Similarity Search in Large Databases

Introduction to Similarity Search

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Outline

1. Similarity Search
   - Intuition
   - Applications
   - Framework

What is Similarity Search?

- Similarity search deals with the question:

  How similar are two objects?

- "Objects" may be
  - strings (`Augsten` $\leftrightarrow$ `Augusten`)
  - tuples in a relational database

    (`Augsten` | `Dominikanerplatz 3` | `204` | `70188`)
    $\leftrightarrow$
    (`N. Augsten` | `Dominikanerpl. 3` | `@` | `70188`)

  - documents (e.g., HTML or XML)
  - ...
- "Similar" is application dependant

Application I: Entity Resolution (ER)

- Problem: (also known as "object identification")
  - Two data items represent the same real world object/entity (e.g., the same person),
  - but they are represented differently in the database(s).
- How can this happen?
  - different coding conventions (e.g., `Gilmstrasse`, `Hermann-von-Gilm-Str.`)
  - spelling mistakes (e.g., `Untervigil`, `Untervigli`)
  - outdated values (e.g., `Siegesplatz` used to be `Friedensplatz`).
  - incomplete/incorrect values (e.g., missing or wrong apartment number in residential address).
- Focus in this course!

Application I: Flavors of Entity Resolution

- Duplicate Detection (also: "dirty ER")
  - one table
  - find all tuples in the table that represent the same thing in the real world
  - Example: Two companies merge and must build a single customer database.
- Similarity Join (also: "clean-clean ER")
  - two tables
  - join all tuples with similar values in the join attributes
  - Example: In order to detect tax fraud, data from different databases need to be linked.
- Similarity Lookup
  - one table, one tuple
  - find the tuple in the table that matches the given tuple best
  - Example: Do we already have customer X in the database?

