

AI in Pharmacoepidemiology

Opportunities for the European Regulatory Network

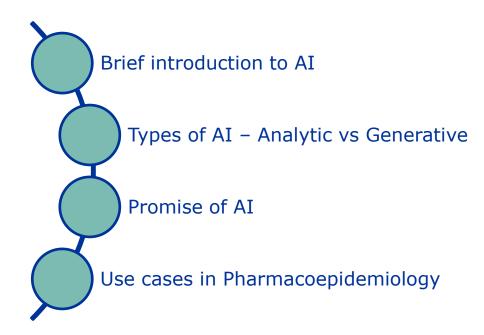
ENCePP Plenary, December 1st, 2023

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Content



AI in Pharmacoepidemiology - ENCePP Plenary Dec 2023

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Brief introduction to AI

AI is a catch-all term for a collection of novel digital technologies and methods

Allow machines to extract rules from data (i.e., learn)

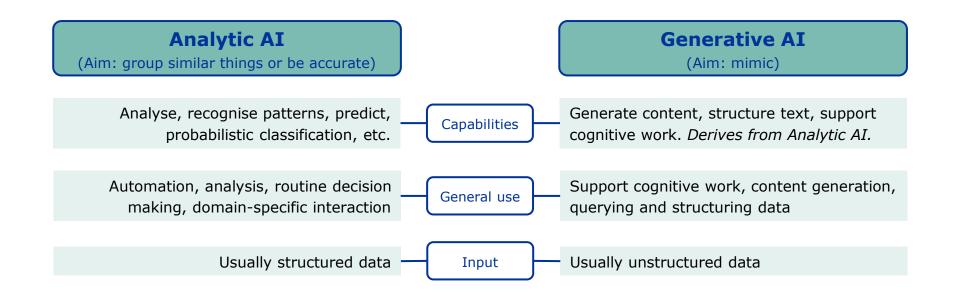
Predict, classify or cluster similar patterns using those rules or execute autonomous actions

AI is data-driven

1 Needs data	2 Typically* needs supervision	B Predicts/ classifies the past	4 Bias in data become rules	5 Needs Human intelligence
(data protection /security)	(establish ground truth)	(performance drops)	(ethical issues)	(design issues)



Artificial intelligence | Types of AI





AI in Medicines Regulation | The Promise



- Automate processes
- Address scalability issues
- Leverage personal assistants (chatbots) Do more things, faster

- Facilitate access to information
- Reduce human cognitive load

Provide information at the fingertip

- Transform text data into structured data
- Reduce dimensionality of data
- Confounding adjustment
- Imputation of missing data

Structure and summarise information

- Probabilistic
 - phenotyping
- Synthetic control arms
- Clinical prediction modelling
- Heterogeneity of treatment effects Predict probability of events



Exposing data | Named Entity Recognition (NER)

Description

NER (and extraction), is a task performed to identify and extract entities.

Entities are objects from some class, such as a disorder, a medicinal product, a person's name, etc.

Pharmacoepidemiology use cases

NER generally an intermediate task – e.g. to expose or present data in a research-ready format

Phenotyping/identification of a patient population

Example

A pregnant 30-year-old woman, had constipation three days after starting iron supplements.

Entity Linking

Mentions are detected with the standard pipeline's mention detector.

А	pregnant EN	NTITY	30-year-	old	woman	ENTI	тү	, had	constipation	ENTITY	three
c	days entity	after s	starting	iron	supplem	ents	ENT	ITY .			



Exposing data | Generative AI (GenAI)

Description

Large language models, facilitate extraction and structuring of information, particularly that which is extensively available in the training data.

LLMs can be used for NER have limitations

Pharmacoepidemiology use cases

Structuring data to be ingested, e.g. in a protocol.

Coding

Screening through information

Example	
json	Copy code
<pre>{ "description": "Anaphylaxis is a severe allergic reaction "symptoms": { "skin": ["hives", "itching", "redness"], "respiratory": ["shortness of breath", "wheezing", "coug "gastrointestinal": ["nausea", "vomiting", "diarrhea"], "cardiovascular": ["weak pulse", "palpitations", "dizzin "other": ["anxiety", "confusion", "loss of consciousness } }</pre>	ghing"], ness"],
sql	🖞 Copy code
<pre>SELECT sex, COUNT(pat_id) AS patient_count FROM person GROUP BY sex;</pre>	

Evample



Data insights | Confounding control

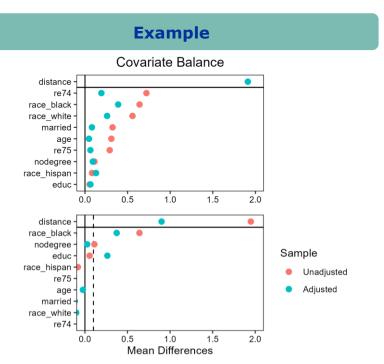
Description

ML models may improve **propensity score estimation** through data-driven confounder selection, better modelling of non-linear effects and interactions

