



OHDSI/OMOP Research Spotlight

OHDSI Community Call
Sept. 29, 2026 • 11 am ET



Upcoming Community Calls

Date	Topic
Sept. 29	OHDSI/OMOP Research Spotlight
Oct. 6	DARWIN EU Progress
Oct. 13	Global Symposium Poster Preview / Final Logistics
Oct. 20	NO CALL – Global Symposium
Oct. 27	Welcome to OHDSI: What We Do, How Can You Make an Impact
Nov. 3	Meet the Titans
Nov. 10	Collaborator Showcase Honoree Presentations
Nov. 17	Early-Stage Researcher Presentations
Nov. 24	Software Demos



Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?



OHDSI Shoutouts!



Congratulations to the team of **Marco Caminati, Jeremy Charriot, Aruna T Bansal, Shane Hanon, Renaud Louis, Florence Schleich, Muriel Delvaux, Guy Brusselle, Stéphanie Ziant, Virginie Paulus, Sanja Grle Popovic, Gordana Pavlisa, Marina Lampalo, Celeste Porsbjerg, Kjell Håkansson, Susanne Hansen, Arnaud Bourdin, Eve Klising, Candice Estellat, Caroline Giboin, Dounya Metdaoui, Zsuzsanna Csoma, Dora Lúðvíksdóttir, Giorgio Walter Canonica, Enrico Heffler, Cristina Cardini, Anna Alloni, Iveta Kroica, Kristina Bieksiene, Romain Tching, Anneke ten Brinke, Jacob Sont, Piotr Kuna, Maria Morawska, Florin Mihaltan, Sanja Hromis, Aleksa Golubovic, Mihailo Stjepanovic, Vojislav Čupurdija, Peter Kopac, Valentyna Yasinska, Fabienne Jaun, Joerg Leuppi, Ebru Damadoglu, Ozlem Goksel, Sabina Skrgat, Ratko Djukanovic, and Bilun Gemicioglu** on the recent publication of **Biologic outcomes in severe asthma patients by smoking status: evidence from SHARP** in the *American Journal of Respiratory and Critical Care Medicine*.

AJRCCM
American Journal of Respiratory and Critical Care Medicine

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JOURNAL ARTICLE ACCEPTED MANUSCRIPT
Biologic outcomes in severe asthma patients by smoking status: evidence from SHARP
[Marco Caminati](#), [Jeremy Charriot](#) , [Aruna T Bansal](#), [Shane Hanon](#), [Renaud Louis](#), [Florence Schleich](#), [Muriel Delvaux](#), [Guy Brusselle](#), [Stéphanie Ziant](#), [Virginie Paulus](#), [Sanja Grle Popovic](#), [Gordana Pavlisa](#), [Marina Lampalo](#), [Celeste Porsbjerg](#), [Kjell Håkansson](#), [Susanne Hansen](#), [Arnaud Bourdin](#), [Eve Klising](#), [Candice Estellat](#), [Caroline Giboin](#), [Dounya Metdaoui](#), [Zsuzsanna Csoma](#), [Dora Lúðvíksdóttir](#), [Giorgio Walter Canonica](#), [Enrico Heffler](#), [Cristina Cardini](#), [Anna Alloni](#), [Iveta Kroica](#), [Kristina Bieksiene](#), [Romain Tching](#), [Anneke ten Brinke](#), [Jacob Sont](#), [Piotr Kuna](#), [Maria Morawska](#), [Florin Mihaltan](#), [Sanja Hromis](#), [Aleksa Golubovic](#), [Mihailo Stjepanovic](#), [Vojislav Čupurdija](#), [Peter Kopac](#), [Valentyna Yasinska](#), [Fabienne Jaun](#), [Joerg Leuppi](#), [Ebru Damadoglu](#), [Ozlem Goksel](#), [Sabina Skrgat](#), [Ratko Djukanovic](#), [Bilun Gemicioglu](#)
[Author Notes](#)
American Journal of Respiratory and Critical Care Medicine, aamag473,
<https://doi.org/10.1093/ajrccm/aamag473>
Published: 22 September 2026 **Article history** ▾

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Abstract
Rationale
The efficacy of biologics remains debatable in current or ex- smokers with severe asthma.
Objectives
This study aimed to evaluate responses to biologics by smoking exposure and to assess variations in management practice across Europe.
Methods
This was a retrospective real-world study of adults with severe asthma from 16 European countries assessed at baseline and after 1-year of biologic treatment. Data were collected within the ERS SHARP (Severe Heterogeneous Asthma Research-Patient Centred) registry, applying the OMOP Common Data Model.



OHDSI Shoutouts!



Congratulations to the team of **Jaleh Shoshtarian Malak, Leonie von Berlin, Irina Balaur, Rada Hussein, Philip Gribbon, Yojana Gadiya, Somayeh Abedian, Andreas Kremer, Stefan Sauermann, Francisco J Núñez-Benjumea, Jens Declerck, Sumit Madan, Hanna Ćwiek-Kupczyńska, Lukas Rohatsch, Holger Fröhlich, Christian Muehlendyck, and Venkata P Satagopam** on the recent publication of **Bridging Gaps in Standards for the Secondary Use of Health Data: Exploratory Standard, Tool Assessment, and Feasibility Study** in *JMIR Formative Research*.

JMIR FORMATIVE RESEARCH

Shoshtarian Malak et al

Early Reports

Bridging Gaps in Standards for the Secondary Use of Health Data: Exploratory Standard, Tool Assessment, and Feasibility Study

Jaleh Shoshtarian Malak¹; Leonie von Berlin²; Irina Balaur¹; Rada Hussein³; Philip Gribbon²; Yojana Gadiya^{2,4}; Somayeh Abedian^{3,5}; Andreas Kremer⁶; Stefan Sauermann⁷; Francisco J Núñez-Benjumea⁸; Jens Declerck^{9,10}; Sumit Madan¹¹; Hanna Ćwiek-Kupczyńska¹; Lukas Rohatsch¹²; Holger Fröhlich^{4,11,13,14}; Christian Muehlendyck¹⁵; Venkata P. Satagopam¹

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OHDSI Shoutouts!



Congratulations to the team of **Jennifer N Hoppe, Jocelyn Lee, Tomi F Akinyemiju, Danielle S Bitterman, Michael Brudno, Michelle F Green, Vojtech Huser, Jafi A Lipson, Sanjay Mishra, Daniel P Nussbaum, Jai N Patel, Valentina I Petkov, Kelli M Rasmussen, Sahussapont Joseph Sirintrapun, Patricia A Spears, Sebastiaan Van Sandijk, Anne-Marie Meyer, Umit Topaloglu, and Jeremy L Warner** on the recent publication of **The GENIE Data Model: A Solid Tumor, Person-Centric Framework for Scalable, Harmonized Precision Oncology Data Collection** in *Cancer Research Communications*.



RESEARCH ARTICLE <https://doi.org/10.1158/2767-9764.CRC-26-0148>

OPEN ACCESS

The GENIE Data Model: A Solid Tumor, Person-Centric Framework for Scalable, Harmonized Precision Oncology Data Collection

Jennifer N. Hoppe¹, Jocelyn Lee², Tomi F. Akinyemiju^{3,4}, Danielle S. Bitterman⁵, Michael Brudno^{6,7}, Michelle F. Green⁸, Vojtech Huser⁹, Jafi A. Lipson¹⁰, Sanjay Mishra^{11,12}, Daniel P. Nussbaum¹³, Jai N. Patel^{14,15,16}, Valentina I. Petkov¹⁷, Kelli M. Rasmussen¹, Sahussapont Joseph Sirintrapun¹⁸, Patricia A. Spears^{19,20}, Sebastiaan Van Sandijk^{9,21}, Anne-Marie Meyer¹⁹, Umit Topaloglu²², and Jeremy L. Warner^{11,12}

ABSTRACT

Adequately powered analyses in precision oncology often require combining cohorts across institutions. However, integration is constrained by the least granular source and may become infeasible when data elements are too heterogeneous to harmonize and map to a common data model. This challenge is acute in multi-institutional precision oncology research, in which real-world evidence requires harmonized clinico-omic data integration. Existing models often lack sufficient treatment patterns, outcomes, and genomic data, limiting interoperability and scalability. To address these gaps, American Association for Cancer Research Project Genomics Evidence Neoplasia Information Exchange (GENIE) developed the GENIE Data Model (GDM), a comprehensive, open-source oncology data model for scalable, consistent, and interoperable data collection across solid tumors, designed to effectively capture the journey of patients with cancer. Through iterative consensus-building, four working groups comprising 13 subject matter experts defined data elements across multiple clinical domains: patient characteristics, imaging, diagnosis, surgery, histopathology, biomarkers, systemic therapy,

radiation, clinical trial history, disease response and outcomes, and social determinants of health. Elements were defined using standardized terminologies and permissible values to support mapping to Health Level 7 Fast Healthcare Interoperability Resources, Observational Medical Outcomes Partnership, and other existing oncology standards. The model architecture distinguishes manually abstracted elements from computationally collected elements, enabling parallel workflows. The GDM provides an extensible framework that addresses critical gaps and enables scalable, harmonized data collection essential for precision oncology and real-world evidence generation.

