Transforming and evaluating the UK Biobank to the OMOP Common Data Model for COVID-19 research and beyond

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Research and Applications

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Transforming and evaluating the UK Biobank to the OMOP Common Data Model for COVID-19 research and beyond

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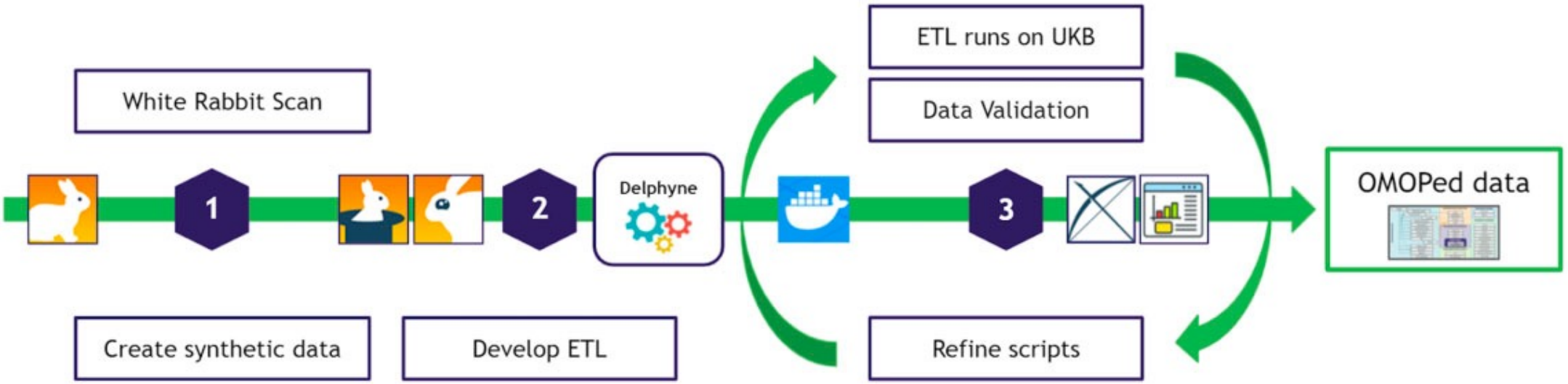
Background

- EHDEN Rapid Collaboration Call
- UK Biobank (~500K)
  - Baseline data (~8k data fields, proprietary dictionaries)
  - EHR from primary care (SNOMED CT, CTV3, EMIS and TPP proprietary codes, dm+d)
  - EHR from hospital care (ICD-10, ICD-9, OPCS4, OPCS3)
  - Mortality register (ICD-10, ICD-9)
  - Cancer register (ICD-O)
  - Covid-19 measurements (EMIS and TPP proprietary codes)
  - ~~Genomic data~~
- OMOP Common Data Model (v5.3)

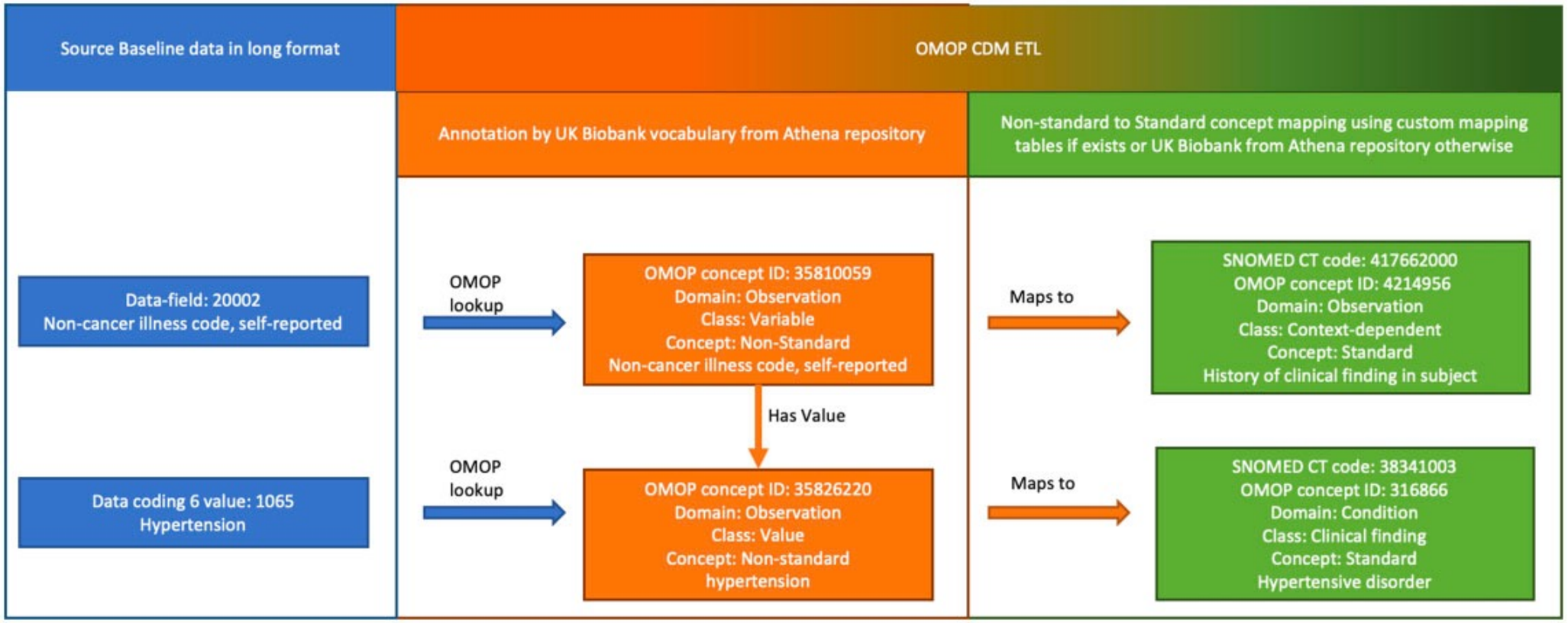
Methods

- ETL
  - Syntactic mapping
  - Semantic mapping
    - Athena Vocabulary repository
    - Bespoke mappings (8 in total)
- Testing and validation
  - Manually written test cases and automated tests on synthetic data
  - OHDSI Achilles, OHDSI DQD and EHDEN CDMInspection
  - Comparing a series of metrics between the raw data and the OMOP converted data

