

Save Our Sisyphus Challenge Week 8: Evidence Synthesis

OHDSI Community Call May 16, 2023 • 11 am ET

in ohdsi



Upcoming Community Calls

Date	Topic
May 16	SOS Week 8 Tutorial: Evidence Synthesis
May 23	SOS Week 9 Tutorial: Interpreting The Results
May 30	Collaborator Showcase Sneak Preview & Rapid Brainstorm
June 6	OHDSI Standardized Vocabularies: Landscape, Roadmap and Community Contributions
June 13	ATLAS: User Input For Community Development
June 20	OMOP Supporting Clinical Registries
June 27	Recent Publication Presentations





May 16: Evidence Synthesis (SOS Week 8)



Marc Suchard

Professor, Departments of Biomathematics & Human Genetics, UCLA

SOS Challenge Weekly Tutorial Schedule

Date	Topic
Mar 28	Initiating A Network Study
Apr 4	Data Diagnostics
Apr 11	Phenotype Development
Apr 18	Phenotype Evaluation
Apr 25	Analysis Design
May 2	Network Execution
May 9	Study Diagnostics
<u>May 16</u>	Evidence Synthesis
May 23	Interpreting Results





Global Tutorials Schedule

Local Time Zone	Session 1: focus on risk of ESRD in antiVEGF treatments for blinding disease	Session 2: focus on risk of aortic aneurysm in fluoroquinalone exposure
Eastern Time (OHDSI in NY, USA) UTC-5	11:00	19:00
PST UTC-8	8:00	16:00
MST UTC-7	9:00	17:00
CST UTC-6	10:00	18:00
BRT UTC-4	12:00	20:00
GMT UTC-0	16:00	0:00
CET UTC+1	17:00	1:00
AST UTC+2	18:00	2:00
IST UTC+5	21:00	5:00
CST UTC+8	0:00	8:00
KST, ACST UTC+9	1:00	9:00
AEST UTC+10	2:00	10:00







Evidence Synthesis Office Hours #1



Yong Chen

Professor of Biostatistics, **Epidemiology &** Informatics, University of Pennsylvania



Martijn Schuemie

Research Fellow, Epidemiology Analytics, Janssen Research and Development

Weekly Tutorial Schedule

Date	Topic
Mar 28	Initiating A Network Study
Apr 4	Data Diagnostics
Apr 11	Phenotype Development
Apr 18	Phenotype Evaluation
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May 2	Network Execution
May 9	Study Diagnostics
<u>May 16</u>	Evidence Synthesis
May 23	Interpreting Results

SOS Challenge

Thursday, 11 am ET

Link Available on the SOS Challenge Homepage





Evidence Synthesis Office Hours #2



Marc Suchard

Professor, Departments of Biomathematics & Human Genetics, UCLA

Thursday, 7 pm ET

Link Available on the SOS Challenge Homepage

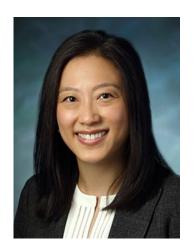
SOS Challenge Weekly Tutorial Schedule

Date	Topic
Mar 28	Initiating A Network Study
Apr 4	Data Diagnostics
Apr 11	Phenotype Development
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May 9	Study Diagnostics
<u>May 16</u>	Evidence Synthesis
May 23	Interpreting Results





May 23: Interpreting the Results (SOS Week 9)



Cindy Cai

Assistant Professor of Ophthalmology, Johns Hopkins University

SOS Challenge Weekly Tutorial Schedule

Date	Topic
Mar 28	Initiating A Network Study
Apr 4	Data Diagnostics
Apr 11	Phenotype Development
Apr 18	Phenotype Evaluation
Apr 25	Analysis Design
May 2	Network Execution
May 9	Study Diagnostics
May 16	Evidence Synthesis
<u>May 23</u>	Interpreting Results





SOS Challenge Homepage





Save Our Sisyphus Challenge

11 am / 7 pm ET

11 am / 7 pm E1

11 am / 7 pm ET

11 am / 7 nm ET

empowering a community to collaboratively generate the evidence that promotes better health decisions and better care. The 2023 Save Our. Sisyphus (SOS) Challenge will try to fulfill that mission, but not through one study at a time.

