Welcome To Phenotype Phebruary II

OHDSI Community Call

Jan. 31, 2023 • 11 am ET

Upcoming OHDSI Community Calls

Date	Topic
Feb. 7	Phenotype Phebruary Weekly Update + Workgroup Plans for 2023
Feb. 14	Phenotype Phebruary Weekly Update + Workgroup Plans for 2023
Feb. 21	Phenotype Phebruary Weekly Update + Workgroup Plans for 2023
Feb. 28	Phenotype Phebruary Weekly Update + Workgroup Plans for 2023

Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?

OHDSI Shoutouts!

Congratulations to the team of **Ines Reinecke, Joscha Siebel, Saskia Fuhrmann, Andreas Fischer, Martin Sedlmayr, Jens Weidner, and Franziska Bathelt** on the publication of **Assessment and Improvement of Drug Data Structuredness From Electronic Health Records: Algorithm Development and Validation** in JMIR Medical Informatics.

Original Paper

Assessment and Improvement of Drug Data Structuredness From Electronic Health Records: Algorithm Development and Validation

Ines Reinecke[1], BA, MA; Joscha Siebel[1]; Saskia Fuhrmann[2,3], Dr Rer Nat; Andreas Fischer[3], MA; Martin Sedlmayr[2], Prof Dr, Dr Rer Nat; Jens Weidner[1], MA; Franziska Bathelt[1], Dr Rer Nat

[1]Institute for Medical Informatics and Biometry, Carl Gustav Carus Faculty of Medicine, Technische Universität Dresden, Dresden, Germany
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[3]Hospital Pharmacy, University Hospital Carl Gustav Carus, Dresden, Germany

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Abstract

Background: Digitization offers a multitude of opportunities to gain insights into current diagnostics and therapies from retrospective data. In this context, real-world data and their accessibility are of increasing importance to support unbiased and reliable research on big data. However, routinely collected data are not readily usable for research owing to the unstructured nature of health care systems and a lack of interoperability between these systems. This challenge is evident in drug data.

Objective: This study aimed to present an approach that identifies and increases the structuredness of drug data while ensuring standardization according to Anatomical Therapeutic Chemical (ATC) classification.

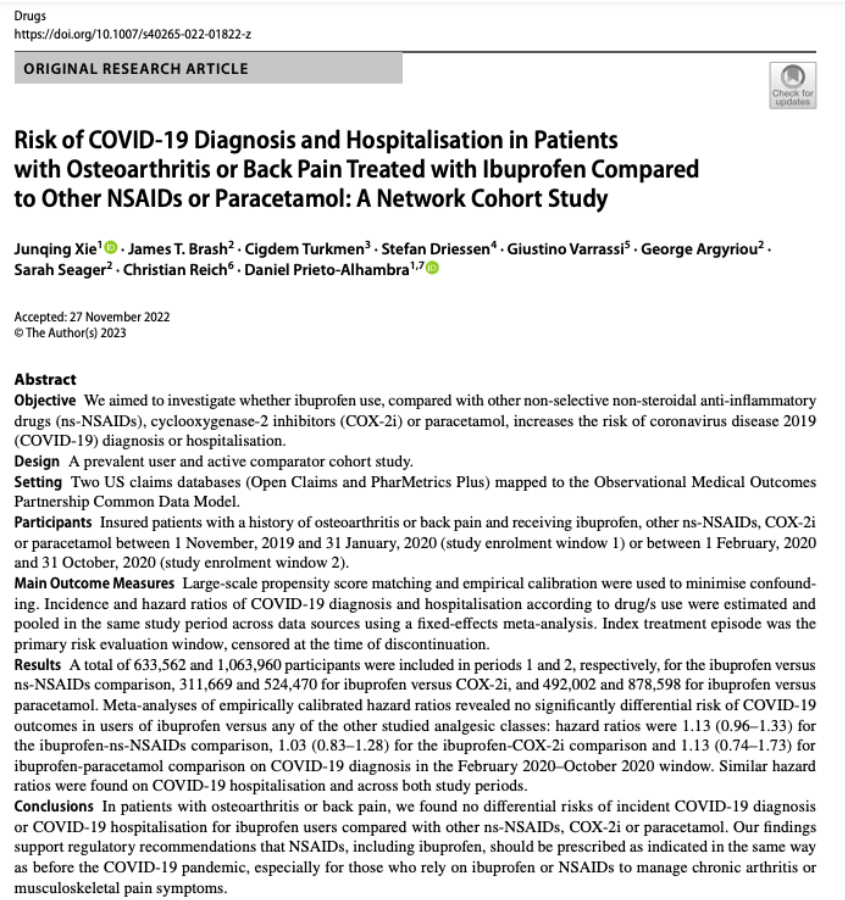
Methods: Our approach was based on available drug prescriptions and a drug catalog and consisted of 4 steps. First, we performed an initial analysis of the structuredness of local drug data to define a point of comparison for the effectiveness of the overall approach. Second, we applied 3 algorithms to unstructured data that translated text into ATC codes based on string comparisons in terms of ingredients and product names and performed similarity comparisons based on Levenshtein distance. Third, we validated the results of the 3 algorithms with expert knowledge based on the 1000 most frequently used prescription texts. Fourth, we performed a final validation to determine the increased degree of structuredness.

Results: Initially, 47.73% (n=843,980) of 1,768,153 drug prescriptions were classified as structured. With the application of the 3 algorithms, we were able to increase the degree of structuredness to 85.18% (n=1,506,059) based on the 1000 most frequent medication prescriptions. In this regard, the combination of algorithms 1, 2, and 3 resulted in a correctness level of 100% (with 57,264 ATC codes identified), algorithms 1 and 3 resulted in 99.6% (with 152,404 codes identified), and algorithms 1 and 2 resulted in 95.9% (with 39,472 codes identified).

Conclusions: As shown in the first analysis steps of our approach, the availability of a product catalog to select during the documentation process is not sufficient to generate structured data. Our 4-step approach reduces the problems and reliably increases the structuredness automatically. Similarity matching shows promising results, particularly for entries with no connection to a product catalog. However, further enhancement of the correctness of such a similarity matching algorithm needs to be investigated in future work.

OHDSI Shoutouts!

Congratulations to the team of **Junqing Xie, James T. Brash, Cigdem Turkmen, Stefan Driessen, Giustino Varrassi, George Argyriou, Sarah Seager, Christian Reich and Daniel Prieto-Alhambra** on the publication of **Risk of COVID-19 Diagnosis and Hospitalisation in Patients with Osteoarthritis or Back Pain Treated with Ibuprofen Compared to Other NSAIDs or Paracetamol: A Network Cohort Study** in Drugs.



Drugs
https://doi.org/10.1007/s40265-022-01822-z

ORIGINAL RESEARCH ARTICLE

Check for updates

Risk of COVID-19 Diagnosis and Hospitalisation in Patients with Osteoarthritis or Back Pain Treated with Ibuprofen Compared to Other NSAIDs or Paracetamol: A Network Cohort Study

Junqing Xie[1] · James T. Brash[2] · Cigdem Turkmen[3] · Stefan Driessen[4] · Giustino Varrassi[5] · George Argyriou[2] · Sarah Seager[2] · Christian Reich[6] · Daniel Prieto-Alhambra[1,7]

Accepted: 27 November 2022

Abstract

Objective We aimed to investigate whether ibuprofen use, compared with other non-selective non-steroidal anti-inflammatory drugs (ns-NSAIDs), cyclooxygenase-2 inhibitors (COX-2i) or paracetamol, increases the risk of coronavirus disease 2019 (COVID-19) diagnosis or hospitalisation.

Design A prevalent user and active comparator cohort study.

Setting Two US claims databases (Open Claims and PharMetrics Plus) mapped to the Observational Medical Outcomes Partnership Common Data Model.

