

# Evidence Network in Action: The Semaglutide Study

OHDSI Community Call Nov. 19, 2024 • 11 am ET



n ohdsi



## **Upcoming Community Calls**

Date	Topic	
Nov. 19	Evidence Network in Action: Semaglutide Study	
Nov. 26	Collaborator Showcase Honorees	
Dec. 3	Recent OHDSI Publications	
Dec. 10	How Did We Do In 2024?	
Dec. 17	Holiday-Themed Final Call of 2024	







## Three Stages of The Journey

# Where Have We Been? Where Are We Now? Where Are We Going?









Pharmacoepidemiology and Drug Safety

WILEY

Congratulations to the team of Francesco Dernie, George Corby, Abigail Robinson, James Bezer, Nuria Mercade-Besora, Romain Griffier, Guillaume Verdy, Angela Leis, Juan Manuel Ramirez-Anguita, Miguel A. Mayer, James T. Brash, Sarah Seager, Rowan Parry, Annika Jodicke, Talita Duarte-Salles, Peter R. Rijnbeek, Katia Verhamme, Alexandra Pacurariu, Daniel Morales, Luis Pinheiro, Daniel Prieto-Alhambra, and Albert Prats-Uribe on the publication of Standardised and Reproducible Phenotyping Using **Distributed Analytics and Tools in the Data Analysis** and Real World Interrogation Network (DARWIN EU) in Pharmacoepidemiology and Drug Safety.

ORIGINAL ARTICLE OPEN ACCESS

#### Standardised and Reproducible Phenotyping Using Distributed Analytics and Tools in the Data Analysis and Real World Interrogation Network (DARWIN EU)

Francesco Dernie<sup>1,2</sup> | George Corby<sup>1,2</sup> | Abigail Robinson<sup>1,2</sup> | James Bezer<sup>1,2</sup> | Nuria Mercade-Besora<sup>2</sup> | Romain Griffier<sup>3</sup> | Guillaume Verdy<sup>3</sup> | Angela Leis<sup>4</sup> | Juan Manuel Ramirez-Anguita<sup>5</sup> | Miguel A. Mayer<sup>4,5</sup> | James T. Brash<sup>6</sup> | Sarah Seager<sup>6</sup> | Rowan Parry<sup>7</sup> | Annika Jodicke<sup>2</sup> | Talita Duarte-Salles<sup>7,8</sup> | Peter R. Rijnbeek<sup>7</sup> | Katia Verhamme<sup>7</sup> | Alexandra Pacurariu<sup>9</sup> | 

<sup>1</sup>Medical Sciences Division, University of Oxford, Oxford, UK | <sup>2</sup>Pharmaco- and Device Epidemiology, Centre for Statistics in Medicines, Nuffield Department of Orthopaedics, Rheumatology and Musculoskeletal Sciences, University of Oxford, Oxford, UK | 3 Public Health Department, Medical Information Service, Medical Informatics and Archiving Unit (IAM), University Hospital of Bordeaux, Bordeaux, France | 4Research Programme on Biomedical Informatics (GRIB), Hospital del Mar Research Institute, Barcelona, Spain | 5Management and Control Department, Consorci Mar Parc de Salut de Barcelona, Barcelona, Spain | 6Real World Solutions, IQVIA, Brighton, UK | 7Department of Medical Informatics, Erasmus University Medical Centre, Rotterdam, The Netherlands | <sup>8</sup>Fundació Institut Universitari per a la Recerca a l'Atencio Primaria de Salut Jordi Gol I Gurina (IDIAPJGol), Universitat Autonoma de Barcelona, Barcelona, Spain | 9Real World Evidence Workstream, European Medicines Agency, Amsterdam, The Netherlands | 10Division of Population Health and Genomics, University of Dundee, Dundee, UK

Correspondence: Daniel Prieto-Alhambra (d.prietoalhambra@darwin-eu.org)

Received: 10 January 2024 | Revised: 2 October 2024 | Accepted: 6 October 2024

Funding: This work is part of the DARWIN EU initiative, funded by the European Medicines Agency. Francesco Dernie, Annika Jodicke, Daniel Prieto-Alhambra and Albert Prats-Uribe receive partial support from the National Institute for Health and Care Research (NIHR) in the form of the Oxford NIHR Biomedical Research Centre

Keywords: pancreatic cancer | phenotyping | systemic lupus erythematosus

#### ABSTRACT

Purpose: The generation of representative disease phenotypes is important for ensuring the reliability of the findings of observational studies. The aim of this manuscript is to outline a reproducible framework for reliable and traceable phenotype generation based on real world data for use in the Data Analysis and Real-World Interrogation Network (DARWIN EU). We illustrate the use of this framework by generating phenotypes for two diseases: pancreatic cancer and systemic lupus erythematosus (SLE). Methods: The phenotyping process involves a 14-steps process based on a standard operating procedure co-created by the DARWIN EU Coordination Centre in collaboration with the European Medicines Agency. A number of bespoke R packages were utilised to generate and review codelists for two phenotypes based on real world data mapped to the OMOP Common Data

Results: Codelists were generated for both pancreatic cancer and SLE, and cohorts were generated in six OMOP-mapped databases. Diagnostic checks were performed, which showed these cohorts had broadly similar incidence and prevalence figures to previously published literature, despite significant inter-database variability. Co-occurrent symptoms, conditions, and medication use were in keeping with pre-specified clinical descriptions based on previous knowledge.

Conclusions: Our detailed phenotyping process makes use of bespoke tools and allows for comprehensive codelist generation and review, as well as large-scale exploration of the characteristics of the resulting cohorts. Wider use of structured and reproducible phenotyping methods will be important in ensuring the reliability of observational studies for regulatory purposes.







Congratulations to the team of Aaron S Eisman, Elizabeth S Chen, Wen-Chih Wu, Karen M Crowley, Dilum P Aluthge, Katherine Brown, and Indra Neil Sarkar on the publication of **Learning health** system linchpins: information exchange and a common data model in JAMIA.

Journal of the American Medical Informatics Association, 2024, 1–11 https://doi.org/10.1093/jamia/ocae277 Research and Applications



#### Research and Applications

### Learning health system linchpins: information exchange and a common data model

Aaron S. Eisman , MD, PhD\*, 1,2,3, Elizabeth S. Chen, PhD1,2,4, Wen-Chih Wu, MD, MPH2,4,5, Karen M. Crowley, MS, PhD1, Dilum P. Aluthge, PhD1,2, Katherine Brown, PhD, MSN, RN1,2, Indra Neil Sarkar, PhD, MLIS1,2,4,6

<sup>1</sup>Center for Biomedical Informatics, Brown University, Providence, RI 02912, United States, <sup>2</sup>The Warren Alpert Medical School, Brown University, Providence, RI 02912, United States, <sup>4</sup>Yale School of Medicine, New Haven, CT 06510, United States, <sup>4</sup>School of Public Health Brown University, Providence, RI 02912, United States, <sup>5</sup>Division of Cardiology, VA Providence Health Care, Providence, RI 02912, United States, <sup>6</sup>Rhode Island Quality Institute, Providence, RI 02912, United States

\*Corresponding author: Aaron S. Eisman, MD, PhD, Center for Biomedical Informatics, Brown University, Providence, RI 02912, United States (aaron.eisman@yale.edu)

#### Abstract

**Objective:** To demonstrate the potential for a centrally managed health information exchange standardized to a common data model (HIE-CDM) to facilitate semantic data flow needed to support a learning health system (LHS).

