Combined Utilization of SNOMED-CT with LOINC for Comparative Effectiveness Research

SNOMED CT Implementation Showcase 2014

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• University of Utah OpenFurther Team members (past & present)
• Apelon

*The opinions expressed [in this presentation] are those of the authors and do not reflect the official position of AHRQ, HHS, NCRR, NCATS, or NIH
Objectives

• Mapping local coding schemata to SNOMED CT and LOINC for better representation of laboratory (lab) results and their enhanced retrieval for clinical research.

• Opportunities for data validation and ontology reasoning on linking SNOMED CT with LOINC.
Overview

• What is PHIS+?
• What is FURTHeR/OpenFurther?
• What problems did we face with lab data?
• How did we use SNOMED-CT to improve LOINC mappings?
• What was another approach we could have used?
• Why was the approach we used using SNOMED-CT was better for our use case?
What is PHIS+?

- An effort to augment the Children’s Hospital Association’s (CHA) existing electronic database of administrative data called the Pediatric Health Information System (PHIS) with clinical data in order to conduct Comparative Effectiveness Research (CER) studies.
- Comparative effectiveness research (CER) is designed to inform health-care decisions by providing evidence on the effectiveness, benefits, and harms of different treatment options.
- University of Utah Biomedical Informatics partnered with CHA in this effort.
- Agency for Healthcare Research and Quality (AHRQ) PROSPECT funded project.
PHIS+ Hospitals

1. Cincinnati Children’s Hospital Medical Center (CCHMC)
2. Children’s Hospital Boston (CHB)
3. Children’s Hospital of Philadelphia (CHOP)
4. Children’s Hospital of Pittsburgh (CHP)
5. Primary Children’s Medical Center, Intermountain Healthcare (PCMC)
6. Seattle Children’s Hospital (SCH)

Pediatric Research in Inpatient Setting (PRIS) Sites
Overview PHIS+

3 Data Streams
- Laboratory
- Microbiology
- Radiology

4 CER Studies
- Pneumonia
- Appendicitis
- Osteomyelitis
- Gastroesophageal Reflux Disease

5 Years Data
- 2007 – 2011
- 2009 – Development
- 2012….
### Electronic Data Sources for PHIS+ Hospitals

<table>
<thead>
<tr>
<th>Site</th>
<th>Lab Information System</th>
<th>Electronic Medical Record</th>
<th>PHIS+ Lab Datasource</th>
</tr>
</thead>
<tbody>
<tr>
<td>CCHMC</td>
<td>Cerner Millenium</td>
<td>Epic</td>
<td>Epic Clarity</td>
</tr>
<tr>
<td>CHB</td>
<td>Cerner Pathnet</td>
<td>Cerner</td>
<td>In-house data warehouse</td>
</tr>
<tr>
<td>CHOP</td>
<td>Meditech</td>
<td>Epic</td>
<td>In-house data warehouse</td>
</tr>
<tr>
<td>CHP</td>
<td>Sunquest</td>
<td>Cerner</td>
<td>Cerner PowerInsight*</td>
</tr>
<tr>
<td>PCMC</td>
<td>Sunquest</td>
<td>In-house system</td>
<td>In-house data warehouse</td>
</tr>
<tr>
<td>SCH</td>
<td>Cerner Pathnet</td>
<td>Cerner</td>
<td>Cerner PowerInsight</td>
</tr>
</tbody>
</table>

Narus et. al, *Federating Clinical Data from Six Pediatric Hospitals: Process and Initial Results from the PHIS+ Consortium*. AMIA 2011
FURTHeR is an informatics platform designed to federate data from heterogeneous data sources.

OpenFurther is an open source version of the platform & is available OpenFurther.org.
Component Overview

- Query Tool
- Federated Query Engine
- Data Source Adapters
- Admin & Security Components
- Virtual Identity Resolution on the GO (VIRGO)
- Quality & Analytics Framework
- Metadata Repository
- Terminology/Ontology Server

Diagram:
- Quality Analysis
- VIRGO
- Security
- Data Sources
- Counts & Data
Developmental Process Overview

FURTHeR was customized to aggregate data for CHA

Narus et. al, Federating Clinical Data from Six Pediatric Hospitals: Process and Initial Results from the PHIS+ Consortium. AMIA 2011

FURTHeR= Federated Utah Research & Translational Health e-Repository
OpenFurther Typical Lab Translation Handling

- OpenFurther translates each local site lab test code to a LOINC code.
- Mappings are manually created by a terminologist.
  - RELMA is helpful but not always used.

