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Development of a SNOMED-CT Mapping Framework for the Interoperability of Biobank Resources in Korea

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Abstract

The existing Systematized Nomenclature of Medicine - Clinical Terms (SNOMED-CT) toolkit includes only a clinical term search, and its output functions are not linked to a particular database, making it difficult for users to map biological data, and the use of biobanks requires much time and effort. This study developed a SNOMED-CT toolkit using an optimized search, allowing users to map clinical items for efficient utilization and standardization of biobank resources. The toolkit was developed using the Java programming language and Java Database Connectivity to connect to a previously developed research database. The user interface was implemented using Swing. The functions and interfaces of the toolkit were developed after a requirement analysis by SNOMED-CT experts. Using the toolkit, the user can search SNOMED-CT concepts. Using pre-and post-coordinated mapping of clinical items with the toolkit, it is possible to maximize the semantic interoperability of the previously developed database.

Keywords: *Biobank, Semantic Interoperability, SNOMED-CT*

1. Introduction

Biobanks worldwide have collaborated to construct a Biobank Information Management System (BIMS) for the efficient management of collected biological data, to enable the development of customized methods for treating and preventing disease. Each BIMS was developed with the aim of providing high-quality information to a large number of researchers, regardless of affiliation. However, the BIMS experienced difficulties with information exchange because incompatibility and database problems between heterogeneous system, such as Electronic Medical Record System (EMRS) [1]. Typically, different institutions and practitioners use various methods to express the same concept of an item or represent it using local code or abbreviations, because BIMS operates based on the range of collected information, content, and format in each biobank. Consequently, this polymorphism of items leads to misinterpretation by researchers and acts as an obstacle to information exchange.

National projects in the United states and Europe have constructed network environments that facilitate the exchange of biological data between biobanks, such as the Cancer Biomedical Informatics Grid (caBIG) [2] and the Biobanking and Biomolecular Resources Research Infrastructure (BBMRI) [3]. Therefore, we studied database development in order to integrate biological data managed by 15 university hospital biobanks in the Republic of Korea, together with the National Biobank of Korea (NBK).

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A three-stage data mining process (specification, classification, and standardization) was used to construct a database composed of 18 tables containing 7,197,252 raw data items. To clarify the meanings of the items, clinical items were defined using the Systematized Nomenclature of Medicine -- Clinical Terms (SNOMED-CT), and specimen items were defined using the Logical Observation Identifiers Names and Codes (LOINC). In total, 2,504 (70.4%) items were mapped and the remainder withheld because of uncertainties in the collected data.

The most efficient means of maximizing the semantic interoperability of a database would be to map the biobank data that could enhance understanding of the significance of an item to the international terminology directly. This necessitates the development of a tool that is easily maintained. However, the existing SNOMED-CT toolkit [4-6] provides only the search concept and term, outputs to the web, and includes an installation program; it is impossible to research and edit the mapped identifier or automatically map the searched concept identifier in conjunction with a specific database. Therefore, this study developed a customized toolkit that enables all users who wish to take advantage of the biological data stored in the biobank to perform clinical item searches and SNOMED-CT mapping, editing, and viewing upon accessing the database. Specifically, experts designed the function and user interface of the toolkit after conducting a requirement analysis and implemented an output function that links the terminology based on previously developed toolkit [7].

2. Methods

2.1. Expert Requirement Analysis

The user requirements were analyzed by three SNOMED-CT experts such that they could develop a toolkit enabling users to utilize the biological data. The toolkit included various functions, such as searching clinical items, mapping clinical items with concept identifiers, viewing concept information, and editing mapped information in connection with the database (Figure 1).

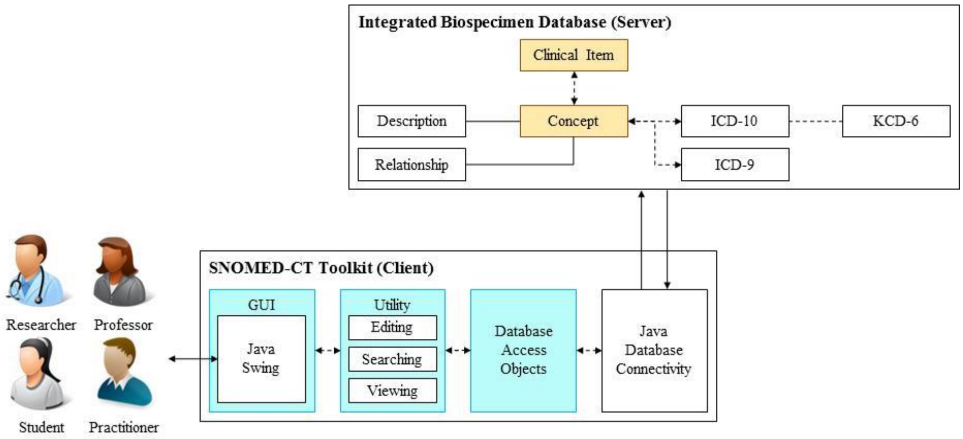


Figure 1. Architecture of SNOMED-CT Toolkit

The detailed function requirements were separated into five domains (Table 1). The search domain included the SNOMED-CT concept, reference terminology, and a clinical item search function, and the output domain included detailed information on the selected SNOMED-CT concept and a clinical item metadata output function. Specifically, we implemented an edit domain function that automatically manages and inputs the mapping results and a reference terminology domain function that utilizes the benefits of SNOMED-CT to differentiate it from existing toolkits.