Materials and Methods: The Rhode Island Quality Institute operates the Rhode Island (RI) statewide HIE, which aggregates RI health data for more than half of the state's population from 47 data partners. We standardized HIE data to the Observational Medical Outcomes Partnership (OMOP) CDM. Atherosclerotic cardiovascular disease (ASCVD) risk and primary prevention practices were selected to demonstrate LHS semantic data flow from 2013 to 2023.

Results: We calculated longitudinal 10-year ASCVD risk on 62,999 individuals. Nearly two-thirds had ASCVD risk factors from more than one data partner. This enabled granular tracking of individual ASCVD risk, primary prevention (ie, statin therapy), and incident disease. The population was on statins for fewer than half of the guideline-recommended days. We also found that individuals receiving care at Federally Qualified Health Centers were more likely to have unfavorable ASCVD risk profiles and more likely to be on statins. CDM transformation reduced data heterogeneity through a unified health record that adheres to defined terminologies per OMOP domain.

**Discussion:** We demonstrated the potential for an HIE-CDM to enable observational population health research. We also showed how to leverage existing health information technology infrastructure and health data best practices to break down LHS barriers.

Conclusion: HIE-CDM facilitates knowledge curation and health system intervention development at the individual, health system, and population levels.

Key words: learning health system; health information exchange; common data model; atherosclerotic cardiovascular disease.







Congratulations to the team of Junqing Xie, Kim López-Güell, Daniel Dedman, Talita Duarte-Salles, Raivo Kolde, Raúl López-Blasco, Álvaro Martínez, Gregoire Mercier, Alicia Abellan, Johnmary T. Arinze, Zara Cuccu, Antonella Delmestri, Dominique Delseny, Sara Khalid, Chungsoo Kim, Ji-woo Kim, Kristin Kostka, Cora Loste, Lourdes Mateu, Miguel A. Mayer, Jaime Meléndez-Cardiel, Núria Mercadé-Besora, Mees Mosseveld, Akihito Nishimura, Hedvig M.E. Nordeng, Jessie O. Oyinlola, Laura Pérez-Crespo, Marta Pineda-Moncusí, Juan Manuel Ramírez-Anguita, Nhung T.H. Trinh, Anneli Uusküla, Bernardo Valdivieso, Theresa Burkard, Edward Burn, Martí Català, Daniel Prieto-Alhambra, Roger Paredes, and Annika M. Jödicke on the publication of Incidence of post-acute COVID-19 symptoms across healthcare settings in seven countries: an international retrospective cohort study using routinely**collected data** in *eClinical Medicine*.

#### Incidence of post-acute COVID-19 symptoms across healthcare settings in seven countries: an international retrospective cohort study using routinely-collected data



Junqing Xie, a.aa Kim López-Güel, a.aa Daniel Dedman, Talita Duarte-Salles, al Raivo Kolde, Raúl López-Blasco, Álvaro Martínez, Gregoire Mercier, Alicia Abellan, Johnmary T. Arinze, Zara Cuccu, Antonella Delmestri, Dominique Delseny, Sara Khalid, Chungsoo Kim, Ji-woo Kim, Kristin Kostka, a.m. Cora Loste, h.w.x.y Lourdes Mateu, h.v.w.x.y Miquel A. Mayer, I Jaime Meléndez-Cardiel, Núria Mercadé-Besora, a.c. Mees Mosseveld, Akihito Nishimura,<sup>s</sup> Hedviq M. E. Nordenq,<sup>o,p</sup> Jessie O. Oyinlola,<sup>b</sup> Laura Pérez-Crespo,<sup>c</sup> Marta Pineda-Moncusí,<sup>a</sup> Juan Manuel Ramírez-Anquita,<sup>n</sup> Nhung T. H. Trinh, anneli Uusküla, Bernardo Valdivieso, t Theresa Burkard, Edward Burn, Martí Català, Daniel Prieto-Alhambra, ad., Roger Paredes, h,q,u,v,x,y,z,ab and Annika M. Jödickea,ab



<sup>a</sup>Nuffield Department of Orthopaedics, Rheumatology and Musculoskeletal Sciences, University of Oxford, Oxford, UK

<sup>b</sup>CPRD, Medicines and Healthcare Products Regulatory Agency, London, UK

Frundació Institut Universitari per a la recerca a l'Atenció Primària de Salut Jordi Gol i Gurina (IDIAPJGol), Barcelona, Spain <sup>d</sup>Department of Medical Informatics, Erasmus University Medical Center, Rotterdam, the Netherlands

Institute of Computer Science, University of Tartu, Tartu, Estonia

Biocomputing Unit, Aragon Health Sciences Institute (IACS), Zaragoza, Spain

<sup>9</sup>The Health Research Institute Hospital La Fe, Avenida Fernando Abril Martorell, 106 Torre A 7a Planta, 46026, Valencia, Spain

<sup>h</sup>Department of Infectious Diseases, Hospital Germans Trias i Pujol, Badalona, Catalonia, Spain

Public Health Department, University Hospital of Montpellier, 34295 Montpellier, France

JDESP, Université de Montpellier, INSERM, 34000, Montpellier, France

<sup>k</sup>Department of Biomedical Sciences, Ajou University Graduate School of Medicine, Suwon, Republic of Korea

Big Data Department, Health Insurance Review and Assessment Service, Wonju, Republic of Korea

<sup>m</sup>The OHDSI Center at the Roux Institute, Northeastern University, Portland, ME, USA

<sup>n</sup>Parc de Salut Mar, Hospital del Mar Medical Research Institute, Barcelona, Spain

<sup>o</sup>Pharmacoepidemiology and Drug Safety Research Group, Department of Pharmacy, Faculty of Mathematics and Natural Sciences

PDepartment of Child Health and Development, Norwegian Institute of Public Health, Oslo, Norway

qCenter for Global Health and Diseases, Department of Pathology, Case Western Reserve University School of Medicine, Cleveland, OH,

'Institute of Family Medicine and Public Health, University of Tartu, Tartu, Estonia

<sup>5</sup>Department of Biostatistics, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD, USA

<sup>t</sup>The University and Polytechnic La Fe Hospital of Valencia, Avenida Fernando Abril Martorell, 106 Torre H 1a Planta, 46026, Valencia,

CIBER Infectious Diseases (CIBERINFEC), Institute of Health Carlos III (ISCIII), Madrid, Spain

VUniversitat Autònoma de Barcelona, Catalonia, Spain

WREICOP (Red de Investigación Covid Persistente), Madrid, Spain

\*Fundació Lluita Contra les Infeccions, Badalona, Catalonia, Spain

<sup>y</sup>Universitat de Vic - UCC, Vic, Catalonia, Spain

<sup>2</sup>IrsiCaixa AIDS Research Institute, Germans Trias i Pujol Research Institute (IGTP), Can Ruti Campus, Badalona, Catalonia, Spain

Background The World Health Organisation (WHO) has identified a range of symptomatic manifestations to aid in the clinical diagnosis of post-COVID conditions, herein referred to as post-acute COVID-19 symptoms. We conducted an international network cohort study to estimate the burden of these symptoms in North American, European, and Asian populations.

eClinicalMedicine 2024:77: 102903

> Published Online xxx https://doi.org/10. 1016/j.eclinm.2024. 102903









Congratulations to the team of Eizen Kimura, Yukinobu Kawakami, Shingo Inoue, and Ai Okajima on the publication of Mapping Drug Terms via Integration of a **Retrieval-Augmented Generation** Algorithm with a Large Language **Model** in *Healthcare Informatics* Research.