<table>
<thead>
<tr>
<th>Local Test Code</th>
<th>Test Description</th>
<th>LOINC Code</th>
<th>LOINC NAME</th>
</tr>
</thead>
<tbody>
<tr>
<td>691225</td>
<td>pH Blood</td>
<td>11558-4</td>
<td>pH of Blood</td>
</tr>
</tbody>
</table>
Terminology Server Perspective
Local Test Code/Single Specimen

Using a terminology system like Apelon DTS we can capture additional properties for a concept.

Notice for this concept there is a single Mapping to LOINC.
**Local Test Code Issues**

<table>
<thead>
<tr>
<th>Local Test Code</th>
<th>Test Description</th>
<th>LOINC Code Generic Specimen</th>
<th>LOINC NAME</th>
</tr>
</thead>
<tbody>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Abdominal</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
</tr>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Ascites</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
</tr>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Chest Fluid</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
</tr>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Joint Fl</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
</tr>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Knee</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
</tr>
</tbody>
</table>

- Local Test Code having multiple specimens
- We could map to LOINC using the most generic specimen that all tests have in common
## Local Test Code Issues

<table>
<thead>
<tr>
<th>Local Test Code</th>
<th>Test Description</th>
<th>Generic Specimen</th>
<th>LOINC NAME</th>
<th>Specific Specimen</th>
<th>LOINC NAME</th>
</tr>
</thead>
<tbody>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Abdominal</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
<td>14621-7</td>
<td>Appearance of Peritoneal fluid</td>
</tr>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Ascites</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
<td>14621-7</td>
<td>Appearance of Peritoneal fluid</td>
</tr>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Chest Fluid</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
<td>14620-9</td>
<td>Appearance of Pleural fluid</td>
</tr>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Joint Fl</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
<td>29605-3</td>
<td>Appearance of Synovial fluid</td>
</tr>
<tr>
<td>699414</td>
<td>Body Fluid Appearance Knee</td>
<td>9335-1</td>
<td>Appearance of Body fluid</td>
<td>29605-3</td>
<td>Appearance of Synovial fluid</td>
</tr>
</tbody>
</table>

- Mapping this more granularly to a specific specimen is more accurate and reflects the true local test.
How can we map identical local codes to LOINC when those local codes represent different lab tests?

Leverage Specimen & Body Site
And... Synergy
Association Qualifiers

- Use **Association Qualifiers** to enable maps & translations to specimen specific LOINC Codes.
- Specimen descriptions from the source sometimes contained just body site information or a combination of specimen & body site.
- Association Qualifiers Used
  - Generic Specimen
    - Body Fluid
  - Specific Specimen
    - Peritoneal Fluid
  - Body Site
    - Tissue Specimen (from some body site)
How OpenFurther Handles Lab Translations in PHIS+ Instance Using Association Qualifiers

Data Needed For Translation
- Local Test Code
- Local Specimen Code

OpenFurther Checks Terminology Server
- hasSpecimenType
- hasBodySite

If hasSpecimenType is mapped it is used

OpenFurther then checks Local Test Code and uses the hasSpecimenType or hasBodySite to check the qualifiers on the mapped LOINC codes

If hasSpecimenType is NOT mapped hasBodySite is used
Test Code with Multiple Specimens

- **Body Fluid RBC Abdominal Fluid**
  - Code: C60
  - ID: 60
  - Namespace: AssociationQualifierTest (Thesaurus, Local, Editable, Not Published)
  - Properties
    - **Description**: Body Fluid Red Cell Count Abdominal Fluid
    - **Name**: Body Fluid Red Cell Count
    - **Specimen**: Peritoneal fluid sample (specimen)
  - Associations
    - ExactMatch [Further]: Erythrocytes [#/volume] in Body fluid [LOINC]
      - **Generic Specimen**: Body fluid (substance)
    - ExactMatch [Further]: Erythrocytes [#/volume] in Peritoneal fluid [LOINC]
      - **Specific Specimen**: Peritoneal fluid sample (specimen)
  - Inverse Associations
    - Child Of: Labs

