Correctness of Voluntary LOINC Mapping for Laboratory Tests in Three Large Institutions

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Abstract

With IRB approval, we obtained de-identified laboratory test data from 3 large institutions (ARUP, Intermountain, and Regenstrief). In this study we evaluated correctness of mapping local laboratory result codes to Logical Observation Identifier Names and Codes (LOINC®). We received 9,027 laboratory tests mapped to 3,669 unique LOINC codes. A one tenth sample (884 tests) was manually reviewed for correctness of the mappings. After review, there were 4 tests mapped to totally unrelated LOINC codes and there were 36 tests containing at least one error in mapping to the 6 axes of LOINC. The errors of LOINC mapping could be categorized into 4 systematic errors: 1) human errors, 2) mapping to different granularity, 3) lack of knowledge of the meaning of laboratory tests and 4) lack of knowledge of LOINC naming rules. Finally, we discuss how these systematic mapping errors might be avoided in the future.

Introduction

Evaluation of Terminological Systems

Many terminological systems (TSs) are used in Electronic Medical Records (EMR) to enable interoperability in health care. International Classification of Disease (ICD), the Systemized Nomenclature of Medicine (SNOMED), and the Logical Observation Identifier Names and Codes (LOINCR®)[1] are examples of widely used TSs. To improve the development of TSs, it is important to evaluate them from two main perspectives: 1) content independent (functional) evaluations, and 2) content dependent evaluations. Content independent evaluation of TSs discusses the requirements of TSs from a functional, structural and policy perspective. Examples are James Cimino's desiderata[2] for controlled medical vocabularies, and the technical specification "Health informatics – Controlled health terminology – Structure and high-level indicator" published by the International Standards Organization (ISO)[3]. Content dependent evaluations focus on concept coverage, term coverage, synonym completeness, etc. Until TSs are in widespread use in health care systems, the usage of TSs can be pooled for analysis. Two examples include the evaluation of the coverage of the Unified Medical Language System (UMLS) for coding of concepts in the Gene Ontology (GO)[4] and analysis of the coding consistency of LOINC in three hospitals[5].

Current LOINC usage and evaluation

The LOINC committee began to develop a universal code system for reporting laboratory and clinical observations in February of 1994. The current LOINC release (version 2.30, February 26, 2010) contains 57,693 active codes, including both laboratory and clinical observation codes. LOINC is widely used in many domains, including major laboratories, hospitals, public health departments, health care provider networks and insurance companies.[6]

Since LOINC is in widespread use, Huff et al. proposed that there were two main perspectives for evaluating LOINC: 1) Coverage 2) Correctness[7]. The goal of LOINC is to provide standard codes to improve interoperability when sharing clinical data. In pursuit of that goal, the LOINC database is designed to support greater accuracy and to decrease the time and cost when mapping from local codes to standard codes[7]. Manual mapping is not usually an easy task. Without a good understanding of content and the design of LOINC codes, using LOINC could have two possible types of errors: 1) human errors: simple typographic or selection errors, 2) semantic errors, where there is a difficulty in choosing the correct LOINC code. The second kind of error can occur if LOINC is too complicated for the average

mapper to understand, or if the codes have ambiguous meaning. Users could have trouble in aligning local information with the six axis model of LOINC codes. Lau et al. at 3M Health Care reported that in a large scale mapping project LOINC mapping was time consuming and laborious, and that human variation caused mapping inconsistencies and errors[8].

Evaluating LOINC mappings using extensional definitions

Evaluating existing LOINC mappings of laboratory systems is not an easy task because of the use of idiosyncratic abbreviations and the lack of available documentation about the test details. For example, "Red blood cells (RBC)" could have different meanings in different systems. It could be "RBC in cerebral spinal fluid" in one system or "RBC in blood" in another. However, by examining how these two tests are actually used we can determine the real meaning. In looking at instances of results we can observe that these two tests have very different values: one is "1492/mm3" and the other is "4.3-10^6/ul". We call the profile of information associated with tests in these systems, such as frequency of testing, mean value, standard deviation of the value, units of measure, value type (coded vs numeric), etc. **extensional definitions** (EDs)[9]. These profiles or extensional definitions reflect the actual meaning of tests in the system. By utilizing EDs, Zollo et al. automatically cross mapped local laboratory codes from 3 institutions with an accuracy of 81%[10].

Problem Statement

The accuracy of mappings from local codes to LOINC codes influences the quality of interoperability in exchanging clinical observations. We wanted to evaluate mapping accuracy in existing systems, so we collected voluntary LOINC mappings of laboratory tests from three large institutions and created extensional definitions associated these tests. We analyzed the correctness of the mappings, identified systematic errors, and then formulated some suggestions that might improve the LOINC mapping process.

