Assessing the re-identification potential of health care data for people with statutory health insurance in Germany (preliminary results)

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Outline

1. Background
2. Methods
3. Results
4. Discussion
Background

- **Illness** might predict or turn into a chronic illness
- Sensitive nature of health care data obliges institutions dealing with them to ensure confidentiality and prevent re-identification
- Assessment of re-identification risk necessary
  - re-identification potential
- Application to German statutory health insurance data
Background

- DaTraV data
- Data from ~70 million people with statutory health insurance in Germany
  - Data generated by physicians, hospitals, pharmacies
    - Invoice services
    - Compensate expenses between health insurance companies
    - Research or controlling → DIMDI
  - Socio-demographics, outpatient medication, inpatient and outpatient diagnoses, health insurance expenses
Background

- **DIMDI**
  - Trust centre
  - Data processing centre
    - Services to authorised institutions → data analysis, result sets
    - Confidentiality
    - Normally: aggregated result sets
    - Exception: analysis on-site
Modelling re-identification risk
Results of an expert survey

- Potentially suitable methods
  - Uniqueness measure (see e.g. Duncan et al. 2011)
  - Special uniques detection algorithm (Elliot et al. 2002)
  - Loglinear models (Skinner & Holmes 1998)
  - Record linkage (Domingo-Ferrer & Torra 2002)
  - Information theoretic approach (Antal et al. 2014)
  - Aggregated individual risk measures

- Importance of appropriate definition of risk scenarios (dependent on context)
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Application of the uniqueness measure

• **Basis** for many methods for modelling re-identification risk
• **Joint consideration** of variables/attributes
• Examination of **attribute patterns**
• **DaTraV data:** sample uniqueness → population uniqueness
• **Rare attribute values or rare attribute combinations** → higher re-identification risk
### Uniqueness measure

#### Example

<table>
<thead>
<tr>
<th>No.</th>
<th>Sex</th>
<th>Born in</th>
<th>Diagnosis 1</th>
<th>Diagnosis 2</th>
<th>Diagnosis 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Male</td>
<td>196X</td>
<td>E10 (diabetes), 1st half-year 20YY, confirmed diagnosis</td>
<td>J06 (upper respiratory infection), 2nd half-year 20YY, primary inpatient diagnosis</td>
<td>E10 (diabetes), 2nd half-year 20YY, secondary inpatient diagnosis</td>
</tr>
<tr>
<td>2</td>
<td>Male</td>
<td>198X</td>
<td>F32 (depression), 2nd half-year 20YY, confirmed diagnosis</td>
<td>J45 (asthma), 2nd half-year 20YY, confirmed diagnosis</td>
<td>J20 (bronchitis), 1st half-year 20YY, confirmed diagnosis</td>
</tr>
<tr>
<td>3</td>
<td>Female</td>
<td>197X</td>
<td>K02 (caries), 1st half-year 20YY, confirmed diagnosis</td>
<td>A09 (gastro-intestinal disease), 1st half-year 20YY, confirmed diagnosis</td>
<td>—</td>
</tr>
<tr>
<td>4</td>
<td>Male</td>
<td>198X</td>
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**Uniqueness measure**

Selection of *key variables*

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Year of birth</td>
<td>Numeric (4 digits)</td>
</tr>
<tr>
<td>Sex</td>
<td>1 – female, 2 – male</td>
</tr>
<tr>
<td>Documented ICD-code</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>Documentation period</td>
<td>Years, half-years, quarters</td>
</tr>
<tr>
<td>Qualification/type of diagnosis</td>
<td>V – suspected, G – confirmed, Z – condition after, A – diagnosis of</td>
</tr>
<tr>
<td></td>
<td>exclusion, O – other</td>
</tr>
<tr>
<td></td>
<td>1 – primary diagnosis, 2 – secondary diagnosis</td>
</tr>
<tr>
<td>Sector</td>
<td>1 – outpatient, 2 – inpatient</td>
</tr>
</tbody>
</table>
## Uniqueness measure

