Towards implementing the OMOP CDM across five European biologic registries

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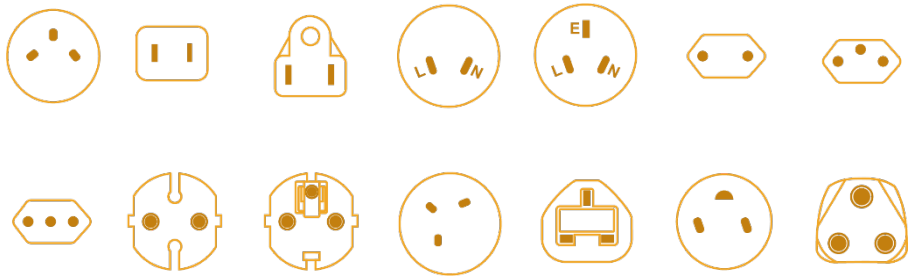
Potential value of a common data model

Implementing the OMOP CDM

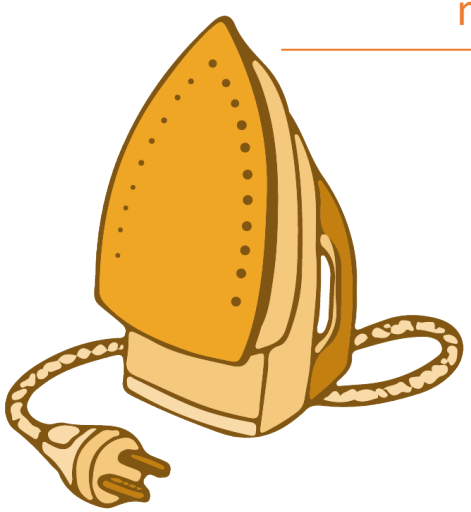
Current approach

- New, script based input data mapping for every study

The data…



