

Trick or Treat

How to use OHDSI tools to quickly generate insights from your OMOP CDM

OHDSI Community Call Oct. 26, 2021 • 11 am ET









Upcoming OHDSI Community Calls

Date	Topic
Oct. 26	Trick or Treat: How to use OHDSI tools to quickly generate insights from your OMOP CDM
Nov. 2	Collaboration Opportunities: Methods Res., Data Standards, Open-Source, Clinical App.
Nov. 9	Demos: Tools for Adoption of OHDSI Data Standards
Nov. 16	Open Network Studies
Nov. 23	History of OHDSI
Nov. 30	Collaborator Showcase Presentations







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Nov. 2: Future Collaboration Opportunity Breakouts

Open-Source



Jenna Reps



Martijn Schuemie



Clair Blacketer

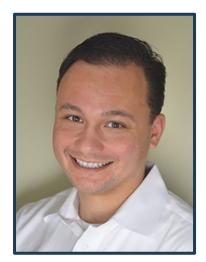


Maxim Moinat

www.ohdsi.org



Adam Black



Anthony Sena



Talita Duarte-Salles



Asieh Golozar

#JoinTheJourney

Clinical



Three Stages of The Journey

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







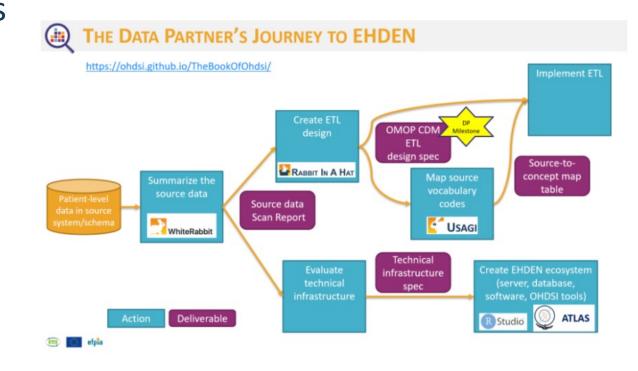
OHDSI Shoutouts!



Congratulations to the EHDEN

Consortium on welcoming 21 new SMEs to support mapping to the OMOP Common Data Model, and perform services in the ecosystem of the EHDEN federated data network.

EHDEN now has a total of 47 SMEs across 19 European nations to assist in real world evidence generation within the community.





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	
Wednesday	10 am	FHIR and OMOP - Digital Quality Measures Subgroup (ZOOM)	
Thursday	8 am	Psychiatry	
Thursday	1 pm	OMOP CDM Oncology – CDM/Vocabulary Subgroup	
Friday	10 am	Electronic Health Record	
Friday	10:30 am	Clinical Trials	
Monday	10 am	GIS-Geographic Information System	
Tuesday	9 am	OMOP CDM Oncology – Genomic Subgroup	

www.ohdsi.org/upcoming-working-group-calls





Get Access To Different Teams/WGs/Chapters

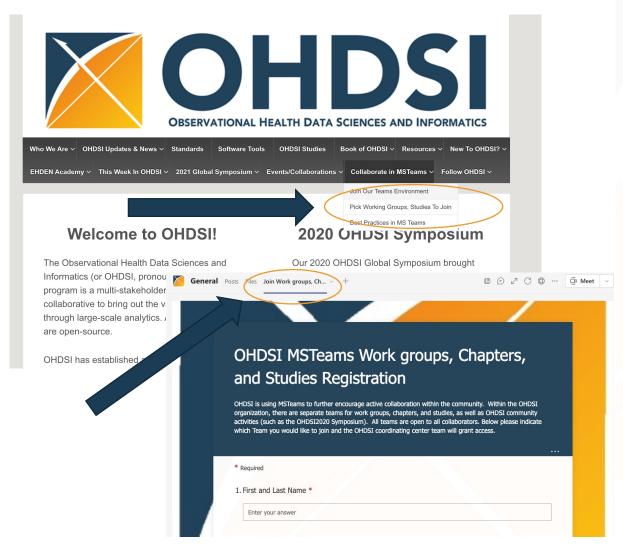


ATLAS		
Clinical Trials		
Common Data Model	Phenotype Development and Evaluation	
Data Quality Dashboard Development	Population-Level Effect Estimation / Patient-Level Prediction	
Early-stage Researchers	☐ Psychiatry	
	Registry (formerly UK Biobank)	
Education Work Group	Surgery and Perioperative Medicine	
Electronic Health Record (EHR) ETL	☐ Vaccine Safety	
Geographic Information System (GIS)	☐ Vaccine Vocabulary	
HADES Health Analytics Data-to-Evidence Suite	☐ Women of OHDSI	
Health Equity		
Latin America	6. Select the chapter(s) you want to join	
Laun America	Africa	
Medical Devices	Australia	
Natural Language Processing	China	
OHDSI APAC	☐ Europe	
OTIDSI AFAC	Japan	
OHDSI APAC Steering Committee	☐ Korea	
OHDSI Steering Committee	Singapore	
Oncology	☐ Taiwan	
Patient-Generated Health Data		
Pharmacovigiliance Evidence Investigation	7. Select the studies you want to join	
Pharmacovigiliance Evidence Investigation	HERA-Health Equity Research Assessment	