#### **Original Article**

Healthc Inform Res. 2024 October;30(4):355-363 https://doi.org/10.4258/hir.2024.30.4.355 pISSN 2093-3681 • eISSN 2093-369X



### Mapping Drug Terms via Integration of a Retrieval-Augmented Generation Algorithm with a Large Language Model

Eizen Kimura<sup>1</sup>, Yukinobu Kawakami<sup>1</sup>, Shingo Inoue<sup>2</sup>, Ai Okajima<sup>2</sup>
<sup>1</sup>Department of Medical Informatics, Medical School of Ehime University, Toon, Ehime, Japan
<sup>2</sup>Yuimedi Inc., Tokyo, Japan

Objectives: This study evaluated the efficacy of integrating a retrieval-augmented generation (RAG) model and a large language model (LLM) to improve the accuracy of drug name mapping across international vocabularies. Methods: Drug ingredient names were translated into English using the Japanese Accepted Names for Pharmaceuticals. Drug concepts were extracted from the standard vocabulary of OHDSI, and the accuracy of mappings between translated terms and RxNorm was assessed by vector similarity, using the BioBERT-generated embedded vectors as the baseline. Subsequently, we developed LLMs with RAG that distinguished the final candidates from the baseline. We assessed the efficacy of the LLM with RAG in candidate selection by comparing it with conventional methods based on vector similarity. Results: The evaluation metrics demonstrated the superior performance of the combined LLM + RAG over traditional vector similarity methods. Notably, the hit rates of the Mixtral 8x7b and GPT-3.5 models exceeded 90%, significantly outperforming the baseline rate of 64% across stratified groups of PO drugs, injections, and all interventions. Furthermore, the r-precision metric, which measures the alignment between model judgment and human evaluation, revealed a notable improvement in LLM performance, ranging from 41% to 50% compared to the baseline of 23%. Conclusions: Integrating an RAG and an LLM outperformed conventional string comparison and embedding vector similarity techniques, offering a more refined approach to global drug information mapping.

Keywords: RxNorm, Machine Learning, Computer Neural Network, Terminology, Controlled Vocabulary







Congratulations to Erica Voss for successfully defending her dissertation at Erasmus University





## Three Stages of The Journey

Where Have We Been? Where Are We Now? Where Are We Going?







## **Upcoming Workgroup Calls**



Date	Time (ET)	Meeting
Tuesday	1 pm	Common Data Model
Wednesday	1 pm	Perinatal & Reproductive Health
Thursday	7 am	India Community Call
Thursday	9 am	OMOP CDM Oncology – Vocabulary/Development Subgroup
Thursday	9:30 am	Themis
Thursday	12 pm	Medical Devices
Thursday	12 pm	HADES
Thursday	7 pm	Dentistry
Friday	9 am	Phenotype Development & Evaluation
Friday	10 am	GIS-Geographic Information System
Friday	11:30 am	Clinical Trials
Friday	11:30 am	Steering
Monday	10 am	CDM Survey Subgroup
Tuesday	9 am	OMOP CDM Oncology – Genomic Subgroup





## **Next CBER Best Seminar: Tomorrow!**

Topic: Statistical methods for improving postlicensure vaccine safety surveillance

Presenter: Jennifer Clark Nelson, PhD, Director of Biostatistics & Senior Investigator, Biostatistics Division, Kaiser Permanente Washington Health Research Institute.

Date/Time: Nov. 20, 11 am ET



ohdsi.org/cber-best-seminar-series



# The Center for Advanced Healthcare Research Informatics (CAHRI) at Tufts Medicine welcomes:



Agnes Kiragga, PhD

Lead - Data Science Program, African Population and Health Research Center (APHRC)

'Promoting Data Science and Data Harmonization in Africa'

November 21, 2024, 11am-12pm EST Virtually via Zoom





## 2024 APAC Symposium

Dec. 4-8 • Marina Bay Sands & National University of Singapore (NUS)

Dec. 4: Tutorial at NUS

Dec. 5-6: Main Conference at Marina Bay Sands

Dec. 7-8: Datathon at NUS





ohdsi.org/APAC2024





## 2024 Global Symposium



### 2024 OHDSI Global Symposium

Oct. 22-24 · New Brunswick, N.J. · Hyatt Regency Hotel

The 10th annual OHDSI Global Symposium brought together more than 470 global collaborators for three days of sharing research, building new connections and pushing forward our mission of improving health by empowering a community to collaboratively generate the evidence that promotes better health decisions and better care.

This page will host all materials from OHDSI2024, including video presentations (when available) from the main conference and tutorials, slide decks, posters, demos and more.

#### State of the Community

Where Have We Gone and Where Are We Going?
(George Hripcsak, Columbia University)

Expand OHDSI Initiative for Eye Care and Ocular Imaging Challenge

(Amberlynn Reed, Natiional Eye Institute)

Titan Awar

(George Hripcsak, Columbia University & Marc Suchard, UCLA)



State of the Community Slides

### Plenary: Value Proposition for Participating in OHDSI Network Studies like LEGEND-T2DM

Introduction to OHDSI Evidence Network / Marketplace (Moderator: Clair Blacketer, Johnson & Johnson)

Reflections from US Department of Veterans Affairs (Scott Duvall, VA)

Reflections from SIDIAP (Spain) (Talita Duarte-Salles, IDIAP)

Reflections from a Global Commercial Data Provider (Atif Adam, IQVIA)



Plenary: Value Proposition for Participating in OHDSI Network Studies like LEGEND-T2DM Slides

#### Plenary Q&A: Lessons Learned on LEGEND-T2DM Journey

Moderator: Fan Bu, University of Michigan

Panelists: LEGEND-T2DM co-authors



Plenary Q&A: Lessons Learned on LEGEND-T2DM Journey Slides

#### Plenary Panel: JACC-OHDSI Partnership

#### Moderators

Nicole Pratt, University of South Australia Marc Suchard, UCLA

#### anelists:

Harlan Krumholz, Yale University Seng Chan You, Yonsei University Yuan Lu, Yale University



Plenary Panel: JACC-OHDSI Partnership Slides

ohdsi.org/OHDSI2024

### 2024 Global Collaborator Showcase Observational Data Standards & Management

- 1 <u>Application of OMOP Common Data Model to Disease Registry Data</u> (Vojtech Huser, Maria Rogozhkina, Vlad Korsik, Teresa A. Simon, Peter Moorthamer, Dan Kiselev, Teresa A. Simon, Anastasia Vakhmistrova, Eugene Paulenkovich, Alexander Davydov, Michel Van Soevbroeck)
- 2 Best Practices for Developing Disease-Specific Federated Networks: Insights from a Systemic Lupus Erythematosus Study (Clair Blacketer, Frank DeFalco, Gowtham A Rao, Anna Sheahan, Michel Van Speybroeck, Martine Lewi, Federico Zazzetti)
- 3 Standardizing Rare Disease Patient Registry data to the OMOP-CDM (Parag Shiralkar, Radhika Lakireddy, Sushma Ghanta, Sanket Kalyankar)
- 4 <u>PHederation</u> the federated network of <u>Pulmonary Hypertension registries</u> (Eva-Maria Didden, Valerie van Baalen, Michel van Speybroeck, Monika Brand)
- 5 Lessons from magoing cancer information from European hospitals to ICD-0-3 conditions in OMOP (Lars Halvorsen, Olivier Bouissou, Elisabeth Ross, Stellos Theophanous, Joëlle Thonnard, Piers Mahon)

