



OHDSI/OMOP Research Spotlight

OHDSI Community Call
March 24, 2026 • 11 am ET



Upcoming Community Calls

Date	Topic
Mar. 24	OHDSI/OMOP Research Spotlight
Mar. 31	Kickoff to Phenotype April
Apr. 7	Phenotype April, Week 1
Apr. 14	Phenotype April, Week 2
Apr. 21	NO MEETING / EUROPE SYMPOSIUM
Apr. 28	Phenotype April, Week 4
May 5	Europe Symposium Review/Phenotype April Finale



Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?



OHDSI Shoutouts!



Congratulations to the team of **Man Young Park, Jaeuk U. Kim, SunMi Choi, Youngheum Yoon, Byung-Kwan Seo, and Sangkwan Lee** on the recent publication of **Transforming Traditional Korean Medicine hospital EHRs into the OMOP common Data Model: methodology and implications** in *BMC Medical Informatics and Decision Making*.

[Home](#) > [BMC Medical Informatics and Decision Making](#) > Article

Transforming Traditional Korean Medicine hospital EHRs into the OMOP common Data Model: methodology and implications

Research | [Open access](#) | Published: 16 March 2026

article number , (2026) [Cite this article](#)

✔ You have full access to this [open access](#) article

[Download PDF](#) ↓

🔖 [Save article](#)

[Man Young Park, Jaeuk U. Kim, SunMi Choi, Youngheum Yoon, Byung-Kwan Seo & Sangkwan Lee](#) ✉

Abstract

Background

Standardizing data from Traditional Korean Medicine (TKM) is essential for enhancing interoperability with international real-world data infrastructures, such as multi-institutional OMOP-CDM databases within the OHDSI network, multinational claims databases, and large-scale clinical data repositories, thereby enabling evidence-based research. This study aimed to convert electronic health records (EHRs) from a TKM hospital into the Observational Medical Outcomes Partnership (OMOP) Common Data Model (CDM).



OHDSI Shoutouts!



Congratulations to the team of **Khaoula El Mekkaoui, Chitra Mukherjee, Clodomir Santana, Hitalo Silva, Arnib Quazi, Meghana Balabhadruni, Aditya Ballal, Shamika Gavaskar, Kea Turqueza, Leslie Molina, Pablo Acevedo, Kay Moua, Omar Dawar, Federico Garcia, Mohammad S Soroya, XiaoDong Zhang, Ezra Amsterdam, Chao-Yin Chen, Padmini Sirish, Leighton Izu, Ronaldo Menezes, Nipavan Chiamvimonvat, Vladimir Filkov, Martin Cadeiras, and David A Liem** on the recent publication of **The impact of the Social Exposome in Cardiovascular Health and Disease** in *The Journal of Precision Health: Health and Disease*.

The Journal of Precision Medicine: Health and Disease 3 (2025) 100015



Contents lists available at ScienceDirect

The Journal of Precision Medicine: Health and Disease

journal homepage: www.sciencedirect.com/journal/the-journal-of-precision-medicine-health-and-disease



The impact of the social exposome in cardiovascular health and disease

Khaoula El Mekkaoui^{a,b,c}, Chitra Mukherjee^a, Clodomir Santana^a, Hitalo Silva^a, Arnib Quazi^a, Meghana Balabhadruni^a, Aditya Ballal^d, Shamika V. Gavaskar^a, Kea T. Turqueza^a, Leslie Molina^a, Pablo E. Acevedo^a, Kay Moua^a, Omar Dawar^a, Federico Garcia^a, Mohammad S. Soroya^a, Xiao-Dong Zhang^a, Ezra A. Amsterdam^a, Chao-Yin Chen^d, Padmini Sirish^a, Leighton T. Izu^d, Ronaldo Menezes^e, Nipavan Chiamvimonvat^{a,f}, Vladimir Filkov^g, Martin Cadeiras^a, David A. Liem^{a,g}

^a Department of Medicine, Division of Cardiovascular Disease, University of California, Davis, USA

^b VTT Technical Research Centre of Finland, Espoo, Finland

^c Department of Computer Science, Aalto University, Espoo, Finland

^d Department of Pharmacology, School of Medicine, University of California, Davis, USA

^e Department of Computer Science, University of Exeter, Exeter, UK

^f Department of Basic Medical Sciences and Translational Cardiovascular Research Center, University of Arizona, College of Medicine, Phoenix, USA

^g Department of Computer Science, University of California, Davis, USA

ARTICLE INFO

Keywords:
Heart disease
Exposome
Social determinants of health
Multimodal data

ABSTRACT

Cardiovascular disease (CVD) remains a leading cause of mortality and morbidity worldwide, influenced by complex interactions between biological, environmental, and social factors. Studies employing traditional genetic approaches are often insufficient to capture the broader context of these heterogeneous factors. We highlight an integrative framework that combines electronic health records (EHRs) with public (census) data on socio-environmental exposures, leveraging the Observational Medical Outcomes Partnership (OMOP) Common Data Model and individual's geolocations linked through ZIP Code Tabulation Area (ZCTA) codes. By incorporating the exposome, including social determinants of health (SDoH), this framework enhances privacy-preserving analysis and improves personalized CVD risk stratification. Furthermore, Precision Medicine aims to identify tailored prevention and therapeutic strategies by considering an individual's unique genetic, environmental, and lifestyle factors in which the exposome plays a pivotal role. Accordingly, in this review we will discuss a holistic precision medicine approach centered around the exposome to address health disparities, to better identify communities at high-risk for CVD, and to advance tailored prevention and intervention strategies.



OHDSI Shoutouts!



Check for updates

Congratulations to the team of **Matthias Vanderkerken, Koen Van Eygen, Veerle Galle, Annelies Verbiest, Ann Janssens, Imke Masuy, Kristof Theys, Tine Cuppens, Katoo Muylle, and Ann De Becker** on the recent publication of **Leveraging Digital Technology and Artificial Intelligence to Describe the Real-World Belgian Chronic Lymphocytic Leukemia Patient Population: The BE-CLLEAR Study** in *JCO Clinical Cancer Informatics*.

Original Reports | Artificial Intelligence

Leveraging Digital Technology and Artificial Intelligence to Describe the Real-World Belgian Chronic Lymphocytic Leukemia Patient Population: The BE-CLLEAR Study

Matthias Vanderkerken, MD, PhD^{1,2}; Koen Van Eygen, MD³; Veerle Galle, MD⁴; Annelies Verbiest, MD, PhD⁵; Ann Janssens, MD, PhD⁶; Imke Masuy, PhD⁷; Kristof Theys, PhD⁸; Tine Cuppens, PhD⁹; Katoo Muylle, PhD⁹; and Ann De Becker, MD, PhD¹⁰

