Coding of Electronic Laboratory Reports for Biosurveillance, Selected United States Hospitals, 2011

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Abstract

Objective: Electronic laboratory reporting has been promoted as a public health priority. The Office of the U.S. National Coordinator for Health Information Technology has endorsed two coding systems: Logical Observation Identifiers Names and Codes (LOINC) for laboratory test orders and Systemized Nomenclature of Medicine-Clinical Terms (SNOMED CT) for test results.

Materials and Methods: We examined LOINC and SNOMED CT code use in electronic laboratory data reported in 2011 by 63 non-federal hospitals to BioSense electronic syndromic surveillance system. We analyzed the frequencies, characteristics, and code concepts of test orders and results.

Results: A total of 14,028,774 laboratory test orders or results were reported. No test orders used SNOMED CT codes. To describe test orders, 77% used a LOINC code, 17% had no value, and 6% had a non-informative value, "OTH". Thirty-three percent (33%) of test results had missing or non-informative codes. For test results with at least one informative value, 91.8% had only LOINC codes, 0.7% had only SNOMED codes, and 7.4% had both. Of 108 SNOMED CT codes reported without LOINC codes, 45% could be matched to at least one LOINC code.

Conclusion: Missing or non-informative codes comprised almost a quarter of laboratory test orders and a third of test results reported to BioSense by non-federal hospitals. Use of LOINC codes for laboratory test results was more common than use of SNOMED CT. Complete and standardized coding could improve the usefulness of laboratory data for public health surveillance and response.

Keywords: Logical Observation Identifiers Names and Codes (LOINC); Systemized Nomenclature of Medicine Clinical Terms (SNOMED CT); electronic laboratory report; computerized medical record systems; biosurveillance

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Introduction

Because Electronic Laboratory Reporting (ELR) has been seen to be more accurate, timely, and cost-effective than reporting by other conventional means (e.g., mail, fax, etc.), ELR adoption has been systematically promoted as a public health priority [1-7]. A major deterrent to laboratory data being used in public health research and biosurveillance programs seems to be the lack of interoperability of automated laboratory information management systems [8-12]. Standardized, universal coding that records laboratory test order and result information in a structured and systematic fashion is an essential component of interoperable ELR systems [9,13,14]. The use of local codes or terminology and unstructured text fields to describe laboratory test orders and results varies widely among laboratories [15,16]. Several coding strategies are available to make electronic laboratory data more computational and thus readily interchangeable electronically. Long established coding systems such as International Classification of Diseases (ICD) and Current Procedural Terminology (CPT) are used for insurance reimbursement and other administrative purposes. ICD codes are primarily designed for classifying diseases and other health conditions while CPT is designed to record a medical service or a procedure. Therefore, coding laboratory information is out of scope for ICD and CPT coding systems. Several coding strategies are available to make electronic laboratory data more computational and thus readily interchangeable electronically; Logical Observation Identifiers Names and Codes (LOINC) and Systemized Nomenclature of Medicine Clinical Terms (SNOMED CT) are the two most comprehensive coding systems representing lab test type and result information.

Therefore, these two information coding systems were specifically recommended for use in coding laboratory information in electronic health records by the U.S. Department of Health and Human Services Office of National Coordinator for Health Information Technology

Established in 1994, LOINC is a coding system designed to identify medical laboratory observations and procedures. LOINC covers both laboratory tests and clinical observations enabling coding of test orders and test results. The system has been endorsed by the American Clinical Laboratory Association and the College of American Pathologists. A LOINC code is composed of six attributes that characterize the details of laboratory test orders and results, namely: component (e.g., *Escherichia coli*, potassium), property (e.g., arbitrary concentration, mass concentration), timing (e.g., point in time, over a span of time), system (e.g., stool, blood), scale (e.g., ordinal, nominal), and method (e.g., culture, microscopy). The most recent version of the LOINC database contains more than 70,000 codes [17-22]. LOINC codes are updated twice a year to reflect changes in diagnostic practices over time.

