

Clinical Mapper: technical description

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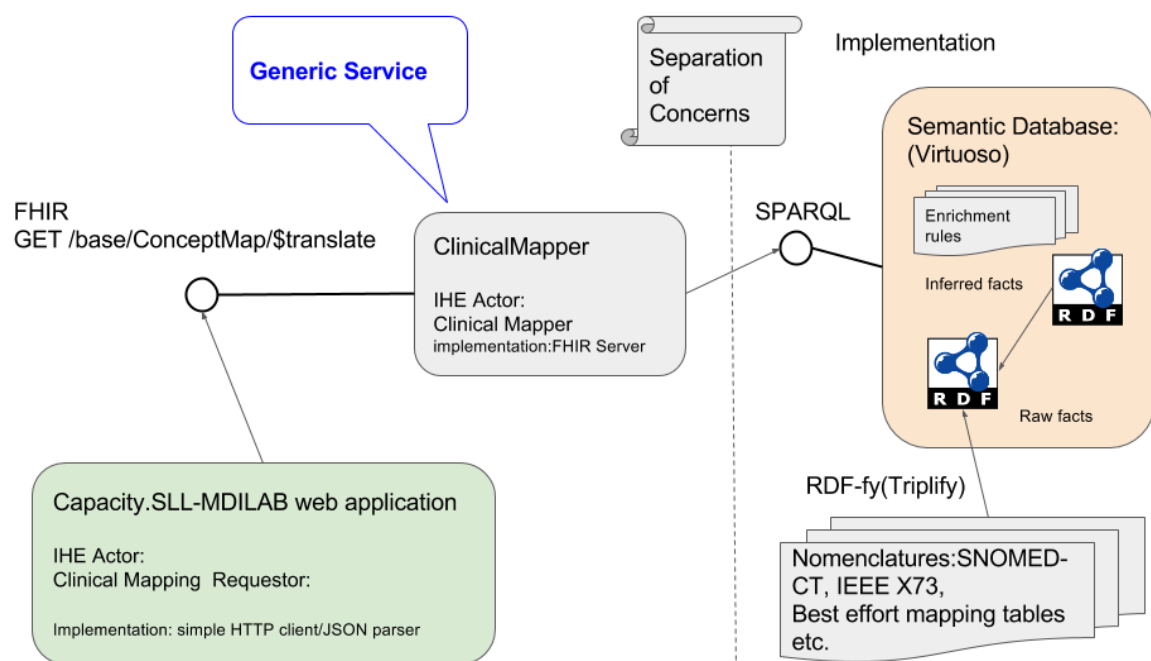
1 Introduction

Clinical Mapper is a system that provides a function of translation of codes between alternate healthcare nomenclatures/coding systems. The goal of the system is demonstrating one feasible technical approach to support the need of semantic interoperability of various medical systems that in they own domain operate within one medical nomenclature and do not support the mapping capability with others.

The system described in this document is a proof-of-concept and is limited to following

1. The subset of codes that are supported is limited to Anatomy/Body Structure/Body Sites
2. Supported coding systems are SNOED-CT, IEEE X73 and proprietary GE Centricity for Critical Care/Clinisoft notation for tagging of clinical impressions on human body.
3. The mapping provided has limitations that are discussed further in this document

2 Architecture



The PoC system consists of three parts

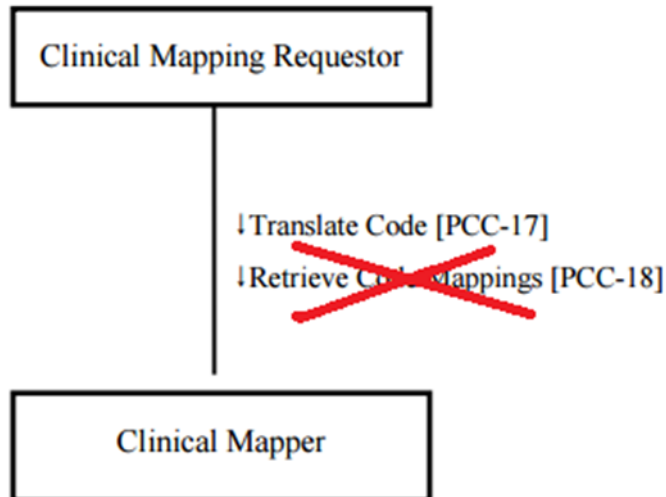
1. A generic REST based service to provide mapping functionality
2. Semantic Database – knowledge base holding the nomenclature code definitions, the mapping rules and materialized mapping assertions.
3. A reference client application that uses the service and provides a GUI to annotate human body with various clinical impressions, where the report of these clinical impressions are available in all three supported coding systems.

2.1 Clinical Mapper service

Clinical Mapper services implements the IHE Clinical Mapping integration profile

http://ihe.net/uploadedFiles/Documents/PCC/IHE_PCC_Suppl_CMAP.pdf

The implementation support only 1-term at the time transaction



It also only supports Simple Transaction

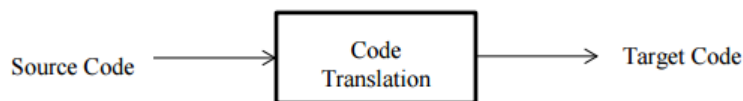
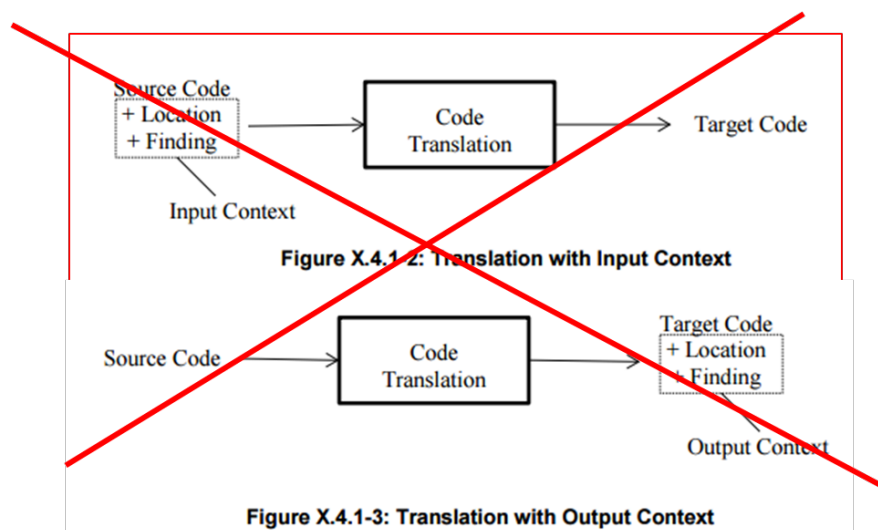


Figure X.4.1-1: Simple Translation

Because IEEE term are pre-coordinated, as well as Clinisoft notation, the system uses pre-coordinated SNOMED-CT terms and does not implement post-coordinated terms mapping



