



Network Studies

(and possible a software demo!)

OHDSI Community Call
Nov. 15, 2022 • 11 am ET



Upcoming OHDSI Community Calls

Date	Topic
Nov. 22	10-Minute Tutorials
Nov. 29	Workgroup Updates
Dec. 6	Fall Publications
Dec. 13	How Did We Do In 2022?
Dec. 20	Holiday-Themed Final Call of 2022



Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?





OHDSI Shoutouts!



Congratulations to the team of **Emily Jefferson, Christian Cole, Shahzad Mumtaz, Sam Cox, Tom Giles, Samuel Adejumo, Esmond Urwin, Daniel Lea, Calum Macdonald, Joseph Best, Erum Masood, Gordon Milligan, Jenny Johnston, Scott Horban, Ipek Birced, Christopher Hall, Aaron S Jackson, Clare Collins, Sam Rising, Charlotte Dodsley, Jill Hampton, Andrew Hadfield, Roberto Santos, Simon Tarr, Vasiliki Panagi, Joseph Lavagna, Tracy Jackson, Antony Chuter, Jillian Beggs, Magdalena Martinez-Queipo, Helen Ward, Julie von Ziegenweidt, Frances Burns, Joanne Martin, Neil Sebire, Carole Morris, Declan Bradley, Rob Baxter, Anni Ahonen-Bishopp, Amelia Shoemark, Ana M Valdes, Benjamin Ollivere, Charlotte Manisty, David Eyre, Stephanie Gallant, George Joy, Andrew McAuley, David W Connell, Kate Northstone, Katie Jeffery, Emanuele Di Angelantonio, Amy McMahon, Mat Walker, Malcolm Gracie Semple, Jessica Mai Sims, Emma Lawrence, Bethan Davies, John Kenneth Baillie, Ming Tang, Gary Leeming, Linda Power, Thomas Breeze, Natalie Gilson, Paul Smith, Duncan Murray, Chris Orton, Iain Pierce, Ian Hall, Shamez Ladhani, Matthew Whitaker, Laura Shallcross, David Seymour, Susheel Varma, Gerry Reilly, Andrew Morris, Susan Hopkins, Aziz Sheikh, and Philip Quinlan** on the publication of **CO-CONNECT: A hybrid architecture to facilitate rapid discovery and access to UK wide data in the response to the COVID-19 pandemic** in the Journal of Medical Internet Research.

The screenshot shows the JMIR Publications website. At the top, there's a navigation bar with 'JMIR Publications', 'SUBMIT', 'MEMBERSHIP', a 'Follow' button, and a search bar. Below this is a header for 'JMIR Preprints'. The main content area displays the article title 'CO-CONNECT: A hybrid architecture to facilitate rapid discovery and access to UK wide data in the response to the COVID-19 pandemic'. It includes metadata: 'Currently accepted at: Journal of Medical Internet Research', 'Date Submitted: Jun 7, 2022', 'Date Accepted: Nov 1, 2022', and 'Date Submitted to PubMed: Nov 2, 2022'. There's a 'Tweet' button. A grey box contains a message: 'This paper has been accepted and is currently in production. It will appear shortly on 10.2196/40035. The final accepted version (not copyedited yet) is in this tab. An "ahead-of-print" version has been submitted to Pubmed, see PMID: 36322788'. Below this is a tabbed interface with 'Preprint' and 'Accepted Manuscript' tabs. The 'Accepted Manuscript' tab is active, showing the full list of authors: Emily Jefferson; Christian Cole; Shahzad Mumtaz; Samuel Cox; Thomas Charles Giles; Sam Adejumo; Esmond Urwin; Daniel Lea; Calum Macdonald; Joseph (Joe) Best; Erum Masood; Gordon Milligan; Jenny Johnston; Scott Horban; Ipek Birced; Christopher Hall; Aaron S Jackson; Clare Collins; Sam Rising; Charlotte Dodsley; Jill Hampton; Andrew Hadfield; Roberto Santos; Simon Tarr; Vasiliki Panagi; Joseph Lavagna; Tracy Jackson; Antony Chuter; Jillian Beggs; Magdalena Martinez-Queipo; Helen Ward; Julie von Ziegenweidt; Frances Burns; Joanne Martin; Neil Sebire; Carole Morris; Declan Bradley; Rob Baxter; Anni Ahonen-Bishopp; Paul Smith; Amelia Shoemark; Ana M Valdes; Benjamin Ollivere; Charlotte Manisty; David Eyre; Stephanie Gallant; George Joy; Andrew McAuley; David Connell; Kate Northstone; Katie Jeffery; Emanuele Di Angelantonio; Amy McMahon; Mat Walker; Malcolm Gracie Semple; Jessica Mai Sims; Emma Lawrence; Bethan Davies; John Kenneth Baillie; Ming Tang; Gary Leeming; Linda Power; Thomas Breeze; Natalie Gilson; Duncan Murray; Chris Orton; Iain Pierce; Ian Hall; Shamez Ladhani; Matthew Whitaker; Laura Shallcross; David Seymour; Susheel Varma; Gerry Reilly; Andrew Morris; Susan Hopkins; Aziz Sheikh; Philip Quinlan.