Established in 1965, SNOMED CT is a coding system designed to identify anatomic and clinical pathology information and laboratory results. The system is a collection of medical terms, codes, findings and procedures. A SNOMED CT code is composed of the following three attributes; unique concepts (e.g., *E. coli*), concept descriptions (e.g., is a), and relationships between concepts (e.g., bacteria present in stool). The system is updated twice a year and currently includes over 300,000 unique concepts [23]. SNOMED CT is the ontological basis of the upcoming International Classification of Diseases 11th Edition (ICD-11) revision spearheaded by the World Health Organization [24,25].

Objective

We examined the use of LOINC and SNOMED CT codes for coding laboratory test orders and results in laboratory reports transmitted to BioSense program from 63 non-federal hospitals in the calendar year 2011. In this report, we present the first national level description of the use of LOINC and SNOMED

CT codes from biosurveillance data to characterize laboratory test orders and results reported by hospital-based laboratories.

Materials and Methods

BioSense is a syndromic surveillance system supported by the U.S. Centers for Disease Control and Prevention (CDC), and it receives daily medical encounter data from participating hospitals. During 2011, 11% of participating non-federal hospitals also shared laboratory data with BioSense [26,27]. Details of the data transmission from hospitals to CDC's BioSense program have been previously described [28-30]. In brief, data reporting standards follow guidance from the Public Health Information Network Messaging System's (PHINMS) syndromic surveillance message guide and are transmitted securely via digital certificates and data encryption [31]. The laboratory reports included in this analysis were transmitted using version 2.3.1 of Health Level 7 (HL7) message formats. All laboratory reports from non-federal hospitals reporting to BioSense from January 1, 2011 through December 31, 2011 were extracted from HL7 messages and converted to SAS analytic data files. Reports included laboratory test orders only, test orders with results, and results only.

Data elements in each laboratory message can be broadly categorized into three sections: 1) administrative data elements, 2) laboratory test order related data elements, and 3) laboratory result related data elements. Administrative data elements include date of visit, type of service facility, testing laboratory ID, and date of HL7 message creation. Laboratory test order data elements include order number, order test name, order test codes (local and "standard"), order test coding system, and segments of coding structure. Laboratory result data elements are grouped into two categories: observation identifier (OBR) and observation value (OBX). Elements of OBR include observation result code, observation result coding system, local observation result code, observation result text (local and "standard"), and observation result type. Elements of OBX include result coding system, result test code (local and "standard"), result status, result notes, result test date, result test name (local and "standard"), result unit, test interpretation, and details of the sample to be tested (component, property, timing, system, scale, method). Additionally, BioSense laboratory message data include site and type of the specimen, diagnostic criteria, and test sequence number.

Each laboratory test result with result code was categorized into one of six result status categories, namely: "final result", "preliminary result", "specimen in the laboratory", "correction", "deletes OBX record", and "result can't be obtained for this observation". Since results identified as "preliminary" constituted almost one-third of all laboratory results reported we analyzed all reported results regardless of their status. Later we compared our analysis with findings from a separate review limited to "final" results.

We analyzed the frequency distribution of laboratory test orders and results to determine characteristics of the test orders and results reported, and to examine the 25 most common test orders and results. Unique LOINC or SNOMED CT codes used in the reports were identified, along with the percentage of reports that were missing a standardized code. For each of the SNOMED CT codes reported without corresponding LOINC codes, we used the Public Health Information Network Vocabulary Access and Distribution System (https://phinvads.cdc.gov) web sites to obtain the SNOMED CT concept or descriptive text. Then each concept was searched in Regenestrief LOINC Mapping Assistant (RELMA®) software version 5.8, to determine if there was a LOINC code that might corresponded to the SNOMED CT concept. Since the value "OTH" in HL7 messages does not clearly indicate a specific laboratory test order or results, rather it indicates concepts not represented by the code system; we

treated reports coded with "OTH" as non-informative data. This analysis was determined to be a public health surveillance activity rather than human subject research requiring institutional board review.