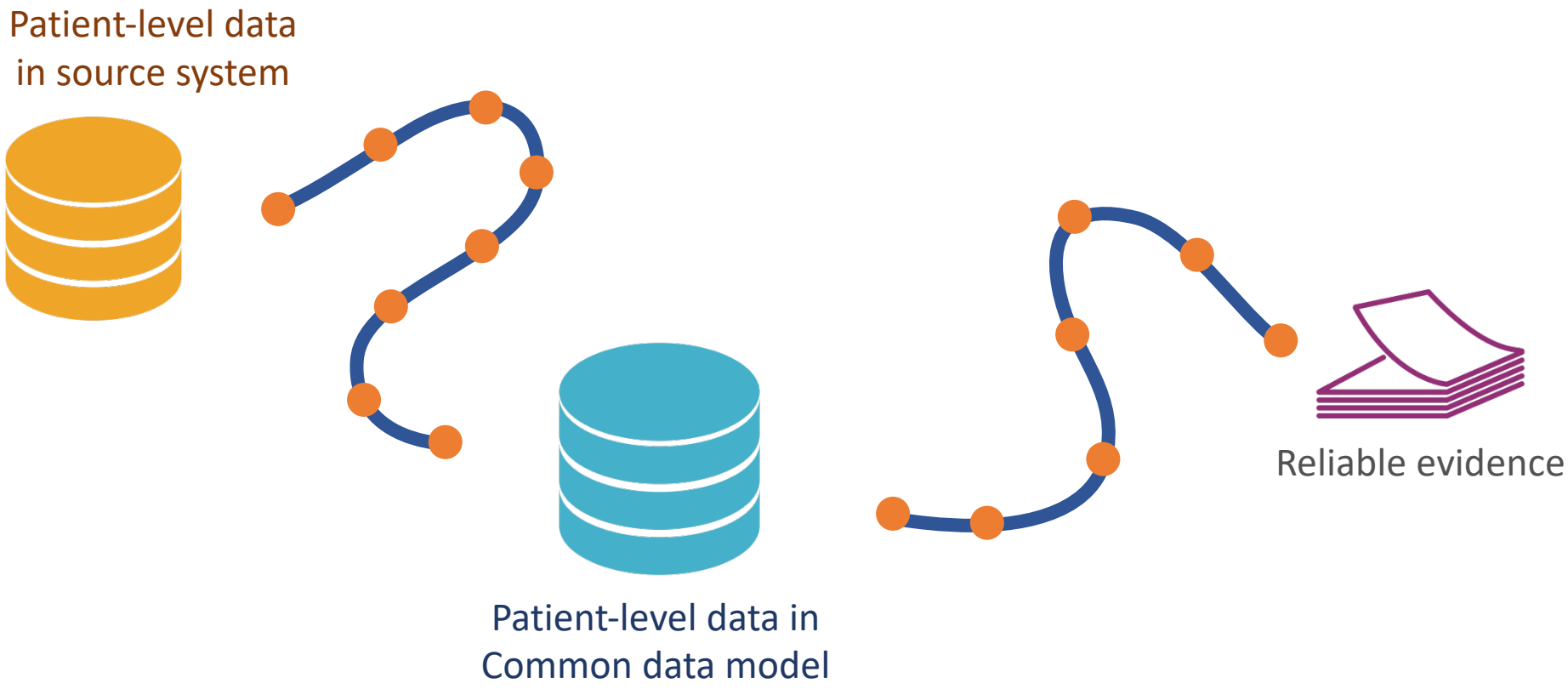
Analytical method



Link to data

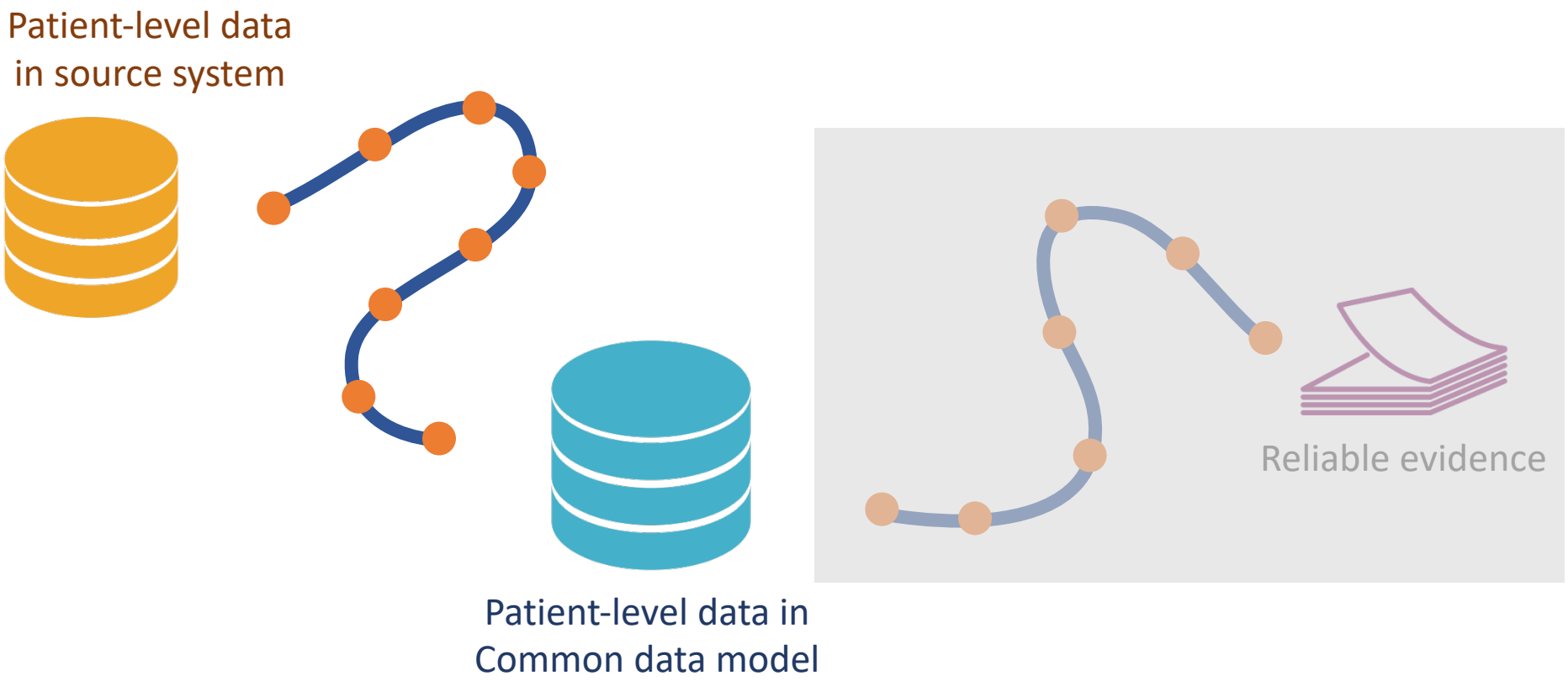
Journey to RWE using a CDM

- Data standardisation enables systematic research

