

Comparative study of LOINC and SNOMED CT in panel mapping: enhancing interoperability in laboratory testing

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ARTICLE INFO

Keywords:

Logical Observation Identifier Names and Codes (LOINC)
SNOMED CT
Panel test
Laboratory data
Interoperability

ABSTRACT

Background: We aimed to evaluate and compare the applicability of Logical Observation Identifiers Names and Codes (LOINC) and SNOMED CT in mapping frequently requested panel tests.

Method: Frequently requested panel tests were identified from the test records of two major referral laboratories. Subsequently, LOINC and SNOMED CT mappings were cross-validated, and the results were classified based on pre-defined criteria. A consensus was reached among the teams. A comparative structural analysis was performed by aligning the mapped SNOMED CT concepts with LOINC codes and visualizing the selected items with conditionality to evaluate the differences in representation.

Results: We conducted 23 panel tests. Exact mapping was achieved for 87.0% of the panel tests using LOINC: two failures were recorded due to the lack of a suitable code, and one panel test was classified as narrowly mapped. In contrast, SNOMED CT achieved the exact mapping for 78.2% of the panel tests, with 12 mappings requiring post-coordination to represent the test concepts. SNOMED CT mapping failures stemmed from missing primitive concepts and limited pre-coordinated codes. LOINC offered detailed component specifications and predefined panel codes. In contrast, SNOMED CT relied on post-coordination to address gaps in the pre-defined codes, allowing the addition of new combinations where necessary.

Conclusion: LOINC demonstrated advantages in mapping frequently performed panel tests with higher exact mapping rates and structured panel codes. However, leveraging SNOMED CT's flexibility through initiatives such as the LOINC Ontology project could enhance interoperability and standardization in laboratory data exchange.

1. Introduction

Laboratory testing is the cornerstone of modern healthcare, influencing over 70 % of medical decisions and playing a pivotal role in diagnostic accuracy, patient management, and treatment planning [1]. As digital health systems evolve, achieving interoperability in laboratory data is essential to enhance their effectiveness [2]. Standardizing test results is critical, and the terminology used to exchange laboratory test names is important [3]. Standardized terminology ensures efficient

data exchange and effective clinical communication across hospitals, thereby enabling the seamless integration of test results within and between healthcare systems [4].

Panel tests, defined as “collections of terms to represent specific sets of information,” pose unique challenges to standardization [5]. Panel tests refer to test sets that are typically requested to diagnose or evaluate a particular disease or symptom [6]. Besides traditional panel tests, such as complete blood cell count (CBC) and urine sediment analysis, the advancement of molecular technologies has led to the introduction of

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<https://doi.org/10.1016/j.ijmedinf.2025.106055>

Received 13 March 2025; Received in revised form 2 July 2025; Accepted 19 July 2025

Available online 21 July 2025

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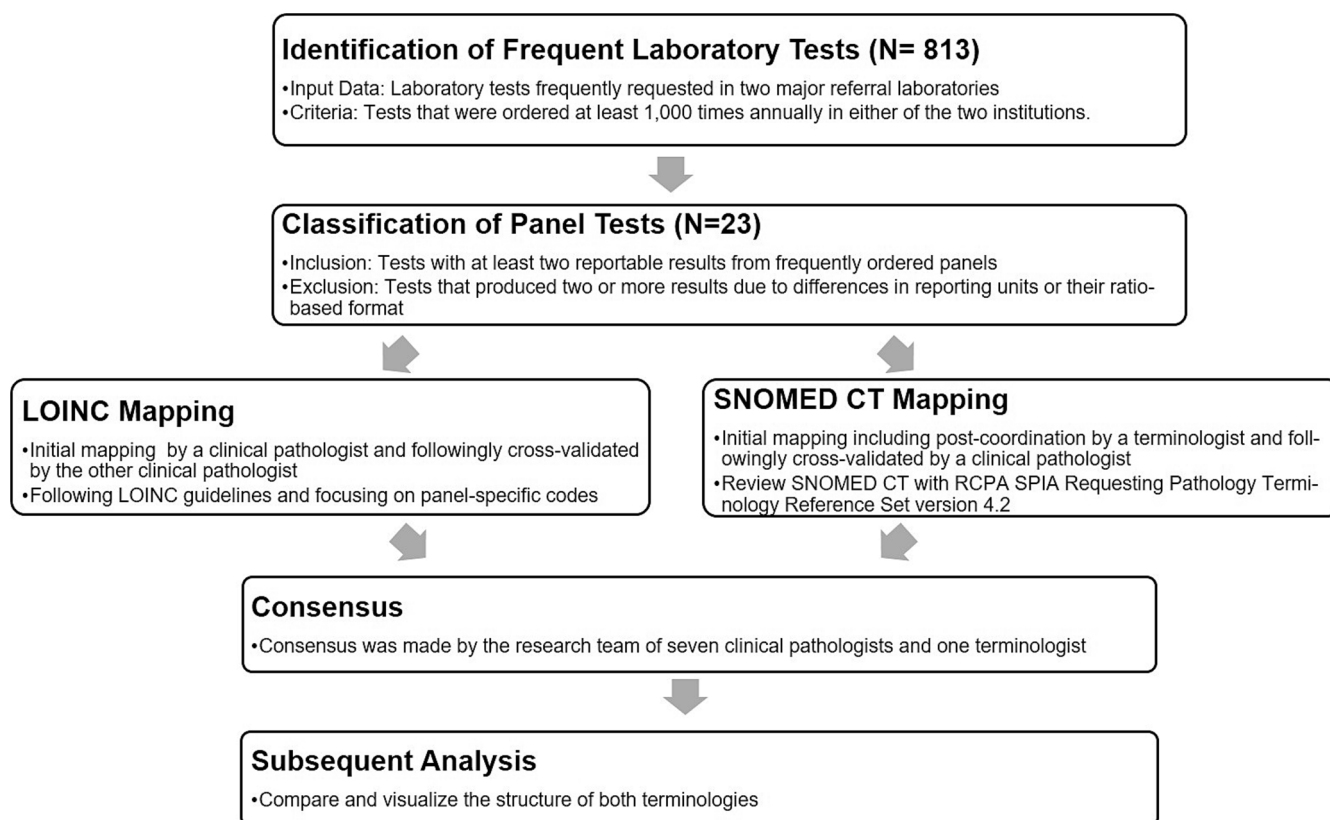