2.2 Semantic database/Knowledge base

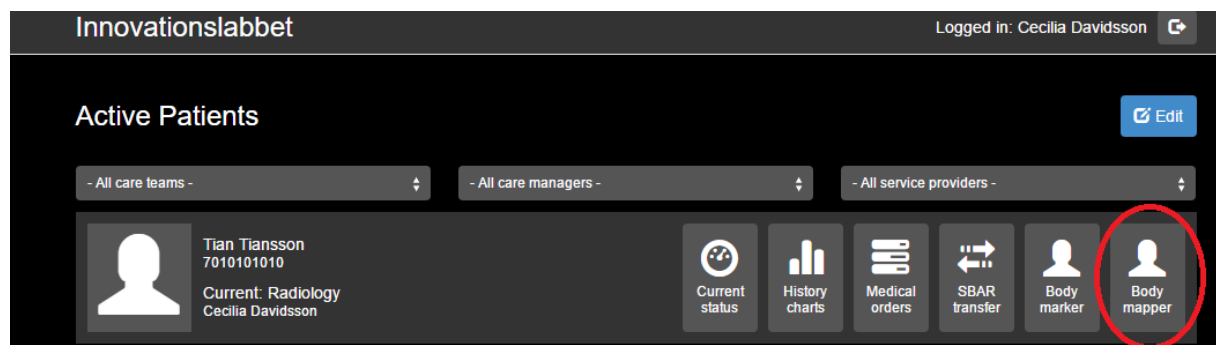
This component provides the separation of concerns for the Clinical Mapper service. It is based on Semantic Technologies such as RDF, OWL and SPARQL. The components used in system is Virtuoso Universal Server from OpenLink software - <http://virtuoso.openlinksw.com/>

The Knowledge Base holds the code definitions in form of RDF triples. The designed data cleaning and matching rules are then applied via SPARQL statements. Clinical Mapper interfaces with the Knowledge Base over the SPARQL protocol

2.3 Capacity.SLL-MDILAB web application

This is a module plugged into the MDILAB reference architecture implementation:

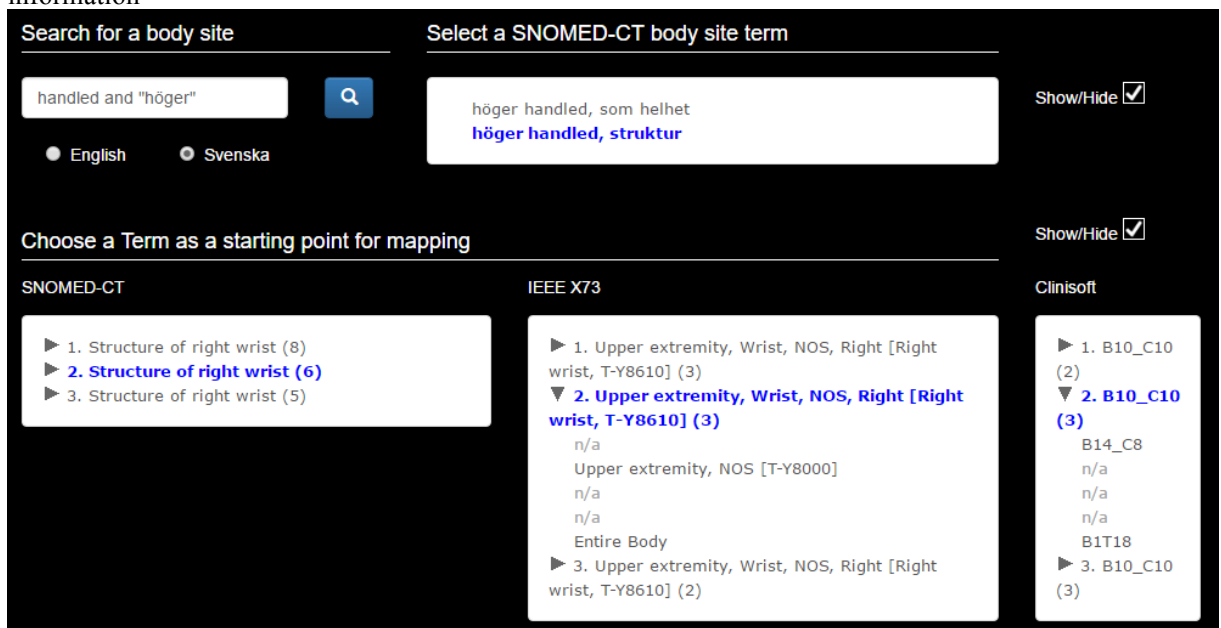
<https://capacity.sll-mdilab.net/#/overview>



This is an AngularJS based web application that provides

Following functionality

1. Text based search in SNOMED-CT body structure terms. Both search by English and Swedish labels are supported.
2. Mapping of the selected term to semantically corresponding IEEE X73 and Clinisoft body sites
3. Pedagogical visualization of mapping quality and relevance, as well as presenting loss of information



4. User interface to make annotations about clinical impression alternatively based on SNOMED-CT terms (text based) or Clinisoft body grid diagram.

Add clinical impressions

| | | |
|------------------------|---|---|
| Arterial line | + | ✕ |
| Bedsore | + | |
| Epidural analgesia | + | |
| Peripheral venous line | + | |
| Tracheal tube | + | |
| Surgical wound | + | |
| Dialysis catheter | + | |

Selected Terms

SNOMED: 9736006

IEEE X73:
MDC_UPEXT_WRIST_R

Clinisoft: B10_C10

Clear

Active clinical impressions

Arterial line

- SNOMED: 9736006
- IEEE: MDC_UPEXT_WRIST_R
- Clinisoft: B10_C10

Delete

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U |
|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 18 | | | | | | | | | | | | | | | | | | | | | |
| 17 | | | | | | | | | | | | | | | | | | | | | |
| 16 | | | | | | | | | | | | | | | | | | | | | |
| 15 | | | | | | | | | | | | | | | | | | | | | |
| 14 | | | | | | | | | | | | | | | | | | | | | |
| 13 | | | | | | | | | | | | | | | | | | | | | |
| 12 | | | | | | | | | | | | | | | | | | | | | |
| 11 | | | | | | | | | | | | | | | | | | | | | |
| 10 | | | | | | | | | | | | | | | | | | | | | |
| 9 | | | | | | | | | | | | | | | | | | | | | |
| 8 | | | | | | | | | | | | | | | | | | | | | |
| 7 | | | | | | | | | | | | | | | | | | | | | |
| 6 | | | | | | | | | | | | | | | | | | | | | |
| 5 | | | | | | | | | | | | | | | | | | | | | |
| 4 | | | | | | | | | | | | | | | | | | | | | |
| 3 | | | | | | | | | | | | | | | | | | | | | |
| 2 | | | | | | | | | | | | | | | | | | | | | |

Legend:

- Arterial line
- Bedsore
- Epidural analgesia
- Peripheral venous line
- Tracheal tube
- Surgical wound
- Dialysis catheter

- Semantically equivalent report generation of the patient's clinical impression summary for all three coding systems.