DOI <https://doi.org/10.1200/JCO.25.00159>

ABSTRACT	ACCOMPANYING CONTENT
<p>PURPOSE Chronic lymphocytic leukemia (CLL) treatment paradigms have evolved significantly, yet real-world evidence (RWE) on guideline implementation and patient characteristics remains limited.</p> <p>MATERIALS AND METHODS This multicenter retrospective study leveraged artificial intelligence (AI) to analyze structured and unstructured data from four Belgian hospitals (January 1, 2018–October 31, 2021). Structured data including diagnosis codes, laboratory results, treatment records, and national registries were standardized using the Observational Medical Outcomes Partnership (OMOP) Common Data Model. Unstructured clinical notes and reports were processed using a transformer-based natural language processing (NLP) pipeline. We examined clinical characteristics, diagnostic testing, and treatment patterns among patients with newly diagnosed CLL.</p> <p>RESULTS Of 22 variable groups analyzed, 50.0% was derived from structured data only, 36.4% from unstructured data only (NLP-extracted), and 13.6% from mixed sources. Five hundred eighty-six patients with CLL were identified, with a median age of 74 years. One hundred seventy-four patients (29.7%) initiated first-line (1L) treatment, and 41 progressed to second-line treatment. Of 1L treated patients, 68.4% had at least one prespecified comorbidity, including 12.1% with significant cardiovascular disease. <i>TP53/del17p</i> testing was documented in 34.3% of patients before 1L treatment, with aberrations detected in 42.8%. Bruton's tyrosine kinase inhibitors (BTKi; 35.6%) were the most common 1L treatment, followed by chemoimmunotherapy (CIT; 25.9%). CIT use declined (30.6% to 17.5%), whereas BTKi use remained stable (34.2% to 38.1%) between 2018 and 2021.</p> <p>CONCLUSION This AI-augmented study demonstrates the feasibility and scalability of combining NLP-derived insights with OMOP-standardized structured data to generate reproducible RWE in hematology. Our results highlight an elderly CLL population with significant comorbidities and a shift toward targeted therapies. While treatment patterns aligned with guidelines, data quality depended on source documentation accessibility. Improved integration of molecular testing into electronic health records is essential for enhancing clinical decision making, patient outcomes, and future research.</p>	<p>Data Supplement</p> <p>Accepted February 9, 2026 Published March 18, 2026</p> <p>JCO Clin Cancer Inform 10:e2500159 © 2026 by American Society of Clinical Oncology</p> <p>Creative Commons Attribution Non-Commercial No Derivatives 4.0 License</p>

Copyright © 2026, American Society of Clinical Oncology. All rights reserved.



OHDSI Shoutouts!



Congratulations to the team of **Francesco Pignatti, Tarec Christoffer El-Galaly, Martin Kaiser, Kimmo Porkka, Robin Doeswijk, Peter Mol, Donna R. Rivera, Catherine C. Lerro, Ulrich-Peter Rohr, Patrice Verpillat, Antonios Valachis, Dario Trapani, Massimo Di Maio, Nicola Latino, Raul Cordoba, Nathan Cherny, Miriam Koopman, Diogo Martins-Branco, George Pentheroudakis, and Douwe Postmus** on the recent publication of **Assessing Overall Survival Benefits in Advanced Cancers: The Role of External Comparator Cohort Studies with Real-World Data** in *Clinical Pharmacology & Therapeutics*.

ARTICLE

Assessing Overall Survival Benefits in Advanced Cancers: The Role of External Comparator Cohort Studies with Real-World Data

Francesco Pignatti^{1*}, Tarec Christoffer El-Galaly², Martin Kaiser³, Kimmo Porkka⁴, Robin Doeswijk⁵, Peter Mol^{6,7}, Donna R. Rivera⁸, Catherine C. Lerro⁸, Ulrich-Peter Rohr⁹, Patrice Verpillat¹, Antonios Valachis¹⁰, Dario Trapani^{11,12}, Massimo Di Maio¹³, Nicola Latino¹⁴, Raul Cordoba¹⁵, Nathan Cherny¹⁶, Miriam Koopman¹⁷, Diogo Martins-Branco¹⁴, George Pentheroudakis¹⁴ and Douwe Postmus⁶

External comparator cohort (ECC) studies with real-world data (RWD) may provide more reliable estimates of treatment differences compared to single-arm trials (SAT), yet they face limitations such as selection bias and data heterogeneity. This study assessed the perceived strength of evidence of ECC studies compared to SAT and randomized controlled studies (RCT). The study included healthcare professionals (HCP) from the European Hematology Association (EHA), the European Society for Medical Oncology (ESMO), and assessors from international regulatory agencies (RA). A conjoint analysis evaluated strength of evidence ratings for establishing an effect on OS for different hypothetical scenarios, based on different designs, RWD quality, and observed OS improvement, for a new cancer treatment for advanced disease and no effective treatments. Participants from HCP organizations rated RWD studies favorably (advantages outweigh disadvantages) more frequently (47.6%; $n=103$) compared to RA participants (12.9%; $n=116$). Compared to a SAT, a high-quality RWD ECC study showing a 1.5-month and 3-month OS improvement had 2.7 (95% CI: 1.9–3.8) and 14.7 (95% CI: 10.0–21.5) times higher odds of receiving a higher strength of evidence rating, respectively. The OR for RCT v. SAT was 36.4 (95% CI: 24.0–55.2) and 358.4 (95% CI: 217.3–591.3), respectively. Strength of evidence ratings were associated with maximum acceptable risk of severe or symptomatic toxicity. In conclusion, when evaluating the OS of new therapies, ECC studies with RWD, especially when based on high-quality RWD or demonstrating a larger OS benefit, were rated as more convincing than SAT without a formal control.



OHDSI Shoutouts!



Congratulations to the team of **Montserrat León-García, Sergio Álvarez-Pérez, Janire Gesto-Gómez, Clara Urbano-Molina, Sonia Soto-Díaz, Juan Cárdenas-Valladolid, Luis Rodríguez-Rodríguez, Antonio Díaz-Holgado, Isabel Del Cura-González, Javier De La Cruz-Bertolo, Noelia García-Barrio, Juan Luis Cruz-Bermúdez, Cristina García-Fernández, Carlos Rodríguez-Antolín, Laila García-Aldars, Elsa María Moreda-Sánchez, Álvaro Roldán López, José María Veganzones Alonso-Cortés, Ana Isabel Gonzalez Gonzalez, Miguel A Salinero-Fort, and the HealthData@MAD-R&I Working Group** on the recent publication of **HealthData@MAD-R&I: Protocol for Design and Development of a Regional Health Data Infrastructure to Enable Secondary Use of Health Data in Research and Innovation** in *JMIR Research Protocols*.



JMIR Publications
Advancing Digital Health & Open Science

Articles Search articles

JMIR Research Protocols Journal Information Browse Journal

Published on 20.Mar.2026 in Vol 15 (2026)

Preprints (earlier versions) of this paper are available at <https://preprints.jmir.org/preprint/82815>, first published 25.Aug.2025.