Results

Out of 569 non-federal hospitals reporting data to BioSense in 2011, 63 (11.1%) hospitals in 14 states submitted 14,028,774 laboratory reports (test orders and/ or results) from 821,108 unique laboratory visits. On average, 38,000 laboratory reports were reported daily. In the reports with at least one result code, the hospital diagnostic service ordering the test was categorized into five groups: microbiology (94.7%), serology (2.8%), outside laboratory (1.7%), virology (0.5%), and immunology (0.4%).The reports consisted of final (68.7%), preliminary (31.0%), specimen in the lab (0.2%) and corrected (0.1%) result status (Table 1).

Table 1. Characteristics of hospital-based laboratory data reported to BioSense, 2011

Characteristics	**N (%)**
Number of reporting hospital laboratories	63 (100)
Number of unique laboratory visits	821,108 (100)
Number of laboratory reports (test orders or test results)	14,028,774 (100)
LOINC order codes	10,776,494 (76.8)
Non-informative order codes (missing or HL7 null code "OTH")	3,252,280 (23.2)
Number of laboratory reports with test results code	9,347,179 (66.6)
LOINC or SNOMED CT or both result codes	4,681,595 (33.4)
Non-informative codes (both missing or one missing and the other is HL7 null code "OTH")	
Number of test results with code by code system	9,347,179 (100)
LOINC codes only	8,584,826 (91.8)
SNOMED CT codes only	69,566 (0.7)
LOINC and SNOMED CT both	692,787 (7.4)
Number of unique LOINC codes for orders	805 (100)
Number of unique codes for results	608 (100)
SNOMED CT codes	1,428 (100)
LOINC codes	
Test result status	9,347,179 (100)
Final result	6,420,538 (68.7)
Preliminary result	2,898,975 (31.0)
Specimen in lab	18,739 (0.2)
Correction	7,011 (0.1)
Deletes observation value (OBX) record*	331 (0.0)
Result can't be obtained for this observation	7 (0.0)
Diagnostic services	9,347,179 (100)
Microbiology	8,849,051 (94.7)
Serology	258740 (2.8)
Outside Laboratory	161,561 (1.7)
Virology	42,974 (0.5)
Immunology	34,853 (0.4)

Among the 14,028,774 laboratory test reports, 76.8% had LOINC order codes, while for the rest either the codes were missing (16.8%) or had the HL7 null code, "OTH" (6.4%). No test orders were reported using a SNOMED CT code. Out of 10,776,494 laboratory test orders with LOINC codes, 9,347,179 (86.7%) also had either LOINC or SNOMED CT or both codes for the test result.

Of all laboratory reports, 9,347,179 (66.6%) had at least one result code (LOINC or SNOMED CT or both); of these, 91.8% had only LOINC codes, 0.7% had only SNOMED CT codes while 7.4% had both codes (Table 1). Of the remaining 4,681,595 laboratory reports, 63.4% were missing a SNOMED or LOINC result code with "OTH" reported as a result value while 36.6% had neither LOINC nor SNOMED codes for the results. Laboratory test results with "final" status comprised the majority (68.7%) of all laboratory reports with result codes (Table 1) Findings from the analysis comparing results with "final" status to all results were comparable except that the number of laboratory test results with only LOINC codes differed (91.8% in all messages versus 61.4% in only "final" result messages). This suggests that results reported as "preliminary" were not updated when result status changed to "final".

Table 2.Twenty five most common hospital-based laboratory order test types reported to BioSense, 2011, with Logical Observation Identifiers Names and Codes (LOINC) codes