We will be collaborating simultaneously on four studies, each of which will be designed. implemented, executed and disseminated by members of the OHDSI global community.

As you can see on the right, there will be two

weekly tutorials, taught by different members of the community, and featuring two of the four studies

that were voted on by the community. Please join either or both each week to learn every step of executing a network study. The earlier session will take place during the weekly global community call, while the later will take place at 7 pm ET. Weekly call invites will go out for both, or you can access either meeting using the links below

Weekly Tutorial Links

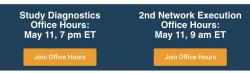
Please remember that each week, there are two seminars focused on the same aspect of running a network study, but featuring different SOS Challenge studies. We want to make sure that regardless of your location, there is a tutorial that is convenient for all hours. All tutorials will also be recorded and posted below.



SOS Challenge Weekly Tutorial Schedule

Office Hours

There will be weekly office hours, corresponding with the topic of the weekly tutorials. Office hours are determined by the availability of each week's tutorial lead. When the next set of office hours are determined, the time and meeting link will be posted to the right.



SOS Challenge Studies

The SOS Challenge was introduced in January 2023, and community members submitted 35 different studies that could be run during the challenge. Four were selected from that group, two of which will be done live during the weekly tutorials, and two that will be done asynchronously. You can learn more about each of the four studies below, and each of the pertinent links (GitHub repo, protocol, Teams channel, etc.) will be linked in the proper section.

Intravitreal Anti-VEGF and Kidney Failure Lead: Cindy Cai









Is fluoroguinolone use really associated with the development of aortic aneurysms Is fluoroquinolone use really associated with the development of aortic aneurysms and aortic dissections? OHDSI Save Our Sisyphus Challenge 2023 Seng Chan You, Seonii Kim, Jung Ho Kim, Jung Ah Lee - Yonsei University Jack Janetzki, Nicole Pratt - University of South Australia MS Teams Channel GitHub Repo

Tutorial Recordings

Week 6: Network Execution

Session 1: Jenna Reps, Jack Brewster (slides)



Session 2: Anthony Sena, Chungsoo Kim (coming soon)



Week 5: Analysis Design

Session 1: Patrick Ryan (slides)



Session 2: Patrick Ryan (slides)



Week 4: Phenotype Evaluation

Session 1: James Gilbert, Azza Shoaibi



Session 2: James Gilbert, Evan Minty



ohdsi.org/sos-challenge

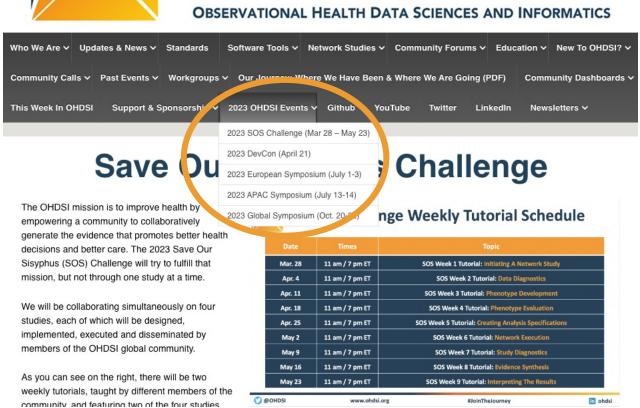






SOS Challenge Homepage









Three Stages of The Journey

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









Congratulations to

Nick Williams on the

publication of **Building the observational medical outcomes partnership's T-**

MSIS Analytic File common data model in Informatics in Medicine Unlocked.



