Robust temporal graph clustering and cluster evaluation measure for group record linkage

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Outline

• Group record linkage and (temporal) constraints

• Temporal constraints based graph clustering
  • Detailed steps of our approach
  • Experimental evaluation on a Scottish data set from the Isle of Skye

• Cluster quality evaluation measure for group record linkage
  • Why traditional evaluation measures might not be adequate
  • A new cluster quality evaluation measure
  • Illustrative use on a Scottish data set

• Conclusions and future work
(Historical) Group Record Linkage

• Record linkage is the process of identifying sets of records that refer to the same entity (person) within one database or across different databases.

• In group record linkage, the aim is to link records for groups of entities, such as families or households.

• Historical record linkage refers to the linkage of historical birth, marriage, and death records for population reconstruction (building family trees), where each record contains information about several people.
Problem Statement

• **Aim**: To identify groups of records that refer to the same entities where there are certain temporal constraints between records.

• **Challenges**:
  - Existing record linkage techniques do not consider constraints that are implied by factors such as time (temporal), culture, or geographic location.
  - Data errors are often introduced when recording and transcribing the data.
  - Missing values in records.
  - Highly skewed frequency distributions of names.

<table>
<thead>
<tr>
<th>First name</th>
<th>Last name</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Father</td>
</tr>
<tr>
<td>John (3,444)</td>
<td>Mcleod (1,571)</td>
</tr>
<tr>
<td>Donald (2,628)</td>
<td>Mcdonald (1,556)</td>
</tr>
<tr>
<td>Alexander (1,665)</td>
<td>Mckinnon (1,168)</td>
</tr>
<tr>
<td>Malcolm (800)</td>
<td>Nicolson (1,047)</td>
</tr>
<tr>
<td>Neil (787)</td>
<td>Mclean (908)</td>
</tr>
</tbody>
</table>
We introduce a novel graph clustering approach for group record linkage which takes temporal constraints into account.

Temporal constraints: The constraints implied by time differences when linking records.

Due to biological limitations, it is temporally not possible for the same mother to have two babies 5 months apart.

Bangladesh woman with two wombs has twins one month after first birth: https://www.bbc.com/news/world-asia-47729118
## Phase 1: Similarity Graph Generation

<table>
<thead>
<tr>
<th>Record ID</th>
<th>Baby’s name</th>
<th>Mother’s name</th>
<th>Father’s name</th>
<th>Date of birth</th>
</tr>
</thead>
<tbody>
<tr>
<td>k</td>
<td>Mary</td>
<td>Kate</td>
<td>John</td>
<td>01/02/1861</td>
</tr>
<tr>
<td>l</td>
<td>Tom</td>
<td>Katy</td>
<td>Johnny</td>
<td>05/07/1863</td>
</tr>
<tr>
<td>m</td>
<td>Pat</td>
<td>Kate</td>
<td>John</td>
<td>12/12/1869</td>
</tr>
<tr>
<td>o</td>
<td>Harry</td>
<td>Peggy</td>
<td>-</td>
<td>03/09/1890</td>
</tr>
<tr>
<td>p</td>
<td>Kate</td>
<td>Peg</td>
<td>Ron</td>
<td>06/11/1896</td>
</tr>
<tr>
<td>q</td>
<td>Lizzy</td>
<td>Peggy</td>
<td>Roger</td>
<td>01/01/1901</td>
</tr>
</tbody>
</table>

### Similarity graph $G$

![Similarity graph $G$](image)
Phase 1: Similarity Graph Generation

- **Records**
  - **Record ID**: k, l, m, o, p, q
  - **Baby's name**: Mary, Tom, Pat, Harry, Kate, Lizzy
  - **Mother's name**: Kate, Katy, Kate, Peggy, Peg, Peggy
  - **Father's name**: John, Johnny, John, Roger, Ron, -
  - **Date of birth**: 01/02/1861, 05/07/1863, 12/12/1869, 03/09/1890, 06/11/1896, 01/01/1901

- **Similarity Graph**
  - **Graph G**
  - **Similarity values**
    - 0.45, 0.55, 0.6, 0.7, 0.75, 0.8, 0.85, 0.9, 0.95

- **Temporally not possible links**
Phase 2 (a): Link Strength Based Edge Classification

- The concept of link strength is first used in record linkage by Saeedi et al. (2018). Only the edges with similarities greater than a user defined threshold are used.

- **Strong**: Edges \((r_i, r_j)\) with the highest similarity with respect to all other edges connected to both \(r_i\) and \(r_j\).