Methods

Data sources

With IRB approval, de-identified patient data were collected from three institutions: 1. Associated Regional and University Pathologists, ARUP Laboratories (Salt Lake City, UT) 2. Intermountain Healthcare, Intermountain (Salt Lake City, UT) 3. Regenstrief Institute, Inc. (Indianapolis, IN). ARUP Laboratories is a national clinical and anatomic pathology reference laboratory and is owned and operated by the Pathology Department of the University of Utah. Intermountain Healthcare is a not-for-profit health care provider organization, with hospitals located in many major cities in Utah. Regenstrief Institute, Inc., an informatics and healthcare research organization, that is located on the campus of the Indiana University School of Medicine in Indianapolis. Regenstrief operates a regional health information exchange in central Indiana called the Indiana Network for Patient Care[new reference] that includes data from more than a hundred source systems and five major hospital systems.

Data scope

This research focused only on mappings related to standard laboratory LOINC codes, i.e. we excluded anatomic pathology and microbiology tests. We chose to focus on laboratory test results because laboratory data is one of the most important kinds of data in the medical record and it has been mapped to LOINC codes more frequently than any other kind of data. At ARUP and Intermountain, the de-identified patient data were collected for the month of April for five consecutive years (each April, from 2003-2007). At Regenstrief, this data was retrieved for a 12 month period (August, 2007 – August 2008). The mappings of local codes to LOINC codes were also collected from the three participating institutions. In this study, we utilized data collected in 2007 from all three institutions.

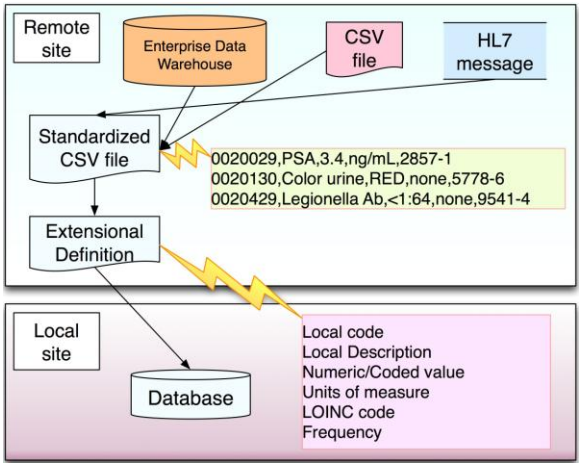

Figure1. Data processing steps.

Collect data and generate extensional definitions

The patient data were initially stored in the source institutions in various formats, with data being stored in an Enterprise Data Warehouse, comma separated values (CSV) files, or HL7 messages. The patient data were retrieved by administrative staff at each

institution. Each individual test result instance included the following database elements: 1.Local code 2.Local description 3.Numeric value 4.Coded variables 5.Units of measure (UOM) 6.LOINC mapping. The retrieved data was transformed into standardized CSV files at each site. The CSV files were then processed to generate extensional definitions (EDs) of each local code. Only EDs were sent to the authors for analysis; no patient identifying information was included (Figure 1). After preparing summary reports, a one tenth sample was examined for LOINC mapping accuracy following explicit review criteria.

Review Criteria

Local Name	Mean	Standard Deviation	Units of Measure	Coded variable	LOINC code
Creatinine, 24 hr urine	1.46	0.54	g/24 h	Null	2162-6
CREAT URINE SEDOUT	0.54	0	Null	See note	2162-6
MACROPHAGE FLUID	18.4	17	%	Null	30427-9

Table 1. The example of some Extensional Definitions (EDs) including mean, standard deviation, units of measure, and coded variable.

We evaluated the accuracy of the mappings based on instantiating the six axis LOINC model for each local code and comparing that local instance to the definition of the LOINC code to which the local code was mapped (Table 1). For each axis we reviewed, we defined 3 categories of review results:

1) **Correct:**. The mapping of a particular axis is correct, e.g. for "Creatinine, 24hr urine" that was mapped to "2162-6:Creatinine:None:MRat:24H:Qn:Urine", the mapping of "Creatinine" for the Analyte is correct.