Table 2. Result of Requirement Analysis

Domain	Requirement
Search	search the SNOMED-CT concept, descriptions using the identifier search the SNOMED-CT concept in accordance with string conditions search the clinical item in accordance with metadata conditions search the reference terminology concept
Output	output the searched SNOMED-CT concept in table form output the hierarchy and top-level information of selected SNOMED-CT concept output the detailed information of selected SNOMED-CT concept output the post-coordinated mapping attributes of selected SNOMED-CT concept output the post-coordinated expression output the clinical item metadata in table form
Edit	pre-coordinated mapping and automatically input post-coordinate mapping and automatically input edit the mapping information of selected clinical item
Reference Terminology	refer the ICD-10 code about selected SNOMED-CT concept refer the KCD-6 code about selected SNOMED-CT concept refer the ICD-9 code about selected SNOMED-CT concept

SNOMED-CT contains 400,000 medical concepts; this vast number includes multiple terms for a single concept [8-9]. It can be mapped to other terminologies, because it consists of a hierarchy of various depths based on 19 top-level concepts. By mapping the International Classification of Diseases (ICD)-10, 9 and the Korean Classification of Diseases (KCD-6) codes corresponding to the identifier of a specific concept, it is possible to attain compatibility with existing terminology. Therefore, the user is not only provided with the detailed SNOMED-CT information for the searched term but also reference information for other terminologies.

2.2. Database Design

To provide clinical item information and database connection, we added nine new tables to the existing entity relationship diagram (ERD) (Figure 2). The ERD of the clinical domain consisted of seven tables, including biobank and document information tables (t_bank, t_document), clinical item classification tables (t_high_class, t_middle_class, and t_low_class), and the t_clinical_item table, which contains metadata for 1,796 clinical items.

The primary key (PK) to the classification tables is t_clinical_item, which includes data on the clinical item, values, descriptions, and SNOMED-CT concept identifier fields.

The three SNOMED-CT tables are t_concepts, t_descriptions, and t_relationships, which contain 397,787, 1,182,734, and 1,454,681 records, respectively. The unique SNOMED-CT concepts are stored in t_concepts, t_descriptions stores multiple terms for a single concept, and t_relationships stores the relationships between the source and target concepts. Therefore, t_descriptions and t_relationships refer to the PK of t_concepts. To meet these requirements, a relationship is created between the concept-id field in t_clinical_item and the PK in t_concepts. Other terminology tables (t_icd9, t_icd10, and t_kcd6) were added, and mapping tables (t_snomed2icd10, t_icd92target, and t_snomed2icd9) were placed between the t_concepts.