Participants Insured patients with a history of osteoarthritis or back pain and receiving ibuprofen, other ns-NSAIDs, COX-2i or paracetamol between 1 November, 2019 and 31 January, 2020 (study enrolment window 1) or between 1 February, 2020 and 31 October, 2020 (study enrolment window 2).

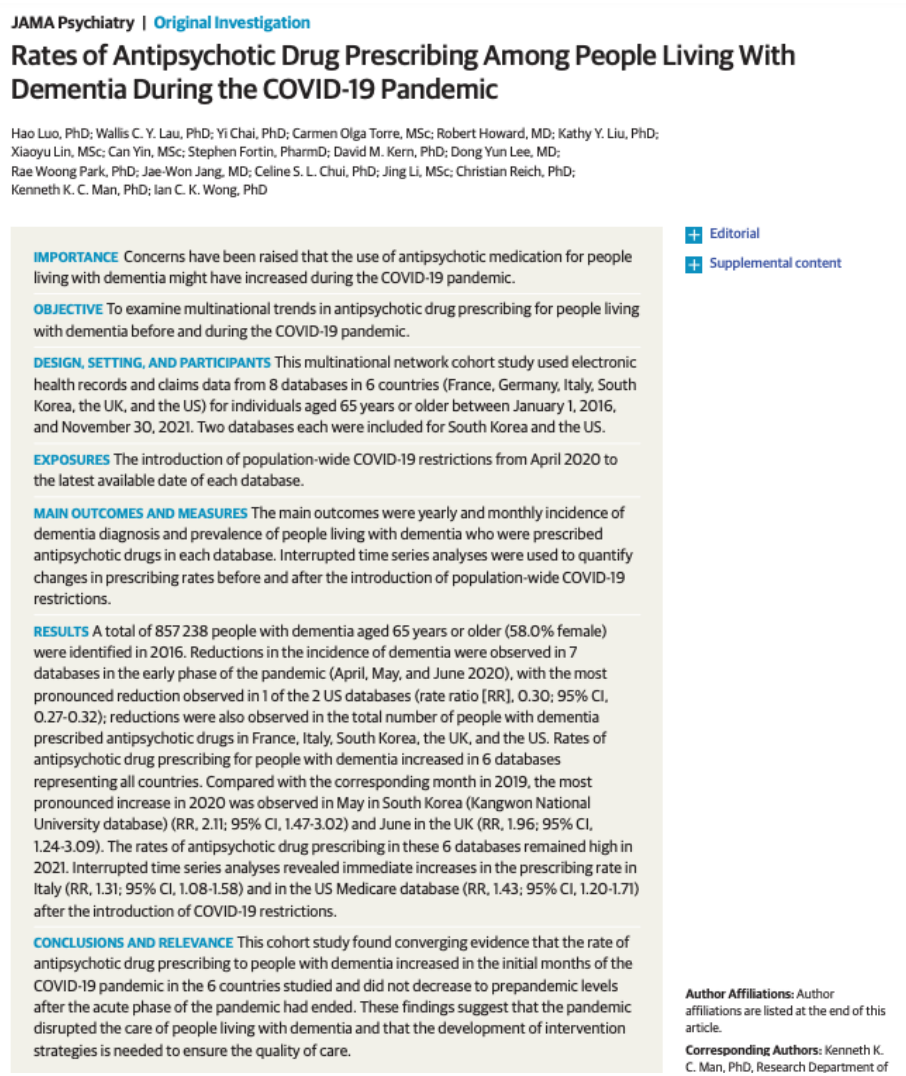
Main Outcome Measures Large-scale propensity score matching and empirical calibration were used to minimise confounding. Incidence and hazard ratios of COVID-19 diagnosis and hospitalisation according to drug/s use were estimated and pooled in the same study period across data sources using a fixed-effects meta-analysis. Index treatment episode was the primary risk evaluation window, censored at the time of discontinuation.

Results A total of 633,562 and 1,063,960 participants were included in periods 1 and 2, respectively, for the ibuprofen versus ns-NSAIDs comparison, 311,669 and 524,470 for ibuprofen versus COX-2i, and 492,002 and 878,598 for ibuprofen versus paracetamol. Meta-analyses of empirically calibrated hazard ratios revealed no significantly differential risk of COVID-19 outcomes in users of ibuprofen versus any of the other studied analgesic classes: hazard ratios were 1.13 (0.96–1.33) for the ibuprofen-ns-NSAIDs comparison, 1.03 (0.83–1.28) for the ibuprofen-COX-2i comparison and 1.13 (0.74–1.73) for ibuprofen-paracetamol comparison on COVID-19 diagnosis in the February 2020–October 2020 window. Similar hazard ratios were found on COVID-19 hospitalisation and across both study periods.

Conclusions In patients with osteoarthritis or back pain, we found no differential risks of incident COVID-19 diagnosis or COVID-19 hospitalisation for ibuprofen users compared with other ns-NSAIDs, COX-2i or paracetamol. Our findings support regulatory recommendations that NSAIDs, including ibuprofen, should be prescribed as indicated in the same way as before the COVID-19 pandemic, especially for those who rely on ibuprofen or NSAIDs to manage chronic arthritis or musculoskeletal pain symptoms.

OHDSI Shoutouts!

Congratulations to the team of **Hao Luo, Wallis C. Y. Lau, Yi Chai, Carmen Olga Torre, Robert Howard, Kathy Y. Liu, Xiaoyu Lin, Can Yin, Stephen Fortin, David M. Kern, Dong Yun Lee, Rae Woong Park, Jae-Won Jang, Celine S. L. Chui, Jing Li, Christian Reich, Kenneth K. C. Man, and Ian C. K. Wong** on the publication of **Rates of Antipsychotic Drug Prescribing Among People Living With Dementia During the COVID-19 Pandemic** in JAMA Psychiatry.



JAMA Psychiatry | Original Investigation

Rates of Antipsychotic Drug Prescribing Among People Living With Dementia During the COVID-19 Pandemic

Hao Luo, PhD; Wallis C. Y. Lau, PhD; Yi Chai, PhD; Carmen Olga Torre, MSc; Robert Howard, MD; Kathy Y. Liu, PhD; Xiaoyu Lin, MSc; Can Yin, MSc; Stephen Fortin, PharmD; David M. Kern, PhD; Dong Yun Lee, MD; Rae Woong Park, PhD; Jae-Won Jang, MD; Celine S. L. Chui, PhD; Jing Li, MSc; Christian Reich, PhD; Kenneth K. C. Man, PhD; Ian C. K. Wong, PhD

IMPORTANCE Concerns have been raised that the use of antipsychotic medication for people living with dementia might have increased during the COVID-19 pandemic.

OBJECTIVE To examine multinational trends in antipsychotic drug prescribing for people living with dementia before and during the COVID-19 pandemic.

DESIGN, SETTING, AND PARTICIPANTS This multinational network cohort study used electronic health records and claims data from 8 databases in 6 countries (France, Germany, Italy, South Korea, the UK, and the US) for individuals aged 65 years or older between January 1, 2016, and November 30, 2021. Two databases each were included for South Korea and the US.

EXPOSURES The introduction of population-wide COVID-19 restrictions from April 2020 to the latest available date of each database.

MAIN OUTCOMES AND MEASURES The main outcomes were yearly and monthly incidence of dementia diagnosis and prevalence of people living with dementia who were prescribed antipsychotic drugs in each database. Interrupted time series analyses were used to quantify changes in prescribing rates before and after the introduction of population-wide COVID-19 restrictions.