HealthData@MAD-R&I: Protocol for Design and Development of a Regional Health Data Infrastructure to Enable Secondary Use of Health Data in Research and Innovation

Montserrat León-García¹; Sergio Álvarez-Pérez¹; Janire Gesto-Gómez¹; Clara Urbano-Molina¹; Sonia Soto-Díaz²; Juan Cárdenas-Valladolid^{2, 3, 4}; Luis Rodríguez-Rodríguez⁵; Antonio Díaz-Holgado⁶; Isabel del Cura-González^{6, 7, 8, 9, 10}; Javier De La Cruz-Bertolo¹¹; Noelia García-Barrio¹¹; Juan Luis Cruz-Bermúdez¹¹; Cristina García-Fernández¹²; Carlos Rodríguez-Antolín¹³; Laila García-Aldars²; Elsa María Moreda-Sánchez²; Álvaro Roldán López²; José María Veganzones Alonso-Cortés¹²; Ana Isabel Gonzalez Gonzalez^{2, 8, 9}; Miguel A Salinero-Fort^{2, 4}; HealthData@MAD-R&I Working Group¹⁴

Article	Authors	Cited by	Tweetations (5)	Metrics
<ul style="list-style-type: none"> Abstract Introduction Methods Results Discussion References Abbreviations 	<p>Abstract</p> <p>Background: The exponential growth of electronic health records (EHRs), together with the recent entry into force of the European Health Data Space (EHDS) Regulation, highlights the urgent need for secure, interoperable environments that support the secondary use of health data. In response, HealthData@MAD-R&I emerges as a pioneering initiative in Madrid (Spain), aligned with the EHDS strategy and the European Commission's vision for data sovereignty and trustworthy data reuse.</p>			



Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?



Upcoming Workgroup Calls

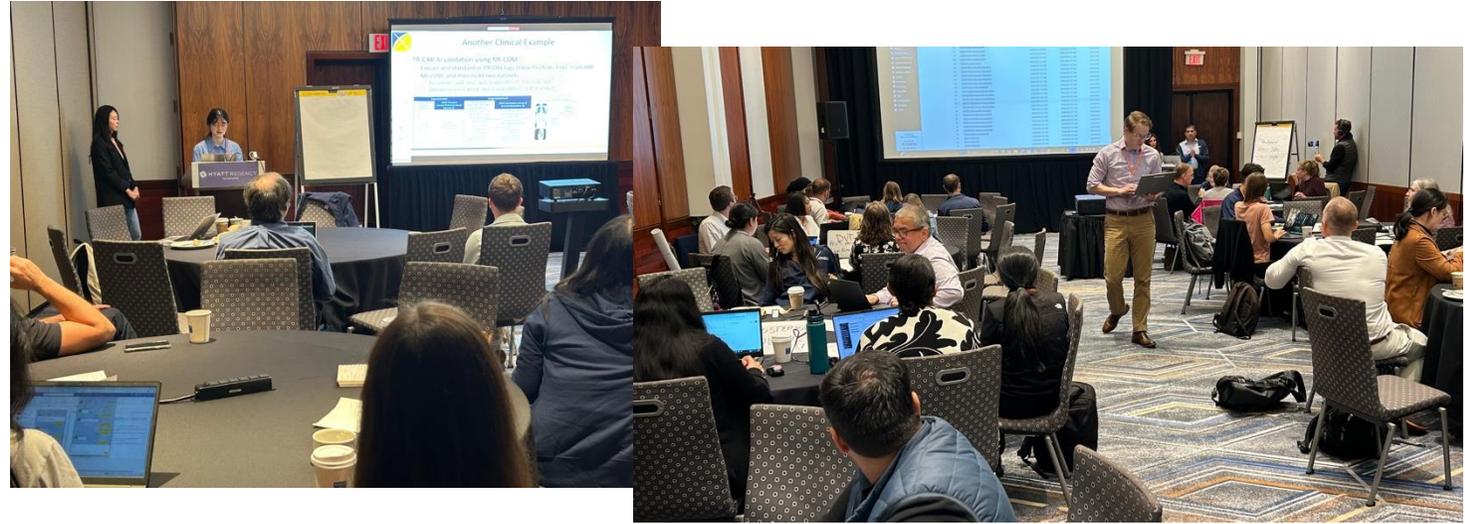


Date	Time (ET)	Meeting
Wednesday	10 am	Surgery and Perioperative Medicine
Wednesday	10 am	Women of OHDSI
Wednesday	10 am	Common Data Model
Wednesday	1 pm	Latin America Chapter
Thursday	6:30 am	India Community Call
Thursday	9 am	Phenotype Development and Evaluation
Thursday	10 am	Africa Chapter (ZOOM)
Thursday	10 am	GIS – Geographic Information System
Thursday	11 am	Perinatal & Reproductive Health
Friday	9 am	Network Data Quality
Friday	11 am	Clinical Trials
Monday	9 am	Vaccine Vocabulary
Tuesday	9 am	Open EHR and OMOP
Tuesday	10 am	CDM Survey



Workgroups Leadership Retreat

Attention, workgroup leads: There will be a workgroup leadership retreat this Friday, March 27, from 10-11:30 am ET in our MS Teams environment. If you didn't receive the call invite, please reach out to Paul Nagy or Craig Sachson.



ohdsi.org/workgroups



UK Symposium Call for Abstracts Opens

HDR UK Event

OHDSI UK 2026

We're delighted to announce that OHDSI UK 2026 will be held on the 18th of September at the University of Nottingham. For the first time, there will also be an OMOP training day on the 17th of September.

Share this page [in](#) [twitter](#)

OHDSI (Observational Health Data Sciences and Informatics, pronounced "Odyssey") is an international community of stakeholders dedicated to unlocking the value of health data through large-scale analytics. OHDSI promotes open science and collaboration in health data research with a key focus on adoption of the OMOP Common Data Model, a global standard for harmonising data and facilitating federated analytics across institutions. [Find out more about OHDSI.](#)

Call for Abstracts

We invite you to submit an abstract for consideration at OHDSI UK 2026. Whether you wish to present a poster, software demo, or lightning talk, we welcome contributions from across the community. Abstract submission is available via [this form](#), and the deadline is 1st May 2026. Please use [this template](#) to prepare your abstract and save it as a PDF, and start your file name with the surname (family name) of the presenting author.

Key dates:

Registration Opens: 20th April 2026

Registration Closes: 4th September 2026

Abstract Submission Opens: 20th March 2026

Abstract Submission Deadline: 1st May 2026

Training day: 17th September 2026

Symposium: 18th September 2026



OMOP School in Stockholm, Sweden

passion2improve



The OMOP School

3+1-day OMOP CDM Bootcamp

A hands-on training and workshop that turns your data harmonization vision into reality.

May 26th – 28th

+ May 29th (optional extra day for Use Cases Deep Dive)

09:00-17:00 Tue-Thu, 09:00-16:00 Fri
Stockholm, Sweden (venue TBD)

Learning objectives:

- Explain the role of standardization in federated research
- Understand the OMOP Common Data Model and how it can be applied
- Perform semantic mapping using OMOP vocabularies
- Design and implement an OMOP ETL process
- Evaluate and improve data quality
- Conduct standardized observational analyses
- Execute an end-to-end mini-harmonization project
- Use selective OHDSI methods and tools

Who to attend?

- Health Data Owners/Data Custodians
- Data Scientists, Clinical Researchers & Epidemiologists
- IT/Data Architects/ETL Developers/Health Informatics Specialists
- Digital Transformation Leads, Registry Directors, Healthcare Strategists
- Healthcare Policy Stakeholders



Lars Halvorsen
Trainer
[edenceHealth NV](#)

Freija Descamps
Trainer
[edenceHealth NV](#)

Christian Högberg
Coordinator
Passion 2 Improve AB

“Walk away with a working understanding of the OMOP Common Data Model, an actionable data harmonization plan, and the tools to execute it.”