Significance: The GDM is an open-source, ready-to-implement, solid tumor framework that standardizes clinical and genomic data capture across institutions to effectively capture the journey of patients with cancer. It enables interoperable mapping to existing standards, accelerates multisite study start-up, and supports scalable real-world evidence generation in precision oncology.



OHDSI Shoutouts!



Congratulations to the team of **Melissa Y Wei, Ashley J Kang, Alexandra M Kломhaus, Lucia Y Chen, Douglas S Bell, David Elashoff, and Chi-Hong Tseng** on the recent publication of **Computable phenotypes for multimorbidity measurement: development and implementation of a new electronic health record-based multimorbidity-weighted index for harmonized Observational Medical Outcomes Partnership data** in *JAMIA*.

Journal of the American Medical Informatics Association, 2026, 1-9
<https://doi.org/10.1093/jamia/ocag161>
Research and Applications

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Computable phenotypes for multimorbidity measurement: development and implementation of a new electronic health record-based multimorbidity-weighted index for harmonized Observational Medical Outcomes Partnership data

Melissa Y. Wei, MD, MPH, MS^{1,2,*}, Ashley J. Kang, BS¹, Alexandra M. Kломhaus, PhD¹, Lucia Y. Chen, MS¹, Douglas S. Bell, MD, PhD¹, David Elashoff, PhD¹, Chi-Hong Tseng, PhD¹

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Abstract

Objective: To develop an electronic health record (EHR)-based multimorbidity-weighted index (eMWI) using computable phenotypes mapped to the Observational Medical Outcomes Partnership (OMOP) common data model and previously validated physical functioning-based condition weights.

Materials and Methods: We constructed eMWI from the previously validated MWI, which includes 76 chronic conditions weighted by their impact on physical functioning. For each condition, we identified validated EHR case algorithms through targeted literature search. For conditions without published algorithms, we performed chart review validation of ICD-based definitions in UCLA EHR. We translated all condition algorithms into OMOP computable phenotypes to enable use across harmonized EHR datasets. We applied eMWI to adults ≥ 18 years with ≥ 2 outpatient encounters between 2012 and 2024 in the University of California Health Data Warehouse (UCHDW), a harmonized dataset spanning 6 health systems.

Results: Validated algorithms were available for 53/76 conditions. Chart review validation supported ≥ 1 International Classification of Diseases, Ninth and Tenth Revisions (ICD-9 and ICD-10) code definitions for 22/23 remaining conditions. We translated 76 condition definitions into OMOP phenotypes and applied eMWI in UCHDW. Final sample included 4 672 662 adults with mean $\pm$ SD age 46.3 ± 16.8 years, eMWI 5.66 ± 7.85 (range 0-91), 55.7% female, and 45.5% non-Hispanic White. eMWI increased with age and social vulnerability and captured wide distributions across population subgroups.

Discussion and Conclusion: eMWI enables scalable implementation of multimorbidity measurement in large harmonized EHR datasets. Its weighting to physical functioning preserves a person-centered approach while adapting disease ascertainment to rich, clinical information in EHRs. eMWI establishes a foundation for rigorous comorbidity adjustment, risk stratification, and population health research across health systems and harmonized EHR datasets.



OHDSI Shoutouts!



Congratulations to the team of **Jungha Min, Sueun Shin, Sohyeon Park, Jeongha Yun, KayInn Park, and Sandy Jeong Rhie** on the recent publication of **Real-World Antidepressant Prescribing Patterns and Comparative Safety Outcomes of Commonly Prescribed Antidepressants in Patients with Depressive Disorder: A Multicenter OMOP-CDM Study in *Pharmaceuticals***.



pharmaceuticals



Article

Real-World Antidepressant Prescribing Patterns and Comparative Safety Outcomes of Commonly Prescribed Antidepressants in Patients with Depressive Disorder: A Multicenter OMOP-CDM Study

Jungha Min ^{1,†}, Sueun Shin ^{1,†}, Sohyeon Park ², Jeongha Yun ² , KayInn Park ² and Sandy Jeong Rhie ^{1,2,*}

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[†] These authors contributed equally to this work.

Abstract

Background/Objectives: Real-world antidepressant use for depressive disorder varies across clinical settings. This study aimed to characterize prescribing pathways and evaluate the comparative safety of frequently prescribed antidepressants in a large multicenter cohort with newly diagnosed depressive disorder. **Methods:** We conducted a retrospective multicenter observational study using electronic health record data standardized to the OMOP Common Data Model (1999–2026) in adults initiating antidepressants. Prescribing patterns among 13,381 patients were visualized using sunburst plots and Sankey diagrams. Comparative safety, escitalopram vs. sertraline and trazodone, was evaluated across 18 hospitals ($n = 44,542$) for nine clinical safety outcomes using propensity score-matched Cox proportional hazards models and empirically calibrated random-effects meta-analysis. **Results:** Selective serotonin reuptake inhibitors, particularly escitalopram (21.4%, $n = 2868$), were the preferred antidepressant. Common adjunctive medications included trazodone (14.6%, $n = 794$) and quetiapine (14.0%, $n = 761$), though utilization varied across hospitals. No clear differences were detected for most safety outcomes between cohorts. However, empirically calibrated QTc prolongation risk was significantly increased with sertraline relative to escitalopram (HR 1.75, 95% CI 1.10–2.78), a signal requiring further confirmation. **Conclusions:** This study demonstrates substantial institutional variation exists in real-world antidepressant treatment pathways and combination strategies. While comparative safety profiles were broadly comparable across evaluated outcomes, the isolated QTc prolongation signal for sertraline warrants targeted external confirmation. Furthermore, trazodone and escitalopram cohorts should not be regarded as clinically interchangeable first-line options, supporting individualized, evidence-based antidepressant selection in routine clinical practice.

Keywords: depressive disorder; antidepressants; prescribing patterns; real-world evidence; safety



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OHDSI Shoutouts!



