



Workgroup Spotlight: Vocabulary and Evidence Network

OHDSI Community Call
May 26, 2026 • 11 am ET



Upcoming Community Calls

Date	Topic
May 26	Workgroup Spotlight: Vocabulary and Evidence Network
June 2	LLM Research Around The World, Session 1
June 9	LLM Research Around The World, Session 2
June 16	LLM Research Around The World, Session 3
June 23	CANCELLED: OHDSI Summer School at Columbia University
June 30	OMOP & OHDSI Research Spotlight



Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?



OHDSI Shoutouts!



Congratulations to the team of **Natthawut Adulyanukosol, Krittaphas Chaisutyakorn, Saknarong Sombutjaroan, Suchanan Kanjanapong and Prapat Suriyaphol** on the recent publication of **Efficient Drug Terminology Mapping with Bidirectional Late-Interaction Reranking and Deterministic Reordering in *Healthcare Informatics Research***.

Original Article

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Efficient Drug Terminology Mapping with Bidirectional Late-Interaction Reranking and Deterministic Reordering

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Objectives: Standardizing medication concepts across heterogeneous vocabularies is essential for interoperable analytics and observational research. In the Observational Medical Outcomes Partnership (OMOP) Common Data Model, local drug codes must be mapped to standardized RxNorm concepts, but automated mapping is challenging because drug strings encode clinically critical attributes, including strength, dosage form/route, release characteristics, and brand. **Methods:** We propose THIRAWAT (Terminology Harmonization using Late-Interaction Reranker With Alignment-tuned Transformers), a fine-tuned ColBERTv1 late-interaction reranker, and embed it within THIRAWAT Mapper, a retrieval-reranking pipeline with deterministic tie-breaking and stable ordering. Candidate generation used approximate nearest-neighbor retrieval with a bi-encoder (SapBERT-XLMR or BioLORD-2023). Candidates were reranked by THIRAWAT models that were fine-tuned using one-sided MaxSim and scored at inference using our adapted Bidirectional MaxSim (BiMaxSim) pooling. Finally, a deterministic tie-breaker extracted clinically salient cues, including strength, dosage form/route, release characteristics, and bracketed brand annotations, to resolve near-ties reproducibly. **Results:** We evaluated three mapping settings: Branded Drugs, Clinical Drugs, and Thai Medicines Terminology (TMT). Using SapBERT-XLMR retrieval with THIRAWAT-SapBERT reranking and deterministic tie-breaking, THIRAWAT Mapper achieved MRR@100 values of 0.954 (95% confidence interval [CI], 0.921–0.983), 0.898 (95% CI, 0.866–0.925), and 0.912 (95% CI, 0.891–0.931), outperforming a lexical term frequency-inverse document frequency baseline (0.491, 0.216, and 0.143, respectively). Hits@1 improved to 0.942 (95% CI, 0.899–0.978), 0.859 (95% CI, 0.817–0.898), and 0.868 (95% CI, 0.838–0.896), respectively. **Conclusions:** BiMaxSim and deterministic tie-breaking improved drug mapping to RxNorm while preserving an efficient runtime profile and stable ordering. Overall, THIRAWAT Mapper offers a pragmatic combination of learned semantic matching and deterministic lexical constraints. Models and code are available on Hugging Face (<https://huggingface.co/collections/sidataplus/thirawat>) and GitHub (<https://github.com/sidataplus/THIRAWAT-mapper>).



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Congratulations to the team of **Ricardo Lourenço Santos and Ricardo João Cruz-Correia** on the recent publication of **An HL7 FHIR® IG for lifestyle medicine in learning health systems: Multi-vendor wearable interoperability with documented terminology gaps in the *International Journal of Medical Informatics*.**

International Journal of Medical Informatics 217 (2026) 106465



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Original research article

An HL7 FHIR® IG for lifestyle medicine in learning health systems:
Multi-vendor wearable interoperability with documented terminology gaps

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HIGHLIGHTS

- IPS-compatible, EHDS-ready HL7 FHIR® IG for patient-generated wearable data.
- Multi-vendor semantic convergence buffer spanning 7 wearable vendors and 11 domains across lifestyle medicine and wearable biometrics.
- Documents critical wearable terminology gaps: RMSSD and pNN50 lack LOINC codes; all SNOMED CT HRV concepts are fetal/obstetric.
- 718 custom codes with 28 ConceptMaps providing declarative migration paths to LOINC, SNOMED CT, and OMOP via OCL governance.
- Iterative terminology audit: 1173 codes refined to 718, with 19 LOINC substitutions across recurrent audit cycles.

ARTICLE INFO

Keywords:
FHIR®
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Patient-generated health data
Lifestyle medicine
Heart rate variability
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LOINC
EHDS

ABSTRACT

Background: Consumer wearable devices collect clinically useful physiological data from patients, yet less than 5% of this patient-generated health data (PGHD) reaches clinical systems. The European Health Data Space (EHDS) Regulation 2025/327 mandates standardized health data exchange, creating an urgent need for validated transformation frameworks.

Objective: To develop and validate a FHIR® R4 Implementation Guide enabling multi-vendor wearable data transformation for lifestyle medicine, while documenting terminology gaps across seven vendor ecosystems.

Methods: We developed FHIR® profiles, extensions, and ConceptMaps using a multi-layer architecture covering eleven domains (six lifestyle medicine pillars and five wearable-specific domains). Technical validation included HL7 IG Publisher compilation, FHIR® Validator conformance testing, and systematic terminology verification.

Results: The IG comprises 74 profiles, 50 extensions, 14 CodeSystems, 174 ValueSets, and 28 ConceptMaps (546 artifacts). A two-phase terminology audit refined 1173 custom codes to 718 without standard direct equivalents, including genuine gaps (RMSSD, pNN50), wearable-specific metrics, and granularity not yet addressed by LOINC or SNOMED CT. Build validation produces 23 errors (all IPS upstream) and 73 warnings (97% non-actionable). Of six core HRV metrics, only SDNN has a LOINC code (80404-7). The multi-layer architecture achieved 75% weighted reuse across seven vendor ecosystems.

Conclusions: This work extends the HL7 Physical Activity IG's "Temporary Codes" pattern into a semantic convergence buffer—a vendor-neutral intermediary CodeSystem with outbound ConceptMap coverage to LOINC, SNOMED CT, and OMOP enabling multi-vendor semantic convergence. The 75% weighted reuse and iterative terminology audits progressively reduce custom codes as standards mature. All profiles are vendor-agnostic and EHDS-compliant.



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Congratulations to the team of **Elisabeth Ross, Olivier Bouissou, Åslaug Helland and Arild Faxvaag** on the recent publication of **From documentation to discovery: clinicians' perspectives on the generation, usability and standardization of real-world data** in the *International Journal of Medical Informatics*.

International Journal of Medical Informatics 217 (2026) 106501

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International Journal of Medical Informatics

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Original Research Article

From documentation to discovery: clinicians' perspectives on the generation, usability and standardization of real-world data

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ARTICLE INFO

Keywords:
Real-world data
Learning health systems
OMOP CDM
Data standardization
Oncology

ABSTRACT

Background: Real-world data (RWD) are increasingly recognized as essential for understanding patient populations underrepresented in clinical trials and for supporting data-driven learning in healthcare. For smaller subgroups, the value of RWD depends on standardization and interoperability that enable meaningful reuse across institutions. This study examines how clinicians perceive the reuse and standardization of RWD within a federated Learning Health System (LHS), with emphasis on data quality, clinical relevance, and implications for continuous learning.

Methods: A qualitative case study was conducted at Oslo University Hospital, informed by Learning Health System theory. Ten oncologists representing seven cancer subspecialties participated in focused, semi structured interviews. Data were analyzed using the stepwise deductive inductive (SDI) method to support empirically grounded conceptual development. The study was situated in the hospital's implementation of the OMOP Common Data Model (CDM) for oncology data.

Results: Clinicians highlighted the value of RWD for capturing patient groups often excluded from clinical trials. They described substantial variation in documentation practices, noting that clinically relevant information is frequently unstructured or inconsistently recorded. Time constraints and uncertainty about documentation requirements were identified as barriers to data quality. When reviewing data transformed into the OMOP CDM, participants generally found the mappings accurate but expressed concerns about loss of nuance and semantic drift. Across interviews, there was strong support for involving domain experts in validation and for using standardized data to enable collaboration and learning across institutions.

Conclusions: RWD can strengthen oncology practice by supporting insights into diverse patient populations and enabling continuous learning. Standardization through models such as OMOP CDM facilitates reuse and cross institutional collaboration, but success depends on structured documentation, semantic fidelity, clinician engagement, and robust technical infrastructure. These findings underscore the sociotechnical conditions required to realize the potential of RWD within emerging frameworks such as the European Health Data Space.



