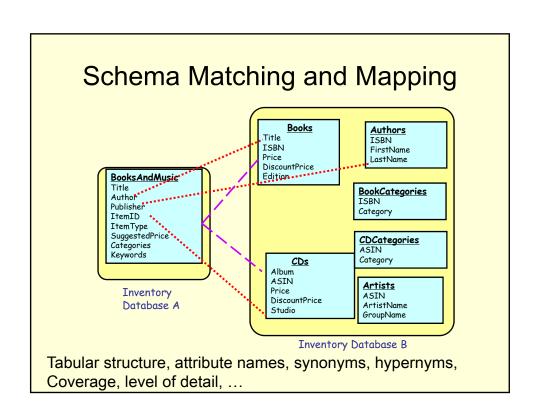
Alon Halevy, David Maier VLDB 2008 Auckland, New Zealand

### **Outline**

- ✓ Dataspaces: why? What are they?
  - Examples and motivation
- Dataspace techniques:
  - √ Locating and understanding data sources
  - Creating mappings and mediated schemas
  - Pay-as-you-go: improving with time
  - Querying dataspaces
- Research challenges on specific dataspaces:
  - Science, the desktop, the Web

### Sub-Outline

- What are schema matches and mappings?
  - Why is it so hard to create them?
- Automatic techniques for creating them
- Probabilistic schema mappings
- Probabilistic mediated schemas
- Trails: mapping hints



# Why is it so Hard?

- Schemas were developed in different contexts for different purposes
- Schemas never fully capture their intended meaning:
  - They're just symbols and structures.
  - Descriptions are:
    - · Often missing,
    - · In plain text, or wrong, or,
    - Don't capture all the semantics

### Schema Mapping Overview

- Step 1: schema matching:
  - Generate correspondences between elements of the two schemas
  - Easier to elicit from designers
  - May actually be all that's needed
- Step 2: create mappings:
  - Decide on joins, unions, filters, ...

User in the loop in both steps

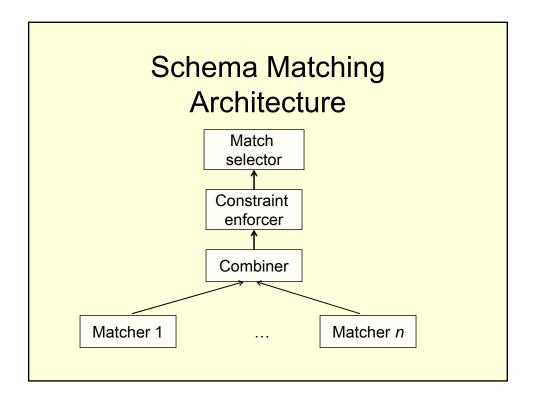
See Chapter 5 of upcoming book

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### Schema Matching overview

- · One trick won't do it all
- Hence:
  - Consider several base matchers
  - And then combine them
- Exploit domain constraints when possible
- We focus on 1-1 matching here
- [See Survey by Rahm & Bernstein, 2001]



### **Basic Matchers**

- · Schema level:
  - Name, description, data type,
  - Constraints (keys, foreign keys, is-a)
  - Schema structure
- · Instance level:
  - Look for common patterns in the data
  - Often more meaningful than the schema

### **Example: Edit Distance**

### Levenshtein Distance:

Number of operations needed to transform one name to the other.

$$edSim(s_1, s_2) = 1 - \frac{edit\_distance(s_1, s_2)}{max(length(s_1), length(s_2))}$$

edSim(discountPrice, discountedPrice)?

### **Instance-Based Matchers**

- Formatting patterns in the data can reveal type:
  - E.g., dates, phone numbers, prices, addresses, names, ...
- What other attribute names were used elsewhere for such values?
  - Additional clues to name matcher
- Consider similarity in values & type between two columns
  - E.g., house price versus # of rooms

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### Probabilistic Schema Mappings

- In a dataspace, we may rely on automatically created schema mappings
   --> uncertainty
- How do we model uncertain mappings?
- How do we answer queries in their presence?

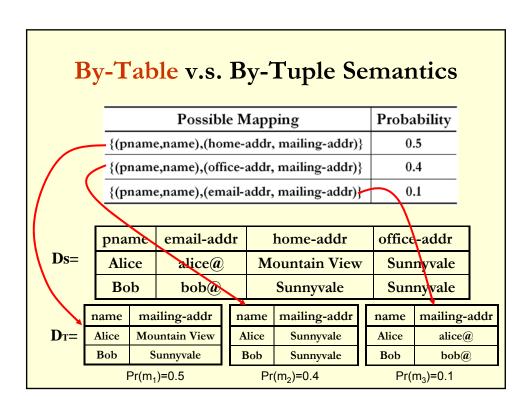
# **Probabilistic Mappings**

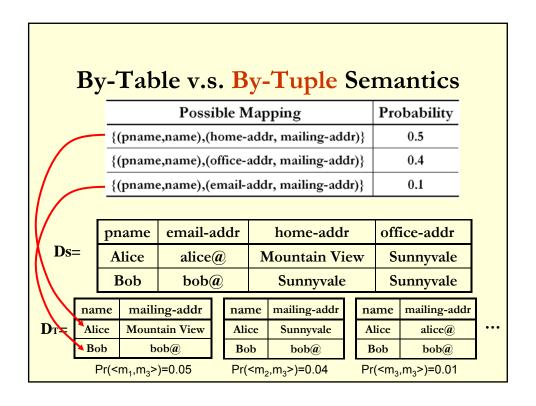
[Dong, H., Yu, VLDB 2007]