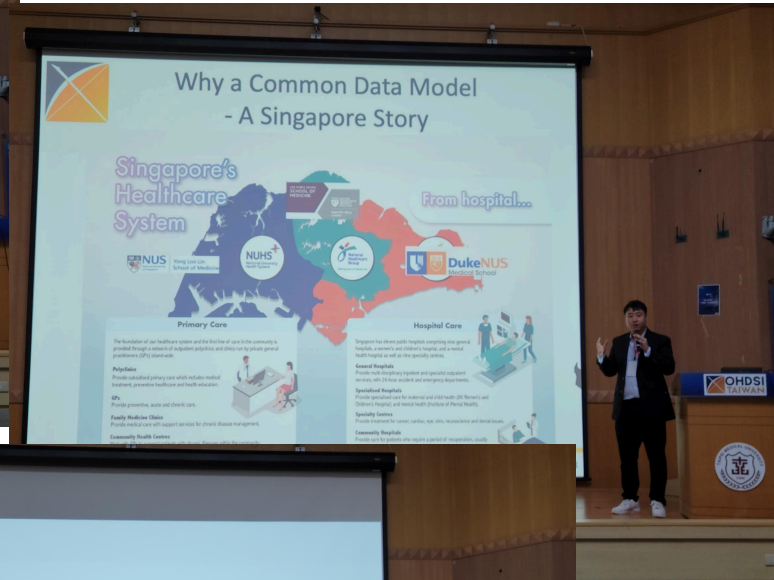


2022 Asia-Pacific (APAC) Symposium



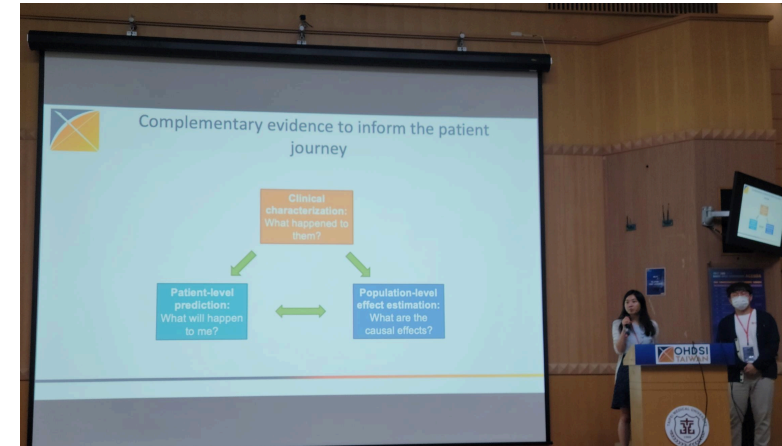
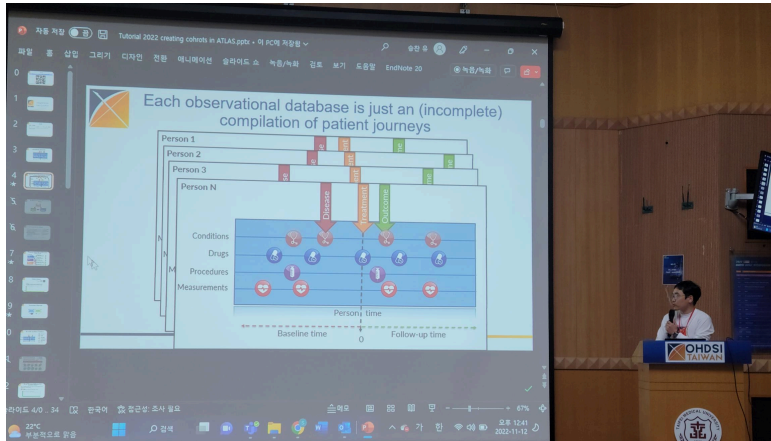