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Congratulations to the team of **Adnan Jouned, Laura Verbei, Florian Katsch, Marta Ferri Peradalta, Sofia Bazakou, Tanja Stamm, Georg Duftschmid and Renske Los** on the recent publication of **Integration of Patient-Reported Outcomes into the OMOP Common Data Model in Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care.**

Opening the Personal Gate between Technology and Health Care
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Integration of Patient-Reported Outcomes into the OMOP Common Data Model

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Abstract. An approach for integrating Patient-Reported Outcomes into the OMOP Common Data Model is presented. Feasibility is demonstrated, although coverage remains constrained by vocabulary gaps. Information loss can be minimized by the consideration of outcome origin, negation, and temporal annotation.

Keywords. Patient-Reported Outcomes, OMOP Common Data Model, CDM



OHDSI Shoutouts!



Congratulations to the team of **Somayeh Abedian** and **Rada Hussein** on the recent publication of **Proposed Schema Extensions and ETL Pathways for Integrating Wearable and Patient-Reported PGHD into OMOP-CDM for Secondary Use in Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care.**

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Proposed Schema Extensions and ETL Pathways for Integrating Wearable and Patient-Reported PGHD into OMOP-CDM for Secondary Use

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Abstract. The rapid expansion of wearable sensing technologies and patient-reported outcomes (PROs) has revealed a persistent gap between high-frequency, context-rich patient-generated health data (PGHD) and standardized data models used for secondary analysis. Although the OMOP Common Data Model (OMOP-CDM) supports large-scale observational research, it does not natively capture key PGHD characteristics such as device provenance, calibration parameters, temporal resolution, and contextual metadata. This paper introduces an extension layer for OMOP-CDM and a direct extract-transform-load (ETL) pathway that enhances its capacity to handle heterogeneous, time-series, and PRO data while maintaining semantic consistency. The approach preserves device traceability, enables flexible data compression, and links PRO instruments with OMOP constructs without altering the core schema, remaining fully compatible with OHDSI analytical tools and aligned with FAIR principles. The model has strong potential for community discussion and future OMOP updates on PGHD.

Keywords. Patient-Generated Health Data (PGHD), Wearables, Interoperability, OMOP Common Data Model, FAIR Principles



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Congratulations to the team of **Stefano Antola, Selene Gallone, Ylenia Murgia, Daniele Roberto Giacobbe, Matteo Bassetti and Mauro Giacomini** on the recent publication of **A Unified Database for a Set of Clinical Studies on the Treatment of Bacterial and Fungal Infections Within the MULTI-SITA Project** in *Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care*.

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A Unified Database for a Set of Clinical Studies on the Treatment of Bacterial and Fungal Infections Within the MULTI-SITA Project

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Abstract. The MULTI-SITA project, an observational pharmacological study involving 30 centers across Italy, required a flexible and scalable data management solution. This paper describes the transition from separate study-specific databases to a unified SQL Server-based system with a modular architecture and a web interface developed in Blazor Server. The new design enhances data interoperability, supports future studies, and simplifies clinician interaction, paving the way for future alignment with the OMOP Common Data Model.

Keywords. Data modelling, interoperability, antibiotics and antifungals use in hospitals



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Congratulations to the team of **Ali Raza,**
Christian Esposito and **Mauro Giacomini**
on the recent publication of **Large
Language Models for Automating
Conformance to Health-Data Standards:
The Interoperability Case of HL7 FHIR
and OMOP** in *Volume 336 of Studies in
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Large Language Models for Automating Conformance to Health-Data Standards: The Interoperability Case of HL7 FHIR and OMOP

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Abstract. Interoperability standards enable different healthcare systems to exchange electronic health information seamlessly, and support large-scale analytics needed for current Secondary uses of healthcare data. Transforming diverse clinical inputs into standards-compliant, analyzable data remains labor-intensive and error-prone. Moreover, the learning curve for their proper exploitation can be steep due to extensive documentation, specific technical requirements, and the need for both semantic and technical integration, making them not fully accessible to practitioners in the healthcare domain unless they undergo extensive training. Our study investigated whether large language models can automate conformance while preserving syntactic validity, semantic correctness, and reproducibility, thereby simplifying the adoption of these standards. Using diabetes measurements as a probe domain, we validated extraction fidelity, coding accuracy against controlled vocabularies, and conformance to the domain's main standards. Our prototype emits FHIR Observations and OMOP MEASUREMENT rows.

Keywords. HL7; OMOP; large language models; data standardization; LOINC; SNOMED CT; diabetes; OGTT.



OHDSI Shoutouts!



Congratulations to the team of **Karen Triep and Olga Endrich** on the recent publication of **Challenging Interoperability: Mapping and Validation of a Swiss Medication Catalogue to RxNorm in Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care.**

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Challenging Interoperability: Mapping and Validation of a Swiss Medication Catalogue to RxNorm

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Keywords. OMOP CDM, RxNorm, Health data interoperability, Semantic interoperability

1. Introduction

To participate in the European Health Data Space and initiatives such as DARWIN EU, Swiss hospitals need medication data that is mappable to internationally used vocabularies [1]. The OMOP Common Data Model (CDM) recommends RxNorm (and, for non-US content RxNorm Extension) as standard drug terminology because it provides cross-links to other terminologies and supports secondary use [2,3]. Using OHDSI's standard tools—Athena [4] for vocabulary distribution and Usagi [5] for semi-automated mapping—offers a community-aligned approach. However, RxNorm is US-centric and does not always reflect Swiss product structures (multi-ingredient products, package sizes, concentrations, brands), which makes validation essential [6,7,8].



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Congratulations to the team of **Sunah Yang, Kwangsoo Kim and Chang Wook Jeong** on the recent publication of **Development of an Airflow-Based Automated Pipeline for Constructing Common Data Model Integrating Structured and Unstructured Medical Data in Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care.**

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Development of an Airflow-Based Automated Pipeline for Constructing Common Data Model Integrating Structured and Unstructured Medical Data

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Abstract

The growing use of multimodal clinical data requires standardized and automated construction of Common Data Models (CDMs). This study presents an Apache Airflow-based automated pipeline for OMOP CDM v5.4 that integrates structured EMR data and unstructured sources. Applied to Seoul National University Hospital data (2004–2024), the pipeline generated 47 CDM tables from approximately 3.7 million patients and incorporated nearly 10 million unstructured data instances. The proposed workflow improves reproducibility and scalability of CDM construction and supports future multi-institutional deployment.

Keywords. OMOP Common Data Model, Airflow, ETL Pipeline



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Congratulations to the team of **Maria Parra Rodriguez-Armijo, Celia Alvarez-Romero, Jan van den Brand, Boris Delange and Carlos Luis Parra-Calderón** on the recent publication of **Design of a Privacy-Preserving ETL Dataflow for Federated ICU Data Reuse in INDICATE** in *Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care*.

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Design of a Privacy-Preserving ETL Dataflow for Federated ICU Data Reuse in INDICATE

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Abstract. The INDICATE project, funded by the European Union under the Digital Europe Programme, develops a federated framework for the secure reuse of intensive care unit (ICU) data within the EHDS. This work presents the design of a privacy-preserving ETL dataflow that standardizes and validates ICU data locally. The process enables harmonization of ICU data into the OMOP Common Data Model, based on HL7 FHIR as well, ensuring semantic interoperability, data quality, and regulatory compliance. Only aggregated study results are uploaded to the INDICATE Portal, ensuring that no patient-level data leave the hospital domain.

Keywords. ETL dataflow, ICU data, federated analytics, OMOP CDM, EHDS.



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Congratulations to the team of **Philip Stampfer, Hendrik Lef, Sai Pavan Kumar Veeranki, Birgit Fürst, Antonia Schelnast, Martina Kroissenbrunner, Elisabeth Mayrhuber, Elske Ammenwerth, Katharina Lichtenegger and Franz Feichtner** on the recent publication of **Cross-Institutional Data Harmonization for AI in Nursing Care Using the OMOP CDM** in *Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care*.

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Cross-Institutional Data Harmonization for AI in Nursing Care Using the OMOP CDM

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Abstract. Artificial Intelligence (AI) offers potential to support and empower nurses, yet its development depends on the availability of high-quality, standardized data. Nursing data are often fragmented, unstructured, and semantically inconsistent, hindering their secondary use. This work aims to harmonize heterogeneous nursing data from hospitals and nursing homes to create an AI-ready data foundation. Following a generic harmonization process, example datasets from two institutions and software systems were extracted and mapped to the Observational Medical Outcomes Partnership Common Data Model (OMOP CDM). Using open-source tools, we performed dataset specification, vocabulary identification, coverage analysis, semantic and structural mapping, and initial ETL implementation. A core dataset was defined, covering key data elements such as demographics, vital signs, and medication. Initial test transfers demonstrated the feasibility of mapping and integrating nursing data, though complex nursing constructs such as care plans and assessments remain challenging. This study establishes a structured methodological approach for cross-institutional nursing data harmonization and lays the groundwork for the development of future AI applications in nursing.