Congratulations to the team of
**Seunggyeong Lee, Yeonju Woo,
and Soojin Lee** on the recent
publication of **Representing
Traditional East Asian Medicine
in International Health
Informatics Standards: A Scoping
Review** in *Healthcare*.



healthcare



Review

Representing Traditional East Asian Medicine in International Health Informatics Standards: A Scoping Review

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Abstract

Background/Objectives: Traditional East Asian medicine (TEAM), comprising traditional Korean medicine (TKM), traditional Chinese medicine (TCM), and Japanese Kampo, is increasingly recorded in electronic health records, and sharing these data depends on interoperability standards. Yet, TEAM concepts rest on conceptual foundations differing from those of biomedical standards. Prior reviews examined traditional medicine's own systems, not how TEAM concepts fit into mainstream biomedical standards. This review examined how TEAM concepts have been mapped or modeled into international health informatics standards. **Methods:** Following JBI methodology and PRISMA-ScR guidelines with a Population, Concept, and Context framework, we searched PubMed, Embase, Scopus, and IEEE Xplore for English reports from January 2016 to March 2026, with gray literature and citation searching. Screening was conducted by a single reviewer with senior verification and a 10% inter-rater reliability check. Findings were synthesized descriptively by functional category and clinical object type. **Results:** Of 16,763 records, 10 studies (2017 to 2026) were included; seven addressed TCM, three TKM, and none Kampo. Terminology work predominated, most often SNOMED CT, UMLS, and MeSH. The OMOP Common Data Model was the only data model, and no exchange standard such as HL7 FHIR appeared. Representability followed a gradient by clinical object type: acupuncture points anchored directly to terminologies, whereas only 1 of 260 ICD-11 Chapter 26 patterns had a SNOMED CT equivalent. Symptoms and disorders fit only partially, and compound herbal medicines required extension or decomposition. Most studies supplemented standards locally, and none of their additions were incorporated into a released standard. **Conclusions:** The work identified here has centered on establishing shared meaning rather than moving data between systems, and because supplementation stays external, the same gaps recur. Because the search covered only English-language, internationally indexed reports, these



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	7 am	Medical Imaging
Wednesday	10 am	Women of OHDSI
Wednesday	10 am	Common Data Model
Wednesday	11:30 am	Surgery and Perioperative Medicine
Wednesday	12 pm	Latin America Chapter
Thursday	10 am	ATLAS/WebAPI
Thursday	10 am	GIS-Geographic Information Systems
Thursday	11 am	Themis
Thursday	11 am	Industry
Thursday	12 pm	Methods Research
Thursday	1 pm	Oncology Vocabulary/Development Subgroup
Thursday	2 pm	Early-Stage Researchers
Thursday	2 pm	REVEAL
Thursday	7 pm	Dentistry
Friday	9 am	Waveform
Friday	9 am	Transplant
Friday	10 am	Respiratory Research
Friday	11:30 am	Steering
Monday	10 am	Health Systems Interest Group
Tuesday	9 am	Data2Evidence



Congratulations to our 2026 Titan Nominees!

ASSURE team, David Bard, Robert Barrett, Clair Blacketer, Rich Boyce, Danielle Boyce, Evanette Burrows, Cindy Cai, Carrot and Bunny Team, Cindy Chen, Pascal Coorevits, Data4Life, Scott Duvall, Noémie Elhadad, Lee Evans, Eye Care and Vision Research WG, FastOMOP, Mornin Feng, Davera Gabriel, Josh Gagne, Sarah Gasman, Lars Halvorsen, Peter Hoffmann, Christian Högberg, Michelle Hribar, Jason Hsu, Ben Illigens, Andy Kanter, Elisse Katzman, Masha Khitrin, Mack Kigada, Chungsoo Kim, Chris Knoll, Haeun (Hannah) Lee, Gaeun Lee, Renske Los, Benjamin Martin, Valentina Martufi, Mind Meets Machine, Evan Minty, Karthik Natarajan, Bill O'Brien, Sean O'Reilly, OHDSI UK organizers, Julio Oliveria, Anna Ostropolets, Woo Yeon (Jen) Park, Rowan Parry, Paul Petraro, Melanie Philofsky, Hanieh Razzaghi, Jenna Reys, Harry Reyes Nieva, Marti Sabate, Craig Sachson, Alexander Saelmans, Martijn Schuemie, Sarah Seager, Anthony Sena, Cynthia Sung, Jim Todd, Mui Van Zandt, Annelies Verbiest, Fleur Vereijken, Katia Verhamme, Ilse Vermeulen, David Vizcaya, Tom White, Qi Yang, Seng Chan You, Bingyu Zhang



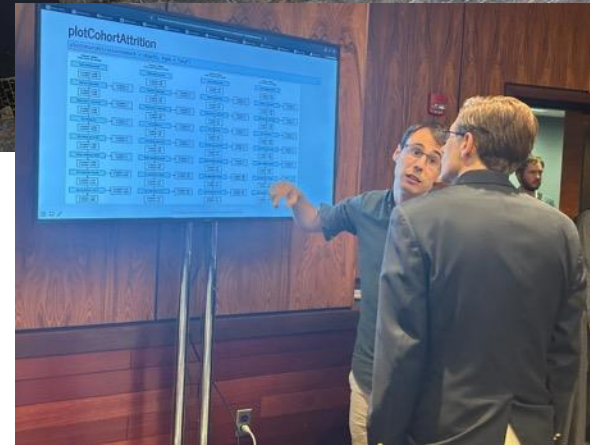
2026 OHDSI Global Symposium

Registration is OPEN for the **2026 OHDSI Global Symposium**, which will be held Oct. 20-22 in New Brunswick, N.J., USA.

Oct. 20: Tutorials

Oct. 21: Plenaries, Showcase

Oct. 22: Workgroup Activities



ohdsi.org/OHDSI2026



2026 Symposium Tutorials – Session 1

- **An Introduction to the Journey from Data to Evidence Using OHDSI**
- **An Introduction to ATLAS**
- **Bringing FAIR to Imaging Research with the Medical Imaging OMOP Extension**
- **Complex Phenotyping at Scale with and without LLMs Using PhenotypeR**
- **OHDSI Leadership Storytelling Workshop**
- **Mastering OMOP: Transforming EHR Data with Practical Strategies, Best Practices, and OHDSI Integration**



2026 Symposium Tutorials – Session 2

- **Building and Using the OHDSI Evidence Network: From Data Partner to Federated Study Execution**
- **From Multi-Modal Data to Real-World Evidence: Hands-on with the Data2Evidence Platform for OMOP Data Curation and Analytics**
- **Integrating Geospatial Data Into OMOP CDM**
- **Introduction to OHDSI Phenotype Development & Evaluation**
- **Using OMOP Model in Registry Context & Clinical Trials Standardization Context: Conventions, Past Use Cases, SDTM & Regulatory Consideration, Challenges**



2026 Global Symposium Agenda

Start	End	Topic	Presenter/Lead
7:15 am	8:00 am	Newcomer Welcome	Paul Nagy/Marc Suchard
8:00 am	8:30 am	State of the Community	George Hripcsak
8:30 am	9:15 am	OHDSI Year In Review	Early-Stage Researcher WG
9:15 am	10:00 am	Collaborator Showcase: Posters and Demos (Session 1)	
10:00 am	11:00 am	Plenary 1: Federated Learning Meets Negative Control Calibration: Toward Reliable Multi-Site Evidence Generation	Yong Chen
11:00 am	12:00 pm	Plenary 2: Beyond the Defaults: How the OHDSI Community is Adapting, Extending, and Reimagining Its Tools	Scott Duvall
12:00 pm	1:00 pm	Network & Lunch	
1:00 pm	2:00 pm	Plenary 3: The role of national initiatives in supporting sustainability, collaboration, and growth of OHDSI	Ed Burn
2:00 pm	2:45 pm	Collaborator Showcase: Lightning Talks (Session 1)	5 presenters
2:45 pm	3:30 pm	Collaborator Showcase: Posters and Demos (Session 2)	
3:30 pm	4:15 pm	Collaborator Showcase: Posters and Demos (Session 3)	
4:15 pm	5:00 pm	Collaborator Showcase: Lightning Talks (Session 2)	5 presenters
5:00 pm	6:00 pm	Titan Awards, Closing	Patrick Ryan
6:00 pm	8:30 pm	Dinner on your own	
8:30 pm	11:00 pm	OHDSI Jam Session	Martijn Schuemie



2026 Symposium Workgroup Activities

Session 1 (8 am – 10 am): Eyecare and Vision Research, GIS – Geographic Information Systems, Early-Stage Researchers, Industry, Tidy R Programming with OMOP, HADES Hackathon, Generative AI and Foundation Models, Phenotype Development and Evaluation, Oncology, Health Equity, Vocabularies, APAC

Session 2 (10:30 am – 12:30 pm): Perinatal and Reproductive Health, Waveform, Medical Imaging, Industry, Tidy R Programming with OMOP, HADES Hackathon, Generative AI and Foundation Models, Phenotype Development and Evaluation, Oncology, Health Equity, Vocabularies, Rare Disease

Session 3 (1:30 pm – 3:30 pm): Dentistry, GIS & Waveform Cross-Pollination Meeting, Evidence Network, Women of OHDSI, Psychiatry, HADES Hackathon, Natural Language Processing, Health Economics & Value Assessment, ATLAS/WebAPI, CDM Survey, Surgery & Perioperative Medicine

Session 4 (3:30 pm – 5 pm): Workgroup Summary Session



APAC Symposium: Nov. 13-15

The 2026 APAC Symposium will be held Nov. 13-15 at Yonsei University in Seoul, South Korea.