Fig. 1. Study workflow for mapping panel tests to LOINC and SNOMED CT. The process involved selecting frequently requested panel tests, applying the mapping criteria, performing cross-validation, and analyzing mapping accuracy. Abbreviations: RCPA, Royal College of Pathologists of Australia; SPIA, Standardized Pathology Informatics in Australia.

syndromic testing and more refined autoantibody tests for autoimmune diseases in clinical practice [7,8]. According to the Korean National Health Insurance claims data (<https://opendata.hira.or.kr/>), >38 % of the total population underwent a CBC test in 2024, highlighting its high utilization rate. For newly introduced tests, the specific components may vary depending on regional epidemiological differences [9], and tests with the same name may serve different purposes depending on the characteristics of the testing hospitals. Because test names are often abbreviated according to institutional policies, they may not fully convey the purpose or targets of the test. Consequently, categorizing panel tests based solely on their names could lead to misclassification, where distinct panel tests are mistakenly considered identical.

In laboratory testing, the Logical Observation Identifier Names and Codes (LOINC) and SNOMED CT are well-known standardized terminologies for laboratory test name standardization [10]. In the United States, LOINC is the mandated standard for laboratory test names under the United States Core Data for Interoperability, a nationally standardized set that includes panel codes [11]. Conversely, in Australia, LOINC is used for reporting results. SNOMED CT is the standard for naming requests for laboratory tests, including panels, as defined by the Royal College of Pathologists of Australasia (RCPA) [12]. LOINC codes were adopted in Korea in 2024 as the standard terminology for laboratory test names, alongside insurance claims codes [13]. A national strategy that specifically addresses the standardization of panel codes remains undeveloped.

Efforts to link LOINC and SNOMED CT in various domains of medicine have gained traction, reflecting a global need for interoperability between the two widely used terminologies [14–16]. Despite this progress [17], research evaluating their applicability or integration, specifically for panel tests, is limited. The absence of comparative evaluations hinders the progress needed to standardize laboratory

panels, leaving institutions with inconsistent implementations that undermine data integration and interoperability.

Therefore, we aimed to evaluate and compare the applicability of LOINC and SNOMED CT in mapping frequently performed panel tests requested in clinical practice. This study seeks to inform strategies for standardizing laboratory panel codes and enhancing interoperability within global digital health systems by analyzing the mapping rate, advantages, and limitations of each term.

2. Methods

2.1. Study design

Fig. 1 illustrates the study design. Frequently requested panel tests were identified in two steps, using test records from two major referral laboratories. The input data consisted of laboratory tests frequently requested in these institutions, and the selection criteria included tests ordered at least 1000 times in primary care settings by 2023 at either of the two institutions. Second, we selected panel tests from among the most frequently requested tests, defining a panel as one that provides at least two distinct analyte measurements. Tests that yielded multiple results solely due to differences in reporting units were excluded, as they are typically designed to assist clinical interpretation rather than represent multiple analytes. Similarly, ratio-based tests such as urine protein/creatinine were excluded, in accordance with LOINC Committee guidance, which considers such tests as single observations (e.g., LOINC 34535-5) and were not included in our analysis [18]. The selected panel tests were categorized according to discipline, and one representative test name and specimen were identified for each category.

Table 1
Panels included in this study by discipline (N = 23).

Discipline (Number of panel tests)	Panel name (Specimen)
Clinical chemistry (8)	Risk of Ovarian Malignancy Algorithm (ROMA) (Serum)
	Risk of Ovarian Malignancy Algorithm (ROMA; premenopausal) (Serum)
	Risk of Ovarian Malignancy Algorithm (ROMA; postmenopausal) (Serum)
	Urine dipstick test (Random urine)
	Urine sediment analysis (Random urine)
	Protein electrophoresis (Serum)
	Neonatal metabolic disease screening test (Dried blood spot)
	Metanephrine fraction (Plasma)
	Complete blood count (Whole blood)
	Peripheral blood differential count (Whole blood)
Diagnostic hematology (7)	Peripheral blood smear (Whole blood)
	Prothrombin time (Plasma)
	Body fluid analysis (Body fluid)
	Body fluid differential count (Body fluid)
	Blood viscosity test (Whole blood)
Diagnostic immunology (1)	Multiple Allergen Simultaneous Test (MAST) (Serum)
Molecular microbiology (7)	Sexually transmitted pathogen screening molecular test (Genital specimen)
	Respiratory viral pathogens screening molecular test (Nasopharyngeal swab)
	Pneumonia pathogen screening molecular test (Respiratory system specimen)
	Mycoplasma macrolide resistance test (Respiratory system specimen)
	Gastrointestinal bacterial pathogens screening molecular test (Stool)
	Gastrointestinal viral pathogens screening molecular test (Stool)
	Clarithromycin resistance mutation test (Tissue)

