FHIR to OMOP Oncology

OHDSI Symposium 2022
October 15, 2022
Agenda

Background 10 min
FHIRE resources and API 15 min
mCODE to OMOP – Introduction and mapping 30 min
Hands-on demo exploration of FHIRE/mCODE and OMOP translations 15 min
General FHIRE to OMOP Guidelines / Patterns 20 min
Areas for further exploration, opportunities, and call for action 20 min
Q&A / Open discussion 15 min
Thanks to our amazing contributors and supporters

- **FHIR-OMOP Oncology sub-group**
  - Guy Livne
  - Qi Yang
  - Jane Pollack
  - Sebastiaan Van Sandjik
  - Andrea Pitkus
  - Anna Aloni
  - Jeff Liu

- **HL7 / OHDSI community**
  - FHIR-OMOP sub-groups: Data Model Harmonization, Vocabulary
  - FHIR-OMOP Genomics
  - FHIR-OMOP Oncology Vocabulary
  - HL7 CodeX FHIR Accelerator / mCODE Communities

- **HL7/OHDSI FHIR-OMOP cross-team and Support**
  - Ben Smith
  - Davera Gabriel
  - Christian Reich
  - Lee Evans

- **...and many others!**
Background
HL7 International and OHDSI Announce Collaboration to Provide Single Common Data Model for Sharing Information in Clinical Care and Observational Research

Health Level Seven International (HL7®) and the Observational Health Data Sciences and Informatics (OHDSI) network today announced a collaboration to address the sharing and tracking of data in the healthcare and research industries by creating a single common data model. The organizations will integrate HL7 Fast Healthcare Interoperability Resources (FHIR®) and OHDSI’s Observational Medical Outcomes Partnership (OMOP) common data model to achieve this goal.

HL7 International CEO Dr. Charles Jaffe, M.D., Ph.D., underscored the significance of this partnership. “The Covid-19 pandemic has emphasized the need to share global health and research data.” He continued, “Collaboration with OHDSI is critical to solving this challenge and will help our mutual vision of a world in which everyone can securely access and use the right data when and where they need it.”

The organizations will align their standards to capture data in a clearly defined way into a single common data model. This will allow clinicians as well as researchers to pull data from multiple sources and compile it in the same structure without degradation of the information. This endeavor has global implications with the potential to permit the clinical community to define the elements they need, package and share them in a consistent single structure.

August 2021: Kick-off

Sept 2021: 2-day working session identified 4 use cases:
- OMOP-to-FHIR (DMH)
- OMOP-FHIR (Vocabulary)
- OMOP-to-FHIR (DQM)
- FHIR-to-OMOP Oncology**
Fast Healthcare Interoperability Resources (FHIR®)

- a next generation standards framework from HL7

- Describes data formats for clinical and administrative healthcare data known as “Resources”

- Data exchange through standardized Representational State Transfer (REST)-based application programming interfaces (APIs)

- Governance, process, and tooling
The Impact of HL7

• **Influence** – in market and regulatory adoption; over 450 organizational members in commercial, non-profit, and government.

• **Penetration** - almost all hospitals in the U.S. use some form of an HL7 data product (HL7v2, CDA)

• **Relevance** - FHIR will increase in relevance for the foreseeable future
Why FHIR?

• A pillar of the National Strategy for Digital Health
• In 2019, **84%** of hospitals and **61%** of clinicians adopted API technology enabled with Health Level Seven (HL7)® Fast Healthcare Interoperability Resources (FHIR)

Why FHIR?

• Write-one, use many
  – Reduce bespoke translations
FHIR Resources and API
Fast Healthcare Interoperability Resources (FHIR®)

- a next generation standards framework from HL7
- Describes data formats for clinical and administrative healthcare data known as “Resources”
- Data exchange through standardized Representational State Transfer (REST)-based application programming interfaces (APIs)
- Governance, process, and tooling
FHIR Patient Resource

- Easy readability
- Extensible
- Represented in multiple formats
  - JSON, XML, Turtle
FHIR API Search Parameters

- REST-based.
- Basic queries with search parameters are standardized.
  - A FHIR client should be able to query this from any conformant FHIR server