Refresh
Save
SNOMED-CT
IEEE X73
Clinisoft

Tian Tiansson
2016-05-20 11:49:33

Arterial line
Structure of right wrist (9736006)

Bedsore
Entire back of head (182322006)

Dialysis catheter
Structure of right half of neck (170303002)

Refresh
Save
SNOMED-CT
IEEE X73
Clinisoft








Tian Tiansson
2016-05-20 11:50:20

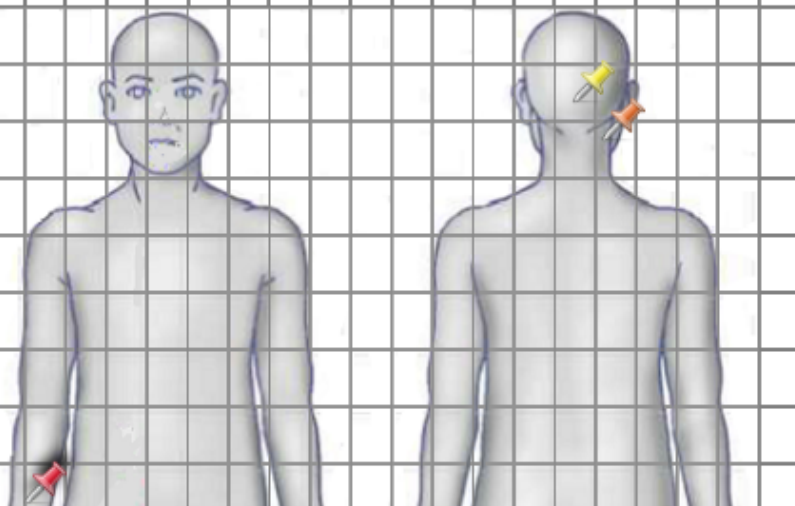
Arterial line
Upper extremity, Wrist, NOS, Right [Right wrist, T-Y8610] (MDC_UPEXT_WRIST_R)

Bedsore
Head, Occipital region [T-Y0140] (MDC_HEAD_OCCIP_REGION)

Dialysis catheter
Head and Neck, NOS [T-Y0000] (e.g., for surgical drainage) (MDC_HEAD_NECK)

Refresh
Save
SNOMED-CT
IEEE X73
Clinisoft

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U | |
|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|--|
| 18 | | | | | | | | | | | | | | | | | | | | | | Legend:  Arterial line  Bedsore  Epidural analgesia  Peripheral venous line  Tracheal tube  Surgical wound  Dialysis catheter |
| 17 | | | | | | | | | | | | | | | | | | | | | | |
| 16 | | | | | | | | | | | | | | | | | | | | | | |
| 15 | | | | | | | | | | | | | | | | | | | | | | |
| 14 | | | | | | | | | | | | | | | | | | | | | | |
| 13 | | | | | | | | | | | | | | | | | | | | | | |
| 12 | | | | | | | | | | | | | | | | | | | | | | |
| 11 | | | | | | | | | | | | | | | | | | | | | | |
| 10 | | | | | | | | | | | | | | | | | | | | | | |



3 Detailed description

3.1 Semantic database/Knowledge base

The Semantic database is Virtuoso Universal server and is installed at <http://10.0.1.209:8890/>

It is the same server that is used by MDILAB Validation System: <https://github.com/sll-mdilab/validation-tool>

For setup and access refer to the documentation provided at <https://github.com/sll-mdilab/validation-tool/wiki/Technical-Guide-for-Administration-and-Extension#virtuoso-setup-and-administration>

3.1.1 Data sources

This chapter details what data sources for were used for respective coding systems.

3.1.1.1 SNOMED-CT

SNOMED-CT body sites nomenclature is loaded from OWL file, which is checked in here:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/RDF/SNOMED_CT.zip

It contains SNOMED-CT Anatomy ontology in 2 different formats: RDF-XML and NT

The NT file was used to load into Virtuoso. The Conductor interface was used for this:

LinkedData/Quad Store Upload

The ontology is loaded into named graph: <http://ihtsdo.org/snomedct/anatomy#graph>

To see all classes for a test run, use the query:

```
SELECT *
WHERE
{
GRAPH <http://ihtsdo.org/snomedct/anatomy#graph>
{
?Cls a owl:Class .
}
}
```

3.1.1.2 IEEEEX73

This nomenclature is originally downloaded as XML file from NIST Rosetta:

<https://rtmms.nist.gov/rtmms/index.htm#!x73>

In order to access this table one needs to login as registered user.

This table was already fetched, triplified and loaded to Virtuoso as a part of Validation Server mentioned above:

https://github.com/sll-mdilab/validation-tool/blob/master/src/main/resources/RDF/X73_abox.ntriple

https://github.com/sll-mdilab/validation-tool/blob/master/src/main/resources/RDF/X73_tbox.tlt

They are loaded to named graph: <http://sll-mdilab.net/hRosetta#graph>

3.1.1.3 Clinisoft human body grid

There initial data file that represent the grid data was generated by a java program <https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/java/net/sllmdilab/clinicalmapper/util/ClinisoftBodyTableGenerator.java>

and is saved at <https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/data/ClinisoftBodyTable.csv>

This CSV file was then triplified and the RDF version is saved at

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/RDF/ABox_ClinisoftBodyTable_0.nt

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/RDF/TBox_ClinisoftBodyTable.nt

These triples were loaded to Virtuoso via Conductor interface (LinkedData/Quad Store Upload) to named graph: <http://sll-mdilab.net/BodySites/Clinisoft#graph>

3.1.1.4 SNOMED-CT Swedish terms

The Swedish translation of SNOMED-CT terms are triplified version of the table on SNOMED-CT Swedish release, from file

\SnomedCT_Release_SE_7.0.1_20151130\SnomedCT_RF2Release_SE1000052_20151130\Full\Terminology\set2_Description_Full-sv_SE1000052_20151130.csv

One needs to apply for the license at <http://www.socialstyrelsen.se/nationellehalsa/snomed-ct>

The triplified files are too big to be checked in to GitHub, so they are at ProjectPlace:

https://service.projectplace.com/pp/pp.cgi/0/1?op=rightclick&link=pp%2Fpp.cgi%2Fd1242745709%2FSDNOMED_CT_SwedishTerms_Triples.zip

3.1.2 Cleaning, Enrichment and Mapping of RDF data

After each source body site nomenclature data was loaded to Triple Store, a sequence of INSERT statements were executed. All these rules are packaged in one file: https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/Enrichment_All_conductor.sparql

The content of this file was copied to Virtuoso ISQL interface **Database/Interactive SQL** and executed.

In this section each rule and its purpose is described.

3.1.2.1 Clearing the graph

The first section sets the database mode to atomic transaction, i.e., row based commit and then clears all

triples from the graph <http://sll-mdilab.net/ClinicalMapping#graph> which contains all generated clinical mapping related triples

The graph <http://snomed.info/sct/se#graph> contains the SNOMED-CT Swedish terms

The graph <http://snomed.info/sct/se/labels#graph> contains the asserted Swedish labels to the SNOMED-CT concepts instances.