2.2. Mapping procedure

Panel tests were mapped to LOINC and SNOMED CT following standard guidelines and procedures (Fig. 1) [19,20]. The results underwent cross-validation, and the final mapping was determined through consensus among the research team. In SNOMED CT, panel test concepts were primarily mapped to procedure-type concepts rather than Observable Entities, since the LOINC codes used describe the act of performing the test rather than its result. Of note, SNOMED CT mappings were conducted using a two-step strategy: precoordinated concepts were prioritized, and post-coordinated expressions were applied when no semantically equivalent precoordinated term existed. Post-coordinated expressions were developed accordingly and reviewed by a SNOMED CT expert in Korea. Notably, when modeling panel tests using SNOMED CT compositional grammar, the “+” symbol was used to denote multiple values under a single attribute—not multiple focus concepts. Therefore, it does not imply a relationship group or multiple distinct procedures, but rather a single procedure involving multiple analytes. Further details on the mapping methodologies are provided in the [Supplementary material](#).

2.3. Mapping classification

LOINC mapping was classified as “exactly mapped” if all panel components matched completely, or “narrowly mapped” if some components were missing. SNOMED CT mapping was classified as exactly, broadly, or narrowly mapped, according to semantic correspondence. Only concepts that exactly matched the test definition were included in the calculation of exact mapping rates. Concepts that were broadly mapped, narrowly mapped, or marked as ‘not available’ were excluded from the exact mapping category. Additional comparison with the RCPA SPIA Requesting Set was performed (detailed criteria available in

[Supplementary material](#)) [12].

2.4. Comparison of LOINC and SNOMED CT

The mapped SNOMED CT concepts were compared with their corresponding LOINC codes by aligning the information provided by the concepts with the six attributes used in LOINC. In addition, the selected items with conditionality were visualized to evaluate the structural differences between the LOINC and SNOMED CT images.

3. Results

3.1. Extraction of study data

Initially, 813 frequently requested laboratory tests were identified, and 26 were screened. However, hemoglobin A1c was excluded due to reporting in multiple units. In addition, the urine protein/creatinine ratio and microalbumin/creatinine ratio tests were excluded due to their ratio-based format. Consequently, 23 frequently requested panel tests were included in this study (Table 1). Of the selected panel tests, molecular tests, newborn metabolic screening tests, and multiple allergen simultaneous tests (MAST) often contain numerous components, with significant variations in their composition depending on the testing institution or the specific test kits used.

3.2. LOINC mapping

For panel tests, exact mapping was achieved in 87.0 % of cases using LOINC. Two mapping failures were recorded in the Peripheral blood smear, Whole blood test and Mycoplasma macrolide resistance test because no suitable LOINC code was available to represent these specific tests. The body fluid analysis item was mapped to LOINC 34557-9 (Cell count and differential panel) and classified as narrowly mapped because this code includes color and turbidity but does not include pH and specific gravity. Although the discouraged LOINC code 34994-4 (Smear morphology panel – Blood) was initially considered for “Peripheral blood smear, Whole blood” due to the lack of a suitable alternative, it was evaluated as a mapping failure. Accordingly, this item was marked as “not available (N/A)”. In addition, four individual test codes were included in the optimal mapping because of the absence of suitable panel codes to represent their corresponding tests. The blood viscosity test, which reports systolic and diastolic results together, was mapped to an individual test code because of the absence of a panel code capable of comprehensively representing this test.

The Risk of Ovarian Malignancy Algorithm (ROMA) tests, which assess risk by measuring carbohydrate antigen 125 (CA125) and human epididymis protein 4 (HE4) for premenopausal and postmenopausal patients, were originally included as subcomponents within the panel code LOINC 104551-7 (ROMA test). A dedicated panel code (LOINC 104551-7) exists for ROMA; however, no specific panel code is available to differentiate between premenopausal and postmenopausal patients. Consequently, the individual test codes LOINC 49569-2 (ROMA, premenopausal) and LOINC 69570-0 (ROMA, postmenopausal) were mapped as the optimal codes despite not being panel codes. In addition, the code for clarithromycin resistance testing was not designated as a panel code but was included in the mapping as an individual test code.

LOINC offers significant advantages for existing panel codes, including detailed specifications of component tests and their requirements. However, molecular microbiology tests with unstandardized components, such as sexually transmitted pathogen screening molecular tests, respiratory viral pathogen screening molecular tests, gastrointestinal bacterial pathogen screening molecular tests, and gastrointestinal viral pathogen screening molecular tests, lack the specification of conditionality in their requirements. These panel codes were introduced in the LOINC versions released after 2.54 (December 2015), which reflects their relatively recent incorporation into the

Table 2
LOINC codes mapped to panels.