2022 Asia-Pacific (APAC) Symposium





2022 Asia-Pacific (APAC) Symposium

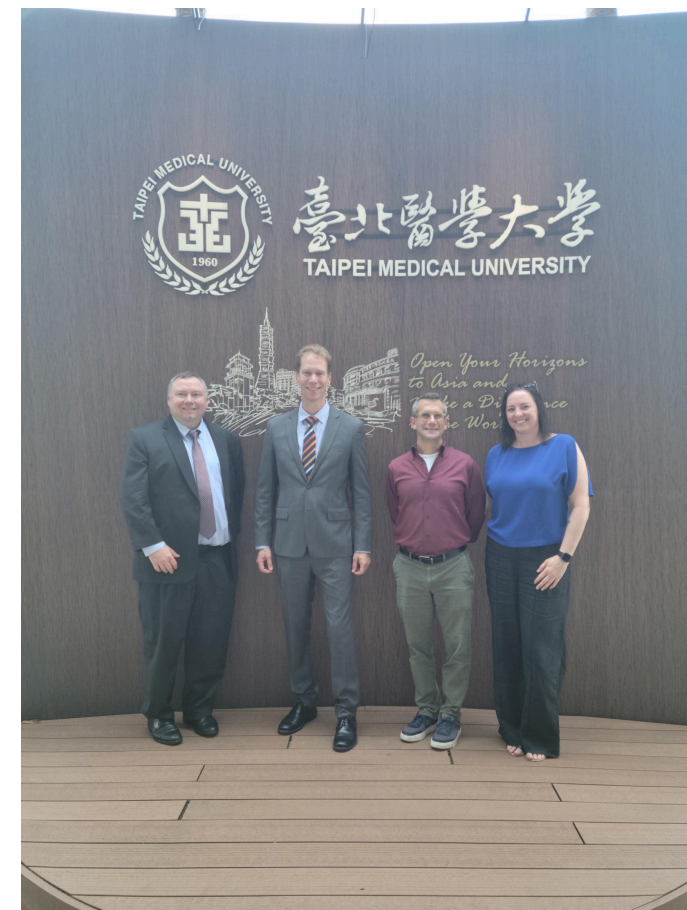


The image shows a presentation of the OHDSI Analysis Viewer. The screen displays the following data:

Model Designs Summary						
ML Model	Num. Development Databases	min AUROC	mean AUROC	max AUROC	Num. Validation Databases	Time at risk
1	1	0.629	0.629	0.629	1	(cohort start + 1) - (cohort start + 365)
1	1	0.751	0.751	0.751	1	(cohort start + 1) - (cohort start + 365)



2022 Asia-Pacific (APAC) Symposium





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	1 pm	Common Data Model
Wednesday	9 am	FHIR and OMOP Data Model Harmonization Subgroup (ZOOM)
Wednesday	12 pm	Health Equity Journal Club
Wednesday	2 pm	FHIR and OMOP Terminologies Subgroup (ZOOM)
Wednesday	7 pm	Medical Imaging
Thursday	10 am	Data Quality Dashboard Development
Thursday	12 pm	HADES
Thursday	1 pm	OMOP CDM Oncology Vocabulary/Development Subgroup
Thursday	7 pm	Dentistry
Friday	9 am	Geographic Information System (GIS)
Monday	10 am	Healthcare Special Interest Group
Tuesday	9 am	OMOP CDM Oncology

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



Open-Source Community WG Meeting

Please join the Nov. 23 Open-Source Community WG meeting, which will include a presentation from 2018 Titan Award winner **Lee Evans** focused on **OHDSI open source software: continuous integration, automated testing, & test database infrastructure.**



Wednesday, Nov. 23 , 11 am ET



Join Anna Ostropolets' Dissertation Defense

OHDSI veteran and 2018 Titan Award winner **Anna Ostropolets** will defend her Columbia University dissertation Wed., Nov. 30, on **Generating Reliable and Responsive Observational Evidence: Reducing Pre-analysis Bias**. The open session will be at 10 am ET on Zoom.



Wednesday, Nov. 30, 10 am ET



#OHDSISocialShowcase This Week



Deployment of an OMOP CDM-compatible NLP system for Rapid Development and Dissemination of a Long-COVID Sign/Symptom Extraction NLP task

Andrew Wen¹, Liwei Wang¹, Huan He, Sunyang Fu, Sijia Liu, Hongfang Liu¹, on behalf of the RECOVER NLP team
Department of AI and Informatics Research Mayo Clinic, Rochester, MN, 55905

INTRODUCTION

The wealth of longitudinal clinical data contained within the Electronic Health Record (EHR) has given rise to tremendous opportunity for both clinical research and practice. A key component to enabling leveraging this data for research in a cross-institutionally portable manner is the Observational Health Data Sciences and Informatics collaborative, with its Observational Medical Outcomes Partnership Common Data Model (OMOP CDM). This standard model for representing clinical data has successfully been leveraged to enable rapid execution of many clinical phenotyping tasks across multiple healthcare institutions with heterogeneous EHR systems. While tremendous effort has been made in ingesting structured portions of EHR data into the OMOP CDM, usage of unstructured data, particularly clinical narratives, in the OMOP CDM is less well defined. Despite the existence of a plethora of clinical natural language processing pipelines, data ingestion and output to these applications vary greatly.

While the OMOP CDM offers some standardization to this process as part of the NOTE and NOTE_NLP tables, integration with existing NLP solutions is limited. As such, neither the ease of adoption of such an integrated NLP solution amongst OMOP sites nor the ability of the existing CDM tables to meet information needs for practical usage are well understood. In order to evaluate the latter problem, the former must first be addressed such that OMOP-compliant NLP data can be processed across a wide variety of sites.

As part of prior work, we developed an NLP framework integrated with the OMOP CDM, the Open Health Natural Language Processing Toolkit (OHNLP toolkit). In this work, we will report on the usage of this toolkit to rapidly develop and prototype an NLP system using this toolkit to execute a clinical phenotyping task to meet a real world information need in the form of extracting signs and symptoms related to long COVID. Additionally, we will demonstrate a federated evaluation of said NLP system across participating sites.