3.1.2.2 Set direct navigation Downwards in SNOMED

This rule creates a materialized direct hierarchy in SNOMED-CT graph structure that allows direct navigation from parent concepts to its children.

3.1.2.3 Insert raw SNOMED ids

This rule extracts from IEEEEX73 term out the substring that contains the SNOMED-CT referenceID, and asserts it explicitly as a datatype property. This is for easier mapping later on.

3.1.2.4 Insert LEFT / RIGHT discriminators

Because the SCT-CT referenceID:s embedded in IEEEEX73 strings contain laterality suffixes, it will be necessary to exclude them later from mapping, and this rule detects them and asserts an explicit laterality property to Term instance.

3.1.2.5 Fix obsolete SMOMED references in IEEEEX73 terms

The following rules provide this task:

Replace T-Y0 with T-D1

Replace T-Y1 with T-D2

Replace T-Y4 with T-D4

Replace T-Y6 with T-D6

Replace T-Y7 with T-D7

Replace T-Y8 with T-D8

Replace T-Y9 with T-D9

All these rules fix the problem that the SCT ReferenceID:s inserted in IEEEEX73 terms have been obsolete and mismatched. Historical analysis and exact reason how and why was out of the scope of the project. Empirically it was discovered consistent pattern of how the code notation had changed. The pattern is not total and complete but good enough for this proof-of-concept system.

All these rules replace a substring in an initial string with a substring that matches the current SNOMED RT identifier.

3.1.2.6 insert relation from IEEE to SNOMED

This rule now matches the cleaned up IEEEEX73 reference to SNOMED with the corresponding property of SNOMED class. The match is materialized and link sameSNOMEDConcept is asserted.

3.1.2.7 insert relation from SNOMED to IEEE

This is a similar rule as the previous one, but from other direction when the link sameIEEEEX73Concept

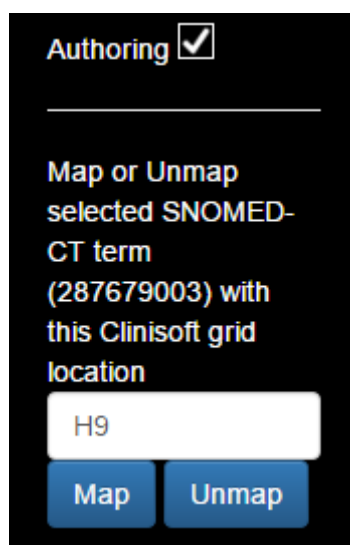
goes from SCT to IEEEX73. The difference here is that laterality based IEEEX73 terms are excluded from mapping, as those would otherwise map to SCT:s laterality neutral concepts, and that would be semantically incorrect.

3.1.2.8 Insert MyRosetta Body Region Structure

This rule creates a “new” body site concept to Rosetta/IEEEX73 – Entire Body. It is needed to provide a mapping between SNOMED-CT: s Body Region Structure top most concept, so that it will be possible to infer the IEEEX73 term hierarchy, which is otherwise explicitly missing.

3.1.2.9 SNOMED - Clinisoft mapping – Predefined

This rule asserts a handful of bi-directional mappings between Clinisoft grid cells and SNOMED-CT concepts. Same result can be achieved by using the “Authoring corner” in Capacity.SLL-MDILAB web application.



3.1.2.10 Insert Swedish labels to SNOMED-CT

This rule adds a data property <http://snomed.info/sct/se/model#term> to the classes of SNOMED-CT anatomy ontology, by matching concept identifiers in that ontology and the Swedish translation source.

3.1.3 State of data

At this point after executing the rules above, the clients can post SPARQL queries to the endpoint

<http://10.0.1.209:8890/sparql>

The rules created mapping between SOMED-CT <-> IEEEX73 and SNOMED-CT <-> Clinisoft.

There is no direct mapping between IEEEX73 and Clinisoft. However, as the SNOMED-CT is used as the canonical anatomical model, then it can be used as an indirect middle man between coding systems that map to SNOED-CT, but not directly to each other.

The Jena API clients would use 10.0.1.209:1111

Some SPARQL example queries will be given here to demonstrate the basics of getting the lists of mapped concepts between code systems

3.1.3.1 Mapping: SNOMED-CT to IEEEEX73

```
# Mapping SNOMED-CT to IEEE - direct
PREFIX rosetta_m: <http://sll-mdilab.net/Rosetta/model#>
SELECT DISTINCT
xsd:string(?sct_label) as ?sct_label
xsd:string(?sct_id) as ?sct_id
xsd:string(?target_this_label) as ?ieeeex73_label
xsd:string(?target_this_id) as ?ieeeex73_id
WHERE
{
?Class0 rdfs:label ?sct_label .
?Class0 <http://ihtsdo.org/snomedct/anatomy#id> ?sct_id .

?Class0 <http://sll-mdilab.net/ClinicalMapping#sameIEEEEX73Concept> ?Term .

?Term rosetta_m:hasTerm_description ?Term_description .
?Term rosetta_m:hasREFID ?REFID .
?REFID rosetta_m:rEFIDValue ?target_this_id .
?Term_description rosetta_m:term_descriptionValue ?target_this_label .
}
```

3.1.3.2 Mapping: Clinisoft to SNOMED-CT

```
#Clinisoft to SNOMED-CT - direct best fit
PREFIX cs_m: <http://sll-mdilab.net/BodySites/Clinisoft/model#>
PREFIX cs_d: <http://sll-mdilab.net/BodySites/Clinisoft/data#>
PREFIX sct_d: <http://ihtsdo.org/snomedct/anatomy#>
PREFIX cmap_m: <http://sll-mdilab.net/ClinicalMapping#>
SELECT DISTINCT
xsd:string(?source_this_id) as ?ClinisoftID
xsd:string(?target_this_label) as ?sct_label
xsd:string(?target_this_id) as ?sct_id
WHERE
```

```
{
?ClinisoftBodyTable <http://sll-mdilab.net/BodySites/Clinisoft/model#horizontal> ?_horizontal .
?ClinisoftBodyTable <http://sll-mdilab.net/BodySites/Clinisoft/model#vertical> ?_vertical .
?ClinisoftBodyTableBroader <http://sll-mdilab.net/ClinicalMapping#sameSNOMEDConcept>
?SnomedTerm .
?SnomedTerm rdfs:label ?target_this_label .
?SnomedTerm <http://ihtsdo.org/snomedct/anatomy#id> ?target_this_id .
?ClinisoftBodyTableBroader cs_m:id ?source_this_id .
}
ORDER BY ASC( ?ClinisoftID )
```

3.2 Clinical Mapper service

This service is implemented by <https://github.com/sll-mdilab/clinical-mapper>

It uses HAPI FHIR library and is a branch of <https://github.com/sll-mdilab/t5-pid-xref-manager>, which is the good source for information how this server is structured.