RESULTS A total of 857 238 people with dementia aged 65 years or older (58.0% female) were identified in 2016. Reductions in the incidence of dementia were observed in 7 databases in the early phase of the pandemic (April, May, and June 2020), with the most pronounced reduction observed in 1 of the 2 US databases (rate ratio [RR], 0.30; 95% CI, 0.27-0.32); reductions were also observed in the total number of people with dementia prescribed antipsychotic drugs in France, Italy, South Korea, the UK, and the US. Rates of antipsychotic drug prescribing for people with dementia increased in 6 databases representing all countries. Compared with the corresponding month in 2019, the most pronounced increase in 2020 was observed in May in South Korea (Kangwon National University database) (RR, 2.11; 95% CI, 1.47-3.02) and June in the UK (RR, 1.96; 95% CI, 1.24-3.09). The rates of antipsychotic drug prescribing in these 6 databases remained high in 2021. Interrupted time series analyses revealed immediate increases in the prescribing rate in Italy (RR, 1.31; 95% CI, 1.08-1.58) and in the US Medicare database (RR, 1.43; 95% CI, 1.20-1.71) after the introduction of COVID-19 restrictions.

CONCLUSIONS AND RELEVANCE This cohort study found converging evidence that the rate of antipsychotic drug prescribing to people with dementia increased in the initial months of the COVID-19 pandemic in the 6 countries studied and did not decrease to prepandemic levels after the acute phase of the pandemic had ended. These findings suggest that the pandemic disrupted the care of people living with dementia and that the development of intervention strategies is needed to ensure the quality of care.

Editorial

Supplemental content

Author Affiliations: Author affiliations are listed at the end of this article.

Corresponding Authors: Kenneth K. C. Man, PhD, Research Department of

OHDSI Shoutouts!

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

Have a study published? Please send to sachson@ohdsi.org so we can share 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	3 pm	OMOP CDM Oncology Outreach/Research Subgroup
Wednesday	2 am	Population-Level Estimation (Eastern Hemisphere)
Wednesday	8 am	Psychiatry
Wednesday	11 am	Open-Source Community
Wednesday	12 pm	Health Equity
Thursday	12 pm	Population-Level Estimation (Western Hemisphere)
Thursday	1 pm	OMOP CDM Oncology Vocabulary/Development Subgroup
Thursday	7 pm	Dentistry
Friday	9 am	GIS – Geographic Information System Development
Friday	11 am	Clinical Trials
Monday	9 am	Vaccine Vocabulary
Monday	10 am	Africa Chapter

ohdsi.org/workgroups

OHDSI HADES releases: SqlRender 1.12.0

SqlRender 1.12.0 | Reference | Articles | SqlDeveloper | Changelog | HADES

SqlRender

R-CMD-check passing | codecov 81% | CRAN_Status_Badge | downloads 3119/month

SqlRender is part of HADES.

Introduction

This is an R package for rendering parameterized SQL, and translating it to different SQL dialects. SqlRender can also be used as a stand-alone Java library and a command-line executable.

Features

- Supports a simple markup syntax for making SQL parameterized, and renders parameterized SQL (containing the markup syntax) to executable SQL
- The syntax supports defining default parameter values
- The syntax supports if-then-else structures
- Has functions for translating SQL from one dialect (Microsoft SQL Server) to other dialects (Oracle, PostgreSQL, Amazon RedShift, Impala, IBM Netezza, Google BigQuery, Microsoft PDW, Snowflake, Azure Synapse, Apache Spark and SQLite)
- Can be used as R package, Java library, or as stand-alone executable through a command-line interface

Links

View on CRAN

Browse source code

Report a bug

Ask a question

License

Apache License 2.0

Citation

Citing SqlRender

Developers

Martijn Schuemie
Author, maintainer

Marc Suchard
Author

OHDSI HADES releases: DatabaseConnector 6.0.0

DatabaseConnector 6.0.0 | Reference | Articles | Changelog | HADES

DatabaseConnector

R-CMD-check passing | codecov 58% | CRAN 6.0.0 | downloads 2158/month

DatabaseConnector is part of HADES.

Introduction

This R package provides function for connecting to various DBMSs. Together with the `SqlRender` package, the main goal of `DatabaseConnector` is to provide a uniform interface across database platforms: the same code should run and produce equivalent results, regardless of the database back end.

Features

- Create connections to the various database platforms:
  - MicrosoftSQL Server
  - Oracle
  - PostgresSql

Links

View on CRAN

Browse source code

Report a bug

Ask a question

License

Apache License

Citation

Citing DatabaseCon

Developers

Martijn Schuemie
Author, maintainer

Marc Suchard
Author

More about authors

OHDSI HADES releases: DatabaseConnector 6.0.0

CirceR 1.0.0 | Reference | Changelog | HADES

CirceR

CirceR is part of HADES.

Introduction

A R-wrapper for Circe, a library for creating queries for the OMOP Common Data Model. These queries are used in cohort definitions (CohortExpression) as well as custom features (CriteriaFeature). This package provides convenient wrappers for Circe functions, and includes the necessary Java dependencies.

Features

- Convert a JSON cohort expression into a markdown print-friendly presentation.
- Convert a JSON cohort expression into SQL.