Test name, specimen	Recommended LOINC in this study Optimal LOINC panel code	Component	Property	Timing	System	Scale	Method	Version First Released	Mapping classification	Conditionality attribute ¹
Complete blood count, Whole blood	58410–2	Complete blood count panel	–	Pt	Bld	–	Automated count	2.3	Exactly mapped	Designated
Peripheral blood differential count, Whole blood	69738–3	Differential panel, method unspecified	–	Pt	Bld	Qn		2.4	Exactly mapped	Designated
Peripheral blood smear, Whole blood	N/A									
Prothrombin time, Plasma	34528–0	PT panel	–	Pt	PPP	Qn	Coag	2.1	Exactly mapped	Designated
Body fluid analysis, Body fluid	34557–9	Cell count & Differential panel	–	Pt	Body fld	Qn		2.1	Narrowly mapped	Designated
Body fluid differential count, Body fluid	29580–8	Differential panel	–	Pt	Body fld	–		2.03	Exactly mapped	Designated
Blood viscosity test, Whole blood	4690–4*	Viscosity	Visc	Pt	Bld	Qn		1.0	Exactly mapped	N/A
Risk of Ovarian Malignancy Algorithm (ROMA), Serum	104551–7	Ovarian malignancy (ROMA) panel	–	Pt	Ser/Plas	–		2.78	Exactly mapped	Not designated
Risk of Ovarian Malignancy Algorithm (ROMA, premenopausal), Serum	69569–2*	Risk of ovarian malignancy algorithm score*premenopausal	Score	Pt	Ser/Plas	Qn		2.40	Exactly mapped	N/A
Risk of Ovarian Malignancy Algorithm (ROMA, postmenopausal), Serum	69570–0*	Risk of ovarian malignancy algorithm score*postmenopausal	Score	Pt	Ser/Plas	Qn		2.40	Exactly mapped	N/A
Urine dipstick test, Random urine	24357–6	Urinalysis macro (dipstick) panel	–	Pt	Urine	–		1.0o	Exactly mapped	Designated
Urine sediment analysis, Random urine	53293–7	Urinalysis microscopic panel	Naric	Pt	Urine sed	Qn	Automated count	2.24	Exactly mapped	Designated
Protein electrophoresis, Serum	24351–9	Protein fractions panel	–	Pt	Ser/Plas	Qn		1.0o	Exactly mapped	Designated
Neonatal metabolic disease screening test, Dried blood spot	57794–0	Newborn screening test results panel	–	Pt	Bld.dot	–		2.29	Exactly mapped	Partially designated
Metanephrine fraction, Plasma	57772–6	Metanephrine.free & Normetanephrine.free panel	SCnc	Pt	Ser/Plas	Qn		2.29	Exactly mapped	Designated
Sexually transmitted pathogen screening molecular test, Genital specimen	91134–7	Sexually transmitted pathogens panel	–	Pt	XXX	–	Probe.amp. tar	2.65	Exactly mapped	Not designated
Respiratory viral pathogens screening molecular test, Nasopharyngeal swab	78922–2	Respiratory pathogens DNA & RNA panel	–	Pt	Nph	–	Probe.amp. tar	2.54	Exactly mapped	Not designated
Pneumonia pathogen screening molecular test, Respiratory system specimen	92143–7	Respiratory pathogens DNA & RNA panel	–	Pt	Respiratory System Specimen	–	Probe.amp. tar	2.66	Exactly mapped	Not designated
Mycoplasma Macrolide resistance test, Respiratory system specimen	N/A									

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Table 2 (continued)

Test name, specimen	Recommended LOINC in this study Optimal LOINC panel code	Component	Property	Timing	System	Scale	Method	Version First Released	Mapping classification	Conditionality attribute [†]
Gastrointestinal bacterial pathogens screening molecular test, Stool	92695–6	Gastrointestinal bacterial pathogens panel	–	Pt	Stool	–	Probe.amp. tar	2.66	Exactly mapped	Not designated
Gastrointestinal viral pathogens screening molecular test, Stool	92696–4	Gastrointestinal viral pathogens panel	–	Pt	Stool	–	Probe.amp. tar	2.66	Exactly mapped	Not designated
Clarithromycin resistance mutation test, Tissue	88509–5*	Helicobacter pylori 23S rRNA clarithromycin resistance mutation	Prid	Pt	Isolate/ Specimen	Nom	Molgen	2.64	Exactly mapped	N/A
Multiple Allergen Simultaneous Test (MAST), Serum	94593–1	Multiplex allergen panel	–	Pt	Ser/Plas	–		2.68	Exactly mapped	Not designated

Abbreviations: N/A, not available; Visc, Viscosity; Naric, Number Aeric (number per area); SCnc, Substance Concentration; Prid, Presence or identity; Pt, Point in time; Bld, Blood; PPP, Platelet poor plasma; Body fld, Body fluid, unsp; Ser/Plas, Serum/Plasma; Urine sed, Urine sediment; Bld.dot, Blood filter paper; XXX, Unknown or not specified; Nph, Nasopharynx; Qn, Quantitative; Nom, Nominal; Coag, Coagulation Assay; Probe.amp.tar, Target amplification followed by probe-based detection; Molgen, Molecular Genetics.

* Although the corresponding result codes were identified for these tests, they were marked because of the absence of a designated panel code.

† Conditionality refers to whether a test within a panel is required, optional, or performed only under specific conditions.

coding system. Table 2 summarizes the attributes and conditions of the LOINC codes mapped to the panel tests included in this study.

3.3. SNOMED CT mapping

Table 3 summarizes the SNOMED CT codes mapped to the panel tests included in this study. Of the 23 panel tests, exact mapping was achieved for 18 (78.2 %) tests. We used 12 post-coordinated expressions, of which nine were classified as exact mapping and three as broadly mapped.

Mapping discrepancies, including discrepancies in cases classified as broadly or narrowly mapped, were primarily due to the absence of pre-coordinated concepts necessary to fully capture the scope of specific tests, as well as the inherent limitations of the existing SNOMED CT framework in representing test components comprehensively. For example, the body fluid differential count was narrowly mapped because it lacked a pre-coordinated concept specific to differential counts, which is essential for accurately reflecting its clinical scope. Similarly, the ROMA test was broadly mapped because SNOMED CT does not have a primitive concept designed for ovarian cancer risk assessment. Post-coordination for the ROMA test was limited to the generation of a combination of concepts representing the measurement of CA125 and HE4 levels. Furthermore, the Mycoplasma macrolide resistance test was broadly mapped because no pre-coordinated concept exists to represent macrolide-resistant *Mycoplasma* within the current SNOMED CT structure.