Nov. 13: Main Conference

Nov. 14: Tutorials, Datathon

Nov. 15: Datathon Team Activities

Registration is open! All details can be found on the event homepage.



ohdsi.org/APAC2026



Canada Symposium: Nov. 17-18

Registration is now open for the 2026 OHDSI Canada Symposium, held Nov. 17-18 in Toronto, Ont.

Nov. 17: Workshops

Track A: From Source Data to OMOP

Track B: From OMOP to Evidence

Nov. 18: Symposium

The main symposium day will bring the Canadian OHDSI community together to share experiences, showcase emerging work, and explore opportunities for collaboration.



JOIN US IN TORONTO THIS NOVEMBER

2026 OHDSI Canada Symposium

DATE
Nov 17–18, 2026

LOCATION
Toronto, ON

Join the OHDSI Canada community in Toronto for two days of hands-on workshops, engaging talks, strategic discussions, and networking.

Workshop Day

Practical sessions on vocabulary mapping, ETL, and using OMOP and OHDSI to answer real-world research questions.

Symposium Day

Presentations, strategic discussions, and opportunities to connect with colleagues from across the OHDSI Canada community.

India Symposium: Dec. 11



OHDSI INDIA SYMPOSIUM 2026

11 DECEMBER 2026

CHENNAI

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WHY TO ATTEND?

- **UNDERSTAND INDIA'S HEALTHCARE DATA LANDSCAPE**
Learn about the current state of healthcare data in India, emerging national priorities, and how global standards are shaping the future of healthcare and research.
- **EXPLORE OMOP AND HEALTHCARE DATA INITIATIVES**
Discover the latest developments in OMOP, Real-World Evidence (RWE), FHIR, AI, and other data standardization initiatives being implemented across India.
- **LEARN HOW YOUR ORGANIZATION CAN PARTICIPATE**
Understand how hospitals, medical colleges, and healthcare organizations can contribute to national data initiatives, multicenter research, training programs, and collaborative projects through OHDSI India.
- **LEARN FROM EXPERTS**
Gain insights from national and international experts on healthcare data standards, OMOP, FHIR, Real-World Evidence, AI, and observational research.
- **NETWORK WITH THE HEALTHCARE COMMUNITY**
Connect with clinicians, researchers, hospitals, academia, industry partners, and global OHDSI leaders to build meaningful collaborations
- **SHOWCASE YOURWORK**
SHOWCASE YOURWORK Present your research through posters, lightning talks, or case studies and receive valuable feedback from the community
- **BUILD FUTURE COLLABORATIONS**
Identify opportunities to participate in multicenter research, training programs, industry collaborations, and Real-World Evidence projects.



Job Openings at Illinois-Chicago



Director of Informatics and Data Science Operations and Development

Chicago, IL, United States | 1042586

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Posted on: 9/22/2026 - Application Deadline: 10/15/2026

The Director of Informatics and Data Science Operations and Development provides strategic leadership and operational management for the Informatics and Data Science Program within the Center for Clinical and Translational Science (CCTS). Funded through the Clinical and Translational Science Awards Program (CTSA), the Program advances the national mission of accelerating the translation of scientific discoveries into improved health outcomes. This is achieved through the development of robust informatics infrastructure, the promotion of interdisciplinary team science, the enablement of high-quality and interoperable data integration, and the support of innovative, rigorous, and reproducible clinical and translational research.

This position bridges advanced technical expertise with real-world health implementation by identifying translational bottlenecks, developing novel methodological and analytic approaches, and advancing informatics initiatives aligned with institutional strategy and national CTSA priorities. In collaboration with Data Science/Informatics Director(s) this role contributes to shaping the scientific direction and growth of informatics-driven research initiatives across the CCTS and the UIC health sciences colleges, strengthening the University's impact within the national translational science ecosystem. The role manages multidisciplinary teams responsible for the design, development, implementation, and oversight of innovative informatics and data science solutions that advance clinical and translational research across the full research continuum.

This is an academic professional, non-faculty position responsible for advancing the institution's clinical and translational research informatics capabilities through strategic management, operational oversight, and collaboration with faculty and institutional leaders.

Responsibilities:

Operational Leadership and Team Management

Provide strategic leadership and day-to-day management for the CCTS Informatics/Data Science team. Supervise, mentor, and develop informatics specialists and staff, including performance management, coaching, and professional development planning. Foster a collaborative, accountable, and high-performing team culture. Establish and enforce team norms, standard operating procedures, and quality standards in alignment with Center policies, Campus guidelines, and state/federal regulations. Oversee resource allocation and project prioritization to ensure timely and high-quality delivery of services. Assign personnel to projects; guide development of project plans and timelines; monitor progress and ensure achievement of strategic objectives. Track and report scientific and operational progress, resource utilization, performance metrics, and quality indicators. Identify operational or scientific barriers and implement solutions to ensure successful project outcomes.

Scientific and Technical Leadership

Advise Center leadership on innovative informatics strategies that align with local and national research priorities and sponsor requirements. Lead needs assessments with investigators to identify opportunities for clinical information systems and data services. Monitor emerging trends in biomedical informatics, clinical data science, AI, and translational research. Oversee the design, development, and implementation of clinical informatics solutions that support research, quality improvement, and health intervention initiatives. Ensure scientific rigor, regulatory compliance, and reproducibility across projects.

Strategic Partnerships and Collaboration

Lead collaborative informatics and data science initiatives with internal and external stakeholders to achieve objectives outlined in the CCTS grant. Partner with the Center and Program leadership to represent CCTS in national networks and collaboratives, including the Clinical and Translational Science Awards Program Consortium. Strengthen institutional partnerships with UI Health IT, UIC's Advanced Cyberinfrastructure for Education and Research (ACER), and the AI Health4All Center. Serve as liaison between campus units and CCTS leadership to ensure alignment of informatics and data science strategies with institutional priorities. Identify, evaluate, and recommend collaborative opportunities through engagement with CTSA hubs, Enterprise Committees, Working Groups, and professional associations. Develop coalitions that expand institutional capabilities and enhance national visibility.



Postdoctoral Research Associate (Hribar Lab) - Ophthalmology & Visual Sciences

Chicago, IL, United States | 1042846

[Apply Now](#)[Share](#)[Save Job](#)

Posted on: 9/15/2026 - Application Deadline: 10/30/2026

Position Summary

The Postdoctoral Research Associate will work on the standardization and integration of electronic health record (EHR) and imaging data in ophthalmology. The focus will be on standardizing to the OMOP common data model to support federated learning and data networks. The position will have the opportunity to work collaboratively with data and AI models at UIC as well as other sites in the OHDSI Eye Care and Vision Research workgroup. In addition, the Postdoc will be using the AI-READI dataset as a test set for the models and federated network.

Duties & Responsibilities

- Perform other related duties and participate in special projects as assigned.

Minimum Qualifications

- PhD, MD, or equivalent terminal degree required
- Informatics, data science, or computer science training and/or experience

The University of Illinois System is an equal opportunity, affirmative action employer dedicated to building a community of excellence, equity, and diversity. We are committed to fostering an inclusive environment and we welcome applications from qualified individuals of all backgrounds and identities. The University of Illinois System does not discriminate against any applicant or employee based on their real or perceived race, color, religion, sex, national origin, ancestry, age, order of protection status, genetic information, marital status, disability, sexual orientation including gender identity, unfavorable discharge from the military or status as a protected veteran and will comply with all federal and state nondiscrimination, equal opportunity and affirmative action laws, orders and regulations. Visit [University of Illinois Non-Discrimination Statement](#)

The University of Illinois System conducts background checks on all job candidates upon acceptance of a contingent offer of employment. Convictions are not a bar to employment. Background checks will be performed in compliance with state and federal law.