Examples

Links

Browse source code at
https://github.com/OHDSI/CirceR/

Report a bug at
https://github.com/OHDSI/CirceR/issues

Ask a question at
http://forums.ohdsi.org

License

Apache License 2.0

Developers

Chris Knoll
Author, maintainer

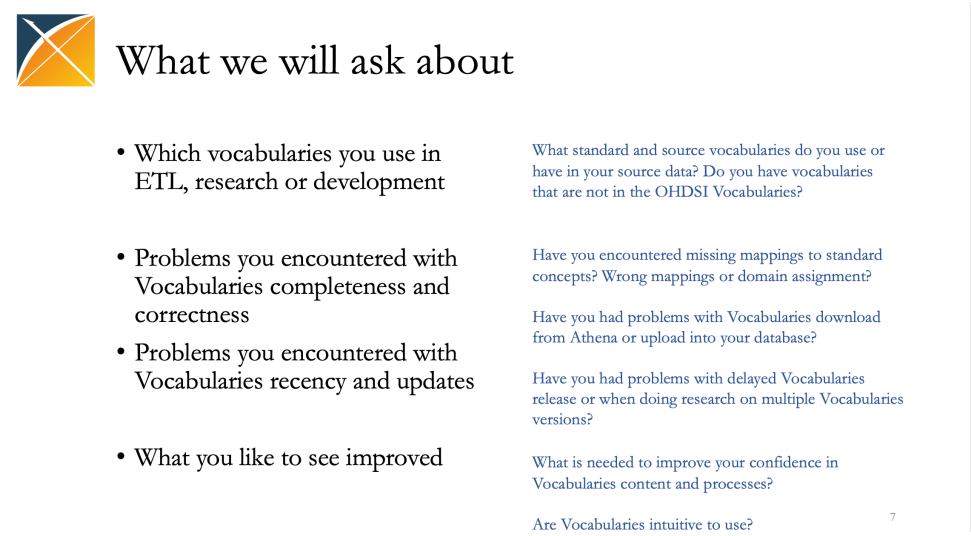
Martijn Schuemie
Author

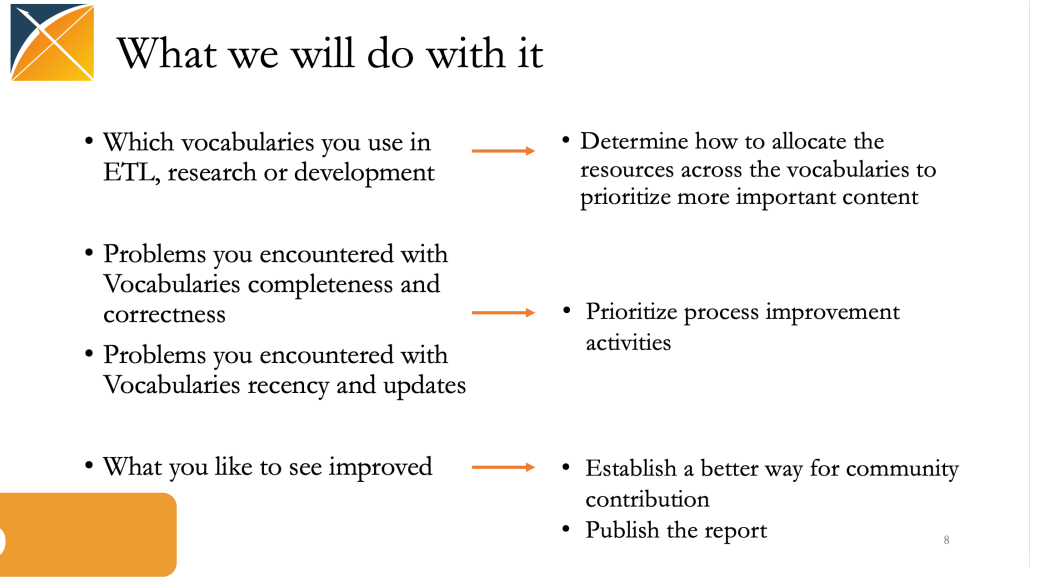
Dev status

Vocabulary Landscape Assessment

Anna Ostropolets introduced a vocabulary landscape assessment survey to directly inform which vocabularies and activities the vocabulary team prioritizes in 2023.

The deadline is Feb. 23.





bit.ly/3iTnyco

Save Our Sisyphus Challenge

Save Our Sisyphus Challenge

The task of taking a research study from idea through design through execution through publication can seem a daunting challenge, much like rolling a boulder up a hill. That task is all the more challenging when researchers try to go it alone, as each step requires a distinct set of skills. Observational study design requires epidemiologic understanding and statistical methodological expertise. Implementing a study design requires statistical programming ability. Interpreting and reporting results requires domain knowledge of the clinical problem.

But when you are part of the OHDSI community, you never have to go it alone. And as a team effort, what seems an arduous task can become an efficient and effective process.

We are seeking important research questions that you want to contribute and participate in to take from idea to publication. The OHDSI community will provide support through every step of the process, working with you to design an appropriate protocol, implement a network analysis package, execute across OHDSI data partners, and prepare a manuscript for publication. Our goal is to collaboratively complete this network study over the course of 8 weeks across April and May, using the open-source tools and process that OHDSI has

https://forms.gle/DySfETJPtmwgquKv9

Save the Date! April 21: DevCon

OHDSI DevCon 2022 Welcomes & Mentors New Contributors To Our Open-Source Environment

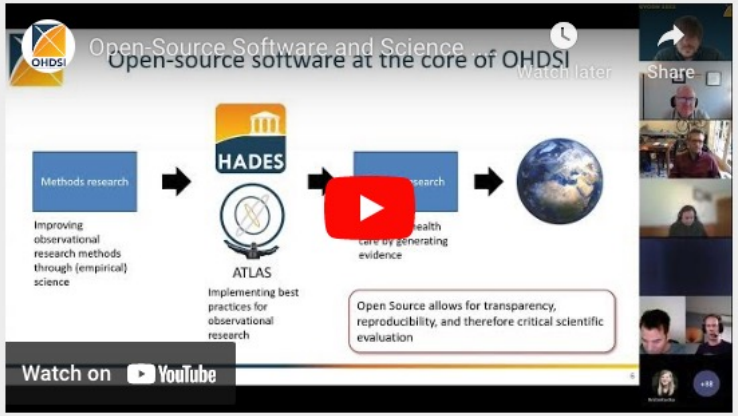
Watch All Eight Workshops, Talks & The Panel From DevCon Below

The Open-Source Community hosted the first Dev Con on Friday, April 22 as a way of accepting and mentoring new contributors to our environment. Organized by **Paul Nagy** and **Adam Black**, the event included eight workshops, talks and a panel discussion to both welcome and engage both current and future developers within OHDSI.

All videos from this session have or will be uploaded to this page. A big announcement from DevCon was the formation of the Khieron Contributor Cohort, which will help onboard and mentor open-source developers in the community. If you are interested in joining the effort, please fill out the application.

To learn more about the Khieron Contributor Cohort, please check out the State of the Open Source Community presentation below.

OHDSI DevCon Keynote

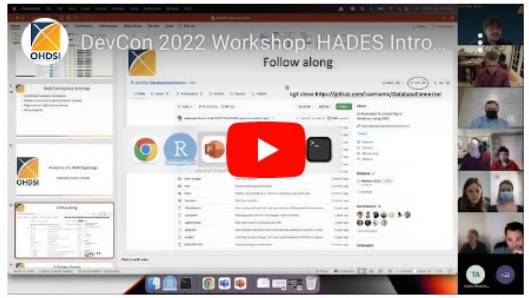


Martijn Schuemie provided the keynote address during DevCon 2022, entitled "Open-Source Software and Science … Obviously." His slides are available here.

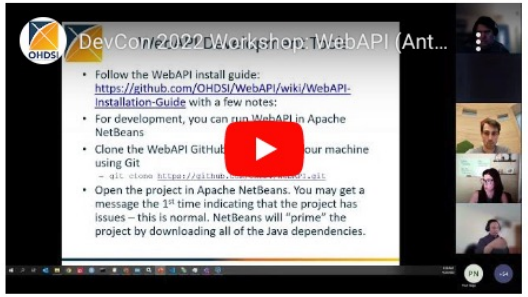
Workshops

ATLAS
(Anthony Sena)

HADES Introduction
(Adam Black)



WebAPI
(Anthony Sena)



Cohort Diagnostics
(James Gilbert)

White Rabbit
(Maxim Moinat)

Patient-Level Prediction
(Jenna Reps)

Teams invite will go out at a later date.

Save the Date!
October 20-22, OHDSI Global Symposium

Location and more details coming soon

Next CBER Best Seminar

The CBER BEST Seminar Series returns Wed., Feb. 8, at 11 am ET, as 2022 Titan Award recipient **Fan Bu** will provide a presentation on Bayesian Safety Surveillance with Adaptive Bias Correction.

Speaker: Dr. Fan Bu (UCLA)

Description: In this presentation, we will discuss a collaborative project with the FDA CBER BEST Initiative to improve on post-market vaccine safety surveillance procedures through Bayesian sequential analysis. Post-market surveillance on approved vaccine products is essential for addressing safety concerns. The goal is to detect rare or high-risk adverse events that often go undetected in clinical trials due to limited sample sizes. Collaborating with FDA CBER, we have developed a Bayesian alternative surveillance procedure that tackles these challenges in sequential analysis of observational data. The standard statistical approach for surveillance is Maximum Sequential Probability Ratio Test (MaxSPRT). Through comprehensive empirical evaluations on large-scale observational healthcare databases, we show that, compared to MaxSPRT, our Bayesian method offers more flexibility on the surveillance schedule, more transparency and interpretability in decision-making, and better error control through statistical correction of bias in observational data.

Job Opening

Job Details

Database Programmer

Nuffield Department of Orthopaedics, Rheumatology and Musculoskeletal Sciences, Botnar Research Centre, Windmill Road, Oxford, OX3 7LD

We are seeking to appoint a highly qualified and dedicated Database Programmer to join the Health Data Sciences research group led by Professor Daniel Prieto-Alhambra at the Botnar Research Centre, Nuffield Department of Orthopaedics, Rheumatology and Musculoskeletal Sciences (NDORMS), Oxford.

You will join an outstanding, multi-disciplinary and friendly Group of motivated and cutting-edge researchers and to contribute to clinical research by providing technical knowledge, software engineering expertise and data insight.