3.4. Comparison with the SPIA Requesting Set

A comparison was conducted with the SPIA Requesting Set to further evaluate the accuracy and comprehensiveness of SNOMED CT mapping. Of the 23 panel tests included in this study, 11 SNOMED CT codes were identified using the SPIA Requesting Set. Of these, six codes were consistent with our mapping results. However, discrepancies were observed in five codes. For example, the peripheral blood differential count was mapped in the SPIA Requesting Set to the code 767002 | white blood cell count |, which represents a broader concept than our intended mapping. Another example of broad mapping is 395142003 | Allergy screening test | used in Australia, which represents a broader concept that may include tests other than MAST. For protein electrophoresis, the

SPIA Requesting Set uses specimen-specific codes, whereas our mapping lacked this specification, causing a discrepancy. To address this, we mapped a post-coordinated expression specifying serum as the specimen because the original code included subcodes for protein fractions, requiring hierarchical preservation and explicit specimen definition. In addition, for molecular screening tests such as the pneumonia pathogen screening molecular test and the gastrointestinal bacterial pathogen screening molecular test, the referenced codes in the SPIA Requesting Set were from the Australian edition of SNOMED CT, which were not included in our mappings.

3.5. Comparison of LOINC and SNOMED CT for panel test mapping

Further challenges were compounded by differences in the level of detail contained in the LOINC and SNOMED CT codes (Fig. 2). For example, in the case of protein electrophoresis, SNOMED CT lacks more granular concepts related to specimen type and quantitative status, which are critical for ensuring interoperability in real-world laboratory settings. LOINC mandates all five attributes except for the method; however, many panel codes lack values in these fields. Another limitation was that quantitative protein tests performed in laboratories for reporting purposes are not a part of protein electrophoresis. SNOMED CT does not include a component in 82962001 | protein electrophoresis (procedure). Furthermore, ROMA mapping revealed significant differences between LOINC and SNOMED CT in the representation of risk-based panel tests. In LOINC, ROMA is structured as a panel code that incorporates the individual biomarker components CA125 and HE4 and risk assessment.

When the SNOMED CT concept models were reviewed for information corresponding to the six LOINC attributes, the SNOMED CT component attribute was related to 18 concepts. However, the system attribute was related to only eight concepts (Table 4). In contrast, in LOINC, all 22 mapped concepts contained a component attribute, with only one specimen lacking a system attribute (Table 2). Further, several concept models, including commonly used tests such as CBC and prothrombin time, lacked information related to the specimen. The method was assigned to all concepts in SNOMED CT; however, they were general concepts including measurement, evaluation, and inspection; therefore, we reviewed the description and attributes, such as the “using device”

Table 3

SNOMED CT codes mapped to panel tests.

Test name, specimen	SNOMED CT code recommended in this study	Mapping classification	SNOMED CT code designated by RCPA	Remark
Complete blood count, Whole blood	26604007 Complete blood count (procedure)	Exactly mapped	26604007 Complete blood count	
Peripheral blood differential count, Whole blood	165511009 Differential white blood cell count procedure (procedure)	Exactly mapped	767002 White blood cell count	
Peripheral blood smear, Whole blood	14768001 Peripheral blood smear interpretation (procedure)	Exactly mapped	14768001 Peripheral blood smear interpretation	
Prothrombin time, Plasma	396451008 Prothrombin time (procedure)	Exactly mapped	396451008 Prothrombin time	
Body fluid analysis, Body fluid	127801007 Body fluid analysis (procedure)	Exactly mapped	N/A	
Body fluid differential count, Body fluid	78951002 Cell count and differential, body fluid (procedure)	Narrowly mapped	N/A	A new concept exclusively for the differential count is needed.
Blood viscosity test, Whole blood	250408005 Blood viscosity measurement (procedure)	Exactly mapped	250408005 Blood viscosity measurement	
Risk of Ovarian Malignancy Algorithm (ROMA), Serum	250724005 Tumor marker measurement (procedure): {246093002 Component (attribute) =(103084007 Cancer antigen 125 (substance) +708046007 Human epididymis protein 4 (substance))}	Broadly mapped	N/A	A new concept for risk of ovarian cancer is needed.
Risk of Ovarian Malignancy Algorithm (ROMA, premenopausal), Serum	250724005 Tumor marker measurement (procedure): {246093002 Component (attribute) =(103084007 Cancer antigen 125 (substance) +708046007 Human epididymis protein 4 (substance)), 246454002 Occurrence (attribute) =309606002 Before menopause (qualifier value) }	Broadly mapped	N/A	A new concept for risk of ovarian cancer is needed.
Risk of Ovarian Malignancy Algorithm (ROMA, postmenopausal), Serum	250724005 Tumor marker measurement (procedure): {246093002 Component (attribute) =(103084007 Cancer antigen 125 (substance) +708046007 Human epididymis protein 4 (substance)), 246454002 Occurrence (attribute) =307429007 After menopause (qualifier value) }	Broadly mapped	N/A	A new concept for risk of ovarian cancer is needed.
Urine dipstick test, Random urine	167226008 Urine dipstick test	Exactly mapped	167226008 Urine dipstick test	
Urine sediment analysis, Random urine	127800008 Microscopic urinalysis	Exactly mapped	127800008 Microscopic urinalysis	
Protein electrophoresis, Serum	82962001 Protein electrophoresis (procedure): {116686009 Has specimen (attribute) = 119364003 Serum specimen (specimen) }	Exactly mapped	4903000 Serum protein electrophoresis	
Neonatal metabolic disease screening test, Dried blood spot	428447008 Newborn blood spot screening (procedure): {363702006 Has focus (attribute) =736652002 Neonatal metabolic disorder (disorder) }	Exactly mapped	N/A	
Metanephrine fraction (Metanephrine.free and Normetanephrine.free), Plasma	412910008 Plasma catecholamine measurement (procedure):{246093002 Component (attribute) = 24427005 Metanephrine (substance) }+104835007 Normetanephrine measurement (procedure):{116686009 Has specimen (attribute) = 119361006 Plasma specimen (specimen) }	Exactly mapped	N/A	
Sexually transmitted pathogen screening molecular test, Genital specimen	104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure): {363702006 Has focus (attribute) = 8098009 Sexually transmitted infectious disease (disorder) }	Exactly mapped		
Respiratory viral pathogens screening molecular test, Nasopharyngeal swab	104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure):{363702006 Has focus (attribute) = 312133006 Viral respiratory infection (disorder) }	Exactly mapped	N/A	
Pneumonia pathogen screening molecular test, Respiratory system specimen	104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure):{363702006 Has focus (attribute) = 53084003 Bacterial pneumonia (disorder) }	Exactly mapped	843441000168103 Respiratory pathogen nucleic acid assay	RCPA code was Australian edition code.
Mycoplasma macrolide resistance test, Respiratory system specimen	117245002 Nucleic acid probe method with target amplification (procedure)	Broadly mapped	N/A	A new concept for macrolide-resistant Mycoplasma is needed.
Gastrointestinal bacterial pathogens screening molecular test, Stool	104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure): {363702006 Has focus (attribute) = 409966000 Acute diarrhea (disorder) }	Exactly mapped	843431000168107 Faecal enteropathogen nucleic acid assay	RCPA code was Australian edition code.
Gastrointestinal viral pathogens screening molecular test, Stool	104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure): {363702006 Has focus (attribute) = 409966000 Acute diarrhea (disorder) }	Exactly mapped	N/A	
Clarithromycin resistance mutation test, Tissue	117245002 Nucleic acid probe method with target amplification (procedure):{246093002 Component	Exactly mapped	N/A	