Contents lists available at ScienceDirect

Informatics in Medicine Unlocked

journal homepage: www.elsevier.com/locate/imu



Building the observational medical outcomes partnership's T-MSIS Analytic File common data model

Nick Williams

National Library of Medicine, Lister Hill National Center for Biomedical Communications, Bethesda, MD, USA

ARTICLE INFO

Keywords:
Common data model
Medicaid
Observational medical outcomes partnership
Centers for medicare and medicaid services
Observational health data sciences and

ABSTRACT

Objectives: This effort used Databricks to create an Observational Medical Outcomes Partnership (OMOP) Common Data Model (CDM) for Transformed MSIS Analytic File (TAF) Medicaid records.

Materials and methods: Our process included data volume and content assessment of TAF, translation mapping of TAF concepts to OMOP concepts and the creation of Extract Transform and Load (ETL) code.

 ${\it Results}. The final CDM contained 119,048,562 individuals and 24,806,828,121 clinical observations from 2014 through 2018.$

Discussion: The transformation of TAF into OMOP can support the generation of evidence with special attention to low-income patients on public insurance. Such patients are perhaps underrepresented in academic medical center patient populations.

Conclusion: Our effort successfully used Databricks to transform TAF records into OMOP CDM. Our CDM can be used to generate evidence for OMOP network studies.

Lay summary

Generating evidence from academic medical centers, rather than safety net insurance programs may bias clinical evidence. Patients who use academic medical centers may differ from safety net patients. Safety net patients have meaningful preexisting conditions, barriers to care and real world precarity which may be lacking in patients who seek services at academic medical centers.

Changing the data source for evidence generation may improve the utility of evidence-based medicine in the United States. Using federal claims data from the Centers for Medicare and Medicaid Services (CMS) as an alternative data source has several barriers to success.

We investigate the complexity of CMS data available to researchers and further attempt to transform current vintage of Medicaid records (TAF) into the Observational Medical Outcomes Partnership's (OMOP) Common Data Model (CDM) for 2014–2018 data years. The OMOP CDM is commonly used by researchers for multi-center network studies and evidence generation. A TAF OMOP CDM can provide over 119 million patients and tens of billions of clinical observations researchers. Further development of Medicare and legacy Medicaid records could see a maximum of 297 million individuals from 1999 through made available to researchers.

Background and significance

Evidence-based medicine requires reoccurring assessments of clinical practice across a diversity of settings and patients to maintain efficacy and respond to change [1-4]. The increase in demand for multi-center network studies has largely been driven by the quality of clinical evidence they provide when compared with single institutions [5,6]. Multi-center network study methodology has improved remarkably over the years allowing for complex, international studies to be delivered. These network studies work by harmonizing retrospective data in electronic health record systems around the world into a specific research study. These studies work across languages and are delivered at highly competitive costs when compared with bedside studies. The Observation Medical Outcomes Partnership (OMOP) offers a Common Data Model (CDM) to support the interoperability of observational research study data [7–10].

The Centers for Medicare and Medicaid Services (CMS) curates' identifiable records for clinical services billed to CMS from 1999 onward to support data reuse research. Made available via the Chronic Conditions Warehouse (CCW), CMS data is traditionally vended as SAS data sets for analysis using SAS Enterprise Guide and SAS Grid [11]. CCW recently transitioned to the 'cloud' and now offers SAS Cloud Studio and Databricks as alternative points of access to CMS data. Databricks is







Congratulations to the team of Raffael Lukas Korntheuer, Florian Katsch, and Georg **Duftschmid** on the publication of **Transforming Documents of the Austrian Nationwide EHR** System into the OMOP CDM Vol. 301 of Studies in Health Technology and Informatics.

Transforming Documents of the Austrian Nationwide EHR System into the OMOP CDM

Authors Raffael Lukas Korntheuer, Florian Katsch, Georg Duftschmid

Pages 54 - 59

DOI 10.3233/SHTI230011

Category Research Article

Series Studies in Health Technology and Informatics

Ebook Volume 301: dHealth 2023

Abstract

The Austrian nationwide EHR system ELGA can contribute valuable data for research due to its high volume of data and broad population coverage. In order to be applicable in international research projects, transformation to a standardized, research-oriented data model such as the OMOP common data model is essential. In this paper we describe our experience with the corresponding transformation task. Using Python scripts, we implemented a prototypical process that extracts, transforms, maps, and loads fully structured sections of ELGA documents to an OMOP database.