As a Database Programmer you will Develop new database applications for big clinical data to meet project requirements and deadlines, provide software feedback and carry out software improvement, extension, integration and further development on existing code. You will contribute to the harmonisation, curation, and processing of large clinical datasets and develop code to validate, test, document and maintain database applications. You will also represent the project, team, and the University in collaboration meetings, conferences and at external meetings.

You will have a Degree in computer science, software engineering, health informatics or an equivalent combination of training and professional experience. Proven understanding and experience in one or more RDBMSs and SQL dialects (e.g. PostgreSQL), excellent skills in at least one high level programming language (e.g. Python, C#, C++) and excellent analytical and problem-solving skills with great attention to detail are essential. Experience in common data models (CDMs) and in the extract, transform, and load (ETL) process, knowledge of R and/or RStudio and working experience in a research environment are desirable.

This is a full-time fixed-term appointment for 2 years.

The closing date for this position is 12 noon on Monday 27 February 2023. You will be required to upload a CV and supporting statement as part of your online application.

Contact Person : HR Team, NDRMS
Contact Phone :
Vacancy ID : 163066
Closing Date & Time : 27-Feb-2023 12:00

ICPE 2023 Abstract Deadline: Feb. 13

pharmacoepi.org/meetings/annual-conference/

#OHDSISocialShowcase This Week

Constructing a vaccine vocabulary hierarchy using formal concept analysis

PRESENTER: **Adam Black**

INTRO:
Vaccine concepts in the OMOP CDM Vocabulary lack a comprehensive and consistent hierarchy. A manually curated hierarchy is difficult to maintain and scale up with proper quality control considering the large number concepts in existing vaccine vocabularies. An automated approach is needed to facilitate the creation of a high-quality and practically useful vocabulary hierarchy.

METHODS

1. "Decompose" each source code into its attributes (e.g. indication, mechanism of action). (This step requires manual work from vaccine experts.)

Table 1: Example vaccine source code "decomposition"

concept_id	concept_name	...	indication 1	indication 2	indication 3	mechanism of action 1
40213291	diphtheria, tetanus toxoids and pertussis vaccine	CVX	diphtheria	tetanus	pertussis	diphtheria toxoid
40213190	bivalent poliovirus vaccine, live, oral	CVX	poliovirus			poliovirus live
40213183	measles, mumps and rubella virus vaccine	CVX	measles	rubella	mumps	
40213169	measles and rubella virus vaccine	CVX	measles	rubella		
40213170	measles virus vaccine	CVX	measles			

2. Convert decomposition to a "formal context"

Table 2: Example vaccine formal context

id	D_measles	D_mumps	D_rubella	D_poliovirus	M_poliovirus_live
1	X				
2	X	X	X		
3	X		X		
4		X			
5				X	X
6				X	
7			X		

3. Run Formal Concept Analysis Algorithm to create hierarchical relationships and "Maps to" table

RESULTS

Automated Vaccine Vocabulary Construction using Formal Concept Analysis

Link to code repository and full results

Formal Concept Analysis

FCA is a rigorous method for building ontologies from a set of items and their attributes. In this work we demonstrate the utility of the algorithm applied to OMOP vaccine vocabularies.

Comparison with manual hierarchy

The hierarchy produced by FCA is guaranteed to be a lattice: every pair of nodes in the resulting graph will have a unique least upper bound and a unique greatest lower bound.

A manually curated hierarchy is difficult to maintain over time and integrate with existing drug hierarchies.

Vaccine code decomposition

Vaccine decomposition is a challenging exercise due to the large number vaccine source codes, implicit attributes not described in the source code name, and ambiguity about which attributes should be considered.

Adam Black, Yupeng Li, Denys Kaduk, Licong Cui, Rashmie Abeysinghe, Lixia Yao

ODYSSEUS DATA SERVICES INC

OHDSI

MONDAY

Constructing vaccine vocabulary hierarchy using formal concept analysis

(Adam Black, Yupeng Li, Denys Kaduk, Licong Cui, Rashmie Abeysinghe, Lixia Yao)

#OHDSISocialShowcase This Week

OHDSI Phenotype Phebruary: lessons learned

Azza Shoaibi, Joel Swerdel, Allan Wu, Gowtham Rao, Adam Black, Evan Minty, Asieh Golozar, Rupa Makadia, Jill Hardin, Voss, Tiffany J. Callahan, Juan Banda, Anna Ostropolets, Claudia Pulgarin, Marcela Rivera, David Vizcaya, Patrick Ryan

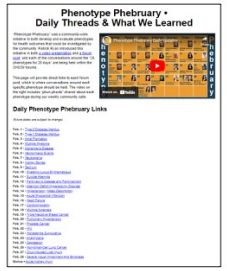
BACKGROUND:

- Phenotypes are the foundational elements in almost every real-world analysis. Yet, the science of phenotype development and evaluation is relatively immature.
- In February of 2022, OHDSI initiated "Phenotype Phebruary: 28 days. 28 phenotypes".
- Each day, an OHDSI collaborator followed a process to phenotype one of the 28 clinical ideas.

METHODS:

clinical description → prior work → cohort definition → evaluate → Discuss & Share

- The community forum served as a platform for all members to collaborate by exploring the posted definitions, reviewing the results provided, replying with reflections or by executing cohort definitions and CohortDiagnostics in additional databases, and sharing consequent learnings.