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Table 3 (continued)

Test name, specimen	SNOMED CT code recommended in this study	Mapping classification	SNOMED CT code designated by RCPA	Remark
Multiple Allergen Simultaneous Test (MAST), Serum	(attribute) =726496002 Clarithromycin resistant Helicobacter pylori (organism) } 116151006 Multi-allergen solid phase immunosorbent assay for immunoglobulin E antibodies (procedure)	Exactly mapped	395142003 Allergy screening test	A new concept for multiple allergen simultaneous test is needed.

Abbreviations: N/A, not available; RCPA, Royal College of Pathologists of Australia.

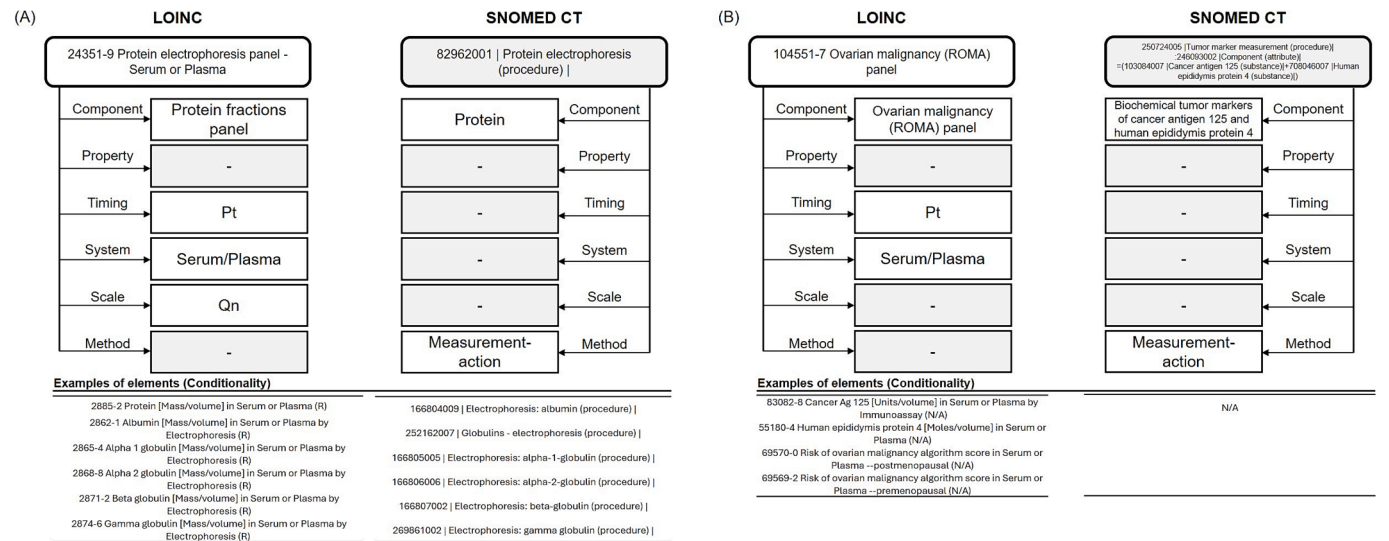


Fig. 2. Representative example of comparative analysis of the structure of LOINC and SNOMED CT codes mapped to panel tests: (A) Protein electrophoresis; (B) ROMA score. The attributes corresponding to LOINC's six-axis model were compared for each code. LOINC mandates all axes except for the method; however, many panel codes had missing values in these fields. In contrast, post-coordinated SNOMED codes often lacked specific attributes. LOINC defines conditionality as shown in A; however, there are cases, as illustrated in B, where conditionality is not available. Abbreviations: N/A, not available; Pt, Point in time; Qn, Quantitative.

attribute for addressing a detailed method. Moreover, SNOMED CT lacks a pre-coordinated concept for ovarian cancer risk, making it impossible to map post-coordinated ROMA expression using its existing concept.