Keywords. Nursing, Data Harmonization, Artificial Intelligence, Real World Data



OHDSI Shoutouts!



Congratulations to the team of **Iiris Karppila, Manu Setälä and Laura-Maria Peltonen** on the recent publication of **Interoperability Barriers in the European Health Data Space: A Scoping Review** in *Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care*.

Opening the Personal Gate between Technology and Health Care

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Interoperability Barriers in the European Health Data Space: A Scoping Review

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Abstract. The European Health Data Space (EHDS) is the EU's most ambitious attempt to standardize cross-border data sharing, yet implementation faces significant interoperability challenges. This scoping review synthesizes literature on EHDS readiness across EU Member States to identify key barriers to seamless data sharing. Using Arksey and O'Malley's five-stage framework, 11 sources addressing EHDS implementation, patient care pathway coordination, and interoperability requirements were analyzed. The findings reveal that while the EHDS addresses technical standardization through frameworks like the European Electronic Health Record exchange Format (EEHRxF), persistent disparities in national implementations create semantic, organizational, and social gaps. Member States show varying adoption of standards such as HL7 FHIR and OMOP, with few shared metadata catalogues. The study contributes a systematic categorization of EHDS interoperability barriers across technical, organizational, and legal dimensions, identifying which challenges the regulation directly addresses versus those requiring additional Member State coordination. These insights inform prioritization strategies for European health informatics standardization efforts.

Keywords. European Health Data Space, EHDS, interoperability, cross-border healthcare, health information systems, health data standardization, scoping review



OHDSI Shoutouts!



Congratulations to the team of **Omid Pournik, Saadullah Farooq Abbasi, Xuefei Ding, Nasim Mahmoodi, Rose Allington, Laura Maria Peltonen, Parisi Gallos, Leila Ghalichi and Theodoros N. Arvanitis** on the recent publication of **Large Language Models for Health Knowledge Modelling in Data Interoperability: A Scoping Review of Methods, Standards, and Applications in Volume 336 of Studies in Health Technology and Informatics: Opening the Personal Gate between Technology and Health Care.**

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1287

Large Language Models for Health Knowledge Modelling in Data Interoperability: A Scoping Review of Methods, Standards, and Applications

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Abstract. Achieving interoperability in healthcare requires semantic alignment of data with standards such as SNOMED CT, LOINC, and FHIR. Manual ontology mapping is slow and inconsistent. Evolving Large Language Models (LLMs) can automate knowledge modelling and data harmonisation. This review explores how LLMs are applied to enhance or automate health knowledge modelling for data interoperability. Following PRISMA-ScR guidance, PubMed and Compendex were searched. Studies applying LLMs to ontology alignment, terminology mapping, schema integration, or knowledge-graph construction were included. From 166 records, 20 studies met the inclusion criteria. Most used GPT-4 or BERT-derived models with retrieval-augmented or embedding-based methods. Reported gains included automation, improved mapping precision, and scalability across standards such as FHIR, OMOP, and UMLS. LLMs show strong potential for automating semantic interoperability in health informatics. Standardised evaluation benchmarks and explainable frameworks are essential for trustworthy adoption.

Keywords. Large Language Models, Data Interoperability, Knowledge Modelling, Ontology Alignment, FHIR, Healthcare



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	8 am	Psychiatry
Wednesday	10 am	Surgery and Perioperative Medicine
Wednesday	10 am	Women of OHDSI
Wednesday	10 am	Common Data Model
Wednesday	1 pm	Latin America Chapter
Wednesday	7 pm	Medical Imaging
Thursday	6:30 am	India Community Call
Thursday	9 am	Phenotype Development and Evaluation
Thursday	10 am	GIS – Geographic Information System
Thursday	10:30 am	Evidence Network
Thursday	11 am	Perinatal & Reproductive Health
Thursday	7 pm	Dentistry
Friday	9 am	Waveform
Friday	10 am	Transplant
Friday	11:30 am	Steering Group
Monday	10 am	Healthcare Systems Interest Group
Tuesday	9 am	Data2Evidence

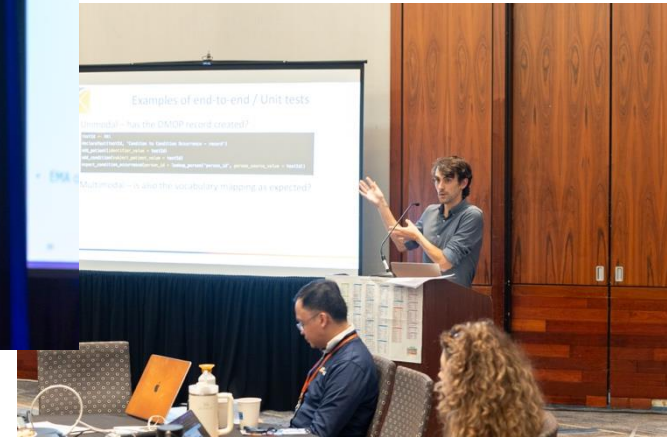


2026 OHDSI Global Symposium

The **call for participation** is open for the 2026 Global Symposium.

The submission deadline is June 5 at 8 pm ET.

10 Days Remaining!



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www.ohdsi.org

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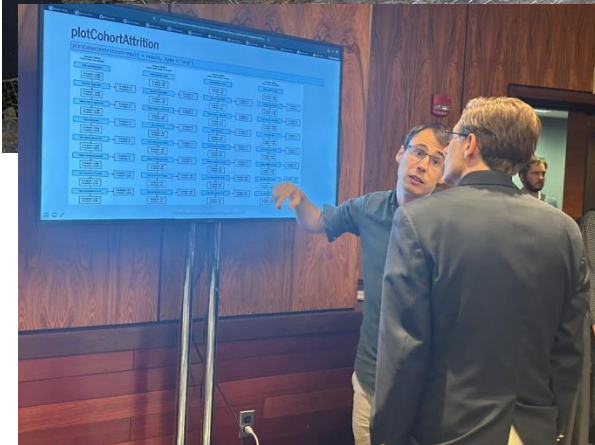
2026 OHDSI Global Symposium

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



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Opening: Data Science Engineer

Position Summary

The Department of Biomedical Informatics at Columbia University is seeking a highly motivated data science engineer to support large-scale observational research within the OHDSI (Observational Health Data Sciences and Informatics) network. This role will focus on the design, implementation, and execution of distributed network studies using electronic health record (EHR) and administrative claims data to generate real-world evidence.

The successful candidate will contribute to characterization, population-level estimation (causal inference), and patient-level prediction analyses across multi-institutional data networks. This position offers a unique opportunity to work at the intersection of biomedical informatics, data science, and clinical research within a leading academic medical center.

This position is a full-time two-year position with a possibility of an extension, contingent on available funding.

Responsibilities

Key Responsibilities

- Design and implement observational network studies using distributed EHR and administrative claims data
- Conduct large-scale characterization, comparative effectiveness and safety estimation, and patient-level prediction analyses
- Develop reproducible analytic pipelines using R and SQL in relational database environments
- Apply and evaluate methods from causal inference (e.g., confounding control, bias assessment, sensitivity analyses)
- Apply machine learning approaches for predictive modeling using high-dimensional healthcare data
- Work with standardized data representations, including the OMOP Common Data Model and standardized clinical vocabularies for conditions, drugs, procedures, and measurements
- Collaborate with interdisciplinary teams including clinicians, statisticians, data engineers, and informaticians
- Contribute to scholarly outputs including manuscripts, presentations, and open-source analytic tools
- Support transparent, reproducible, and scalable research practices across distributed data networks

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557250

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- Bargaining Unit:
- Regular/Temporary: Regular
- End Date if Temporary:
- Hours Per Week: 35
- Standard Work Schedule: Monday - Friday
- Building: PH-20
- Salary Range: \$160,000 - \$180,000

The salary of the finalist selected for this role will be set based on a variety of factors, including but not limited to departmental budgets, qualifications, experience, education, licenses, specialty, and training. The above hiring range represents the University's good faith and reasonable estimate of the range of possible compensation at the time of posting.