- S=(pname, email-addr, home-addr, office-addr)
- T=(name, mailing-addr)

Possible Mapping	Probability
{(pname,name),(home-addr, mailing-addr)}	0.5
{(pname,name),(office-addr, mailing-addr)}	0.4
{(pname,name),(email-addr, mailing-addr)}	0.1

### Semantics? by table or by tuple?





### Complexity of Query Answering By-table By-tuple **PTIME Data Complexity** #P-complete Mapping Complexity **PTIME PTIME** Works for Results extend compressed to more PTIME for representations complex important of mappings mapping special cases too. languages.

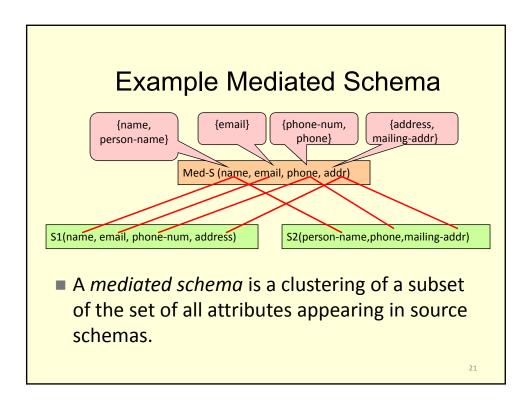
### Sub-Outline

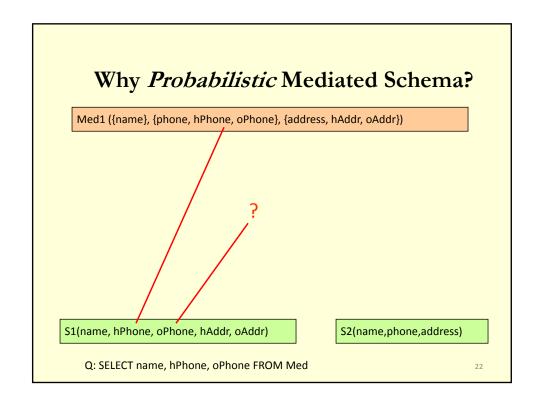
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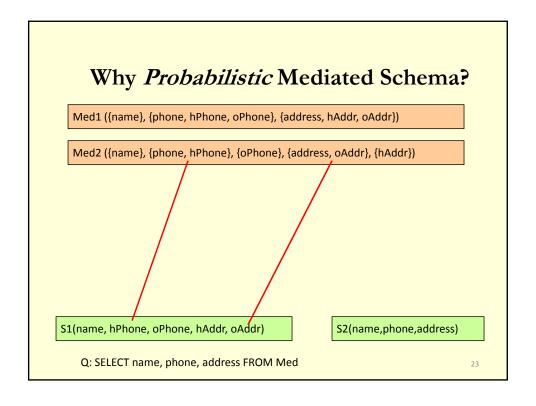
### Creating the Mediated Schema

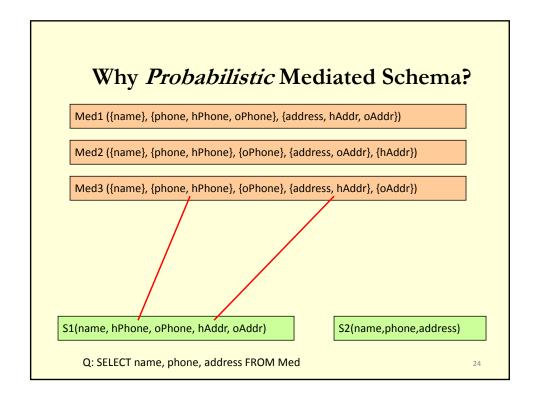
[Das Sarma, Dong, H., SIGMOD 2008]

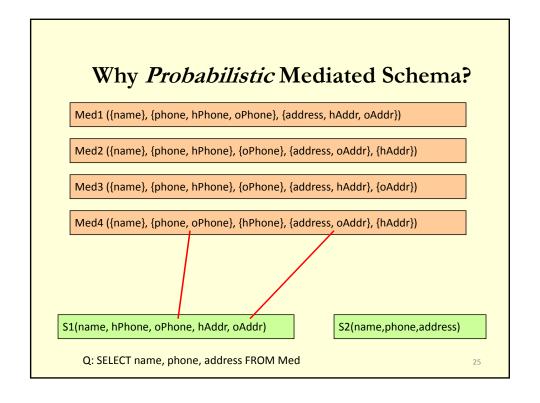
- Mediated schema creation: up front effort.
- Can we create it automatically?
  - If we can, then we can completely bootstrap data integration.
- Probabilistic mediated schemas:
  - manage the uncertainty involved.