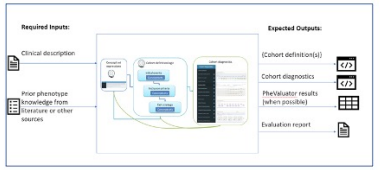
Step	Tips	Strategies	Debates, Challenges & Opportunities
Clinical description	Specify clinical terms that are related to the clinical idea (synonyms, sub-types) Covers known and established epidemiology/trends	Phenotype development should not be attempted before a clear shared understanding of the clinical description and its scope.	Ill-specified phenotype target can lead to an uninformative clinical description. A specific issue for "symptoms" and "syndromes". *(ex. Hemorrhage.*)
Phenotype development	Cannot solely rely on the SNOMED hierarchy to drag in all related concepts. PHOEBE can recommend concepts that you might otherwise missed. *Ex. Type 1 and 2 DM.* Whether or not to include a specific code(s) is a clinical choice which the material consequences should be empirically investigated using tools like CD. *EX. Atrial fibrillation, Delirium).* Prior source code lists can (most of the time) be 100% replicated using standard vocabulary, and the mapping can be easily checked in Atlas. Use SQL when you need to work with lists of codes and perform bulk operations on the list. Since the OHDSI vocabularies are stored in a relational database, this is a perfect task for SQL- then one can copy/paste them into ATLAS *(ex. Multiple Myeloma)* The notion of relying on 'primary position' has been extensively applied in observational research of US administrative claims data, and for some conditions, it has been shown upon validation that codes using primary position led to more specific phenotypes than codes using the secondary diagnosis positions. However, two major issues should be considered: 1) imposing a rule that increases specificity may come at the cost of sensitivity, and that tradeoff should be empirically evaluated, and 2) many databases in the world do not follow the same notion of 'primary position', so this algorithm may not be generalizable. An alternative definition that one could evaluate would be to simply focus on hospitalizations that contain any of the codes. But if one needs to designate 'primary' position, use the CONDITION_STATUS_CONCEPT_ID field *(ex. Hemorrhagic events)* When phenotyping clinical events that can reoccur, model all events (take all occurrences in Atlas) and then use the exit criteria in Atlas to decide on how long the event lasts. Finally, use the era collapse gap size to combine records that may be part of the same episode. *(Ex. Kidney stone).* When using measurement, specify units for measurements, then specify the value for each unit listed. You can specify the value as a range to overcome some data quality problems. To help determine plausible values in a database use ACHILLES browser, the ATLAS data sources tab, via ARES. *(ex. Neutropenia)*	Prior published phenotypes can be a good starting point. OHDSI tools can help implement and evaluate the starting point. One can use prior published phenotypes to identify their clinical intent and try to improve their code sets or logic. When there are multiple published papers, one can use the union of all published codes as a basis to determine which codes can be included. One should differentiate between situations where one data base is not "fit-for use" and situations where the logic makes the implementation of the definition in a data base unfeasible. ex. In the case of bleeding, if the phenotype target is 'bleeding-related hospitalizations', then use of a database without hospitalizations would not be fit-for-use. But if the phenotype target is 'bleeding events' more broadly, then one could consider another an alternative definition. The clinical idea should determine if a phenotype need to include "all events" or only the "earliest event". If the event (ex. disease) can reoccur then it should be modeled as such. When modelling recurrent events, one should pay attention to the "exit strategy". We should balance the potential errors of falsely combining separate events into a single episode. The following inputs are useful to decide on exit criteria and gaps allowed between episodes: 1. Understanding of the biological phenomenon 2. understand how healthcare data may be captured for the clinical event of interest 3. Test the impact of multiple alternative gap size windows on the number of events that are identified and rates of reoccurrence. *(Ex. Kidney stone).* There is tremendous diversity in measurements and units used across datasets and doing a network study with measurements can require iterations of CD execution on the target databases to make sure that your definition is inclusive of what's out there. When building phenotypes for a network study where there can be substantial variation on what specific data are available, we should consider the components that can be used to make up the definition	Do we customize phenotypes to specific data sources, or do we follow a standardized approach across sources? Do we customize phenotypes to analytical use (specific use in studies) or do we follow a standardized approach across use cases? How to consider interpreting results across a collection of databases when capture of inpatient/outpatient labs can be so variable? What logic belongs in ETL and what logic belongs in phenotype definitions? (e.g. pregnancy, mother-child linkages, oncology regimen detection) Sometimes in the attempt of improving specificity one can utilize a logic that when implemented can influence the interpretation of the clinical target. *Ex: hemorrhage:* One could argue that it changes the phenotype target when you go from 'any bleed' to 'any bleed requiring health service utilization' to 'any bleed requiring hospitalization'. In the context of measurements, we need to identify the set of measurements that can yield the value of interest; LOINC provides a robust set of potential measurements, and SNOMED also provides some standard measurement concepts, and the task is to identify the superset of relevant concepts. we add an inclusion criterion that requires some period of prior observation (usually 365), with the intent to give confidence that the event is new. The length of that period can affect the sensitivity of the phenotype. The community can systematically assess multiple periods and recommend one. Develop a PubMed search strategy for finding papers with published/evaluated phenotypes Automated diagnostics execution across a distributed network of databases would speed up phenotype development process (Opportunity).
phenotype evaluation	The use of patient profile, even when built on only structured data- can provide a strong sense about the validity of a case and can approximate manual chart review. *(ex. Multiple myeloma)* Whenever evaluating two cohorts where one is broader than the other, check covariate distribution plot in cohort diagnostic. If indeed the two cohorts had very similar covariate distribution, that may suggest that they are the same type of people, then I would lean toward going with the broad definition. Use cohort diagnostic -incidence rate to see how smooth the transition between ICD9 and ICD10 and to check if the observed trends over time, sex and age groups is consistent with known trends. *(ex. Delirium)* Use cohort diagnostic temporal characterization to assess index event misclassification by examining if there are markers of the condition of interest that proceeded the index date. *(ex SLE)* Phenotype algorithm performance (magnitude of errors of sensitivity, specificity, index date misclassification) is not database agnostic.	Evaluate multiple dimensions of measurement error: sensitivity specificity and index date misclassification (did the person enter the cohort on the right date?) Index event misclassification is commonly observed upon evaluation using OHDSI tools. Current approaches for phenotype development/evaluation rarely address this type of misclassification. In prediction analysis, cleaning out the target cohort from index event misclassification is important to get an honest performance estimate of predicting future outcomes that are truly new. 'Bounding' analyses with a sensitive algorithm and a specific algorithm is a good strategy to consider when trying to evaluate the potential bias caused by measurement error. Use patient profile to propose structure disqualifying criteria in the phenotype logic *Ex. Multiple myeloma* In the presence of alternative cohort definitions, CohortDiagnostics can be very useful to run across a network of databases because the impact of these alternatives can vary There is value in systematically applying PheValuator across multiple definitions and multiple databases. Sometimes you have to let the data tell you what is happening in the real world, rather than you telling the data what you are looking for. *ex. ADHD*	How should we handle codes of 'complication due disease X' and the notion of incident vs. prevalent disease status? How do we balance between the competing tradeoff that comes with consistency of having a definition that is applied and understood vs. variance that is introduced by changing phenotype at the same time of changing the research question? True misdiagnosis and broad coding can result in misclassification *(ex: Type 1 diabetes)* Data might not be able to differentiate between events causing hospitalization vs events occurring during hospitalization *(ex: Delirium)* Outcomes may have poor sensitivity even if your conceptset is exhaustive because events occur outside of the healthcare system. *(ex: suicide).* Improving sensitivity can come at consequence of decreased sensitivity due to misclassification by related conditions *(ex: Alzheimer)* Event exit can be difficult to evaluate *(ex: Kidney stone)* Complete structured "tour" of CohortDiagnostics- that is build out a structured and comprehensive guidance of how to use CD. Explore the potential to use patient chart review to build a phenotype/cohort definition validity tools.

RESULTS :

- Table 1 summarizes the 29 phenotypes that were discussed by the community. Table 2 summarizes lessons learned with the following structure: clinical description, phenotype development and phenotype evaluation. The themes identified belonged to 5 different types of lessons: tips, strategies, debatable topics, challenges, and opportunities.

CONCLUSIONS:

- Phenotyping is complex, multidimensional and requires exchange of knowledge, learnings and insights across collaborators from different background and expertise
- Large scale characterization (e.g.CD), Diagnostic predictive models (e.g., PheValuator) and structured review of patient's profile are potentially effective and novel strategies for phenotype evaluation.
- We are getting closer to a standardized process. But further collaboration is needed to formalize a scalable and reproducible processes and establish empirically-driven objective diagnostics

