

Name:	Jon Duke
Affiliation:	Regenstrief Institute
Email:	jonduke@regenstrief.org
Presentation type (select one):	Collaborator Demonstration

TxPath: An Open-Source Tool for Conducting Treatment Pathway Analyses Using the OHDSI Framework

Jon D. Duke, MD¹, Alex Asiimwe PhD², Gunnar Brobert PhD², Leif Friberg MD, PhD³, Paul Petraro, ScD², Chen Wen¹, Ken Spry¹, MPH, Patrick Ryan PhD⁴

¹Regenstrief Institute, Indianapolis IN; ²Bayer Healthcare Pharmaceuticals, Whippany, NJ; ³Karolinska Institute, Stockholm, Sweden; ⁴Janssen Research and Development, Titusville, NJ;

Abstract

We propose a collaborator demonstration of a generalizable tool for performing treatment pathway analyses using the OHDSI framework.

Introduction

The seminal OHDSI study by Hripesak et al explored treatment patterns for 3 chronic diseases (diabetes mellitus, hypertension, and depression) across 250 million patients in 11 OMOP CDM datasets¹. This remarkable study raised interest amongst the OHDSI community regarding what other clinical domains and therapeutic classes could be explored in a similar manner. In this demonstration we will unveil TxPath, a generalized treatment pathway analysis tool that leverages the OMOP CDM and OHDSI framework.

TxPath Design

TxPath was designed to enable data holders with data in OMOP CDM v5 format to assess patterns of usage of any set of medications or procedures across any patient cohort. The application leverages the existing concept set creation and cohort definition features of OHDSI (i.e., Atlas/Circe). Once a user has defined a concept set of interest (e.g., oral diabetes medications) and a cohort (e.g., patients with a diagnosis of type 2 diabetes), they can use the TxPath tool to build a custom analysis (Figure 1A). Once the user has specified the study duration (e.g., 3 years following cohort index date), TxPath will cull from the drug_era and procedure_occurrence tables all matching data for the patient cohort and present the results through a series of tables and visualizations (Figure 1B).

The results section includes the following components:

- Overview of the selected cohort and concept set
- Interactive ‘Sunburst’ visualization of all treatment pathways (including combination treatments)
- Interactive ‘Sunburst’ visualization of all unique treatments
- Distribution of treatment regimens by drug including number of patients on regimen, mean days from index to treatment start, mean days on treatment, and frequency of treatment switches, additions, and drops following that regimen

As the number of potential pathways can grow quite extensive (see Hripcsak et al), TxPath allows users to filter results by minimum number of patients taking a given drug combination or minimum days of use. These filters prune the resulting pathways to avoid the myriad unique paths that represent for example only a single patient.

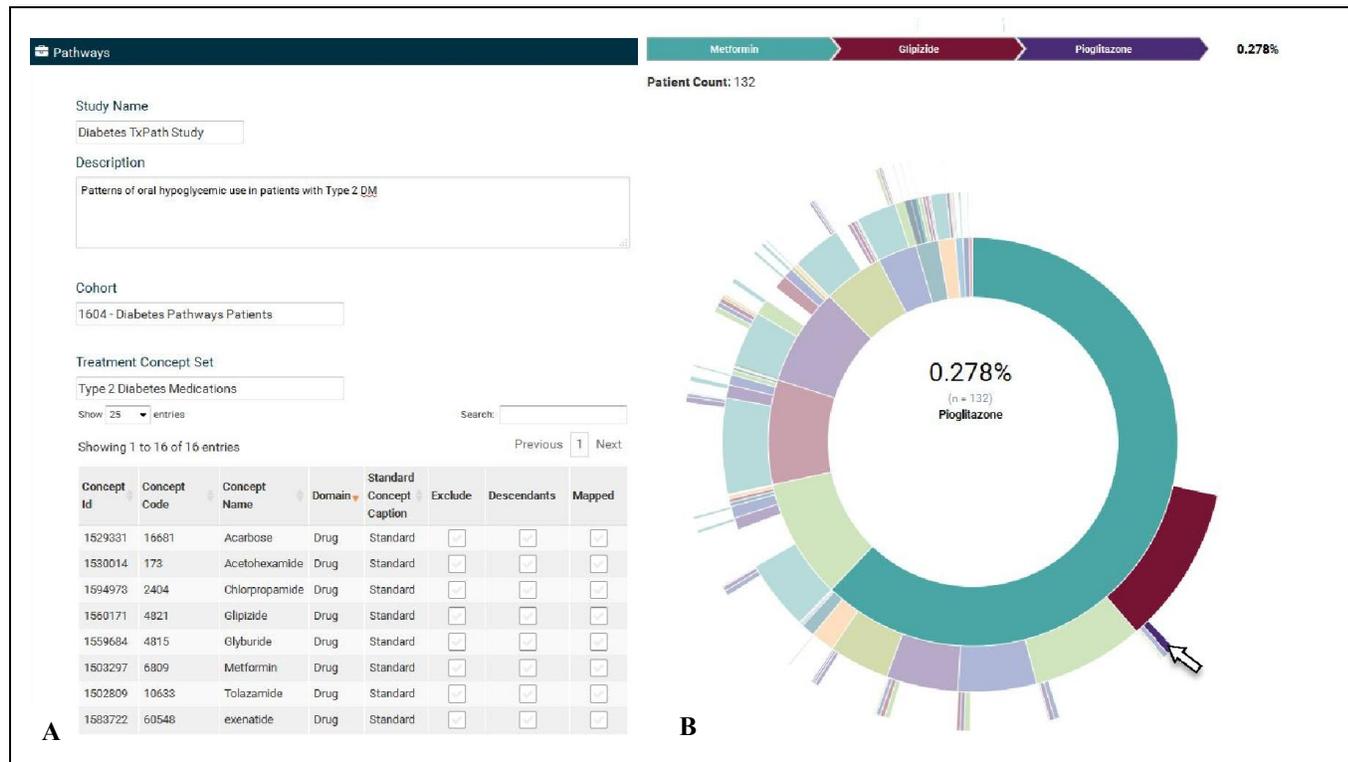


Figure 1. A) TxPath study definition interface. B) Sunburst visualization example from TxPath results view.

TxPath Demonstration

In the proposed collaborator demonstration, we will walk through the configuration of a TxPath study from concept set definition and cohort creation through configuration of a treatment pathways analysis. We will then explore the results report and visualizations. Finally, we will demonstrate how filtering can be used to prune the pathways results.

Conclusion

The capability to analyze OHDSI cohorts for treatment patterns is valuable to numerous stakeholders as reflected by the great interest in the recent PNAS publication. We have developed a generalizable open-source tool to bring these capabilities to the OHDSI community,

References

1. Hripcsak G, Ryan PB, Duke JD, Shah NH, Park RW, Huser V, Suchard MA, Schuemie MJ, DeFalco FJ, Perotte A, Banda JM. Characterizing treatment pathways at scale using the OHDSI network. Proceedings of the National Academy of Sciences. 2016 Jun 6:201510502.