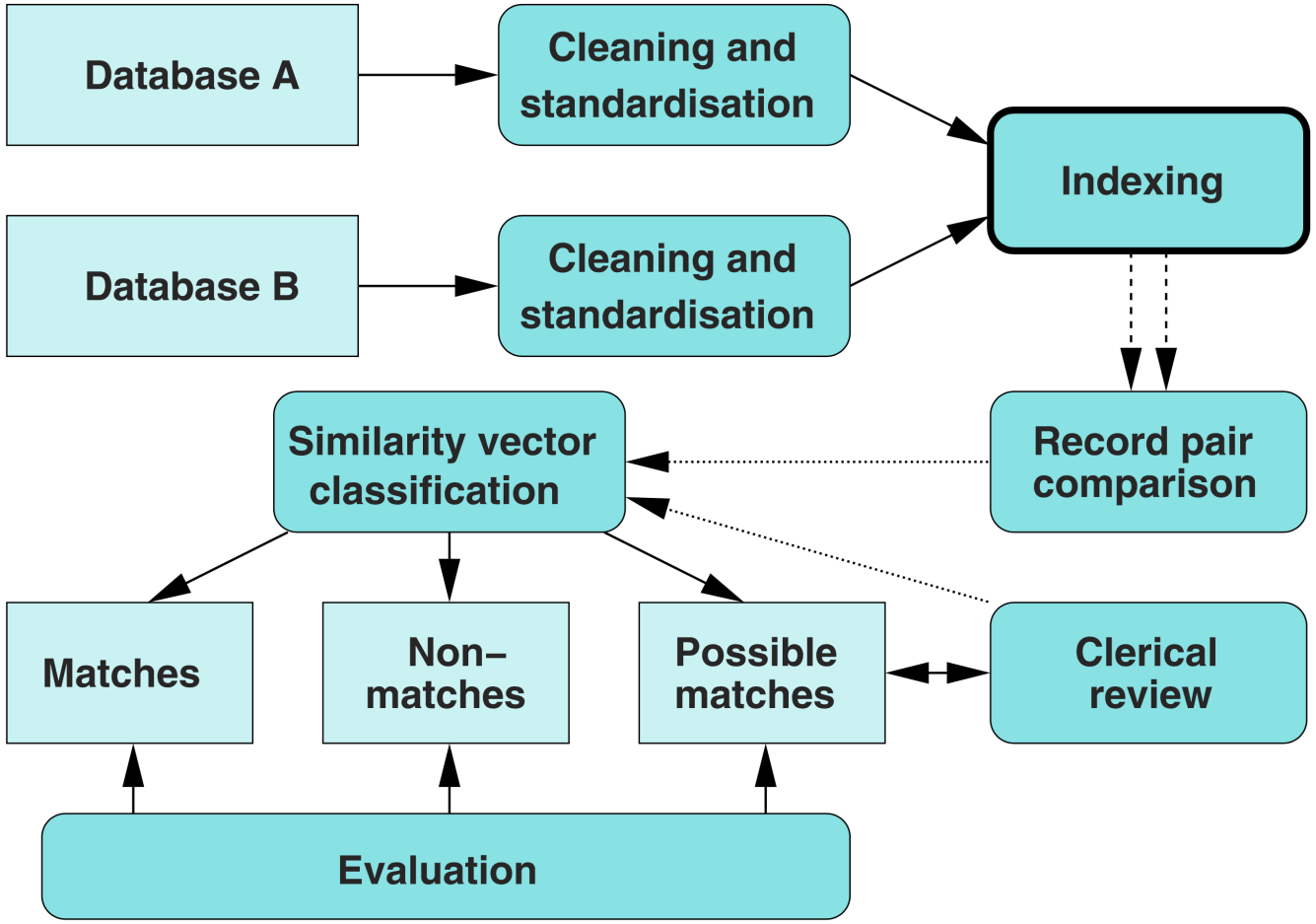
Application II: Computational Biology

- DNA and protein sequences
  - modelled as text over alphabet (e.g. $\{A, C, G, T\}$ in DNA)
- Application: Search for a pattern in the text
  - look for given feature in DNA
  - compare two DNAs
  - decode DNA
- Problem: Exact matches fail
  - experimental measures have errors
  - small changes that are not relevant
  - mutations
- Solution: Similarity search
  - Search for *similar* patterns
  - *How similar* are the patterns that you found?

Application III: Error Correction in Signal Processing

- Application: Transmit text signal over physical channel
- Problem: Transmission may introduce errors
- Goal: Restore original (sent) message
- Solution: Find correct text that is closest to received message.

Framework for Similarity Search / 1



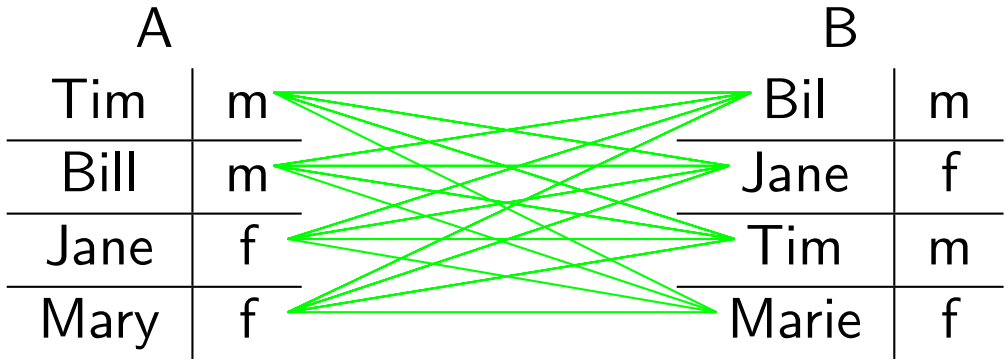
Source figure: [Chr12].

Framework for Similarity Search / 2

1. Preprocessing: Cleaning and standardization, e.g.
   - lowercase all values: `Augsten` → `augsten`
   - standardize values: {`f`, `w`, `female`, `weiblich`} → {`f`}
   - standardize encoding: `K.Wolf Strasse` → `Karl-Wolf-Str.`
2. Indexing for Search Space Reduction
   - blocking
   - sorted-neighborhood
   - filter ing (pruning)
   - nearest neighbor search
3. Compute Distances
   - compare record/tuple pairs
4. Find Matches: Classification
   - classify record/tuple pairs based on a distance or a vector of distances

Search Space Reduction: Brute Force

- We consider the example of similarity join.
- Similarity Join: Find all pairs of similar tuples in tables A and B.
  - Search space: $A \times B$ (all possible pairs of tuples)
  - Complexity: compute $|A||B|$ distances $\rightarrow$ expensive!
    ($|A| = 30k$, $|B| = 40k$, $1ms$ per distance $\Rightarrow$ join will run for 2 weeks)
- Example: 16 distance computations!