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Congratulations to the team of **Emmanuelle** Kempf, Morgan Vaterkowski, Damien Leprovost, Nicolas Griffon, David Ouagne, Stéphane Breant, Patricia Serre, Alexandre Mouchet, Bastien Rance, Gilles Chatellier, Ali Bellamine, Marie Frank, Julien Guerin, Xavier Tannier, Alain Livartowski, Martin Hilka, and Christel Daniel on the publication of How to **Improve Cancer Patients Enrollment in Clinical Trials From rEal-Life Databases Using** the Observational Medical Outcomes Partnership Oncology Extension: Results of the PENELOPE Initiative in Urologic Cancers in JCO Clinical Cancer Informatics.

JCO[®] Clinical Cancer Informatics An American Society of Clinical Oncology Journal









JAMIA Open, 6(2), 2023, ooad032 https://doi.org/10.1093/jamiaopen/ooad032 Brief Communications





Congratulations to the team of Matthew Spotnitz, Nripendra Acharya, James Cimino, Shawn Murphy, Bahram Namjou, Nancy Crimmins, Theresa Walunas, Cong Liu, David Crosslin, Barbara Benoit, Elisabeth Rosenthal, Jennifer Pacheco, Anna Ostropolets, Harry Reyes Nieva, Jason Patterson, Lauren Richter, Tiffany Callahan, Ahmed Elhussein, Chao Pang, Krzysztof Kiryluk, Jordan Nestor, Atlas Khan, Sumit Mohan, Evan Minty, Wendy Chung, Wei-Qi Wei, Karthik Natarajan, and Chunhua Weng on the publication of A metadata framework for

computational phenotypes in JAMIA Open.

Brief Communications

A metadata framework for computational phenotypes

Matthew Spotnitz ®¹, Nripendra Acharya¹, James J. Cimino², Shawn Murphy³.⁴, Bahram Namjou⁵, Nancy Crimmins⁵, Theresa Walunas⁶, Cong Liu¹, David Crosslin², Barbara Benoit³, Elisabeth Rosenthal⁶, Jennifer A. Pacheco¹₀, Anna Ostropolets ®¹, Harry Reyes Nieva ®¹, Jason S. Patterson¹, Lauren R. Richter¹, Tiffany J. Callahan¹, Ahmed Elhussein¹, Chao Pang¹, Krzysztof Kiryluk¹¹, Jordan Nestor ®¹¹, Atlas Khan¹¹, Sumit Mohan¹¹¹,² Evan Minty¹³, Wendy Chung¹⁴, Wei-Qi Wei¹⁵, Karthik Natarajan¹, and Chunhua Weng¹

¹Department of Biomedical Informatics, Vagelos College of Physicians & Surgeons, Columbia University Irving Medical Center, New York, New York, USA, ²Informatics Institute, Heersink School of Medicine, University of Alabama at Birmingham, Birmingham, Alabama, USA, ³Laboratory of Computer Science, Mass General Brigham, Boston, Massachusetts, USA, ⁵Department of Pediatrics, Cincinnati, Children's Hospital Medical Center, Cincinnati, Ohio, USA, ⁶Department of Medicine, Feinberg School of Medicine, Northwestern University, Chicago, Illinois, USA, ⁷Division of Biomedical Informatics and Genomics, Tulane University School of Medicine, New Orleans, Louisiana, USA, ⁸Department of Research Information Science & Computing, Mass General Brigham, Boston, Massachusetts, USA, ⁸Division of Genetics, University of Washington, Seattle, Washington, USA, ¹⁰Center for Genetic Medicine, Northwestern University, Chicago, Illinois, USA, ¹¹Division of Nephrology, Department of Medicine, Vagelos College of Physicians & Surgeons, Columbia University Irving Medical Center, New York, New York, USA, ¹³Department of Epidemiology, Columbia University Mailman School of Public Health, New York, New York, USA, ¹³Department of Medicine, University of Calgary, Calgary, Alberta, Canada, ¹⁴Department of Pediatrics, Vagelos College of Physicians & Surgeons, Columbia University Irving Medical Center, New York, New York, USA, and ¹⁵Department of Biomedical Informatics, Vanderbilt University, Nashville, Tennessee, USA