The University of Illinois System requires candidates selected for hire to disclose any documented finding of sexual misconduct or sexual harassment and to authorize inquiries to current and former employers regarding findings of sexual misconduct or sexual harassment. For more information, visit [Policy on Consideration of Sexual Misconduct in Prior Employment](#).

As a qualifying federal contractor, the University of Illinois System uses E-Verify to verify employment eligibility.

Artificial Intelligence (AI) tools may be used in some portions of the candidate review process for this position; however, all employment decisions will be made by a person.

The university provides accommodations to applicants and employees. [Request an Accommodation](#)

Preferred Qualifications



#OHDSISocialShowcase This Week

Monday

PandemicPrediction: three-year temporal validation of Seek- COVER models during the COVID-19 pandemic

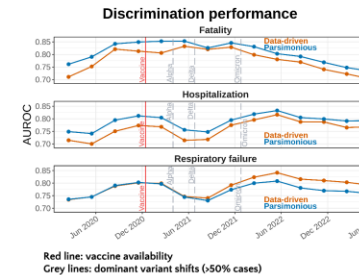
(Egill Fridgeirsson, Ross Williams,
Jenna Reps)

Influenza-proxy Seek-COVER models remained
useful through three years of COVID-19.

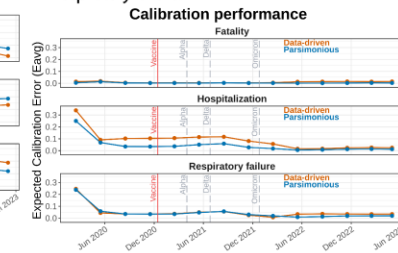
*PandemicPrediction: three-year temporal validation of Seek-COVER
models during the COVID-19 pandemic*

Background: Seek-COVER used influenza as a proxy when SARS-CoV-2 data were scarce. We examined whether those fixed parsimonious and data-driven models still performed adequately as COVID-19 care, vaccination, and dominant variants changed from January 2020 to June 2023.

Discrimination peaked around Alpha/Delta and
declined by early 2023 across outcomes.



Calibration was stable for fatality, but early
2020 error was large for hospitalization and
respiratory failure.



Influenza-proxy models transported surprisingly well despite
major distribution shifts during the pandemic.

Study Design

1. Fixed Seek-COVER models
Parsimonious and data-driven
Seek-COVER models for fatality,
hospitalization, and respiratory
failure.
2. Quarterly COVID-19 cohorts
Optum Clinformatics patients with
COVID-19, split into 14 non-
overlapping 3-month cohorts from
Jan 2020 to Jun 2023.
3. Validation outputs
Apply models without retraining.
AUROC measures discrimination;
Eavg measures calibration in the
figures above.

Limitation: This is a single-database temporal validation in Optum Clinformatics. Future work should compare influenza-proxy models with SARS-CoV-2-trained models and determine when enough COVID-19 data existed to retrain.



Egill A. Fridgeirsson¹, Ross D. Williams¹, Jenna Reps^{1,2}
¹: Medical Informatics, Erasmus University Medical Center; ²: JNJ, Raritan, New Jersey





#OHDSISocialShowcase This Week

Tuesday

Comparing Human and AI-Derived DRG Severity of Illness Using OMOP CDM: A Belgian APR-DRG Case Study

(**Peter Heirman**, Philippe Kolh, Ittoo Ashwin)

AI vs Human Coding in DRG Severity: A Real-World OMOP CDM Study (Belgium)

AI-assisted coding identifies clinically valid missed diagnoses, increasing DRG severity and hospital capacity by +15% — but requires human validation to avoid errors.

PROBLEM & METHODS

Why this matters

DRG & SOI drive hospital financing in Belgium

Manual coding is:
Time-consuming
Variable
Incomplete

AI can detect diagnoses from clinical text

But impact on DRG/SOI is unclear

Study Design

18,515 hospitalizations (2025, CHU Liège)

Compared:
Human-coded ICD-10
AI-coded (Solventum 360)

Derived:
APR-DRG
Severity of Illness (SOI)

Validation

Selected 2,563 cases where:

AI → higher SOI

Reviewed by:

25 professional coders

Checked:

Real diagnosis vs hallucination

OMOP Innovation

Stored different DRG/SOI in:
OMOP OBSERVATION table
Linked to hospital stay

Enables:

Multi-source comparison
Full provenance tracking

Future:
- AI benchmarking
- Multi-center OMOP studies
- ICD-11/ SNOMED integration

RESULTS & IMPACT

Key Findings

→ identical DRG (AI vs human)
10,312 / 18,515

→ In higher AI-SOI cases:
→ many AI diagnoses were clinically valid

Impact

→ **+15% increase in effective justified capacity**

Equivalent to: **+7.67 hospital beds**
Mean LOS: 5.79 days

Driven by:

Additional **secondary diagnoses**
Improved SOI classification

Interpretation

✗ AI alone → not reliable
✓ Human alone → incomplete

→ **Best approach: Hybrid Human + AI**

Takeaways

AI improves **coding completeness**
Human ensures **clinical validity**

OMOP enables:

Transparent comparison
Scalable evaluation



Peter Heirman, Philippe Kolh, Ashwin Ittoo. (CHU Liège · Uliège)



#OHDSISocialShowcase This Week

Wednesday

A SNOMED CT Template-Based Interoperability Framework for Multi-Standard Outputs

(**T. Helleputte**, M. Borshchivska, G. Vanhalst, R. Verschuren, T. Klein, O. Latignies, F. Daue, A. Vandenberghe)

SNOMED CT Template-Based Interoperability for Multi-Standard Outputs

A semantic-first framework bridging unstructured clinical data and interoperable health data standards

Background: Traditional medical data integration relies on one-to-one mappings between source data and target models such as OMOP CDM or FHIR, often leading to loss of clinical context and limited reusability. We propose a novel interoperability framework using SNOMED CT templates as a central, model-agnostic semantic layer to preserve clinical meaning and enable multi-standard outputs.

Method

Clinical information is extracted from unstructured medical texts using a Large Language Model (Mistral Small 3), deployed on-premise to ensure data privacy. The model produces structured outputs (JSON schema) capturing entities, attributes, and relationships.

Results

The framework enables the generation of standardized, context-preserving clinical representations from free-text data. Compared to traditional mapping approaches, it significantly reduces information loss and improves data completeness.



Extracted data are transformed into SNOMED CT expressions using domain-specific templates (allergies, vaccination, oncology). An automated SNOMED-ization process assigns concepts with confidence scores, supported by expert-annotated training data and validation thresholds.

Validated SNOMED expressions are then converted into multiple standardized formats, including OMOP CDM tables and FHIR resources. This pipeline is fully modular, allowing independent improvement of extraction, semantic modeling, and transformation components. In addition, the use of structured templates ensures consistency across heterogeneous data sources while maintaining fine-grained clinical detail.

The approach successfully captures complex clinical constructs across domains, including allergy reactions and causative agents, vaccination status and events, and oncological topography and morphology. The SNOMED-based layer allows seamless and reusable transformation into both OMOP CDM and FHIR outputs.

Preliminary evaluations show improved semantic fidelity and reduced need for manual post-processing compared to conventional pipelines.

The unified representation also facilitates extension to new domains without requiring redesign of downstream mappings.

Conclusion: This work introduces a scalable interoperability paradigm that decouples clinical meaning from technical representations. By leveraging SNOMED CT templates and LLM-based extraction, the framework preserves semantic richness while enabling flexible, multi-standard data integration. This approach supports both clinical research and secondary use of healthcare data and can be extended to additional domains and standards.