There are still places open!

Registration page:
<https://omop.se/education>



First Latin America Symposium – July 30-31

1ST SYMPOSIUM LATIN AMERICA
OHDSI 2026
30-31 July
Salvador,
Brasil

Organized by:

- cidacs
Centro de Investigación en Salud y Conocimiento para Todos
- FIOCRUZ | Bahia
- PRECISION DATA
BRIDGING PEOPLE AND DATA

LATIN AMERICA

The poster features a large, stylized map of Latin America in the background, composed of orange dots. A dark blue diagonal band with a crowd of people is on the left. The OHDSI logo is in the top right, and a smaller version is at the bottom center.



2026 Europe Symposium

The 2026 OHDSI Europe Symposium returns to Rotterdam next year and will be held **April 18-20**.

Registration is open on the **OHDSI & OHDSI Europe** web sites.

Time	Symposium Agenda - Monday April 20, 2026	Location
8:00	Registration and Coffee	Queen's Lounge
9:00	Welcome to OHDSI Europe <i>Dr. Renske Los, Department of Medical Informatics, Erasmus MC</i> <i>Dr. Aniek Markus, Department of Medical Informatics, Erasmus MC</i>	Theatre
9:05	Journey of OHDSI <i>Prof. Peter Rijnbeek, Chair Department of Medical Informatics, Erasmus MC</i>	Theatre
9:30	Collaborator Showcase - part 1 Moderated by <i>Dr. Egill Fridgeirsson, Department of Medical Informatics, Erasmus MC</i>	Theatre
10:00	Speed networking	Theatre
10:15	Coffee Break & posters National Nodes	Queen's Lounge
11:15	Collaborator Showcase - part 2 Moderated by <i>Dr. Egill Fridgeirsson, Department of Medical Informatics, Erasmus MC</i>	Theatre
11:45	Dreaming about the OHDSI journey ahead <i>Dr. Patrick Ryan, Vice President, Observational Health Data Analytics, Johnson & Johnson</i> <i>Dr. Renske Los, Department of Medical Informatics, Erasmus MC</i>	Theatre

12:15	Lunch break & networking & posters/demo's <i>(Early investigator meeting - 13:00-13:45 Queen's Lounge)</i>	La Fontaine & Odyssee Room
13:45	From dreams to reality <i>OHDSI Titan Award winners</i>	Theatre
14:30	Propositions for collaboration from the National Nodes <i>National Node leads</i>	Theatre
14:45	Coffee break & posters/demo's	La Fontaine & Odyssee Room
16:15	The OH Factor <i>To be announced</i>	Theatre
17:00	Closing	Theatre
17:15	Networking reception	Queen's Lounge



2026 Global Symposium

The 2026 OHDSI Global Symposium will return to the Hyatt Regency Hotel in New Brunswick, N.J., on **Oct. 20-22.**





#OHDSISocialShowcase This Week

Monday

Building the OHDSI Evidence Network – A Global, Open, Federated Collaboration

(**Clair Blacketer**, Haeun Lee, Benjamin Martijn, Evanette Burrows, Patricia Mabry, Deran McKeen, Sam Patnoe, Ben Gerber, Pantelis Natsiavas, Aamirah Vadsariya, Hanieh Razzaghi, Paul Nagy)

Building the OHDSI Evidence Network: A Global, Open, Federated Collaboration

PRESENTER: Clair Blacketer

INTRODUCTION

- Real-world data is plentiful and reflects natural conditions, but is siloed, due to privacy concerns, preventing the benefits of dataset integration from being realized, e.g. study of rare events, generalizability, use of data-hungry AI tools to reveal new insights
- Federated networks address this problem by sharing only aggregated results (not record level data) to preserve data privacy
- The OHDSI Evidence Network was launched in 2024 inspired by the success of other federated networks, e.g., European Health Data and Evidence Network (EHDEN) and the Data Analysis and Real World Interrogation Network (DARWIN EU).

METHODS

- The Evidence Network (EN) is composed of "Data Partner Organizations" (DPOs) who volunteer to run analytic code on their organization's data.
- Membership in EN is voluntary - no contracts or centralized data sharing!
- Governance is decentralized; each DPO adheres to its local IRB requirements.
- To catalog data available in the EN, each DPO is sent a Database Diagnostics software package which they run locally to produce a standardized DbProfiles - aggregated metadata describing the DPO's database(s)
- All EN activities are opt-in and include EN workgroup meetings, steering committee representation, monthly data partner calls, and EN study co-development
- A pilot study, "Save Our Sisyphus", measured partner engagement. Results led to the adoption of best practices by the EN (learning, clear protocols, transparent communication).

The OHDSI Evidence Network demonstrates that open, federated, community-led research is inclusive and effective on a global scale



Take a picture to learn more

Start making steps to join today!



RESULTS

- 28 DPOs onboarded since inception, contributing access to 48 databases across 4 continents (see map)
- The EN supported 20 rapid fit-for-purpose assessments and study co-developments in 2025



Figure 1: Global map of current OHDSI Evidence Network data partner organizations.

KEY LESSONS:

- Decentralized, federated, community-led governance is feasible and effective at a global scale
- Trust and transparency drive collaboration
- Low-burden participation lowers barriers
- Shared tools enable shared learning

FUTURE GOALS:

- Address funding/sustainability challenges
- Develop and test a process for study development and support
- Refine DPO-study matching
- Expand DPO membership

Clair Blacketer^{1,2,4}, Haeun Lee^{1,8}, Benjamin Martijn^{1,8}, Evanette Burrows^{1,4}, Patricia Mabry^{1,10}, Deran McKeen^{1,10}, Sam Patnoe^{1,10}, Elizabeth Grossman^{1,10}, Ben Gerber^{1,5}, Pantelis Natsiavas^{1,6}, Aamirah Vadsariya^{1,7}, Hanieh Razzaghi^{1,9}, Paul Nagy^{1,9}

1. OHDSI Collaborators, Observational Health Data Sciences and Informatics (OHDSI), New York, NY, USA 2. Department of Medical Informatics, Erasmus University Medical Center, Rotterdam, NL 3. Department of Biomedical Informatics, Columbia University, New York, NY, USA 4. Johnson & Johnson, Raritan, NJ, USA 5. Department of Population and Quantitative Health Sciences, UMass Chan Medical School, Boston, MA, USA 6. Institute of Applied Bioscience, Centre for Research & Technology Hellas, Thessaloniki, GR 7. Clinical Informatics Center, University of Texas Southwestern Medical Center, Dallas, TX, USA 8. Johns Hopkins University, Baltimore, MD, USA 9. Applied Clinical Research Center, Children's Hospital of Philadelphia, Philadelphia, PA 10. Health Partners Institute, Bloomington, MN, USA





#OHDSISocialShowcase This Week

Tuesday

Bridging FHIR and OMOP: Data Lineage for Observational Data Conversion

(Benjamin Berk, Melissa Benzie, Bindu Bolisetty, Scott Favre, Jeremy Fortune, Jeremy Goslin, Vik Kheterpal, Kathleen Marinar, Anne Marsan, Ed Ramos, Sunanda Venumuddula, John Wyderko)

