Where Can We Go Together in 2026?

OHDSI Community Call

Jan. 13, 2026 • 11 am ET

OHDSI
OBSERVATIONAL HEALTH DATA SCIENCES AND INFORMATICS

Upcoming Community Calls

Date	Topic
Jan. 13	Where Can We Go Together in 2026?
Jan. 20	Connections for Future Collaborations
Jan. 27	Education and Innovation Brainstorm
Feb. 3	2026 Workgroup Objectives & Key Results, Part 1
Feb 10	2026 Workgroup Objectives & Key Results, Part 2

Three Stages of The Journey

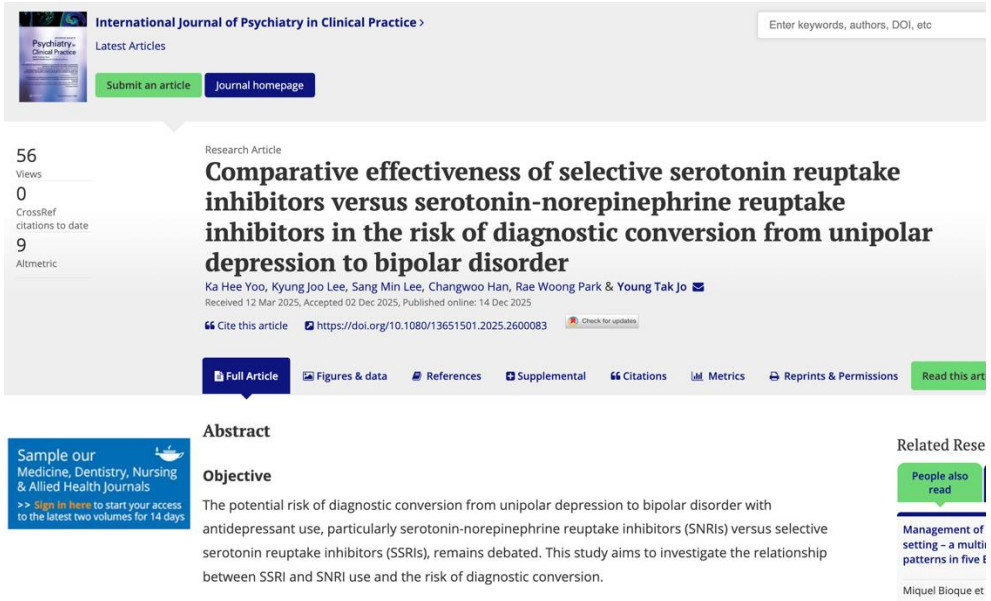
Where Have We Been?

Where Are We Now?

Where Are We Going?

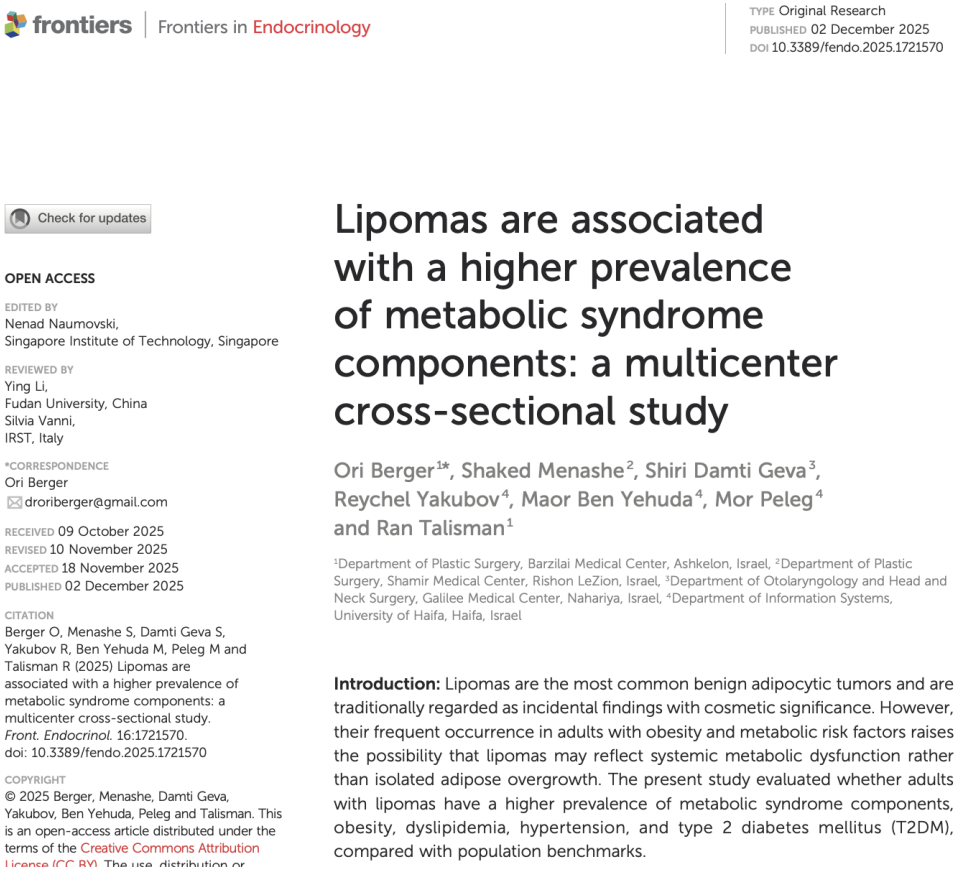
OHDSI Shoutouts!

Congratulations to the team of **Ka Hee Yoo, Kyung Joo Lee, Sang Min Lee, Changwoo Han, Rae Woong Park and Young Tak Jo** on the publication of **Comparative effectiveness of selective serotonin reuptake inhibitors versus serotonin-norepinephrine reuptake inhibitors in the risk of diagnostic conversion from unipolar depression to bipolar disorder** in the *International Journal of Psychiatry in Clinical Practice*.



OHDSI Shoutouts!

Congratulations to the team of **Ori Berger, Shaked Menashe, Shiri Damti Geva, Reychel Yakubov, Maor Ben Yehuda, Mor Peleg, and Ran Talisman** on the publication of **Lipomas are associated with a higher prevalence of metabolic syndrome components: a multicenter cross-sectional study** in *Frontiers in Endocrinology*.



frontiers | Frontiers in Endocrinology

TYPE Original Research
PUBLISHED 02 December 2025
DOI 10.3389/fendo.2025.1721570

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OPEN ACCESS

EDITED BY
Nenad Naumovski,
Singapore Institute of Technology, Singapore

REVIEWED BY
Ying Li,
Fudan University, China
Silvia Vanni,
IRST, Italy

*CORRESPONDENCE
Ori Berger
droriberger@gmail.com

RECEIVED 09 October 2025
REVISED 10 November 2025
ACCEPTED 18 November 2025
PUBLISHED 02 December 2025

CITATION
Berger O, Menashe S, Damti Geva S, Yakubov R, Ben Yehuda M, Peleg M and Talisman R (2025) Lipomas are associated with a higher prevalence of metabolic syndrome components: a multicenter cross-sectional study. *Front. Endocrinol.* 16:1721570. doi: 10.3389/fendo.2025.1721570

Lipomas are associated with a higher prevalence of metabolic syndrome components: a multicenter cross-sectional study

Ori Berger[1*], Shaked Menashe[2], Shiri Damti Geva[3], Reychel Yakubov[4], Maor Ben Yehuda[4], Mor Peleg[4] and Ran Talisman[1]

[1]Department of Plastic Surgery, Barzilai Medical Center, Ashkelon, Israel, [2]Department of Plastic Surgery, Shamir Medical Center, Rishon LeZion, Israel, [3]Department of Otolaryngology and Head and Neck Surgery, Galilee Medical Center, Nahariya, Israel, [4]Department of Information Systems, University of Haifa, Haifa, Israel

Introduction: Lipomas are the most common benign adipocytic tumors and are traditionally regarded as incidental findings with cosmetic significance. However, their frequent occurrence in adults with obesity and metabolic risk factors raises the possibility that lipomas may reflect systemic metabolic dysfunction rather than isolated adipose overgrowth. The present study evaluated whether adults with lipomas have a higher prevalence of metabolic syndrome components, obesity, dyslipidemia, hypertension, and type 2 diabetes mellitus (T2DM), compared with population benchmarks.

OHDSI Shoutouts!

Congratulations to the team of **Ever Augusto Torres-Silva, Juan José Gaviria-Jiménez, Ana María Guevara-Zambrano, Laura Herrera-Almanza, and José Flórez-Arango** on the publication of **Synthetic data from a common data model for artificial intelligence applications in maternal health: experience report in the Colombian context** in *Biomedica*.

Biomédica. 2025;45(Supl.3):71-82
https://doi.org/10.7705/biomedica.7937

Artículo original

Datos sintéticos de un modelo de datos común para las aplicaciones de inteligencia artificial en salud materna: reporte de experiencia en el contexto colombiano

Ever Augusto Torres-Silva[1], Juan José Gaviria-Jiménez[2], Ana María Guevara-Zambrano[3], Laura Herrera-Almanza[4], José Flórez-Arango[5]

[1] Futuro, Netux S.A.S., Medellín, Colombia
[2] Facultad de Medicina, Universidad de Antioquia, Medellín, Colombia
[3] Ginecología y Obstetricia, Hospital Pablo Tobón Uribe, Medellín, Colombia
[4] Investigación, Clínica Universitaria Bolivariana, Medellín, Colombia
[5] Population Health Sciences, Weill Cornell Medicine, New York, USA

Introducción. Los datos sintéticos en salud son una alternativa para generar registros clínicos que permitan obtener historias clínicas similares a las reales y que puedan ser usadas en diferentes situaciones clínicas.
Objetivo. Formular un modelo basado en la generación de datos sintéticos para el proceso de atención de la gestación en Colombia y adaptarlo al modelo de datos común de la *Observational Medical Outcomes Partnership* (OMOP) para facilitar su integración en aplicaciones de inteligencia artificial en salud materna.
Materiales y métodos. Se realizó un estudio de caso de formulación de datos completamente sintéticos, en el cual se incluyeron algunos de los desenlaces y condiciones más frecuentes de la gestación durante un proceso típico de atención de mujeres gestantes en Colombia. La propuesta se complementó con la generación de un modelo común de datos para facilitar la integración de los datos en futuras aplicaciones

Recibido: 08/04/2025
Revisado: 26/08/2025
Aceptado: 18/09/2025
Publicado: 19/09/2025

OHDSI Shoutouts!