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2026 Maternal Health Fellowship

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- Create evidence from real-world data
- Leverage standard data models for reproducible research
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Practice



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- Master OHDSI tools
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#OHDSISocialShowcase This Week

Monday

Bridging Standards: Transforming Consolidated Clinical Document Architecture (C-CDA) Data via Health Information Networks to OMOP

(Xiaohan Tanner Zhang, Chris Roeder, Stephanie Hong, Thanaphop Na Nakhonphanom, Adam Lee, Richard Moffitt, Josh Lemieux, James Cavallon, Monique Bangudi, Lakshmi Anandan, Rob Schuff, Bill Hogan, Chris Chute, Emily Pfaff, Melissa Haendel)

PRESENTER: Tanner Zhang MD, MS

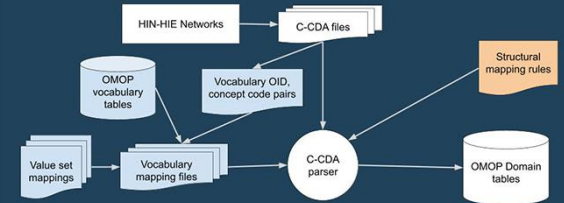
INTRODUCTION

- The Problem:** The All of Us (AoU) program collects patient data from many sources to populate an OMOP data warehouse for use by researchers. The Center for Linkage and Acquisition of Data (CLAD) program acquires additional data through many avenues including HIN-HIE networks where much of it requires parsing the HL7 C-CDA format. The format is complex, and the data are often inconsistent, presenting a challenge for harmonizing and mapping structure and vocabulary.
- The Goal:** Create an effective and transparent mechanism for transforming high-volumes of C-CDA data into the OMOP CDM to enable critical research (phenotyping, comparative studies, etc.)

METHODS

- Approach:** A rule-based, multi-stage ETL pipeline using Python and SQL, scaled using PySpark.
- Core Components:**
 - Vocabulary Mapping:** Standardizes terminologies using custom maps, OID translation, and advanced code/format normalization.
 - Structural Mapping:** rule driven process uses XPath to parse C-CDA structure with transparent mapping.
- Key Graphics:**
 - The ETL Flowchart visually illustrates this two-part method.
 - An abbreviated set of mapping rules for the observation table shows the source for observation_id, person_id and observation_concept_id in the C-CDA document drawing from an observation element within a results section.
- Vocabulary Nuance:** A custom C-CDA Value Set Mapping Table was created to accurately handle non-standard HL7-specific and EPIC internal vocabularies, increasing semantic precision.
- Advanced Data Cleaning:**
 - Code System Normalization:** Standardizes vocabulary names (e.g., "CPT" vs. "CPT4").
 - Pattern Recognition:** Uses regex to automatically correct misclassified codes (e.g., ICD-9 vs. ICD-10).
 - Format Normalization:** Standardizes various NDC and ICD code formats.
- Flexible Structural Rules:** Concise rules show mapping from C-CDA to OMOP. The rules use distinct field types for adaptability: FIELD (direct copy), DATE (parses dates), DERIVED (handles complex transformations), etc.
- Key Takeaway:** The successful pilot offers a flexible and viable mechanism to convert C-CDA to OMOP, providing a reusable framework for broader OHDSI initiatives.
- Source Code Availability** A PyPi package for structural mapping is in development.

Bridging Standards: Transforming Consolidated Clinical Document Architecture (C-CDA) Data via Health Information Networks to OMOP



Simplified C-CDA Document Results Section (input)

```
<section>
  <root>
    <templateId root="2.16.840.1.113883.10.20.22.2.3.1"/>
    <code code="30954-2" codeSystem="2.16.840.1.113883.6.1"/>
    <entry typeCode="DRIV">
      <organizer classCode="BATTERY" moodCode="EVN">
        <templateId root="2.16.840.1.113883.10.20.22.4.1"/>
        <id root="7d5a02b0-67a4-11db-bd13-0800200c9a66"/>
        <code xsi:type="CE" code="43789009"
              codeSystem="2.16.840.1.113883.6.9"/>
        <statusCode code="completed"/>
        <component>
          <observation classCode="OBS" moodCode="EVN">
            <templateId root="2.16.840.1.113883.10.20.22.4.2"/>
            <id root="01c2d0c0-67a5-11db-bd13-0800200c9a66"/>
            <code xsi:type="CE" code="30313-1"
                  codeSystem="2.16.840.1.113883.6.1"/> <code3
            <statusCode code="completed"/>
            <effectiveTime value="20120810"/>
            <value xsi:type="PQ" value="10.2" unit="g/dl"/>
          </observation>
        </component>
      </organizer>
    </entry>
  </root>
</section>
```

Simplified OMOP Measurement table (output)

measurement_id	person_id	measurement_concept_id	value_as_number
(hash of) 107c2d0c-67a5-11db-bd13-0800200c9a66	(not shown)	3002173	10.2

Structural Mapping rules for Measurement table

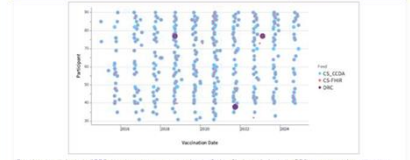
```
Measurement: {
  'root': {
    'conf': 'ROOT',
    'expected_domain_id': 'Measurement',
    'element':
      ("ClinicalDocument/component"
       "structuredBody/component/section"
       "entry/organizer/component/observation")
  },
  'measurement_id_root': {
    'conf': 'FIELD',
    'attribute': 'root',
    'measurement_id_extension': {
      'conf': 'FIELD',
      'element': 'id',
      'attribute': 'extension',
      'measurement_id': {
        'conf': 'FIELD',
        'hash': {
          'measurement_id_root', 'measurement_id_extension',
          'order': 1},
        'person_id': {
          'conf': 'FK',
          'FK': 'person_id',
          'order': 2},
        'measurement_concept_code': {
          'conf': 'FIELD',
          'attribute': 'code',
          'measurement_concept_code_system': {
            'conf': 'FIELD',
            'attribute': 'codeSystem',
            'measurement_code': {
              'conf': 'FIELD',
              'attribute': 'codeSystem',
              'measurement_concept_id': {
                'conf': 'DERIVED',
                'FUNCTION': 'VT_codemap_xwalk_concept_id',
                'argument_names': [
                  'concept_code', 'measurement_concept_code',
                  'vocabulary_oid', 'measurement_concept_codeSystem'
                ],
                'order': 3},
                'value_as_number': {
                  'conf': 'FIELD',
                  'data_type': 'FLOAT',
                  'element': 'value',
                  'attribute': 'value',
                  'order': 9
                }
              }
            }
          }
        }
      }
    }
  }
}
```

RESULTS

Data Source	OMOP Table	Total Records	Mapping Rate	Notes
Site B	Drug Exposure	52,823	100%	Complete mapping achieved.
Site B	Measurement	5,329,582	100%	Complete mapping achieved.
Site B	Condition	235,216	100%	Complete mapping achieved.
Site B	Procedure	193,634	100%	Complete mapping achieved.
Site B	Visit Occurrence	903,854	98.20%	High mapping success. Unmapped due to non-standard 6.80% encodings.
Site B	Observation	529,567		

Data Source	OMOP Table	Total Records	Mapping Rate	Notes
Site A	Drug Exposure	2,020,862	100%	Complete mapping achieved.
Site A	Measurement	842,392	100%	Complete mapping achieved.
Site A	Condition	49,610	100%	Complete mapping achieved.
Site A	Procedure	383,513	99.96%	Complete mapping achieved.
Site A	Observation	163,124		99.96% Minor unmapped due to data quality.
Site A	Visit Occurrence	708,297	0.01%	Significant mapping limitation identified.

Cedars Sinai FHIR vs Cedars Sinai C-CDA vs DRC: Influenza vaccine records for 60 random patients



Based on the relative lack of DRC data shown here, we assume that the Cedars Sinai submission to the DRC may not contain vaccine data. Cedars Sinai C-CDA and FHIR feeds clearly and significantly overlap in terms of records received by the already held by the OHDSI C-CDA and FHIR mostly overlap here, with a few exceptions (e.g., patient 70), whose vaccines only appear in the C-CDA feed.

LIMITATIONS

- Mapping non-standard vocabularies can require extensive manual effort.
- Identifiers within the documents can have varying quality. On-going work addresses these issues with data providers, and investigates ways to mitigate them.
- On-going work retrieves and counts concepts and values directly and simply from the C-CDA documents for comparison in data quality efforts that validate the resulting OMOP tables contain what the documents do.

Xiaohan Tanner Zhang MD, MS, Chris Roeder MS, Stephanie Hong MS, FAMILA, Thanaphop Na Nakhonphanom MS, MMedSc, MD, Adam Lee PhD, Richard Moffitt PhD, Josh Lemieux BA, James Cavallon BS, Monique Bangudi MPH, Lakshmi Anandan MPH, Rob Schuff MS, Bill Hogan MD, MS, Chris Chute MD, DrPH, Emily Pfaff MS, PhD, Melissa Haendel PhD



Please contact Melissa Haendel, PhD for future collaboration work. This work was funded by NIH AoU CLAD program.