ETL Workflow



Semantic mapping example



Results	Source UK Biobank data	OMOP-Transformed UK Biobank data	Transformed UK Biobank COVID-19 positive sub population
Patients	502,505	502,504	3,086
% Female	54.4	54.4	48.76
Median age (IQR)	58 (13)	58 (13)	58 (15)
Median Townsend deprivation index (IQR)	-2.135 (4.18)	-2.135 (4.18)	-1.111 (5.19)
BMI median - baseline (IQR)	26.652 (5.72)	26.65 (5.70)	27.7 (6.21)
BMI median - GP EMIS (IQR)	27.2 (6.9)	27.3 (6.84)	28.89 (8)
SBP median - baseline (IQR)	136 (26)	136 (26)	136 (25)
DBP median - Baseline (IQR)	81 (14)	81 (14)	82 (14)

Results

	Source UK Biobank data	OMOP-Transformed UK Biobank data	Transformed UK Biobank COVID-19 positive sub population
Smoking status			
– Not answered	2,276	Not mapped	Not mapped
– Never	317,891	317,891	1,676
– Previous	197,949	197,949	1,323
– Current	55,676	55,676	395
Comorbidities			
T2DM	40,433 (8.04%)	40,476 (8.05%)	453 (14.67%)
HF	8,068 (1.60%)	8,053 (1.6%)	140 (4.53%)
AMI	10,593 (2.10%)	10,749 (2.13%)	110 (3.56%)
COPD	22,364 (4.45%)	22,367 (4.45%)	328 (10.62%)
HT	175,449 (34.91%)	175,539 (34.93%)	1,571 (50.9%)

Results

- 690 baseline datafields with 2898 values encoded by proprietary coding system mapped

Source Vocab	Used source terms #	Mapped used terms # (%)	Events #	Mapped event # (%)
Baseline ethnic status	22	10 (45.45%)	533,612	512,158 (95.97%)
Self-reported non-cancer illness	446	351 (78.69%)	1,127,434	946,053 (83.91%)
Self-reported cancer	82	48 (58.53%)	53,384	37,802 (70.81%)
Self-reported medication	3,737	1,100 (29.43%)	1,381,148	1,218,935 (88.25%)
Self-reported procedures	254	128 (50.39%)	994,355	864,788 (86.96%)
Haematology samples	124	93 (75%)	61,119,731	45,629,849 (74.65%)
Hospital EHR admission source	86	44 (51.16%)	3,541,594	282,505 (7.97%)
Hospital EHR admission method	63	58 (92.06%)	3,541,610	3,540,046 (99.95%)
Hospital EHR discharge destination	91	56 (61.53%)	3,484,435	3,189,509 (91.53%)

Results

- A small number of patients identified in converted data only
- Successfully transformed
  - Hospital care
    - 99.9% ICD-10; 91% ICD-9
    - 89.32% OPCS4; 77% OPCS3
  - 99.95% Death events
  - Primary care
    - 97.67% SNOMED CT; 97.78% CTV3
    - 98.74% dm+d
    - 0.19% TPP and EMIS
- DQD
  - 3399 checks passed
  - 18 failed

Discussion

Published

Observational Study > Drug Saf. 2022 Jun;45(6):685-698. doi: 10.1007/s40264-022-01187-y. Epub 2022 Jun 2.

Phenotype Algorithms for the Identification and Characterization of Vaccine-Induced Thrombotic Thrombocytopenia in Real World Data: A Multinational Network Cohort Study

Azza Shoaibi [1 2], Gowtham A Rao [3 4], Erica A Voss [3 4], Anna Ostropolets [4 5], Miguel Angel Mayer [6], Juan Manuel Ramírez-Anguita [6], Filip Maljković [7], Biljana Carević [8], Scott Horban [9], Daniel R Morales [9], Talita Duarte-Salles [10], Clement Fraboulet [11], Tanguy Le Carrour [12], Spiros Denaxas [13], Vaclav Papez [13], Luis H John [14], Peter R Rijneek [14], Evan Minty [15], Thamir M Alshammari [4 16], Rupa Makadia [3 4], Clair Blacketer [3 4], Frank DeFalco [3 4], Anthony G Sena [3 4], Marc A Suchard [4 17], Daniel Prieto-Alhambra [18], Patrick B Ryan [3 4]

Affiliations + expand

PMID: 35653017 PMCID: PMC9160850 DOI: 10.1007/s40264-022-01187-y Paperpile

Free PMC article

In preparation

Evaluating the impact of alternative phenotype definitions on incidence rates across a global data network

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OHDSI

1 List of Abbreviations
2 Responsible Parties
3 Amendments and Updates
4 Milestones
5 Rationale and Background

RESEARCH PROTOCOL

Adverse Events of Special Interest within COVID-19 Subjects

Version: 1.0.1

Under review

Contextualizing adverse events of special interest: A multinational cohort study to characterize the baseline incidence rates in 24 million COVID-19 infected subjects across 26 databases

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