- **Body Fluid RBC Chest Fluid**
  - Code: C59
  - ID: 59
  - Namespace: AssociationQualifierTest (Thesaurus, Local, Editable, Not Published)
  - Synonyms
    - **Synonym**: Body Fluid RBC Chest Fluid (Preferred)
  - Properties
    - **Description**: Body Fluid Red Cell Count Chest Fluid
    - **Name**: Body Fluid Red Cell Count
    - **Specimen**: Pleural fluid (substance)
    - **Unit of Measure**: /mm3
  - Associations
    - ExactMatch [Further]: Erythrocytes [#/volume] in Body fluid [LOINC]
      - **Generic Specimen**: Body fluid (substance)
    - ExactMatch [Further]: Erythrocytes [#/volume] in Pleural fluid [LOINC]
      - **Specific Specimen**: Pleural fluid (substance)
  - Inverse Associations
    - Child Of: Labs

**ExactMatch Association with Generic Specimen Qualifier of ‘Body Fluid’**

**Same ‘Code’, different ‘Specimen’**
Test Code with Body Site

- **Nasopharyngeal Swab**
  - Code: C1272
  - ID: 1272
  - Namespace: Seattle (Thesaurus, Local, Editable, Not Published)
  - **Synonyms**
    - Synonym: Nasopharyngeal Swab (Preferred)
  - **Properties**
    - Code: 312624 AssociationQualifierTest (Thesaurus, Local, Editable, Not
    - Code: 740247
    - Code: Nasopharyngeal Swab
    - Description: Nasopharyngeal Swab
    - Name: Admit Nasal Culture
    - Name: Nasopharyngeal Swab
  - **Associations**
    - hasBodySite [Further]: Entire nasopharynx (body structure) [SNOMED CT]
    - hasSpecimenType [Further]: Nasopharyngeal swab (specimen) [SNOMED CT]
  - **Inverse Associations**
    - Child Of: Specimen
Test Code with Body Site
Another Approach

### Anatomy of a LOINC Term

<table>
<thead>
<tr>
<th>5193-8</th>
<th>Hepatitis B virus surface Ab</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACnc</td>
<td></td>
</tr>
<tr>
<td>Pt</td>
<td></td>
</tr>
<tr>
<td>Ser</td>
<td></td>
</tr>
<tr>
<td>Qn</td>
<td></td>
</tr>
<tr>
<td>EIA</td>
<td></td>
</tr>
</tbody>
</table>

**LOINC Code**

- Component
- Property Measured
- Timing
- System
- Scale
- Method

*There are six major LOINC axes*

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Comparison

• 100 System Sample Types (System) Listed in LOINC User Manual

• 1329 possible specimens with SNOMED-CT
  – 36 Different options containing the word “Blood”

• >10000 possible body sites with SNOMED-CT
Our Approach Using SNOMED-CT Provides

- Two dimensions to query data for clinical research cohorts (using specimens and then tests or the reverse).

- SNOMED-CT hierarchy supports inclusion of specific tests that have child specimen/body site concepts that are not so obvious in LOINC (Subsumption e.g. arterial blood is_a child of blood). Other SNOMED-CT relations could also be used.

- Data Quality - If a blood glucose test has a urine specimen, we know that there is a data quality issue

- There isn’t information loss as SNOMED-CT most times allows mapping to the same level of granularity of specimens/body sites as the local specimen descriptions.
Conclusion

• Mapping the specimen of LOINC to SNOMED-CT offers flexibility that is difficult or not possible by using LOINC alone.
• Mapping other axes of LOINC to SNOMED-CT might also be useful
• Mappings such as this could be shared and curated by the informatics community
Thank you!
Questions/Comments

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@RyanxButcher

www.OpenFurther.org
@OpenFurther on Twitter
References

• Gouripeddi R, Mitchel JA, Narus SP et al. Federating Clinical Data from Six Pediatric Hospitals: Process and Initial Results for Microbiology from the PHIS+ Consortium AMIA Annu Symp Proc. 2012 (Accepted).