Congratulations to the team of **Ylenia Murgia, Roberta Gazzarata, Mario Ciampi, Mario Sicuranza, Franco Cirillo, Christian Esposito, Norbert Maggi, Gabriella Balestra, Lucia Sacchi, and Mauro Giacomini** on the publication of **The challenges of national health data ecosystems in feeding the European health data space: the Italian example** in *Frontiers in Medicine*.

frontiers | Frontiers in Medicine

TYPE Hypothesis and Theory
PUBLISHED 08 December 2025
DOI 10.3389/fmed.2025.1644719

OPEN ACCESS

EDITED BY
Beatriz S. Lima,
Research Institute for Medicines (iMed.ULisboa), Portugal

REVIEWED BY
Gunnar Piho,
Tallinn University of Technology, Estonia
Mikhail Shifrin,
National Association of Medical Informatics, Russia

*CORRESPONDENCE
Mauro Giacomini
mauro.giacomini@unige.it

RECEIVED 10 June 2025
REVISED 18 September 2025
ACCEPTED 11 November 2025
PUBLISHED 08 December 2025

CITATION
Murgia Y, Gazzarata R, Ciampi M, Sicuranza M, Cirillo F, Esposito C, Maggi N, Balestra G, Sacchi L and Giacomini M (2025) The challenges of national health data ecosystems in feeding the European health data space: the Italian example. *Front. Med.* 12:1644719. doi: 10.3389/fmed.2025.1644719

The challenges of national health data ecosystems in feeding the European health data space: the Italian example

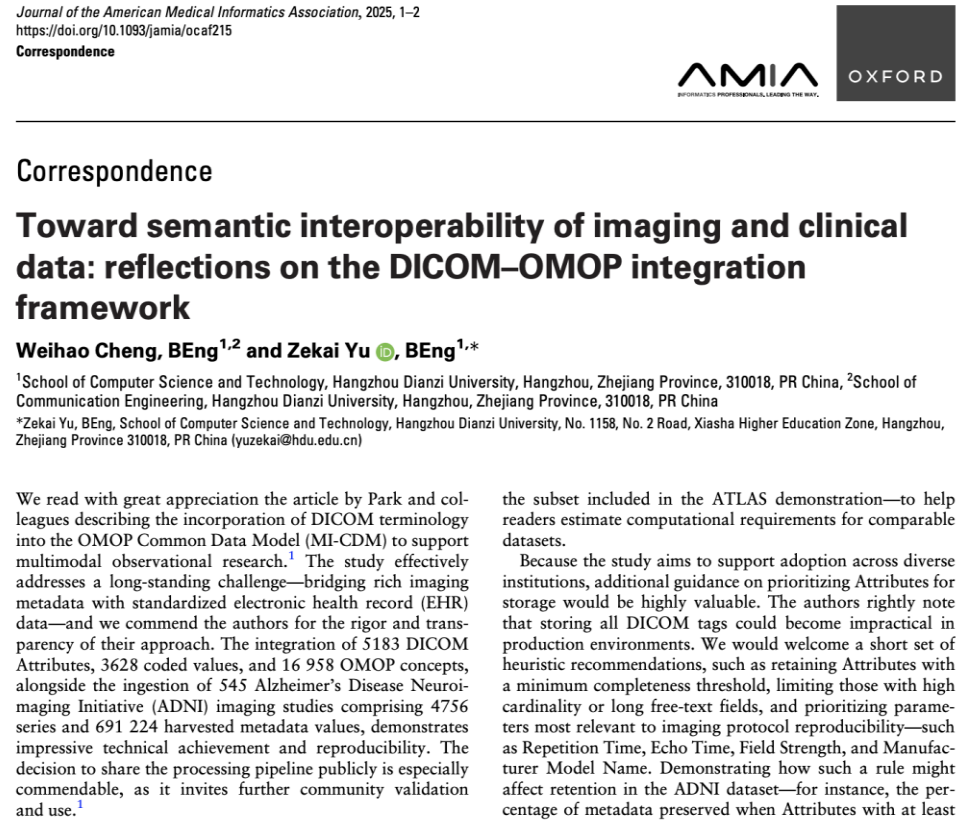
Ylenia Murgia[1], Roberta Gazzarata[2,3,4], Mario Ciampi[4,5], Mario Sicuranza[4,5], Franco Cirillo[6], Christian Esposito[6], Norbert Maggi[1,2], Gabriella Balestra[7,8], Lucia Sacchi[8,9,10] and Mauro Giacomini[1,8]*

[1]Department of Informatics, Bioengineering, Robotics and System Engineering (DIBRIS), University of Genoa, Genoa, Italy, [2]Healthropy, Savona, Italy, [3]HL7 Europe, Brussels, Belgium, [4]HL7 Italy, Rome, Italy, [5]Institute for High Performance Computing and Networking, National Research Council of Italy (ICAR-CNR), Naples, Italy, [6]Department of Computer Science, University of Salerno, Fisciano, Italy, [7]PoliToBIOMedLab, Department of Electronics and Telecommunications, Politecnico di Torino, Turin, Italy, [8]Italian Scientific Society of Biomedical Informatics (SIBIM), Pavia, Italy, [9]Department of Industrial and Information Engineering, University of Pavia, Pavia, Italy, [10]OHDSI Italian National Node, Italy

The European Health Data Space (EHDS) is an European Union (EU) initiative, aimed at helping facilitate the secure and standardized sharing of health data to improve continuity of care, research and innovation. However, the successful implementation of such an ecosystem requires the active participation and cooperation of EU Member States (MS), each of which needs to adapt its local health data infrastructure to meet the requirements at the European level. The specific characteristics of the various European countries, such as size, number of citizens, and internal organization greatly influence the ease with which a country can integrate its health data structure into this supra-national system. States with higher levels of local autonomy are experiencing significant challenges in this process. For instance, the Italian National Healthcare System (NHS) is highly decentralized, with significant variability among regions and

OHDSI Shoutouts!

Congratulations to the team of **Weihao Cheng and Zekai Yu** on the publication of **Toward semantic interoperability of imaging and clinical data: reflections on the DICOM-OMOP integration framework** in *JAMIA*.



Journal of the American Medical Informatics Association, 2025, 1–2
https://doi.org/10.1093/jamia/ocaf215
Correspondence

AMIA INFORMATICS PROFESSIONALS, LEADING THE WAY. OXFORD

Correspondence

Toward semantic interoperability of imaging and clinical data: reflections on the DICOM–OMOP integration framework

Weihao Cheng, BEng[1,2] and Zekai Yu, BEng[1,*]

[1]School of Computer Science and Technology, Hangzhou Dianzi University, Hangzhou, Zhejiang Province, 310018, PR China, [2]School of Communication Engineering, Hangzhou Dianzi University, Hangzhou, Zhejiang Province, 310018, PR China

*Zekai Yu, BEng, School of Computer Science and Technology, Hangzhou Dianzi University, No. 1158, No. 2 Road, Xiasha Higher Education Zone, Hangzhou, Zhejiang Province 310018, PR China (yuzekai@hdu.edu.cn)

We read with great appreciation the article by Park and colleagues describing the incorporation of DICOM terminology into the OMOP Common Data Model (MI-CDM) to support multimodal observational research.[1] The study effectively addresses a long-standing challenge—bridging rich imaging metadata with standardized electronic health record (EHR) data—and we commend the authors for the rigor and transparency of their approach. The integration of 5183 DICOM Attributes, 3628 coded values, and 16 958 OMOP concepts, alongside the ingestion of 545 Alzheimer's Disease Neuroimaging Initiative (ADNI) imaging studies comprising 4756 series and 691 224 harvested metadata values, demonstrates impressive technical achievement and reproducibility. The decision to share the processing pipeline publicly is especially commendable, as it invites further community validation and use.[1]

the subset included in the ATLAS demonstration—to help readers estimate computational requirements for comparable datasets.

Because the study aims to support adoption across diverse institutions, additional guidance on prioritizing Attributes for storage would be highly valuable. The authors rightly note that storing all DICOM tags could become impractical in production environments. We would welcome a short set of heuristic recommendations, such as retaining Attributes with a minimum completeness threshold, limiting those with high cardinality or long free-text fields, and prioritizing parameters most relevant to imaging protocol reproducibility—such as Repetition Time, Echo Time, Field Strength, and Manufacturer Model Name. Demonstrating how such a rule might affect retention in the ADNI dataset—for instance, the percentage of metadata preserved when Attributes with at least

OHDSI Shoutouts!

Congratulations to the team of **Srinivas R. Sadda, Charles C. Wykoff, Itay Chowers, Jean-Francois Korobelnik, Raja Narayana, Rajeev R. Pappuru, Frank G. Holz, Robyn Guymer, Chui Ming Gemmy Cheung, David S. Boyer, Michael Ip, Heiko G. Niessen, Nancy Holenkamp, Mary Durbin, Stephanie Magazzeni, Anne-Marie Cairns, Carlos Ciller, Natasa Jovic, Joseph Blair, Sandro De Zanet & Aaron Y. Lee** on the publication of **Initiation of a global consortium to study the progression of age-related macular degeneration: RIMR AMD consortium report # 1** in *Graefe's Archive for Clinical and Experimental Ophthalmology*.