- Parameters provide standardized sorting and filtering queries

**HTTP GET**

```http
http://myexamplefhirendpoint.com/Patient/glossy
```

**HTTP Response**

```xml
<FHIR client>
  <Patient xmlns="http://hl7.org/fhir">
    <id value="glossy"/>
    <meta>
      <lastUpdated value="2014-11-13T11:41:05+11:00"/>
    </meta>
    <status value="generated"/>
    <div xmlns="http://www.v3.org/2004/08/vsn1"

<p>Henry Levitt the 7th</p>
</div>
</extension>
<identifier>
  <use value="usual"/>
  <type>
    <coding>
      <code value="http://hl7.org/fhir/v2/0203"/>
      <code value="NHS"/>
    </coding>
  </type>
</identifier>
</Patient>
</FHIR client>
```

<table>
<thead>
<tr>
<th>Search Parameter Types</th>
<th>Parameters for all resources</th>
<th>Search result parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number</td>
<td>_id _lastUpdated _tag</td>
<td>_sort _count _include _revinclude _summary _total</td>
</tr>
<tr>
<td>Date/DateTime</td>
<td>_profile _security _source</td>
<td>_elements _contained _containedType</td>
</tr>
<tr>
<td>String</td>
<td>_text _content _has _type</td>
<td></td>
</tr>
<tr>
<td>Token</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reference</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Composite</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Quantity</td>
<td></td>
<td></td>
</tr>
<tr>
<td>URI</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Special</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
## Let’s Explore FHIR

### FHIR Patient Resource


<table>
<thead>
<tr>
<th>Name</th>
<th>Flags</th>
<th>Card.</th>
<th>Type</th>
<th>Description &amp; Constraints</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patient</td>
<td></td>
<td></td>
<td>DomainResource</td>
<td>Information about an individual or animal receiving health care services</td>
</tr>
<tr>
<td>identifier</td>
<td>Σ</td>
<td>0..255</td>
<td>Identifier</td>
<td>An identifier for this patient</td>
</tr>
<tr>
<td>active</td>
<td>?!</td>
<td>0..1</td>
<td>boolean</td>
<td>Whether this patient’s record is in active use</td>
</tr>
<tr>
<td>name</td>
<td>Σ</td>
<td>0..255</td>
<td>HumanName</td>
<td>A name associated with the patient</td>
</tr>
<tr>
<td>telecom</td>
<td>Σ</td>
<td>0..255</td>
<td>ContactPoint</td>
<td>A contact detail for the individual</td>
</tr>
<tr>
<td>gender</td>
<td>Σ</td>
<td>0..1</td>
<td>code</td>
<td>male</td>
</tr>
<tr>
<td>birthDate</td>
<td>Σ</td>
<td>0..1</td>
<td>date</td>
<td>The date of birth for the individual</td>
</tr>
<tr>
<td>deceased[x]</td>
<td>?!</td>
<td>0..1</td>
<td>boolean</td>
<td>Indicates if the individual is deceased or not</td>
</tr>
<tr>
<td>deceasedboolean</td>
<td></td>
<td></td>
<td>boolean</td>
<td></td>
</tr>
<tr>
<td>deceasedDateTime</td>
<td></td>
<td></td>
<td>dateTime</td>
<td></td>
</tr>
<tr>
<td>address</td>
<td>Σ</td>
<td>0..255</td>
<td>Address</td>
<td>An address for the individual</td>
</tr>
<tr>
<td>maritalStatus</td>
<td>Σ</td>
<td>0..1</td>
<td>CodeableConcept</td>
<td>Martial (civil) status of a patient</td>
</tr>
<tr>
<td>multipleBirth[x]</td>
<td></td>
<td></td>
<td>boolean</td>
<td>Whether patient is part of a multiple birth</td>
</tr>
<tr>
<td>multipleBirthboolean</td>
<td></td>
<td></td>
<td>boolean</td>
<td></td>
</tr>
<tr>
<td>multipleBirthInteger</td>
<td></td>
<td></td>
<td>integer</td>
<td></td>
</tr>
<tr>
<td>photo</td>
<td>Σ</td>
<td>0..255</td>
<td>Attachment</td>
<td>Image of the patient</td>
</tr>
<tr>
<td>contact</td>
<td>Σ</td>
<td>0..1</td>
<td>BackboneElement</td>
<td>A contact party (e.g. guardian, partner, friend) for the patient</td>
</tr>
<tr>
<td>relationship</td>
<td>Σ</td>
<td>0..255</td>
<td>CodeableConcept</td>
<td>The kind of relationship</td>
</tr>
<tr>
<td>name</td>
<td>Σ</td>
<td>0..1</td>
<td>HumanName</td>
<td>A name associated with the contact person</td>
</tr>
<tr>
<td>telecom</td>
<td>Σ</td>
<td>0..1</td>
<td>ContactPoint</td>
<td>A contact detail for the person</td>
</tr>
<tr>
<td>address</td>
<td>Σ</td>
<td>0..1</td>
<td>Address</td>
<td>Address for the contact person</td>
</tr>
<tr>
<td>gender</td>
<td>Σ</td>
<td>0..1</td>
<td>code</td>
<td>male</td>
</tr>
<tr>
<td>organization</td>
<td>Σ</td>
<td>0..1</td>
<td>Reference(Organization)</td>
<td>Organization that is associated with the contact</td>
</tr>
<tr>
<td>period</td>
<td>Σ</td>
<td>0..1</td>
<td>Period</td>
<td>The period during which this contact person or organization is valid to be contacted relating to this patient</td>
</tr>
<tr>
<td>communication</td>
<td>Σ</td>
<td>0..1</td>
<td>BackboneElement</td>
<td>A language which may be used to communicate with the patient about his or her health</td>
</tr>
<tr>
<td>language</td>
<td>Σ</td>
<td>0..1</td>
<td>CodeableConcept</td>
<td>The language which can be used to communicate with the patient about his or her health</td>
</tr>
<tr>
<td>preferred</td>
<td>Σ</td>
<td>0..1</td>
<td>boolean</td>
<td>Language preference indicator</td>
</tr>
<tr>
<td>generalPractitioner</td>
<td>Σ</td>
<td>0..1</td>
<td>Reference(Practitioner</td>
<td>Patient’s nominated primary care provider</td>
</tr>
<tr>
<td>managingOrganization</td>
<td>Σ</td>
<td>0..1</td>
<td>Reference(Organization)</td>
<td>Organization that is the custodian of the patient record</td>
</tr>
<tr>
<td>other</td>
<td>Σ</td>
<td>0..1</td>
<td>Reference(Patient</td>
<td>RelatedPerson)</td>
</tr>
<tr>
<td>type</td>
<td>Σ</td>
<td>0..1</td>
<td>code</td>
<td>replaced-by</td>
</tr>
</tbody>
</table>
Let’s Explore FHIR