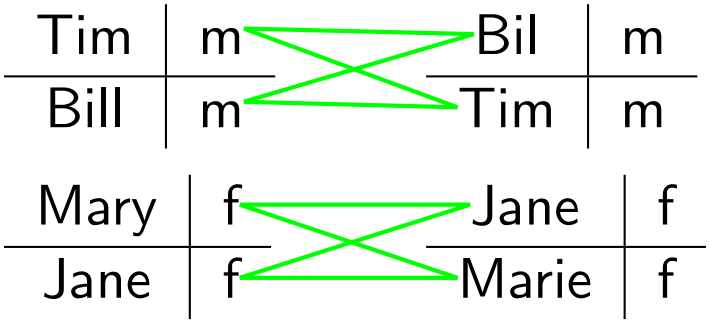


- Goal: Reduce search space!

Search Space Reduction: Blocking

- Blocking
  - Generate blocks for A and B (seperately):
    1. compute one or more block keys for each tuple
    2. each distinct block key represents one block
    3. assign each tuple to all blocks of its block keys
  - Compare only tuples of block pairs with the same block key.
- Example: Attribute blocking: block key is value of a chosen attribute.

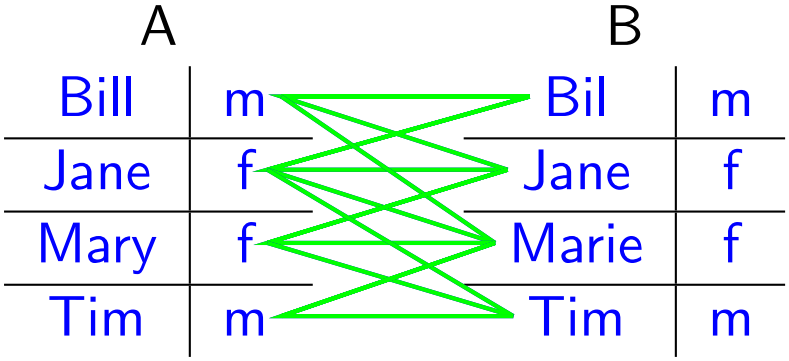
  Block by "gender" attribute:



- Improvement: 8 distance computations (instead of 16)!

Search Space Reduction: Sorted Neighborhood

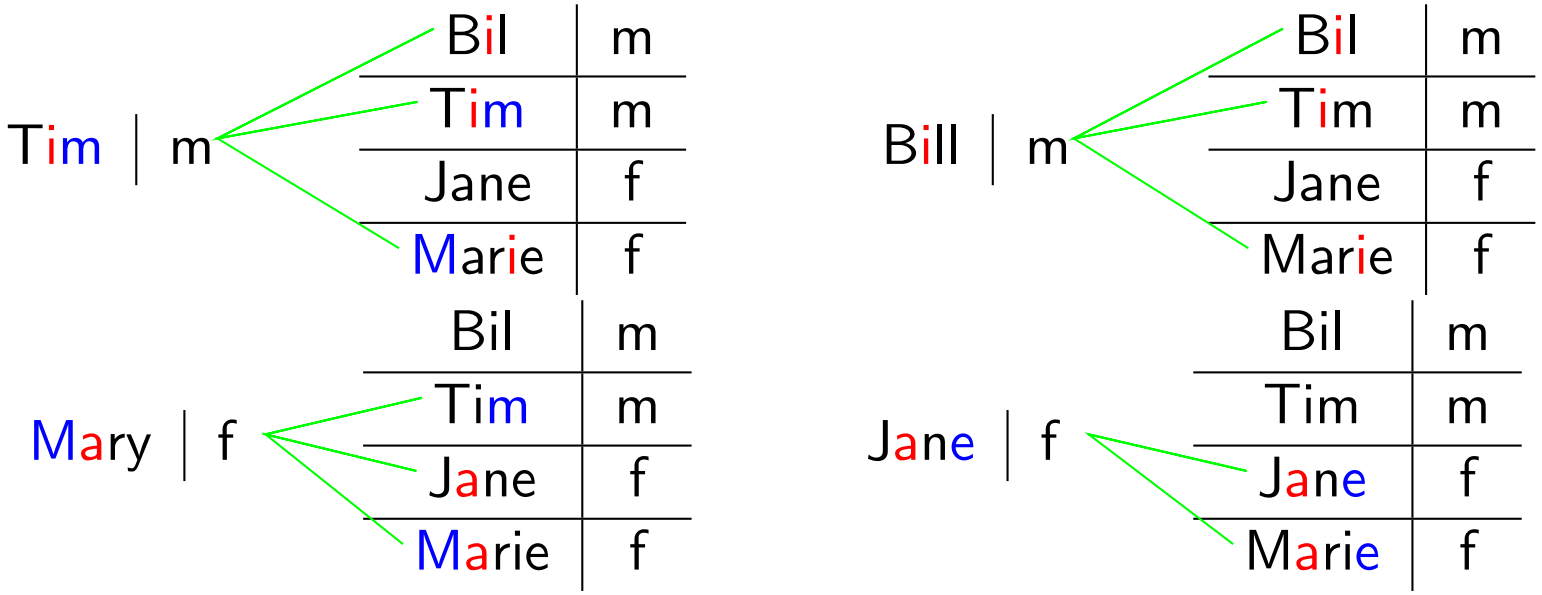
- Sorted Neighborhood
  - Sort A and B (e.g., by one of the attributes).
  - Move a window of fixed size over A and B.
    - move A-window if sort attribute of next tuple in A is smaller than in B
    - otherwise move B-window
  - Compare only tuples within the windows.
- Example: Sort by name, use window of size 2:



- Improvement: 12 distance computations (instead of 16)!

Search Space Reduction: Filtering

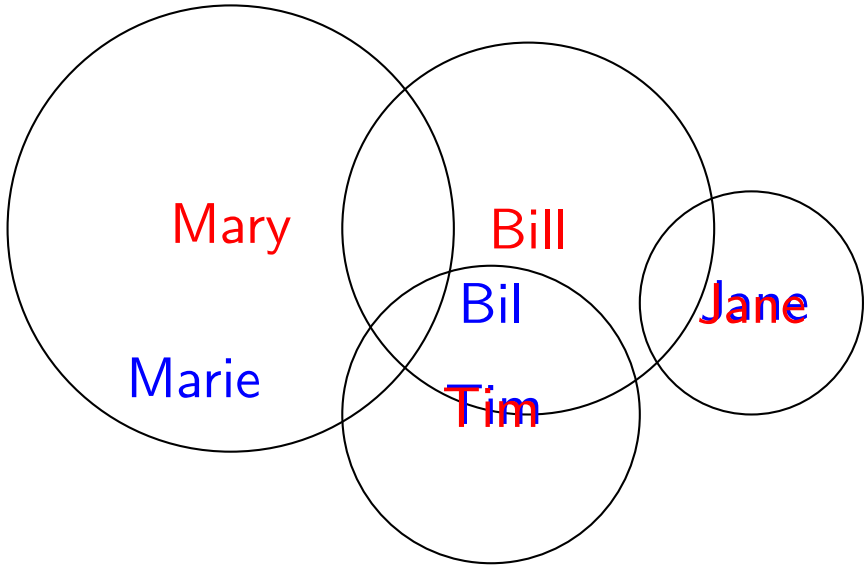
- Filtering (Pruning)
  - Filter: quick check if tuple pair is "promising" (i.e., distance is expected to be small enough).
  - Do not compute distance function if filter check fails.
  - Idea: filter is faster than distance function. Overhead for filtering is amortized by avoided distance computations.
- Example: Do not match names that have no character in common:



- Improvement: 11 distance computations (instead of 16)!

Search Space Reduction: Nearest-Neighbor Search

- Represent tuples in some vector space or metric space.
- For each tuple t in A:
  - search for all tuples in B that are close to tuple t of A
  - distance to t is evaluated only for these tuples of B
- Example: Search for tuples of A in tuples of B.



- Improvement: 6 distance computations (instead of 16)!

Distance Computation

Definition (Distance Function)

Given two sets of objects, A and B, a *distance function* for A and B maps each pair $(a, b) \in A \times B$ to a positive real number (including zero).

$$\delta : A \times B \to \mathbb{R}_0^+$$

- We will define distance functions for
  - sets
  - strings
  - trees

Distance Matrix

Definition (Distance Matrix)

Given a distance function δ for two sets of objects, $A = \{a_1, \ldots, a_n\}$ and $B = \{b_1, \ldots, b_m\}$.
The *distance matrix* D is an $n \times m$-matrix with

$$d_{ij} = \delta(a_i, b_j),$$

where d_{ij} is the element at the i-th row and the j-th column of D.