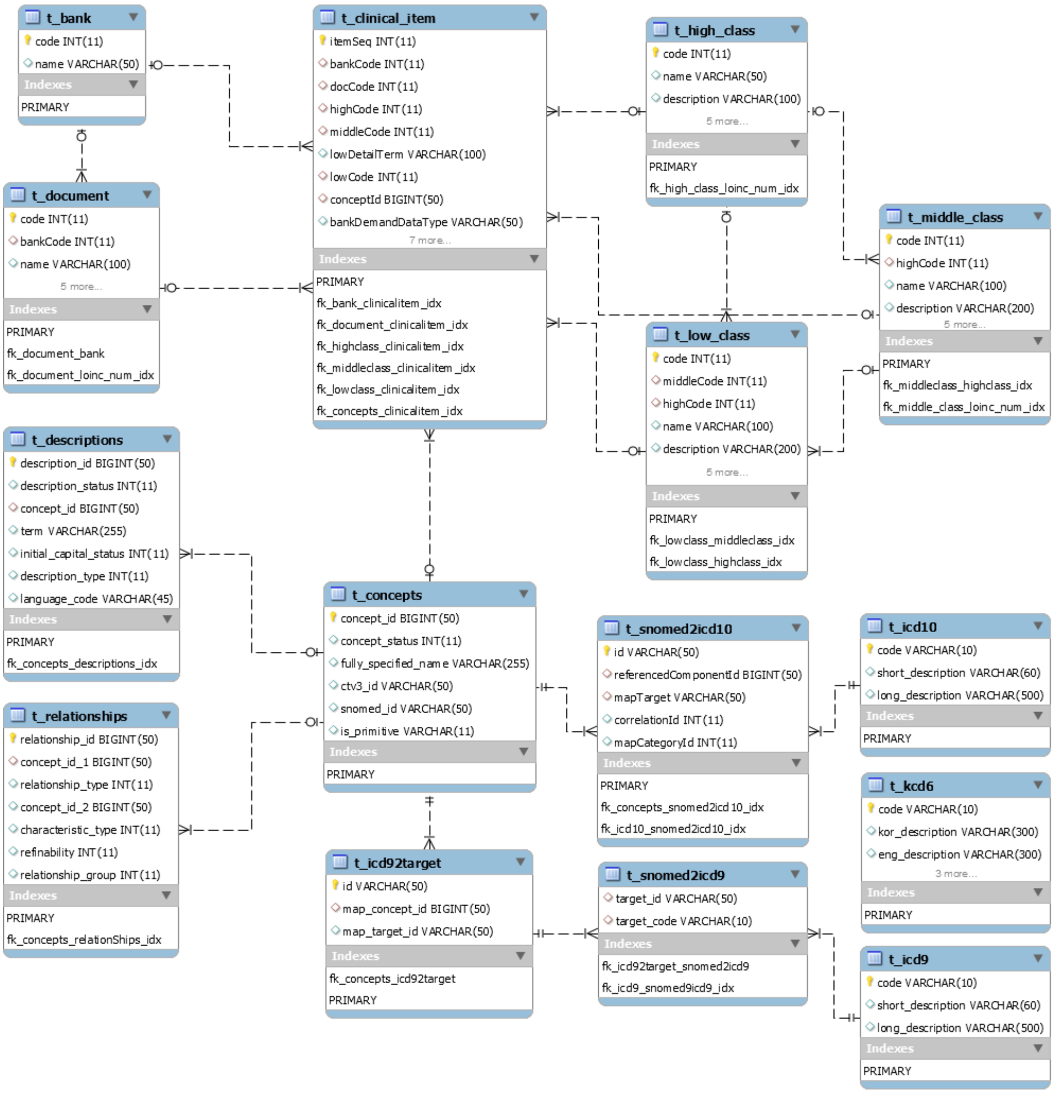


Figure 2. Entity Relationship Diagram of SNOMED-CT Toolkit

The mapping tables used were derived from an official source in the Unified Medical Language System (UMLS), which is updated regularly [9]. Each table was mapped to other terminologies to appropriately determine the depth of the SNOMED-CT hierarchy using predetermined rules. For example, ICD-10 was mapped to 54,262 of the 69,902 codes, which belong to three top-level concepts (51,900 clinical findings, 1,008 events, and 1,354 situations with explicit context). KCD-6 might be compatible with SNOMED-CT without the use of a mapping table by using the ICD-10 mapping table, because KCD-6 is a set of Korean diseases within the ICD-10.

2.3. Concept Hierarchy Algorithm

The SNOMED-CT concept consists of a hierarchy that source-target concepts using an “is-a” relationship from the “SNOMED-CT Concept” root concept. The 19 top-level concepts connected directly to the root concept with “is-a” relationships are clearly divided into those involving a semantic relationship, while the remainder are connected hierarchically with “is-a” relationships through a descendant of one or more of the top-level concepts (Figure 3). For example, “lung abscess” is the top level concept of “clinical finding”; parent concepts are “lung disorder”, “inflammatory disorder of the respiratory tract", and "thoracic abscess", and the child concepts include "abscess of lung and mediastinum", "single lung abscess", *etc*.