LOINC Test Name	LOINC Code	Test Orders N (%)
Bacteria identified (Blood)	600-7	3770050 (35.0)
Bacteria identified (Urine)	630-4	1637400 (15.2)
Bacteria identified- Respiratory culture	32355-0	522495 (4.8)
Bacteria identified- Wound culture	6462-6	459784 (4.3)
Antibiotic- Agar diffusion	45187-2	328113 (3.0)
Fungus Identified- Culture	580-1	291370 (2.7)
Mycobacterium sp identified	543-9	284631 (2.6)
Bacteria identified (Anaerobic+Aerobic)- Culture	21020-3	283577 (2.6)
Staphylococcus aureus methicillin resistant isolate- Culture	13317-3	207718 (1.9)
Bacteria identified- Body fluid culture	611-4	186589 (1.7)
Microscopic observation- Wet preparation	680-9	174113 (1.6)
Bacteria identified- Stool culture	625-4	159657 (1.5)
Chlamydia trachomatis + *Neisseriagonorrhoeae*- Probe	36902-5	155606 (1.4)
Bacteria identified- Aerobic culture (Wound)	632-0	145213 (1.3)
Bacteria identified- CSF culture	606-4	139418 (1.3)
Bacteria identified (Anaerobic)- Culture	635-3	112496 (1.0)
Bacteria identified (Aerobic)- Culture	634-6	92773 (0.9)
Streptococcus pyogenes Ag – EIA	6558-1	89173 (0.8)
Microscopic observation (Gram Stain)	664-3	81129 (0.8)
Bacteria identified- Culture (system- xxx)	6463-4	67118 (0.6)
Antibiotic- Minimum inhibitory concentration	21070-8	58891 (0.5)
Bacteria identified- Culture	43408-4	57084 (0.5)
Bacteria identified (Sputum)- Respiratory culture	624-7	56906 (0.5)

Clostridium difficile toxin A+B (Stool)	34713-8	55567 (0.5)
Bacteria identified- Throat culture	626-2	50977 (0.5)

For test orders, 805 unique LOINC codes were used. After excluding "OTH" and missing, values, LOINC codes to identify bacteria in blood (35.0%), urine (15.2%), respiratory specimens (4.8%), or wounds (4.2%), and to test antibiotic susceptibilities by agar diffusion (3.0%), were the five most frequent laboratory orders reported (Table 2). Fourteen hundred twenty eight unique LOINC and 608 unique SNOMED CT codes were used to describe laboratory test results. For results with LOINC codes, the five most commonly reported tests were: bacteria identified by blood culture (12.2%), microscopic observation of unspecified specimen by Gram stain (8.9%), appearance of unspecified specimen (7.6%), microorganism identified in unspecified specimen by culture (7.5%), and bacteria identified by urine culture (6.6%)(Table 3a). For results with SNOMED CT codes, a qualifier for antimicrobial susceptibility (10.4%), *Escherichia coli* (10.4%), a qualifier for bacterial sensitivity (9.9%), *Staphylococcus aureus* (9.7%), and a qualifier for non-reactive status (6.5%) were the five most frequent codes (Table 3b).

Table 3a. Twenty five most common hospital-based laboratory result types reported to BioSense, 2011, with Logical Observation Identifiers Names and Codes (LOINC) codes

LOINC Long Name	LOINC Code	Test Results N (%)
Bacteria identified in blood by culture	600-7	1128381(12.2)
Microscopic observation in unspecified specimen by gram stain	664-3	823440 (8.9)
Appearance of unspecified specimen	33511-7	707650 (7.6)
Microorganism Identified in unspecified specimen by culture	11475-1	696652 (7.5)
Bacteria identified in urine by culture	630-4	611553 (6.6)
Specimen Source of unspecified specimen	31208-2	532232 (5.7)
Bacteria identified in unspecified specimen	41741-0*	271916 (2.9)
Service comment[#]	8251-1	176943 (1.9)
Bacteria identified in unspecified specimen by respiratory culture	32355-0	148069 (1.6)
Fungus identified in unspecified specimen by culture	580-1	140800 (1.5)
Bacteria identified in blood by aerobe culture	17928-3	127807 (1.4)
Microscopic observation in unspecified specimen by other stain	11546-9	115486 (1.2)
Bacteria identified in wound by aerobe culture	632-0	110500 (1.2)
Microorganism or agent Identified in unspecified specimen	41852-5	107766 (1.2)
Mycobacterium SP Identified in unspecified specimen by culture	543-9	106956 (1.2)
Bacteria identified in wound by culture	6462-6	103717 (1.1)
Bacteria identified in blood by anaerobe culture	17934-1	98539 (1.1)
Microscopic observation in wound by Gram stain	10357-2	98288 (1.1)
Microscopic observation in unspecified specimen by wet preparation	680-9	93901(1.0)
Gentamycin susceptibility	18928-2	75789 (0.8)
Microscopic observation in unspecified specimen by acid fast stain	11545-1	70546 (0.8)
Trimethoprim + Sulfamethoxazole susceptibility	18998-5	68972 (0.7)
Microorganism identified in stool by culture	625-4	64295 (0.7)