2) **Error:** The mapping of the axis is incorrect, e.g. a test, "ISLET CELL Ab, IgG" was mapped to "33563-8:Pancreatic islet cell Ab.IgG:None:ACnc:Pt:Qn:Ser", but the test result values are "1:4;1:8;1:16", which are "Titer(s)" and are not "ACnc"; so the mapping is in error. We also considered it an error if a more specific test is mapped to a more general concept, e.g. "Ab.IgG" is mapped to just "Ab". This is considered and error because it represents a loss of meaning when going from the specific code to the more general code.

3) **Unknown:** The mapping of the axis could not be verified due to insufficient information, e.g. a test, "Succinic acid" was mapped to "Succinate/Creatinine (Ratio)". Because the test description only contains "Succinic acid", we cannot confirm to the association to "Creatinine". It is often the case that there is only very general information contained in local test code descriptions.

Results

After collecting the data from all three institutions, 9,027 local laboratory tests mapped to 3,669 unique LOINC codes. A one tenth sample of these 3,669 unique LOINC codes contained 884 laboratory tests that were manually reviewed for correctness of the LONC mappings.

We found 4 tests mapped to totally unrelated LOINC codes: 1) "Cannabinoids" was mapped to "Bacteria identified:Culture:Prid:Pt:Nom:Thrt", but "Cannabinoids" is a chemical substance in the nervous and immune systems and not a bacteria. 2) There are two tests having identical test names in one institutions, "EPI CELL-UR" with UOM "/HPF" that was mapped to "Epinephrine:None: MCnc:Pt:Qn:Urine". Based on the local description and UOM, "EPI CELL-UR" should mean "Epithelia Cell of Urine" per high power field (HPF) using light microscopy. and 3) "Estrogen receptor IP" was mapped to "Basement membrane Ab.IgG:IF:ACnc:Pt:Ord:Ser" and "Estrogen receptor IP" should mean a estrogen receptor, not a basement membrane, which is a thin sheet of fibers underlying the epithelium.

After excluding the above 4 tests, 880 tests were then reviewed by each axis of LOINC mapping (Table 2). Among 880 tests, there are 36 tests containing at least one error in one of the six axes.

	Analyte	**Method**	**Property**	**Time**	**Scale**	**System**
C	755	733	860	869	877	310
U	111	140	10	11	3	562
E	14	7	10	0	0	8

Table 2. The review results of 880 tests by examining each axis of LOINC mapping. The review results were categorized into 3 categories: 1) Correct **(C)** - The mapping is correct, 2) Unknown **(U)** – The

information is insufficient for review, and 3) Error **(E**) – The mapping is error.

The followings are examples of errors of each axis from the above review:

A) Analyte:

1.“Glucose 30 Minute **75 g** Glucose PO, Serum or Plasma” was mapped to “Glucose^30M post dose glucose”. The correct mapping is “Glucose^30M post 75g glucose PO”.

2.“ISLET CELL Ab, **IgG**” was mapped to “Pancreatic islet cell Ab”. The correct analyte is “Pancreatic islet cell Ab.IgG”

3.” Beta Hydroxybutyrate/Creatinine” was mapped to “3-hydroxy-2-methylbutyrate”. The correct analyte is “3-hydroxy,3-methylglutarate/Creatinine”

B) Method:

1.”Bartonella Henselae Ab IgM, Serum Quantitative **EIA**” was mapped to “Bartonella henselae Ab.IgM:IF:Titr:Pt:Qn:Ser:”. The correct method is “EIA”

2.”Cocaine Screen” was mapped to ”Cocaine:None:ACnc:Pt:Ord:Urine”. The correct mapping is “Cocaine: ACnc:Pt:Ord:Urine :Screen”. The correct method is “Screen”.

C) Property:

1.“ISLET CELL Ab, IgG” has tests value “1:4,1:8,1:16,1” and was mapped to “Pancreatic islet cell Ab.IgG:None:**ACnc**:Pt:Qn:Ser”. The correct property should be “Titr”, not “ACnc”.

2. “SEROTYPE 3 (3)” has UOM “ug/ml” and was mapped to “Streptococcus pneumoniae 3 Ab.IgG:None:ACnc:Pt:Qn:Ser”. The correct property is “MCnc” based on its UOM

D) System.

1.” **CSF**-MONOS” was mapped to “26486-1:Monocytes/100 leukocytes:None:NFr:Pt:Qn:**Bld**”. The correct system is “CSF”

2.” pH Temperature Corrected, **Arterial Cord Blood** Quantitative” is mapped to “pH^^adjusted to patients actual temperature:None:SCnc:Pt:Qn:**BldCo**:”. The correct system should be “BldCoA”

Discussion

Mapping is not perfect yet

After reviewing voluntary LOINC mapping of three institutions, we found relatively few errors (less than 5%), but that the mappings are not perfect yet.