It is a Tomcat web app and is deployed to AWS Elastic Beanstalk. These are its environmental parameters:

| Property Name | Property Value |
|--|---|
| JDBC_CONNECTION_STRING Connection string to JDBC database (e.g. RDS) for application use. | <input type="text"/> |
| T5_RDF_HOST | <input type="text" value="10.0.1.209"/> ✕ |
| T5_RDF_PASSWORD | <input type="text" value="dba"/> ✕ |
| T5_RDF_PORT | <input type="text" value="1111"/> ✕ |
| T5_RDF_USER | <input type="text" value="dba"/> ✕ |
| T5_XREF_API_KEY | <input type="text"/> ✕ |
| T5_XREF_OAUTH_AUTHORIZE_URI | <input type="text"/> ✕ |
| T5_XREF_OAUTH_CLIENT_ID | <input type="text"/> ✕ |
| T5_XREF_OAUTH_CLIENT_SECRET | <input type="text"/> ✕ |
| T5_XREF_OAUTH_INTROSPECTION_URL | <input type="text"/> ✕ |
| T5_XREF_OAUTH_TOKEN_URI | <input type="text"/> ✕ |

3.2.1 FHIR implementation

This FHIR server implements Concept Map resource: <https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/java/net/sllmdilab/clinicalmapper/resourceprovider/ConceptMapResourceProvider.java>

It implements two operations - /\$translate and /\$map

3.2.2 /\$translate

This is the operation described in FHIR specification and in IHE profile:

<https://www.hl7.org/fhir/conceptmap-operations.html#translate>

The functionality needed by the PoC application is greater than what IHE Clinical Mapper profile depicts. It goes beyond of 1 to 1 mapping of a single codes between two coding systems. The following is the list of queries that is supported, depicting the search parameters and response payload, and also providing the SPARQL query executed against Knowledge Base that returns the requested data.

3.2.2.1 SNOMED-CT free text search

By this query the Client can search SNOMED-CT terms that match the given free text search string

In parameters

| parameter | value | comment |
|-------------|--|---|
| equivalence | search | It is a custom parameter |
| label | Free text search string, i.e. “left and hip”, where operators like AND, OR, NOT can be used. Even wildcard endings with at least 4 leading characters are supported. The syntax is what Virtuoso specifies. Example: left and "fore*" | It is a custom parameter |
| lang | [en,sv,""] | It is a custom parameter. If it is omitted then the search will be by English labels. |
| target | http://snomed.info/sct | |
| _format | [json,xml] | ClinicalMapper server uses XML |

Example:

[https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\\$translate?equivalence=search&label=left and hip&lang=en&target=http://snomed.info/sct&_format=xml](https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/$translate?equivalence=search&label=left and hip&lang=en&target=http://snomed.info/sct&_format=xml)

Response

Response is a json or xml document according to Out Parameters in FHIR specification.

The Clinical Mapper uses HAPI FHIR library and its API does not seem to be totally in synch with the specification. There was not enough time to sort out the discrepancy and the implementation adjusts to what HAPI FHIR creates. HAPI FHIR library only supports the *parameter.part* construction, and each parameter has @name attribute, instead of sub elements as described in FHIR specification,

The **match.equivalence** is set to “specializes”, as the term specializes the free text search string:s meaning.

Example:

```
{
  "resourceType": "Parameters",
  "parameter": [
    {
      "name": "result",
      "valueBoolean": true
    },
    {
      "name": "match",
      "part": [
        {
          "name": "equivalence",
          "valueCode": "specializes"
        },
        {
          "name": "concept",
          "valueCoding": {
            "code": "287679003",
            "display": "Left hip region structure"
          }
        }
      ]
    }
  ]
}
```

3.2.2.1.1 SPARQL query

The corresponding SPARQL query is saved here:

English:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/SNOMED_CT_term_label_search.sparql

Swedish:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/SNOMED_CT_term_label_search_Swedish.sparql

3.2.2.2 SNOMED-CT to IEEE X73 mapping with Wider Hierarchy

This search provides mapping from SNOMED-CT to IEEE X73. The returned matches provide entire hierarchy from given SCT-CT code upwards until the root (concept 52530000/Body region structure) is reached. The query returns all paths between the given code and the root concept. For each element in each path an IEEE X73 term is provided (or n/a element), so that even IEEE X73 term hierarchy is inferred and provided. The client can now present and choose the best fit mapping for given SCT-CT term. This is especially useful if there is no direct SCT-CT and IEEE X73 mapping for the given concept. Then the closest IEEE term in hierarchy is the best fit.

In parameters

| parameter | value | comment |
|-------------|--------------------------------------|--|
| equivalence | wider | It is a custom parameter, but the value is from the list: https://www.hl7.org/fhir/valueset-concept-map-equivalence.html |
| code | SNOMED-CT identifier, i.e. 287679003 | |
| system | http://snomed.info/sct | |
| target | urn:std:iso:11073 | |
| _format | [json,xml] | ClinicalMapper server uses XML |

Example

[https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\\$translate?equivalence=wider&code=287679003&system=http://snomed.info/sct&target=urn:std:iso:11073&_format=xml](https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/$translate?equivalence=wider&code=287679003&system=http://snomed.info/sct&target=urn:std:iso:11073&_format=xml)

Response

The response document provides the each path in one **parameter** element. Within each parameter with name="match", the source (SCT-CT) and target (IEEE X73) are provided in adjacent **part** elements, where the first part name="concept" holds target code and the second part name="product" holds the source code.

Example:

```
<parameter>
  <name value="match"/>
  <part>
    <name value="equivalence"/>
```

```

    <valueCode value="wider"/>
  </part>
  <part>
    <name value="concept"/>
    <valueCoding>
      <code value="n/a"/>
      <display value="n/a"/>
    </valueCoding>
  </part>
  <part>
    <name value="product"/>
    <part>
      <name value="concept"/>
      <valueCoding>
        <code value="287679003"/>
        <display value="Left hip region structure"/>
      </valueCoding>
    </part>
  </part>
  <part>
    .....

```

For getting the full payload example, execute the provided example search call in REST client such as POSTMAN.

3.2.2.2.1 SPARQL query

The corresponding SPARQL query is saved here:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/SNOMED_IIEX73_hierarchy_UP.sparql

3.2.2.3 SNOMED-CT to Clinisoft mapping with Wider Hierarchy

This service similar to the service described in previous chapter, just that instead of IEEE X73 the mapping is performed against Clinisoft body site nomenclature.