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#OHDSISocialShowcase This Week

Tuesday

Leveraging Epic's Native ETL Infrastructure for OMOP CDM Implementation: A Collaborative Experience

(**Lauren N. Cooper**, Aamirah Vadsariya, Mereeja Varghese, Bhavini Nayee, Jessica Moon, Chaitanya Katterapalli, Clark Walker, Chris Gonzalez, Sonam Sohal, Christoph U. Lehmann, Ferdinand Velasco, Mujeeb Basit, DuWayne Willett)

Title: Leveraging Epic's native ETL infrastructure for OMOP CDM implementation: a collaborative experience
Subtitle: Building a Reproducible OMOP Pipeline Across Health Systems

PRESENTER: **Clark Walker, MPH**

INTRO: Electronic health records hold valuable information but sharing and analyzing that data across organizations is difficult and often resource-intensive. We describe how UT Southwestern and Texas Health Resources used Epic's built-in extract-transform-load (ETL) tools to convert their records into the OMOP Common Data Model, enabling secure collaboration through the OHDSI network. This approach improved data quality and performance while cutting development, operational, and maintenance costs.

METHODS



Figure 1. Epic Caboodle ETL data flow for both (A) Texas Health Resources (THR) and (B) the University of Texas Southwestern Medical Center. A Pre-OMOP Caboodle ETL data flow is shown on the left of Figure 1B.

RESULTS

Person Count (n)	
Texas Health Resources (THR)	7,361,120
University of Texas Southwestern Medical Center (UTSW)	5,617,846
Drug Exposure Count (n)	
Texas Health Resources (THR)	164,888,002
University of Texas Southwestern Medical Center (UTSW)	128,141,943

How we used Epic's built-in data pipeline to create an OMOP database together

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OmopConditionOccurrenceFactX

Duration	
Texas Health Resources (THR)	3h 1m
University of Texas Southwestern Medical Center (UTSW)	3h 7m
Rows extraction (n)	
Texas Health Resources (THR)	246,266,249
University of Texas Southwestern Medical Center (UTSW)	269,116,345
Records created (n)	
Texas Health Resources (THR)	766,066
University of Texas Southwestern Medical Center (UTSW)	20,699
Records modified (n)	
Texas Health Resources (THR)	206,356
University of Texas Southwestern Medical Center (UTSW)	10,449

Table 2. Performance metrics for the ETL of OMOP CDM table, OmopConditionOccurrenceFactX for both Texas Health Resources executed on March 16, 2025, and the University of Texas Southwestern Medical Center, executed on March 24, 2025.

Texas Health Resources	Validations			Total		
	Pass	Fail	Total %	Pass	Fail	Total %
Plausibility	237	5	242	98	0	98
Completeness	265	14	279	98	2	100
Consistency	247	11	258	95	5	100
Total	1349	36	1385	97	3	99

University of Texas Southwestern Medical Center	Validations			Total		
	Pass	Fail	Total %	Pass	Fail	Total %
Plausibility	176	0	176	100	0	100
Completeness	204	11	215	94	6	100
Consistency	214	12	226	94	6	100
Total	1134	13	1147	99	1	100

Aamirah Vadsariya, RN MSN, Mereeja Varghese, MS Bhavini Nayee, BS, Jessica Moon, BS, Chaitanya Katterapalli, MS, Clark Walker, MPH, Chris Gonzalez, LPN, Sonam Sohal, MHS MBA, Christoph U. Lehmann, MD, Ferdinand Velasco, MD, Mujeeb Basit, MD, DuWayne Willett, MD





#OHDSISocialShowcase This Week

Wednesday

Onto-OMOP: An Automatic Pipeline for Generating Classification Level Terms and Relationships for OHDSI Vaccine Concepts Using the Vaccine Ontology

(Jie Zheng, Alexander Davydov, Anna Ostropolets, Qi Yang, Yongqun He)



Onto-OMOP - An Automatic Pipeline for Generating Classification Level Terms and Relationships for OHDSI Vaccine Concepts Using the Vaccine Ontology

Jie Zheng, PhD¹, Alexander Davydov, MD², Anna Ostropolets, PhD³, Qi Yang, MD, PhD⁴, Yongqun He, PhD⁵

¹University of Michigan Medical School, Ann Arbor, MI, USA; ²Thesaurus Health, New York, NY, USA; ³Odyssey Data Services, Inc., Cambridge, MA, USA; ⁴QVIA, Inc., Durham, NC, USA.

Background

The OHDSI OMOP CDM¹ is a widely recognized open-science community data model, standardizing data from diverse clinical domains and sources to support robust and reliable analysis. This is achieved through the OHDSI Standardized Vocabularies—a globally harmonized set of medical vocabularies, coding systems, and ontologies. The vocabulary system is a cornerstone of OHDSI and required for all data sources in the network.

As an Open Biomedical Ontologies (OBO) Foundry² library ontology, the Vaccine Ontology (VO)³ represents various types of licensed vaccines, research and clinical trial vaccines, vaccine components, and vaccine responses. VO has incorporated vaccine-related concepts from RxNorm and RxNorm Extension^{4,5}, the two OMOP Standardized Vocabularies. Additionally, VO includes many intermediate classification terms and relationships not present in the OHDSI Standardized Vocabularies, which support better classification of vaccine concepts.

In this study, we introduce the Onto-OMOP pipeline, which automatically retrieves classification terms and relationships from an ontology, demonstrated here in the vaccine domain using the VO. The extracted concepts and relationships are intended for submission to the OHDSI Standardized Vocabularies to better support vaccine classification and analysis.

Methods

Figure 1 illustrates the Onto-OMOP pipeline applied to the VO.

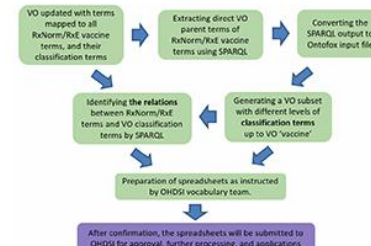
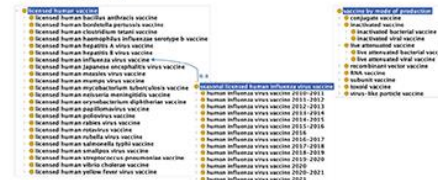


Figure 1. Illustration of automatic Onto-OMOP pipeline with the vaccine use case.

Contact: iezhen@umich.edu, yongqunh@med.umich.edu

Results

The Onto-OMOP pipeline automatically retrieved 666 VO terms used to classify RxNorm and RxNorm Extension vaccine concepts. Figure 2 highlights the main vaccine classification terms, including categories based on targeted pathogen, influenza vaccination season, and vaccine platform.



(A) vaccine against pathogen (B) influenza vaccine by flu season (C) vaccine by platform
Figure 2. VO vaccines used for grouping RxNorm and RxNorm Extension concepts (A) vaccines grouping by vaccine against pathogen; (B) influenza vaccines grouping by the flu season they are used for; (C) vaccines grouping by the methods they are produced.

The retrieved VO OMOP subset is available at: https://github.com/vaccineontology/VO/blob/master/OMOP_classification/OMOP_classification.owl.

Figure 3 illustrates examples of submissions using the OHDSI vocabulary submission template, which can be automatically populated using the Onto-OMOP pipeline. These submissions will include VO classification terms, along with their relationships to RxNorm and RxNorm Extension concepts.

(A) Concept

concept_name	concept_code	vocabulary_id	domain_id	concept_class_id
concept code from your source vocabulary	your source	short name (e.g. your vocabulary)	domain of your source concept; has to be an existing OHDSI domain	has to be an existing OHDSI concept class
max 255 characters	max 50 characters	max 20 characters	max 20 characters	max 20 characters

(B) Concept relationship

concept_code_1	vocabulary_id_1	relationship_id	concept_code_2	vocabulary_id_2	concept_code_3	vocabulary_id_3
codes from your source vocabulary	your source	short name (e.g. your vocabulary)	vocabulary you map to (SSE)	concept code in the OHDSI Standardized Vocabulary	concept code in the OHDSI Standardized Vocabulary you map to	OHDSI Vocabulary you map to
max 50 characters	max 20 characters	max 50 characters	max 50 characters	max 20 characters	max 20 characters	max 20 characters

Figure 3. OHDSI vocabulary submission (A) Concept (B) Concept relationships.