Wei-Qi Wei, Karthik Natarajan, and Chunhua Weng contributed equally to this work and senior authors.

Corresponding Author: Matthew Spotnitz, MD, MPH, Department of Biomedical Informatics, Columbia University Irving Medical Center, 630 W 168th Street, New York, NY 10032-3784, USA; mes2165@cumc.columbia.edu

Received 10 February 2023; Revised 10 April 2023; Editorial Decision 18 April 2023; Accepted 21 April 2023

ARSTRACT

With the burgeoning development of computational phenotypes, it is increasingly difficult to identify the right phenotype for the right tasks. This study uses a mixed-methods approach to develop and evaluate a novel metadata framework for retrieval of and reusing computational phenotypes. Twenty active phenotyping researchers from 2 large research networks, Electronic Medical Records and Genomics and Observational Health Data Sciences and Informatics, were recruited to suggest metadata elements. Once consensus was reached on 39 metadata elements, 47 new researchers were surveyed to evaluate the utility of the metadata framework. The survey consisted of 5-Likert multiple-choice questions and open-ended questions. Two more researchers were asked to use the metadata framework to annotate 8 type-2 diabetes mellitus phenotypes. More than 90% of the survey respondents rated metadata elements regarding phenotype definition and validation methods and metrics positively with a score of 4 or 5. Both researchers completed annotation of each phenotype within 60 min. Our thematic analysis of the narrative feedback indicates that the metadata framework







Any shoutouts from the community? Please share and help promote and celebrate **OHDSI** work!

Do you have anything you want to share? Please send to sachson@ohdsi.org so we can highlight during this call and on our social channels. Let's work together to promote the collaborative work happening in OHDSI!





Three Stages of The Journey

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







Upcoming Workgroup Calls



Date	Time (ET)	Meeting
Tuesday	12 pm	Common Data Model Vocabulary Subgroup
Tuesday	1 pm	Common Data Model
Tuesday	7 pm	SOS Challenge Tutorial: Evidence Synthesis
Wednesday	7 am	Medical Imaging
Wednesday	1 pm	Perinatal & Reproductive Health
Thursday	9 am	1st Evidence Synthesis Office Hours
Thursday	9 am	OMOP CDM Oncology Vocabulary/Development Subgroup
Thursday	12 pm	HADES
Thursday	7 pm	Dentistry
Thursday	7 pm	2nd Evidence Synthesis Office Hours
Friday	9 am	GIS – Geographic Information Systems General
Friday	10 am	Education
Friday	10:30 am	Open-Source Community
Friday	11 am	Clinical Trials
Monday	10 am	Healthcare Systems Interest Group
Monday	4 pm	Eyecare & Vision Research
Tuesday	9 am	OMOP CDM Oncology Genomic Subgroup





OHDSI HADES releases: DataQualityDashboard 2.2.0

EvidenceSynthesis 0.5.0 **MHADES** Reference Articles ▼ Video vignette Changelog Changelog Contents Source: NEWS.md 0.5.0 0.4.1 0.4.0 EvidenceSynthesis 0.5.0 0.3.0 0.2.3 0.2.2 Changes 0.2.1 1. Supporting Bayesian adaptive bias correction in sequential analysis by adding fitBiasDistribution(), sequentialFitBiasDistribution() and biasCorrectionInference() functions 0.2.0 2. Added relevant plotting functions, plotBiasDistribution() and plotBiasCorrectionInference(). 0.1.0 0.0.5 3. Added a vignette on Bayesian adaptive bias correction. EvidenceSynthesis 0.4.12023-04-05 Changes 1. Added a video vignette.