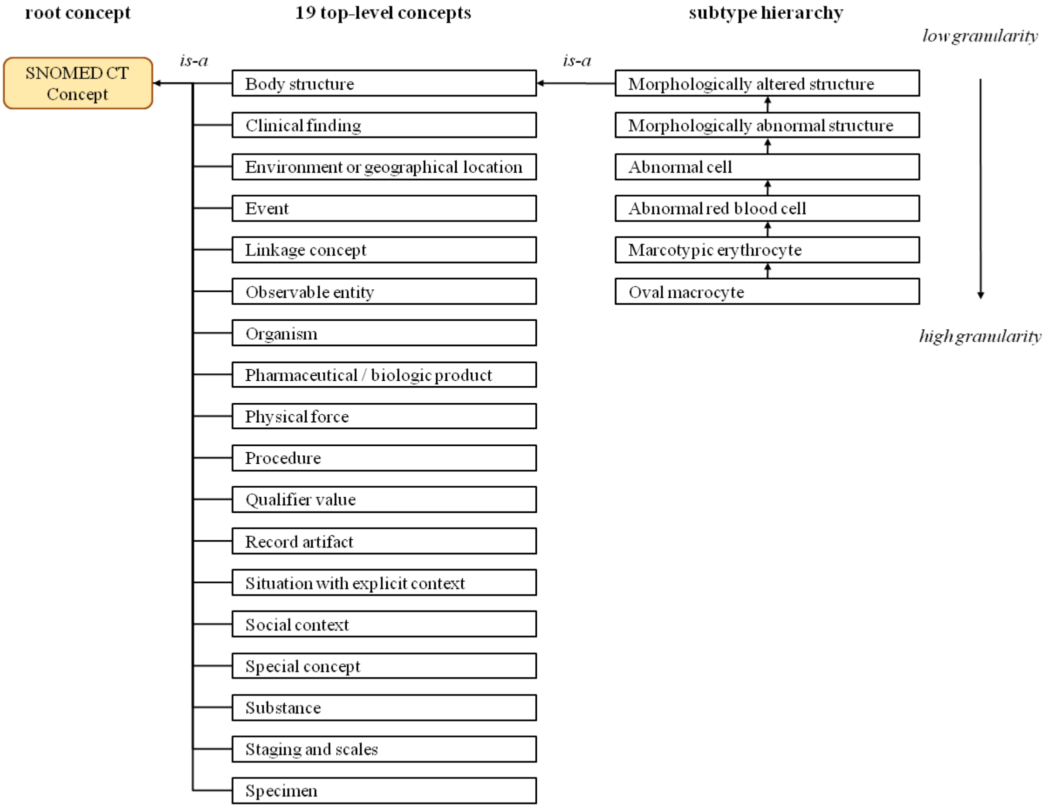


Figure 3. Hierarchy of SNOMED-CT

The SNOMED-CT concept needs to decipher the meaning of a term through its relative position in the hierarchy and detailed information, because it does not have a clear definition. However, due to the enormous number of concepts and the complex hierarchy of SNOMED-CT, a user cannot remember all of the parents or children of a specific concept. Therefore, it is necessary to display multiple parents and children in a sub-graph for a selected concept to enable rapid understanding by the user. SNOMED-CT stores a variety of relationships and attribute types for the source and target concepts in t_relationships. Any efficient method for generating a hierarchy has to explore the source and target concepts using an "is-a" relationship_type field. The toolkit was designed as a concept hierarchy algorithm that explores the parent and children of the selected concept based on "is-a" concept identifiers (Figure 4).

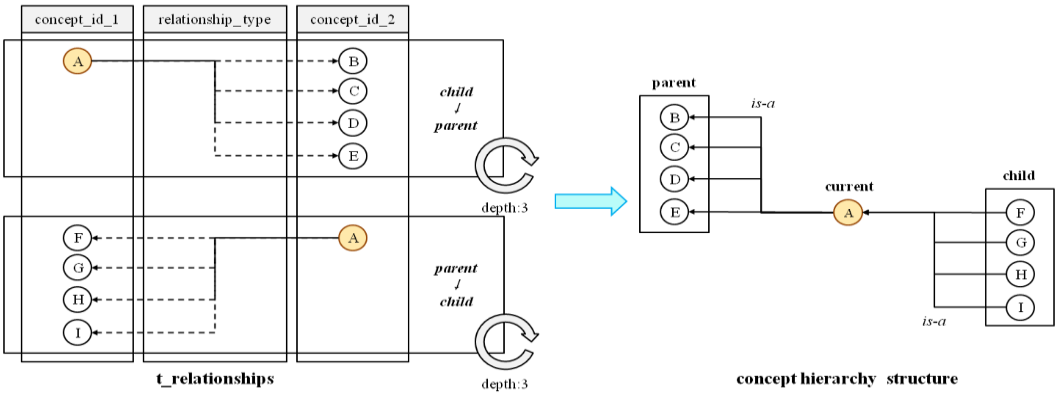


Figure 4. Algorithm of SNOMED-CT Hierarchy

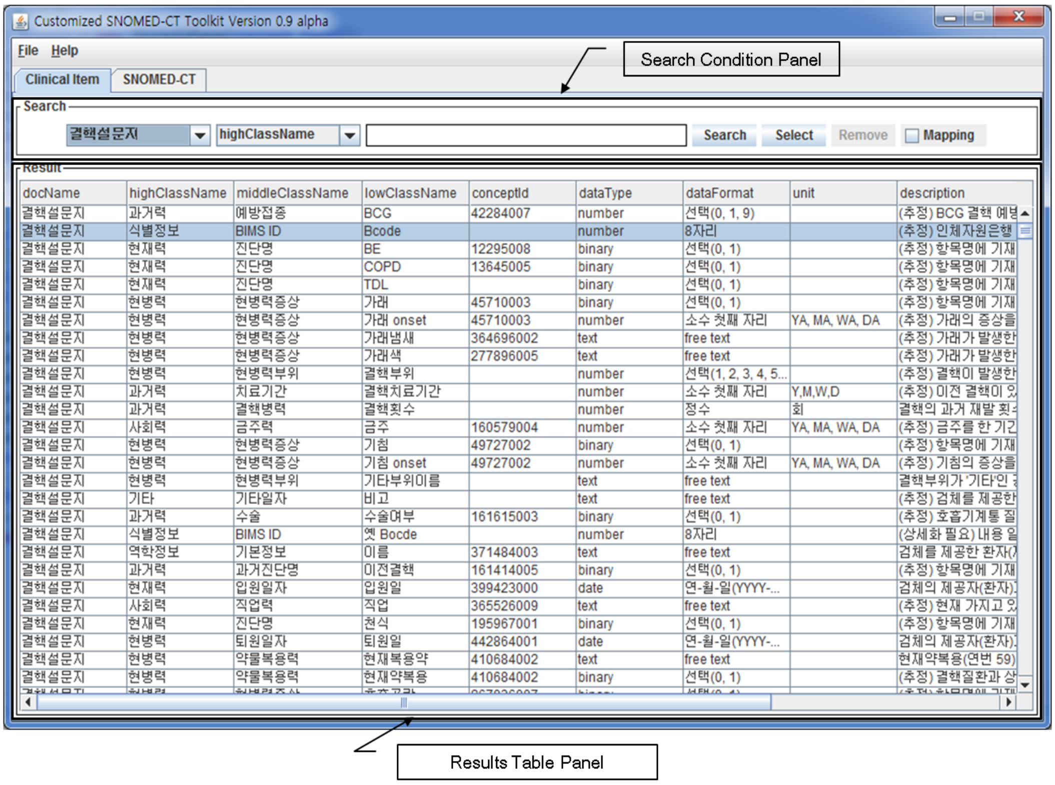
The designed algorithm was divided into search areas for the parent and child concepts using two threads, and a node in the sub-tree search was performed using a recursive call method [11]. The parent concept searches the concept_id_2 field (target concept) after setting the selected concept to the concept_id_1 field (source concept). This process is repeated until the next target concept is the root concept. By contrast, the child concept is repeated until there is no next source concept after setting the selected concept to the target concept. Since the number of parent and child concepts makes the search very inefficient, we added a terminate condition that is a recursive call that continues until there is a maximum of three levels between the current concept and the parent and child concepts. In addition, if the parent and child concepts are selected, the research on the parent and child concepts has optimized the production rate of the hierarchy.