Get Access To Different Teams/WGs/Chapters



ATLAS		
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OHDSI Steering Committee	Singapore	
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2021 APAC Symposium • Nov. 18

Nov. 18 (APAC Time Zone)	Time (Korea time)	Contents	Speaker(s)
	9:00 – 9:25 am	OHDSI State of the Community	George Hripcsak/Patrick Ryan
	9:25 – 9:50 am	OHDSI APAC State of the Community	Mui Van Zandt
	9:50 – 10:00 am	Energy Break	
	10:00 – 10:25 am	EHDEN	Peter Rijnbeek
Morning	10:25 – 10:50 am	FHIR and OHDSI Collaboration	Christian Reich
	10:50 – 11:00 am	Energy Break	
	11:00 - 12:30 pm	APAC Chapter Visions for 2022	Chapter Leads
Lunch Break	12:30 – 13:00 pm		
Afternoon (in	13:00 – 14:00 pm	Workgroup Sessions (Medical Image, FHIR, CDM Tables)	
GatherTown)	14:00 – 15:00 pm	Collaboration Showcase	
	15:00 – 16:00 pm	APAC Study Sessions	

www.ohdsi.org/apac







Association Rule and Frequent Pattern Mining using the OMOP- CDM

PRESENTER: Solomon Ioanno

INTRODUCTION

To better understand the cooccurrence of data elements and their sequence, association rules analysis and frequent pattern analysis are powerful tools.

An Association Rule analysis answers the question "Given a cohort of patients, what are the most associated concepts that occur together?"

A Frequent Pattern analysis answers the question "What are the most common sequences of concepts observed in a cohort of patients"?

Potentially, they are also promising tools to improve other data mining tasks such as patient-level prediction.

We introduce here an open-source analytics framework, an R package, for performing Association Rule and Frequent Pattern mining using data in the OMOP-CDM

METHODS

- The AssociationRuleMining R package makes use of the open source SPMF Java library by Phillippe Fournier-Viger that implements a large collection of association rule and frequent pattern mining algorithms.
- Using standard HADES packages the user can connect to a database, create the cohort/s of interest and extract relevant covariates.
- Functionalities within the package allow efficient preparation of the input datasets and analysis using the algorithm of choice.

Workflow Description

Create a cohort using one of OHDSI's tool of choice

Extract covariates using the FeatureExtraction package.

- For Association Rule Mining, extracting the first occurrence of an event (diagnosis, drug subscription, etc) will suffice to perform the analysis.
 - For Frequent Pattern Mining, the order of events matters, therefore extracting temporal covariates is essential.

Choose an algorithm for the relevant analysis and set its parameters.

- A required parameter to extract highly occurring itemsets or frequent patterns is minimum support, which acts as the threshold for the minimum number of patients that should have the concept set in their medical history, e.g., (obesity, diabetes)
 - Algorithms that extract either association rules or frequent patterns require also to specify minimum confidence, which is the threshold for determining how often the left side of the rule occurs together with the right side, e.g., (obesity, diabetes) -> (heart failure)

Prepare input datasets and run the analysis.

- The package provides specific functionalities to prepare the input datasets to the necessary format and execute the algorithm.
- Based on the size of the cohort, an iterative procedure to select the optimal value for minimum support and minimum confidence may be applied.

Viewing and exploring the results through interactive plots.





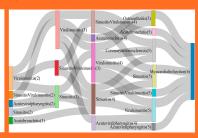


Figure 2: Frequent patterns indicating the chronological ordering of events.

RESULTS

- Depending on the size of the cohort to be analyzed, the number of concepts included, and the values of predefined parameters of minimum support and minimum confidence, a huge number of rules or patterns can be revealed.
- Currently results are presented in lists for further processing and use such as, covariates in prediction

 problems.

 The processing are properties.

 The problems are problems.

 The problems are problems.
- Interactive visualizations are also implemented to explore the results graphically.

How can this tool be used?

- We are exploring the possibilities of using these methods for characterization purposes.
- Another research direction is the added predictive value, especially of frequent patterns, in clinical prediction problems.