OHDSI HADES releases: PheValuator 2.2.8

PheValuator 2.2.8 Reference Articles → Changelog hadesLogo

PheValuator

PheValuator is part of HADES.

Introduction

The goal of PheValuator is to produce a large cohort of subjects each with a predicted probability for a specified health outcome of interest (HOI). This is achieved by developing a diagnostic predictive model for the HOI using the PatientLevelPrediction (PLP) R package and applying the model to a large, randomly selected population. These subjects can be used to test one or more phenotype algorithms.

Process Steps

The first step in the process, developing the evaluation cohort, is shown below:

Step 1: Develop Evaluation Cohort from Diagnostic Predictive Model

Create Evaluation Cohort of 1M randomly selected subjects from

Links

Browse source code

Report a bug

Ask a question

License

Apache License 2.0

Citation

Citing PheValuator

Developers

Joel N. Swerdel Maintainer

Dev status









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OHDSI HADES releases: DatabaseConnector 6.2.1

MHADES DatabaseConnector 6.2.1 Reference Articles -Changelog DatabaseConnector 6.2.1 Contents 6.2.1 Bugfixes: 6.2.0 1. Workaround for rJava and rlang interaction causing no field, method or inner class called 6.1.0 'use_cli_format' errors to be thrown when Java throws an error. 6.0.0 5.1.0 DatabaseConnector 6.2.02023-04-13 5.0.4 5.0.3 Changes: 5.0.2 1. Can now use downloadJdbcDrivers() to download BigQuery drivers (directly from Google). 5.0.1 2. Updating Spark JDBC driver to latest version. 5.0.0 4.0.2 Bugfixes: 4.0.1 1. Not asking to delete old files when not in interactive mode and calling downloadJdbcDrivers(). 4.0.0 2. Fixing error in RStudio table preview on Postgres when database name contains uppercase characters. 3.0.0 3. Several bugfixes for Spark. 2.4.4 2.4.3 DatabaseConnector 6.1.02023-03-15 % 2.4.2







Publications Dashboard





OHDSI Publications Ehden Courses Network Studies Phenotype Library

Opportunities

Publication PubMed Publication Tracking highlights scholarship

generated using the OMOP Common Data Model. OHDSI tools, or the OHDSI network. These publications represent scientific accomplishments across areas of data standards, methodological research, open-source development, and clinical applications. We provide the resource to search and browse the catalogue of OHDSI-related publications by date, author, title, journal, and SNOMED terms. We monitor the impact of our community using summary statistics (number of publications and citations), and the growth and diversity of our community with the number of distinct authors. Searches for new papers are performed daily, and citation counts are updated



