FHIR to OMOP Cookbook - Mapping mCODE FHIR Resources for Observational Research

Yang, Q., Livne, G., van Sandijik, S., Terry, M.
IQVIA, Ministry of Health Israel, Odysseus Data Services, MITRE Corporation

Background

How aligned are FHIR and the OMOP CDM for use in oncology observational studies? This was explored with two well-recognized standards - the minimum Common Oncology Data Elements (mCODE) Health Level 7 (HL7) Fast Healthcare Interoperability Resources (FHIR) specification and the OMOP Common Data Model (CDM).

mCODE has been adopted by at least 30 organizations and specified in United States federal initiatives like the Office of the National Coordinator (ONC) USCDI+ for Cancer and the CMS Enhancing Oncology Model (EOM) [1]. The OHDSI framework, built on the Observational Medical Outcomes Partnership (OMOP) Common Data Model (CDM), has been widely and internationally adopted as a standard for large-scale collaboration for healthcare observational research and analytics. While both FHIR and OHDSI frameworks have been recognized as complementary and fit for purpose, it is unclear how well a model initially designed for EHR capture and data exchange is well suited for observational studies [2].

Methods

The oncology sub-group performed gap analysis using an approach for mapping from FHIR to OMOP that includes the identification of FHIR constructs and patterns for translation to OMOP tables and elements based on the extracted concept from FHIR resources.

We created a repeatable approach to evaluating FHIR structural and semantic constructs to identify gaps and inform translations between FHIR and OMOP, summarized in the steps below:

1. Define the information elements that are relevant to represent in OMOP in observational studies.
2. Identify the OMOP concept that best matches each of the FHIR code elements in its context FHIR record.
3. Analyze the corpus between the content inventory FHIR codeable Concept with the OMOP Ontology for gaps and misaligned domains.
4. Determine the OMOP CDM table based on the OHDSI-assigned domain for the OMOP concept.
5. Map the element related FHIR resources / profile elements to the OMOP CDM table required fields.
6. Populate the OMOP CDM records at the atomic/record level.
7. Preserve references and relationships among FHIR resources in cases where the concepts are qualifiers or modifiers to a clinical domain from the original resource where possible (meas_event_id, observation_event_id, fact_relationship, etc.). Maintain provenance to the originating FHIR resources by ensuring references to the FHIR id within the OMOP record.

8. Test OMOP CDM integrity and completeness.
9. Compare FHIR and OMOP representations for a known set of patient information (condition, test results, procedures, observations, etc.) for accuracy and identify gaps.

Our approach was tested in a FHIR Connectathon with three organizations. The test environment provided a common FHIR test dataset and a shared OMOP vocabulary schema to mitigate semantic version discrepancies among ETL developers. Each participant was provisioned a dedicated OMOP v5.4 schema to test their ETL code against our recommended mappings. We compared the number of records translated for the OMOP PERSON and CONDITION_OCCURRENCE tables as well as the representation of key fields in each table, including PERSON birth date, race, and gender as well as CONDITION concepts and dates. We captured issues and questions related to our mappings during the development of their ETL code.

Results

We analyzed, mapped over half of the mCODE elements to the OMOP CDM [Figure 1]. As part of this work, we identified several patterns that also apply to general FHIR principles and representation patterns. These were formalized in a FHIR-to-OMOP Cookbook document as guidance for implementers.

mCODE Profile	Status
Cancer Disease Status Profile	2
Cancer Patient Profile	3
Cancer-Related Medication Administration Profile	2
Cancer-Related Medication Request Profile	1
Cancer-Related Surgical Procedure Profile	1
Cancer Stage Group Profile	2
Comorbidities Elixhauser Profile	D
ECOG Performance Status Profile	1
Genomic Region Studied Profile	2
Genomic Specimen Profile	2
Genomic Variant Profile	2
Genomics Report Profile	2
Karnofsky Performance Status Profile	1

mCODE Profile	Status
mCODE Patient Bundle Profile	D
mCODE Patient Group Profile	D
Primary Cancer Condition Profile	3
Radiotherapy Course Summary Profile	1
Radiotherapy Volume Profile	1
Secondary Cancer Condition Profile	0
TNM Distant Metastases Category Profile	0
TNM Primary Tumor Category Profile	0
TNM Regional Nodes Category Profile	0
Tumor Profile	2
Tumor Marker Test Profile	2
Tumor Size Profile	2
Tumor Specimen Profile	2

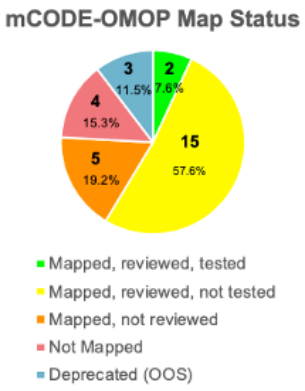

Figure 1. FHIR to OMOP Mapping

Several FHIR-to-OMOP axioms and patterns were identified, some of which are listed below in Table 1. A detailed list is available in the FHIR-to-OMOP cookbook.

Category	Description	Guidance

Axioms	Protected Health Information (PHI) data is generally not mapped to OMOP.	Assume the following patient-level data elements will **NOT** be present in the OMOP CDM: ● Patient and patient contact names ● Addresses ● Telecom ● Medical record numbers ● Government-issued identifiers (e.g.: social security number, driver's license number, etc.)
	Not all FHIR metadata is relevant to OMOP.	Maintain the provenance to the FHIR resource instance id in the mapped OMOP record if needed.
Mapping Patterns	OMOP assumes that observations and measurements are completed or final while FHIR observations can be preliminary.	ETL logic should filter for a FHIR Observation.status code of *final* or *amended*. Use of preliminary values that may be overridden should be documented.

Table 1. FHIR to OMOP Axioms and Patterns

Conclusion

We concluded that it is feasible for FHIR to be used for oncology observational research, however the FHIR-to-OMOP mappings should consider patterns of representation, and be captured in an implementation guide such as the FHIR-to-OMOP Cookbook to ensure that researchers understand the context and assumptions made in translating from its FHIR source to the OMOP CDM.

Since our initial release of the FHIR-to-OMOP Cookbook, we revisited some of our assumptions and identified patterns with updates in mCODE STU3 and new mapping techniques. We found that it is more possible to capture complex patterns since our initial work and most of the patterns identified in the cookbook still apply.

Limitations and Opportunities

We briefly considered mappings to the OMOP Oncology cancer modifiers, but focused mostly on the methodology related to the OMOP tables. We should also compare our approach, which was started in 2022, with newer approaches for converting FHIR to OMOP. Updated versions of the FHIR-to-OMOP

cookbook could both align with and provide additional guidance to several initiatives in further identifying oncology-specific guidelines for translation. These include OHDSI THEMIS [3], MEDOC, as well as other FHIR-to-OMOP initiatives like OSIRIS [4] and the HL7 Vulcan FHIR-to-OMOP sub-group [5] in their efforts to formalize an implementation guide.

Supporting Materials

- FHIR-to-OMOP Cookbook

References

1. Osterman TJ, Terry M, Miller RS. Improving cancer data interoperability: the promise of the Minimal Common Oncology Data Elements (mCODE) Initiative. JCO Clin Cancer Inform. 2020;4:993-1001. doi:10.1200/CCI.20.00059
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4. OSIRIS. https://github.com/InstitutNationalduCancer
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