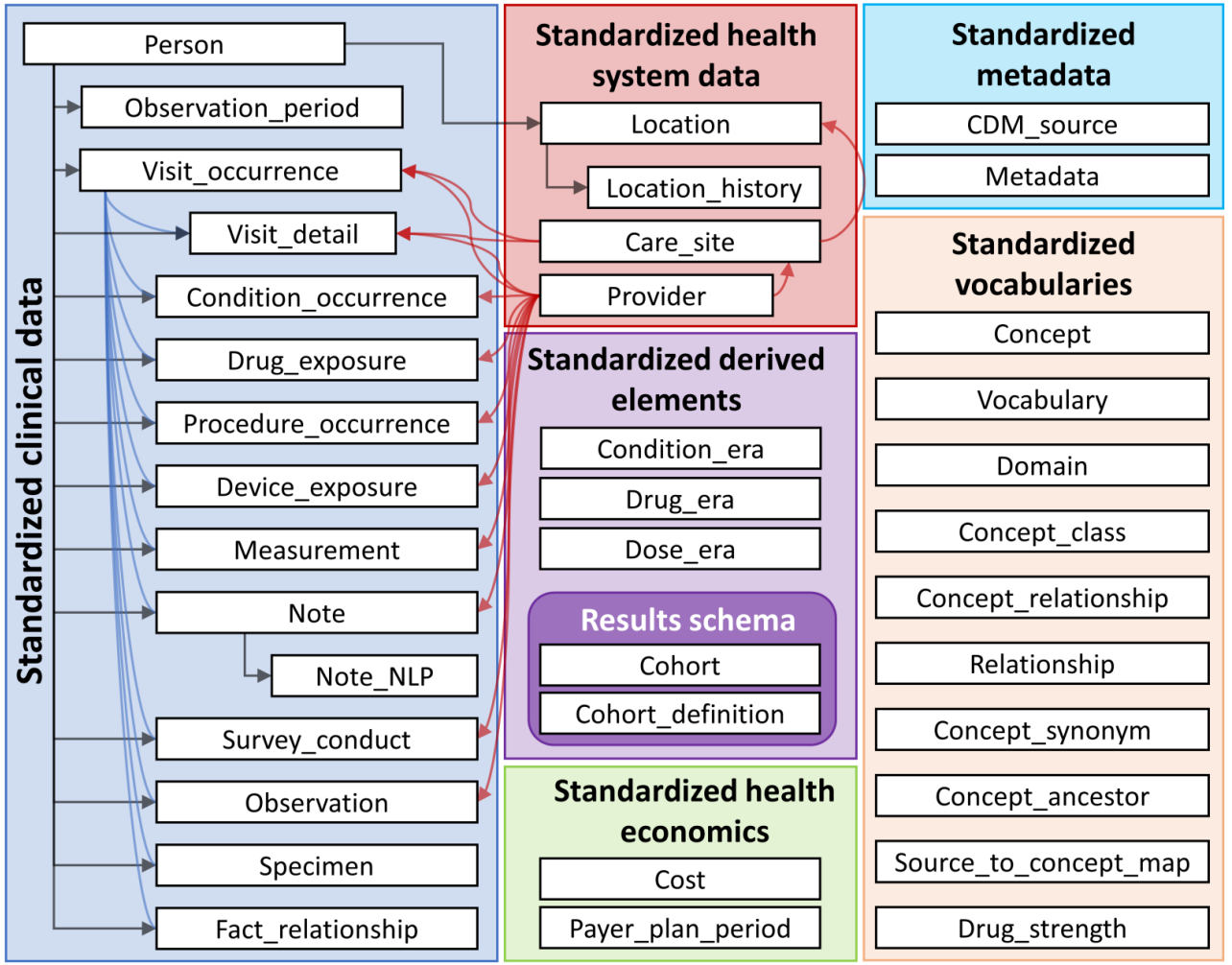


Journey to RWE using a CDM

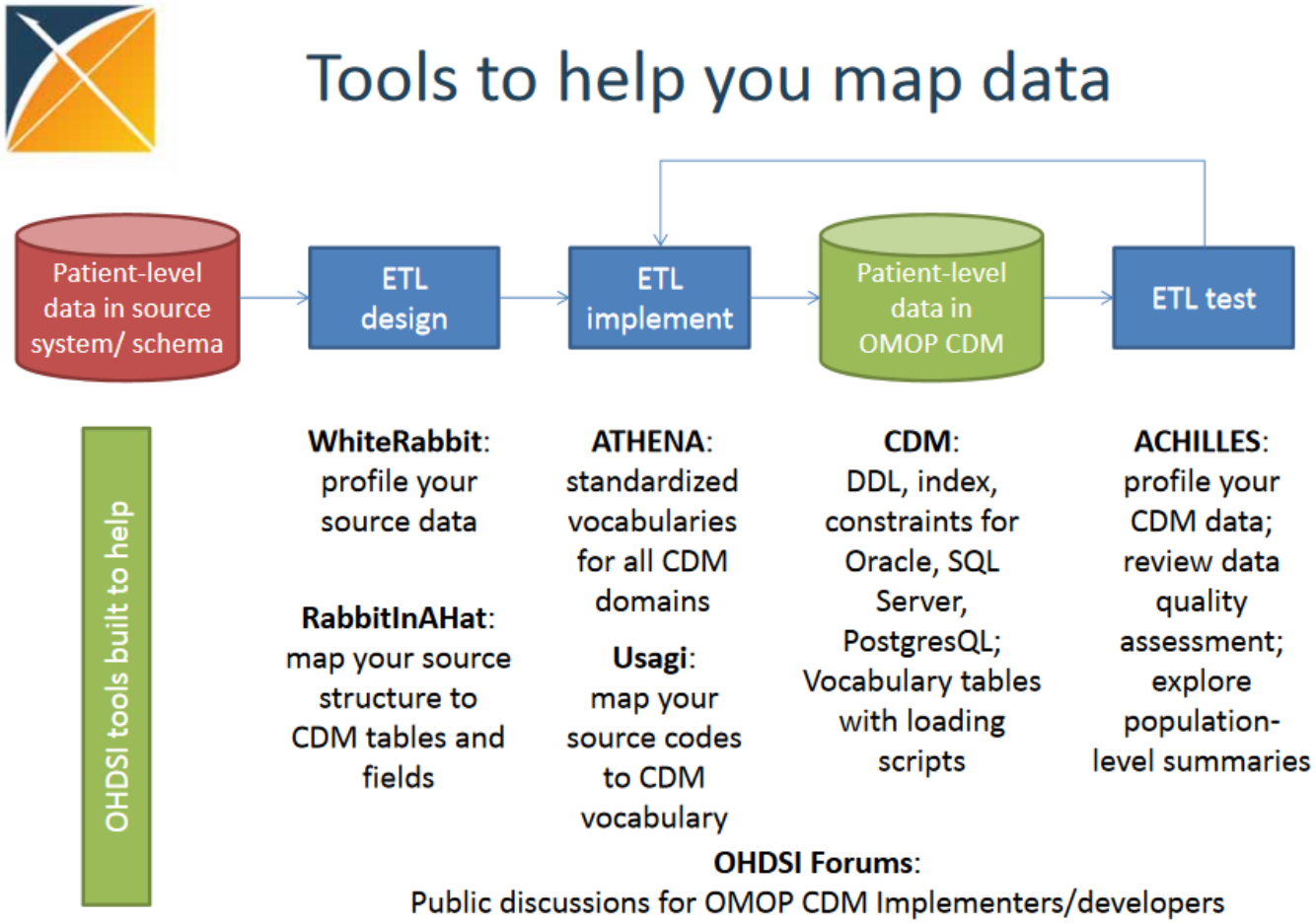
- Data standardisation enables systematic research