  6 SMEs optimization with high precision data inpastion of CAPriCORN CDM onto OMOP at AllianceChicago (Andrew Hamilton, Amro Hassan,
- Davera Gabriel, Guy Tsafnat)
- 7 <u>Process of Conversion of Ukrainian Medical Data to OMOP CDM Format</u> (Bohdan Khilchevskyi, Denys Kaduk, Maksym Trofymenko, Polina Talapova, Tetiana Nesmilan, Max Ved, Inna Ageeva, Pavlova Olga, Holovko Tetiana, Shevchenko Natalia)
- 8 An evaluation of the transformation of large German EHR database to OMOP CDM (Andreas Ochs, Milou Brand, Jack Brewster, Methosdios Typou, Meda Sandu, Joe Maskell, Meghan Pettine, Atif Adam, George Kafatos)
- 9 Adopting the OMOP Oncology CDM at the Helsinki University Hospital (Valtteri Nieminen, Alexey Ryzhenkov, Johanna Sanoja, Salma Rachidi, Juho Lähteenmaa, Joonas Laitinen, Samu Eränen, Tomi Mäkelä, Eric Fey, Kimmo Porkka)
- 10 Going global, redeeming the local: an innovative approach to implement the OMOP CDM in two countries of the Global South (Valentina Martuf, Emma Kalk, Enny S. Cruz, Juliana Araújo Prata de Faria, Adalton do Anjos Fonseca, Maurício L. Barreto, Maria Yury Travassos Ichihara, Jessica Gammon, Nicri Fiftin, Chris Fourie, Danio Luis Cerqueira Dias, Denise Moraes Pimenta, Tsaone Tamuhla, Andrew Boulle, Themba Mutemaringa, Juan-Paul Hynek, Muzzammil Ismail, Julio Barbour Oliveira, Ricardo Felix Monteiro Neto, Júlia Pescarini, Fernanda Revoredo de Sousa, Marianne Costa e Sliva Lage, Adam Loff, Melvin Moodley, Elzo Pereira Pinto Junior)
- 11 <u>Transforming Clinical Trial Data to the OMOP CDM</u> (Cynthia Sung, Mike Hamidi, Zhen Lin, Tom Walpole, Rebecca Baker, Melissa Cook, Shital Desai, Priya Gopal, Dan Hartley, Voltech Huser, Priya Meghrajani, Tra Nguyen, Paul Orona12, Katy Sadowski, Sebastiaan van Sandijk, Philip Soloveye, Ramona Walls, Kenneth J. Wilkins, Gi Yanq)
- 12 Streamlining Research Data Standardization: Al-READI Survey Instrument Data Elements and MoCA Measurement Data Elements are curated and magged utilizing a Standardized Value Set Magging Table for transformation into the OMOP Common Data Model (Stephanie S. Hong, James Cavallon, Yvette Chen, Monique Bangudi, Jessica Mitchell, Dawn Matthies, Steven Chamberlin, Aaron Cohen, Julie Owens, Abigail Lucero, Sally Baxter, Christopher G Chute, Cecilia S. Lee, Aaron Lee, Al-READI consortium)
- 13 Institutionalizing data interogerability and the application of common data models in a health data and research center: CIDACS' experience in Brazil (Valentina Martufi, Juliana Araújo Prata de Faria, Danilo Luis Cerqueira Dias, Elzo Pereira Pinto Junior, Roberto Carreiro, Pablo Ivan Ramos, Maurcio L. Barreto)
- 14 OMOP GIS Vocabulary Package for Observational Studies in Health Care and Public Health (Maksym Trofymenko, Polina Talapova, Andrew Williams)
- 15 Enhancing Infectious Disease Data Integration and management through OMOP-CDM in South Korea (Min Ho An, Seok Kim, ByungJin Choi,Sooyoung Yoo,Rae Woong Park,Ji Seon Oh)
- 16 FHIR to OMOP Cookbook Mapping mCODE FHIR Resources for Observational Research (Qi Yang, Guy Livne, Sebastian van Sandijik, May
- 17 <u>Towards Reproducible Imaging Research: Implementation of DICOM to OMOP CDM</u> (Woo Yeon Park, Ben Martin, Gabriel Salvador, Blake Dewey, Teri Sippel Schmidt, Paul Nagy)
- 18 Leveraging UDI for Advanced Medical Device Tracking in OMOP-CDM (Seojeong Shin, Yiju Park, Sujeong Eom, Kyulee Jeon, Seng Chan You)
  19 Inclusion of intraocular pressure data into the University of California Health Data Warehouse (William Halfpenny\*, Shahin Hallaj\*, Ayan Patel,
- Catherine Q. Sun, Kerry Goetz, Michelle Hribar, Sally L. Baxter, on behalf of the OMOP Eye Care & Vision Research Workgroup)
  20 A Collaborative Analytic Enclave for the Metabolic Dysregulation and Obesity Cancer Risk Program (MeDOC) Consortium: Extensions of the
- OMOP Common Data Model for Translational Research (Madhan Subramanian, Nisha Grover, Maddie Wheeler, Marinella Temprosa)

  21 Expanding the OMOP Common Data Model to support Extracorporeal Life Support research (Clemens Rieder, Oleg Zhuk, Ahmed Said, Peta
- M.A. Alexander, Dominik J. Hoechter)
- 22 ETling from your OMOP CDM to your OMOP CDM? An efficient solution to vocabulary migration (Clair Blacketer, Anton Ivanov, Evanette Burrows, Dmitry Dymshyts, Frank DeFalco)
- 23 Evaluating the impact of different vocabulary versions on cohort definitions and CDM (Dmitry Dymshyts, Frank DeFalco, Anna Ostropolets, Gowtham Rao, Azza Shoaibi, Clair Blacketer)





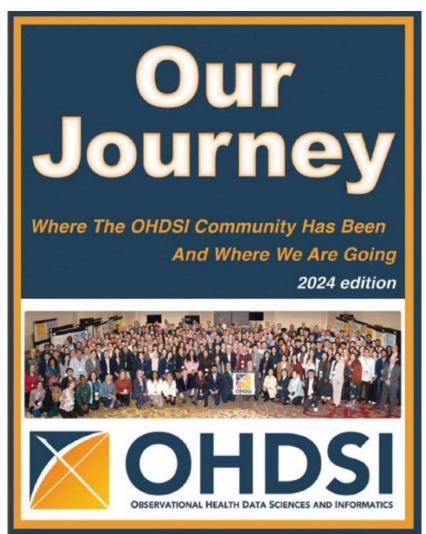


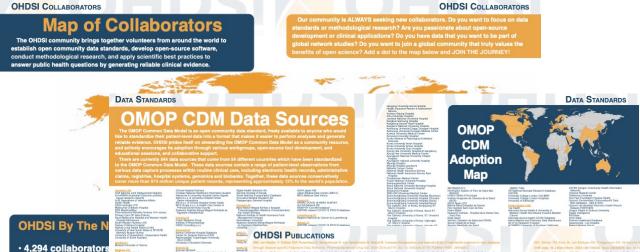
## 2024 Our Journey is Online

· 83 countries

 21 time zones · 6 continents

1 community





Princen P, Reich C, Raffaele Resta G, Ribal MJ, Gómez Rivas J, Smith E, Snijder R, Steinbeisser C, Vanderberghe F, Comford P, Evans-Axetsson S, N'Dow J, Willernes P.