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METHODS

Due to PASC's international recognition, many useful literature resources have been developed. A recent literature review¹ identified 303 articles published before April 29, 2021, curated 59 relevant manuscripts that described clinical manifestations in 81 cohorts of individuals three weeks or more following acute COVID-19, and mapped 287 unique clinical findings to Human Phenotype Ontology (HPO) terms. Another study² consolidated 355 long COVID symptoms from 1,520 UMLS concepts of 16,466 synonyms, which were identified from 328,879 clinical notes of 26,117 COVID-19 positive patients from their post-acute infection period (day 51-110 from first positive COVID-19 test).

These resources were used as a base concept list, which was then cross-referenced with the Unified Medical Language System (UMLS) version 2021AB to obtain an algorithmically-derived base dictionary. Lexical variant generation was then run on these terms to obtain normalized forms and used as a base NLP system. The coverage of this NLP system was then compared against an annotated 98 document clinical narrative set from the Post COVID Care Clinic at the Mayo Clinic, and NLP system finetuning was done using this narrative set to obtain the NLP system used for distribution across the RECOVER team.

This NLP system was then distributed alongside the OHNLP toolkit to 10 RECOVER sites for deployment. A subset of 5 RECOVER sites conducted federated evaluation by manually annotating 10 notes locally each with 2 annotators + 1 adjudicator and returned result coverage statistics to the Mayo Clinic.

1. Deer RR, Rock MA, Vasilevsky N, Carmody L, Rando H, Anzalone AJ, et al. Characterizing long covid: Deep phenotype of a complex condition. *eBioMedicine*. 2021;74:103722.
2. Wang L, Forer D, MacPhail E, Lu Y-C, Bates DW, Zhou L, Pastick A. Comprehensive post-acute sequelae of Covid-19 (PASC) symptom lexicon derived from electronic health record clinical notes. *Journal of Biomedical Informatics*. 2022;125:103951.

RESULTS

TABLE 1: Dictionary Coverage Statistics

	Site 1	Site 2	Site 3	Site 4	Site 5
# Annotations	126	23	171	118	73
# Dictionary Entries	77	20	138	84	65
Coverage %	61.1%	87.0%	80.7%	71.2%	89%

TABLE 2: Dictionary Coverage Statistics

	Site 1	Site 2	Site 3	Site 4	Site 5
# Annotations missed by NLP	49	3	33	34	8
Missed Concepts	55.1%, 27	66.7%, 2	27.3%, 9	11.8%, 4	12.5%, 1
Missed Lexical Variants	40.8%, 20	33.3%, 1	51.5%, 17	76.5%, 26	50.0%, 4
Annotation error	4.1%, 2	0	21.2%, 7	11.8%, 4	37.5%, 3

DISCUSSION

The usage of a common data model for data ingest/output in the NLP pipeline greatly facilitated deployment of the developed NLP system across a wide variety of clinical healthcare sites. Additionally, our results fundamentally demonstrate the advantage of this high degree of portability when discussing generalizable NLP solutions: while the initial Mayo-developed NLP system performs decently across the RECOVER sites that returned evaluation results, not all information needs are met in terms of dictionary coverage. Refinement is thus vastly simplified as gaps in data coverage is assessed across a variety of differing healthcare institutions, thus granting greater confidence in the wide-range generalizability of the final solution.

While the OHNLP toolkit is only one example of how NLP systems can prospectively integrate with the OMOP CDM, we believe that the rapid deployment and ease of refinement demonstrates the importance of such solutions. Additionally, as many sites are now providing this data centrally back to the N3C collaborative for long COVID research use cases, we can begin examining the problem of whether the existing CDM tables NOTE and NOTE_NLP meet information needs for practical usage.

Installation scripts and source code for the OHNLP toolkit and associated NLP algorithms can be found at https://www.github.com/OHNLP/OHNLPKIT_RECOVER and <https://www.github.com/OHNLP/Backbone/MedTagger/> respectively

ACKNOWLEDGEMENTS

Many thanks to the sites participating in the federated evaluation subtask: University of Kentucky, University of Minnesota, Stony Brook, University of Michigan, and Columbia University

MONDAY

Deployment of an OMOP CDM-compatible NLP system for Rapid Development and Dissemination of a Long-COVID Extraction NLP task

(Andrew Wen, Liwei Wang, Huan He, Sunyang Fu, Sijia Liu, Hongfang Liu)



#OHDSISocialShowcase This Week

Impact of random oversampling and random undersampling on the performance of prediction models developed using observational health data

PRESENTER: Cynthia Yang

INTRO:

- Many datasets used for clinical prediction modelling are imbalanced.
- In the machine learning literature, it has been suggested that developing models using resampled data may improve prediction performance.
- Our aim is to empirically investigate the impact of random oversampling and random undersampling on the performance of prediction models using observational health data.

METHODS:

- We used the PatientLevelPrediction (PLP) framework and a sample of 100,000 patients from each database: CCAE, MDCR, MDCD and IQVIA Germany. We investigated 21 binary outcomes within a target population of people suffering from depression.
- The imbalance ratio (IR) is defined as $IR = (\# \text{ patients who do not experience the outcome}) / (\# \text{ patients who do experience the outcome})$. For these tasks, the original IR ranged from 8.6 to 245.3 with a median of 84.0.
- We investigated lasso logistic regression, random forest, and XGBoost. 75% of the data was used for training (including 3-fold cross-validation for hyperparameter tuning) and the remaining 25% was used for testing. Random sampling was only applied to the training folds, where we varied target IR = $\min(\text{original IR}, x)$ with $x \in \{20, 10, 2, 1\}$. We evaluated the area under the receiver operating characteristic curve (AUROC) and inspected calibration plots.