Graefe's Archive for Clinical and Experimental Ophthalmology
https://doi.org/10.1007/s00417-025-07081-4

RETINAL DISORDERS

Initiation of a global consortium to study the progression of age-related macular degeneration: RIMR AMD consortium report # 1

Srinivas R. Sadda[1,2,3] · Charles C. Wykoff[4] · Itay Chowers[5] · Jean-Francois Korobelnik[6,7] · Raja Narayana[8] · Rajeev R. Pappuru[8] · Frank G. Holz[9] · Robyn Guymer[10] · Chui Ming Gemmy Cheung[11] · David S. Boyer[12] · Michael Ip[1,2,3] · Heiko G. Niessen[13] · Nancy Holenkamp[14] · Mary Durbin[15] · Stephanie Magazzeni[16] · Anne-Marie Cairns[17] · Carlos Ciller[18] · Natasa Jovic[18] · Joseph Blair[18] · Sandro De Zanet[18] · Aaron Y. Lee[1,19]

Received: 27 August 2025 / Revised: 6 November 2025 / Accepted: 10 December 2025

Abstract

Purpose To describe the design and organizational structure of a global collaborative consortium aimed at aggregating longitudinal multimodal imaging data to better understand the progression of age-related macular degeneration (AMD) and facilitate therapeutic development.

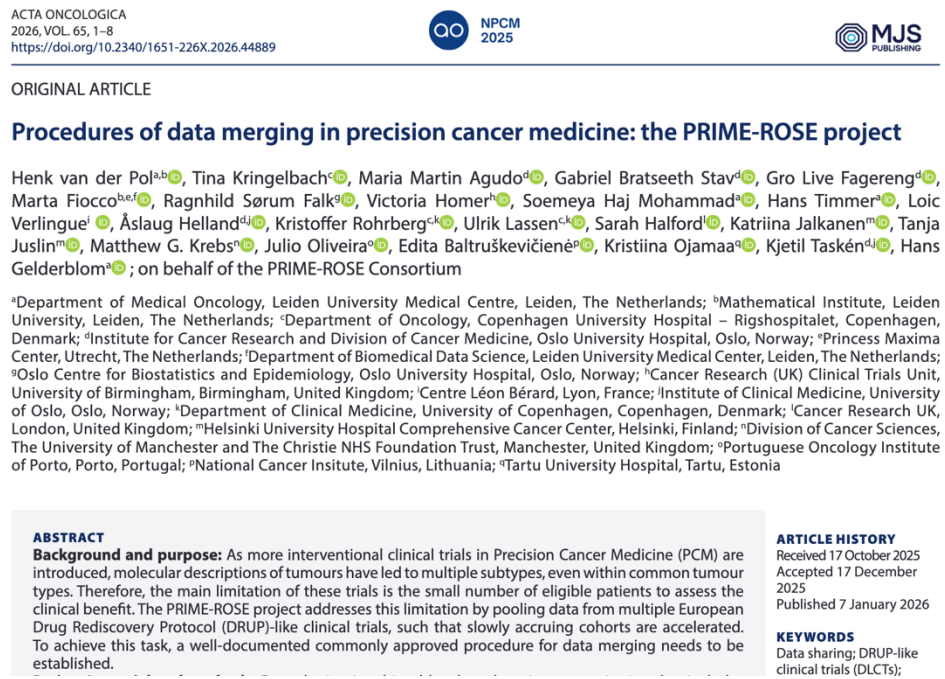
Methods The Ryan Initiative for Macular Research (RIMR) AMD Consortium was established as a nonprofit organization, bringing together academic institutions, biopharmaceutical companies, and imaging technology providers. The consortium collects, de-identifies, and harmonizes longitudinal optical coherence tomography (OCT) data, as well as associated clinical metadata, from multiple international clinical centers using a cloud-based infrastructure. Imaging data is converted and stored in DICOM format, and associated clinical data is mapped to the OMOP Common Data Model. All analyses are conducted within a secure cloud environment, supporting both built-in and member-contributed artificial intelligence (AI) tools.

Results As of the time of reporting, the Consortium has ingested over 100,000 OCT volumes from more than 5,000 subjects across 7 global cohorts spanning 4 continents and 3 major OCT platforms. Based on information provided by the data providers, the dataset encompasses a wide range of AMD stages, from normal aging to late-stage neovascular or atrophic AMD, with longitudinal follow-up extending beyond 15 years for some subjects. A data harmonization pipeline has been established to convert all ingested OCT data to the DICOM standard and is thus ready for automated analysis to gain disease-related insights.

Conclusions The RIMR AMD Consortium represents a novel model for global collaboration in AMD research, enabling the pooling and analysis of heterogeneous imaging data while addressing privacy, regulatory, and interoperability challenges. This framework may serve as a model for similar initiatives in other ocular diseases.

OHDSI Shoutouts!

Congratulations to the team of **Henk Van der Pol, Tina Kringelbach, Maria Martin Agudo, Gabriel Bratseth Stav, Gro Live Fagereng, Marta Fiocco, Ragnhild Sørum Falk, Victoria Homer, Soemeya Haj Mohammad, Hans Timmer, Loic Verlingue, Åslaug Helland, Kristoffer Rohrberg, Ulrik Lassen, Sarah Halford, Katriina Jalkanen, Tanja Juslin, Matthew G Krebs, Julio Oliveira, Edita Baltruskeviciene, Kristiina Ojamaa, Kjetil Taskén, and Hans Gelderblom** on the publication of **Procedures of data merging in precision cancer medicine: the PRIME-ROSE project** in *Acta Oncologica*.



ACTA ONCOLOGICA
2026, VOL. 65, 1–8
https://doi.org/10.2340/1651-226X.2026.44889

NPCM 2025

MJS PUBLISHING

ORIGINAL ARTICLE

Procedures of data merging in precision cancer medicine: the PRIME-ROSE project

Henk van der Pol[a,b], Tina Kringelbach[c], Maria Martin Agudo[d], Gabriel Bratseeth Stav[d], Gro Live Fagereng[d], Marta Fiocco[b,e,f], Ragnhild Sørum Falk[g], Victoria Homer[h], Soemeya Haj Mohammad[a], Hans Timmer[a], Loic Verlingue[i], Åslaug Helland[d,j], Kristoffer Rohrberg[c,k], Ulrik Lassen[c,k], Sarah Halford[l], Katriina Jalkanen[m], Tanja Juslin[m], Matthew G. Krebs[n], Julio Oliveira[o], Edita Baltruškevičienė[p], Kristiina Ojamaa[q], Kjetil Taskén[d,j], Hans Gelderblom[a]; on behalf of the PRIME-ROSE Consortium

[a]Department of Medical Oncology, Leiden University Medical Centre, Leiden, The Netherlands; [b]Mathematical Institute, Leiden University, Leiden, The Netherlands; [c]Department of Oncology, Copenhagen University Hospital – Rigshospitalet, Copenhagen, Denmark; [d]Institute for Cancer Research and Division of Cancer Medicine, Oslo University Hospital, Oslo, Norway; [e]Princess Maxima Center, Utrecht, The Netherlands; [f]Department of Biomedical Data Science, Leiden University Medical Center, Leiden, The Netherlands; [g]Oslo Centre for Biostatistics and Epidemiology, Oslo University Hospital, Oslo, Norway; [h]Cancer Research (UK) Clinical Trials Unit, University of Birmingham, Birmingham, United Kingdom; [i]Centre Léon Bérard, Lyon, France; [j]Institute of Clinical Medicine, University of Oslo, Oslo, Norway; [k]Department of Clinical Medicine, University of Copenhagen, Copenhagen, Denmark; [l]Cancer Research UK, London, United Kingdom; [m]Helsinki University Hospital Comprehensive Cancer Center, Helsinki, Finland; [n]Division of Cancer Sciences, The University of Manchester and The Christie NHS Foundation Trust, Manchester, United Kingdom; [o]Portuguese Oncology Institute of Porto, Porto, Portugal; [p]National Cancer Insitute, Vilnius, Lithuania; [q]Tartu University Hospital, Tartu, Estonia

ABSTRACT

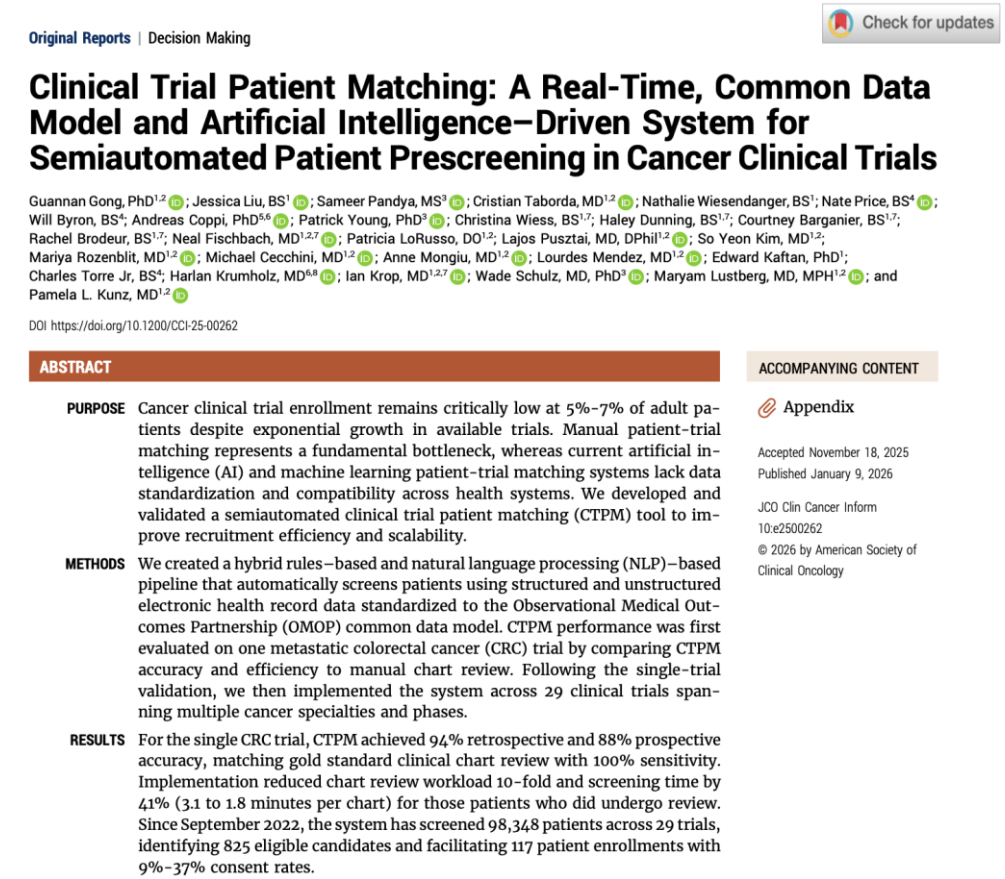
Background and purpose: As more interventional clinical trials in Precision Cancer Medicine (PCM) are introduced, molecular descriptions of tumours have led to multiple subtypes, even within common tumour types. Therefore, the main limitation of these trials is the small number of eligible patients to assess the clinical benefit. The PRIME-ROSE project addresses this limitation by pooling data from multiple European Drug Rediscovery Protocol (DRUP)-like clinical trials, such that slowly accruing cohorts are accelerated. To achieve this task, a well-documented commonly approved procedure for data merging needs to be established.