- **Norm**: Edges \((r_i, r_j)\) with the highest similarity with respect to all other edges connected to either \(r_i\) or \(r_j\), but not both.

- **WeakHigh**: Edges which are neither strong nor normal.

- **Strong**: \(c, b\) with similarity 0.95
- **Norm**: \(f, h\) with similarity 0.9
- **WeakHigh**: \(a, k\) with similarity 0.6
Phase 2 (b): Base Cluster Generation

Iterative Cluster Refinement:
• The temporal implausibilities of connected components are eliminated in this step.
• For each connected component, nodes involved in implausible connections are ordered to determine the best sequence to iteratively remove non-temporal edges.
Phase 3: Iterative Cluster Merging

- Pairwise base cluster similarity is a combination of the similarity and the coverage.

- Similarity can be calculated as:
  - Maximum – maximum similarity among edges between two clusters (complete-link)
  - Minimum – minimum similarity among edges between two clusters (single-link)
  - Average – average similarity across edges between two clusters (average-link)

- Coverage = \[
\frac{\text{Number of edges of the selected link strength between two clusters}}{\text{Number of all edges between two clusters (with respect to the similarity graph } G)}\]
Experimental Setup

• Data set
  • For evaluation we used a real Scottish birth data set with 17,614 birth certificates, covering the population of the Isle of Skye from 1861 to 1901.
  • Each birth certificate contains personal details about a baby and its parents such as their names, address, marriage date, occupations, and the baby's date of birth.
  • We used six different attribute combinations for similarity calculation: all (parents names, addresses, occupations, and marriage dates), parent names with addresses, and parent names only, with and without weighting (Fellegi and Sunter, 1969).

• Evaluation measures:

<table>
<thead>
<tr>
<th>Precision</th>
<th>Recall</th>
<th>Area under the precision-recall curve (AUC-PR)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TP/(TP+FP)</td>
<td>TP/(TP+FN)</td>
<td>A summary measure of the precision and recall values across different similarity thresholds</td>
</tr>
</tbody>
</table>

TP – True matching record pairs, FP – Wrongly matched record pairs, FN – Wrongly non-matched record pairs
• Results are shown only for base clusters created with 'Strong' edges, since they showed highest precision (95%). Since the variation across similarity calculation methods was minimal, we have shown curves only for the 'average' similarity method.
• Surprisingly, better results were obtained with fewer attributes for similarity graph generation!
Area Under the Precision-Recall Curve (AUC-PR)

<table>
<thead>
<tr>
<th>Similarity graph</th>
<th>Temporal</th>
<th>Non-temporal</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Connected component</td>
<td>Connected component</td>
</tr>
<tr>
<td>All (UW)</td>
<td>0.72 ± 0.012</td>
<td>0.64 ± 0.005</td>
</tr>
<tr>
<td>All (W)</td>
<td>0.77 ± 0.014</td>
<td>0.69 ± 0.005</td>
</tr>
<tr>
<td>Names and addresses (UW)</td>
<td>0.87 ± 0.006</td>
<td>0.83 ± 0.002</td>
</tr>
<tr>
<td>Names and addresses (W)</td>
<td>0.86 ± 0.007</td>
<td>0.80 ± 0.003</td>
</tr>
<tr>
<td>Names only (UW)</td>
<td>0.88 ± 0.002</td>
<td>0.85 ± 0.001</td>
</tr>
<tr>
<td>Names only (W)</td>
<td>0.80 ± 0.002</td>
<td>0.73 ± 0.001</td>
</tr>
<tr>
<td>Averages</td>
<td>0.82 ± 0.064</td>
<td>0.76 ± 0.083</td>
</tr>
<tr>
<td></td>
<td>Star</td>
<td>Star</td>
</tr>
<tr>
<td></td>
<td>0.70 ± 0.003</td>
<td>0.63 ± 0.003</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.68 ± 0.004</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.73 ± 0.003</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.72 ± 0.007</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.78 ± 0.015</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.69 ± 0.019</td>
</tr>
</tbody>
</table>

- We compared this novel approach against our recently proposed temporal star clustering approach (Nanayakkara et al. 2018).
- There are no other temporal clustering approaches that we are aware of.
- Our new temporal approach achieved the highest average AUC-PR value of 0.88, compared to the previous temporal star clustering approach.
Are Precision and Recall Suitable for Evaluating Group Record Linkage?