https://api.logicahealth.org/mcdesitru2/open/Patient?given:contains=Jenny&_format=json

```json
{
  "resourceType": "Bundle",
  "id": "e21c296f-9761-40a0-902b-eb43db4007cf",
  "meta": {
    "lastUpdated": "2022-10-15T01:55:29.433+00:00"
  },
  "type": "searchset",
  "total": 1,
  "link": [
    {
      "relation": "self",
      "url": "https://api.logicahealth.org/mcdesitru2/open/Patient?_format=json&given%3Acontains=Jenny"
    }
  ],
  "entry": [
    {
      "fullUrl": "https://api.logicahealth.org/mcdesitru2/open/Patient/cancer-patient-jenny-m",
      "resource": {
        "resourceType": "Patient",
        "id": "cancer-patient-jenny-m",
        "meta": {
          "versionId": "2",
          "lastUpdated": "2022-10-06T21:13:55.000+00:00",
          "source": "#yqx1GX3vxh98qap",
          "profile": [
          ]
        },
        "text": {
          "status": "generated",
```

---

These are the JSON responses for the FHIR API call to search for a patient named Jenny. The JSON structure includes details such as the resource type, ID, meta data, and links to related resources.
What if FHIR doesn’t quite fit what I need?

- too loose...
  - create constraints...
    - e.g.: limit cardinality, limit code choices, make specific elements required
  - need a modifier or qualifier...
    - add a standard extension
    - create a new extension...