Clinical relevance

- Characterising frequent patterns and associations in health data can help to identify different types of patients that may need different types of treatment.
- Frequent pattern analyses could help to generate new hypothesis for the pathogenesis of diseases.

The European Health Data & Evidence Network has received funding from the Innovative Medicines Initiative 2 Joint Undertaking (UI) under grant agreement No 806968. The JU receives support from the European Union's Horizon 2020 research and innovation programme and EFPIA.

Solomon Ioannou, Egill Fridgeirsson, Jan Kors, Peter Rijnbeek



(a) EHDEN

#JoinTheJourney



MONDAY

Association Rule and Frequent Pattern Mining using the OMOP CDM Authors: Solomon Ioannou, Egill Fridgeirsson, Jan Kors, Peter Rijnbeek



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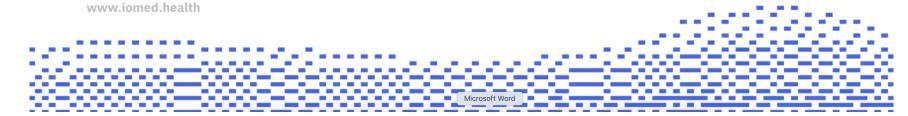
Extending the OMOP CDM to store the output of NLP pipelines

Mónica Arrúe, Sandra Pulido, Alvaro Abella, Gabriel Maeztu, Alberto Labarga

2021 OHDSI Collaborator Showcase



Accelerating Clinical Research



TUESDAY

Extending the OMOP CDM to store the output of natural language processing pipelines Authors: Monica Arrue (presenter), Sandra Pulido, Alvaro Abella, Gabriel Maeztu, **Alberto Labarga**



Title: CQL Scripting
From Atlas Cohort
DefinitionsMichael Riley

INTRO:

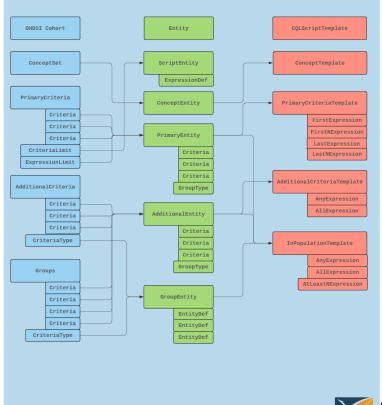
 Who cares? CQL is a complete language for defining logical inferences from medical datasets. Atlas Cohort Definitions are a quick structure-based definition to quickly and easily define a population set. By translating Atlas Cohort Definitions to CQL, we can use the various measure libraries available in CQL, as well as expand cohort definitions into a form that invites comparison to other measures.

METHODS

We captured the cohort definitions from atlas-ohdsi as a JSON definition. From this definition we parsed to a set of interal entities describing the concepts, primary criteria, and additional criteria used. We then use a set of cql formatting templates to convert the criteria into CQL definitions and craft a final InPopulation definition given the criteria groupings from the original cohort.

RESULTS

Translation was tested on 11 different cohort definitions with a variety of criteria sets. Preliminary results comparing the accuracy of the CQL definition vs the original cohort are pending.



- ConceptSet With SystemURI Definitions were automatically expanded into ConceptEntities using VSAC Terminology Service
- ExpressionLimit(First/La st/FirstN/LastN) Used as a global definition applied to primaryEntity
- GroupEntity Defines
 Grouping of
 AdditionalCriteria while
 AdditionalEntity
 collects temporal and
 value based filtering on
 the entity
- InPopulation Subsumes final definition from Primary, Additional, and Group Entities
- Patient CQL Context
 used, Population CQL
 Context feature in
 development

Michael Riley (Michael.Riley@gtri.gatech.ed u)



WEDNESDAY

Authors: Michael Riley, Jon Duke





Best of Intent, Worst of Both Worlds: Why Sequentially Combining Epidemiological Methods Does Not Improve Signal Detection in Vaccine Surveillance

PRESENTER: Faaizah Arshad

INTRO

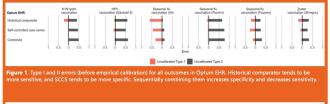
- There is a clinical intuition that combining sensitive and specific methods will improve vaccine safety signal detection.
- Little is known on the comparative performance of methods with real-world data.

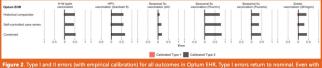
METHODS

- We evaluated six vaccine exposures: H1N1pdm, seasonal flu (Fluvinin), seasonal flu (Fluzone), seasonal flu (All), zoster (Shingrix), HPV (Gardasil 9) across four databases (CCAE, IBM MDCR, IBM MDCD, Optum EHR).
- All data partners used the Observational Medical Outcomes Partnership (OMOP) common data model (CDM).
- We generated a set of negative control and imputed positive control outcome:
- We defined a time-at-risk of 1-28 days after vaccination.
- 5. We used R programming to compute and compare the one-sided p values and type I and II errors (with and without empirical calibration) of a highly sensitive method (historical comparator), a highly specific method (self-controlled case series), and a method that sequentially combines the two.