Title: Bridging FHIR & OMOP: Data Lineage for Observational Data Conversion

PRESENTER: Benjamin Berk MD

INTRO

While FHIR excels as a clinical data exchange standard, OMOP provides a standardized format optimized for observational research. Converting data between these models presents significant challenges in maintaining data integrity and traceability. In converting from FHIR to OMOP, we would like to capture:

- **Data Source Provenance:** Tracking source system provenance of each element.
- **Entity Lineage:** Maintaining traceability from FHIR resources to OMOP table rows.
- **Concept Standardization:** Recording source codes to OMOP standard concepts.
- **Processing Events:** Logs of transformation decisions, including warnings, informational messages, errors, and documentation of unmapped FHIR resources

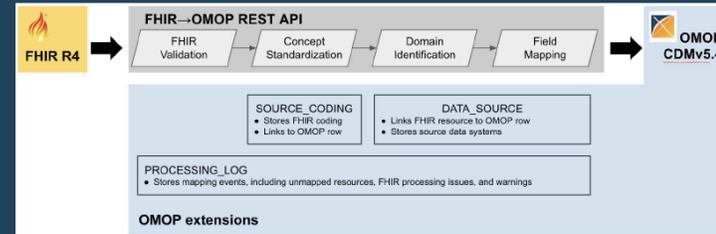
METHODS

1. Developed REST-based FHIR→OMOP conversion API that implements a data transformation pipeline
2. Source codes mapped to OMOP standard concepts via CareEvolution Orchestrate Terminology API (using exact code and display matching & natural language processing)
3. Worked with HL7 Vulcan FHIR→OMOP Working Group to develop a standard implementation guide for this transformation (now in HL7 Balloting)
4. Captured data lineage in 3 extension tables
5. Tested with data collected from PRediction Of Glycemic RESponse Study (PROGRESS) study conducted by Scripps Digital Clinical Trials Center using CareEvolution's MyDataHelps research platform

RESULTS

- Processed over 2.8 million FHIR resources, generating comprehensive lineage data through three extension tables.
- 1.1 million FHIR resource IDs linked to corresponding OMOP table rows
- 3.8 million source codings, including successful standardizations and unmappable source codes

Proposal: Integrate data lineage tables into CDM for FHIR→OMOP conversion



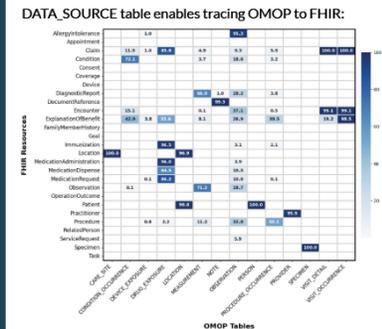
SOURCE_CODING		DATA_SOURCE		PROCESSING_LOG	
omop_table_name	string NN	omop_table_name	string NN	omop_table_name	string
omop_fk_id	integer 1 0..1	omop_fk_id	integer 1 1	omop_fk_id	integer
omop_concept_column_name	string NN	omop_person_id	integer 1 1	omop_person_id	integer NN
source_system	string	fhir_path	string NN	level	string NN
source_code	string	fhir_data_source	string	type	string NN
source_display	string			system	string NN
				code	string NN
				fhir_path	string
				text	string NN

data_source_type	person_id
Other FHIR	632
Phys	563
Phys (Other)	77
Carrier	24
Payer (CMS)	19
Athava	19
NextGen	7
eClinicalWorks	5
Abraxis	1

665 individuals sourced via participant-mediated exchange using MyDataHelps platform from diverse EMRs and other FHIR providers

More than 99% of all non-duplicate resources generated rows in OMOP tables

level	type	code	fhir_resource
Error	Processing	DuplicateFhirElement	585
		FhirProcessingIssue	1
Information	Processing	NoActionTaken	1678
		ProviderMissing	1748
		ProviderNotReferenced	2178
		ResourceRemovedBecauseOfIgnoreCode	32
		ResourceRemovedBecauseOfStatusCode	4322
		ResourceRemovedBecauseOfVerificationCode	1644
		RowCreated	2160867
		RowDuplicatesMerged	522315
		ValueTruncated	405761
		VisitFuture	2
		VisitMissingStartDate	342
Warning	Processing	FhirProcessingIssue	71665
		PatientMissingDateOfBirth	14
		PatientMissingDateOfDeath	1



Berk BB, Benzie M, Bolisetty B, Favre S, Fortune J, Goslin J, Kheterpal V, Marinar K, Marsan A, Ramos E, Venumuddula S, Wyderko J
All authors: CareEvolution, Ann Arbor, MI, USA; *Also affiliated with: Digital Trials Center, Scripps Research Translational Institute, La Jolla, CA, USA



Take a picture to download the full paper



Now Under Ballot:
<https://build.fhir.org/ig/HL7/fhir-omop-ig>
<https://www.hl7.org/ballotdesktop/>





#OHDSISocialShowcase This Week

Wednesday

Creating a Standardized EHR Analytics Data Source for the National Cancer Institute's Connect for Cancer Prevention Study

(Edward A. Frankenberg, Jacob M. Peters, Nicole M. Gerlanc)

Creating a Standardized EHR Analytics Data Source for the National Cancer Institute's Connect for Cancer Prevention Study

Edward A. Frankenberg¹, Jacob M. Peters¹, Nicole M. Gerlanc¹
¹National Institutes of Health (NIH), National Cancer Institute (NCI)

Background

Connect is an NCI-led, multi-site prospective cohort (target 200,000 participants; 25+ years) study collecting biospecimens, surveys, and OMOP-formatted EHR data. To maximize participation, sites maintain independent OMOP ETLs and – unlike *N3C* or *All of Us* – may use any version of the CDM and vocabulary. To create a single OMOP instance, we developed an automated open-source pipeline to validate and standardize incoming OMOP datasets of varying versions and quality.

Challenges

- **Any CDM, any vocab:** sites deliver any CDM version with mixed vocabulary releases
- **Black-box ETLs:** site-specific interpretations and implementation errors
- **Schema drift:** column order, data types, & required fields often off-spec
- **Semantic drift:** deprecated/non-standard concepts; domain-table misplacements
- **One target needed:** stable OMOP v5.4 with consistent vocabulary

Pipeline Architecture

- **Ingress:** sites drop flat files to Google Cloud Storage
- File(s) representing individual tables are processed through series of **step-wise tasks**
- **File-centric parallelism:** each file processing task is an independent job run on a single node
- **Orchestration:** an Airflow DAG drives task progression
- **OLAP engine:** DuckDB performs transformations on data files
- **Outputs & provenance:** unified OMOP 5.4 in BigQuery + delivery report + processing artifacts + logs



Validation

- Convert incoming file(s) to Parquet
- Identify unexpected or missing tables and columns
- Obtain basic descriptive statistics (row counts, etc.)