ARTICLE HISTORY
Received 17 October 2025
Accepted 17 December 2025
Published 7 January 2026

KEYWORDS
Data sharing; DRUP-like clinical trials (DLCTs);

OHDSI Shoutouts!

Congratulations to the team of **Guannan Gong, Jessica Liu, Sameer Pandya, Cristian Taborda, Nathalie Wiesendanger, Nate Price, Will Byron, Andreas Coppi, Patrick Young, Christina Wiess, Haley Dunning, Courtney Barganier, Rachel Brodeur, Neal Fischbach, Patricia LoRusso, Lajos Pusztai, So Yeon Kim, Mariya Rozenblit, Michael Cecchini, Anne Mongiu, Lourdes Mendez, Edward Kaftan, Charles Torre Jr, Harlan Krumholz, Ian Krop, Wade Schulz, Maryam Lustberg, and Pamela L Kunz** on the publication of **Clinical Trial Patient Matching: A Real-Time, Common Data Model and Artificial Intelligence-Driven System for Semiautomated Patient Prescreening in Cancer Clinical Trials** in *JCO Clinical Cancer Informatics*.



Original Reports | Decision Making

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Clinical Trial Patient Matching: A Real-Time, Common Data Model and Artificial Intelligence–Driven System for Semiautomated Patient Prescreening in Cancer Clinical Trials

Guannan Gong, PhD[1,2]; Jessica Liu, BS[1]; Sameer Pandya, MS[3]; Cristian Taborda, MD[1,2]; Nathalie Wiesendanger, BS[1]; Nate Price, BS[4]; Will Byron, BS[4]; Andreas Coppi, PhD[5,6]; Patrick Young, PhD[3]; Christina Wiess, BS[1,7]; Haley Dunning, BS[1,7]; Courtney Barganier, BS[1,7]; Rachel Brodeur, BS[1,7]; Neal Fischbach, MD[1,2,7]; Patricia LoRusso, DO[1,2]; Lajos Pusztai, MD, DPhil[1,2]; So Yeon Kim, MD[1,2]; Mariya Rozenblit, MD[1,2]; Michael Cecchini, MD[1,2]; Anne Mongiu, MD[1,2]; Lourdes Mendez, MD[1,2]; Edward Kaftan, PhD[1]; Charles Torre Jr, BS[4]; Harlan Krumholz, MD[6,8]; Ian Krop, MD[1,2,7]; Wade Schulz, MD, PhD[3]; Maryam Lustberg, MD, MPH[1,2]; and Pamela L. Kunz, MD[1,2]

DOI https://doi.org/10.1200/CCI-25-00262

ABSTRACT

PURPOSE Cancer clinical trial enrollment remains critically low at 5%–7% of adult patients despite exponential growth in available trials. Manual patient-trial matching represents a fundamental bottleneck, whereas current artificial intelligence (AI) and machine learning patient-trial matching systems lack data standardization and compatibility across health systems. We developed and validated a semiautomated clinical trial patient matching (CTPM) tool to improve recruitment efficiency and scalability.

METHODS We created a hybrid rules–based and natural language processing (NLP)–based pipeline that automatically screens patients using structured and unstructured electronic health record data standardized to the Observational Medical Outcomes Partnership (OMOP) common data model. CTPM performance was first evaluated on one metastatic colorectal cancer (CRC) trial by comparing CTPM accuracy and efficiency to manual chart review. Following the single-trial validation, we then implemented the system across 29 clinical trials spanning multiple cancer specialties and phases.

RESULTS For the single CRC trial, CTPM achieved 94% retrospective and 88% prospective accuracy, matching gold standard clinical chart review with 100% sensitivity. Implementation reduced chart review workload 10-fold and screening time by 41% (3.1 to 1.8 minutes per chart) for those patients who did undergo review. Since September 2022, the system has screened 98,348 patients across 29 trials, identifying 825 eligible candidates and facilitating 117 patient enrollments with 9%–37% consent rates.

ACCOMPANYING CONTENT

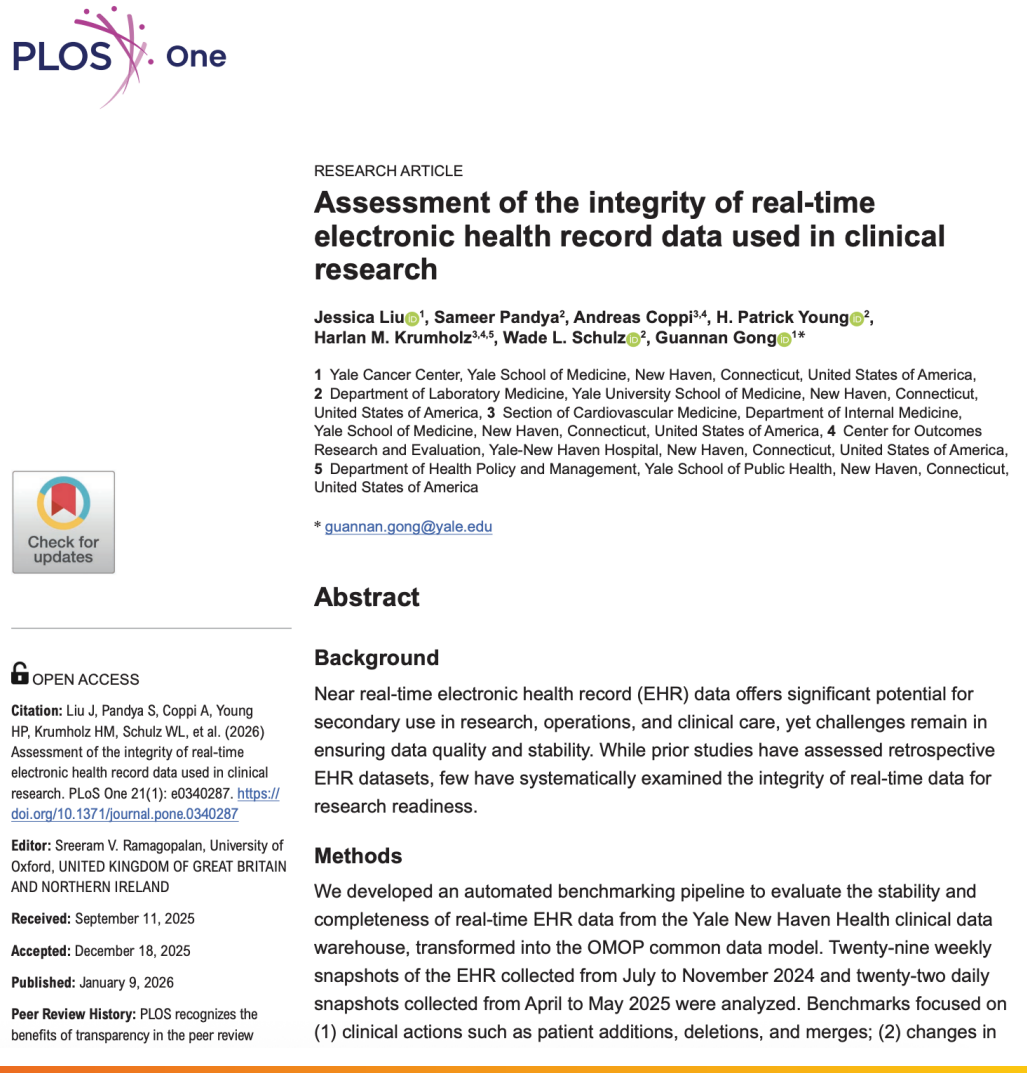
Appendix

Accepted November 18, 2025
Published January 9, 2026

JCO Clin Cancer Inform
10:e2500262

OHDSI Shoutouts!

Congratulations to the team of **Jessica Liu, Sameer Pandya, Andreas Coppi,H. Patrick Young, Harlan M. Krumholz, Wade L. Schulz, Guannan Gong** on the publication of **Assessment of the integrity of real-time electronic health record data used in clinical research** in *PLOS One*.



PLOS One

RESEARCH ARTICLE

Assessment of the integrity of real-time electronic health record data used in clinical research

Jessica Liu[1], Sameer Pandya[2], Andreas Coppi[3,4], H. Patrick Young[2], Harlan M. Krumholz[3,4,5], Wade L. Schulz[2], Guannan Gong[1]*

1 Yale Cancer Center, Yale School of Medicine, New Haven, Connecticut, United States of America, **2** Department of Laboratory Medicine, Yale University School of Medicine, New Haven, Connecticut, United States of America, **3** Section of Cardiovascular Medicine, Department of Internal Medicine, Yale School of Medicine, New Haven, Connecticut, United States of America, **4** Center for Outcomes Research and Evaluation, Yale-New Haven Hospital, New Haven, Connecticut, United States of America, **5** Department of Health Policy and Management, Yale School of Public Health, New Haven, Connecticut, United States of America

* guannan.gong@yale.edu

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OPEN ACCESS

Citation: Liu J, Pandya S, Coppi A, Young HP, Krumholz HM, Schulz WL, et al. (2026) Assessment of the integrity of real-time electronic health record data used in clinical research. PLoS One 21(1): e0340287. https://doi.org/10.1371/journal.pone.0340287

Editor: Sreeram V. Ramagopalan, University of Oxford, UNITED KINGDOM OF GREAT BRITAIN AND NORTHERN IRELAND

Received: September 11, 2025

Accepted: December 18, 2025

Published: January 9, 2026

Peer Review History: PLOS recognizes the benefits of transparency in the peer review

Abstract

Background

Near real-time electronic health record (EHR) data offers significant potential for secondary use in research, operations, and clinical care, yet challenges remain in ensuring data quality and stability. While prior studies have assessed retrospective EHR datasets, few have systematically examined the integrity of real-time data for research readiness.