### Definition of risk scenarios

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Scenario 1</th>
<th>Scenario 2</th>
<th>Scenario 3</th>
<th>Scenario 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Year of birth</td>
<td></td>
<td>Yes</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td>Yes</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Documented ICD-codes</td>
<td></td>
<td></td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>Documentation period</td>
<td>Quarters</td>
<td>Quarters</td>
<td>Half-years</td>
<td>Year</td>
</tr>
<tr>
<td>Qualification/type of diagnosis</td>
<td>All qualifications incorporated</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sector</td>
<td></td>
<td></td>
<td>Separate consideration</td>
<td></td>
</tr>
<tr>
<td>Number of considered ICD-codes</td>
<td>4 diagnoses, with chronological order</td>
<td>2 diagnoses, with chronological order</td>
<td>2 diagnoses, with chronological order</td>
<td>2 diagnoses, without chronological order</td>
</tr>
</tbody>
</table>

→ Multiple patterns per person, analysis in batches
Outline

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Uniqueness measure
Calculation of re-identification potential for selected cohorts

<table>
<thead>
<tr>
<th>Cohort</th>
<th>Number of insurants</th>
<th>Number of attribute patterns</th>
</tr>
</thead>
<tbody>
<tr>
<td>Women born 1980</td>
<td>428,979</td>
<td>3,015,917,360</td>
</tr>
<tr>
<td>Men born 1980</td>
<td>351,513</td>
<td>540,947,537</td>
</tr>
<tr>
<td>Women born 1970</td>
<td>477,394</td>
<td>6,922,749,866</td>
</tr>
<tr>
<td>Men born 1970</td>
<td>383,280</td>
<td>2,063,101,723</td>
</tr>
<tr>
<td>Women born 1960</td>
<td>544,015</td>
<td>19,050,562,520</td>
</tr>
<tr>
<td>Men born 1960</td>
<td>450,564</td>
<td>8,469,607,592</td>
</tr>
</tbody>
</table>

Tab. 1: Number of attribute patterns in scenario 1 for different cohorts in the DaTraV dataset for one reporting year.
Results: Uniqueness measure

Fig. 1: Proportion of attribute patterns depending on the frequency of occurrence in the reporting year for persons with year of birth 1960.
Results: Uniqueness measure

Fig. 2: Proportion of attribute patterns depending on the frequency of occurrence in the reporting year for women and men with year of birth 1960.
Results: Uniqueness measure

Fig. 3: Proportion of unique attribute patterns in the reporting year for each cohort.
Results: Uniqueness measure

Fig. 4: Proportion of insured persons with at least X unique attribute patterns in the reporting year for birth cohorts 1960, 1970 and 1980.
Results: Uniqueness measure

Fig. 5: Proportion of insured persons with at least X unique attribute patterns in the reporting year for women and men of birth cohorts 1960, 1970 and 1980.
Outline

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Summary

Results obtained so far

- Many attribute patterns
  - … more for women than for men
  - … slightly more for older cohorts

- Proportion of unique or rare patterns was very high

- Scenario 1:
  - Almost the entire dataset consisted of unique patterns
  - More than half of the statutory insured people had 50 or more unique attribute patterns
Implications for re-identification potential and actual risk

- Basic individual risk measure that is linked to uniqueness of attribute patterns is
  \[ \frac{1}{\text{frequency of that pattern in the population}} \]
- Assumption: Data processor randomly knows at least one specific pattern and is able to find it in the dataset → strong assumption with multiple patterns
- Unique patterns mainly caused by patterns of diagnoses (special uniques)
Implications for statistical disclosure control

• Minimum cell count rule
• Prevention of (approximate) recalculations/derivations
Limitations and further steps

- Inpatient and outpatient diagnoses
- Coarser definition of diagnoses
- Record linkage simulations

→ Based on the achieved results we hope to find a way to better estimate the re-identification risk with
  → the re-identification potential,
  → the intended utilisation
  → and the settings in which the data and the result sets are distributed and handled.
Thank you for your attention.

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References