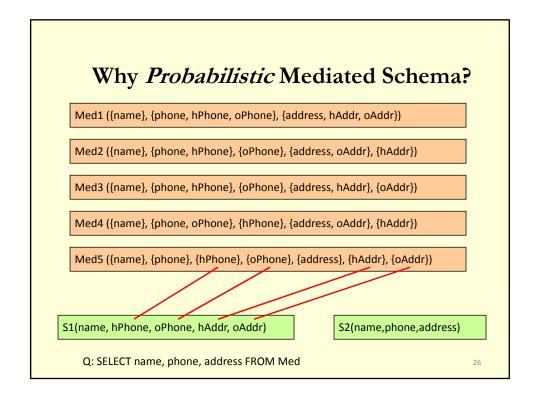


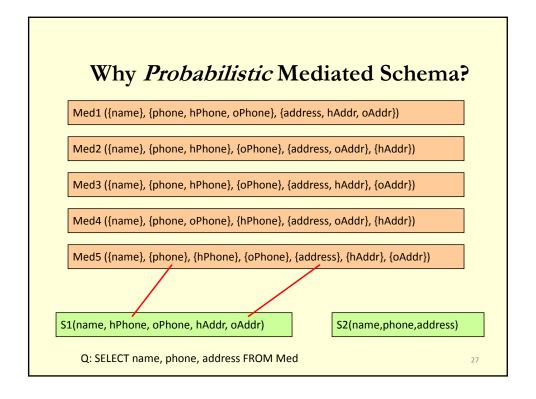


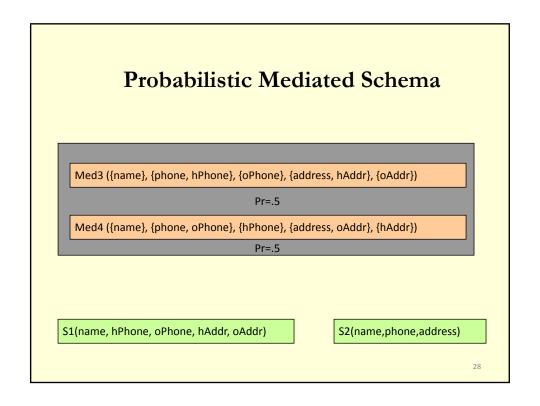












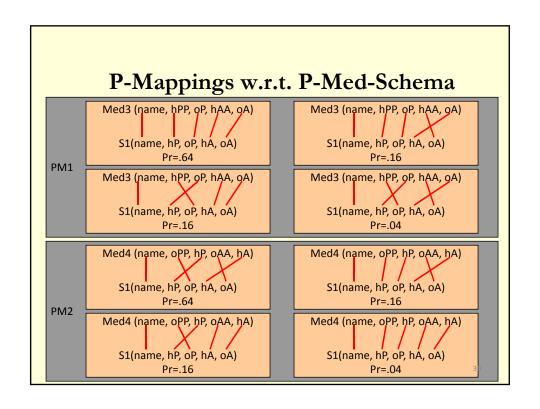
### Probabilistic Mediated Schema

• A p-med-schema is a set

$$\mathbf{M} = \{ (M_1, Pr(M_1)), ..., (M_l, Pr(M_l)) \}$$
 where

- M<sub>i</sub> is a med-schema; i≠j => M<sub>i</sub>≠ M<sub>j</sub>
- $Pr(M_i) \in (0,1]; \Sigma Pr(M_i) = 1$

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### **Bootstrapping Data Integration**

- Need to choose a mapping based on the correspondences:
  - One that minimizes entropy
- Consolidate probabilistic med schemas into one -- for the user.
- Between 0.85 and 0.95 P/R for queries on collections of 50-800 tables from the Web.

### Sub-Outline

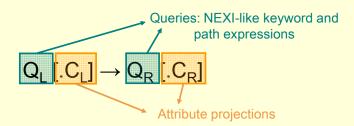
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# iTrails: Add Integration Hints Incrementally [Vas Salles et al., VLDB 06, 07]

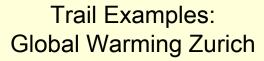
- Step 1: Provide a search service over all the data
  - Use a general graph data model (see VLDB 2006)
  - Works for unstructured documents, XML, and relations
- Step 2: Add integration semantics via hints (trails) on top of the graph
  - Works across data sources, not only between sources
- Step 3: If more semantics needed, go back to step 2
- Impact:
  - Smooth transition between search and data integration
  - Semantics added incrementally improve precision / recall