Methods

We developed an automated benchmarking pipeline to evaluate the stability and completeness of real-time EHR data from the Yale New Haven Health clinical data warehouse, transformed into the OMOP common data model. Twenty-nine weekly snapshots of the EHR collected from July to November 2024 and twenty-two daily snapshots collected from April to May 2025 were analyzed. Benchmarks focused on (1) clinical actions such as patient additions, deletions, and merges; (2) changes in

Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?

Upcoming Workgroup Calls

Date	Time (ET)	Meeting
Tuesday	12 pm	ATLAS/WebAPI
Thursday	8 am	India Community Call
Thursday	12 pm	HADES
Friday	10 am	GIS– Geographic Information System
Friday	10:30 am	Open-Source Community
Monday	9 am	Africa Chapter

ATHENA Survey

Athena user survey

Help us understand how to make Athena better

When you submit this form, it will not automatically collect your details like name and email address unless you provide it yourself.

* Required

1. If you are open to follow-up about your feedback, please provide your email address

Enter your answer

2. How do you use athena.ohdsi.org? *

- [ ] Search concepts
- [ ] Download current version of vocabularies
- [ ] Download previous version of vocabularies
- [ ] Other

3. What do you athena.ohdsi.org for? *

- [ ] ETL data
- [ ] Search concepts to create mappings
- [ ] Search concepts for concept sets (value sets, code lists)
- [ ] Translate concepts to other languages/find translations
- [ ] Use as knowledge graph outside of OMOP CDM
- [ ] Other

4. On average, how often do you access athena.ohdsi.org? *

- ◯ Every day
- ◯ Once a week
- ◯ A few times a month
- ◯ Once a month
- ◯ Once 6 month or less
- ◯ Other

5. If there was an Athena API, how would you use it and what would you use it for? *

Enter your answer

6. Anything else you'd like to tell us? *

Enter your answer

You can print a copy of your answer after you submit

Submit

LATAM Steering

Columbia DBMI Summer School

The 2026 Summer School in Observational Health Data Science & Informatics, AI, and Real World Evidence

COLUMBIA | COLUMBIA UNIVERSITY DEPARTMENT OF BIOMEDICAL INFORMATICS

OHDSI
OBSERVATIONAL HEALTH DATA SCIENCES AND INFORMATICS

June 22–26, 2026, Columbia Biomedical Informatics

The Columbia OHDSI Summer School provides health professionals, researchers, and industry practitioners with an immersive, hands-on training to working with real-world health data and generating real-world evidence (RWE). Participants will explore the types of healthcare data captured during routine clinical care—such as electronic health records and administrative claims—and learn how to standardize these data using the OMOP Common Data Model to support collaborative, distributed research as part of a data network.

Over the course of the week, participants will engage with three real-world analytic use cases:

- **Clinical characterization** – using descriptive epidemiology to study disease natural history and treatment patterns
- **Population-level estimation** – applying causal inference to assess drug safety and comparative effectiveness
- **Patient-level prediction** – leveraging machine learning for early disease detection and precision medicine

Participants will be guided through the full RWE study lifecycle: from designing observational studies tailored to each use case, to applying open-source tools form the OHDSI community, and executing analyses across real-world data sources.

The curriculum combines foundational lectures on analytical methods with hands-on, interactive, faculty-led group exercises. In addition, participants will have dedicated time to develop and advance their own study concepts with personalized feedback and mentoring.

Oxford Summer School Registration Opens

Oxford Summer School 2026: Real World Evidence using the OMOP Common Data Model

COURSE DIRECTORS

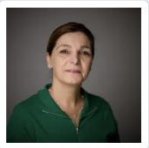
Daniel Prieto-Alhambra

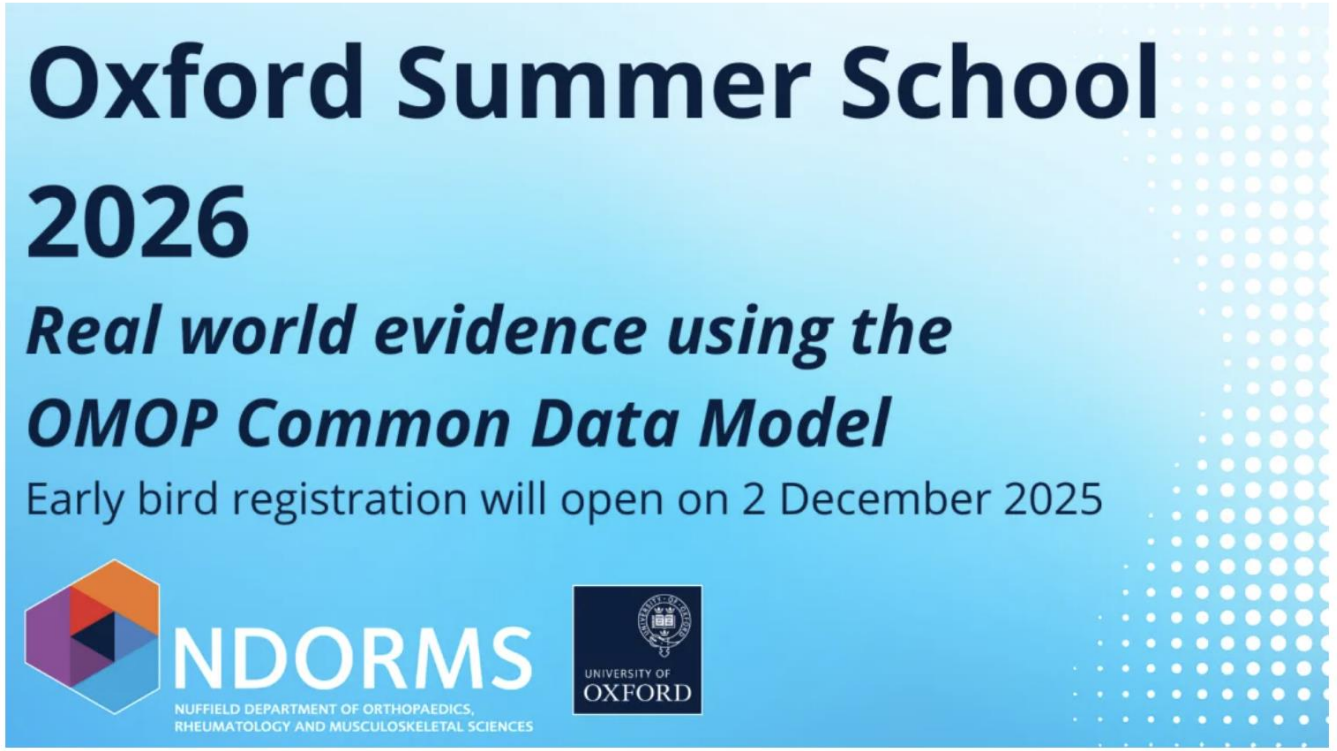
Professor of Pharmaco- and Device Epidemiology

COURSE ADMINISTRATOR

Mahkameh Mafi

Personal Assistant to Professor Prieto-Alhambra





2026 Global Symposium

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

2026 Global Symposium

2026 OHDSI Global Symposium Call for Plenary Sessions

Symposium plenaries provide opportunities to share innovative, community-developed content to empower researchers to generate reliable real-world evidence. The community is currently seeking proposals for our #OHDSI2026 plenaries. These sessions will be 60 minutes in duration and must touch on at least two of following pillars of our community:

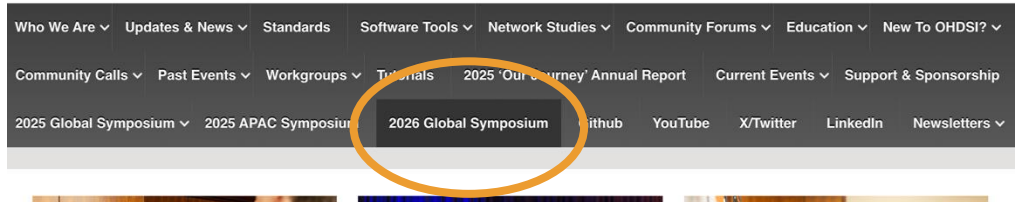
- Open community data standards
- Methodological research
- Open-source development
- Clinical applications

Plenary sessions must also involve three or more on-stage participants across at least two organizations. Sessions may include a combination of keynote talks, panel discussions, interactive activities, and more. We strongly encourage using multiple formats and synthesizing completed research, current perspectives and future calls-to-action to maximize community engagement.

The deadline for proposal submissions is January 30, 2026. Please use the link below to submit your proposal by answering the following questions:

- Name(s) of plenary session organizers:
- Your email address(es):
- Short (2,500 character max) description / abstract of your proposed session:
- Which pillars are you targeting:
- One sentence “pitch” of your session to excite the community:
- Names and roles of individuals who have tentatively agreed to participate in your session:

Deadline to submit proposals for #OHDSI2026 plenaries or tutorials is Jan. 30, 2026!



2026 OHDSI Global Symposium

Oct. 20-22 • New Brunswick, N.J. • Hyatt Regency Hotel

2026 OHDSI Global Symposium Call for Tutorials

Tutorial sessions aim to deliver educational content, led by community members who wish to train our global collaborators on scientific, technical, and other skills that can support advancing OHDSI’s mission and the effective use of real-world data and the generation and dissemination of reliable real-world evidence. Examples of prior tutorials offered are provided here: https://www.ohdsi.org/tutorials.