3. Results

This study developed a SNOMED-CT toolkit based on the designed ERD that met the cited requirements, using the Java programming language. We used the JDBC-MySQL Connector to connect to a database server developed using MySQL Server 6.0, and implemented the user interface by using SWING. The developed toolkit consist of a clinical item tab and a SNOMED-CT tab, and it is automatically executed when you log in to the previously database server using the account information that is given to each biobank users.

3.1. Clinical Item Tab

The clinical item tab consists of a search condition panel and a results table panel (Figure 5). The search condition panel can filter the mapping of clinical items using the combo boxes, check box, and text field. The combo boxes consist of items that document the appropriate biobank and items for the fields (high class, middle class, low class, data types, value type, units, and concept identifier) to search in conjunction with a text field. The user can filter the clinical items in a specified document using a document combo box, and the search can be divided into items not mapped and items mapped to SNOMED-CT using the combo box.



Search Condition Panel

docName	highClassName	middleClassName	lowClassName	conceptId	dataType	dataFormat	unit	description
결핵설문지	과거력	예방접종	BCG	42284007	number	선택(0, 1, 9)		(추정) BCG 결핵 예
결핵설문지	식별정보	BIMS ID	Bcode		number	8자리		(추정) 인체자원은행
결핵설문지	현재력	진단명	BE	12295008	binary	선택(0, 1)		(추정) 항목명에 기재
결핵설문지	현재력	진단명	COPD	13645005	binary	선택(0, 1)		(추정) 항목명에 기재
결핵설문지	현재력	진단명	TDL		binary	선택(0, 1)		(추정) 항목명에 기재
결핵설문지	현병력	현병력증상	가래	45710003	binary	선택(0, 1)		(추정) 항목명에 기재
결핵설문지	현병력	현병력증상	가래 onset	45710003	number	소수 첫째 자리	YA, MA, WA, DA	(추정) 가래의 증상을
결핵설문지	현병력	현병력증상	가래냄새	364696002	text	free text		(추정) 가래가 발생한
결핵설문지	현병력	현병력증상	가래색	277896005	text	free text		(추정) 가래가 발생한
결핵설문지	현병력	현병력부위	결핵부위		number	선택(1, 2, 3, 4, 5...		(추정) 결핵이 발생한
결핵설문지	과거력	치료기간	결핵치료기간		number	소수 첫째 자리	Y,M,W,D	(추정) 이전 결핵이 있
결핵설문지	과거력	결핵병력	결핵횟수		number	정수	회	결핵의 과거 재발 횟수
결핵설문지	사회력	금주력	금주	160579004	number	소수 첫째 자리	YA, MA, WA, DA	(추정) 금주를 한 기간
결핵설문지	현병력	현병력증상	기침	49727002	binary	선택(0, 1)		(추정) 항목명에 기재
결핵설문지	현병력	현병력증상	기침 onset	49727002	number	소수 첫째 자리	YA, MA, WA, DA	(추정) 기침의 증상을
결핵설문지	현병력	현병력부위	기타부위이름		text	free text		결핵부위가 '기타'인
결핵설문지	기타	기타일자	비고		text	free text		(추정) 검체를 제공한
결핵설문지	과거력	수술	수술여부	161615003	binary	선택(0, 1)		(추정) 호흡기계통 질
결핵설문지	식별정보	BIMS ID	옛 Bocde		number	8자리		(상세화 필요) 내용 일
결핵설문지	역학정보	기본정보	이름	371484003	text	free text		검체를 제공한 환자(
결핵설문지	과거력	과거진단명	이전결핵	161414005	binary	선택(0, 1)		(추정) 항목명에 기재
결핵설문지	현재력	입원일자	입원일	399423000	date	연-월-일(YYYY-...		검체의 제공자(환자)
결핵설문지	사회력	직업력	직업	365526009	text	free text		(추정) 현재 가지고 있
결핵설문지	현재력	진단명	천식	195967001	binary	선택(0, 1)		(추정) 항목명에 기재
결핵설문지	현병력	퇴원일자	퇴원일	442864001	date	연-월-일(YYYY-...		검체의 제공자(환자)
결핵설문지	현병력	약물복용력	현재복용약	410684002	text	free text		현재약복용(연번 59)
결핵설문지	현병력	약물복용력	현재약복용	410684002	binary	선택(0, 1)		(추정) 결핵질환과 상