Community Dashboard Citation **OHDSI** SNOMED Terms (n) Matthew Spotnitz, Nripendra Acharva, James J Cimino. Publications Shawn Murphy, Bahram Namjou, Nancy Crimmins, Theresa Walunas, Cong Liu, David Crosslin, Barbara Benoit, Elisabeth Rosenthal, Jennifer A Pacheco, Anna Ostropolets, A metadata framework Harry Reyes Nieva, Jason S Patterson, Lauren R Richter, JAMIA open for computational Tiffany J Callahan, Ahmed Elhussein, Chao Pang, Krzysztof phenotypes. Ehden Courses Kirvluk, Jordan Nestor, Atlas Khan, Sumit Mohan, Evan Minty, Wendy Chung, Wei-Qi Wei, Karthik Natarajan, Network Studies Chunhua Weng Transforming Studies in health Documents of the Phenotype Library Raffael Lukas Korntheuer Florian Katsch, Georg 2023/05/12 technology and Austrian Nationwide Duftschmid EHR System into the informatics Opportunities OMOP CDM. Byungjin Choi, Ah Ran Oh, Jungchan Park, Jong-Hwan Lee, Perioperative adverse Kwangmo Yang, Dong Yun Lee, Sang Youl Rhee, Sang-Soo cardiac events and Korean journal of Kang, Seung Do Lee, Sun Hack Lee, Chang Won Jeong, mortality after non-Burnhee Park, Soobeen Seol, Rae Woong Park, Seunghwa cardiac surgery: a multicenter study. How to Improve Cance Patients ENrollment in Clinical Trials From rEa Emmanuelle Kempf, Morgan Vaterkowski, Damien Life Databases Using Leprovost, Nicolas Griffon, David Ouagne, Stephane Breant, JCO clinical cancer the Observational Patricia Serre, Alexandre Mouchet, Bastien Rance, Gilles Medical Outcomes informatics Chatellier, Ali Bellamine, Marie Frank, Julien Guerin, Xavier Partnership Oncology Tannier, Alain Livartowski, Martin Hilka, Christel Daniel Extension: Results of the PENELOPE Initiative in Urologic Cancers. Feasibility of Linking AMIA ... Annual Xinzhuo Jiang, Maura A Beaton, Jake Gillberg, Andrew Symposium Area Deprivation Index 2023/05/02 Williams, Karthik Natarajan proceedings AMIA Data to the OMOP Common Data Mode Symposium Hierarchy-aware Venkata Joopudi, Bharath Dandala, Ching-Huei Tsou, Adverse Reaction Symposium proceedings. AMIA Jennifer II jang Embeddings for Signal

OHD

OBSERVATIONAL HEALTH DATA SCIENCES AND INFORMATICS



Welcome to OHDSI!

The Observational Health Data Sciences and Informatics (or OHDSI, pronounced "Odyssey") program is a multi-stakeholder, interdisciplinary collaborative to bring out the value of health data through large-scale analytics. All our solutions are open-source.

OHDSI has established an international network of researchers and observational health databases with a central coordinating center housed at Columbia University.

Building A He Toge

The 2022 OHDSI Symposium focused on the theme of "Building A Healthier World Together" and it featured presentations and researchers from collaborators around the world. Please visit the symposium homepage to see the videos, slides and all other output from this three-day



2023 OHDSI Symposium Schedule



European Symposium

July 1-3 • Rotterdam, Neth.

ohdsi-europe.org



Asia-Pacific Symposium

July 13-14 • Sydney, Australia

ohdsi.org/2023apacsymposium



Global Symposium

Oct. 20-22 • East Brunswick, NJ, USA

ohdsi.org/ohdsi2023



Job Opening

Research Programmer Analyst (RPA) Remote/Hybrid

IT EDW Operations Full Time 72973BR

Job Summary

Work as a Research Programmer Analyst (RPA) on a small team to develop, operate, and maintain ETL processes, clinical data warehouses, and associated data products for health research.

The RPA's role is multi-faceted, involving domain knowledge (clinical data, research informatics), technical expertise, and communication skills. The RPA will operate, monitor, and enhance existing ETL processes and infrastructure, develop data profiles, perform quality assessments, investigate data anomalies, and create/maintain related documentation and annotated data dictionaries. The RPA will routinely communicate with researchers, clinicians, data scientists, and other stakeholders to stay aligned with needs and understand data requirements and translate them into efficient, well-documented ETL solutions.

The RPA will support multiple projects and data assets, including the PCORnet CDM (and related research projects), the UC Health Data Warehouse (UC HDW Operational OMOP), and the "All of Us" Research Program.