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There are four types of systematic errors identified so far: **1) Human errors**: There were 4 tests mapped to totally unrelated LOINC codes. The reasons might be the misunderstanding of meaning of acronym or simply picking up the wrong LOINC codes. **2) Mapping to different granularity:** These types of errors mainly happen when there is a group of LOINC codes having similar analyte but varying degrees of specificity. For example, LOINC codes were not chosen correctly according to the specific subtype of analyte e.g. Ab.IgG was mapped to Ab, instead of Ab.IgG. Currently the LOINC database provides a multi-axial hierarchy of LOINC codes. When exploring LOINC codes, the parent-child relationship of LOINC codes could be displayed for choosing the correct granularity of mapping. **3) Lack of knowledge of the meaning of laboratory tests:** The laboratory methods are still developed actively, e.g. there are enzyme immunoassay (EIA), Western blot, and indirect immunofluorescene (IF) for detecting antibodies. Without understanding the detail of the test itself, it is hard to distinguish the various methods and choose the correct LOINC code. **4) Lack of knowledge of LOINC naming rules:** Measuring the same analyte could be mapped to different LOINC codes for different purposes, e.g. “BENZODIAZEPINES, URINE” has three candidate LOINC codes “19283-1:Benzodiazepines cutoff:Screen:MCnc:Pt:Qn:Urine”, “19284-9:Benzodiazepines-cutoff:Confirm: MCnc:Pt:Qn:Urine”;”19064-5:Bezodiazepines cutoff:null:MCnc:Pt:Qn:Urine” one is for “Screen”, one is for “Confirm”, and another is for “Null”. The methods for “Screen” and “Confirm” could be different, so the sensitivity and precision of tests might be different; therefore two LOINC codes have been created. Without knowing the LOINC naming rules, users cannot choose the correct method among “Screen”, “Confirm” or “Null” appropriately.

Improving the correctness of LOINC mapping

Medline indexing consistency can be used as a model for evaluating LOINC mappings. Funk et al. concluded that high quality MEDLINE indexing

requires an excellent controlled vocabulary, exemplary quality control and highly trained indexers[11]. Based on the above conclusions, LOINC mapping could be improved by five possible approaches: **1) Use more specific naming conventions for local descriptions:** Based on above results, many tests do not have a specific description, e.g. 562 tests out of 880 tests do not contain information about "System" (Specimen types) and it is hard to guess which specimen types from EDs. To include more specific information for each axis could save time and improve the quality of mapping. **2) Develop automated mapping tools:** Mapping is a labor intensive job and human errors can cause careless mapping errors. Automated mapping tools can facilitate mapping processes and reduce human errors. For example, local mappers should use the Regenstrief LOINC Mapping Assistant (RELMA) for semi-automated mappings. **3) Use extensional definitions to validate LOINC mapping:** Some parts of EDs explicitly identify the LOINC axis, e.g. a test with UOM, "mcg/24 h" indicates the property, time aspect, and scale type of LOINC mapping are "MRat","24H" and "Qn". By implementing validation rules into mapping tools, we can detect the invalid mapping when choosing inappropriate codes according to EDs of tests. Furthermore, as more EDs are collected from different places, a reference ED for each LOINC code, e.g. reference mean and standard deviation, UOM, etc. could be distributed with the LOINC database to help build validation rules. **4) Develop enhanced quality control:** Since current LOINC mapping still contains errors, manually evaluating the correctness of LOINC mappings to detect any possible systematic errors and use this information to benchmark the performance of mappings and **5) Provide better training:** Provide better training to teach users to avoid making common errors when mapping. Many errors are caused by lack of knowledge of LOINC code usage. Evaluating voluntary LOINC mappings across institutions can identify common errors users make, e.g. failure to choose correct granularity of Antibody IgG or choose inappropriate "Screen" or "Confirm" for the method.

Limitations

We only utilized local names and EDs to evaluate the correctness of the LOINC mappings in this study. To conduct a more thorough evaluation, would require complete information, such as "subtype of analyte", "method", "timing" and "system" for all tests. To accomplish this would require cooperation with laboratory technicians and administrative staff who would create local test definitions that describe the complete meaning of all test codes.

Conclusion

By using EDs of laboratory tests, we evaluated the correctness of voluntary LOINC mappings of three large institutions and identified several common errors that occur in current mappings. Understanding those errors can help in the development of better LOINC codes, automated tools, evaluation methods, and training courses to reduce systematic errors in LOINC mapping.

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