**FHIR Profile**

- Additional “rules” that further extend or constrain FHIR base resources
- Represented as a FHIR profile.
- Specifications are published in a FHIR Implementation Guide (IG)
Example: Patient

http://hl7.org/fhir/patient.html

https://build.fhir.org/ig/HL7/US-Core/StructureDefinition-us-core-patient.html

This structure is derived from Patient.
FHIR Registries

- Where to find profiles and IGs in progress

`http://fhir.org/guides/registry/`

**Implementation Guide Registry**

The base [FHIR Specification](http://fhir.org/) is a platform specification - a specification on which all sorts of different solutions are built. The specification focuses on defining capabilities, and creating an ecosystem. National standards, vendor consortiums, clinical societies, etc publish “implementation guides” that define how the capabilities defined by the FHIR specification are used in particular data exchanges, or to solve particular problems. Here is a list of some of the implementation guides defined by the FHIR community:

In addition to this list of Implementation Guides, the full FHIR registry is at [http://registry.fhir.org/](http://registry.fhir.org/).
Oncology on FHIR

mCODE™
People’s lives are depending on what we do and what this data tells us.

DR. MONICA BERTAGNOLLI
Chief of Surgical Oncology, Dana-Farber Cancer Institute/Brigham and Women’s Hospital
Professor of Surgery, Harvard Medical School
President, Alliance for Clinical Trials in Oncology

minimal Common Oncology Data Elements

Every patient’s journey improves all future care
A Fast Healthcare Interoperability Resources (FHIR®)-based core set of common data elements for cancer that is standardized, computable, clinically applicable and available in every electronic health for patients with a cancer diagnosis

**A standard health record** for oncology

The **minimal set of data elements** applicable to all cancers, and collected for:

- Standardized information exchange
- Use-case driven and targeted use

Oncology data element domains: **patient, disease, treatment, outcomes, genomics, lab/vital**

Building an Engaged Network of Health System Solutions

- **Active** – Committed or actively participating in planning, design, development, piloting
- **Engaged & Previously Expressed Interest** – Engaged in multiple conversations and/or in the process of being Active

**ICAREdata**
**Trial Matching**
**Registry Reporting**
**Radiation Therapy Treatment Data**

**Brigham and Women’s Hospital**
**City of Hope**
**Dana Farber Cancer Institute**
**Duke University**
**Heartland Cancer Research**
**Massachusetts General Hospital**
**McGill University**
**MD Anderson Cancer Center**
**Metro-Minnesota Community Oncology**
**Missouri Baptist**
**Northwell Health**
**Rush University Medical Center**
**Saint Joseph Mercy Health System**
**The Ohio State University**

**The University of Chicago Medicine**
**ThedaCare**
**Trinity Health**
**UNC Lineberger Comprehensive Cancer Center**
**University of California San Francisco**
**University of Kansas Medical Center**
**University of Michigan**
**University of Pennsylvania**
**University of Texas Southwestern**
**Veterans Health Administration**
**Virginia Commonwealth University**
**Wake Forest University**
**Washington University in St Louis**

**Onoclinicas**
**Taiwan Cancer Registry**
**Netherlands Cancer Registry**
**UC Los Angeles**
**Mayo Clinic**

**Scaling through Industry Implementations**

- **CancerInsights**
- **Cerner**
- **Clinical Pipe**
- **Elekta**
- **Elsevier**
- **Epic**
- **Flatiron**
- **IQVIA**
- **Jitterbit**
- **MassiveBio**
- **Mettle Solutions**
- **Microsoft**
- **NeuralFrame**
- **Nuance**
- **PatientLink**
- **Pfizer**
- **RaySearch**
- **Roche**
- **Semedy**
- **Syntropy**
- **Tempus**
- **Trial Scope**
- **TrialJectory**
- **Varian**
- **Varian**
- **Wemedoo**
mCODE is a FHIR Publication

http://hl7.org/fhir/us/mcode/
FHIR to OMOP – Oncology Use Case

- standardized exchange of cancer data for large-scale observational studies
- use of study results as actionable data to drive oncology treatment decisions and monitoring
Integrative Use Cases

Option 1: Provider uses portal
- Request “Patients Like Mine” (Phenotypes, Cancer Diagnosis, Stage, Biomarker, etc.)
- Match study based on phenotypes

Option 2: EHR proxy to portal
- Updates cancer patient diagnosis, treatment, etc., data
- Request Studies
- Match study based on phenotypes
mCODE and OMOP CDM