In parameters

| parameter | value | comment |
|-------------|---|--|
| equivalence | wider | It is a custom parameter, but the value is from the list: https://www.hl7.org/fhir/valueset-concept-map-equivalence.html |
| code | SNOMED-CT identifier, i.e. 287679003 | |
| system | http://snomed.info/sct | SNOMED-CT uri |
| target | http://sll-mdilab.net/BodySites/Clinisoft | Clinisoft body site nomenclature uri, invented by this project |
| _format | [json,xml] | ClinicalMapper server uses XML |

Example

https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\$translate?equivalence=wider&code=287679003&system=http://snomed.info/sct&target=http://sll-mdilab.net/BodySites/Clinisoft&_format=xml

Response

See the full response by running the http call in an example. Below is a fragment of how one hierarchy path is returned. Note how the levels without corresponding Clinisoft code is given as "n/a".

```
<parameter>
  <name value="match"/>
  <part>
    <name value="equivalence"/>
    <valueCode value="wider"/>
  </part>
  <part>
    <name value="concept"/>
    <valueCoding>
      <code value="H9"/>
      <display value="left hip front"/>
    </valueCoding>
  </part>
  <part>
    <name value="product"/>
```

```

<part>
  <name value="concept"/>
  <valueCoding>
    <code value="287679003"/>
    <display value="Left hip region structure"/>
  </valueCoding>
</part>
</part>
<part>
  <name value="concept"/>
  <valueCoding>
    <code value="n/a"/>
    <display value="n/a"/>
  </valueCoding>
</part>
<part>
  <name value="product"/>
  <part>
    <name value="concept"/>
    <valueCoding>
      <code value="61379005"/>
      <display value="Structure of left side of trunk"/>
    </valueCoding>
  </part>
</part>
<part>
  <name value="concept"/>
  <valueCoding>
    <code value="n/a"/>
    <display value="n/a"/>
  </valueCoding>

```

```

</part>

<part>

  <name value="product"/>

  <part>

    <name value="concept"/>

    <valueCoding>

      <code value="31156008"/>

      <display value="Structure of left half of body"/>

    </valueCoding>

  </part>

</part>

<part>

  <name value="concept"/>

  <valueCoding>

    <code value="n/a"/>

    <display value="n/a"/>

  </valueCoding>

</part>

<part>

  <name value="product"/>

  <part>

    <name value="concept"/>

    <valueCoding>

      <code value="423857001"/>

      <display value="Structure of half of body lateral to midsagittal plane"/>

    </valueCoding>

  </part>

</part>

<part>

  <name value="concept"/>

  <valueCoding>

```

```

<code value="B1T18"/>
<display value="Entire Body"/>
</valueCoding>
</part>
<part>
<name value="product"/>
<part>
<name value="concept"/>
<valueCoding>
<code value="52530000"/>
<display value="Body region structure"/>
</valueCoding>
</part>
</part>
</parameter>

```

3.2.2.3.1 SPARQL query

The corresponding SPARQL query is saved here:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/SNOMED_Clinisoft_hierarchy_UP.sparql

3.2.2.4 SNOMED-CT to IEEE X73 mapping with Narrower Hierarchy

This search provides mapping from SNOMED-CT to IEEE X73. The returned matches provide entire hierarchy from given SCT-CT code **downwards** until the atomic concepts (without children/specialized concepts). The query returns all branches that originate from the given code, however the SPARQL query used has set a limit to 25 branches for not overloading the GUI application. For each element in each path an IEEE X73 term is provided (or “n/a” element), so that even IEEE X73 term hierarchy is inferred and provided. The client can now present and choose the best fit mapping for specialized terms of the given SCT-CT term. It may happen that there are no specialized terms in IEEE X73 for a given SCT-CT branch.

In parameters

| parameter | value | comment |
|-------------|--|--|
| equivalence | narrower | It is a custom parameter, but the value is from the list: https://www.hl7.org/fhir/valueset-concept-map-equivalence.html |
| code | SNOMED-CT identifier, i.e. 85562004 | |

| | | |
|---------|------------------------|--------------------------------|
| system | http://snomed.info/sct | |
| target | urn:std:iso:11073 | |
| _format | [json,xml] | ClinicalMapper server uses XML |

Example

https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\$translate?equivalence=narrower&code=85562004&system=http://snomed.info/sct&target=urn:std:iso:11073&_format=xml

Response

Run the example HTTP request above in some client and see the returned payload. The structure is same as in **wider** queries, just that the sequence of <part> elements follows the downward path, i.e. specialization.

3.2.2.4.1 SPARQL query

The corresponding SPARQL query is saved here:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/SNOMED_IEEEEX73_hierarchy_DOWN.sparql

3.2.2.5 SNOMED-CT to Clinisoft mapping with Narrower Hierarchy

This service similar to the service described in previous chapter, just that instead of IEEE X73 the mapping is performed against Clinisoft body site nomenclature.

In parameters

| parameter | value | comment |
|-------------|---|--|
| equivalence | narrower | It is a custom parameter, but the value is from the list: https://www.hl7.org/fhir/valueset-concept-map-equivalence.html |
| code | SNOMED-CT identifier, i.e. 85562004 | |
| system | http://snomed.info/sct | |
| target | http://sll-mdilab.net/BodySites/Clinisoft | |
| _format | [json,xml] | ClinicalMapper server uses XML |

Example

https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\$translate?equivalence=narrower&code=85562004&system=http://snomed.info/sct&target=http://sll-mdilab.net/BodySites/Clinisoft&_format=xml

Response

Run the example HTTP request above in some client and see the returned payload. The structure is same as in **wider** queries, just that the sequence of <part> elements follows the downward path, i.e. specialization.

3.2.2.5.1 SPARQL query

The corresponding SPARQL query is saved here:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/SNOMED_Clinisoft_hierarchy_DOWN.sparql

3.2.2.6 Direct SNOMED-CT to IEEE X73 mapping

This search provides direct mapping from SNOMED-CT code to IEEE X73 term. If the match result is a failure (the given SCT-CT code does not have explicitly defined mapping IEEE X73 term), then the client should try to get the best fit by using “wider” query.

In parameters

| parameter | value | comment |
|-------------|--|--|
| equivalence | equal | It is a custom parameter, but the value is from the list: https://www.hl7.org/fhir/valueset-concept-map-equivalence.html |
| code | SNOMED-CT identifier, i.e. 85562004 | |
| system | http://snomed.info/sct | |
| target | urn:std:iso:11073 | |
| _format | [json,xml] | ClinicalMapper server uses XML |

Example

[https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\\$translate?equivalence=equal&code=85562004&system=http://snomed.info/sct&target=urn:std:iso:11073&_format=xml](https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/$translate?equivalence=equal&code=85562004&system=http://snomed.info/sct&target=urn:std:iso:11073&_format=xml)

Response

The response document provides one mapping or failure. Note that the source code is also given in the part where name=”product” element.

Example of success:

```
<Parameters
  xmlns="http://hl7.org/fhir">
  <parameter>
    <name value="result"/>
    <valueBoolean value="true"/>
  </parameter>
</Parameters>
```



```

</parameter>
<parameter>
  <name value="match"/>
  <part>
    <name value="equivalence"/>
    <valueCode value="equal"/>
  </part>
  <part>
    <name value="concept"/>
    <valueCoding>
      <code value="MDC_UPEXT_HAND"/>
      <display value="Upper extremity, Hand, NOS [T-Y8700]"/>
    </valueCoding>
  </part>
  <part>
    <name value="product"/>
    <part>
      <name value="concept"/>
      <valueCoding>
        <code value="85562004"/>
        <display value="Hand structure"/>
      </valueCoding>
    </part>
  </part>
</parameter>
</Parameters>

```

Example of failure:

```

<Parameters
  xmlns="http://hl7.org/fhir">
  <parameter>
    <name value="result"/>

```

```
<valueBoolean value="false"/>

</parameter>

</Parameters>
```

3.2.2.6.1 SPARQL query

The corresponding SPARQL query is saved here:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/SNOMED_CT_to_IEEE_X73_direct.sparql

3.2.2.7 Direct IEEE X73 to SNOMED-CT mapping

This search is just reverse of the previous one.