Tutorial sessions are 4 hours in duration. Registrants for your tutorial will be requested to pay a registration fee. The fees will be used to offset the costs of the symposium and other OHDSI expenses. Sessions may include a combination of talks, interactive activities, and more. We strongly encourage using multiple formats to maximize community engagement. Your session must include at least three people from at least two different organizations.

The deadline for tutorial proposal submissions is January 30, 2026. Please use the link below to submit your proposal by answering the following questions:

- Name(s) of tutorial session organizers:
- Your email address(es):
- Short (2,500 character) description / abstract of your proposed session:
- Names and roles of individuals who have tentatively agreed to participate in your session:

2026 Europe Symposium

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

The deadline for abstract submissions will be Feb. 6, 2026.

#OHDSISocialShowcase This Week

Monday

Preserving the DNA of Clinical Intent: Integrating IMO Health API services into OHDSI Extract-Transform-Load Process

(Evan Sholle, David Haines, Chandan Ravishankar, Tejaswini Viswanath, Merlin Simoes, Daniel Timke, Sajjad Abedian, Frank Naeymi-Rad)

Preserving the DNA of Clinical Intent
Integrating IMO Health API services into OHDSI Extract-Transform-Load Process

PRESENTER: **Evan Sholle**

INTRO:
While the OHDSI community has established a well-validated library of techniques for generating evidence from real-world data, the value of data sets mapped to the model is constrained by data quality issues[1] attributable to a host of factors, including factors derived from source data systems and those introduced by the mapping process.
Specifically, within the Condition domain, mapping physician documented clinical terms ("interface terms") to OHDSI standard terms often involves a "step down" into a less granular intermediate terminology - ICD-10 - prior to mapping to SNOMED.[2]
We hypothesized that by incorporating IMO Health terminology services into the ETL process and mapping IMO-derived interface terminology items directly to SNOMED, rather than stepping through ICD-10, we could preserve diagnostic granularity, better reflect physician intent, and improve the performance of computable phenotyping techniques executed against the resultant data set.

METHODS

1. ETL Comparison:
   As illustrated in Figure 1, we developed two pipelines for mapping EHR diagnoses to the OHDSI CDM: a "legacy" ETL representative of current standard practice reliant on ICD-10-CM → SNOMED mapping, and an "Enhanced" ETL using IMO Precision Normalize™ API for direct interface-term → SNOMED mapping with bidirectional ICD-10-CM crosswalks to derive the *condition_source_concept_id*.
2. Patient Impact Analysis:
   After conducting the ETL, we measured the number of unique interface terminology items present within the source data. We then calculated the number of unique SNOMED and ICD-10 codes these terminology items mapped to for each of the two techniques. We also measured the impact of the different ETL techniques on specific ICD-10 codes that were highly impacted by the change.

Mapping diagnoses into the CDM through ICD-10 incurs real data granularity loss! Using IMO Health's suite of terminology services, we can map clinical terms directly to preserve important diagnostic details.

Take a picture to download the full paper

Results
As detailed in Figure 2, the Enhanced ETL technique resulted in a significantly more granular data set. The 162,501 unique interface terminology items in the source data set were mapped to 45,561 unique SNOMED codes and 29,751 ICD-10 codes using the Enhanced ETL technique, while the legacy ETL technique resulted in only 11,389 unique SNOMED codes and 29,348 ICD-10 codes.

Figure 1

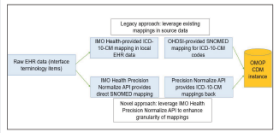


Figure 2

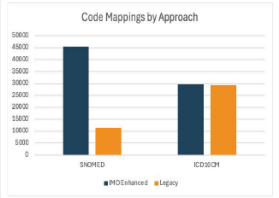


Table 1

ICD-10 code	Diagnosis name	Count of patients with legacy ETL method	Count of patients with enhanced ETL method
Z40.00	Encounter for prophylactic removal of unspecified organ	3	6,336
H44.50	Unspecified degenerated conditions of globe	1	8510
Z00.71	Encounter for examination for period of delayed growth in childhood with abnormal findings	0	783
H55.9	Unspecified disorder of globe	0	6932
S70.001A	Unspecified injury of muscle, fascia and tendon of right hip, initial encounter	1	162

1. Blackstor C, Defalco FJ, Ryan PB, Rijnbeek PR. Increasing trust in real-world evidence through evaluation of observational data quality. J Am Med Inform Assoc. 2021 Sep 18;28(10):2251-2257. doi: 10.1093/jamia/ocab132. PMID: 34313749; PMCID: PMC8449528.
2. Weiskopf NG, Weng C. Methods and dimensions of electronic health record data quality assessment: enabling reuse for clinical research. J Am Med Inform Assoc. 2013 Jan 1;20(1):144-51. doi: 10.1136/amiajnl-2011-000681. Epub 2012 Jun 25. PMID: 22733976; PMCID: PMC3555312.

Evan Sholle, David Haines, Chandan Ravishankar, Tejaswini Viswanath, Merlin Simoes, Daniel Timke, Sajjad Abedian, Frank Naeymi-Rad

#OHDSISocialShowcase This Week

Tuesday

Prediction of Hyperuricemia and Its Association with Renal failure, Cardiovascular Prognosis in Adults with Type 2 Diabetes mellitus

(Sujin Gan, Dong Yun Lee, Rae Woong Park)

Prediction of Hyperuricemia and Its Association with Renal failure, Cardiovascular Prognosis in Adults with Type 2 Diabetes mellitus

Sujin Gan[1,4,5], Dong Yun Lee[2,3], and Rae Woong Park[1,2,4,5]

[1] Department of Biomedical Sciences, Ajou University Graduate School of Medicine, Suwon, Korea; [2] Department of Biomedical Informatics, Ajou University School of Medicine, Suwon, Korea
[3] Bongdam forest mental health clinic, Hwaseong, Korea; [4] Center for Biomedical Informatics Research, Ajou University Medical Center, Suwon, Korea; [5] BK21 R&E Initiative for Advanced Precision Medicine, Suwon, Korea

Background

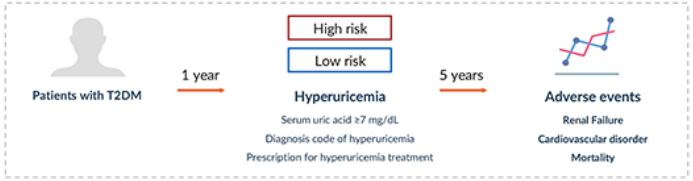
- Accurate prediction of disease progression in T2DM is essential for personalized treatment, yet the prognostic value of hyperuricemia as a potential biomarker remains unclear.

We aimed to:

- Develop and externally validate a machine learning model predicting hyperuricemia within 1 year of T2DM diagnosis.
- Evaluate associations between predicted hyperuricemia and long-term outcomes

Methods

1. Data sources
- OMOP-CDM databases from **4 Korean healthcare institutions** (N = 6,108,232 patients)
  - Model development: Ajou University School of Medicine (AUSOM)
  - External validation: Kangdong Sacred Heart Hospital (KDH), Sejong General Hospital Bucheon (SJBCN), Wonkwang University Hospital (WKUH)



2. Study population
- Target cohort: Adults (≥18 years) with newly diagnosed T2DM
  - Inclusion criteria: ≥ 1 year prior observation; ≥1 serum uric acid measurement within one year post-diagnosis
  - Exclusion criteria: prior hyperuricemia, gout, cancer, renal, cardiovascular, or cerebrovascular disease

3. Model development
- XGBoost, LASSO, Random Forest (in 3-fold Cross validation with 75/25 train-test split)
  - Features: Demographics, Conditions, Drugs, Observations, Procedures (30-day and 365-day windows)
  - Performance metrics: AUROC, AUPRC, F1-score, Accuracy

4. External validation & Long-term Outcomes
- Kaplan–Meier survival estimates and Cox proportional hazards regression
- **Meta-analysis** performed to generate pooled hazard ratios across databases

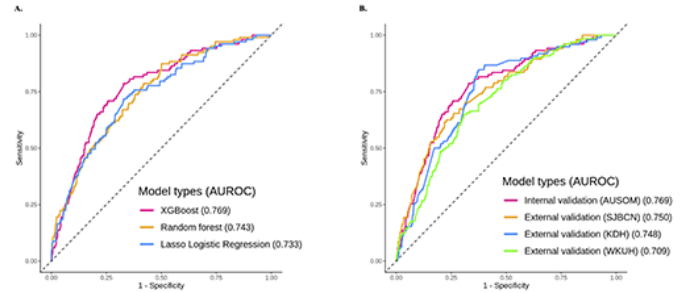
Conclusions

- This study developed and externally validated a robust prediction model for one-year hyperuricemia in newly diagnosed T2DM patients.
- Importantly, predicted hyperuricemia was associated with a significantly elevated risk of renal failure, cardiovascular complications, and death over 5 years, suggesting that early identification of hyperuricemia risk may inform risk stratification and long-term management strategies in T2DM.
- **Findings highlight hyperuricemia as a prognostic biomarker for adverse outcomes in diabetes.**

Results

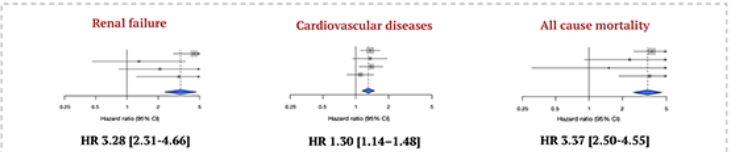
1. Study population characteristics
- In the AUSOM cohort (n = 5,263), 413 patients (7.85%) developed hyperuricemia within one year of T2DM diagnosis. These patients were more likely to be male (67.3%) compared to those without hyperuricemia (47.4%, p < 0.001), but no significant age difference was observed.