Responsibilities include, but are not limited to the following:

- 1. Work closely with researchers, data scientists, and other stakeholders to understand their data requirements and translate them into efficient ETL solutions.
- 2. Develop, implement, and maintain ETL processes using SSIS and t-SQL stored procedures to extract, transform, and load data from Epic EHR and other sources into common data models like PCORnet CDM and OHDSI's OMOP.
- 3. Ensure data quality and integrity throughout the ETL process by performing data mapping, transformation, and validation.
- 4. Optimize ETL processes for performance, scalability, and reliability, identifying and resolving bottlenecks as needed.
- 5. Collaborate with team members to integrate data from disparate sources and ensure seamless data flow for research purposes.
- 6. Maintain up-to-date knowledge of the healthcare domain, including clinical terminologies, workflows, data standards, and regulations.
- 7. Adhere to data security best practices and ensure compliance with privacy regulations like HIPAA.
- 8. Provide (and request) technical support and guidance to (and from) other team members as needed.
- 9. Contribute to project management, setting priorities, and meeting deadlines.

To see the salary range for this position (we recommend that you make a note of the job code and use that to look up): TCS Non-Academic Titles Search (ucop.edu)

Please note: The compensation ranges listed online for roles not covered by a bargaining unit agreement are very wide, however a job offer will typically fall in the range of 80% - 120% of the established mid-point. An offer will take into consideration the experience of the final candidate AND the current salary level of individuals working at UCSF in a similar role.

For roles covered by a bargaining unit agreement, there will be specific rules about where a new hire would be placed on the range.

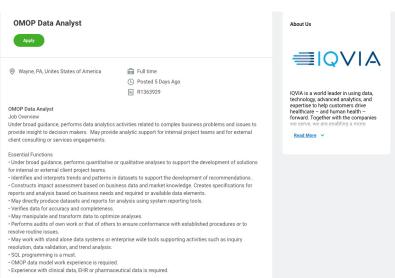
To learn more about the benefits of working at UCSF, including total compensation, please visit: https://ucnet.universityofcalifornia.edu/compensation-and-benefits/index.html







Job Openings – This Week In OHDSI page







Boehringer Ingelheim is an equal opportunity global employer who takes pride in maintaining a diverse and inclusive culture. We embrace diversity of perspectives and strive for an inclusive environment which benefits our employees, patients and communities.

Senior Associate Director, Real World Data & Analytics (Remote)-232633

Description:

The purpose of this job is to:

• Generate real world evidence (RWF) to support in line and nineline products

Centerate real world evidence (1994) to support a raise and pipeline products.

Provide statistical advice on the analysis of real world data (RWD) to various internal and external stakeholders.

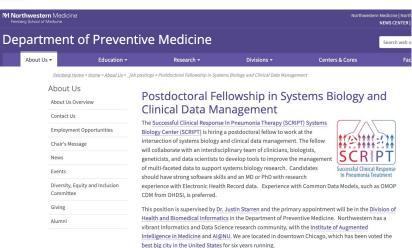
Contribute to the RWD acquisition strategy and tool evaluation.

Participate in the development and presentation of RWE trainings

As an employee of Destringer Ingeltenin, you will actively contribute to the discovery, development and delivery of our products to our patients and continents. Our global presence provides operating for all employees to collaborate international, offering visibility and opportunity to directly contribute to the companient's access. We realize that our strength and competitive advantage lie with our people. We support our employees in a number of ways to foster a healthy working environment, meaningful work, deventry and inclusion, mobility, inclusiving and work-life balance. Our competitive compensation and benefit programs and rediscipations of the production in patients and several productions.

Duties & Responsibilities

Provide expert advice in the analysis of real world data (such as medical claims, electronic health records, registries) for stakeholders in epidemiolic market access / HEOR, medical affairs, and other functional areas. These analyses may include:



Software Dev Analyst II - Res - G&C - CTSI

Job ID: REF9053H Date posted: 2/20/2023

Employment Type: Full Time

Shift: Days

Location: Boston, MA







Where Are We Going?

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







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May 16: Evidence Synthesis (SOS Week 8)



Yong Chen

Professor of Biostatistics, Epidemiology & Informatics, University of Pennsylvania



Martijn Schuemie

Research Fellow, Epidemiology Analytics, Janssen Research and Development

SOS Challenge Weekly Tutorial Schedule

Date	Topic
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