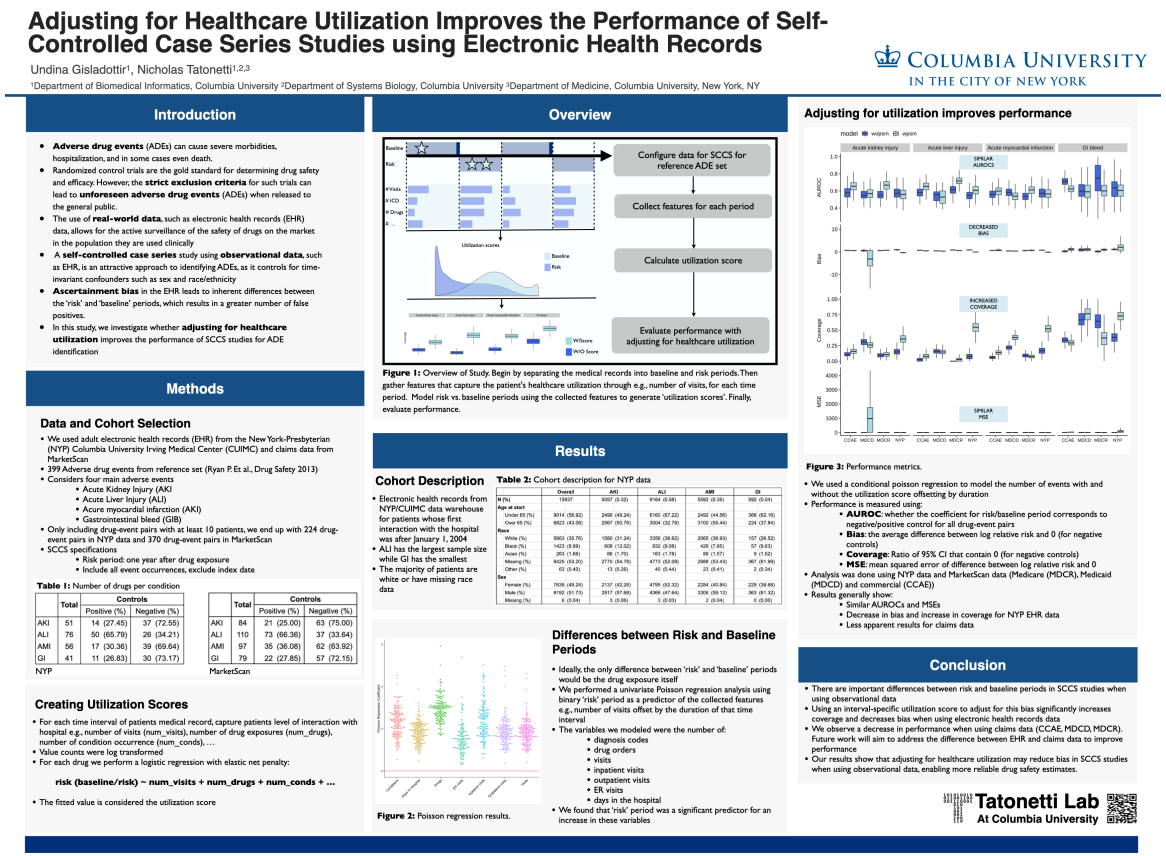


Scan the QR code for additional information

TUESDAY

OHDSI Phenotype Phebruary: lessons learned (Azza Shoaibi, Joel Swerdel, Allan Wu, Gowtham Rao, Adam Black, Evan Minty, Asieh Golozar, Rupa Makadia, Jill Hardin, Erica Voss, Tiffany J. Callahan, Juan Banda, Anna Ostropolets, Claudia Pulgarin, Marcela Rivera, David Vizcaya, Patrick Ryan)

#OHDSISocialShowcase This Week



Adjusting for Healthcare Utilization Improves the Performance of Self-Controlled Case Series Studies using Electronic Health Records

Undina Gisladottir[1], Nicholas Tatonetti[1,2,3]

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COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

Introduction

- **Adverse drug events** (ADEs) can cause severe morbidities, hospitalization, and in some cases even death.
- Randomized control trials are the gold standard for determining drug safety and efficacy. However, the **strict exclusion criteria** for such trials can lead to **unforeseen adverse drug events** (ADEs) when released to the general public.
- The use of **real-world data**, such as electronic health records (EHR) data, allows for the active surveillance of the safety of drugs on the market in the population they are used clinically
- A **self-controlled case series** study using **observational data**, such as EHR, is an attractive approach to identifying ADEs, as it controls for time-invariant confounders such as sex and race/ethnicity
- **Ascertainment bias** in the EHR leads to inherent differences between the 'risk' and 'baseline' periods, which results in a greater number of false positives.
- In this study, we investigate whether **adjusting for healthcare utilization** improves the performance of SCCS studies for ADE identification

Methods

Data and Cohort Selection

- We used adult electronic health records (EHR) from the New York-Presbyterian (NYP) Columbia University Irving Medical Center (CUIMC) and claims data from MarketScan
- 399 Adverse drug events from reference set (Ryan P. Et al., Drug Safety 2013)
- Considers four main adverse events
  - Acute Kidney Injury (AKI)
  - Acute Liver Injury (ALI)
  - Acure myocardial infarction (AKI)
  - Gastrointestinal bleed (GIB)
- Only including drug-event pairs with at least 10 patients, we end up with 224 drug-event pairs in NYP data and 370 drug-event pairs in MarketScan
- SCCS specifications
  - Risk period: one year after drug exposure
  - Include all event occurrences, exclude index date

Table 1: Number of drugs per condition

	Total	Controls	
		Positive (%)	Negative (%)
AKI	51	14 (27.45)	37 (72.55)
ALI	76	50 (65.79)	26 (34.21)
AMI	56	17 (30.36)	39 (69.64)
GI	41	11 (26.83)	30 (73.17)

NYP

	Total	Controls	
		Positive (%)	Negative (%)
AKI	84	21 (25.00)	63 (75.00)
ALI	110	73 (66.36)	37 (33.64)
AMI	97	35 (36.08)	62 (63.92)
GI	79	22 (27.85)	57 (72.15)

MarketScan

Creating Utilization Scores

- For each time interval of patients medical record, capture patients level of interaction with hospital e.g., number of visits (num_visits), number of drug exposures (num_drugs), number of condition occurrence (num_conds), …
- Value counts were log transformed
- For each drug we perform a logistic regression with elastic net penalty:

$$\text{risk (baseline/risk)} \sim \text{num\_visits} + \text{num\_drugs} + \text{num\_conds} + \ldots$$

- The fitted value is considered the utilization score

Overview

Figure 1: Overview of Study. Begin by separating the medical records into baseline and risk periods. Then gather features that capture the patient's healthcare utilization through e.g., number of visits, for each time period. Model risk vs. baseline periods using the collected features to generate 'utilization scores'. Finally, evaluate performance.

Results

Cohort Description

- Electronic health records from NYP/CUIMC data warehouse for patients whose first interaction with the hospital was after January 1, 2004
- ALI has the largest sample size while GI has the smallest
- The majority of patients are white or have missing race data

Table 2: Cohort description for NYP data

	Overall	AKI	ALI	AMI	GI
N (%)	18837	9057 (0.32)	9164 (0.68)	9362 (0.35)	9362 (0.04)
Age at start					
Under 65 (%)	9014 (58.92)	2490 (49.24)	6160 (67.22)	2492 (44.56)	368 (52.10)
Over 65 (%)	6823 (43.08)	2567 (50.76)	3004 (32.78)	3100 (55.44)	224 (37.84)
Race					
White (%)	5663 (35.76)	1590 (31.24)	3356 (36.62)	2065 (36.93)	157 (26.52)
Black (%)	1423 (8.99)	606 (12.02)	832 (9.08)	428 (7.65)	57 (9.63)
Asian (%)	263 (1.66)	86 (1.70)	163 (1.78)	88 (1.57)	9 (1.52)
Missing (%)	8425 (53.20)	2770 (54.76)	4773 (52.08)	2988 (53.43)	367 (61.99)
Other (%)	63 (0.40)	13 (0.26)	40 (0.44)	23 (0.41)	2 (0.34)
Sex					
Female (%)	7639 (48.24)	2137 (42.28)	4795 (52.32)	2284 (40.84)	229 (38.68)
Male (%)	8192 (51.73)	2917 (57.68)	4366 (47.64)	3306 (59.12)	363 (61.32)
Missing (%)	6 (0.04)	3 (0.06)	3 (0.03)	2 (0.04)	0 (0.00)

Figure 2: Poisson regression results.

Differences between Risk and Baseline Periods

- Ideally, the only difference between 'risk' and 'baseline' periods would be the drug exposure itself
- We performed a univariate Poisson regression analysis using binary 'risk' period as a predictor of the collected features e.g., number of visits offset by the duration of that time interval
- The variables we modeled were the number of:
  - diagnosis codes
  - drug orders
  - visits
  - inpatient visits
  - outpatient visits
  - ER visits
  - days in the hospital
- We found that 'risk' period was a significant predictor for an increase in these variables

Adjusting for utilization improves performance

Figure 3: Performance metrics.