• Precision and recall (as used before) have traditionally been employed to evaluate linkage quality in situations where ground truth data is available.
  • True Positives (true matching record pairs – correct matches).
  • False Positives (wrongly matched record pairs – false matches).
  • False Negatives (wrongly non-matched record pairs – missed matches).
• These metrics measure the quality of links between records.
• For group record linkage, however, we want the quality of clusters (groups) of records.
• Precision and recall can be ambiguous and not meaningful.
Examples of Different Cluster Predictions with same Precision and Recall Results

- The number of correct true matches (true positives) is 6 (solid lines).
- The number of false matches (false positives) is 4 (dotted lines).
- The number of missed matches (false negatives) is 3.
- Precision is 6/10 and recall is 6/9 for all three cluster predictions.
Record Based Cluster Evaluation Measures

• We need measures that assess the quality of clusters based on the records within them – with regard to ground truth clusters.

• This is a more complex undertaking, as there can be some correctly and some wrongly linked records in a cluster.

• The number of predicted clusters can also be higher or lower than the number of ground truth clusters.
  • In some applications this is problematic.
  • For example, in our birth bundling linkage we cannot have several clusters associated with a single mother.
Seven Categories of Predicted Clusters (1)

- Correct singleton (SS): Records in clusters of size 1 in both ground truth and predicted clusters.

- Wrongly grouped singleton (SG): Records in clusters of size 1 in ground truth but size larger than 1 (groups) in predicted clusters.

- Missed group member (GS): Records in clusters larger than size 1 in ground truth but size 1 in predicted clusters.

- Wrongly assigned member (GG_W): Records from a ground truth cluster of size larger than 1 are assigned to a wrong predicted group (not singleton).
Seven Categories of Predicted Clusters (2)

• Exact group match (\textbf{GG\_E}): Clusters of size larger than 1 which are the same in ground truth and predicted clusters.

• Majority group match (\textbf{GG\_M}): Clusters of size larger than 1 in both ground truth and predicted clusters, where the majority of records are the same.

• Minority group match (\textbf{GG\_m}): Clusters of size larger than 1 in both ground truth and predicted clusters, where the majority of records are not the same.
Categorising Records based on Thresholds

• As with traditional record linkage, we can classify record pairs as matches or non-matches based on different similarity thresholds.

• This will result in different numbers of records being classified into the seven categories.
Areas Under the Curves

• As with the AUC-PR, we can summarise these lines as areas under the curves over a range of different similarity thresholds (and normalised into the 0..1 range).

• Better clustering results will have higher values for \( SS \), \( GG_E \), \( GG_M \) and \( GG_m \), and lower values for \( SG \), \( GS \), and \( GG_W \).

<table>
<thead>
<tr>
<th>Clustering technique</th>
<th>AUC-PR</th>
<th>SS</th>
<th>GG_E</th>
<th>GG_M</th>
<th>GG_m</th>
<th>SG</th>
<th>GS</th>
<th>GG_W</th>
</tr>
</thead>
<tbody>
<tr>
<td>Connected components</td>
<td>0.744</td>
<td>0.036</td>
<td>0.206</td>
<td>0.077</td>
<td>0.010</td>
<td>0.087</td>
<td>0.017</td>
<td>0.567</td>
</tr>
<tr>
<td>Star clustering</td>
<td>0.775</td>
<td><strong>0.046</strong></td>
<td>0.367</td>
<td><strong>0.333</strong></td>
<td>0.020</td>
<td><strong>0.077</strong></td>
<td>0.020</td>
<td>0.137</td>
</tr>
<tr>
<td>Robust graph clustering</td>
<td><strong>0.885</strong></td>
<td>0.044</td>
<td><strong>0.413</strong></td>
<td>0.298</td>
<td><strong>0.027</strong></td>
<td>0.077</td>
<td>0.017</td>
<td><strong>0.124</strong></td>
</tr>
</tbody>
</table>
Conclusions and Future Work

• We proposed:
  • A novel temporal graph clustering approach for group record linkage, which addresses the previously highlighted challenges in this domain.
  • Our proposed approach takes advantage of the link strength categorisation in the record grouping, which improves clustering quality.
  • Experimental results show that our approach achieves improved linkage quality with respect to non-temporal clustering approaches, and substantially outperforms a previous temporal clustering approach for group record linkage.
  • A novel record based cluster evaluation measure for group record linkage which classifies records into one of seven categories.

• Future work:
  • Conduct empirical evaluations for different data sets and parameter settings.
  • Develop an adaptive technique to learn temporal constraints for different time intervals using ground truth data.
  • Investigate record linkage evaluation measures when no ground truth data are available.
Questions?

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