4. Discussion

This study evaluated the applicability of LOINC and SNOMED CT in frequently performed panel tests. With rapid advancements in laboratory testing and the increasing number of test items, panel tests have become indispensable [21,22]. However, there is a lack of research on coding systems that should be used to ensure interoperability among these test items. Studies have primarily focused on specific laboratory tests or assessed interoperability within limited scopes [14,16,23,24]. This study systematically examined the applicability of LOINC and SNOMED CT in frequently performed panel tests, providing a comprehensive approach to addressing interoperability challenges.

Mapping panel tests to LOINC was achieved at a higher rate than with SNOMED CT, underscoring the suitability of LOINC for representing laboratory panel tests. This advantage stems largely from the structure of the LOINC terminology, which employs a six-axis model—component, property, timing, system, scale, and method—specifically designed for laboratory testing [25]. The existence of predefined panel codes and clear relationships between panels and their components facilitates consistent encoding and makes LOINC particularly effective for representing ordered test panels in laboratory information systems. However, this structured model also presents limitations, particularly when flexible composition or post-coordination is required. To address these challenges, ongoing efforts are focused on transforming LOINC into an ontology-based terminology in collaboration with

SNOMED International. SNOMED CT, with its ontological framework, allows dynamic composition of test elements and the creation of new concepts through post-coordination. Moving forward, mapping to an integrated framework—such as the emerging LOINC Ontology or an expanded SNOMED CT Observable Entity model—may be necessary to enhance both semantic richness and interoperability. However, certain challenges remain unaddressed. For instance, LOINC 34994-4 (Smear morphology panel-blood) was evaluated as a mapping failure, because this code was marked as discouraged by LOINC guidelines. This illustrates a limitation of LOINC's current repository, where certain specialized tests lack updated or recommended alternatives. Even well-mapped LOINC codes sometimes have missing attributes inherent to panel codes because they often report qualitative and quantitative results together or include results with different properties under a single code, even if they are quantitatively measured. Furthermore, LOINC provides significant granularity and standardization; however, the absence of certain codes and challenges in creating new ones suggests that minor adaptations or extensions may be required for seamless adoption in local healthcare systems [26]. In Korea, pH and specific gravity are considered subcomponents in body fluid analysis. This illustrates how the components of certain panels vary by country. However, as an international terminology system, LOINC cannot fully accommodate such regional variations. The lack of a local extension is a significant limitation in this regard. Creating new codes requires approval from the LOINC system, which makes it less flexible [27].

Approximately 4000 active panel codes exist in the latest LOINC v.2.78, a significant increase from the 148 panel codes in v.2.3 in 2004 [28]. Over time, numerous codes have been added to LOINC, including those for molecular microbiology, MAST, and ROMA tests, which were

Table 4
Mapping of SNOMED CT concept models to LOINC's six attributes.

SNOMED CT concept models mapped in this study	Component	Property	Timing	System	Scale	Method
26604007 Complete blood count (procedure)	Blood cell					Measurement - action
165511009 Differential white blood cell count procedure (procedure)	Leukocyte					Measurement - action
14768001 Peripheral blood smear interpretation (procedure)				Peripheral blood specimen		Evaluation - action
396451008 Prothrombin time (procedure)						Evaluation - action
127801007 Body fluid analysis (procedure)				Body fluid specimen		Evaluation - action
78951002 Cell count and differential, body fluid (procedure)	Blood cell			Body fluid specimen		Evaluation - action
250408005 Blood viscosity measurement (procedure)	Substance					Measurement - action
250724005 Tumor marker measurement (procedure): {246093002 Component (attribute) =(103084007 Cancer antigen 125 (substance) +708046007 Human epididymis protein 4 (substance))}	Biochemical tumor marker					Measurement - action
250724005 Tumor marker measurement (procedure): {246093002 Component (attribute) =(103084007 Cancer antigen 125 (substance) +708046007 Human epididymis protein 4 (substance) , 246454002 Occurrence (attribute) =309606002 Before menopause (qualifier value) }	Cancer antigen 125& Human epididymis protein 4					Measurement - action
250724005 Tumor marker measurement (procedure): {246093002 Component (attribute) =(103084007 Cancer antigen 125 (substance) +708046007 Human epididymis protein 4 (substance) , 246454002 Occurrence (attribute) =307429007 After menopause (qualifier value) }	Biochemical tumor marker					Measurement - action
167226008 Urine dipstick test	Cancer antigen 125& Human epididymis protein 4*postmenopausal					Measurement - action
127800008 Microscopic urinalysis	Substance			Urine specimen		Dipstick
82962001 Protein electrophoresis (procedure): {116686009 Has specimen (attribute) = 119364003 Serum specimen (specimen) }	Protein			Urine specimen		Inspection - action
428447008 Newborn blood spot screening (procedure): {363702006 Has focus (attribute) = 736652002 Neonatal metabolic disorder (disorder) }	Neonatal disorder			Serum specimen		Microscope, device
412910008 Plasma catecholamine measurement (procedure): {246093002 Component (attribute) =24427005 Metanephrine (substance) } +104835007 Normetanephrine measurement (procedure): {116686009 Has specimen (attribute) =119361006 Plasma specimen (specimen) }	Catecholamine			Plasma specimen		Measurement - action
104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure): {363702006 Has focus (attribute) = 8098009 Sexually transmitted infectious disease (disorder) }	Metanephrine					
104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure): {363702006 Has focus (attribute) =312133006 Viral respiratory infection (disorder) }	Normetanephrine					
104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure): {363702006 Has focus (attribute) =53084003 Bacterial pneumonia (disorder) }	Microbial identification					nucleic acid probe, with amplification (polymerase chain reaction)
117245002 Nucleic acid probe method with target amplification (procedure)	Sexually transmitted infectious disease					
104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure): {363702006 Has focus (attribute) = 409966000 Acute diarrhea (disorder) }	Microbial identification					nucleic acid probe, with amplification (polymerase chain reaction)
104170007 Microbial identification by nucleic acid probe, with amplification (polymerase chain reaction) (procedure): {363702006 Has focus (attribute) = 409966000 Acute diarrhea (disorder) }	Viral respiratory infection					nucleic acid probe, with amplification (polymerase chain reaction)
117245002 Nucleic acid probe method with target amplification (procedure): {246093002 Component (attribute) =726496002 Clarithromycin resistant Helicobacter pylori (organism) }	Microbial identification					Nucleic acid probe method with target amplification
116151006 Multi-allergen solid phase immunosorbent assay for immunoglobulin E antibodies (procedure)	Bacterial pneumonia					
	Clarithromycin resistant Helicobacter pylori					
	Allergen specific immunoglobulin E					Measurement - action
						Multi-allergen solid phase immunosorbent assay