**OHDSI PUBLICATIONS** 

Bacry E, Hughes N, Freeberg MA, Schaffhauser B, Wagener H, Sánchez-Pla A, Bertolini G, Panagiotopoulou M. Sharing sensitive data in life sciences: an overview of







## **Monday**

**FHIR to OMOP Cookbook - Mapping** mCODE FHIR **Resources for Observational** Research

(Qi Yang, Guy Livne, Sebastian van Sandijik, May Terry)

#### FHIR-to-OMOP Cookbook a cohesive approach to mapping FHIR Resources for Observational Research

PRESENTERS: Guy Livne, May Terry,

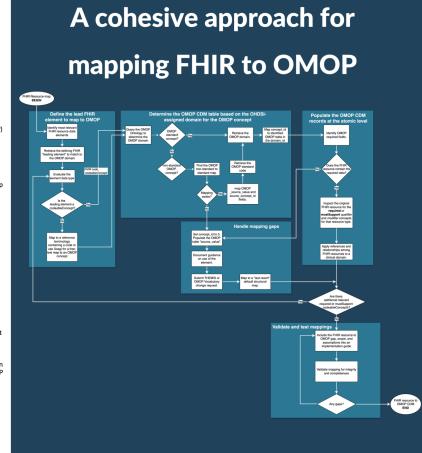
#### **BACKGROUND**

The conversion of Electronic Health Record (EHR) data from Health Level 7 (HL7®) Fast Healthcare Interoperability Resources (FHIR®) to the Observational Medical Outcomes Partnership (OMOP) Common Data Model (CDM) is becoming increasingly standardized for research, though inconsistencies exist among implementers. To address this, HL7 and the Observational Health Data Sciences and Informatics (OHDSI) formed a partnership in 2021, focusing on better alignment between FHIR and the OMOP CDM, including mapping minimum Common Oncology Data Elements (mCODE™) v2.0 FHIR resources to OMOP CDM v5.4. These efforts led to the creation of the FHIR-to-OMOP Cookbook, a guide for providing best practices for seamless integration of FHIR resources with the OMOP CDM

#### PRINCIPAL ARTIFACTS

- 1. Holistic mapping approach
- 2. Starter guide for implementers
- 3. Step-by-step practical guidelines

- 1. Define the FHIR elements that are relevant to represent in OMOP.
- 2. Identify the OMOP concept that best matches each of the FHIR element.
- 3. Determine the OMOP CDM table based on the OHDSI-assigned domain for the OMOP
- 4. Map related FHIR resources to the OMOP CDM table required fields.
- 5. Populate the OMOP CDM records at the atomic/record level.
- 6. Apply references and relationships among FHIR resources to a clinical domain from the original resource where possible.
- 7. Test OMOP CDM integrity and completeness
- 8. Compare FHIR and OMOP representations for a known set of patient information for accuracy and identify gaps.



Scan to download the FHIR-to-OMOP Cookbook

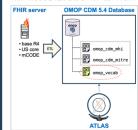
#### COOKBOOK VISION

Starter guide for implementers seeking to convert HL7 FHIR resources to the OMOP CDM.

The Cookbook compares the purpose design principles of both FHIR and OMOP CDM. It proposes a methodology for mapping with example use cases and patterns in mapping FHIR resources to equivalent OMOP CDM elements.

#### **TEST ENVIRONMENT**

The FHIR-to-OMOP Cookbook methodology was tested in the May 2022 HL7 FHIR Connectathon with mappings from mCODE v2.0 and OMOP CDM v5.4.



#### RESULTS

Over 80% of the mCODE FHIR-based elements were mapped. Gaps and learnings from the mapping and testing process were documented in the FHIR-to-OMOP Cookbook.

#### CONCLUSION

Although FHIR and OMOP are widely adopted standards, their purpose and data modeling differences require further guidance, including a methodology on how to integrate both process and technical transformations. The FHIR-to-OMOP Cookbook is an initial step in providing this guidance, and can be used to inform other nteroperability efforts such as the HL7 Vulcan FHIR to OMOP initiative.

Livne, G.1, Terry, M.2, Yang, Q.3 <sup>1</sup> Kineret, Israel, <sup>2</sup> MITRE, Bedford, MA, <sup>3</sup> IQVIA, Durham, NC











## Tuesday

Enabling Clinical Trial Feasibility and Patient Finding Through the Use of the OMOP CDM

(Mui Van Zandt, Jason Hsu, Alex Nguyen, Gyeol Song, Sabrina Cheema, Michael Krupnick) Enabling Clinical Trial Feasibility and Patient Finding Through the Use of the OMOP CDM

PRESENTER: Mui Van Zandt

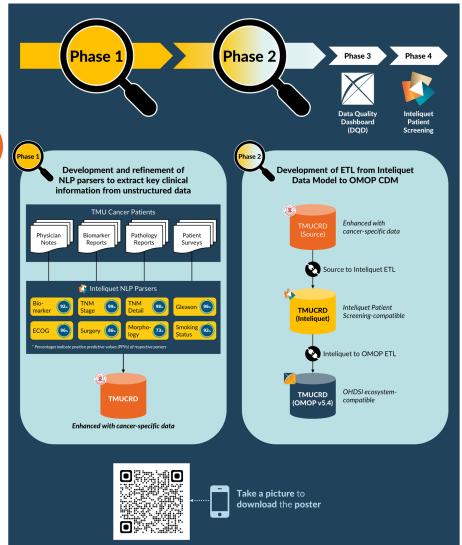
#### INTR



- Recruitment for clinical trials in cancer pose further difficulties due to the complexity and specificity of eligibility criteria
- Data-centric and technologyenabled approaches can tackle these challenges

#### METHODS

- Phase 1: IQVIA and Taipei Medical University (TMU) teams are currently collaborating to develop and refine natural language processing (NLP) parsers to extract key clinical information from unstructured data of cancer patients. These parsers enable extraction of cancer-specific data, such as biomarker and TNM information, from various sources. Cancer-specific data extracted will be used to enhance TMUCRD¹.
- Phase 2: Using the enhanced TMUCRD, IQVIA and TMU are also in parallel developing 2 ETLs:
   (1) TMUCRD source to Inteliquet for compatibility with the Inteliquet Patient Screening? tool and;
   (2) Inteliquet to OMOP CDM v5.4 for compatibility with the OHDSI ecosystem and its tools.



#### METHODS (Continued)

- Phase 3: Post the development of the Inteliquet to OMOP CDM v5.4 ETL, conversion will be validated using OHDSI's Data Quality Dashboard (DOD) package.
- Phase 4: Once all ETLs are validated, the Inteliquet Patient Screening tool will be installed and implemented into the clinical trial workflows of TMU.