FHIRE Base Resources

mCODE STU 2

OMOP Common Data Model (CDM)*

Legend:
- mCODE-relevant OMOP CDM “base”
- mCODE-relevant OMOP CDM “Oncology Extension”
mCODE derives from FHIR Base Resources
### mCODE to OMOP Alignment Progress

<table>
<thead>
<tr>
<th>mCODE Profile</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cancer Disease Status Profile</td>
<td>2</td>
</tr>
<tr>
<td>Cancer Patient Profile</td>
<td>3</td>
</tr>
<tr>
<td>Cancer-Related Medication Administration Profile</td>
<td>2</td>
</tr>
<tr>
<td>Cancer-Related Medication Request Profile</td>
<td>1</td>
</tr>
<tr>
<td>Cancer-Related Surgical Procedure Profile</td>
<td>1</td>
</tr>
<tr>
<td>Cancer Stage Group Profile</td>
<td>2</td>
</tr>
<tr>
<td>Comorbidities Elixhauser Profile</td>
<td>D</td>
</tr>
<tr>
<td>ECOG Performance Status Profile</td>
<td>1</td>
</tr>
<tr>
<td>Genomic Region Studied Profile</td>
<td>2</td>
</tr>
<tr>
<td>Genomic Specimen Profile</td>
<td>2</td>
</tr>
<tr>
<td>Genomic Variant Profile</td>
<td>2</td>
</tr>
<tr>
<td>Genomics Report Profile</td>
<td>2</td>
</tr>
<tr>
<td>Karnofsky Performance Status Profile</td>
<td>1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>mCODE Profile</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>mCODE Patient Bundle Profile</td>
<td>D</td>
</tr>
<tr>
<td>mCODE Patient Group Profile</td>
<td>D</td>
</tr>
<tr>
<td>Primary Cancer Condition Profile</td>
<td>3</td>
</tr>
<tr>
<td>Radiotherapy Course Summary Profile</td>
<td>1</td>
</tr>
<tr>
<td>Radiotherapy Volume Profile</td>
<td>1</td>
</tr>
<tr>
<td>Secondary Cancer Condition Profile</td>
<td>1</td>
</tr>
<tr>
<td>TNM Distant Metastases Category Profile</td>
<td>1</td>
</tr>
<tr>
<td>TNM Primary Tumor Category Profile</td>
<td>1</td>
</tr>
<tr>
<td>TNM Regional Nodes Category Profile</td>
<td>1</td>
</tr>
<tr>
<td>Tumor Profile</td>
<td>2</td>
</tr>
<tr>
<td>Tumor Marker Test Profile</td>
<td>2</td>
</tr>
<tr>
<td>Tumor Size Profile</td>
<td>2</td>
</tr>
<tr>
<td>Tumor Specimen Profile</td>
<td>2</td>
</tr>
</tbody>
</table>

### mCODE-OMOP Map Status

- Mapped, reviewed, tested: 3 (11.5%)
- Mapped, reviewed, not tested: 2 (7.6%)
- Mapped, not reviewed: 4 (15.3%)
- Not Mapped: 5 (19.2%)
- Deprecated (OOS): 15 (57.6%)
Demo
Patient Jenny M. is a 55 year old non-Hispanic white female with a past medical history significant for depression, a 20-pack-year history of smoking (current smoker), anxiety, and hypertension. Her family history was significant for a maternal aunt with ovarian cancer at age 69, a sister with breast cancer at age 64, and deceased paternal uncle due to pancreatic cancer.
FHIR-OMOP Testbed

- FHIR server
- OMOP CDM 5.4 Database
- ATLAS

- base R4
- US core
- mCODE

- onco
- omop_cdm_mhi
- omop_cdm_mitre
- omop_vocab

- FHIR server
- OMOP CDM 5.4
- Database
- ATLAS

- FHIR server
- OMOP CDM 5.4
- Database
- ATLAS
mCODE example in ATLAS
Design Considerations
Disclaimers

• General
  – Mappings based on “plain vanilla” OMOP CDM 5.4
  – Alignment with OMOP Oncology cancer modifiers is an ongoing and future effort
Example Patterns for Discussion

- ID management
- Handling Cardinality
- The postcoordination/precoordination issue
- Missing data
PrimaryCancerCondition does not limit cancer code to one vocabulary