Results Table Panel

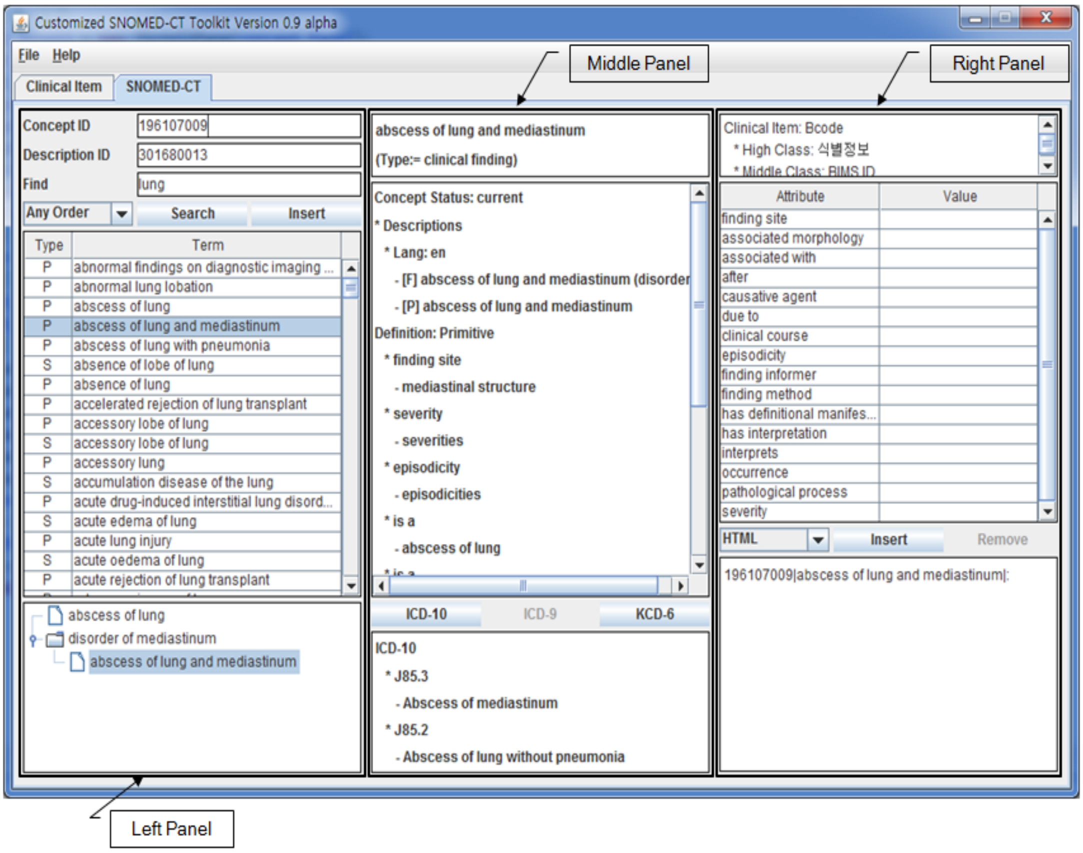
Figure 5. Screen of Clinical Item Tab

By entering a string in the text field, it is possible to search only the corresponding clinical items. It other words, the component selected by the user is added to the conditional query statement and the database server returns the results. Specifically, pressing the deletion button removes the mapping information of the selected clinical items, and pressing the selection button transmits the current output results to the SNOMED-CT tab to be mapped automatically by the recording unit.

The results table panel outputs clinical item metadata regarding the corresponding search condition in table form. The fields in the table consist of document, high class, middle class, low class values and concept identifier, data types, value type, units, and descriptions. These can be filtered to output the result through combo boxes and a check box placed on top by using the relationship between t_clinical_item and the adjacent tables.

3.2. SNOMED-CT Tab

The SNOMED-CT tab consists of three detail panels, which provide the functions of analyzed requirement (Figure 6). The left panel provides three functions: *i.e.*, identifier of concept and description input, term input, search results table, and the hierarchy output function of the selected concept. An term added to the query statement with search condition in the combo box returns the results from t_descriptions, and provides a search results table.