In parameters

| parameter | value | comment |
|-------------|----------------------------------|--|
| equivalence | equal | It is a custom parameter, but the value is from the list: https://www.hl7.org/fhir/valueset-concept-map-equivalence.html |
| code | IEEE X73, i.e. MDC_UPEXT_HAND | |
| system | urn:std:iso:11073 | |
| target | http://snomed.info/sct | |
| _format | [json,xml] | ClinicalMapper server uses XML |

Example

[https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\\$translate?equivalence=equal&code=MDC_UPEXT_HAND&system=urn:std:iso:11073&target=http://snomed.info/sct&_format=xml](https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/$translate?equivalence=equal&code=MDC_UPEXT_HAND&system=urn:std:iso:11073&target=http://snomed.info/sct&_format=xml)

Response

```
<Parameters
  xmlns="http://hl7.org/fhir">
  <parameter>
    <name value="result"/>
    <valueBoolean value="true"/>
  </parameter>
  <parameter>
```

```

<name value="match"/>
<part>
  <name value="equivalence"/>
  <valueCode value="equal"/>
</part>
<part>
  <name value="concept"/>
  <valueCoding>
    <code value="85562004"/>
    <display value="Hand structure"/>
  </valueCoding>
</part>
<part>
  <name value="product"/>
  <part>
    <name value="concept"/>
    <valueCoding>
      <code value="MDC_UPEXT_HAND"/>
      <display value="Upper extremity, Hand, NOS [T-Y8700]"/>
    </valueCoding>
  </part>
</part>
</parameter>
</Parameters>

```

3.2.2.7.1 SPARQL query

The corresponding SPARQL query is saved here:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/IEEEX73_to_SNOMED_CT_direct.sparql

3.2.2.8 Direct Clinisoft to SNOMED-CT

This search provides direct mapping from Clinisoft grid single cell to SNOMED-CT code. This query also finds a best fit, in terms that in case where there is no direct mapping from given cell to a SCT-CT concept, the query finds a smallest rectangle in Clinisoft grid that has the mapping. In worst case the whole body, i.e. “Body Region structure” is returned.

In parameters

| parameter | value | comment |
|-------------|---|--|
| equivalence | equal | It is a custom parameter, but the value is from the list: https://www.hl7.org/fhir/valueset-concept-map-equivalence.html |
| code | Clinisoft body site grid cell identifier, i.e. H9 | |
| system | http://sll-mdilab.net/BodySites/Clinisoft | |
| target | http://snomed.info/sct | |
| _format | [json,xml] | ClinicalMapper server uses XML |

Example

[https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\\$translate?equivalence=equal&code=H9&system=http://sll-mdilab.net/BodySites/Clinisoft&target=http://snomed.info/sct&_format=xml](https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/$translate?equivalence=equal&code=H9&system=http://sll-mdilab.net/BodySites/Clinisoft&target=http://snomed.info/sct&_format=xml)

Response

The response document provides one mapping. Note that the source code is also given in the part where name="product" element.

Example:

```
<Parameters
  xmlns="http://hl7.org/fhir">
  <parameter>
    <name value="result"/>
    <valueBoolean value="true"/>
  </parameter>
  <parameter>
    <name value="match"/>
    <part>
      <name value="equivalence"/>
      <valueCode value="equal"/>
    </part>
    <part>
      <name value="concept"/>
```

```

<valueCoding>
  <code value="287679003"/>
  <display value="Left hip region structure"/>
</valueCoding>
</part>
<part>
  <name value="product"/>
  <part>
    <name value="concept"/>
    <valueCoding>
      <code value="H9"/>
      <display value="left hip front"/>
    </valueCoding>
  </part>
</part>
</parameter>
</Parameters>

```

3.2.2.8.1 SPARQL query

The corresponding SPARQL query is saved here:

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/Clinisoft_SNOMED_direct.sparql

3.2.3 /\$map

This operation is not defined in FHIR, but is made up for this PoC system for providing a similar service in order to add and remove mappings between two code systems.

3.2.3.1 Map Clinisoft grid to a SNOMED-CT concept

This service creates a bi-directional relation between a given SNOMED-CT concept and Clinisoft grid cell (or multiple cells forming a rectangle).

In parameters

| parameter | value | comment |
|-----------|-------|--------------------------|
| direction | map | It is a custom parameter |

| | | |
|--------------|---|--|
| sourcecode | 287679003,9736006 | It is a custom parameter |
| targetcode | Clinisoft grid cell identifier, or a notion of the rectangle H9, B10_C10 | It is a custom parameter The rectangle is given by left upper corner cell and right lower corner cell separated by underscore |
| sourcesystem | http://snomed.info/sct | It is a custom parameter |
| targetsystem | http://sll-mdilab.net/BodySites/Clinisoft | It is a custom parameter |

Example

Mapping left foot (SCT-CT 22335008) to Clinisoft grid cell G1

[https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\\$map?direction=map&sourcecode=22335008&sourcesystem=http://snomed.info/sct&targetcode=G1&targetsystem=http://sll-mdilab.net/BodySites/Clinisoft](https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/$map?direction=map&sourcecode=22335008&sourcesystem=http://snomed.info/sct&targetcode=G1&targetsystem=http://sll-mdilab.net/BodySites/Clinisoft)

Response

The response document provides status – true is success and false is failure

Example:

```
<Parameters
  xmlns="http://hl7.org/fhir">
  <parameter>
    <name value="result"/>
    <valueBoolean value="true"/>
  </parameter>
</Parameters>
```

3.2.3.1.1 SPARQL query

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/INSERT_SNOMED_Clinisoft_mapping.sparql

3.2.3.2 Unmap Clinisoft grid from a SNOMED-CT concept

This service removes an existing bi-directional relation between a given SNOMED-CT concept and Clinisoft grid cell (or multiple cells forming a rectangle).

