Feasibility of Executing Phenotype Algorithms Based on Clinical Quality Language against the OMOP Common Data Model

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Introduction

The goal of the Phenotype Execution and Modeling Architecture (PhEMA) project (https://projectphema.org/) is to improve the portability of electronic health record (EHR)-based phenotyping algorithms using healthcare data standards. The Clinical Quality Language (CQL) is a Health Level Seven (HL7) standard used to represent electronic clinical quality measures (eCQMs). CQL has a prescribed syntax that allows the algorithm logic to be authored in a human readable format, which may be then parsed into the HL7 Expression Language Model (ELM) - a computable format represented using XML. A software system would then be able to interpret the ELM and execute queries against a data repository. The objective of study is to test feasibility of executing phenotype algorithms written in CQL against a data repository based on the Observational Medical Outcomes Partnership (OMOP) common data model (CDM).

Methods

We used the cql-to-elm open source program - developed by the Clinical Quality Framework - to transform the CQL file into the ELM format. We then developed an execution pipeline (https://github.com/PheMA(elm-to-ohdsi-executer) that performs the following steps: 1) read the ELM file and value set definition and then map the logic encoded by the ELM to a JSON format used by ATLAS, including the specification of all value sets (called concept sets within OHDSI); 2) submit the JSON via the OHDSI WebAPI to create a cohort definition; 3) submit a request through the WebAPI to generate the cohort from the cohort definition; 4) use the WebAPI to poll the service for the execution status; 5) retrieve the cohort record count. (Figure 1).

Figure 1. Workflow to transform and execute a phenotype algorithm in CQL in an OHDSI environment

Results and Discussion

We created a simple phenotype algorithm to retrieve patients diagnosed with type 1 diabetes mellitus. A value set of 9 concepts from SNOMED CT and Columbia International eHealth Laboratory (CIEL) were selected to define the query. Manual verification showed that the OHDSI definition generated by our program matched the natively authored definition using the ATLAS user interface. Both the CQL-to-OHDSI translation and the OHDSI authored version of the phenotype generated a cohort of 246 patients with type 1 diabetes mellitus in this test case. The 246 patient identifiers for each result set were compared and the cohorts were found to have 100% overlap. We demonstrated the ability to convert CQL-based logic to the JSON format used by the OHDSI ATLAS application. This is an important proof-of-concept in our goals to improve portability of phenotypes across CDMs. Future work will focus on more complex algorithms, incorporating inclusion and exclusion criteria, temporal relationships and multiple value sets. Our ongoing work also includes porting our existing i2b2 translation engine to incorporate CQL-to-i2b2 translations. We will also consider other repositories based on PCORnet CDM and FHIR to execute CQL.

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