#### Supplementary Information

- Taipei Medical University Clinical Research Database (TMUCRD) is an integrated database consisting of electronic medical records (EMRs) from three TMU affiliated hospitals - Taipei Medical University Hospital (TMUH), Wan-Fang Hospital (WFH) and Shuang-Ho Hospital (SHH). As of today, the database covers a vast range o medical records for approximately 4.15 million patients, spanning from the year 2004 to 2021.
- 2. Inteliquet Patient Screening is an application that sits behind clinical trial sites' firewalls and is used to assist site staff with querying for eligible patients and matching patients to clinical trials. The tool has a with a graphical user interface (GUI) that allows users to easily and quickly conduct prescreening for clinical trials and identify potentially eligible patients. Users may also digitize protocols to automatically and continuously match patients to inclusion/exclusion criteria in the protocol against new data being ingested by the tool.
- Mui Van Zandt, Jason Hsu, Alex Nguyen, Gyeol Song, Sabrina Cheema, Michael Krupnick











## Wednesday

## **Utility of Large Language Models for Concept Set Curation**

(Adit Anand, Anna Ostropolets, Patrick Ryan, George Hripcsak)

#### COLUMBIA COLUMBIA COLUMBIA UNIVERSITY IRVING MEDICAL CENTER

#### **Utility of Large Language Models for Concept Set Curation**



- 1. Department of Biomedical Informatics, Columbia University, New York, NY, USA
- 2. Janssen Research & Development, Raritan, NJ, USA

#### **Key Points**

- We evaluate large-language models' (LLMs) ability to curate concepts for EHR phenotyping from PHOEBE recommendations.
- ChatGPT-3.5-Turbo performs better than ChatGPT-4o, with varying performance across conditions, and ChatGPT-3.5-Turbo has better sensitivity than specificity when refining concept sets.
- Further work is needed to identify generalizable prompt engineering strategies across LLMs and determine the optimal role(s) LLMs should play in streamlining EHR phenotyping.

#### Background

- Constructing rule-based EHR phenotypes requires substantial informatics and clinical expertise. As a result, phenotyping algorithms are currently manually validated in an iterative manner to refine a phenotype's criteria.
- PHOEBE is a concept recommender system that facilitates developing clinical concepts in ATLAS.
- Efforts to generate rule-based phenotyping algorithms with LLMs have recognized the need for a "human-in-the-loop" approach to construct concepts sets.
- . Using 2 different versions of ChatGPT, we explore the utility of LLMs to curate clinical concepts for EHR phenotyping from PHOFRE recommendations

#### **Methods**

- For each of 4 phenotypes, PHOEBE recommends an initial set of OMOP concepts belonging to the Condition domain.
- For each recommended concept, we prompt zero-shot ChatGPT-3.5 and ChatGPT-40 to generate a True/False answer for whether a recommended concept is specific to the phenotype.
- The concepts that ChatGPT approves are inputted into PHOEBE to produce a second set of recommended Condition concepts.
- This second list is validated by ChatGPT with the same prompt engineering strategy, and the approved concepts from each pass comprise the final concept set
- · We calculate the sensitivity, specificity, and AUROC for each final concept set using a manually-curated, gold-standard concept set.

Results						
	ChatGPT-3.5-Turbo			ChatGPT-4o		
	Sensitivity	Specificity	AUROC	Sensitivity	Specificity	AURO
Acute Myocardial Infarction	0.879	0.479	0.679	0.094	0.985	0.539
Pulmonary Hypertension	0.000	0.693	0.347	0.000	1.000	0.500
Rheumatoid Arthritis	0.941	0.430	0.686	0.185	1.000	0.593
Type 1	0.952	0.684	0.819	0.000	1.000	0.500

Table 1. Sensitivity, specificity, and AUROC of the concept set generated by PHOEBE recommendations and zero-shot ChatGPT prompting for each phenotyp

Phenotype	Concept Name	ChatGPT-4o Explanation
Acute Myocardial Infarction	First myocardial infarction	A "first myocardial infarction" refers to the initial occurrence of a myocardial infarction (heart attack) in an individual. While having a first myocardial infarction means that the person has experienced an acute myocardial infarction (AMI), it is not specific to AMI in the sense that it does not exclusively indicate the presence of AMI. The term "first myocardial infarction simply denotes the initial event of a heart attack and does not imply that every instance of AMI is a first myocardial infarction. Therefore, the condition "first myocardial infarction" is not specific to the malady "acute myocardial infarction" is not specific to the malady in acute myocardial infarction "because it does not mee the criterion that if you have the condition, you definitely have the malady.
Rheumatoid Arthritis	Bilateral deformity of hands due to rheumatoid arthritis	While bilateral deformity of the hands can be a consequence of rheumatoid arthritis (RA), it is not specific to RA. This condition can also be seen in other forms of arthritis and joint diseases, such as osteoarthritis or sporatial carthritis. Therefore, having bilateral deformity of the hands does not definitively mean that a person has RA, even though it is a common manifestation in advanced cases of RA.
Type 1 Diabetes Mellitus	Type 1 diabetes mellitus uncontrolled	The condition "Type 1 diabetes mellitus uncontrolled" is not specific to Type 1 Diabetes Mellitus (T1DM) in the sense that having uncontrolled T1DM does not definitionly mean your have T1DM. The term

However, the presence of "uncontrolled" diabetes doe not provide new diagnostic information about the type of diabetes; it only describes the state of management of an already diagnosed condition. Therefore, it does not meet the criteria of being specific to T1DM because it does not independently confirm the diagnosis of T1DM. It merely describes the status of a pre-existing

"uncontrolled" simply indicates that the diabetes,

managed or regulated, leading to poor blood glucose

which is already diagnosed as T1DM, is not well-

Table 2. The concept names and explanations for three phenotypically-relevant clinical concepts assessed by ChatGPT-40 to be not specific to their corresponding phenotype

#### Results

- Table 1 demonstrates how the concept sets derived from using ChatGPT-40 have negligible sensitivity and thus have a statistically insignificant AUROC.
- These findings highlight that ChatGPT-40 performs worse relative to ChatGPT-3.5-Turbo for concept set validation.
- Chat-GPT-3.5 Turbo distinguishes symptoms indicating a condition's onset and risk factors from the disease itself
- ChatGPT-3.5-Turbo overestimates the specificity of symptoms which arise from the phenotype of interest. • To identify what causes ChatGPT-4o to underperform, Table 2
- highlights 3 PHOEBE-recommended concepts that ChatGPT-4o falsely identifies as not specific to their corresponding phenotype
- ChatGPT-4o fails to account for concepts' semantic similarity and overvalues the distinctness of new information or modifiers.