CDM version 6.0

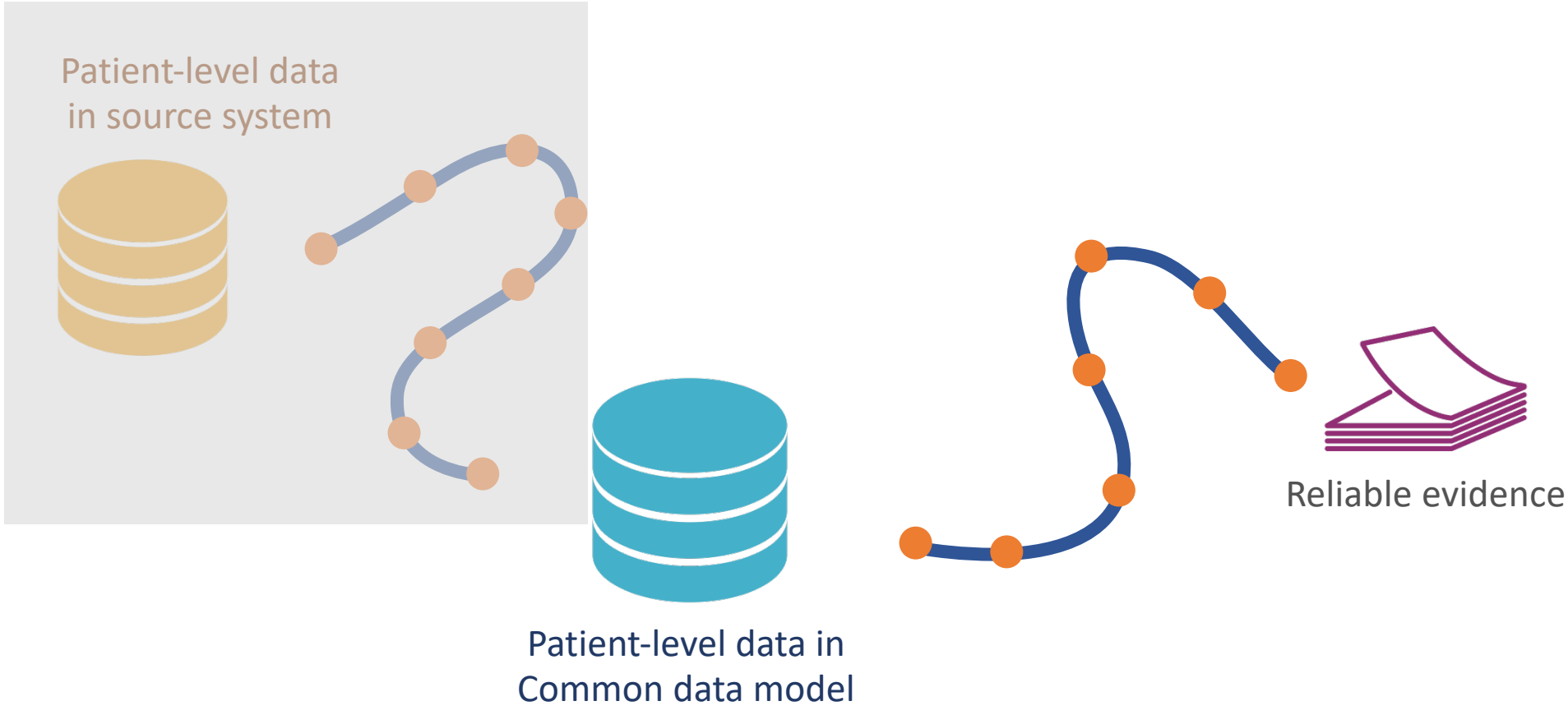


Getting to mapped data

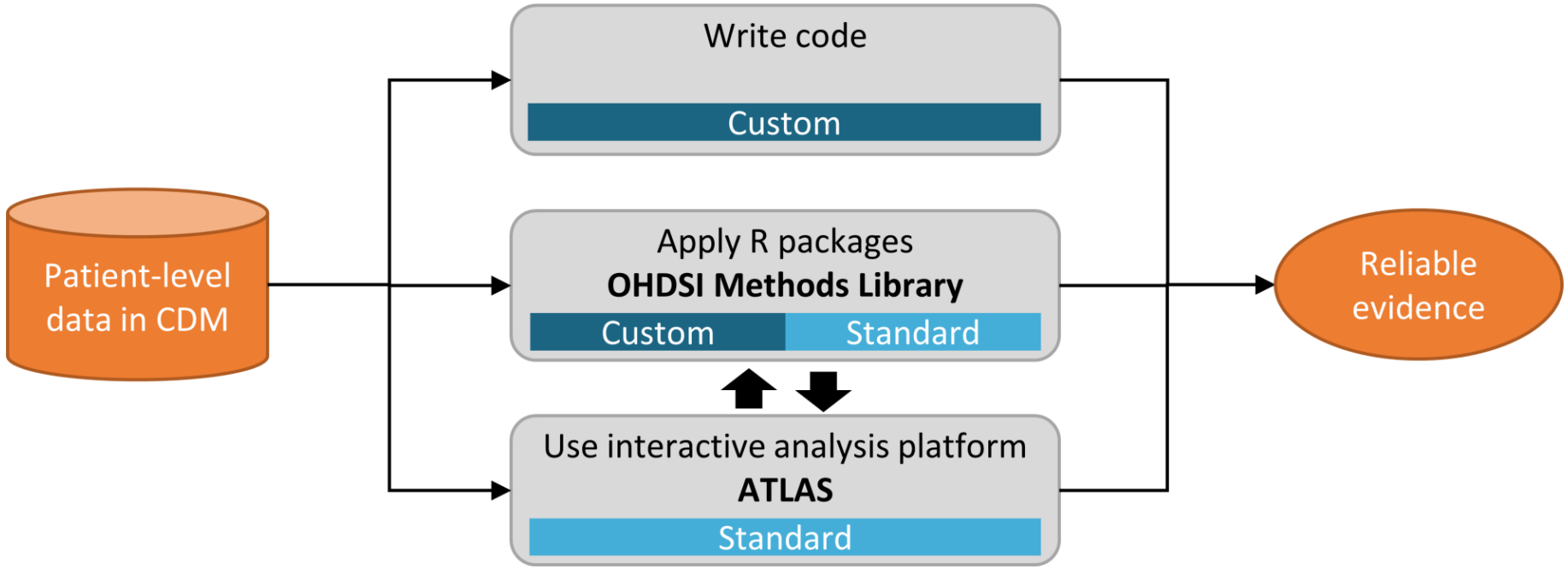


Journey to RWE using a CDM

- Data standardisation enables systematic research



Using the CDM



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Potential value of a common data model