Don't over- or undersample when developing prediction models using large observational health data.

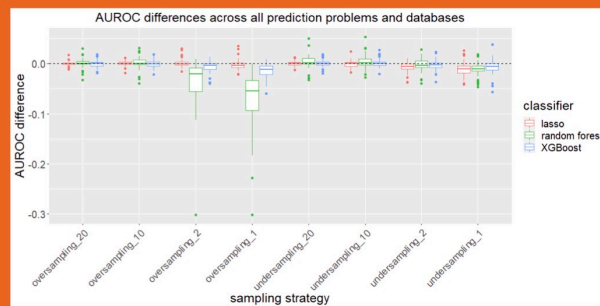


Figure 1. AUROC differences across all prediction problems and databases for each sampling strategy and classifier.

RESULTS:

- Figure 1 shows the AUROC difference (= test AUROC with sampling - test AUROC without sampling) across all prediction problems and databases for each sampling strategy and classifier on internal validation. On average, random oversampling and random undersampling did not improve the AUROC. For random oversampling with random forest, we observed a larger impact on model discrimination.
- We inspected the calibration plots before and after recalibration towards the original imbalance ratios on internal validation. The calibration plots before recalibration indicate increased overestimation for random oversampling or random undersampling towards smaller target IRs, compared to the original data model, for all three classifiers. We found that after recalibration, the calibration plots resembled those of the original data models, although for random oversampling with random forest the models appeared to slightly underestimate risks instead.

Cynthia Yang, MSc,
Egill A. Fridgeirsson, MSc,
Jenna M. Reips, PhD,
Jan A. Kors, PhD,
Peter R. Rijnbeek, PhD



TUESDAY

Impact of random oversampling and random undersampling on the development and validation of prediction models using observational health data (Cynthia Yang, Egill A. Fridgeirsson, Jan A. Kors, Jenna M. Reips, Peter R. Rijnbeek)



#OHDSISocialShowcase This Week

KorNER:
Building Korean NER models for a manually annotated corpus from clinical notes using cross-lingual transfer learning

PRESENTER: **Jimyung Park**

BACKGROUND:

- A lot of studies have been explored on NER to extract important clinical concepts like Problem, Tests, and Treatments in English clinical notes
- However, very limited NER research has been carried out on clinical notes written in Korean, much less in a standardized way in OMOP CDM.

OBJECTIVE:

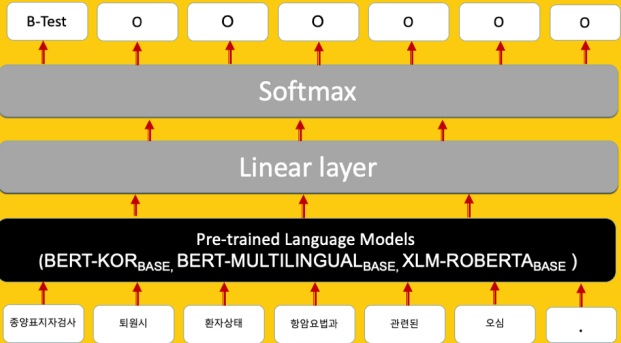
- To develop an efficient and reusable Korean NER framework to extract important clinical concepts based in OMOP-CDM

METHODS

- Data Source**
 - Used 500 discharge summaries from the Korean tertiary hospital database, Ajou University School of Medicine (AUSOM)
 - Important clinical concepts Problem, Tests, and Treatments were identified
 - Annotation was performed using CLAMP
- Model development**
 - Train, test, and validation were set as 6:2:2 in 5-fold
 - Three state-of-the-art pre-trained transformer-based language models were explored: BERT-KOR_{BASE}, BERT-MULTILINGUAL_{BASE}, and XLM-ROBERTA_{BASE}. An additional BI-LSTM-CRF model was trained and taken as baseline
 - Precision, recall, and F1-score are used for model performance evaluation
 - KorNER application was developed based on OMOP-CDM and named as KorNER

KorNER can extract important clinical concepts from Korean discharge summaries in OMOP-CDM

KorNER – An efficient and reusable Korean NER framework based on common data model



Take a picture to download the full paper

This research was funded by the Bio Industrial Strategic Technology Development Program (20003983, 20000221) funded by the Ministry of Trade, Industry & Energy (MOTIE, Korea). This research received a grant from the Korea Health Technology R&D Project through the Korea Health Industry Development Institute (KHIDI), funded by the Ministry of Health & Welfare, Republic of Korea (grant number: HI19C0001). This research was supported by a grant of the project for Infectious Disease Medical Safety, funded by the Ministry of Health, Republic of Korea (grant number: H02200004).