Conclusions

1. The Onto-OMOP pipeline automatically extracts intermediate classification terms and their relationships from the VO to categorize RxNorm and RxNorm Extension vaccine concepts.
2. These intermediate VO terms provide classifications not present in OHDSI Vocabularies, such as vaccine platforms, targeted pathogens, and seasonal flu vaccines.
3. The inclusion of intermediate vaccine classifications and their relationships improves the exploration and analysis of vaccine information.
 - The VO systematically classified various COVID-19 vaccines, which improved the identification of COVID-19 vaccine cases from the national COVID cohort collaborative (N3C) EHR resource.⁶
 - This makes the VO OMOP subset a valuable addition to OHDSI Vocabularies.

Future works

- Incorporate VO classification terms and relationships into the OHDSI Standardized Vocabularies and the OHDSI ATLAS system.
- Enable concept queries that utilize VO classification terms in OHDSI ATLAS.

Acknowledgement

This project is supported by a NIH-NIAID U24 grant (U24AI171008). We also appreciate the guidance, discussion, and support from the OHDSI Vocabulary working group.

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#OHDSISocialShowcase This Week

Thursday

Assessing Temporal Data Quality of Rheumatoid and Psoriatic Arthritis Patients in the All of Us Research Program

(Matthew Spotnitz, John Giannini, Emily Clark, Yechiam Ostchega, Tamara R Litwin, Lewis Berman)



Assessing Temporal Data Quality of Rheumatoid and Psoriatic Arthritis Patients in the All of Us Research Program

Matthew Spotnitz, MD, MPH¹, John Giannini, PhD¹, Emily Clark, MPH², Yechiam Ostchega, PhD, RN (retired)¹, Tamara R Litwin, PhD, MPH¹, Lewis Berman, PhD, MS (retired)¹

¹All of Us Research Program, Office of the Director, National Institutes of Health, ²GAP Solutions, Inc.



Key Points

- Data quality assessments are essential for rigorous and reproducible observational healthcare research.
- However, many of those assessments lack an evaluation of temporality, which is a measure of whether the data elements follow an expected temporal order.
- In this analysis, we present a novel temporality assessment for rheumatoid and psoriatic arthritis cohorts.

Background

- Rheumatoid and Psoriatic Arthritis (RA and PsA) are autoimmune diseases that have overlapping clinical symptoms and can cause debilitating joint pain [1,2].
- Previously, we used a data quality framework, to evaluate cohorts of All of Us participants who had a ductal carcinoma in situ (DCIS) diagnosis, a mastectomy procedure, and multiple surgical oncology procedures [3 - 5].
- In this analysis we assessed the data quality of participant diagnoses for RA and PsA with the portion of the framework that focused on temporality.

Methods

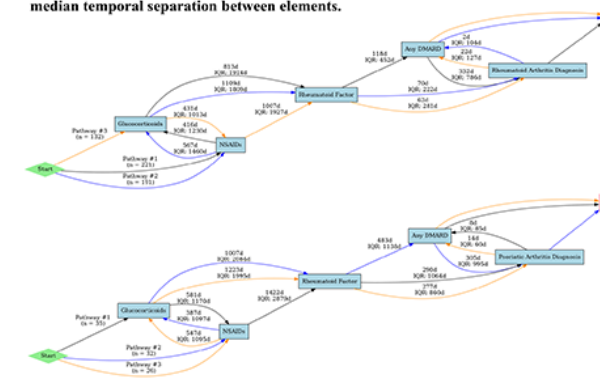
- Phenotype definition: The first occurrence of an ICD-9 or SNOMED CT diagnosis code for RA or PsA in adult All of Us Research Program participants.
- Temporality was measured by calculating the median intervals in days between the following five clinical concept sets: 1) Nonsteroidal anti-inflammatory drugs (NSAIDs), 2) glucocorticoids, 3) rheumatoid factor, 4) any disease-modifying antirheumatic drug (DMARD), and 5) diagnosis. The interval and count calculations are shown in the table.
- We plotted the temporal order of those concept sets for the subset of participants who had data on all of them. The plots were generated using the Python graphviz library. No automated tools were used. The three most common pathways are shown in the figure.

Results

Table: Counts and median intervals in days for Rheumatoid Arthritis and Psoriatic Arthritis cohorts in different temporal analyses.

Analysis	Rheumatoid Arthritis No. (%)	Median (IQR) (In Days)	Psoriatic Arthritis No. (%)	Median (IQR) (In Days)
RF to Diagnosis	4638 (43.1)	19.4 (779.8)	585 (31.9)	62.3 (929.6)
Diagnosis to csDMARD	4856 (45.2)	0 (535.5)	705 (38.4)	0 (557.9)
Diagnosis to NSAID	8714 (81.1)	-279.3 (2094.4)	1394 (76.0)	-588 (-2417.1)
Diagnosis to Glucocorticoids	9123 (84.9)	-117.6 (1852.2)	1491 (81.3)	-560 (-2198)
RF to csDMARD	2780 (25.9)	46.9 (593.6)	314 (17.1)	126 (827.4)
RF to Biologic DMARD	1415 (13.2)	461.3 (1682.1)	296 (16.1)	304.5 (1260.7)
RF to NSAID	4042 (37.6)	-492.4 (2112.6)	497 (27.1)	-685.3 (2517.9)
RF to Glucocorticoids	4126 (38.4)	-212.5 (1871.8)	509 (27.8)	-851.9 (2377.9)

Figure: Timeline analysis in days of subsets of Rheumatoid (top) and Psoriatic (bottom) Arthritis cohorts with representative concept sets. For subset cohorts where participants have all relevant concept sets, these timelines show the most common orderings and median temporal separation between elements.



Abbreviations: Rheumatoid factor = RF; conventional synthetic disease-modifying antirheumatic drug = csDMARD; disease-modifying antirheumatic drug = DMARD; nonsteroidal anti-inflammatory drug = NSAID; interquartile range = IQR; count = n; days = d. Data source = The All of Us Research Program.

Discussion

- We have shown successful implementation of our data quality dimensions analysis to evaluate temporality of RA and PsA cohorts.
- For the subgroup of participants in the cohorts with all five clinical concept sets, the general chronological progression was from symptomatic management to laboratory tests to DMARD therapy or diagnosis.
- The lag between symptomatic treatment and diagnosis ranged from 4 to 5 years in the RA subgroups and was 6 years in the PsA subgroups.
- Our methods can be used to compare the temporality of cohorts from different data sources, including gold standard data sources.
- Our analysis was limited by the amount of data available and manual concept selection. Also, it is unclear if alternative phenotype definitions would have yielded different results.

Conclusions

We have shown successful implementation of our data quality dimensions analysis to evaluate temporality of RA and PsA cohorts. Our findings may have implications for whether RA and PsA diagnosis codes are fit for use as temporal anchors.

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#OHDSISocialShowcase This Week

Friday

Characterizing Acute STEMI Patients Across Multi-Country Real-World Data Sources: A Comparative Analysis

(Milou Brand, Atif Adam, Linying Zhang, Ruochong Fan, Jin Choi, Seng Chan You, Sumin Lee, Ana Danilovic Bastic, Filip Maljkovi, Mirza Khan)

Characterizing Acute STEMI Patients Across Multi-Country Real-World Data Sources: A Comparative Analysis

Milou Brand¹, Atif Adam¹, Linying Zhang², Ruochong Fan³, Jin Choi³, Seng Chan You⁴, Sumin Lee⁴, Ana Danilovic Bastic⁵, Filip Maljkovi⁶, Mirza Khan⁷
 IQVIA, Washington University School of Medicine, Ajuo University Medical Center, Yonsei University College of Medicine, University Clinical Hospital Center Zvezdara, University of Missouri-Kansas City, Saint Luke's Mid America Heart Institute



BACKGROUND AND OBJECTIVES

Cardiovascular diseases accounted for 17.9 million deaths globally in 2019, with the vast majority (85%) attributed to acute myocardial infarction. ST-elevation myocardial infarction (STEMI), a severe AMI subtype, results from acute coronary artery blockage, often due to plaque rupture and thrombosis^{1,2,3}. The 4th Universal Definition of Myocardial Infarction defines STEMI by elevated cardiac troponin and clinical evidence of ischemia. Presentations can vary significantly, from classic chest pain to dyspnea, nausea, or weakness⁴.

Despite global STEMI registries, real-world characterization remains fragmented due to heterogeneous definitions, resource-intensive abstraction, and inability to compare across healthcare systems.

This study aims to accurately identify and characterize STEMI cases using multi-country real-world data, enabling a comprehensive and comparative assessment of STEMI patient characteristics and management.