#### Conclusions

- Filtering PHOEBE concept recommendations with ChatGPT-3.5-Turbo or ChatGPT-40 is a promising method to curate concept sets for phenotyping algorithms.
- Ongoing work is needed to develop generalizable, robust prompt engineering or few-shot prompting methods.
- These LLM-curated concept sets should be used in phenotyping algorithms and evaluated with existing OHDSI tools.
- Reproducing this study across multiple clinical domains within the OMOP CDM (e.g., Procedure, Drug, Measurement, etc.) would provide a more holistic assessment of our methodology

#### References

1. Hripcsak G, Albers DJ. Next-generation phenotyping of electronic health records. J Am Med Inform Associated

2. Hripcask G, Duke JD, Shah NH, Reich CG, Huser V, Schuemie MJ, et al. Observational Health Data Sciences and Informatics (OHDSI): Opportunities for Observational Researchers. Stud Health Technol Inform. 2015;216:574–8. 3. Banda JM, Seneviratne M, Hernandez-Boussard T, Shah NH, Advances in Electronic Phenotyping: From Rule-Based Definitions to Machine Learning Models. Annu Rev Blomed Data Sci. 2018 Jul 20;1(Volume 1, 2018):53–68.

4. Zheng NS, Feng Q, Kerchberger VE, Zhao J, Edwards TL, Cox NJ, et al. PheMap: a multi-resource knowledge base for high-throughput phenotyping within electronic health records. J Am Med Inform Assoc. 2020 No

1.27(11):1675–87.

5. Wu P, Gifford A, Meng X, Li X, Campbell H, Varley T, et al. Mapping ICD-10 and ICD-10-CM Codes to Phecode 6. Ostropolets A, Hripcsak G, Knoll C, Ryan P. PHOEBE 2.0: selecting the right concept sets for the right patient using lexical, semantic, and data-driven recommendations. [cited 2024 Jun 7]; Available from:

https://www.ohdsi.org/wp-content/uploads/2022/10/6-Ostropolets\_Phoebe2.0-abstract.pdf
7. Yan C, Ong HH, Grabowska ME, Krantz MS, Su WC, Dickson AL, et al. Large language models facilitate the generation of electronic health record phenotyping algorithms. J Am Med Inform Assoc. 2024 Apr 13;ocae072. 8. Overhage JM, Ryan PB, Reich CG, Hartzema AG, Stang PE. Validation of a common data model for active safety surveillance research. J Am Med Inform Assoc. 2012 Jan. 1;191(3):34–60. V. ChatGPT [Internet]. Clied 20:30 Be 13]. Available from: https://chat.openal.com

Contact: adit.anand@columbia.edu







## **Thursday**

**Electronic Frailty** index and hazard of with MACE event in patients with Type 2 diabetes melitus

(Daeun Hyeon, Sujin Gan, Rae Woong Park)



#### Electronic Frailty index and hazard of with MACE event in patients with Type 2 diabetes mellitus

Daeun Hyeon<sup>1</sup>, Sujin Gan<sup>1</sup>, Rae Woong Park <sup>1,2</sup>

- <sup>1</sup> Department of Biomedical Informatics, Ajou University School of Medicine, Suwon, Republic of Korea
- <sup>2</sup> Department of Medical Sciences, Graduate School of Ajou University, Suwon, Republic of Korea



#### Background

- Type 2 diabetes mellitus (T2DM) significantly increases the risk of cardiovascular disease (CVD), particularly in older individuals with frailty and multimorbidity
- · Traditional frailty assessment tools are often complex and time-consuming, highlighting the need for EMR-based frailty indices to identify at-risk patients more efficiently.
- · This study aims to investigate the association between frailty, as measured through electronic medical records (EMRs), and major adverse cardiovascular events (MACE) in T2DM patients.

#### Methods

#### 1. Data preparation

- Observational medical outcomes partnership common data model (OMOP-CDM) database at Ajou University School of Medicine (AUSOM)
- Inclusion criteria
- 1) 40 years and older
- 2) Diagnosed with type 2 diabetes mellitus (T2DM)
- (MACE) ; myocardial infarction, cardiovascular disorders, acute ischemic heart disease, chronic ischemic heart disease and acute myocardial infarction.

#### 2. Outcome

- · Occurrence of MACE
- 3. .Sensitivity analysis
- · Dividing the participants into two age groups 65 years and younger and 66 years and older.

#### 3. Frailty index calculation

- · Electronic medical record (EMR) data was used to calculate the Electronic Frailty Index (eFI).
- · The eFI was calculated by summing binarized variables, resulting in a score ranging from 0 to 1.
- . This score was divided by the number of variables per patient, excluding missing values.
- 3) No history of major adverse cardiovascular events The maximum value of eFI was divided into thirds, stratifying patients into three groups based on each
  - Patients were categorized as normal, pre-frailty, or frailty based on their FI score

- · Cox proportional hazards regression model
- Kaplan-Meier survival curves
- Log-rank test

#### Conclusions

- · This study shows an association between increasing eFI and the occurrence of MACE in patients with T2DM aged 40 years or older
- The eFI used in this study has the advantage of not requiring separate frailty testing, and it showed the feasibility of using eFI in OMOP-CDM to screen for CVD risk groups in patients with T2DM.

#### Acknowledgement

- This research was funded a grant from the Korea Health Technology R&D Project through the Korea Health Industry Dev elopment Institute (KHIDI), funded by the Ministry of Health & Welfare, Republic of Korea (grant number: HR16C0001).
- This research was supported by a Government-wide R&D Fund project for infectious disease research (GFID), Republic o f Korea (grant number: HG22C0024).

#### Results

· The risk of MACE was significantly higher in the frailty group compared to the normal group (Hazard Ratio [HR]: 1.68, 95% Confidence Interval [CI]: 1.38-2.04; P < 0.05) and in the pre-frailty group compared to the normal group (HR 1.44 (1.35-1.55); P < 0.05).



Figure 1. Classification of T2DM patients based on electronic Frailty Index

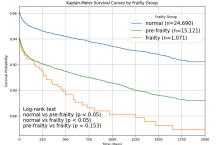


Figure 2. Survival probability curve for normal, pre-frailty, and frailty group

Age	Frailty category	N	Hazard ratio (95%, CI)
Below 65	Normal	15,714	1.0 (ref)
	Pre-Frailty	8,028	1.26 (1.13-1.40)
	Frailty	505	1.28 (0.90-1.83)
Over 65	Normal	8,976	1.0 (ref)
	Pre-Frailty	7,093	1.46 (1.33-1.61)
	Frailty	566	1.70 (1.34-2.16)

Table 1. Hazard ratio for MACE in Subgroup







## Friday

**Comparing IRB Review** of OHDSI Network **Studies: Sharing Experience and** Guidance

(Ben Martin, Will Kelly, Christopher Mecoli, Khyzer Aziz, Haeun Lee, Star Liu, Paul Nagy)

#### Title: Communicating **OHDSI Network Studies to** Local IRBs

PRESENTER: Ben Martin

Progress in data standardization and the adoption of CDMs like OMOP have enabled observational study execution times to go from months to a matter of days. With these robust studies becoming the norm rather than remarkable achievements, it is imperative that informatics faculty and observational health researchers work to optimize their processes for working with the IRB

#### METHODS:

- · This project involved the collation experience and identification of important considerations for IRB review of OHDSI network studies.
- · Individual experiences with the submission of OHDSI network study protocols for IRB review were shared amongst clinical research teams at Johns Hopkins.
- · Feedback and guidance from data governance board members and IRB reviewers were examined across different projects and common issues and unique considerations were summarized.
- required for IRB application was compared, and key considerations were compiled to develop a general-purpose IRB template (available below)



www.ohdsi.org



## Comparing IRB Review of **OHDSI Network Studies:** Sharing **Experience** & **Guidance**

### ID OHDSI Network Study

Dermatomyositis Phenotype Development and

- Impact of concomitant use of proton pump inhibitors and antiplatelet agents on
- cardiovascular adverse outcomes A multicenter, multinational study using common Estimating the risk of adverse drug events
- pediatric patients with sepsis