introduced after v.2.54. However, these codes have yet to establish a well-defined conditionality. Given the incomplete state of detailed information on LOINC panel codes, continuous updates and refinements are necessary.

In this study, SNOMED CT demonstrated a lower mapping rate compared with LOINC, partly due to its lack of detailed specifications for tests requiring precise definitions. In addition, SNOMED CT lacks a pre-coordinated concept related to panel tests, highlighting the need for further refinement of SNOMED CT concepts to accommodate specific laboratory test concepts. SNOMED CT allows the creation of new concepts through post-coordination, enhancing the adaptability and descriptive capability of SNOMED CT, enabling it to accommodate better the increasing number of new concepts arising in clinical practice and making it a widely used standard across various healthcare domains [14,29,30]. SNOMED CT is a comprehensive ontology covering general medicine rather than being specifically focused on laboratory testing. Consequently, it lacks detailed descriptions for attributes other than the component among LOINC's six attributes. Initiatives aimed at improving interoperability between LOINC and SNOMED CT, such as the LOINC Ontology project [17], enable a more effective alignment of LOINC terms with SNOMED CT in the future, facilitating seamless integration into health-information systems and enhancing the utilization of SNOMED CT in laboratory settings.

Urine dipstick tests were labeled as "urine general tests" or "routine urine tests" by the referral laboratories but were initially mapped to "Urinalysis" by the research team. This designation was based on the Korean National Health Insurance nomenclature, where the test is listed as "NU-225 Routine Urinalysis." However, the term "Urinalysis" typically encompasses urine dipstick tests and microscopic urinalysis, suggesting a broader scope [31]. During the mapping process, if the initial test name is incorrectly assigned or broadly defined, mapping accuracy can be compromised [13]. This highlights the critical importance of accurately defining test names and ensuring precise mapping during the standardization process to achieve reliable interoperability and data consistency.

This study had certain limitations. A limited number of test items were analyzed; however, panel tests were selected from laboratory tests that were each claimed over 1,000 times per year at two major referral laboratories in Korea, collectively representing 88.3 % of the total test volume in the national health insurance claims data. This approach ensured that the selected panel tests reflect routine clinical practice. Nevertheless, to improve generalizability, future studies should include a more diverse set of panels from a broader range of institutions. In addition, the dynamic nature of databases, such as LOINC, means that the current mapping accuracy may continually evolve, emphasizing the importance of continuous evaluation and refinement to maintain alignment with updated standards. Furthermore, variations in regional naming conventions and insurance claim codes may restrict the generalizability of these findings across diverse healthcare systems, underscoring the need for localized adaptations to harmonize effectively with international standards and enhance interoperability.

5. Conclusions

For frequently performed panel tests, LOINC demonstrated a higher exact mapping rate than SNOMED CT, highlighting its strength in structured test representation. However, including discouraged codes in this study due to the lack of suitable alternatives reveals areas where LOINC could benefit from further refinement. SNOMED CT exhibited a lower mapping rate; however, its hierarchical structure and widespread use across the medical field provide strong advantages in compatibility and interoperability despite its limitations in detailed representation when using only the pre-coordinated concept. Initiatives such as the LOINC Ontology project [17] show promise for aligning LOINC terms with SNOMED CT and addressing the current gaps in standardization. Future efforts should prioritize the continued development of SNOMED

CT and LOINC alongside collaborative integration initiatives to drive progress and enhance interoperability in laboratory data exchange.

CRedit authorship contribution statement

Hyejin Ryu: Writing – original draft, Investigation, Data curation. **Sumi Sung:** Writing – review & editing, Data curation. **Kuenyoul Park:** Writing – review & editing, Investigation, Conceptualization. **Min-Sun Kim:** Investigation. **YeJin Oh:** Investigation. **Shinae Yu:** Investigation. **Eun-Jung Cho:** Investigation. **Sollip Kim:** Writing – review & editing, Supervision, Investigation.

Funding

This research was supported by a grant from the National Healthcare Standardization Project through the Korea Health Information Service, funded by the Ministry of Health & Welfare, Republic of Korea (grant number: 2024060D571–00).

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

None.

Data availability

The data underlying this article will be shared on reasonable request to the corresponding author.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.ijmedinf.2025.106055>.

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