# **Defining Trails**

· Basic form of a Trail



 Intuition: When I query for Q<sub>L</sub> [.C<sub>L</sub>], you should also query for Q<sub>R</sub> [.C<sub>R</sub>]



global warming zurich



### **Temperatures**

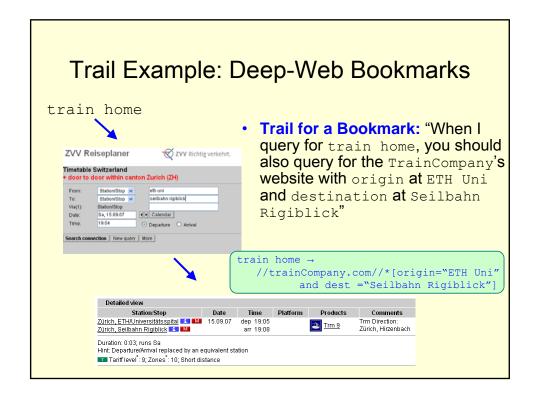
date	city	region	celsius
24-Sep	Bern	BE	20
24-Sep	Uster	ZH	15
25-Sep	Zurich	ZH	14
26-Sep	Zurich	ZH	9

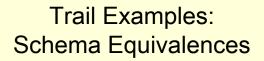
Trail for Implicit Meaning:
"When I query for global
warming, you should also
query for Temperature data
above 10 degrees"

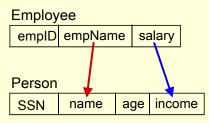
global warming → //Temperatures/\*[celsius > 10]

 Trail for an Entity: "When I query for zurich, you should also query for references of zurich as a region"

zurich → //\*[region = "ZH"]







Trail for schema match on names:
 "When I query for
 Employee.empName, you should also
 query for Person.name"

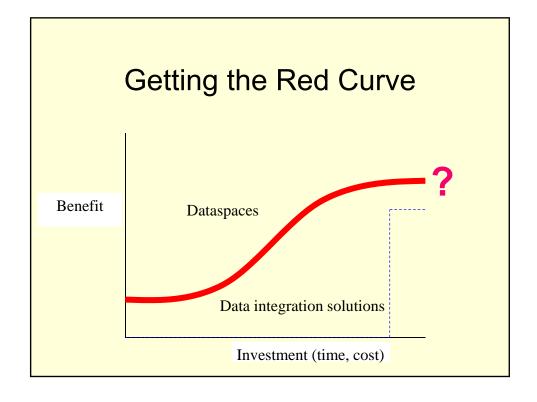
Trail for schema match on salaries:
"When I query for Employee.salary,
you should also query for
Person.income"

### More on Trails

- Creation:
  - Given by the user explicitly or by relevance feedback
  - (Semi-)Automatically: information extraction, schema matching, user communities, ontologies.
- Uncertainty on trails: some paths are better than others.
- Query reformulation: avoid cycles. (see paper)

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# Reusing Human Attention

- Principle:
  - User action = statement of semantic relationship
  - > Leverage actions to infer other semantic relationships
- Examples
  - Providing a semantic mapping
    - · Infer other mappings
  - Writing a query
    - · Infer content of sources, relationships between sources
  - Creating a "digital workspace"
    - · Infer "relatedness" of documents/sources
    - · Infer co-reference between objects in the dataspace
  - Annotating, cutting & pasting, browsing among docs
- ESP [von Ahn], mass collaboration [Doan+], active learning for record matching [Sarawagi et al.]

# Learning Schema Mappings [Doan et al., 2001] Mediated schema Classifiers for mediated schema Training examples: manually created schema matches Technique: multi-strategy learning. Use different learners and combine their predictions. Used in Transformic Inc. to create thousands of mappings.

### Soliciting User Feedback

[Jeffrey, Franklin, H., SIGMOD 2008]

- After bootstrapping, we need help from users to improve.
  - Reference reconciliation
  - Schema matches
  - Extractions from text
- What questions should we ask the users?

### The Most Beneficial Match

Decision theory to the rescue!

→ Value of Perfect Information (VPI)

"What is the benefit of resolving an unknown?"

### Intuition:

```
Benefit(match m_j) = Utility(m_j confirmed)(p_{correct}) +

Utility(m_j disconfirmed)(1 - p_{correct}) -

Utility(without asking)
```

# Utility of a Dataspace

- · Focus on queries!
- 2 components:
  - Result quality
  - Query importance

$$U(D,M) = \sum_{(Q_i,w_i) \in W} r(Q_i,D,M)w_i$$

Look at allQuery resultQuery queries in theuality (eignportance workloadrecision/recall)

# Challenges

- How to estimate benefit without computing all queries?
- Don't want to check all possible resulting dataspaces when a match is confirmed.
- Result: much faster dataspace improvement
  - Experiments on GoogleBase data.