Normalization

- Add missing/remove unexpected columns
- Coerce data types and isolate non-conforming rows
- Set standard default values for NULL required fields

Structural Upgrade

- Convert all incoming CDM versions to v5.4 (unchanged tables pass through; changed tables use specific SQL; tables removed in 5.4 are dropped)
- Enforce consistent column order and letter casing

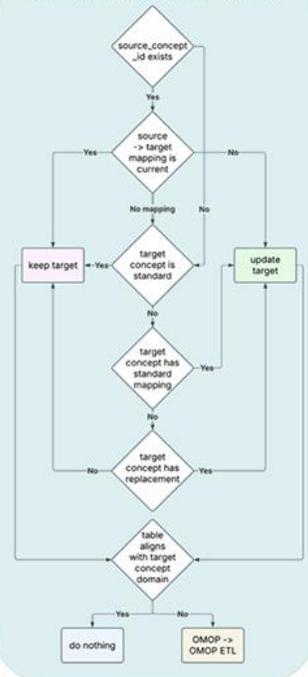
Vocabulary Harmonization

- Remap source_concept_id to new target concepts
- Find replacements for deprecated target concepts
- Move data across tables based on domain changes

Derived Data

- Create standardized observation_period records following THEMIS guidelines
- Generate condition and drug era records
- Future state: precompute cohorts

Vocabulary Harmonization Process





#OHDSISocialShowcase This Week

Thursday

Evaluating the Quality of Positive Unlabeled Learning Methods if Unlabeled Instances Cannot be Validated

(Praveen Kumar, Kristan A Schneider, Fariha Moomtaheen, Rajesh Upadhayaya, Scott A. Malec, Jeremy J. Yang, Cristian G. Bologa, Yiliang Zhu, Mauricio Tohen, Gerardo Villarreal, Douglas J. Perkins, Elliot M. Fielstein, Sharon E. Davis, Michael E. Matheny, Christophe G. Lambert)



Evaluating the Quality of Positive Unlabeled Learning Methods if Unlabeled Instances Cannot be Validated

Praveen Kumar¹, Kristan A. Schneider¹, Fariha Moomtaheen¹, Rajesh Upadhayaya¹, Scott A. Malec¹, Jeremy J. Yang¹, Cristian G. Bologa¹, Yiliang Zhu¹, Mauricio Tohen², Gerardo Villarreal^{2,3}, Douglas J. Perkins¹, Elliot M. Fielstein¹, Sharon E. Davis¹, Michael E. Matheny^{4,5}, Christophe G. Lambert¹

¹University of New Mexico, Department of Internal Medicine, Albuquerque, NM, USA, ²University of New Mexico, Department of Psychiatry & Behavioral Sciences, Albuquerque, NM, USA, ³Va New Mexico Healthcare System, Albuquerque, NM, USA, ⁴Vanderbilt University Medical Center, Department of Biomedical Informatics, Nashville, TN, USA, ⁵Tennessee Valley Healthcare System VA, Nashville, TN, USA



Abstract

The absence of a diagnosis in patient health records does not imply the absence of disease, creating a challenge for supervised learning approaches that rely on both positive and negative labels. The absence of negative labels leads to the problem of Positive and Unlabeled (PU) learning. However, validating the performance of PU learning is difficult, as in conditions such as depression, bipolar disorder, or post-traumatic stress disorder (PTSD). We propose a regression-based framework to evaluate PU learning algorithms by systematically manipulating labeled positives. When a subset of positives is relabeled as unlabeled, the proportion of unlabeled positives increases by a known fraction, which can be used to validate the PU learning methods through linear regression. Regression of the estimated PU fraction against the fraction of relabeled instances provides two key measures: the slope, which reflects algorithmic bias (no bias = 1), and the intercept, which estimates the true fraction of unlabeled positives. Using synthetic data and three benchmark datasets (With remote sensing, MAGIC gamma telescope, and mouse protein expression), we evaluated PU learning algorithms. Results show that the regression approach reliably identifies bias in PU learning methods, and the slope can be used to correct the estimates. This regression-based validation method offers a strategy to assess and improve PU learning algorithms, enabling robust application to empirical health data where unlabeled cases cannot be validated directly.

Background

While clinical diagnoses can confirm the presence of a medical condition, the absence of a diagnosis does not necessarily imply the absence of disease. This principle extends to electronic healthcare records (EHRs): the absence of an International Classification of Diseases (ICD) code does not indicate the absence of the underlying medical condition. When attempting to automatically classify medical conditions in the growing field of health informatics, this asymmetry in diagnostics and coding—or more generally, labeling—creates a fundamental problem for traditional supervised learning, which assumes the availability of both positive and negative examples. The absence of the latter leads to the problem of positive unlabeled (PU) learning. Recently, novel methods to estimate the fraction of positive instances within unlabeled data have been proposed²⁻³. However, the performance of such methods is difficult to assess when unlabeled cases cannot be validated, as is often the case for psychological conditions such as depression, bipolar disorder, and post-traumatic stress disorder (PTSD)⁴.

In this study, we propose a regression-based validation method that identifies bias in PU learning algorithms and provides a strategy to evaluate them, enabling robust application to empirical health data where unlabeled cases cannot be validated directly.

Materials and Methods

- We used synthetic data and three benchmark datasets [With remote sensing⁵ (N=4,839; #features=5, positive=4,576, unlabeled=263), Magic gamma telescope⁶ (N=19,020; #feat.=10, pos.=12,332, unlabeled=6,688) Mouse protein expression⁷ (N=1,080, #feat.=77, pos.=570, unlabeled=510)] to validate the three PU learning algorithms (PULSCAR⁸, DEDPUL⁹, and TIC¹⁰).
- Consider a sample of size N, with N₁ labeled positive, N₂ unlabeled positive, and N₃ unlabeled negative instances (N=N₁+N₂+N₃; the sum N₂+N₃, i.e., the number of unlabeled instances, is known, while N₂ and N₃ are unknown). When removing the labels of x labeled positive instances (0 < x < N₁), the modified data set contains N₁-x labeled positive and N₂+x unlabeled positive instances. Hence, the fraction of unlabeled positive instances increases by x/N.

Size	Labeled	Unlabeled	True parameter	Estimates
N	N ₁	N - N ₁ = N ₂ + N ₃	$\alpha = \frac{N_2}{N_2 + N_3}, p_2$	$\hat{\alpha}, \hat{p}_2 = \hat{\alpha}(1 - p_1)$
N	N ₁ - x	N - N ₁ + x = N ₂ + N ₃ + x	$\alpha^{(x)} = \frac{N_2 + x}{N_2 + N_3 + x}, p_2^{(x)} = p_2 + \frac{x}{N_2 + N_3 + x}$	$\hat{\alpha}^{(x)}, \hat{p}_2^{(x)} = \hat{\alpha}^{(x)}(1 - p_1 + \xi)$

- PU learning method is executed for a range of values of x (0.01 ≤ x/N ≤ 0.10). For each x, several data sets are randomly created. A regression model is then fit with the fraction of removed labels (x/N) as independent and the estimated percentage of PU cases as the dependent variable.
- The slope of the straight line regression reflects algorithmic bias (no bias = 1) and the intercept corresponds to the true fraction of PU instances.