Levofloxacin susceptibility	20629-2	60212 (0.7)
Ciprofloxacin susceptibility:	18906-8	51448 (0.6)

*- LOINC code 41741-0 has been deprecated and superseded by LOINC code 23667-9.

#- LOINC code for Service Comment terms indicates user-defined text.

Among the 608 unique SNOMED CT codes used to report laboratory test results, 498 (81.9%) had corresponding LOINC codes reported. For the 108 SNOMED codes that did not have corresponding LOINC codes in the reported laboratory results, we found that 49 (45.4%) of the SNOMED CT concepts could be associated with at least one LOINC code. The majority of SNOMED CT concepts matched to LOINC (47 of 49) were microorganism related, while one was an anatomical structure (urethra) and one was a system concept (blood). Among 49 SNOMED CT concepts that matched to LOINC codes, 27 concepts matched to more than one LOINC code, depending on other LOINC components including property, timing, system, scale, and method. Among 59 SNOMED CT concepts not identified in mapping to LOINC codes, 47 were for microorganisms, seven were for qualifiers, three were for anatomical structures, and two were for systems.

Table 3b. Twenty five most common hospital-based laboratory results types reported to BioSense, 2011, with Systemized Nomenclature of Medicine Clinical Terms (SNOMED CT) codes

Observation Identifier (OBS) Text	SNOMEDCT Code	Test Results N (%)
Susceptible	131196009	79465 (10.4)
Escherichia coli	112283007	79255 (10.4)
Sensitive	83185005	75142 (9.9)
Staphylococcus aureus	3092008	74216 (9.7)
Non-Reactive	131194007	49852 (6.5)
Resistant	30714006	44504 (5.8)
None*	260413007	39924 (5.2)
Pseudomonas aeruginosa	52499004	30555 (4.0)
Gram-negative bacillus	87172008	18016 (2.4)
Leukocyte	52501007	17678 (2.3)
Staphylococcus, coagulase negative	116197008	16094 (2.1)
Proteus mirabilis	73457008	14522 (1.9)
Reactive	11214006	13693 (1.8)
Klebsiella pneumoniae	56415008	13446 (1.8)
Staphylococcus epidermidis	60875001	13182 (1.7)
Enterococcus fecalis	78065002	12610 (1.7)
Klebsiella pneumonia ss. pneumoniae	18400002	9681 (1.3)
Yeast	62093005	8457 (1.1)
Enterococcus species	131297007	7733 (1.0)
Enterobacter cloacae	14385002	6794 (0.9)
Enterococcus	2785000	5720 (0.8)
Candida albicans	53326005	5446 (0.7)
No organism seen	27863008	5139 (0.7)

Staphylococcus species	116499001	4362 (0.6)
Stenotrophomonas maltophilia	113697002	4342 (0.6)
Streptococcus agalactiae	43492007	4113 (0.5)

*- "None" is a SNOMED CT qualifier value for "absence findings"

Discussion

The hospitals included in our study used LOINC as the coding system to record laboratory test orders. Laboratory test results were coded using both LOINC and SNOMED CT coding systems, though, the use of LOINC was much more common. Our findings indicate that participating hospital laboratories undertook reporting of laboratory test orders and results as recommended in ELR HL7 messaging guidance [32]. However, missing or non-informative codes comprised almost a quarter of laboratory test orders and a third of test results from hospitals reporting to BioSense in 2011.