Concept ID 196107009
Description ID 301680013
Find lung

Type	Term
P	abnormal findings on diagnostic imaging ...
P	abnormal lung lobation
P	abscess of lung
P	abscess of lung and mediastinum
P	abscess of lung with pneumonia
S	absence of lobe of lung
P	absence of lung
P	accelerated rejection of lung transplant
P	accessory lobe of lung
S	accessory lobe of lung
P	accessory lung
S	accumulation disease of the lung
P	acute drug-induced interstitial lung disord...
S	acute edema of lung
P	acute lung injury
S	acute oedema of lung
P	acute rejection of lung transplant

abscess of lung
disorder of mediastinum
abscess of lung and mediastinum

abscess of lung and mediastinum
(Type:= clinical finding)

Concept Status: current
* Descriptions
* Lang: en
- [F] abscess of lung and mediastinum (disorder
- [P] abscess of lung and mediastinum
Definition: Primitive
* finding site
- mediastinal structure
* severity
- severities
* episodicity
- episodicities
* is a
- abscess of lung

ICD-10
* J85.3
- Abscess of mediastinum
* J85.2
- Abscess of lung without pneumonia

Clinical Item: Bcode
* High Class: 식별정보
* Middle Class: BIMS ID

Attribute	Value
finding site	
associated morphology	
associated with	
after	
causative agent	
due to	
clinical course	
episodicity	
finding informer	
finding method	
has definitional manifes...	
has interpretation	
interprets	
occurrence	
pathological process	
severity	

196107009|abscess of lung and mediastinum|;

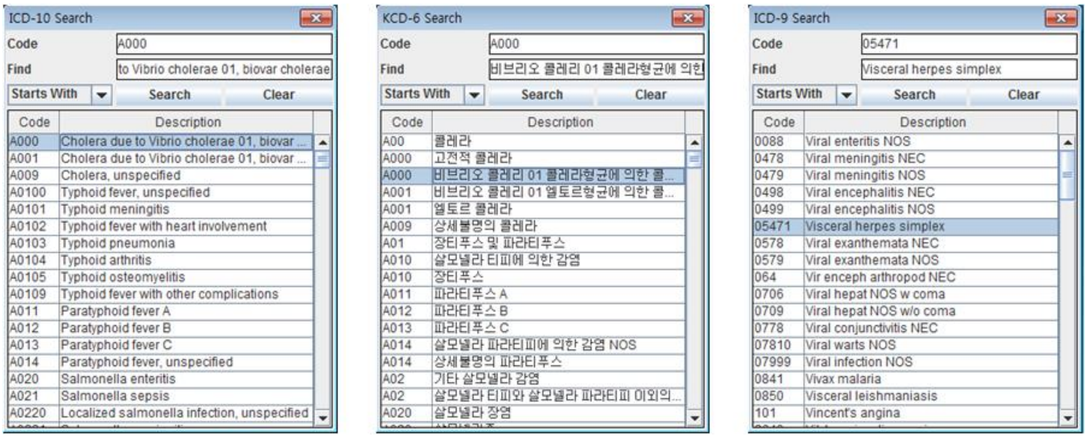
Figure 6. Screen of SNOMED-CT Tab

The search function using the description identifier outputs detailed information regarding the corresponding concept by simply comparing the value of the description_id field in t_descriptions. However, the concept identifier can have a number of descriptions for a single concept, and thus the middle panel must select detailed information to output. Therefore, the toolkit was designed such that the information on the unique fully specified name (FSN) outputs descriptions for the search for the concept identifier. The combo box contains four condition items (any order, starts with, ends with, and identical), and a wildcard can be added to the term field based on selected item.

The search results table outputs information on the searched term using the term and description_type fields of t_descriptions. The types of terms are divided into preferred term and synonym, and these are output to S and P, respectively. If an outputted term exceeds the size of the table, it is outputted to the tooltip box. Specifically, the left panel manages the information output by another panel, and therefore the concept identifier of the term selected by the user should be shared by all instances. Therefore, the value of concept_id field was stored in class variables.

The hierarchy function outputs parent-child concepts with an “is-a” relationship using the t_relationships fields based on the selected concept. The hierarchy outputs the concept of multiple parents and children in the form of a JTree using the designed algorithm. The parent and child nodes that are outputted to JTree are updated using the information from the other panel using the concept identifier based on the event selected by the user.

The center panel provides three functions: the top level of the selected concept, detailed information about the concept, and information on other terminology. The top level outputs information about the corresponding concept of the 19 top-level concepts using a recursive call method as used for exploring the parent concept in the designed algorithm. Top-level information is output along with the FSN of the selected concept, which uses the fully_specified_name field of the t_concept. Detailed concept information outputs the preferred term, synonym, FSN, parent concept, and relationship type of the selected concept by using all fields in the SNOMED-CT key tables. Other terminology is output to the code and description of the term through the activated button when the identifier of the selected concept is present in the mapping tables. Also, the user can search for other than the mapped terms by using the dialog output through the ICD-10, KCD-6, ICD-9 item in the help menu at the top (Figure 7).