RESULTS

- XLM-ROBERTA_{BASE} model achieved the best performance
- Both XLM-ROBERTA_{BASE} and BERT-MULTILINGUAL_{BASE} models outperform the baseline BI-LSTM-CRF model
- BI-LSTM-CRF model outperforms BERT-KOR_{BASE} model

Table 1. Overall model performance*

Model	P	R	F1
BERT-KOR _{BASE}	0.741 (0.829)	0.779 (0.874)	0.760 (0.851)
BERT-MULTILINGUAL _{BASE}	0.787 (0.861)	0.816 (0.894)	0.801 (0.877)
XLM-ROBERTA _{BASE}	0.808 (0.878)	0.835 (0.908)	0.821 (0.893)
BI-LSTM-CRF	0.782 (0.837)	0.792 (0.870)	0.786 (0.853)

* The strict and relaxed overall performances (P/R/F1) on the test sets of the corpus. Numbers in the parentheses are results based on the relaxed matching criteria.

Jianfu Li^{1*}, Jimyung Park^{2*}, Xinyue Hu¹, Jingqi Wang³, Rae Woong Park^{2,4}, Hua Xu¹

¹School of Biomedical Informatics, University of Texas Health Science Center at Houston

²Department of Biomedical Sciences, Ajou University Graduate School of Medicine

³Melax Technologies Inc

⁴Department of Biomedical Informatics, Ajou University School of Medicine

*These authors contributed equally to the work.



WEDNESDAY Building Korean NER models for a manually annotated corpus from clinical notes using cross-lingual transfer learning (Jianfu Li, Jimyung Park, Xinyue Hu, Jingqi Wang, Rae Woong Park, Hua Xu)



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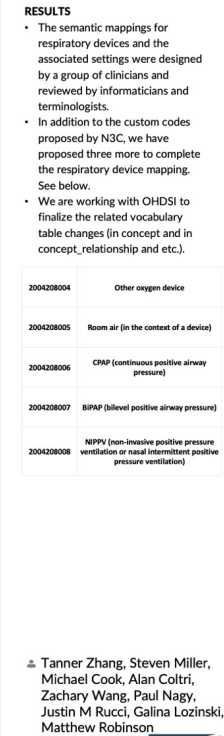
#JoinTheJourney



ohdsi



THURSDAY

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#OHDSISocialShowcase This Week

COVID-19 Vaccine Treatment Pathways in US Administrative Claims

PRESENTER: Kevin Haynes

INTRO:

- Real world data are messy
- The COVID-19 vaccine administration schedule provides a predictable utilization pathway
- The ATLAS Cohort Pathways tool may provide a useful assessment of data quality

METHODS

- Three Databases
 - HealthVerity COVID-19 Database
 - IBM® MarketScan® Commercial Claims and Encounters Database (IBM_CCAE)
 - Optum De-identified Clinformatics® Data Mart Database - Date of Death (DOD) (OPTUM_DOD)
- Four Index Cohorts
 - Pfizer
 - Moderna
 - Janssen
 - Multiple brand

More than one brand on the same date

3. Descriptive study aimed to explore heterogeneity across data resources and vaccine brands

4. Explored the person-time between 1st dose and 2nd dose for mRNA and booster dose regimens of 2nd dose to 3rd dose for mRNA and 1st dose to 2nd dose for Ad26.COV2.S vaccine

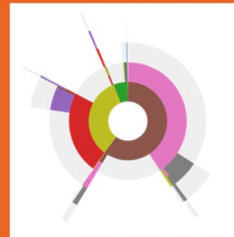
RESULTS

Table 1: Index COVID-19 Vaccine Dose

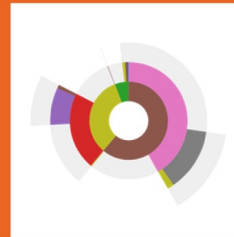
Dose 1	HealthVerity	CCAЕ	Optum-DOD
Pfizer	9,733,844	5,521,742	2,845,264
Moderna	5,498,547	2,996,585	1,585,121
Janssen	941,766	513,362	273,613
Multiple Brand	22,681	2067	1045

ATLAS Cohort Pathways can be used to evaluate data quality by identifying potentially implausible pathways.

HealthVerity



IBM CCAE



Optum DoD



Brand	Dose 1	Dose 2	Dose 3
Pfizer			
Moderna			
Janssen			

Table 2: Dose 1 to Dose 2 Paths

Class	Dose 1	HealthVerity	CCAЕ	Optum-DOD
Pfizer	No	2,894,198	1,728,363	855,354
Pfizer	Record	28,792	131,252	63,157
Pfizer	Pfizer	6,811,751	3,772,647	1,879,514
Pfizer	Moderna	75,052	68,757	68,957
Pfizer	Janssen	22,833	20,816	10,689
Pfizer	Multiple	1,531	508	254
Moderna	No	3,473	581	333
Moderna	Record	1,721,817	1,040,207	531,267
Moderna	Moderna	31,170	124,757	63,957
Moderna	Pfizer	3,747,271	1,842,481	1,040,086
Moderna	Janssen	98,270	84,857	68,057
Moderna	Multiple	23,329	12,960	7167
Moderna	Brand	1693	445	286
Moderna	Brand	4057	492	321
Janssen	No	748,885	356,185	208,204
Janssen	Record	79,632	68,437	67,457
Janssen	Janssen	73,585	29,056	11,158
Janssen	Moderna	7,857	6,747	6,157
Janssen	Pfizer	50,365	56,124	24,892
Janssen	Multiple	46,474	7,463	31,158
Janssen	Brand	1389	134	81
Multiple	No	7682	683	449
Multiple	Record	4087	611	281
Multiple	Pfizer	4087	611	281
Multiple	Moderna	3689	562	157
Multiple	Janssen	219	24	7
Multiple	Brand	7044	187	151