2. Model performance
- The XGBoost model achieved the best performance, with an AUROC of 0.769 (95% CI: 0.723–0.815), AUPRC of 0.205, F1-score of 0.278, and accuracy of 0.681. In external validation, robust performance was observed.



- Key predictive features included male sex, use of sulfonylureas or insulin, bacterial infections, hemoglobin levels, and prescriptions of diuretics or anti-tuberculosis drugs.
- Consistent top predictors were identified across XGBoost, LASSO, and Random Forest models.

3. Long term outcomes
- Over a five-year follow-up period, predicted hyperuricemia was strongly associated with adverse outcomes.
- Meta-analysis across four databases confirmed these associations, yielding pooled HRs of 3.28 (95% CI: 2.31–4.65) for renal failure, 1.30 (95% CI: 1.14–1.48) for cardiovascular disease, and 3.37 (95% CI: 2.50–4.56) for mortality.



Fundings: This work was supported by the National Research Foundation of Korea(NRF) grant funded by the Korea government(MOE)(NO : 2120240615426, BK21 R&E Initiative for Advanced Precision Medicine), the Korea Health Technology R&D Project through the Korea Health Industry Development Institute (KHIDI), funded by the Ministry of Health & Welfare, Republic of Korea (grant number: RS-2024-00335936), a grant (25212MFDS002) from Ministry of Food and Drug Safety in 2025, and the NRF grant funded by the Korea government(MSIT)(grant numbers RS-2025-20552981 and RS-2025-16070957).

#OHDSISocialShowcase This Week

Wednesday

Real-World Treatment Pathways of Lung Cancer Patients in Taiwan: A Common Data Model Analysis Using TMUCRD

(Nguyen Thi Kim Hien, Thanh-Phuc Phan, Nam Hoai Vo, Muhammad Solihuddin Muhtar, Christianus Heru Setiawan, Septi Melisa, Jason C. Hsu)

Real-World Treatment Pathways of Lung Cancer Patients in Taiwan: A Common Data Model Analysis Using TMUCRD

PRESENTER: Nguyen Thi Kim Hien

INTRO

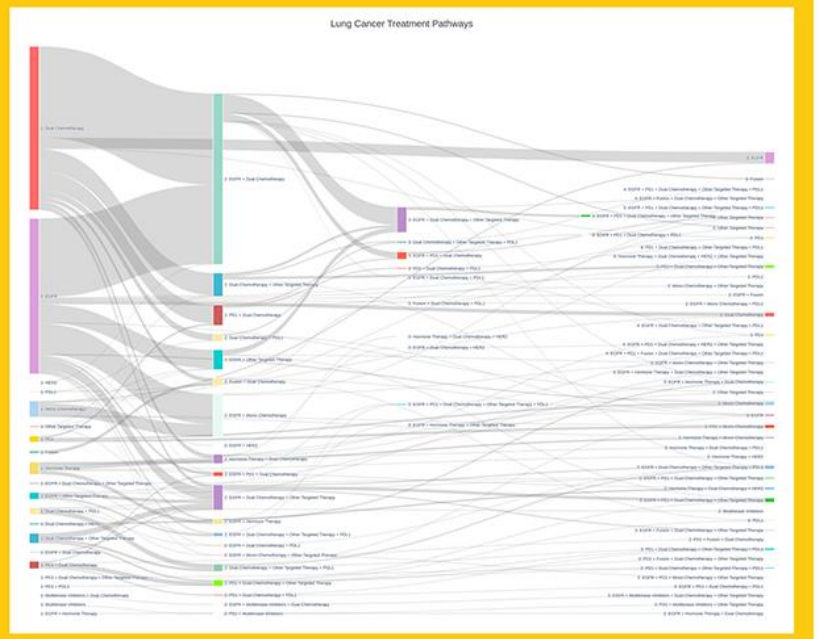
- Lung cancer is the leading cause of cancer deaths globally (1.8M deaths, 18.7% in 2022).
- Clinical trials often don't reflect real-world care.
- Treatment pathway analysis bridges the gap between evidence-based guidelines and actual practice.

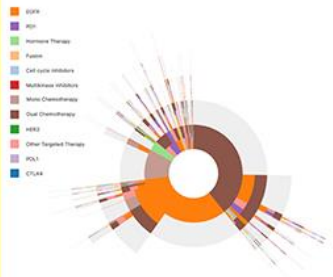
METHODS

1. Data source: TMUCRD (Taipei Medical University Hospital, Shuangho, Wanfang) 2005–2020.
2. Format: Transformed into OMOP CDM for standardized OHDSI analysis.
3. Patients: 1,895 adults with primary lung cancer, ≥18 years, treated pharmacologically.
4. Analysis tools: ATLAS, R (TreatmentPatterns), Python.
5. Therapy categories:
   - ❖ Mono- & dual chemotherapy
   - ❖ EGFR inhibitors
   - ❖ Fusion / HER2 / other targeted agents
   - ❖ Immune checkpoint inhibitors (PD-1/PD-L1/CTLA-4)
   - ❖ Hormonal therapy
6. Pathways: Up to 5 sequential treatment steps visualized.

Chemotherapy and **EGFR inhibitors** dominate **first-line therapy** for lung cancer treatment, but real-world treatment sequences are **highly heterogeneous.**

Substantial patient drop-off beyond second line.





RESULTS

First-line therapies:

- Dual chemotherapy: 39.2%
- EGFR inhibitors: 33.8%
- Mono chemotherapy: 10%

Transitions:

- Patients on dual chemo → often switched to EGFR regimens.
- Patients on EGFR inhibitors → often cycled back to dual chemo.

CONCLUSION

This study highlights the heterogeneous nature of real-world lung cancer treatment pathways, with chemotherapy and EGFR inhibitors as predominant first-line therapies and a gradual integration of targeted and immunotherapies in later lines.

Nguyen Thi Kim Hien, Thanh-Phuc Phan, Nam Hoai Vo, Muhammad Solihuddin Muhtar, Christianus Heru Setiawan, Septi Melisa, Jason C. Hsu*

#OHDSISocialShowcase This Week

Thursday

Empowering Trial by Multi-source Multi-site Real-world Data: A Negative Control-Calibrated Digital Twin Approach

(Dazheng Zhang, Huiyuan Wang, Yiwen Lu, Yong Chen)

OHDSI

Empowering Trial by Multi-source Multi-site Real-world Data: A Negative Control-Calibrated Digital Twin Approach

Dazheng Zhang[a], Huiyuan Wang[a], Yiwen Lu[a], Jingyue Huang[a], Yong Chen[a]

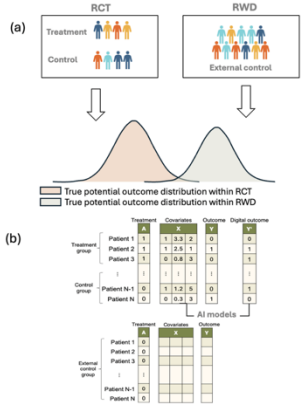
[a] The Center for Health Analytics and Synthesis of Evidence (CHASE), University of Pennsylvania, Philadelphia, PA, USA

Background

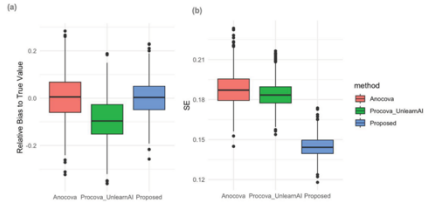
- **Randomized controlled trials** (RCTs) ensure robust causal inference through randomization but often lack generalizability due to strict inclusion criteria, high costs, and limited scalability.
- **Real-world data (RWD)** offer broader population coverage and longitudinal follow-up at lower cost, but are prone to bias due to non-randomization and incomplete data access.
- **Integrating external controls from RWD** can enhance the statistical efficiency of RCTs by reducing required sample sizes and costs.
- **Digital twin technology**, originating from engineering, uses machine learning on high-dimensional RWD to simulate patient-specific counterfactuals and treatment responses. The PROCOVA[1] method applies this by creating virtual control groups to improve trial efficiency[7]. However, discrepancies between trial and real-world populations can introduce bias, necessitating careful calibration.
- We propose a novel framework that corrects **model shift bias** in RCT-RWD integration using digital twins and negative control outcomes.

Method

- We introduce the concept of **NCOs**, outcomes that are theoretically unaffected by treatment assignment, allowing for an empirical estimate of the model shift bias. The observed discrepancy in NCO distributions between RCT and RWD serves as a diagnostic tool for identifying systematic shifts in outcome distributions.
- We utilize predictive modeling within the RWD to construct a **digital twin**—an individualized outcome model for RCT participants. More details about the proposed method can be found the Methods Section. By systematically calibrating for model shift, our method facilitates more robust and generalizable treatment effect estimation in hybrid trial designs.

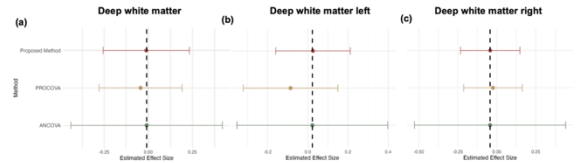


Contact: dazheng.zhang@pennmedicine.upenn.edu and ychen123@upenn.edu



- We illustrate the performance of the proposed method in comparison to baseline methods, including PROCOVA—an approach that does not account for model-shift bias—and ANCOVA.
- The ANCOVA method relies solely on RCT data, making its point estimates the gold standard due to the inherent randomization in RCTs.
- The proposed method achieves a 39.9% relative efficiency gain compared to ANCOVA. In contrast, the PROCOVA method, which is affected by model-shift bias, shows minimal efficiency improvement over ANCOVA.

Results



- As ANCOVA relies solely on RCT data, its estimates serve as the gold standard due to the benefits of randomization.
- The PROCOVA method incorporates external real-world data (RWD) but does not account for model-shift bias, leading to potential inaccuracies.
- The proposed method, by addressing model-shift bias, produces estimates that align closely with ANCOVA while achieving notable efficiency gains. Across all panels, the proposed method consistently yields more precise estimates and avoids the potential distortions observed in PROCOVA.