RESULTS

 Using a highly sensitive method followed by a highly specific method did not compensate for the individual flaws of each method alone. Applying a sensitive method followed by a specific method does not improve signal detection for adverse events under vaccine surveillance.





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Figure 3. Type I and II errors without empirical calibration across databases. Historical comparator is not always more sensitive than SCCS, and SCCS is not always more specific than historical comparator.



Figure 4. Type I and II errors for all outcomes with empirical calibration across databases. Type I error returns to nominal.

DISCUSSION

- The use of real-world data mapped to the CDM allows for replicability and transparency.
- One limitation was the lack of COVID-19

CONCLUSION

 Our findings oppose clinical advice to use a serial method in signal detection.

≜ AUTHORS

Faaizah Arshad¹,

Martijn J. Schuemie^{1,3}, Marc A. Suchard^{1,2} on behalf of the EUMAEUS task force





THURSDAY

Best of intent, worst of both worlds: why sequentially combining epidemiological methods does not improve signal detection in vaccine surveillance

Authors: Faaizah Arshad, Lana YH Lai, George Hripcsak, Daniel Prieto-Alhambra, Martijn J. Schuemie, Marc A. Suchard

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Predicting risk of recurrence after surgery for colorectal







INTRO Risk of recurrence after colorectal cancer surgery is the main driver of long-term morbidity and mortality

Following curative intended surgery, up to 15-20% of patients will experience recurrence. Knowing which patients will have a low risk of recurrence could decide which type of surgery a patient should undergo, where an older frail patient with low risk of recurrence could be offered a small resection. instead of the standard approach of removing large portions of the bowel. However, presently no tools exist to predict which

patients are at risk of recurrence at the preoperative

A CDM was built from the validated Danish Colorectal Cancer Group (DCCG) Database, containing 99% of all colorectal cancer surgeries in Denmark since 2001.

Recurrence was estimated in the DCCG database by applying the validated algorithm by Lash et al. ATLAS and OHDSI prediction-level package was use to create natient-level prediction models using preoperatively available variables to predict risk of recurrence. We applied the LASSO logistic regression model using default settings and a three-foldcross



RESULTS

- From 2001-2019, 25,290 patients underwer surgery with curative intent for colorectal cancer
- 5,717 experienced a recurrence event The PLP was able to predict patients at elevated risk using only preoperatively known variables with risk of recurrence (AUROC: 0.65 (0.63 0.66), PRROC-0.34], with good calibration and a Brief

Preoperative variables can decently predict the risk of

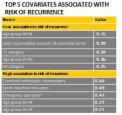
recurrence after surgery for colorectal cancer.

Increased risk can be taken into consideration for clinical decision-making

to identify patients that might benefit from:



smaller resections



CLINICAL USE OF PREDICTION MODELS

In the clinical setting, the absolute risk of recurrence is valuable, why we note that our model had a good calibration despite subpar discrimination.

A patient's individual prediction can be used in the multidisciplinary team (MDT) meeting prior to surgery as well as with the patient in a preoperative discussion on treatment planning.

- recurrence, the patient could be offered extensive surgery with an intensive surveilla program and adjuvant chemotherapy.
- of recurrence. the decision could be to contain the disease for now with a local procedure considering the possible complications of a large

calibration, but is not ready for clinical usage. even though that DCCG contains some genor information, we know that a deep phenotypical understanding of the tumor microenvironment is Incorporating this in our CDM is in our pipeline



FRIDAY

Predicting risk of recurrence after surgery for colorectal cancer

Authors: Mikail Gögenur, Viviane Lin, Adamantia Tsouchnika, Eldar Allakhverdiiev, Andreas Weinberger Rosen, Karoline Bendix Bräuner, Julie Sparholt Walbech, Ismail Gögenur





Where Are We Going?

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

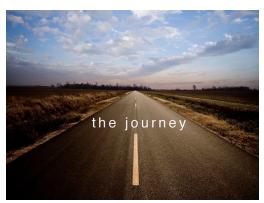






Three Stages of The Journey

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







Oct. 26 Community Call: Trick or Treat

On Tuesday, Oct. 26 (11 am ET), Patrick Ryan will lead a Halloween-themed interactive demonstration of how you can use the OHDSI tools to quickly generate insights from your OMOP CDM.

We hope you'll learn a TRICK or two, and that it will be a TREAT.

