Towards implementing the OMOP CDM across five European biologic registries

Edward Burn1,2, Lianne Kearsley-Fleet3, Kimme L. Hyrich3,4, Martin Schaefer5, Doreen Huschek6, Anja Strangfeld6, Jakub Závada6, Markéta Lagová6, Delphine S. Courvoisier7, Christoph Tellenbach7, Kim Lauper3,7, Carlos Sanchez-Piedra9, Nuria Montero9, Jesús-Tomás Sánchez-Costa9, Daniel Prieto-Alhambra1,10

1NDORMS, University of Oxford, UK, 2Fundació Institut Universitari per a la recerca a l’Atenció Primària de Salut Jordi Gol i Gurina (IDIAPJGol), Barcelona, Spain, 3Centre for Epidemiology Versus Arthritis, The University of Manchester, Manchester Academic Health Science Centre, Manchester, UK, 4National Institute of Health Research Manchester Biomedical Research Centre, Manchester University NHS Foundation Trust, Manchester, UK, 5Epidemiology Unit, German Rheumatism Research Center Berlin, Berlin, Germany, 6Institute of Rheumatology, Prague, Czech Republic, 7Division of Rheumatology, University Hospitals of Geneva, Switzerland, 8Swiss Clinical Quality Management in Rheumatic Diseases, Zurich, Switzerland 9Research Unit, Spanish Society of Rheumatology, Madrid, Spain, 10GREMPAL Research Group, Idiap Jordi Gol and CIBERfes, Universitat Autonoma de Barcelona and Instituto de Salud Carlos III, Barcelona, Spain
Towards implementing the OMOP CDM across five European biologic registries

Potential value of a common data model

Implementing the OMOP CDM
Current approach

- New, script based input data mapping for every study

The data...

Link to data

Analytical method
Journey to RWE using a CDM

- Data standardisation enables systematic research
Journey to RWE using a CDM

- Data standardisation enables systematic research

Patient-level data in source system

Patient-level data in Common data model

Reliable evidence
CDM version 6.0
Getting to mapped data

Tools to help you map data

- **WhiteRabbit**: profile your source data
- **RabbitInAHat**: map your source structure to CDM tables and fields
- **ATHENA**: standardized vocabularies for all CDM domains
- **Usagi**: map your source codes to CDM vocabulary
- **CDM**: DDL, index, constraints for Oracle, SQL Server, PostgreSQL; Vocabulary tables with loading scripts
- **ACHILLES**: profile your CDM data; review data quality assessment; explore population-level summaries

**OHDSI Forums**: Public discussions for OMOP CDM Implementers/developers

[http://github.com/OHDSI](http://github.com/OHDSI)
Journey to RWE using a CDM

- Data standardisation enables systematic research
Using the CDM

Patient-level data in CDM

Write code
- Custom

Apply R packages
- OHDSI Methods Library
  - Custom
  - Standard

Use interactive analysis platform
- ATLAS
  - Standard

Reliable evidence
Towards implementing the OMOP CDM across five European biologic registries

Potential value of a common data model

Implementing the OMOP CDM
Objective

To map national biologic registry data collected from different European countries to the OMOP CDM.

Five biologic registries are currently being mapped:

1. The Czech biologics register (ATTRA)
2. Registro Español de Acontecimientos Adversos de Terapias Biológicas en Enfermedades Reumáticas (BIOBADASER)
3. British Society for Rheumatology Biologics Register for Rheumatoid Arthritis (BSRBR-RA)
4. German biologics register ‘Rheumatoid arthritis observation of biologic therapy’ (RABBIT)
5. Swiss register ‘Swiss Clinical Quality Management in Rheumatic Diseases’ (SCQM)
Methods

Data collected at baseline are being mapped first.
Results

A total of 64,901 individuals are included in the 5 registries being mapped to the OMOP CDM.

<table>
<thead>
<tr>
<th>Registry</th>
<th>Number of individuals</th>
<th>Number of unique mapped baseline conditions</th>
<th>Number of unique mapped baseline medications</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATTRA</td>
<td>5,326</td>
<td>26</td>
<td>26</td>
</tr>
<tr>
<td>BIOBADASER</td>
<td>6,496</td>
<td>30</td>
<td>51</td>
</tr>
<tr>
<td>BSRBR-RA</td>
<td>21,695</td>
<td>17</td>
<td>802</td>
</tr>
<tr>
<td>RABBIT</td>
<td>13,062</td>
<td>108</td>
<td>78</td>
</tr>
<tr>
<td>SCQM</td>
<td>18,322</td>
<td>26</td>
<td>33</td>
</tr>
</tbody>
</table>
Discussion

Opportunities

- Facilitating collaboration
- Utilising existing tools for assessing data quality and running analyses

Challenges

- Difficulty in mapping source codes to standard concepts
- Need to retain an understanding of the source data at the analysis stage
Acknowledgements

• ATTRA: Jakub Závada, Markéta Lagová
• BIOBADASER: Carlos Sanchez-Piedra, Nuria Montero, Jesús-Tomás Sánchez-Costa
• BSRBR-RA: Lianne Kearsley-Fleet, Kimme L. Hyrich, Kim Lauper
• RABBIT: Martin Schaefer, Doreen Huschek, Anja Strangfeld
• SCQM: Delphine S. Courvoisier, Christoph Tellenbach, Kim Lauper