Code A000

Find to Vibrio cholerae 01, biovar cholerae

Starts With

Code	Description
A000	Cholera due to Vibrio cholerae 01, biovar ...
A001	Cholera due to Vibrio cholerae 01, biovar ...
A009	Cholera, unspecified
A0100	Typhoid fever, unspecified
A0101	Typhoid meningitis
A0102	Typhoid fever with heart involvement
A0103	Typhoid pneumonia
A0104	Typhoid arthritis
A0105	Typhoid osteomyelitis
A0109	Typhoid fever with other complications
A011	Paratyphoid fever A
A012	Paratyphoid fever B
A013	Paratyphoid fever C
A014	Paratyphoid fever, unspecified
A020	Salmonella enteritis
A021	Salmonella sepsis
A0220	Localized salmonella infection, unspecified

Code A000

Find 비브리오 콜레리 01 콜레라형균에 의한

Starts With

Code	Description
A00	콜레라
A000	고전적 콜레라
A000	비브리오 콜레리 01 콜레라형균에 의한 콜...
A001	비브리오 콜레리 01 엘토르형균에 의한 콜...
A001	엘토르 콜레라
A009	상세불명의 콜레라
A01	장티푸스 및 파라티푸스
A010	살모넬라 티피에 의한 감염
A010	장티푸스
A011	파라티푸스 A
A012	파라티푸스 B
A013	파라티푸스 C
A014	살모넬라 파라티피에 의한 감염 NOS
A014	상세불명의 파라티푸스
A02	기타 살모넬라 감염
A02	살모넬라 티피와 살모넬라 파라티피 이외의...
A020	살모넬라 장염

Code 05471

Find Visceral herpes simplex

Starts With

Code	Description
0088	Viral enteritis NOS
0478	Viral meningitis NEC
0479	Viral meningitis NOS
0498	Viral encephalitis NEC
0499	Viral encephalitis NOS
05471	Visceral herpes simplex
0578	Viral exanthemata NEC
0579	Viral exanthemata NOS
064	Vir enceph arthropod NEC
0706	Viral hepat NOS w coma
0709	Viral hepat NOS w/o coma
0778	Viral conjunctivitis NEC
07810	Viral warts NOS
07999	Viral infection NOS
0841	Vivax malaria
0850	Visceral leishmaniasis
101	Vincent's angina

Figure 7. Screen of ICD-10, KCD-6, ICD-9 Dialog

The right panel provides two functions for SNOMED-CT mapping: clinical item metadata output and post-coordinated mapping. Clinical item metadata output is a function for automatically outputting information relating to the items necessary for SNOMED-CT mapping by the recording unit, which utilizes the results of the item selected in the clinical item tab. Thus, the user select one of the concept from the outputted results table through the appropriate search, the concept identifier is automatically stored in the conceptId field of t_clinical_item when the insert button pressed. Post-coordinated mapping is a method for information not represented in pre-coordinated mapping or expressing a concept in detail. It is expressed by repetition of one or more attribute concepts and the corresponding value concepts related to the selected concept.

The structure of the post-coordinated expression is of the form “concept id|concept FSN|:attribute concept id|attribute concept FSN|=value concept id|value concept FSN|”.

The attribute concept can be used for only 9 of the 19 top levels (clinical finding, procedure, evaluation procedure, specimen, body structure, pharmaceutical biological product, situation with explicit, event, and physical object); “clinical finding” includes finding site, due to, severity, *etc*. These concepts output the array of attributes stored in accordance with the top-level concepts of the selected concept in table form.

4. Conclusions

The aim of this research was to maximize the semantic interoperability of a database developed previously that presented a customized SNOMED-CT toolkit for efficient use of biobank resources by users. The requirement analysis by SNOMED-CT experts ensured that the developed toolkit provides optimal functionality to users. Users can easily search clinical item metadata using the developed toolkit, and SNOMED-CT concept searching, pre-coordinated mapping, and post-coordinated mapping can be used for non-mapped items. Unlike existing toolkits, it is possible to confirm the reference terminology information of the selected concept by using mapping tables (ICD-10, KCD-6, ICD-9), and to search the reference terminology, by selecting the appropriate item from a menu. Therefore, users can efficiently search and map international terminology, while maximizing their utilization of biobank data with the developed toolkit, which meets all of the predetermined requirements.

In this work, a customized toolkit was developed for SNOMED-CT as a solution to the semantic interoperability issues that must be addressed in the utilization and sharing of biobank data. The developed toolkit was designed to use only information stored in existing databases to enable optimal user functionality. Since SNOMED-CT uses international terminology that can be applied to various domains and in all medical institutions with a biobank, a plug-and-play function must be added to the developed toolkit to improve its versatility regardless of the type and structure of the database. In the future, we plan to extend the toolkit such that it can be linked directly to a user's database via a web application.

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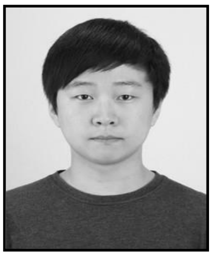

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