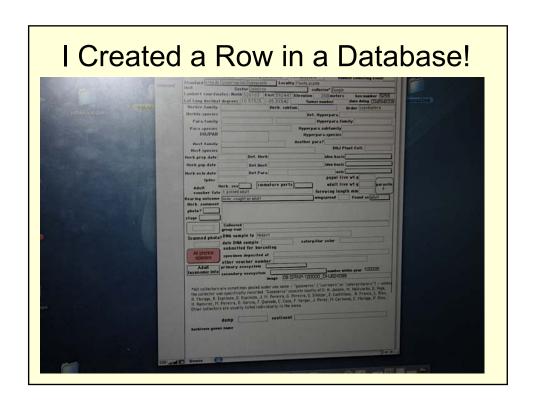
# Outline

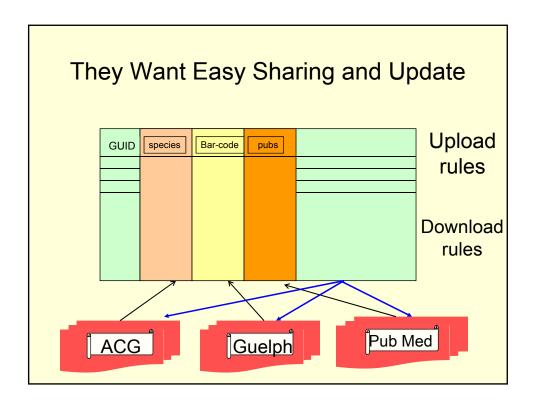
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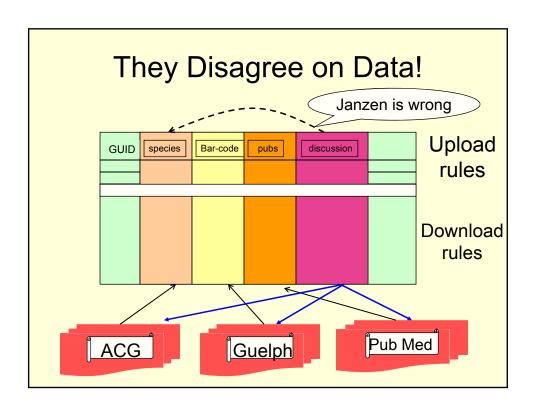


Looking for data management problems in the rainforest in Costa Rica









### **Querying Dataspaces**

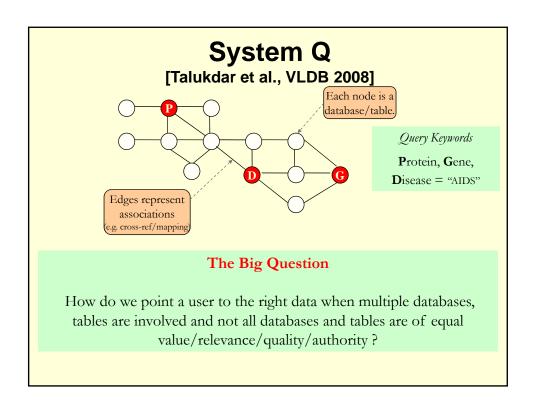
- We'll talk about the 'how' in a moment, but let's set expectations first.
- Recall that uncertainty is everywhere:
  - Data, mappings, query formulation
- · Hence, results need:
  - To be ranked
  - Come with their provenance & explanation
    - See tutorial by Tan & Buneman, SIGMOD 2007.
  - They won't be sets of tuples necessarily.

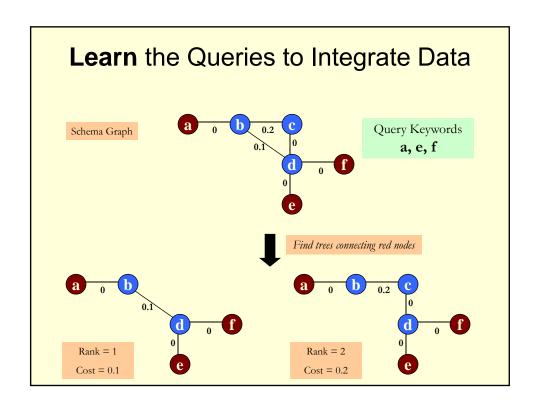
### **Query Mechanisms**

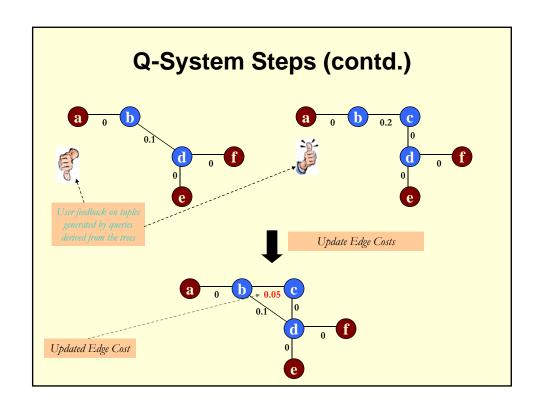
- Keyword search over structured data
  - BANKS (Mumbai), Xrank (Cornell), Discover (Hristidis and Papakonstantinou), Naga (Kasneci et al.)
- Keywords as a starting point:
  - Find the relevant data source and reformulate the query
    - · Examples below
  - Find appropriate structured queries over multiple sources
    - · System Q