T. Helleputte, M. Borshchivska, T. Klein, G. Vanhalst, R. Verschuren, M. Bastin, O. Latignies, F. Daue, A. Vandenberghe



#OHDSISocialShowcase This Week

Thursday

MedValence: A Distributed Methodological Framework for Developing and Validating Personalized Prediction Models of Drug Efficacy and Safety Using Real-World Data

(**Nguyen Phung-Anh**, Phan Thanh-Phuc, Christianus Heru Setiawan, Septi Melisa, Nguyen Thi Kim Hien, Balqis Istiqomah Gusbela, Muhammad Solihuddin Muhtar, Jason C. Hsu)

MedValence: A Distributed Methodological Framework for Developing and Validating Personalized Prediction Models of Drug Efficacy and Safety Using Real-World Data

Background:

- With the rapid growth in availability and scale of real-world data (RWD), clinical decision support is increasingly shifting from population-average analyses toward individualized, patient-centered predictive applications.
- However, most existing multi-institutional or multinational observational studies continue to focus on population-level associations or average treatment effect estimates, providing limited support for individualized prediction of drug efficacy and safety in real-world clinical settings.
- Clinicians and policy makers require predictive models that can generate patient-level outcome estimates while demonstrating robustness, reproducibility, and transportability across heterogeneous healthcare systems.

Figure 1. MedValence Distributed Workflow for Personalized Prediction Model Development and Validation

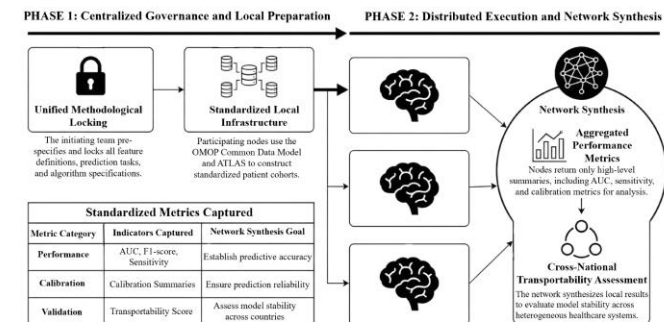


Table 1. Cross-National, Multi-Center Performance and Transportability of Drug-Specific Prediction Models

Category	Endpoint	Data node (country / center)	Sample size (N)	AUC	Sensitivity	Specificity	F1-score	Calibration	Transportability
Efficacy	Endpoint A	Site A (Country 1)	...	...	...	...	...	...	...
		Site B (Country 2)	...	...	...	...	...	...	...
		Site C (Country 3)	...	...	...	...	...	...	...
	Network summary	...	...	Median (range) ...	...	...	...	Overall stable	High
Safety	Endpoint B	Site A (Country 1)	...	...	...	...	...	...	...
		Site B (Country 2)	...	...	...	...	...	...	...
		Site C (Country 3)	...	...	...	...	...	...	...
	Network summary	...	...	Median (range) ...	...	...	...	Overall stable	High



Nguyen Phung-Anh; Phan Thanh-Phuc; Christianus Heru Setiawan; Septi Melisa; Nguyen Thi Kim Hien; Balqis Istiqomah Gusbela; Muhammad Solihuddin Muhtar; Jason C. Hsu*





#OHDSISocialShowcase This Week

Friday

Scaling laws for autoregressive foundation models on observational health event streams

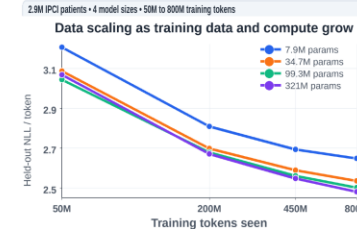
(Egill Fridgeirsson, Peter Rijnbeek)

More tokens reduce loss, but bigger models do not win at fixed compute.

Scaling laws for autoregressive foundation models on observational health event streams

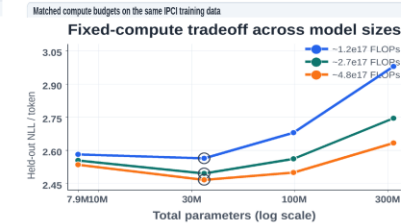
Background: We tested whether autoregressive foundation models trained on 2.9M IPCI patient timelines show predictable scaling under deterministic held-out evaluation.

Within the tested range, more training data continued to reduce held-out loss.



More training data kept improving loss, indicating pretraining had not yet saturated.

At fixed compute, balancing model size and token budget beat scaling parameters alone.

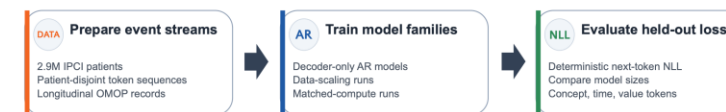


Balanced model size and token budget beat scaling parameters alone at fixed compute.

Value tokens remained hardest to predict



Scaling setup



Limitation: These results are based on deterministic held-out next-token loss in IPCI event streams. Future work should test whether the same scaling patterns hold across other datasets, architectures, and downstream tasks.



Egill A. Fridgeirsson¹, Peter Rijnbeek¹
¹Erasmus MC
²Medical Informatics, Erasmus University Medical Center





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?



Sept. 29: OHDSI/OMOP Research Spotlight



Irene López Sánchez

Predoctoral Researcher, IDIAP Jordi Gol

Temporal trends in epidemiology and patient characteristics of 36 cancers: a protocol for a multinational population-based cohort study using OMOP-standardised databases to investigate CANcer (OMOPCAN) (*BMJ Open*)



Fan Bu

Assistant Professor, Biostatistics, University of Michigan

Comparative Cardiovascular Effectiveness of Glucagon-Like Peptide 1 Receptor Agonists and Sodium-Glucose Cotransporter 2 Inhibitors in Diabetes Mellitus (*JACC*)



Adit Anand

PhD Student, Department of Biomedical Informatics, Columbia University

Completeness of Common Data Elements for Breast Cancer Clinical Trials in Observational Databases (*Proceedings — AMIA Joint Summits on Translational Science*)



Dave Kern

Senior Director, Epidemiology, Neuroscience, Johnson & Johnson Innovative Medicine

REWARD—an open-source framework for identifying the unknown benefits of existing medications to inform drug discovery, development, and repurposing (*JAMIA*)



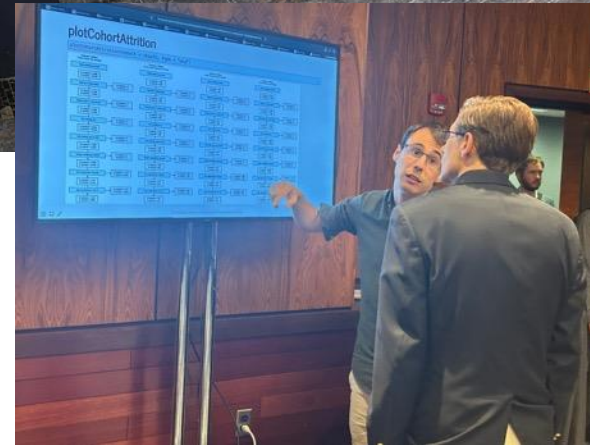
2026 OHDSI Global Symposium

Registration is OPEN for the **2026 OHDSI Global Symposium**, which will be held Oct. 20-22 in New Brunswick, N.J., USA.

Oct. 20: Tutorials

Oct. 21: Plenaries, Showcase

Oct. 22: Workgroup Activities



ohdsi.org/OHDSI2026

An Introduction to the Journey from Data to Evidence Using OHDSI



Meet the people behind this journey

Five perspectives. One OHDSI journey: from data to evidence.