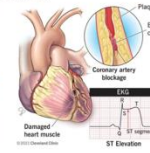


Table 1. Characteristics of STEMI patients

	WashU	Hospital CDM	Open Claims	PMTX w/ AmbEMR	CHCZ	AUSOM	YUHS
N	485	15,870	273,622	63,555	231	348	621
Medication at index date							
Aspirin	92.4%	85.3%	10.3%	7.8%	99.6%	98.3%	96.8%
PAI	92.4%	90.4%	10.3%	4.9%	24.2%	99.1%	99.2%
Statins	59.0%	56.0%	14.2%	8.7%	<5%	49.7%	60.2%
Beta blockers	88.0%	73.3%	28.8%	16.2%	36.4%	95.7%	97.6%
ACEI	80.4%	74.7%	37.2%	23.7%	56.3%	69.3%	59.6%
ARB	47.2%	30.0%	30.1%	18.8%	24.7%	65.9%	38.6%
MRA	2.5%	1.1%	1.3%	0.6%	10.4%	1.7%	3.4%
Comorbidities within 1y prior to index							
Type 2 diabetes	29.1%	17.6%	31.1%	28.1%	10.4%	19.8%	13.0%
Hypertlipidemia	70.3%	25.3%	53.2%	72.9%	20.3%	3.7%	16.6%
Obesity	25.1%	7.3%	10.5%	23.0%	<2%	<2%	<1%
Symptoms at index event							
Chest pain	71.1%	5.4%	59.4%	48.1%	10%	33.6%	13%
Angina pectoris	9.3%	1.0%	10.5%	15.0%	5.6%	30.8%	9.5%
Dyspnea	16.1%	1.5%	10.8%	8.6%	<2%	<2%	1%
Nausea and vomiting	6.4%	1.2%	4.0%	2.0%	<2%	0%	<1%

CONCLUSIONS

- This study underscores the substantial influence that database type has on the characterization of STEMI patients, with 10-fold variations in medication documentation and 6-fold variations in diagnostic testing between data sources.
- The observed variability in the recording of diagnostic procedures, treatments, symptoms, and comorbidities highlight that simple database classifications fail to predict complexity.
- Different data sources answer different questions: hospital EMRs capture acute care, claims reflect longitudinal adherence, and hybrid sources provide complementary perspectives—none is universally "accurate."
- These findings emphasize the importance of selecting appropriate data sources when conducting research on acute cardiovascular conditions.

References
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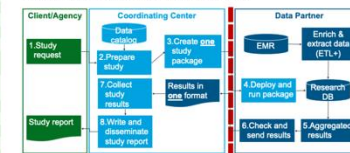
METHODOLOGY

A retrospective cohort study was conducted using real-world data from over 1.2 billion patients. Inclusion criteria were a STEMI diagnosis, age ≥18 years, receipt of an electrocardiogram within days 0-3, inpatient visit on day 0, and catheterization on day 0 of the clinical encounter. The study period spanned from January 1, 2016, to most recent data available.



Seven observational databases, Washington University in St. Louis (WashU), IQVIA Hospital CDM, IQVIA Open Claims, IQVIA Pharmacy linked with Ambulatory EMR, Cleveland Hospital Center Zvezdara (CHCZ), Ajuo University School of Medicine (AUSOM), and Yonsei University Health Systems (YUHS), formatted in the Observational Medical Outcomes Partnership (OMOP) common data model—were analyzed using the OHDSI CohortDiagnoses module via the Strategus framework. Baseline characteristics were summarized per database.

Figure 1. Outline of a federated network study



RESULTS

Patient Demographics: Patient demographics were consistent across databases, with mean ages ranging from 58.8 to 65.2 years, predominantly male (61.5–78.8%).

Medication Documentation: Aspirin documentation varied dramatically: WashU (92.4%), Hospital CDM (85.3%), CHCZ (99.6%), AUSOM (98.3%), and YUHS (96.8%) showed high capture rates, while Open Claims (10.3%) and PMTX w/AmbEMR (7.8%) showed minimal documentation. Platelet aggregation inhibitor (PAI) patterns were similarly complex: WashU (92.4%), Hospital CDM (90.4%), AUSOM (99.1%), and YUHS (99.2%) demonstrated high rates, while Open Claims (10.3%), PMTX w/AmbEMR (4.9%), and notably CHCZ (24.2%) showed lower documentation despite CHCZ being a hospital-based system.

Diagnostic Testing: Troponin was tested in 58.1–97.4% of patients in the four hospital-based databases, but only in 14.7–27.1% of patients in other databases.

Symptom Documentation: Chest pain documentation varied widely from 5.4% (Hospital CDM) to 71.1% (WashU) with no consistent pattern. Other symptoms including dyspnea, nausea, and vomiting were documented in ≤16% across all databases.

Comorbidity Capture: Hyperlipidemia was documented in 53.2–72.9% of patients in Open Claims, PMTX w/AmbEMR, and WashU, compared to 3.7–25.3% in AUSOM, YUHS, CHCZ, and Hospital CDM.





Where Are We Going?

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



2026 OHDSI Vaccine Vocabulary WG

WG Co-Leads: Yongqun “Oliver” He & Alexander Davydov

- History of OHDSI Vaccine Vocabulary WG:
 - The ultimate challenge: classification and standardization of OHDSI vaccines.
 - 2021: [Issues identified by Merck Lixia Yao group](#)
 - 2022: Semi-automated method proposed by Licong Cui et al. PMID: [36029954](#)
 - 2022: Identification of missing hierarchical links in the Vaccine Ontology. PMID: [35964149](#).
 - Jan 2023 - May 2026: Oliver He and Asiyah Yu Lin co-chaired the WG:
 - Members: Alexander Davydov, **Qi Yang (IQVIA)**, **Jie Zheng (U-M)**, Penny Pan, Lixia Yang, Anna Ostropolets, etc.
 - Key idea: Improve and use the Vaccine Ontology (VO) to support OHDSI vaccine classification.
 - We presented posters at the annual OHDSI Symposium every year.
 - Organized a Vaccine Vocabulary WG meeting in 2024.
 - Attended the OHDSI Vocabulathon in 2025.
 - Vaccine Ontology (VO) published in *Nature Scientific Data*: <https://www.nature.com/articles/s41597-026-07298-w> . PMID: [42062309](#).
- Since May 2026, Oliver He and Alexander Davydov have co-chaired the Vaccine Vocabulary WG
 - Overall Goal: Implement the VO vaccine classification system for practical OHDSI use.



Summary of Vaccines in Vaccine Ontology (VO)

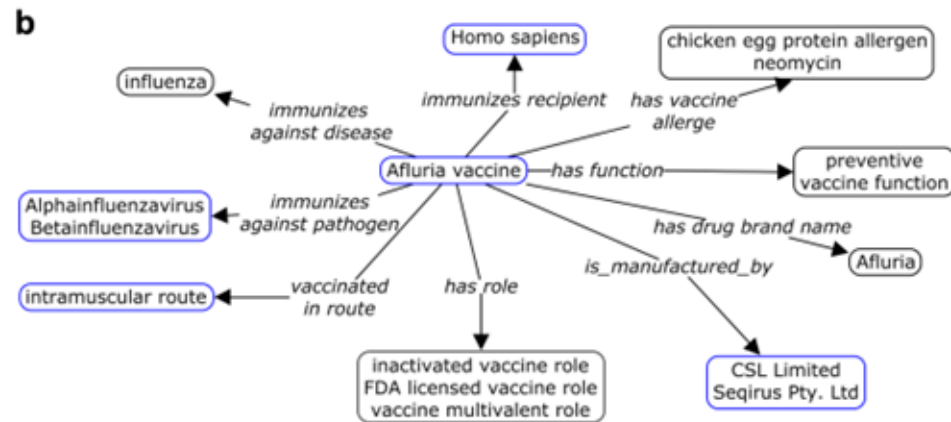
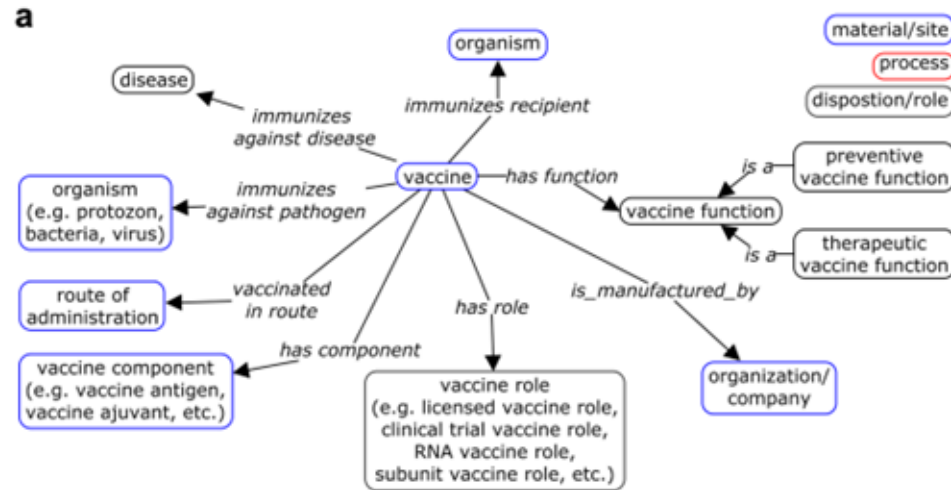
Development phase	Target host	Term resource	Vaccine Count	Total
Licensed/Authorized	Human	FDA	122	6,848
		CVX code	272	
		RxNorm	2,029	
		RxNorm Extension	4,074	
		Other	350	
	Veterinary animals	USDA	788	875
		Other	87	
In Clinical trial	Human	clinicaltrials.gov & NCI Thesaurus	427	805
	Human	Other	378	
In Research	Human + Veterinary animals	Literature and VO users	1,273	1,273