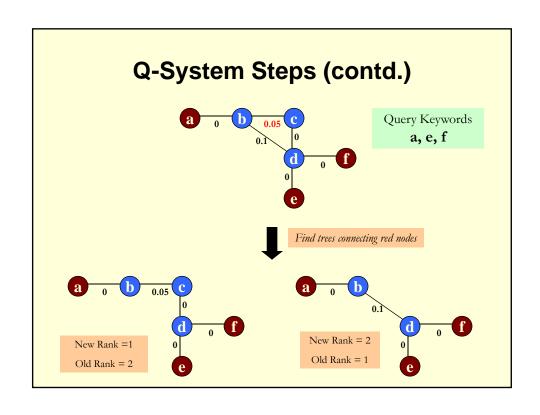


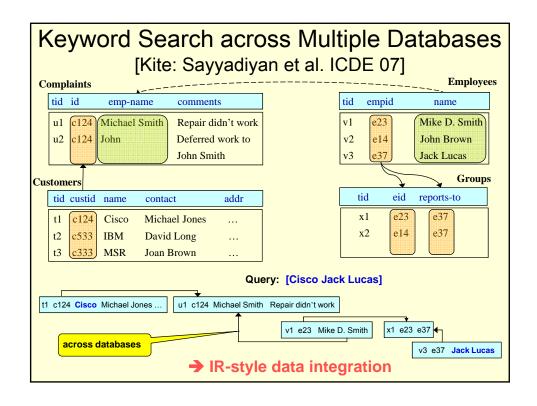


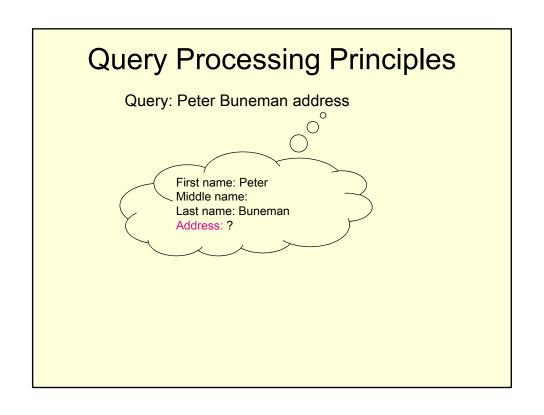


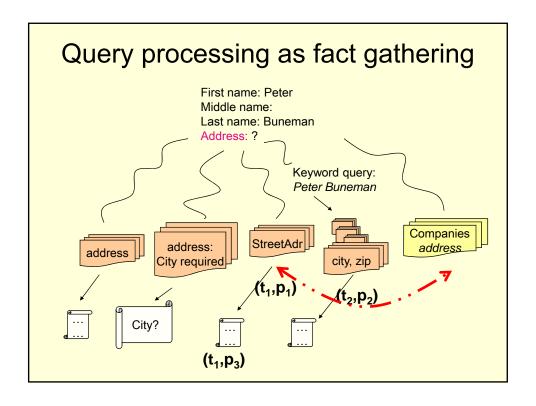






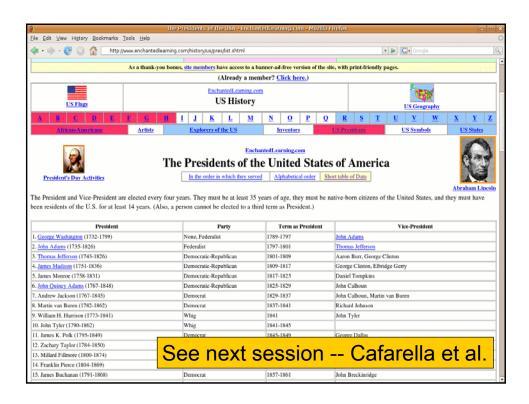






### **Outline**

- ✓ Introduction
- ✓ Dataspace principles through data integration
- Research challenges on specific dataspaces:
  - Dataspaces on the Web,
  - in Science, and
  - for Personal Information Management



# Dataspaces on the Web

- The Deep Web (yesterday, Madhavan et al.):
  - Millions of forms.
- · Main challenges:
  - The domain of everything
  - The context of the data carries semantics
  - Need to live with the rest of web data
- Opportunities:
  - Scale: stuff you can do with millions of schemas, forms

### Issues in Science Dataspaces

Concepts are still gelling, or have multiple abstractions

E.g., Gene

- · Coding region of a chromosome
- Particular transcription and splicing of a region
- · Particular variant of the region
- Product (usu. protein) coded by the region
- Whether they should be treated the same can depend on task or even query
- Makes schemas complex