- Fully identifiable OMOP projection . Lead site for a network study;
- . Lead site for a network study
- C associated with broad-spectrum antibiotics in
- D Characterization of Maternal Health Outcomes
- E Toxicity of time for Planned Tracheostomy
- DbDiagnostics for the OHDSI Data Partner
- G Semaglutide and NAION & DR progression

- **Key IRB Framing Summary** Specific Considerations **Review Type** Use of the patient-level prediction algorithm
- in the Phevaluator package raised Full Review Characterization via executing CohortDiagnostics and concerns about FDA regulations around software as a medical device
- Use of the patient-level prediction algorithm · Aggressively deidentified OMOP projection prompted requests for more information around FDA software as a medical device Expedited Review · Patient-level prediction study of adverse drug events regulations Evaluation of adverse drug events for a broad category of drugs
- Evaluation of a drug efficacy prompted full Aggressively deidentified OMOP IRB review; the specificity of drug Full Review Data partner for an external network study evaluation was also a difference between
- Aggressively deidentified OMOP projection Single site study; descriptive analysis only Exempt Status Aggressively deidentified OMOP projection
- Single site study; descriptive analysis and Characterization of outcomes and healthcare serv Exempt Status phenotype evaluation using PheValuator utilization, phenotype evaluation
- · Aggressively deidentified OMOP projection Multi-site study; submission of concept- Data partner for an external network study: · Submission of dbDiagnostics profile
- · Aggressively deidentified OMOP projection . Data partner for an external network study:
- Population-level effect estimation
- level counts only (dbDiagnostics profile)
  - Multi-site study; execution of CohortMethod Change in Research to and SelfControlledCaseSeries modules
    - Ben Martin; Will Kelly; Christopher Mecoli; <sup>1</sup>Khyzer Aziz; <sup>1</sup>Haeun Lee; <sup>1</sup>Star Liu; <sup>1</sup>Paul Nagy
      - 1. Johns Hopkins School of Medicine Baltimore, MD, USA



Exempt Status

Take a picture to

As was expected with IRB review of

the degree of data deidentification

observational research, the most commor

request from IRB reviewers was around

At IHU, the OMOP data resources are

available as separate projections with

1) Fully identifiable projection of

the OMOP CDM. This CDM

does not contain any direct

identifiers such as MRN, or

contain fields such as date

patient names, but does

of birth and encounter

2) OMOP CDM Limited Data

Clinical Research Data

Aggressively deidentified

OMOP CDM; which has

been determined by the

Core for Clinical Research

Data Acquisition to meet

criteria for a limited datase

and has had sensitive data

removed to further prevent

reidentification.

determined by the Core for

Acquisition to meet criteria

for a HIPAA limited dataset.

Set; which has been

three distinct levels of patient health

information (PHI) sensitivity:

download the



A generalized OHDSI IRB Protocol Template developed at Johns Hopkins from this compiled experience is publicly available for data partner support.

Accessible on the OHDSI Evidence Network GitHub repository

optimizing our collaborations with local IRB review processes by continuing to share knowledge and experience in this domain.

It is vital that the OHDSI community

continues to support each other in







## **Job Opening**

### Senior Program Officer, Clinical Al Innovation, Gates Foundation

#### Senior Program Officer, Public Health Surveillance, Data Integration, and Artificial Intelligence



#### What You'll Do

Are you passionate about using the power of information technology to support better surveillance and public health decision making and thereby improve health and reduce inequality in low- and middle-income countries? Do you have experience working in low- and middle-income countries on AI or digital public health initiatives? If so, we want you to join our team at the largest nonprofit fighting poverty, disease, and inequity around the world.

The Senior Program Officer, Public Health Surveillance, Data Integration, and Artificial Intelligence is a key member of the foundation's Surveillance unit in the Pneumonia and Pandemic Preparedness Team. This role will focus on public health informatics and Al for the Foundation's cross-cutting public health surveillance initiative and will also support other groups in PPP that are considering investments in public health informatics and AI. Beyond the PPP portfolio, this role requires cross-foundation collaboration with surveillance activities with other teams, including Africa Regional Office; Genomics, Epidemiology, & Modeling; Global Policy & Advocacy; and Global Health Agencies & Funds. This role also collaborates with the AI Core Team and Program Strategy Teams on other infectious disease surveillance programs to ensure coordination and integration of surveillance activities. Taking advantage of the promise of AI and preventing an AI digital divide in Africa and other areas of the global south is a high priority area for the Foundation. As such, this role will be responsible for developing our overarching strategy for public health surveillance applications in AI, as well as other applications of information technology to public health surveillance and epidemic readiness. This person will also provide technical assistance to other PSTs and advocate for the safe, responsible use of AI as a force multiplier to improve public health surveillance in LMICs

- Create and implement a strategy for digital innovation, including AI, to improve actionable, integrated, and timely information for public health decision-makers in the global south
  - Develop a strategy for the Foundation's work on public health informatics and AI for public health surveillance, consistent with our theory of change, with quantifiable impact goals
  - Develop a clear understanding of specific ecosystem constraints and opportunities related to AI for public health surveillance
  - Map the pathways by which promising public health surveillance technologies transition from small, defined proof-of concepts to minimal viable products and ultimately scaled products/applications that are sustainable across multiple countries
  - Identify a key set of partners and stakeholders for success in this focus area across the technical, advocacy, government, academic and funding spheres
- Use your scientific and technical expertise to identify, develop, and manage a portfolio of strategic investments related to our strategy
  - Review submitted concept notes and grant proposals to support projects and programs on public health informatics for surveillance, including global and national data architecture, norms, and standards; unique health ID and privacy-preserving record linkage; early warning systems for outbreak detection and notification
  - Shape and manage investments on AI tool effectiveness, safety, and regulatory strategies for AI-informed public health surveillance in LMICs
  - Develop an overarching evaluation plan to understand the viability of tools deployed in LMIC settings and why they succeed or fail
  - Ensure that funding is appropriately managed and where appropriate, done in collaboration with other foundation teams and external funders





## 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?







# Nov. 19: Evidence Network in Action The Semaglutide Study



**Cindy Cai** 

Assistant Professor of Ophthalmology
Wilmer Eye Institute at Johns Hopkins Hospital

**Topic: Semaglutide and NAION: An OHDSI** 

**Network Study** 



**Paul Nagy** 

Program Director for Graduate Training in Biomedical Informatics and Data Science Johns Hopkins University

**Topic: Evidence Network** 



**Linying Zhang** 

Assistant Professor of Biostatistics Washington University

**Topic: Methods** 



**Anthony Sena** 

Director, Observational Health Data Analytics
Johnson & Johnson

**Topic: Strategus** 



**Ben Martin** 

Postdoctoral Fellow Johns Hopkins University

**Topic: Using the Results Schema** 



**Erik Westlund** 

Assistant Scientist
Johns Hopkins University

**Topic: Using the Results Schema** 

n ohdsi



# 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