VO includes vaccines from different development phases and term resources

<https://www.nature.com/articles/s41597-026-07298-w>



Vaccine Ontology (VO) Design Pattern



c

Afluria vaccine — VO:0000006 — <http://purl.obolibrary.org/ontology/vo/>

Annotations Usage

Annotations: Afluria vaccine

Annotations +

rdfs:label [in vaccine]
Afluria vaccine

Description: Afluria vaccine

SubClass Of +

- 'has drug brand name' value Afluria
- 'has function' some 'preventive vaccine function'
- 'has role' some 'FDA licensed vaccine role'
- 'has role' some 'inactivated vaccine role'
- 'has role' some 'vaccine multivalent role'
- 'has vaccine allergen' some 'chicken egg protein allergen'
- 'has vaccine allergen' some neomycin
- 'immunizes against disease' some influenza
- 'immunizes against pathogen' some 'Influenza A virus'
- 'immunizes against pathogen' some 'Influenza B virus'
- 'immunizes recipient' some 'Homo sapiens'
- 'trivalent influenza vaccine'
- 'vaccinated in route' some 'intramuscular route'
- is_manufactured_by value 'CSL Limited'
- is_manufactured_by value 'Seqirus Pty. Ltd'
- 'inactivated influenza vaccine'
- 'licensed human influenza virus vaccine'
- 'multivalent vaccine'
- 'prophylactic vaccine'
- 'USA licensed human vaccine'

<https://www.nature.com/articles/s41597-026-07298-w>



Integration and Semantic Querying of OHDSI Vaccine Terminologies within VO

<https://www.nature.com/articles/s41597-026-07298-w>

a OHDSI COVID-19 vaccines under the VO hierarchical structure

- COVID-19 vaccine
 - authorized COVID-19 vaccine ← RxE: OMOP5042939
 - authorized COVID-19 DNA vaccine
 - ZyCoV-D vaccine ← CVX code: 514
 - authorized COVID-19 recombinant vector vaccine
 - authorized COVID-19 RNA vaccine
 - 0.25 ML SARS-CoV-2 (COVID-19) vaccine, mRNA-1273OMICRON (XBB.1.5) 0.1 MG/ML Injection ← RxNorm: 2664729
 - 0.3 ML SARS-CoV-2 (COVID-19) vaccine, mRNA-BNT162b2OMICRON (XBB.1.5) 0.0333 MG/ML Injection ← RxNorm: 2664832
 - 0.3 ML SARS-CoV-2 (COVID-19) vaccine, mRNA-BNT162b2OMICRON (XBB.1.5) 0.1 MG/ML
 - ...
 - SARS-COV-2 (COVID-19) vaccine UNSPECIFIED ← CVX code: 213

b Find influenza vaccines in OHDSI vocabularies

```
Query Text
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX obo: <http://purl.obolibrary.org/obo/>
SELECT DISTINCT ?VO_ID ?OMOP_Concept_ID ?CVX_code ?RxNorm_CUI ?RxNorm_Extension_ID ?name
FROM <http://purl.obolibrary.org/obo/merged/VO>
WHERE {
  ?entity rdfs:subClassOf* obo:VO_0003495 ; # human influenza virus vaccine
  rdfs:label ?name ;
  obo:VO_0010151 ?OMOP_Concept_ID .
  BIND(COALESCE(IF(CONTAINS(STR(?entity), "?obo/"), STRAFTER(STR(?entity), "?obo/"), ?entity)) AS ?VO_ID)
  OPTIONAL { ?entity obo:VO_0005438 ?CVX_code }
  OPTIONAL { ?entity obo:VO_0003198 ?RxNorm_CUI }
  OPTIONAL { ?entity obo:VO_0010152 ?RxNorm_Extension_ID }
  ORDER BY ASC(?OMOP_Concept_ID)
```

Query Results

VO_ID	OMOP_Concept_ID	CVX_code	RxNorm_CUI	RxNorm_Extension_ID	name
VO_0018874	"1146353"		"2379630"		"influenza A virus A/Guangdong-Maonan/SWL1536/2019 (H1N1) antigen 0.03 MG/ML"
VO_0018875	"1146354"		"2379631"		"influenza A virus A/Hong Kong/2671/2019 (H3N2) antigen 0.03 MG/ML"
VO_0019759	"1146356"		"2379635"		"influenza A virus A/Guangdong-Maonan/SWL1536/2019 (H1N1) antigen 0.03 MG/ML /

c Find human influenza virus vaccines used in flu season 2022-2023 using DL query

DL query

Query (class expression)
'human influenza virus vaccine' and 'has flu season' value 'flu season 2023'

Execute Add to ontology

Query results

Subclasses (10 of 11)

- 0.5 ML influenza A virus A/Darwin/9/2021 (H3N2) antigen 0.03 MG/ML / influenza A virus A/Sydney/5/2021 (H1N1) antigen 0.03 MG/ML / influenza B virus B/Michigan/01/2021 antigen 0.03 MG/ML / influenza B virus B/Phuket/3073/2013 antigen 0.03 MG/ML Prefilled Syringe [Fluzone Quadrivalent 2023 Southern Hemisphere]
- 0.7 ML influenza A virus A/Darwin/9/2021 (H3N2) antigen 0.0857 MG/ML / influenza A virus A/Sydney/5/2021 (H1N1) antigen 0.0857 MG/ML / influenza B virus B/Michigan/01/2021 antigen 0.0857 MG/ML / influenza B virus B/Phuket/3073/2013 antigen 0.0857 MG/ML Prefilled Syringe [Fluzone Quadrivalent 2023 Southern Hemisphere]
- Fluzone Quadrivalent 2023 Southern Hemisphere vaccine
- influenza A virus (H1N1) antigen / influenza A virus (H3N2) antigen / influenza B virus antigen Injectable Suspension [Fluzone Quadrivalent 2023



2026 OHDSI Vaccine Vocabulary WG OKR

Objective 1: Re-examine and refine the **Vaccine Ontology (VO)** semantic and hierarchical model of licensed human vaccine terms **mapped to OMOP** vaccine standards (CVX, RxNorm, RxNorm Extension).

Key results:

1. Scheduled to present at the June OHDSI Vocabulary Workgroup meeting.
Timeline: June 2026.
2. Submit an abstract(s) to the [OHDSI 2026 Symposium](#). Deadline: June 5, 2026.
3. Reach agreement with the OHDSI Vocabulary WG. Timeline: Summer 2026.



2026 OHDSI Vaccine Vocabulary WG

Objective 2: Prepare a **submission** for the inclusion of VO to the OHDSI Vocabularies as a **non-standard/classification vocabulary**.

Key results:

1. Agree on pilot 2-3 use cases (e.g., using IQVIA and N3C OMOP data) with Workgroups and research leads.
2. Prepare a pilot submission, socialize and test it via a pre-release.
Timeline: Summer 2026.
3. Execute a community contribution for VO inclusion to OMOP.
Timeline: Q2-3 2026.
 - *We will refine and use our automated computational approach for a community contribution submission via a scripting pipeline or simple forms*



2026 OHDSI Vaccine Vocabulary WG

Objective 3: Use Case **Studies** and Dissemination of **Results**.

Key results:

1. Develop and evaluate the use of the VO vaccine classification for EHR data analysis using IQVIA and N3C data in OMOP format. Timeline: Q2-4 2026.
2. Attend and present at the **OHDSI 2026 symposium**. Timeline: Oct 20-22, 2026, New Brunswick, N.J. <https://www.ohdsi.org/ohdsi2026/>
3. Prepare a journal article. Timeline: Q3-4 2026.



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-2026



Find your workgroup.

Fuel our mission.

ohdsi.org/workgroups