References

- Kumar P, Lambert CG. 2024. Positive Unlabeled Learning Selected Not All Random (PULSAR): class proportion estimation without the selected complexity of random sampling. *Front Computer Science* 12:2421. <https://doi.org/10.3389/fcsc.2024.12421>
- Harrell B. 2015. *Regression Modeling Strategies: With Medical Applications*. Springer, 2015. 848 pp.
- Belletti G, Davis S. 2023. Estimating the Class Prior in Positive and Unlabeled Data Through Synthetic Free Methods. *Proceedings of the AAAI Conference on Artificial Intelligence*, 2023. 12121-12128. <https://doi.org/10.26434/chemrxiv-2023-12121>
- Martino AL, Laksono MS, Ramak S, Lu CY, Sumner 3R. Mining clinical and behavioral health data in a large electronic health record (EHR) system. *14th IEEE International Conference on e-Healthcare*, 2012. 144-149. <https://doi.org/10.1109/EHEALTH.2012.6262622>
- Johnson B. 2018. *WIT Remote Sensing*. <https://doi.org/10.24123/witpress.com>
- Blank A. 2019. MAGIC Gamma Telescope. <https://doi.org/10.26434/chemrxiv-2019-03080>
- Nguyen C, Guillet R, and Cox R. 2015. *Mouse Protein Expression*. <https://doi.org/10.26434/chemrxiv-2015-03080>

Results

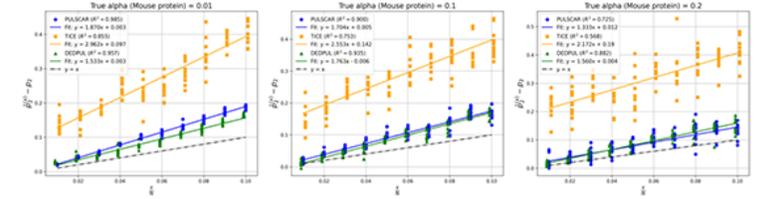


Figure 1: Linear regression plots based on the mouse protein expression dataset for three proportions of positive examples within the unlabeled set: 1%, 10%, and 20%. For each x/N value, the experiment was repeated 10 times with data shuffled using different random seeds.

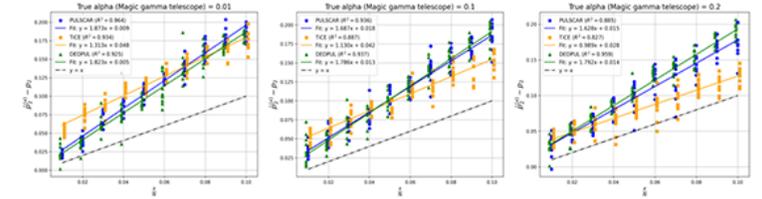


Figure 2: Linear regression plots based on the magic gamma telescope dataset for three proportions of positive examples within the unlabeled set: 1%, 10%, and 20%. For each x/N value, the experiment was repeated 10 times with data shuffled using different random seeds.

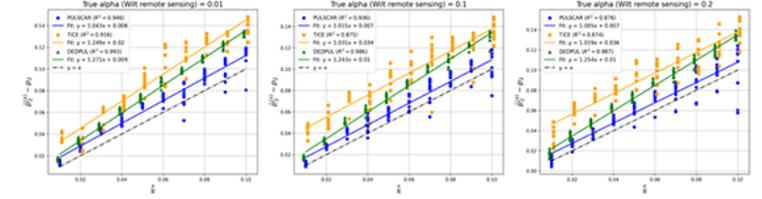


Figure 3: Linear regression plots based on the with remote sensing dataset for three proportions of positive examples within the unlabeled set: 1%, 10%, and 20%. For each x/N value, the experiment was repeated 10 times with data shuffled using different random seeds.

Discussion and Conclusions

- The results show that the linear regression approach presented here is well-suited to identify bias in PU learning algorithms, effectively exposing algorithmic bias.
- High R² is indicative for a good model performance, the regression slope can then be used to bias correct estimates.
- The method performs well on synthetic and benchmark datasets, where the true labels of all instances are known.
- As expected, overestimation by a PU method yields a slope > 1, while underestimation yields a slope < 1.
- The agreement between theoretical predictions and observations in these datasets suggests that the proposed method is suitable for evaluating the performance of PU learning algorithms on empirical data, where the status of unlabeled instances cannot be directly assessed, as in cases of depression, bipolar disorder, or PTSD.

Acknowledgments: This research was supported by funding from the US National Institutes of Health, specifically, the National Institute of Mental Health grant R01MH122764, the National Library of Medicine grant R01LM13387, and infrastructure support from the National Center for Advancing Translational Science grant UL1TR001888.





#OHDSISocialShowcase This Week

Friday

Agentic conversation on OMOP CDM: the OMCP-A2A foundation library

(Niko Möller-Grell, Shihao Shenzhang, Zhangshu Joshua Jiang, Vishnu V Chandrabalan, Richard Dobson)

OMCP-A2A: LLM Agent Collaboration on OMOP CDM Question Answering

Niko Möller-Grell¹; Shihao Shenzhang¹; Zhangshu Joshua Jiang⁷; Richard Dobson^{1,2,3,4,5,6}; Vishnu V Chandrabalan^{7,8}

<https://github.com/fastomop/fastomop>

¹ King's College London, Institute of Psychiatry, Psychology and Neuroscience, Department of Biostatistics and Health Informatics, 2 Institute for Health Informatics, University College London, London, UK, 3 NHR Biomedical Research Centre, University College London Hospitals National Health Service Foundation Trust, London, UK, 4 Health Data Research UK London, University College London, London, UK, 5 NHR Biomedical Research Centre, South London and Maudsley National Health Service Foundation Trust, London, UK, 6 Department of Biostatistics and Health Informatics, Institute of Psychiatry, Psychology and Neuroscience (IoPPN), King's College London, London, UK, 7 Lancashire Teaching Hospitals NHS Foundation Trust, 8 Lancaster University

Background

The Observational Medical Outcomes Partnership Common Data Model (OMOP CDM) has advanced healthcare analytics by standardising electronic health record (EHR) data, enabling cross-institutional interoperability and large-scale observational research¹. Advances in large language models (LLMs) and agentic artificial intelligence (AI) are now transforming how users interact with data, replacing the need for SQL expertise with natural language interfaces. Converting clinical and research questions directly into OMOP CDM queries, these text-to-SQL tools are democratizing access to advanced EHR analytics – bridging the gap between complex data structures and actionable insights².

Methods

Fastomop leverages a robust multi-agent framework to enable secure and explainable analysis of clinical data. Our methodology is divided into two key components: the multi-agent workflow for task orchestration, and a secure tool calling protocol that ensures safety and reliability.



Clinical Query

Agentic workflow

FastOMOP

Our framework utilizes a multi-agent system to tackle complex clinical queries, breaking them down into discrete, manageable tasks.

- **Orchestrator Agent:** The central control agent that receives the initial user query and directs the workflow by delegating tasks to specialized agents.
- **Semantic Agent:** Specializes in processing and enriching the natural language query, mapping medical terms to standardized OMOP vocabulary and concepts for accurate querying.
- **Database Agent:** Responsible for the secure and validated retrieval of data from the OMOP CDM. It handles all direct interactions with the database.
- **Specialized Agents:** We use additional specialized agents for complex analytical tasks. For example, a "Researcher Agent" could perform statistical analysis or machine learning on the retrieved data to produce actionable insights.
- **Agent Communication:** The agents communicate seamlessly and securely using the Agent-to-Agent (A2A) protocol, which enables vendor-agnostic collaboration. This ensures the system is modular and scalable³.