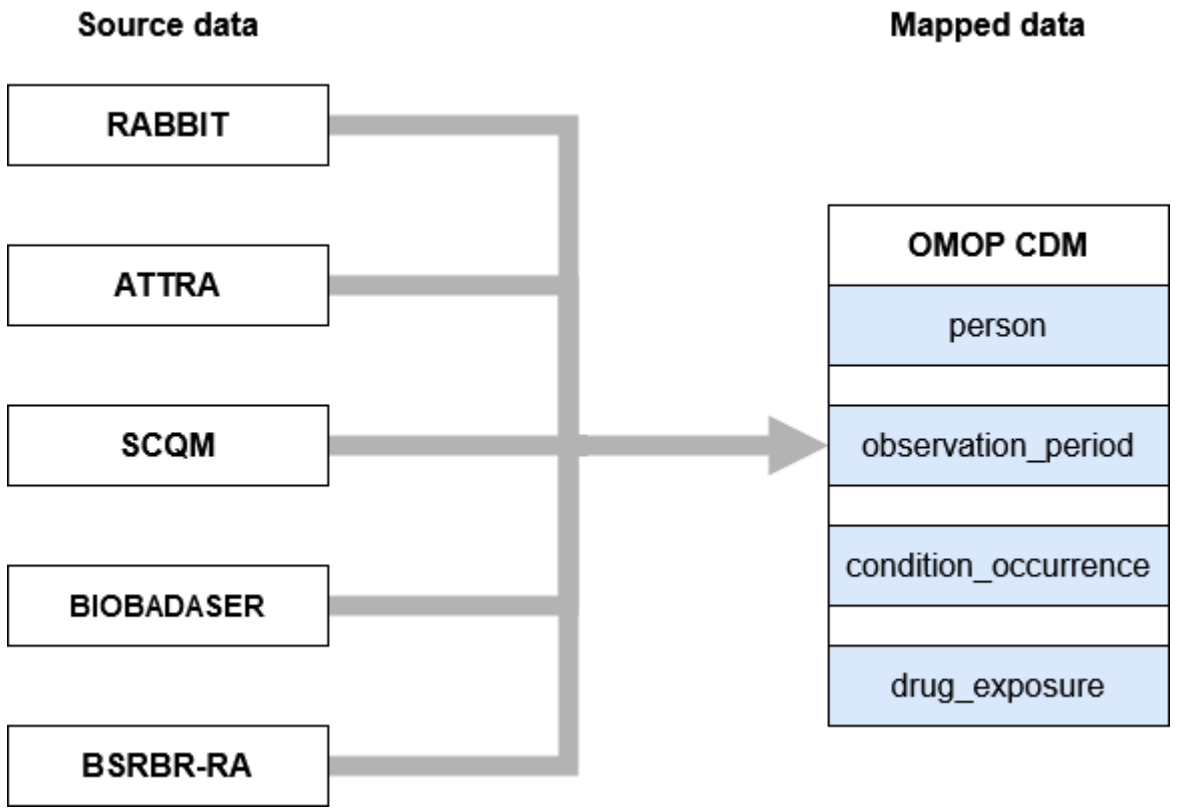
Implementing the OMOP CDM

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.

Registry	**Number of individuals**	**Number of unique mapped baseline conditions**	**Number of unique mapped baseline medications**
ATTRA	5,326	26	26
BIOBADASER	6,496	30	51
BSRBR-RA	21,695	17	802
RABBIT	13,062	108	78
SCQM	18,322	26	33

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

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