### Science DS Issues, Cont.

### Identification is hard

- No common identification scheme yet Hsp10, HSP10, CPN10, Yor020p, ch10\_yeast [Jagadish, Chapman+ SIGMOD 07]
- Comparisons are on complex structures
   Sequence, molecule, 3-D structure
- Slight variants are different entities in rw Gene homologs

On-the-fly matching difficult
Want to reuse manual work

# Scientific DS Issues, cont.

# Complex schemas make query hard Michigan Molecular Interactions (MiMI)

[Jayapandian, Chapman+ Nucleic Acids Res. 2007]

- Use abstracted schema for overview (and now query)
- Multiple query interfaces: form, XQuery, keyword, MQuery (graphical)

But – "same" query gives different answers in different interfaces

### The Other "DataSpace"

- What's the minimum infrastructure for initial transformation, cleaning and exploratory analysis?
- Data sets often too big to replicate, but even fast channels are hard to exploit for on-the-fly combination

[Grossman, Mazzucco IEEE Comp in Sci & Eng 2002]

### **Universal Keys**

- Devise one or more domain-specific universal keys
- Treat data as distributed columns associated with one or more UKs
- Fast transfer and merge-join on keys; templated transform and display ops

Later version called *Sector* with more parallelism

[Grossman, U Penn II Workshop 2006]

### **Supporting Analysis**

Scenario: Domain experts who are unfamiliar with schema, need to make equivalence judgments

- None, <1 pack, 1-2packs, >2 packs
- Never smoked, smoker, quit
- GUAVA: GUI as View Apparatus Query through the data-entry screen
- MultiClass: Save and reuse domain mapping decisions

[Terwilliger, Delcambre+ EDBT Workshops 2006]

## Other Science DS Work

- Multiple Genomes and Meta-genomes
   [Markowitz U Penn II Workshop 06]
  - Have "coarse annotation" in some components while refining annotation (perhaps even manually) in others
- Science dataspaces on the Grid [Elsayed, Brezany+ DEXA 2006]
- Ontologies in science dataspaces [Ning, Wang ICPCA 2007]

## Personal DS Issues

Many territorial entities in your dataspace

- Device boundaries: laptop vs. PDA
- Document boundaries: directory vs. cells
- Server boundaries: files vs. email

Desktop search doesn't solve it all.

# Issue: Reconciling References

- References might have small numbers of attributes
- Not a lot of data to train on or analyze
- · References evolve
  - People move
  - Documents go through versions (think about your interview talk)

## Issue: One-time Query

- Standard information integration often starts by listing frequent queries that are anticipated
- In a personal DS, you might want to ask a query once over a particular combination of sources

"What exam questions do I have that weren't in the HW, weren't on the practice exam, weren't used in class, aren't in the back of the book, aren't examples in the book?"

# **SEMEX: Semantic Exploration**

- Extract objects and relationships automatically and cast into a personal information model [Dong, Halevy CIDR 2005]
- Reference reconciliation is critical

```
First: Mike, Last:Carey, Loc: IBM
First: Michael, Last:Carey
Last: Carey, Email: <u>carey@ibm.com</u>
Email: <u>carey@ibm.com</u>, Loc: Almaden
```

## Reference Merging

Combine references, allow multivalues

```
First: Mike, Last: Carey, Loc: IBM

First: {Mike, Michael},

Last: Carey, Loc: IBM

First: Michael, Last: Carey

First: {Mike, Michael}, Last: Carey,

Email: carey@ibm.com

Loc: {IBM, Almaden}

Last: Carey, email: carey@ibm.com

Loc: Almaden

Email: carey@ibm.com, Loc: Almaden
```

# **Evolving Objects**

- · Do fine-grained reconciliation
- Look for evidence to build chains that represent versions of objects.

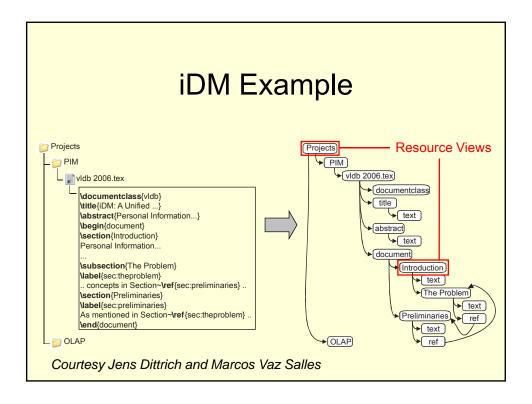
Emails for Carey from ibm.com don't overlap in time with emails for Carey from bea.com

## **iMeMex**

- You saw this previously in iTrails [Dittrich, Vaz Salles VLDB 06]
- Try to over come the document boundary

Why is the file-system directory hierarchy different than the element hierarchy in an XML document?

iMeMex Data Model (iDM)