Table 3: Time between Dose 1 and Dose 2

Dose 1	Dose 2	HealthVerity	CCAЕ	Optum-DOD
		mean (sd)	mean (sd)	mean (sd)
		median (QQR)	median (QQR)	median (QQR)
Pfizer	Pfizer	26.5 (28.8)	31.8 (42.8)	31.4 (42.0)
Pfizer	Moderna	21 (21,22)	21 (21,23)	21 (21,23)
Pfizer	Janssen	153 (103,2)	214 (77,9)	205 (79,6)
Pfizer	Multiple	198 (26,207)	231 (107,249)	229 (203,292)
Moderna	Moderna	98.4 (89.5)	127 (86.4)	108 (93.0)
Moderna	Pfizer	63 (21,146)	102 (32,218)	71.5 (22,199)
Moderna	Janssen	36 (39.0)	39 (45.1)	38.7 (44.1)
Moderna	Multiple	28 (28,29)	28 (28,29)	28 (28,29)
Moderna	Brand	128 (106)	137 (66.4)	180 (97.3)
Moderna	Brand	97 (23,230)	225 (153,361)	219 (72,252)
Moderna	Brand	89.2 (87.7)	137 (88.2)	107 (89.2)
Moderna	Brand	47 (21,146)	124 (37,228)	72 (28,186.8)
Janssen	Janssen	133 (106.1)	225 (51.6)	200 (43.4)
Janssen	Moderna	181 (5,232)	232 (208,352)	228 (207,244)
Janssen	Pfizer	221 (53.1)	241 (14,4)	228 (38.4)
Janssen	Multiple	230 (207,251)	241 (218,366)	232 (213,252)
Janssen	Brand	235 (47.8)	241 (28.9)	230 (34.4)
Janssen	Brand	231 (210,252)	239 (220,264)	233 (215,252)

Additional Findings

- >80% of mRNA homologous dose 2 users followed guidelines
- Time between dose analysis identified areas for further investigation

Kevin Haynes¹, Christopher Knoll¹, Rupa Makadia¹, Patrick Ryan¹
¹Janssen Research & Development, Titusville, NJ



FRIDAY


COVID-19 Vaccine Administration Pathways in US Administrative Claims
(Kevin Haynes, Christopher Knoll, Rupa Makadia, Patrick Ryan)



Opening: Northeastern University





Northeastern University invites applications for multiple tenured/ tenure-track faculty positions in support of an Impact Engine centered on large-scale observational health data science and informatics to start in the fall of 2023. These faculty will be core members of our Real-World Healthcare Navigator (RWHN) Impact Engine which aims to change how research is translated into clinical practice by establishing a sustainable service that leads the way in fully reproducing health studies.


 Careers


Open Rank Professor of Large Scale Observational Data Science

Apply

 Boston, MA (Main Campus)

 Full time

 Posted 14 Days Ago

 R110388

About the Opportunity

About Northeastern

Founded in 1898, Northeastern is a global research university and the recognized leader in experience-driven lifelong learning. Our world-renowned experiential approach empowers our students, faculty, alumni, and partners to create impact far beyond the confines of discipline, degree, and campus. Our locations—in Boston; Oakland; Arlington, Charlotte, North Carolina; London; Portland, Maine; Oakland; San Francisco; Seattle; Silicon Valley; Toronto; Vancouver; and the Massachusetts communities of Burlington and Nahant—are nodes in our growing global university system. Through this network, we expand opportunities for flexible, student-centered learning and collaborative, solutions-focused research.

Northeastern's comprehensive array of undergraduate and graduate programs—in a variety of on-campus and online formats—lead to degrees through the doctorate in nine colleges and schools. Among these, we offer more than 195 multi-discipline majors and degrees designed to prepare students for purposeful lives and careers.

Responsibilities

Responsibilities will include teaching undergraduate and graduate courses, conducting an independent and externally funded research program, and participating in departmental, college, and university service. Qualified candidates must have expertise in, or a demonstrated commitment to, working with diverse student populations and/or in a culturally diverse work and educational environment.

Qualifications


- PhD or equivalent in Statistics, Bioinformatics, Data Science, Epidemiology, Computer Science, Computer Engineering, or similar field.
- Expertise working with large relational databases (e.g., EHRs, Medicare) preferred.
- Advanced knowledge of analytic approaches including data wrangling, visualization, and machine learning preferred.
- Expertise in either R or Python.