This introduces variations in the source data

<table>
<thead>
<tr>
<th>Encoding</th>
<th>Code</th>
<th>Histology Morphology Behavior Extension</th>
<th>Body Site</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNOMED Encoded</td>
<td>Any descendant of 363346000 &quot;Malignant neoplastic disease (disorder)&quot;</td>
<td>Any descendant of 367651003 &quot;Malignant neoplasm of primary, secondary, or uncertain origin (morphologic abnormality)&quot;</td>
<td>Any descendant of 123037004 &quot;Body structure&quot;</td>
</tr>
<tr>
<td>ICD-10-CM Encoded</td>
<td>Any ICD-10-CM primary code (precoordinated)</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>ICD-O-3 Encoded</td>
<td>The code 363346000 &quot;Malignant neoplastic disease (disorder)&quot;</td>
<td>Any ICD-O-3 Morphology Code (including /1, /2, or /3 suffix for primary cancers, and /6 suffix for secondary cancers)</td>
<td>Any ICD-O-3 Topology Code</td>
</tr>
</tbody>
</table>
mCODE
Primary Cancer Condition

OMOP CDM

Post-Coordination/Pre-Coordination
Missing Vocabularies

Example: GenomicsVariant
Missing OMOP Concepts

- Usagi used for human review of mapped FHIR-to-OMOP concepts
- ECOG score and Interpretation are separate tables with link.
- OMOP does not have answer list identifiers (LL-xxxx)
- LOINC answer identifiers (LA-xxxx) are an OMOP Meas Value.
- Use the relationship “Answer of” to find the concept to identify the domain/table for that concept.
- Link the interpretation for ECOG through obs_meas_event.
Handling Observation Components

http://build.fhir.org/ig/HL7/genomics-reporting/Observation-Pgx-var-1011.html
based on http://build.fhir.org/ig/HL7/genomics-reporting/StructureDefinition-variant.html

Example Observation: Pgx-var-1011

Generated Narrative

status: Final
category: Laboratory
code: Genomic variant assessment
subject: Patient(PatientExample) - "EVERYMAN"
effective: 2020-01-01
value: Present (LOINC:62963-4)
method: Sequencing (LOINC:43425-0)

code: Genomic reference sequence (ID) (LOINC:41001-7)
value: 10754 (HUG001000100)

code: Genomic coordinate system (Type) (LOINC:95282-6)
value: 1-based character counting (LOINC:852102-0)

code: Genomic allele start-end (LOINC:81254-5)
value: 95521657-95521657

code: Genomic ref allele (ID) (LOINC:97457-8)
value: C

code: Genomic alt allele (ID) (LOINC:97551-0)
value: C
### Handling FHIR Observation Components

#### mCODE STU2 Data Dictionary and OMOP Mapping Genomics

<table>
<thead>
<tr>
<th>Component</th>
<th>Description</th>
<th>Code</th>
<th>Value</th>
<th>Component</th>
<th>Description</th>
<th>Code</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>measurement_id</td>
<td></td>
<td>12345678</td>
<td></td>
<td>component</td>
<td>Gene studied (ID)</td>
<td>LOINC484018-6</td>
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#### Observation table column FHIR

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#### Example Observation: Pgx-var-1011

- Category: Laboratory (Observation Category Codes 
- Code: Genetic variant assessment (LOINC:82154-5)
- Value: Present (LOINC:82154-5)

- Method: Sequencing (LOINC:82154-5)
- Component code: Gene studied (ID) (LOINC:82121-5)
- Value: >20

- Component code: Allele read depth (LOINC:82121-5)
- Value: >20

- Component code: DNA Change Type (LOINC:82121-5)
- Value: wild type (sequenceontology.org#ID:00007073)

- Component code: Variable name (LOINC:82121-5)
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- Component code: Gene studied (ID) (LOINC:82121-5)
- Value: >20

- Component code: Allele read depth (LOINC:82121-5)
- Value: >20

- Component code: DNA Change Type (LOINC:82121-5)
- Value: wild type (sequenceontology.org#ID:00007073)
General Guidelines Summary FHIR-OMOP