Overfitting less of a problem

Pharmacoepidemiology use cases

Structuring data that can be ingested, e.g. in a protocol or coding





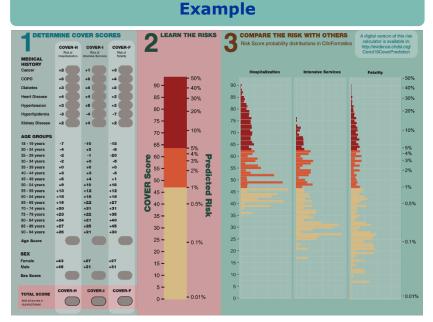
Data insights | Clinical prediction models

Description

Algorithmic risk scores not new to medicine and public health. ML models add the possibility to **predict probability of a clinical outcome** purely from a data-driven perspective

Pharmacoepidemiology use cases

Prediction of the probability of a clinical outcomes or behaviour (e.g. risk of abuse of opioids)



Seek COVER: Development and validation of a personalised risk calculator for COVID-19 outcomes in an international network

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Data insights | Probabilistic phenotyping

Description

Example

In probabilistic phenotyping the ML identifies patterns in the characteristics of a population of interest and **predicts the likelihood that a patient is an element of that population**

Pharmacoepidemiology use cases

Cohort development – populations that share similar traits, particularly for phenotypes that have complex logic or are not directly identifiable from existing diagnostic/laboratory codes (e.g., gestational age) An Application of Machine Learning in Pharmacovigilance: Estimating Likely Patient Genotype From Phenotypical Manifestations of Fluoropyrimidine Toxicity

Luis Correia Pinheiro^{1,*}, Julie Durand¹ and Jean-Michel Dogné^{2,3}

Dihydropyrimidine dehydrogenase (DPD)-deficient patients might only become aware of their genotype after exposure to dihydropyrimidines, if testing is performed. Case reports to pharmacovigilance databases might only contain phenotypical manifestations of DPD, without information on the genotype. This poses a difficulty in estimating the cases due to DPD. Auto machine learning models were developed to train patterns of phenotypical manifestations of toxicity, which were then used as a surrogate to estimate the number of cases of DPD-related toxicity. Results indicate that between 8,878 (7.0%) and 16,549 (13.1%) patients have a profile similar to DPD deficient status. Results of the analysis of variable importance match the known end-organ damage of DPD-related toxicity, however, accuracies in the range of 90% suggest presence of overfitting, thus, results need to be interpreted carefully. This study shows the potential for use of machine learning in the regulatory context but additional studies are required to better understand regulatory applicability.

Data insights | Causal inference

Description

Machine learning identifies relations and patterns within data, not focused on causation but correlation

Targeted Maximum Likelihood Estimation allows

use of ML with few assumptions on data distribution

Pharmacoepidemiology use cases

Being explored for association studies with highdimensional data with complex, non-linear relationships

Example

ORIGINAL ARTICLE

OPEN

Targeted Maximum Likelihood Estimation for Pharmacoepidemiologic Research

Menglan Pang,^{a,b} Tibor Schuster,^{a,b} Kristian B. Filion,^{a,b,d} Maria Eberg,^a and Robert W. Platt^{b,c,e}

Background: Targeted maximum likelihood estimation has been proposed for estimating marginal causal effects, and is robust to misspecification of either the treatment or outcome model. However, due perhaps to its novelty, targeted maximum likelihood estimation has not been widely used in pharmacoepidemiology. The objective of this study was to demonstrate targeted maximum likelihood estimation in a pharmacoepidemiological study with a high-dimensional covariate space, to incorrovare the use of hish-dimensional provensity ecores into this method Results: Through a real example, we demonstrated the double robustness of targeted maximum likelihood estimation. We showed that results with this method and inverse probability weighting differed when a large number of covariates were included in the treatment model. Conclusions: Targeted maximum likelihood can be used in highdimensional covariate settings. In high-dimensional covariate settings, differences in results between targeted maximum likelihood and inverse probability weighted estimation are likely due to sensitiv-

Summary

- Several, and increasing number of, opportunities to leverage AI for pharmacoepidemiology
 - Generative AI will likely increase productivity/efficiency but will likely still play a limited role in the actual analytics real-world data where data tends to be structured
 - Machine learning will become increasingly part of the analytical arsenal of the pharmacoepidemiologist but not likely to replace existing tools (e.g., for the most part, logistic regression models still are the best option)
- Experimentation and collaboration will be essential a European Medicines Regulatory Network workplan including experimentation and fora for interactions with, e.g. Academics, is being prepared



Any questions?

Further information

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