- We used a conditional poisson regression to model the number of events with and without the utilization score offsetting by duration
- Performance is measured using:
  - **AUROC**: whether the coefficient for risk/baseline period corresponds to negative/positive control for all drug-event pairs
  - **Bias**: the average difference between log relative risk and 0 (for negative controls)
  - **Coverage**: Ratio of 95% CI that contain 0 (for negative controls)
  - **MSE**: mean squared error of difference between log relative risk and 0
- Analysis was done using NYP data and MarketScan data (Medicare (MDCR), Medicaid (MDCD) and commercial (CCAE))
- Results generally show:
  - Similar AUROCs and MSEs
  - Decrease in bias and increase in coverage for NYP EHR data
  - Less apparent results for claims data

Conclusion

- There are important differences between risk and baseline periods in SCCS studies when using observational data
- Using an interval-specific utilization score to adjust for this bias significantly increases coverage and decreases bias when using electronic health records data
- We observe a decrease in performance when using claims data (CCAE, MDCD, MDCR). Future work will aim to address the difference between EHR and claims data to improve performance
- Our results show that adjusting for healthcare utilization may reduce bias in SCCS studies when using observational data, enabling more reliable drug safety estimates.

Tatonetti Lab At Columbia University

WEDNESDAY

Adjusting for Healthcare Utilization Improves the Performance of Self-Controlled Case Series Studies using Electronic Health Records (Undina Gisladottir, Nicholas Tatonetti)

#OHDSISocialShowcase This Week

Delirium prediction in trauma center and nontrauma center

PRESENTER: **Su Jin Gan**

INTRO

1. Background
- Delirium is highly prevalent in trauma settings
- Screening tools can help predict delirium, however, this area of studies for patients with trauma has lacked, despite distinct traits of patients with trauma

2. Objectives
- To develop delirium prediction models for trauma and non-trauma centers separately
- To compare delirium predictors between trauma center and nontrauma centers

METHODS

1. Data sources
- Ajou University School of Medicine (AUSOM) database
  - Electronic health records
  - Collected from 1996-2021
  - OMOP-CDM v5.3.1
- Target cohorts
  - Inpatients in trauma center, general wards, and intensive care units
- Outcome cohorts
  - Delirium occurrences within 28 days after the hospitalization

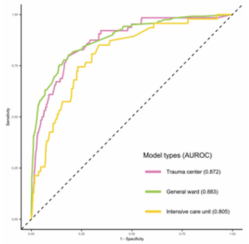
2. Model development
- LASSO logistic regression models
- Covariates
  - The data recorded within 365 days prior to the index date
    - Included in domains of demographics, condition, observation, drug, measurement, and procedure domains
- Data split
  - 75:25 (train/test) set with 3-fold cross validation
- **Top 10 features** were selected based on the feature importance and clinical relevance

3. Model evaluation
- Internal validation
  - Area under the receiver operating curve (AUROC) – Primary metric
  - Area Under Precision – Recall Curve (AUPRC); F1 score; Accuracy
- External validation
  - To evaluate **the consistency of model performance across other patient traits** based on AUROC of the model trained on different cohorts (i.e., AUROC of the model trained on the trauma center cohort when validated in the data set of the general ward cohort

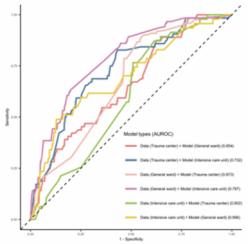
Trauma center needs different delirium screening tools than other wards

- **Model performance**

Internal validation



External validation



- **Delirium predictors**

	Trauma center	General ward	Intensive care unit
1	Non - smoker	Lorazepam	Non - drinker
2	Multiple injuries	Non - smoker	Lactic acid measurement
3	Age group: 75 - 79	CT angiography of head	Normal range of Potassium in Serum or Plasma
4	Normal range of Prothrombin time (PT)	Above normal range of AST in Serum or Plasma	Female
5	Non - drinker	pH of Arterial blood	Anesthetics, general
6	Normal range of serum lactate	Below normal range of Hematocrit [Volume Fraction] of Blood by Automated count	Normal range of Sodium in Serum or Plasma
7	Patient transfer	Male	Insertion of nontunneled central venous catheter
8	Antihemorrhagics	Insertion of indwelling urethral catheter	Insertion of indwelling urethral catheter
9	Below normal range of Calcium.ionized in Serum or Plasma	Psycholeptics	Normal range of Albumin in Serum or Plasma
10	Sulfonamides and potassium in combination	Muscle relaxants	Normal range of Calcium.ionized in Serum or Plasma

Demographics | Condition | Observation | Drug | Measurement | Procedure

RESULTS

The prevalence rate of delirium
- Delirium was **most prevalent** in the **trauma center** (1.3%), which was 1.6 to 13 times higher than in the non -trauma centers

Model performance

1. Internal validation
- The final models had 0.872, 0.883, and 0.805 of AUROC for the trauma center, general ward, and ICU patients, respectively

Table 2. Performance metrics of delirium prediction model in trauma center, general ward, and intensive care unit.

Model	Trauma center	General ward	Intensive care unit
AUROC	0.872	0.883	0.805
AUPRC	0.106	0.033	0.039
F1 score	0.102	0.009	0.039
Accuracy	0.816	0.814	0.665

2. External validation
- **The AUROC of models decreased** when externally validated
  - Trauma center model had the biggest drop compared to nontrauma centers

Table3. The extents to which AUROC of the external validation models have decreased.

Model	AUROC differences in external validation		
	Trauma center	General ward	Intensive care unit
Trauma center	-	- 0.218	- 0.140
General ward	- 0.210	-	- 0.096
Intensive care unit	- 0.203	- 0.109	-

Delirium predictors
- The delirium predictors of trauma center differ in that their traits were more traumatic
- The most frequent domains in each center were different
- Only some features in trauma center were consistent with the results from previous studies

Take a picture
to **download** the **full paper**

Su Jin Gan1, Dong Yun Lee2, Jimyung Park1, Rae Woong Park1,2

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THURSDAY Delirium prediction in patients with trauma and comparison of predictors across trauma center and non-trauma center (Su Jin Gan, Dong Yun Lee, Jimyung Park, Rae Woong Park)

#OHDSISocialShowcase This Week

Welcome to the OHDSI Community Dashboard

PubMed OHDSI Manuscripts	YouTube Videos	Ehden Courses	Working Groups
515 (2,092 authors)	820 (211K+ hours watched)	19 (3,276+ course completions)	28 (3000+ members)

Data as of: 01-30-2023

Observational Health Data Sciences and Informatics (OHDSI) is an open science community. OHDSI's mission is to improve health by empowering a community to collaboratively generate the evidence that promotes better health decisions and better care. The OHDSI Community Dashboard is a tool to highlight the progress we are making toward this mission and the collective accomplishments and impact of our community. A goal of the dashboard is help our community identify how members can see the OHDSI eco-system as an interconnected system to make a larger impact. We hope you find these tools useful staying up to date with all the activities in OHDSI as well as finding new colleagues in our community to collaborate with. Dashboards are developed to represent various aspects of the OHDSI community activities.

FRIDAY

The OHDSI Community Dashboard: Tracking the Health and Impact of the Open Science Observational Health Data Sciences and Informatics Community (Star Liu, Asieh Golozar, Jody-Ann McLeggon, Adam Black, Paul Nagy)

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?

Jan. 31: Introduction to Phenotype Phebruary

Patrick Ryan

Vice President, Observational Health Data Analytics, Janssen Research and Development, Inc.; Adjunct Assistant Professor, Columbia University

Gowtham Rao

Senior Director, Observational Health Data Analytics, Janssen Research and Development, Inc.; Phenotype Development & Evaluation Workgroup Lead

Azza Shoaibi

Associate Director, Observational Health Data Analytics, Janssen Research and Development, Inc.; OHDSI2022 presenter on “OHDSI Phenotype Phebruary: lessons learned”