MCP tool calling

Result synthesising

OMCP

The Model Context Protocol (MCP) ensures all tool interactions are secure, explainable, and reliable by governing the communication between our agents and external tools⁴.

- **Building Trust and Explainability:**
 - **Deterministic tool calls** ensure that all interactions are predictable and verifiable.
 - **Traceability** logs every step of the agent's reasoning and actions, creating a clear audit trail.
 - **Separation of concerns** isolates sensitive tasks in dedicated servers, protecting them from the LLM.
 - **Rigorous validation** prevents security vulnerabilities by sanitizing all data entering and leaving a tool call.
- **OMCP Servers:**
 - **Python/R Sandbox:** Provides a secure, isolated environment for executing code.
 - **Semantic Server:** Maps natural language to medical concepts and enriches queries.
 - **Database Server:** Acts as a secure gateway for retrieving and executing SQL queries against the OMOP CDM.

Evaluation

Evaluation was performed comparing system generated queries and results against manually curated gold standard dataset of 50 NL-SQL-pairs derived from NOSTOS (v)

Results

Category	Count	Accuracy	Time
Overall	27	94% accuracy	20.6 seconds
drug	27	95.3% accuracy	22.2 seconds
condition	13	100% accuracy	21.5 seconds
demographics	4	100% accuracy	13.7 seconds
small evaluation dataset	1	100% accuracy	18 seconds
single execution reasoning	5	60% accuracy	15.2 seconds

References:

¹ OHDSI Collaborators. The Book of OHDSI: Observational Health Data Science and Informatics (OHDSI), 2019.

² Yu, P., Xu, H., Fu, X., & Dang, C. Leveraging generative AI and large language models: a comprehensive roadmap for healthcare integration. *Healthcare* 11, 2776 (2023).

³ Google. *A2A: Ask-to-Answer*. GitHub: <https://github.com/google/a2a> (2023).

⁴ Model Context Protocol. *Introduction to Model Context Protocol*. <https://modelcontextprotocol.ai/introduction/v0.1.0/>

⁵ Romero Galvis, M. et al. NOSTOS: Navigating OMOP-structured data via text-to-SQL. GitHub: <https://github.com/OHDSI/nostos> (2024).

Acknowledgements:

This work was supported by the UK Engineering and Physical Sciences Research Council (EP/S010319/1) Centre for Doctoral Training in Data-Driven Health (DRIVE) (Health) at King's College London, with additional support from the National Institute for Health and Care Research (NIHR) Biomedical Research Centre (BRC) (210023) and Lancaster Teaching Hospitals NHS Foundation Trust. The views expressed are those of the author(s) and not necessarily those of the NHS, the NIHR, the Department of Health and Social Care, or Lancaster Teaching Hospitals NHS Foundation Trust.



Where Are We Going?

**Any other announcements
of upcoming work, events,
deadlines, etc?**



Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?



Community Dashboard

Community Intelligence

Discover and explore research, tools, and knowledge from the global OHDSI community. Access 2833 articles, studies, and resources.

Search for OMOP CDM, Atlas, HADES, authors, or any OHDSI topic...


2833
Total Content


1097
Research Papers

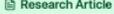

811
Videos


920
Repositories

[View All Content](#) →

Recent Articles

Showing 1097 articles from the OHDSI community

 Research Article 97%

Comorbidities, medication use, and overall survival in eight cancers: a...

BACKGROUND: Real-world evidence provides valuable insights into cancer burden, presentation, and care variations. Through a...

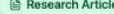
↳ López-Sánchez, Irene, Palomar-Cros, Anna,...

📅 Apr 1, 2026

Methodological research

Observational data standards and management

[Share](#) [View Source](#)

 Research Article 98%

Implementation of OMOP and ConCEPTION Common Data Models...

The impact of the choice of common data model (CDM) approach on the study results in a real-world evidence (RWE) study is unknown...

↳ Hunt, Nicholas B, Souverein, Patrick, Bazelier,...

📅 Mar 7, 2026

Methodological research

Open-source analytics development

[Share](#) [View Source](#)

 Research Article 93%

Comparative risk of the neurodegenerative outcomes...

OBJECTIVE: Type 2 diabetes mellitus has been associated with an increased risk of cognitive decline and dementia, with patients being 1.5-...

↳ Park, Sang Joon, Kim, Hye Jeong, Seo, Miha,...

📅 Feb 22, 2026

Clinical applications

Methodological research

[Share](#) [View Source](#)

 Research Article 68%

Experiences With Integrating Medical Terminologies Into User Interfaces fo...

BACKGROUND: Clinical decision support systems (CDSSs) have shown promise in improving diagnosis in primary care, particular...

↳ Neff, Michaela Christina, Schaaf, Jannik,...

📅 Feb 20, 2026

Observational data standards and management

[Share](#) [View Source](#)

 Research Article 88%

Hypertensive Disorders of Pregnancy and Premature Cardiovascular...

BACKGROUND: Cardiovascular disease (CVD) prevalence is rising among younger women in the United States. Hypertensive disorders of...

↳ Boyer, Theresa M, Barrett, Robert B, Xiong,...

📅 Feb 17, 2026

Methodological research

Observational data standards and management

[Share](#) [View Source](#)

 Research Article 98%

Transforming nursing documentation data into the Observational Medical...

BACKGROUND: Electronic health records (EHRs) provide clinical evidence for observational studies. Of these, nursing...

↳ Jung, Hyesil, Yoo, Sooyoung, Kim, Seok +2,...

📅 Feb 16, 2026

Methodological research

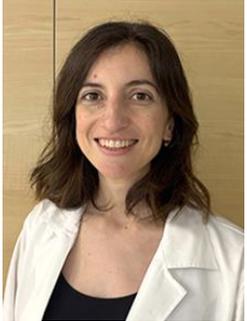
Observational data standards and management

[Share](#) [View Source](#)

dash.ohdsi.org



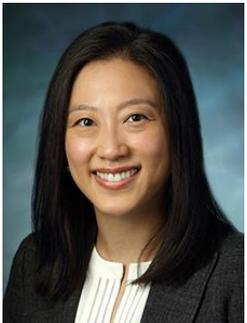
March 24: OHDSI/OMOP Research Spotlight



Berta Cuyàs

Hospital de la Santa Creu i Sant Pau, Autonomous University of Barcelona, CIBERehd

Trends in incidence, prevalence, and survival of primary liver cancer in the United Kingdom (2000–2021)
• *European Journal of Public Health*



Cindy Cai

Johns Hopkins University

Semaglutide and diabetic retinopathy: an OHDSI network study • *BMJ Open Diabetes Research & Care*



Matthew Spotnitz

Department of Health and Human Services, National Institutes of Health

Trends in incidence, prevalence, and survival of primary liver cancer in the United Kingdom (2000–2021)
• *European Journal of Public Health*



**The weekly OHDSI community call is held
every Tuesday at 11 am ET.**

Everybody is invited!

Links are sent out weekly and available at:

ohdsi.org/community-calls-2026



Find your workgroup.

Fuel our mission.

ohdsi.org/workgroups