Erica Voss

Johnson & Johnson



The transformer



Data standards & transformation

Ross Williams

Erasmus MC



The analyst



Network research & prediction

Katy Sadowski

Boehringer Ingelheim



The builder



Data quality & open-source tools

Mitchell Conover

Johnson & Johnson



The evidence maker



Clinical applications & causal inference

Ilse Vermeulen

Erasmus MC / OHDSI BE



The connector



Community & implementation



An Introduction To ATLAS

Preliminary Agenda

8:00am – 8:15am	Introduction • Who should be using Atlas	Chris
8:15am – 9:00am	The CDM & Data Sources • The CDM Data model • Database Characterization in Atlas	Chris
9:00am – 9:30am	Vocabulary, Concepts and Concept Sets • Vocabulary Overview (Domains, Codes) • Concepts: Standard vs. Non-Standard • Searching and Filtering • Record Counts (Record and Descendants) • Building Concept Sets	Jack
9:30am – 11am	Cohort Definitions • What is a Phenotype? • Cohort Definitions: Logic to build a Phenotype • Generation and Reports	Peter
11:00am – 11:45am	Analytics • Characterization • Incidence Rates • Pathways	Jack
11:45am – 12:00pm	Question & Answer	All



Bringing FAIR to Imaging Research with the Medical Imaging OMOP Extension

Participants will learn how to:

- Understand the design principles of the Medical Imaging OMOP extension (MI-CDM)
- Index and characterize DICOM archives from clinical or research repositories
- Standardize DICOM metadata using OMOP-compatible terminology
- Load imaging metadata into searchable OMOP tables
- Represent imaging-derived features while preserving provenance
- Perform multimodal analyses by combining imaging, clinical, and demographic data using standard OHDSI tools such as ATLAS
- Apply FAIR principles to imaging data within the OMOP ecosystem

Who should attend?

- OHDSI community members interested in medical imaging
- Researchers conducting observational or multimodal studies
- Data engineers and informaticians responsible for imaging ETL pipelines
- Institutions planning to integrate imaging into their OMOP CDM

By the end of the tutorial, attendees will be able to:

- Build an imaging-enhanced OMOP dataset from DICOM archives
- Integrate imaging features with clinical data for downstream analyses
- Apply reproducible, FAIR-aligned workflows for imaging research within OHDSI



OHDSI Change Leaders & Leadership

Amplifying our impact, through your ability to lead and create change.



TUTORIAL
Tuesday 20th (4h)



Interactive
Hands-on



Not recorded • Needs physical participation

Strengthen your ability to **drive change**, **engage stakeholders**, and **grow adoption** of OHDSI and OMOP in your environment.

You'll work on **YOUR priorities** and leave with practical tools, methods, insights, and a **concrete action plan** to can execute.



Who Should Attend

- National Node Leaders (Both current & Newly Becoming)
- Aspiring Change Leaders (Researchers, Data Scientists & Engineers)
- Anyone Supporting OHDSI Growth & Adoption (Industry, Innovators...etc)



Your Faculty

- Liesbet Peeters - NN Lead Belgium & Professor University of Hasselt
- Christian Hogberg - NN Lead Sweden & Change Leader Expert
- Chris Baldwin - Commercial Director Unison & Communication Expert



Become a stronger advocate, connector, facilitator & change leader.

What You'll Do — 4 Interactive Parts

Part I



Start with the End in Mind

Define your personal goal & pick your priority use case to work on.

Part II



Becoming a Change Leader

Apply change management & leadership best practices.

Part III



Building the Bridge from You to Them

Craft a narrative for your stakeholders that communicates value for them.

Part IV



Bringing It All Together

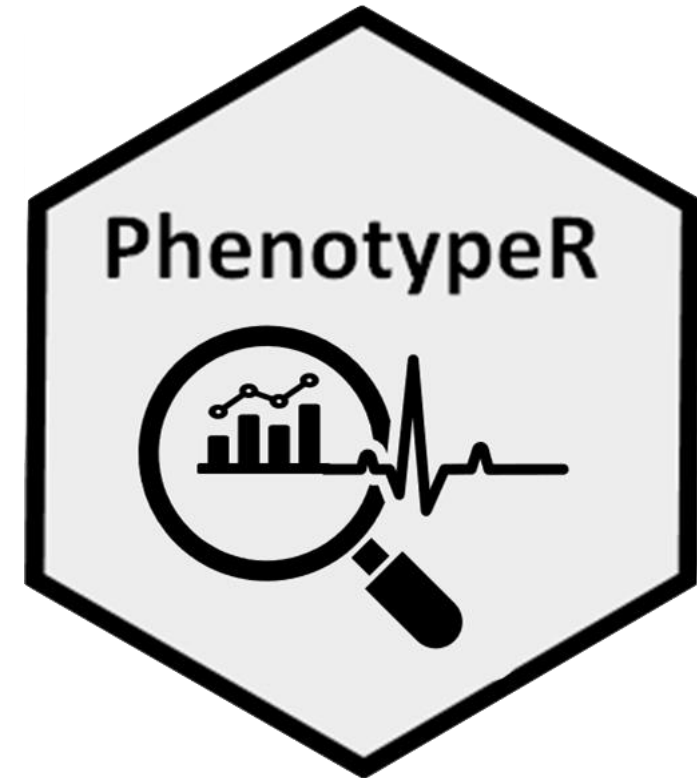
Refine your action plan & get peer + facilitator feedback.

GO!

Your stakeholders are ready & waiting — act now.

Complex Phenotyping at Scale with and without LLMs Using PhenotypeR

- Understand best practices for designing and evaluating clinical phenotypes
- Learn how to use the PhenotypeR R package to generate phenotype diagnostics
- Discover approaches to generating clinical expectations for diagnostics using human experts, LLMs, or both
- Gain experience in reviewing whether diagnostics match clinical expectations



<https://ohdsi.github.io/PhenotypeR>

Morning Session (8 am - 12 pm ET)

Mastering OMOP

Transforming EHR Data with Practical Strategies,
Best Practices, and OHDSI Integration

8am – 12pm on October 20th

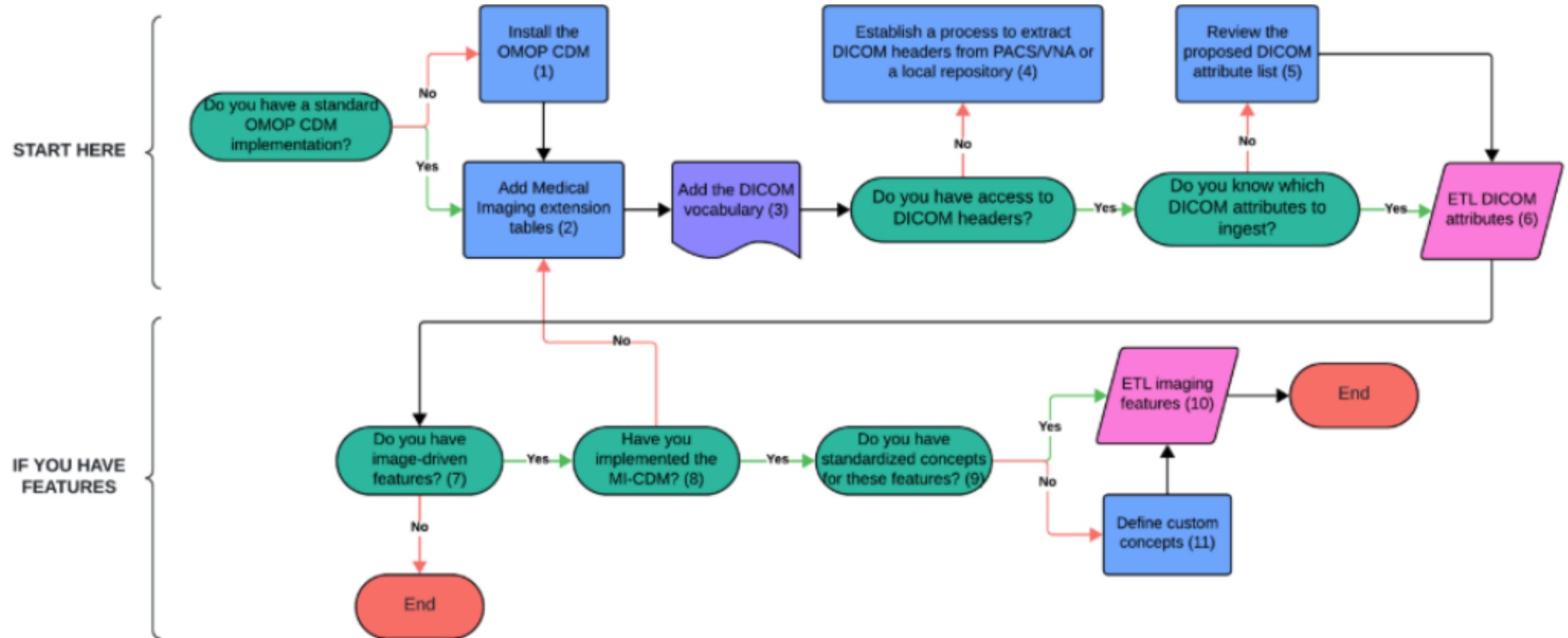


- Strategic Institutional Value (ROI & Impact)
- OMOP vs. EHR Fundamentals
- Theory to Practice
- Empowering Modern, Standardized Research