- **Cookbook steps:**
  - identify the questions/information elements needed for the observational study
  - create the content inventory to support the study
  - analyze the corpus between the content inventory FHIR codeableConcept with the OMOP Ontology for gaps and misaligned domains.
  - identify the FHIR elements that support the study
  - Generate a FHIR profile for the study to ensure translation among multiple data sources to the OMOP CDM.
  - Map the relevant FHIR resources / profiles to OMOP CDM
  - Populate the OMOP CDM records at the atomic level
  - Preserve the FHIR relationships (or provenance) from the original resource where possible (meas_event_id, observation_event_id, fact_relationship, etc.)
  - For OHDSI Network Studies, test data quality and consistency in FHIR-OMOP data translation using a common test data set relevant to the network study.
OHDSI Takeaways for HL7 Community

- generally a relational database design
- driven by a "semantic first" mapping – the concept determines the structural binding – results in complex concept conversion logic
- Concepts are “closed world” scoped to the study
- Terminologies not recognized by OMOP concept impact the effectiveness and reuse of the cohort definitions and characterizations.
- FHIR-to-OMOP lossiness is acceptable as long as it’s sufficient for the study
HL7 Takeaways for OHDSI Community

• **FHIR implementation guides can be inconsistent**
  - Multiple ways to represent data models and loose terminology bindings create a lot of complexity ETL logic cohort definitions.
    - Possible mitigation: Tighten IGs to minimize variation
  - HL7 adopts many code systems which are not recognized in OMOP. Results in unstructured text and complicates cohort definitions.
    - Recommendation: HL7 Healthcare Terminology Authority and OMOP Vocabulary to create a content inventory of all internal and external terminologies.
Recommendations

1. **Short-term: Clearer mapping guidance**
   - Create *overarching design and implementation principles* for FHIR and OMOP alignment.
     - Scope
     - General design patterns/best practices
   - Create a terminology content inventory of HL7 and OMOP vocabularies

2. **Longer-term: Alignment towards a common model**
   - compile the list of mapping gaps for the long journey of consensus
   - Data quality validation in federated environments: Example - Create a “standard-test dataset” that can QA test federated deployments and ensure that ETL logic comes to similar conclusions.
Recommendations (cont’d)

3. Agree to the **vocabulary versions** for translating from FHIR-OMOP.
   - Enforce inclusion of versions in FHIR codeableConcepts.

4. Create **starter heuristics and guidelines** for how to deal with
   - variations
   - semantic drift and version discrepancies

5. A **baseline set of test data** and QA to ensure an “apples-to-apples” comparison.
Knowledge exchange of tools and Implementation Best Practices

**OHDSI**

**HL7**

**OHDSI: ATLAS**

**HL7: CDS Connect**

**OHDSI: HADES**

**HL7: CQL**
What’s Next
The FHIR-OMOP Cookbook
aka: “Project Prometheus”

- A guide to designing and deploying a FHIR-to-OMOP implementation.
- Based on the Book of OHDSI.
- A living document in early stages.
Advancing the Cause
Open Call to Participate

• Multiple “on-ramps”
  – Reviewer / Subject Matter Expert
    • use case development, persona building, clinical guidance
  – Informatics
    • structural and semantic analysis and mapping
  – Integration
    • infrastructure setup and maintenance: FHIR server, OMOP DB, ATLAS, ETL conversion scripts,
  – Developer / Researcher
    • data visualization, research
    • cohort / phenotype development
Communications

- Weekly: **Thursdays at 12p ET**
- Confluence page
  - https://confluence.hl7.org/display/OOF/FHIR-OMOP+Oncology+Use+Case
- Zulip:
  - https://chat.fhir.org/#narrow/stream/286658-omop-.2B.20fhir

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**FHIR-OMOP Oncology Use Case**

**Table of Contents**
- Goals and Objectives
- Initial Use Case:
- Meeting Minutes
- Useful Links
  - HL7
  - OHDSI-OMOP

**Goals and Objectives**

To align FHIR and the OMOP CDM for the purposes of building an oncology learning health system that exchanges patient data for large scale observational studies and analytics.

**Initial Use Case:**

Provider-driven Oncology EHR that captures basic oncology diagnosis and staging information is sent as a set of FHIR resources that is translated to the OMOP CDM for use in observational research. Elements for mapping include:

- cancer conditions and staging
- treatments
- tumor markers and genomic variants

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**JOIN US!**
Thank You!