Conclusion

- In summary, our proposed digital twin framework with negative control outcome calibration effectively addresses model shift bias in RCT-RWD integration.
- Applied to brain imaging data from SPRINT-MIND and iSTAGING, the method achieved treatment effect estimates that closely aligned with RCT-based ANCOVA while offering improved statistical precision.
- This approach enhances the validity and efficiency of hybrid trial designs, paving the way for more reliable real-world evidence for OHDSI community.

Reference

Schuler A, Walsh D, Hall D, Walsh J, Fisher C, Initiative ADN. Increasing the efficiency of randomized trial estimates via linear adjustment for a prognostic score. *Int J Biostat* 2022; **18**: 329–56

#OHDSISocialShowcase This Week

Friday

How do changes in vocabulary mapping and database release versions affect cohort composition in real-world data?

(Jill Hardin, Evanette Burrows, Azza Shaoibi, Clair Blacketer)

Title: How do changes in vocabulary mapping and database release versions affect cohort composition in real-world data?

PRESENTER: **Jill Hardin**

INTRODUCTION:

1. Challenges exist in assessing effects of vocabulary and database version changes in the analysis observational data.
2. Gaining an understanding of the influence on cohort composition is critical for epidemiological research.
3. This study compares incidence rates (IR) of condition (n=239) and drug (n=198) phenotypes across vocabulary versions and database releases for 13 different data sources.
4. Absolute percent difference was calculated to quantify IR changes.

METHODS:

1. 13 observational health data sources standardized to the OMOP Common Data Model (CDM) (1) v5.4 to derive IRs.
2. Two versions of each data source were created by mapping the native data to standard concepts using two vocabulary versions: February 29, 2024, and February 27, 2025.
3. 437 phenotypes were evaluated: 239 outcomes and 198 drug exposures across the 13 data sources x 2 vocabulary versions.
4. The population at risk (target cohort) was subjects with an observation period between January 1, 2016, and December 31, 2022.
5. ATLAS (2) and the Strategus incidence rate module was used for phenotype development and IR calculation.
6. OHDSI best practices was used to develop the phenotypes.
7. The absolute percent difference between IRs for each vocabulary and database release version was calculated using the formula:

$$\frac{(IR\_new\_vocab - IR\_prior\_vocab)}{IR\_prior\_vocab} \times 100$$

8. Per 100 person years unit used

RESULTS:

1. Most phenotypes (31-85%) showed absolute percent differences of 0-5%.
2. Larger changes (>5%) were seen in Optum EHR (12.6%) and CPRD (7.3%).
3. Phenotypes with greatest differences: heavy menstrual bleeding in Optum EHR & CPRD, and epoprostenol in JMDC.

Table 1: The number (%) of phenotypes by categories of absolute percent difference between incidence rates.

Database	The number (%) of phenotypes by category of absolute percent difference in incidence rates											
	>0-5		>5-10		>10-20		>20-50		>50+		NA*	
	N	%	N	%	N	%	N	%	N	%	N	%
CPRD	261	59.7%	13	3.0%	12	2.7%	6	1.4%	1	0.2%	144	32.9%
France Disease Analyzer	205	46.9%	0	0.0%	2	0.5%	5	1.1%	2	0.5%	223	51.0%
German Disease Analyzer	278	63.6%	5	1.1%	2	0.5%	5	1.1%	3	0.7%	144	32.9%
Health Verity CC	370	84.7%	10	2.3%	5	1.1%	3	0.7%	0	0.0%	49	11.2%
JMDC	277	63.4%	6	1.4%	7	1.6%	6	1.4%	7	1.6%	134	30.6%
LPD Australia	136	31.1%	0	0.0%	0	0.0%	0	0.0%	0	0.0%	301	68.8%
CCAE	367	84.0%	2	0.5%	11	2.5%	2	0.5%	0	0.0%	55	12.6%
MDCR	351	80.3%	3	0.7%	8	1.8%	1	0.2%	0	0.0%	74	16.9%
MDCD	369	84.4%	3	0.7%	7	1.6%	3	0.7%	0	0.0%	55	12.6%
Optum EHR	342	78.3%	24	5.5%	22	5.0%	7	1.6%	2	0.5%	40	9.1%
Optum DOD	372	85.1%	2	0.5%	8	1.8%	3	0.7%	0	0.0%	52	11.9%
Optum SES	372	85.1%	2	0.5%	8	1.8%	3	0.7%	0	0.0%	52	11.9%
Premier	283	64.8%	8	1.8%	6	1.4%	1	0.2%	0	0.0%	139	31.8%

*NOTE: NA bin is created when the incidence rate on new and old vocabulary are equal to 0

Phenotype composition is stable across data releases and vocabulary updates.

Figure 1. Condition phenotypes with absolute percent difference values >5% by database

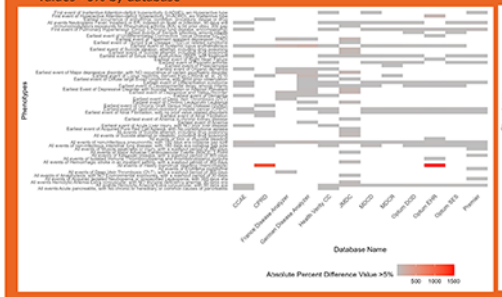
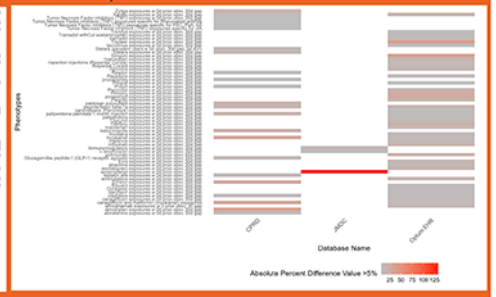


Figure 2. Drug exposure phenotypes with absolute percent difference values >5% by database



Take a picture to download the poster

RESULTS cont:

1. Optum EHR & CPRD use SNOMED; others use ICD10.
2. JMDC data showed drug mappings added across releases, especially for epoprostenol, mapped to English codes.

CONCLUSIONS:

1. Phenotype composition is stable across data releases and vocabulary updates.
2. Certain phenotypes may be sensitive to vocabulary or release changes due to shifts in SNOMED concepts or drug mappings.
3. Data sources using native SNOMED are more affected by hierarchy changes.
4. This study highlights the need to monitor and understand the impacts of vocabulary and data releases in real-world data analysis.
5. The approach provided can help develop standardized methods to assess these effects on phenotype definitions.

FUTURE WORK:

1. Incorporate this approach into a standardized tool

REFERENCES:

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Jill Hardin[1,2], Evanette Burrows[1,2], Azza Shaoibi[1,2], Clair Blacketer[1,2]
[1]Observational Health Data Analytics, Global Epidemiology, Johnson & Johnson Research and Development, Raritan, NJ, USA; [2]Observational Health Data Sciences and Informatics, New York, NY, USA;

Johnson&Johnson Global Epidemiology Organization

OHDSI Network Study: 2025 Bridging Evidence Gaps

Comparative Risk of Infection in Rheumatic Disease Patients Initiating Immunosuppressive Therapy

Background

- Rheumatic/autoimmune diseases (including myositis, scleroderma, lupus, uveitis) are a group of conditions associated with high morbidity and mortality
- Majority of patients are treated with immune-suppressing medications
- Infectious complications are a major contributor to adverse outcomes, driven largely by the immunosuppressive therapies used for treatment

Gaps in Current Evidence/Guidelines

Major gaps remain in comparative safety across rheumatic disease medications, including a lack of head-to-head data

There is also insufficient evidence on optimal vaccination strategies and antimicrobial prophylaxis

Quantification of risk largely unknown; “rare”, “sometimes”

Study Design

- **Population:** Adults aged ≥18 years with prevalent rheumatic disease, including systemic lupus erythematosus (SLE), systemic sclerosis (SSc), inflammatory myositis (IM), or non-infectious uveitis, identified using previously validated OHDSI phenotype algorithms
- **Comparators**: Two complementary analytic aims will be pursued:
  - Aim 1 (Monotherapy comparisons): New users of mycophenolate mofetil (MMF), rituximab (RTX), intravenous immunoglobulin (IVIG), or Janus kinase inhibitors (JAKi; tofacitinib, baricitinib)
  - Aim 2 (Combination therapy comparisons)**:** Prevalent users of a conventional immunosuppressant (MMF, methotrexate [MTX], or azathioprine [AZA]) who initiate a second immunosuppressive agent (e.g., RTX, IVIG, JAKi), compared across alternative add-on strategies
- **Outcomes:**
  - Varicella zoster virus infection (shingles)
  - Hospitalized infection (composite)
  - Progressive multifocal leukoencephalopathy (PML)
  - Pneumocystis jirovecii pneumonia (PJP)
- **Design:** New-user and new-user/active-comparator designs. Time-to-event analyses will be conducted using propensity score–adjusted Cox proportional hazards models, with large-scale propensity scores derived from all available covariates in the OMOP-CDM. Negative control outcomes, subgroup analyses (e.g., vaccination and prophylaxis status), and multiple sensitivity analyses will be performed to assess robustness and residual confounding.

Participating Sites (thus far)

- Johns Hopkins
- Jansen (Johnson & Johnson)
- Columbia University
- Stanford University
- University of Southern California
- Penn State University
- UT Southwestern

The ask of the OHDSI Community:

1. Feedback on protocol:
    - design
    - assumptions
    - concept sets
    - analysis plans

2. Feedback on code (Strategus):
    - Does it match protocol intent?
    - Can it be more efficient?

3. If interested, participate as a data partner!

If you're still listening and interested…

- Protocol and code published to Microsoft teams page, OHDSI Forums, and GitHub

- Teams meetings on January 26th 10 AM EST and January 28th 11 AM EST for those interested:

  - OHDSI Rheumatology Network Study Feedback - January 26th
  - OHDSI Rheumatology Network Study Feedback - January 28th

- Message me at cmecoli1@jhmi.edu with questions

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?

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-2025