Imaging Evidence Network - getting started

- <https://github.com/OHDSI/ImageWG/wiki/>





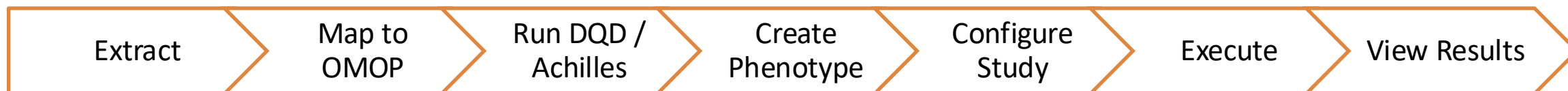
From Multi-Modal Data to Real-World Evidence: Hands-on with the Data2Evidence Platform for OMOP

The dataset

GUSTO - Growing Up in Singapore Towards healthy Outcomes - follows more than 1,100 children from birth since 2009, pairing clinical records, questionnaires and biosamples with longitudinal imaging.

What sets this session apart

Most sessions go deep on one stage of the journey. This one runs its full length: a single dataset travelling from raw files to a shareable evidence artifact in one sitting, with the developers in the room.



Notes: No prior OMOP CDM experience required · laptop and setup instructions provided in advance



Introduction to OHDSI

Phenotype Development & Evaluation

Accurate phenotyping is a cornerstone of reliable observational research, yet it remains one of the greatest methodological challenges in real-world data analytics. Observational data are inherently prone to misclassification and these errors can meaningfully influence study validity. This mid-level OHDSI tutorial is designed for participants who are familiar with OHDSI standardized vocabularies and already comfortable developing cohorts in ATLAS, and who now seek to deepen their scientific understanding and strengthen their applied phenotype development skills. The tutorial will begin with an overview of the science of misclassification error, covering key concepts such as sensitivity, specificity, predictive value, and index event misclassification. Participants will learn how these errors arise within observational data sources and how they directly affect effect estimation, transportability, and downstream decision-making. Building on this foundation, the session will transition to OHDSI's established best practices for phenotype development and evaluation. Using real examples, we will walk through tools and methods that support transparent, reproducible, and scalable phenotype definitions—including cohort diagnostics, standard vocabulary exploration, benchmarking against population characteristics. The latter portion of the tutorial introduces an emerging opportunity for improving phenotype development: an AI-aided iterative workflow. We will demonstrate how AI/LLM can support iterative refinement as part of phenotype development.

By the end of this tutorial, participants will have a richer understanding of the scientific foundations of phenotype misclassification, practical experience applying OHDSI best practices, and early exposure to how AI-enabled workflows can enhance rigor and reproducibility. This session is ideal for researchers ready to advance from simply using ATLAS to mastering phenotype design as a scientific discipline.



2026 OHDSI Global Symposium

Oct 20–22 • New Brunswick, NJ • Hyatt Regency Hotel

Integrating Geospatial Data into OMOP CDM: A Hands-On Tutorial with the OHDSI GIS and GAIA Toolchain

Join the GIS Workgroup Team on
October 20, 2026 | 1–5pm EST

Register now at ohdsi.org/ohdsi2026



Jared
Houghtaling
Johnson &
Johnson



Robert Miller
Miller Data
Solutions, LLC



Polina
Talapova
SciForce



Tim Norris
University
of Miami



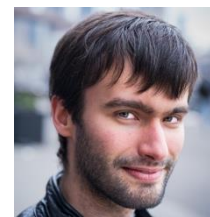
Jay
Greenfield
CODATA



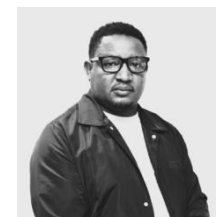
Jim Phuong
University
of Washington



Tim Rossi
Architectural
Medicine, LLC



Jacob Zelko
Northeastern
University



David Amadi
CODATA



Jiawen Liao
Cleveland
Clinic Research



Using OMOP Model in Registry Context & Clinical Trials Standardization Context: Conventions, Past Use Cases, SDTM & Regulatory Consideration, Challenges

Registry and clinical trial (CT) data often need to fill the gap not covered by traditional RWD. If RWD follows OMOP, using the same model for harmonization of registry and CT data has advantages.

Outline:

1. Special considerations found in registry and CT data (e.g., converting relative dates to OMOP compliant dates, CRF data, adverse drug event (seriousness, severity, and relatedness between drug and AE))
2. Use of 2B concepts (custom vocabularies) vs OMOP vocabularies
3. Use cases published in literature (e.g., UK Biobank, OHDSI 2024 poster: Application of OMOP Common Data Model to Disease Registry Data, AllOfUs)
4. Other use cases (AACR GENIE)
5. OMOP and SDTM comparison (+ FDA regulatory considerations)
6. Combining trial and RWD data (external control arm) considerations (data granularity mismatch, RWD limited to routine healthcare, lack of advanced COAs, data collection not regulatory grade)



2026 Global Symposium Agenda

Start	End	Topic	Presenter/Lead
7:15 am	8:00 am	Newcomer Welcome	Paul Nagy/Marc Suchard
8:00 am	8:30 am	State of the Community	George Hripcsak
8:30 am	9:15 am	OHDSI Year In Review	Early-Stage Researcher WG
9:15 am	10:00 am	Collaborator Showcase: Posters and Demos (Session 1)	
10:00 am	11:00 am	Plenary 1: Federated Learning Meets Negative Control Calibration: Toward Reliable Multi-Site Evidence Generation	Yong Chen
11:00 am	12:00 pm	Plenary 2: Beyond the Defaults: How the OHDSI Community is Adapting, Extending, and Reimagining Its Tools	Scott Duvall
12:00 pm	1:00 pm	Network & Lunch	
1:00 pm	2:00 pm	Plenary 3: The role of national initiatives in supporting sustainability, collaboration, and growth of OHDSI	Ed Burn
2:00 pm	2:45 pm	Collaborator Showcase: Lightning Talks (Session 1)	5 presenters
2:45 pm	3:30 pm	Collaborator Showcase: Posters and Demos (Session 2)	
3:30 pm	4:15 pm	Collaborator Showcase: Posters and Demos (Session 3)	
4:15 pm	5:00 pm	Collaborator Showcase: Lightning Talks (Session 2)	5 presenters
5:00 pm	6:00 pm	Titan Awards, Closing	Patrick Ryan
6:00 pm	8:30 pm	Dinner on your own	
8:30 pm	11:30 pm	OHDSI Jam Session	Martijn Schuemie



2026 Symposium Workgroup Activities

Session 1 (8 am – 10 am): Eyecare and Vision Research, GIS – Geographic Information Systems, Early-Stage Researchers, Industry, Tidy R Programming with OMOP, HADES Hackathon, Generative AI and Foundation Models, Phenotype Development and Evaluation, Oncology, Health Equity, Vocabularies, APAC

Session 2 (10:30 am – 12:30 pm): Perinatal and Reproductive Health, Waveform, Medical Imaging, Industry, Tidy R Programming with OMOP, HADES Hackathon, Generative AI and Foundation Models, Phenotype Development and Evaluation, Oncology, Health Equity, Vocabularies, Rare Disease

Session 3 (1:30 pm – 3:30 pm): Dentistry, GIS & Waveform Cross-Pollination Meeting, Evidence Network, Women of OHDSI, Psychiatry, HADES Hackathon, Natural Language Processing, Health Economics & Value Assessment, ATLAS/WebAPI, CDM Survey, Surgery & Perioperative Medicine

Session 4 (3:30 pm – 5 pm): Workgroup Summary Session



**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