- Example distance matrix, $A = \{a_1, a_2, a_3\}$, $B = \{b_1, b_2, b_3\}$:

	b_1	b_2	b_3
a_1	6	5	4
a_2	2	2	1
a_3	1	3	0

Finding Matches

	b_1	b_2	b_3
a_1	6	5	4
a_2	2	2	1
a_3	1	3	0

- Once we know the distances – which objects match?
- Distance matrix and search space reduction:
  - matrix may be only partially filled at the time of computing matches
  - missing distance values are treated as infinite

Finding Matches: Threshold Matching

	b_1	b_2	b_3
a_1	6	5	4
a_2	2	2	1
a_3	1	3	0

- Threshold Approach:
  - fix threshold τ
  - for a given object, all objects with a distance range of τ are matched
- Algorithm: produces n:m matching

  foreach $d_{ij} \in D$ **do**
    if $d_{ij} \leq \tau$ **then** match (a_i, b_j)

- Example with $\tau = 2$: $\{(a_2, b_1), (a_2, b_2), (a_2, b_3), (a_3, b_1), (a_3, b_3)\}$

Finding Matches: k-Nearest Neighbor Matching

	b_1	b_2	b_3
a_1	6	5	4
a_2	2	2	1
a_3	1	3	0

- k-Nearest-Neighbor (kNN) Matching:
  - fix number of neighbors k
  - for a given object, form a match with its k nearest neighbors
- Algorithm: produces 1:k matching

  foreach row i of distance matrix D **do**
  find column IDs $c_1, c_2, \ldots, c_k$ of k smallest values in row i of D
  form k matches $(a_i, b_{c_1}), (a_i, b_{c_2}), \ldots, (a_i, b_{c_k})$
- Properties:
  - not symmetric: transposed matrix D^T may give a different result
  - ties affect the matching (only for k-th neighbor)
- Example $k = 2$: $\{(a_1, b_3), (a_1, b_2), (a_2, b_3), (a_2, b_1), (a_3, b_3), (a_3, b_1)\}$

Finding Matches: Global Greedy

- Global Greedy Approach
  - form object pair with smallest distance first
  - matched objects are removed
- Algorithm: produces 1:1 matching

$M \leftarrow \emptyset$
$A \leftarrow \{a_1, a_2, \ldots, a_n\}$; $B \leftarrow \{b_1, b_2, \ldots, b_m\}$
create sorted list L with all $d_{ij} \in D$
while $A \neq \emptyset$ **and** $B \neq \emptyset$ **do**
  $d_{ij} \leftarrow$ deque smallest element from L
  if $a_i \in A$ **and** $b_j \in B$ **then**
    $M \leftarrow M \cup (a_i, b_j)$
    remove a_i from A and b_j from B
return M

- Properties: must deal with ties when sorting list L, e.g., sort ties randomly, sort ties by i and j
- Example (sort ties by i, j): $\{(a_3, b_3), (a_2, b_1), (a_1, b_2)\}$

	b_1	b_2	b_3
a_1	6	5	4
a_2	2	2	1
a_3	1	3	0

Overview: Matching Techniques

- Threshold Matching:
  - all objects with distance within τ match
  - n:m-matching
  - symmetric, not affected by ties
- k-Nearest Neighbor Matching:
  - each object is matched to its k closest objects
  - 1:k-matching
  - not symmetric, affected by ties
- Global Greedy Approach:
  - pair with smallest distance is matched first and removed
  - 1:1-matching
  - symmetric, affected by ties

Conclusion

- Framework for similarity queries:
  1. Preprocessing: Cleaning and standardization
  2. Indexing for Search Space Reduction
     - blocking
     - sorted-neighborhood
     - filtering (pruning)
     - nearest neighbor search
  3. Compute Distances
  4. Find Matches: Classification
     - threshold-based
     - k-nearest-neighbor
     - global greedy

Peter Christen.

A survey of indexing techniques for scalable record linkage and deduplication.

IEEE Trans. Knowl. Data Eng., 24(9):1537–1555, 2012.