By design, the primary objectives of BioSense program were to monitor clinical syndromes related to infectious diseases for early outbreak detection and ongoing situational awareness [27-29]. Therefore, Biosense recommended that participating hospitals preferentially report laboratory information related to infectious diseases. As a result, the majority of the laboratory reports in this analysis were microbiology related. We examined both test orders and preliminary and final test results. Monitoring laboratory test orders could provide early warning signals of suspicion of infectious disease, while monitoring results could contribute to biosurveillance by providing increased diagnostic specificity to automated syndromic case definition algorithms based on chief complaint text fields [26,33-35]. Laboratory data could also be used to evaluate interventions, and to monitor disease trends and progression, which might result in timely more effective outbreak response and management [1,13].

In ELR reporting, the debate over the definition of "questions" (orders) and "answers" (results) is far from over. It has been suggested that LOINC is used for coding laboratory "questions" while SNOMED CT is used for coding the "answers". [22] Laboratory reports from hospitals in our analysis indicate that LOINC codes are used to code laboratory orders as well as results, illustrating LOINC's potential to provide codes for "questions" as well as "answers". On the other hand, there may be unique situations where a SNOMED CT code is required in combination with a LOINC code to fully represent a lab test result. For example, the SNOMED CT system allows coding for certain clinical structures (cervix, urethra), and for certain conditions (e.g., hyperbilirubinemia), that are currently not accounted for in the LOINC system.

Several earlier reports have suggested different mapping strategies to associate laboratory codes to diseases or health conditions [20,36-41]. Our findings suggest that the BioSense surveillance program might be able to focus on a small subset of LOINC and SNOMED CT codes related to diseases or syndromes of interest, as evidenced by the use of a relatively small number of unique LOINC (n= 1,428) and SNOMED CT (n= 608) codes in the data we analyzed compared to the number of codes available. To determine if laboratory data improves syndromic surveillance performance for enhanced outbreak detection and improved situational awareness, an evaluation of syndromic case definitions that incorporate laboratory test order or result information is required.

Some limitations in interpreting our findings should be noted. Non-federal hospitals who participated in BioSense are not a representative sample of all the U.S. hospitals. Use of the convenience sample of facilities that are able and willing to share electronic laboratory data with CDC may limit the generalizability of our findings. Furthermore, laboratory data in this analysis were primarily collected

for infectious disease syndromic surveillance purposes. Therefore our findings may not be representative of the use of LOINC and SNOMED CT codes for ELR for all hospital laboratory testing. Completeness of ELR data in BioSense has not been validated prior to this study, which shows that one-third of electronic laboratory records are missing standardized codes or are coded as HL7 null "OTH" for result information that would be necessary for interpretation for surveillance. We are unable to report specific accuracy metrics such as specificity or sensitivity related to LOINC and SNOMED CT due to lack of a reference "gold standard".

The current analysis has several important strengths, beginning with computability of the coded laboratory test order and result information in the HL7 messaging format that supports automated categorization for surveillance. Consequently, we were able to merge data files from different hospitals to create one large laboratory data repository and apply standard criteria that could potentially augment information from other surveillance data sources. Laboratory reports in this analysis derived from local hospitals illustrate the potential value of standardizing laboratory data to provide timely information to hospital based infection preventionists and local health departments for situation awareness and early response, as well as contributing to national biosurveillance. Most importantly this study adds value to existing scientific knowledge by describing the use of LOINC and SNOMED CT codes in ELR contributed by select U.S. hospitals as healthcare organizations move towards implementing Meaningful Use and health information exchange [42,43].

Conclusion

We analyzed more than 14 million laboratory reports from non-federal hospital to assess the use of two structured coding systems, SNOMED CT and LOINC. The LOINC system was used more commonly than SNOMED system in the hospitals studied. Missing data and differences in representing laboratory test orders and results may inhibit effective analysis of electronic laboratory data. Increased completeness of coded lab data, data management tools that translate locally coded laboratory test information into LOINC or SNOMED CT codes, and increased participation of hospitals laboratories are needed to fully realize the value of laboratory data in public health practice and syndromic surveillance.

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SD, SB, CW and SG contributed equally in conceptualizing, analyzing, and interpreting data. SD drafted the manuscript. All authors including AD, UA contributed in revising it critically for important intellectual content of the paper. All authors have approved the final version of the paper submitted for publication.

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