In parameters

| parameter | value | comment |
|-----------|-------|--------------------------|
| direction | unmap | It is a custom parameter |

| | | |
|--------------|---|--|
| | | |
| sourcecode | 287679003,9736006 | It is a custom parameter |
| targetcode | Clinisoft grid cell identifier, or a notion of the rectangle H9, B10_C10 | It is a custom parameter The rectangle is given by left upper corner cell and right lower corner cell separated by underscore |
| sourcesystem | http://snomed.info/sct | It is a custom parameter |
| targetsystem | http://sll-mdilab.net/BodySites/Clinisoft | It is a custom parameter |

Example

Removing mapping between left foot (SCT-CT 22335008) to Clinisoft grid cell G1

[https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/\\$map?direction=unmap&sourcecode=22335008&sourcesystem=http://snomed.info/sct&targetcode=G1&targetsystem=http://sll-mdilab.net/BodySites/Clinisoft](https://clinicalmapper.sll-mdilab.net/fhir/ConceptMap/$map?direction=unmap&sourcecode=22335008&sourcesystem=http://snomed.info/sct&targetcode=G1&targetsystem=http://sll-mdilab.net/BodySites/Clinisoft)

Response

The response document provides status – true is success and false is failure

3.2.3.2.1 SPARQL query

https://github.com/sll-mdilab/clinical-mapper/blob/master/src/main/resources/sparql_queries/DELETE_SNOMED_Clinisoft_mapping.sparql

3.3 Capacity.SLL-MDILAB web application

This is implemented as a module of the **fhirCapacityApp** : <https://github.com/sll-mdilab/fhir-capacity-app>

The following links are provided in **fhir-capacity-app\app\index.html**

Stylesheet:

```
<link rel="stylesheet" href="styles/body_mapper.css">
```

Javascript that implements controller:

```
<script src="scripts/controllers/body_mapper.js"></script>
```

The module is registered at \overview\overview.html :

```
<div class="overview-application-box light-grey-background"
  ng-click="vm.goToApp('body-mapper', episode)">
  <span class="glyphicon glyphicon-user" aria-hidden="true"></span>
  <p>Body mapper</p>
</div>
```

And at fhir-capacity-app\app\app.js

```
(function () {
  'use strict';
  angular
    .module('fhirCapacityApp', [
      .....
    ])
    .config(function ($stateProvider, $urlRouterProvider, fhirConfigProvider, fhirAPI) {

      $urlRouterProvider.otherwise('/overview');

      $stateProvider
      .....
      .state('body-mapper', {
        url: '/body-mapper',
        views: {
          "": {
            templateUrl: '../views/body-mapper/body-mapper.html',
            controller: 'BodyMapperCtrl',
            controllerAs: 'vm',
            title: 'Body Mapper | Innovationsplatsen'
          },
          'header@body-mapper': {
            templateUrl: '../views/misc/header.html'
          }
        }
      })
    })
  })
```

The body-mapper module uses the angular tree view component:

<https://github.com/wix/angular-tree-control>

The HTML markup is those in

<https://github.com/sll-mdilab/fhir-capacity-app/blob/master/app/views/body-mapper/body-mapper.html>

The controller and behavioral logic is in

https://github.com/sll-mdilab/fhir-capacity-app/blob/master/app/scripts/controllers/body_mapper.js

The FHIR client implementation that communicates with the FHIR Clinical Mapper server is in

<https://github.com/sll-mdilab/fhir-capacity-app/blob/master/app/scripts/services/fhir-data-services/fhirconceptmap.js>

3.4 SPARQL queries explained

The SPARQL queries that fetch data for Clinical Mapper service are of various complexity. The simpler ones are standard and do not require explanation. The queries that navigate the hierarchical structures (wider, narrower) and create corresponding paths for two code systems however may need handles.

3.4.1 Virtuoso proprietary functions

If a function in the query has a prefix **bif:** or **sql:** - then this function comes from Virtuoso library and those are described here: <http://docs.openlinksw.com/virtuoso/functions.html>

3.4.2 bif:contains

This is a Virtuoso special free text search and uses the special free text index that Virtuoso creates for string literals. Look at the document http://docs.openlinksw.com/virtuoso/fn_contains.html for the syntax.

It is not mention but relevant to know that if the word contains a non-ASCII character, then it must be put in quotes in the search string: 'handled and "höger"

3.4.3 property paths

In hierarchy queries a special Virtuoso construction is used:

<http://virtuoso.openlinksw.com/dataspace/doc/dav/wiki/Main/VirtsubClassOfOrientedSubsumptionTransitiveOptions>

3.4.3.1 Navigation Upwards

For the “wider” queries the nested SELECT query finds all paths between given concept (<CODE>) and the selected top most concept (52530000) by letting the transitive traversal go via rdfs:subClassOf property.

The query also sets a limit to maximum 15 levels.

```
SELECT DISTINCT ?s ?path ?link ?dist
WHERE
{
?s rdfs:subClassOf ?o
OPTION (transitive, t_distinct, t_in(?s), t_out(?o), t_no_cycles, t_min(1), t_max(15),
t_step(?s) as ?link ,
t_step('path_id') as ?path ,
t_step('step_no') as ?dist ,
t_direction 3) .
FILTER (?s= <http://ihtsdo.org/snomedct/anatomy#<CODE>>
&& ?o = <http://ihtsdo.org/snomedct/anatomy#52530000>
```

```
)
}
```

3.4.3.2 Navigation Downwards

For the “narrower” queries the nested SELECT query finds all paths between given concept (<CODE>) and until the leaf is found, letting the transitive traversal go vi <http://ihtsdo.org/snomedct/anatomy#broader> property. The query also sets a limit to maximum 3 levels down.

```
SELECT DISTINCT ?s ?path ?link ?dist
WHERE
{
?s <http://ihtsdo.org/snomedct/anatomy#broader> ?o
OPTION (transitive, t_distinct, t_in(?s), t_out(?o), t_no_cycles, t_min(1), t_max(3),
t_step(?s) as ?link ,
t_step('path_id') as ?path ,
t_step('step_no') as ?dist ,
t_direction 3) .
FILTER ( ?s = <http://ihtsdo.org/snomedct/anatomy#<CODE>>> )
}
```

3.5 Clinisoft body sites explained

The Clinisoft Body sites are described by a grid where rows run by numbers (18 to 1 from top down) and columns run by letters (B to T from left to right). Each combination provide a body site location and the cell identifier is the Clinisoft code. However, even any rectangle consisting of multiple cells is defined as Clinisoft body site, so that hierarchy can be inferred, and if the one cell level identifier is not mapped to SNOMED, then the smallest rectangle containing the given cell is matched against SNOMED-CT term. If the mapping exists then that SNOMED-CT term provides the current “best match” for this cell.

Example:

This is a hierarchy between whole body, trunk and left hip as they are mapped to canonical SNOMED-CT hierarchy

- B1T18
 - D14_R9
 - H9

| SNOMED-CT | Clinisoft |
|---|---|
| <ul style="list-style-type: none"> ▼ 1. Left hip region structure (5) <ul style="list-style-type: none"> Structure of left side of trunk Structure of left half of body Structure of half of body lateral to midsagittal plane Body region structure ▼ 2. Left hip region structure (6) <ul style="list-style-type: none"> Structure of left side of trunk Structure of half of trunk lateral to midsagittal plane Trunk structure Body part structure Body region structure | <ul style="list-style-type: none"> ▶ 1. H9 (2) ▼ 2. H9 (3) <ul style="list-style-type: none"> n/a n/a D14_R9 n/a B1T18 ▶ 3. H9 (2) ▶ 4. H9 (2) ▶ 5. H9 (2) |

In case one want to put an annotation to the left hip, then corresponding SNOMED concept to H9 cell is “Left hip region structure”. If one want to put an annotation to entire left side of the trunk, then as there is no mapping for H11, then the best fit is D14_R9 and this returns “Trunk structure” from SNOMED-CT concepts.