# Ask Us Questions ...

... or straighten us out

# **Backup Slides**

And Extras

## **Query Answering Semantics**

- Input:
  - Source S, query Q
  - P-med-schema  $\mathbf{M} = \{ (M_1, Pr(M_1)), ..., (M_{\nu}Pr(M_{\nu})) \}$
  - P-mappings **pM** = { $pM(M_1)$ , ...,  $pM(M_1)$ }
- Output probability of tuple t:
  - $p = \sum Pr(t|M_i) * Pr(M_i)$

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## **Query Answering**

**S1** 

name	hPhone	oPhone	hAddr	oAddr
Alice	123-4567	765-4321	123, A Ave.	456, B Ave

Q

SELECT name, phone, address FROM Med-S

**Answers** 

Tuple	Probability
('Alice', '123-4567', '123 A Ave.')	0.34
('Alice', '765-4321', '456 B Ave.')	0.34
('Alice', '765-4321', '123 A Ave.')	0.16
('Alice', '123-4567', '456 B Ave.')	0.16

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# Expressive Power of P-Med-Schema v.s. P-Mapping

Theorem 1. For one-to-many mappings:

(p-med-schema + p-mappings)

- = (mediated schema + p-mapping)
- > (p-med-schema + mappings)

Theorem 2. When restricted to one-to-one mappings:

(p-med-schema + p-mappings)

- = (p-med-schema + mappings)
- > (mediated schema + p-mapping)

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### Creation: 1) Creating a Single Med-Schema

• Input: Single-table source schemas  $S_1, ..., S_n$ 

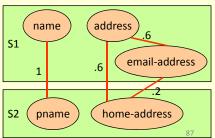
Output: Single-table mediated schema M

- Algorithm
- 1. Remove all infrequent attributes

2. Find *similarity* between every pair of attributes and construct a weighted graph

3. Remove edges with weight below  $\tau$  (e.g.,  $\tau$ =.5)

4. Each connected component is a cluster



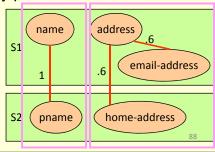
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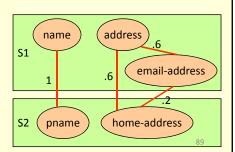


### Creation: 2) Creating All Possible Med-Schemas

- Algorithm
- 1. Remove all infrequent attributes
- 2. Find *similarity* between every pair of attributes and construct a weighted graph
- 3. For each edge
  - (weight  $\geq \tau + \epsilon$ )  $\rightarrow$  retain
  - (weight  $< \tau \epsilon$ )  $\rightarrow$  drop
  - (τ-ε ≤ weight < τ+ε) → uncertain edge

(e.g., 
$$\tau$$
 =.6,  $\epsilon$  = .2)

4. Clustering for each combo of including/excluding uncertain edges

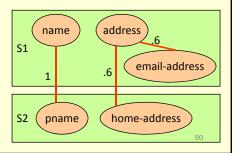


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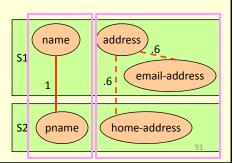


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- 3. For each edge
  - (weight ≥ τ+ε) → retain
  - (weight  $< \tau \epsilon$ )  $\rightarrow$  drop
  - (τ-ε ≤ weight < τ+ε) → uncertain edge

(e.g., 
$$\tau$$
 =.6,  $\epsilon$  = .2)

 Clustering for each combo of including/excluding uncertain edges

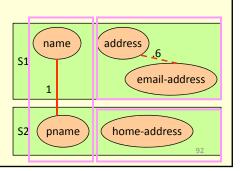


### Creation: 2) Creating All Possible Med-Schemas

- Algorithm
- 1. Remove all infrequent attributes
- 2. Find *similarity* between every pair of attributes and construct a weighted graph
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  - (weight  $< \tau \epsilon$ )  $\rightarrow$  drop
  - $(T-\epsilon \le weight < T+\epsilon) \rightarrow$  uncertain edge

(e.g., 
$$\tau$$
 =.6,  $\epsilon$  = .2)

4. Clustering for each combo of including/excluding uncertain edges

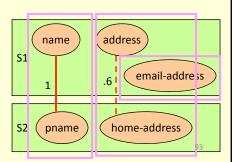


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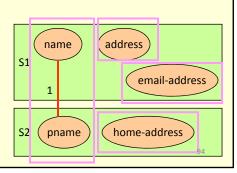


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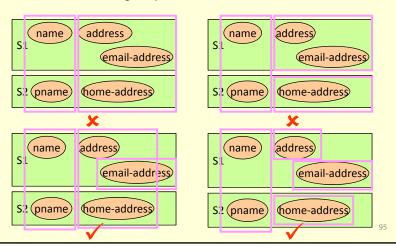
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### Creation: 3) Computing Probabilities

 Mediated schema M and source S are consistent if no two attributes of S are grouped into same cluster in M



### Creation: 3) Computing Probabilities

 Assign probabilities to each M proportional to the number of sources it is consistent with.