Opening: Northeastern University





The OHDSI Center at the Roux Institute seeks a postdoctoral fellow to join their team focused on developing statistical methods and applying them to observational data from large-scale federated datasets (e.g. electronic health records and administrative claims data), with specific applications to the safety of biologics. This research will directly improve our ability to use real world data to characterize patient populations, construct population level estimates relating exposures to health outcomes, and to enhance clinical decision making through improved patient-level predictions.


 Careers


Postdoctoral Research Fellow, Observational Health Data Science and Informatics

[Apply](#)

 Portland, ME

 Full time

 Posted 30+ Days Ago

 R109484

About the Opportunity

Job Summary:

The Observational Health Data Science and Informatics (OHDSI) Center housed within the Roux Institute at Northeastern University (NU) is a new administrative hub of the largest observational health research community in the world. The OHDSI Center @ the Roux Institute works to advance OHDSI's research mission of improving health by empowering a community that collaboratively generates evidence that promotes better health decisions and better care. As part of a multi-institution team, the OHDSI Center is participating in a project to provide support to the U.S. Food and Drug Administration's Biologics Effectiveness and Safety (BEST) program. The mission of the BEST program is to conduct safety and effectiveness surveillance of biologic products, such as vaccines, tissues, and advanced therapeutics.

Responsibilities:

This fellow will collaborate with a growing OHDSI Center team of faculty, staff, postdocs, and students to develop and test statistical methodologies related to the use of real world data (e.g. electronic health records and administrative claims data) to better analyze observational health studies. Fellows will be expected to publish and present their work in leading journals and conferences, participate in departmental seminars, and meet regularly with the OHDSI Center research team. There are also opportunities to mentor junior team members and provide educational support across the Center. The ideal candidate will have a strong statistical and computational background, experience processing and analyzing large datasets, and outstanding communication skills.

Qualifications:

- Ph.D. or equivalent degree in Biostatistics, Data Science, Statistics, Epidemiology, Computer Science, or related fields
- Research experience in observational health data theory/methods
- Demonstrated experience working with large observational health databases and/or medical claims data
- Advanced experience in statistical programming languages such as R or Python and familiarity with version control (i.e., Git/Github)
- Excellent writing and communication skills



Opening: FDA/CDER



FDA/CDER's Division of Hepatology and Nutrition is seeking a clinician with bioinformatics or biostatistics training to work with the Drug-Induced Liver Injury (DILI) Team to evaluate large datasets of liver-related data, collaborate on the Team's review of drugs with hepatotoxicity signals, and help develop informatics-based processes in DILI evaluation across the Agency.

Contact **Judy Racoosin** at judith.racoosin@fda.hhs.gov for information about the application process (that will be through USAJOBS).



Opening: Tufts Medicine



Andrew Williams recently announced two exciting new openings at Tufts Medicine.

1) Senior Project Manager for a multisite multiyear grant standardizing critical care EHR and waveform data. (CHoRUS Bridge2AI)

2) Lead software developer and research data warehouse manager for Tufts Medicine's OMOP instance and related services.

Remote work is possible for both positions.

1. Link for Senior Project Manager position: <https://smrtr.io/bBVzh>
2. Link for Lead Software Developer and Research Data Warehouse Manager position: <https://jobs.smartrecruiters.com/TuftsMedicalCenter1/743999857980631-software-development-lead-res-g-c-ctsi>

Andrew's email:
awilliams15@tuftsmedicalcenter.org



Openings: Johns Hopkins University

Research Associate (Data Scientist/Statistical Engineer), Johns Hopkins inHealth and Biostatistics Center

- Execute OHDSI studies (e.g. for cohort characterizations and comparative effectiveness) on Johns Hopkins's EHR data to support clinicians;
- Collaborate with statisticians and clinicians to continuously integrate state-of-the-art statistical tools to the inHealth/OHDSI tool stack for deployment;
- Mentor trainees on data science and software development skills;
- Co-teach courses on observational health data analytics and data science skills at School of Medicine and Public Health;
- Facilitate adoption of the inHealth tools among the broader OHDSI community by contributing to OHDSI's Health Analytics Data-to-Evidence Suite.
- <https://apply.interfolio.com/114436>



Where Are We Going?

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





Three Stages of The Journey

Where Have We Been?

Where Are We Now?

Where Are We Going?





Nov. 15: Open Network Studies



Expanding maternal and infant data from EHRs for pregnancy research

- Safety and Effectiveness of Anti-Hypertensive Medications in Pregnancy
- Project to Characterize Anti-Hypertensive, Anti-Coagulant, Anti-Diabetic and Antibiotic Medication Usage During Pregnancy and Postpartum



Alison Callahan (Instructor, Medicine • Stanford University)

Stephanie Leonard (Instructor, Obstetrics & Gynecology • Stanford University)

Louisa Smith (Assistant Professor, Health Sciences • Northeastern University)



Relative Risk of Cervical Neoplasms Associated with Copper and Levonorgestrel Secreting Intrauterine Devices: Real World Evidence from the OHDSI Network

Matthew Spotnitz (Postdoctoral Research Fellow • Columbia University)