

Querying Data with SPARQL

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A project of

Outline

- Introduction to SPARQL 1.1
- Query examples:
 - Patient allergic to Peanuts
 - Patient allergic to Pulse Vegetables
 - Patient with specific lab tests

Introduction to SPARQL 1.1

Introduction to SPARQL

<?> SPARQL Protocol and RDF Query Language

- standard querying language for RDF
- declarative language part of the W3C standards:
<https://www.w3.org/TR/sparql11-query/>
- queries based on graph pattern matching finding
- syntax similar to Turtle (but not exactly the same!)



Structure of a query in SPARQL 1.1

prefix dc: <...>

Prefix declarations

prefix uni: <...>

SELECT ...

Declare type of query: SELECT, ASK, DESCRIBE, CONSTRUCT

FROM <...>

Define dataset

FROM NAMED <...>

WHERE { ... }

Graph pattern (in the form of triples)

ORDER BY ...

Query modifiers

HAVING ...

GROUP BY ...

LIMIT ...

OFFSET ...

BINDINGS ...

Four types of SPARQL queries

SELECT get results for requested variables → output is a table

ASK check for matches, gives boolean 'yes/no' result

CONSTRUCT get specific parts of a graph + manipulate graph by creating new triples

DESCRIBE get basic information about a variable

Query formation: other possible constructs

- Nested queries: with SPARQL subquery - one 'SELECT' inside another 'SELECT'
→ more on: <https://www.w3.org/TR/sparql11-query/#subqueries>
- Federated SPARQL: query different SPARQL endpoints in the same query using a 'SERVICE' clause
→ more on: <https://www.w3.org/TR/sparql11-federated-query/>
- ...

Some tips...

'a' is a shortcut for 'rdf:type'

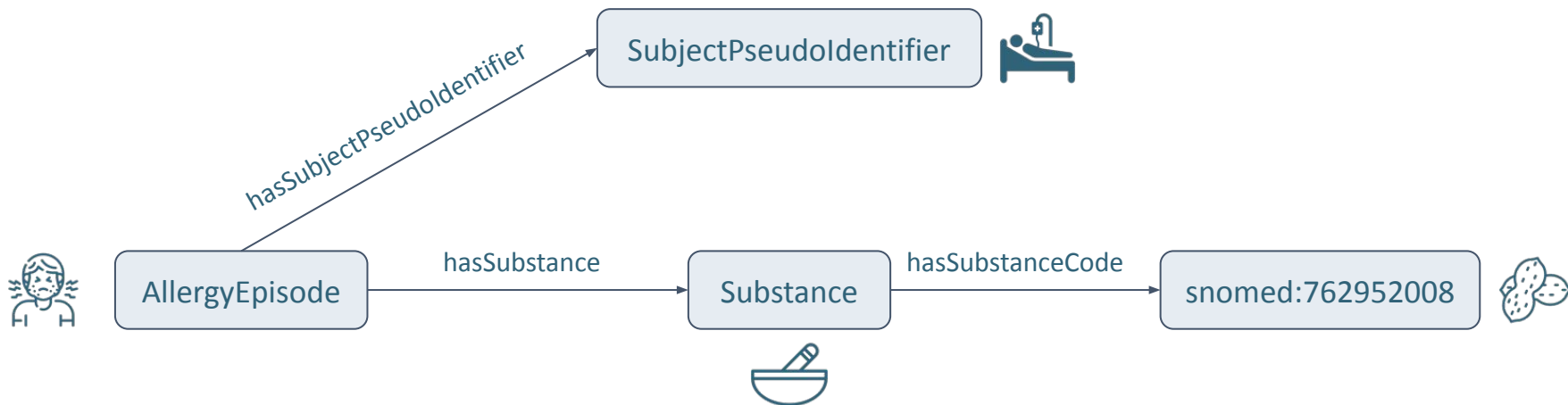
Prefixes are highly recommended for better readability

Being familiar with the dataset structure helps to write a query

```
?patient rdf:type https://biomedit.ch/rdf/sphn-ontology/SubjectPseudIdentifier  
?patient a sphn:SubjectPseudIdentifier
```


Query examples

Patients allergic to Peanuts



Patients allergic to Peanuts

PREFIX rdf:<<http://www.w3.org/1999/02/22-rdf-syntax-ns#>>

PREFIX rdfs:<<http://www.w3.org/2000/01/rdf-schema#>>

PREFIX sphn:<<https://biomedit.ch/rdf/sphn-ontology/sphn#>>

PREFIX resource:<<https://biomedit.ch/rdf/sphn-resource/>>

PREFIX xsd:<<http://www.w3.org/2001/XMLSchema#>>

PREFIX snomed: <<http://snomed.info/id/>>

Patients allergic to Peanuts

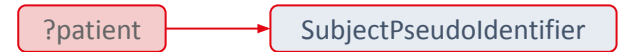
PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
SELECT distinct ?patient



?patient

Patients allergic to Peanuts

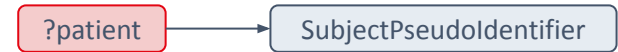
```
PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
SELECT distinct ?patient
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
```



Patients allergic to Peanuts

```

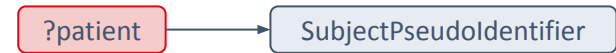
PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
SELECT distinct ?patient
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
    ?allergy_episode a sphn:AllergyEpisode .
  
```



Patients allergic to Peanuts

```

PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
SELECT distinct ?patient
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
    ?allergy_episode a sphn:AllergyEpisode .
    ?substance a sphn:Substance .
  
```



Patients allergic to Peanuts

```

PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>

```

```
SELECT distinct ?patient
```

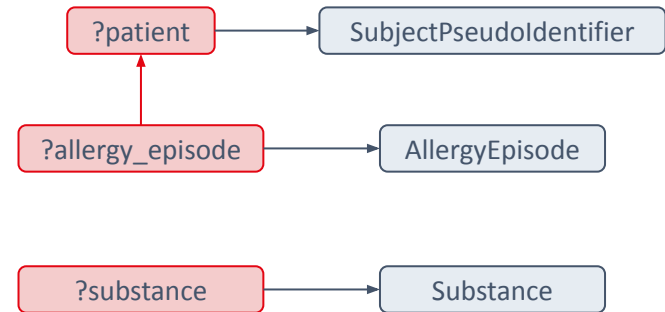
```
WHERE {
```

```
    ?patient a sphn:SubjectPseudoidentifier .
```

```
    ?allergy_episode a sphn:AllergyEpisode .
```

```
    ?substance a sphn:Substance .
```

```
    ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
```



Patients allergic to Peanuts

```
PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
```

```
SELECT distinct ?patient
```

```
WHERE {
```

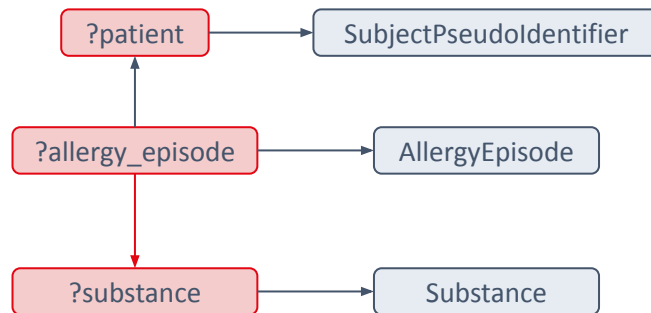
```
    ?patient a sphn:SubjectPseudoidentifier .
```

```
    ?allergy_episode a sphn:AllergyEpisode .
```

```
    ?substance a sphn:Substance .
```

```
    ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
```

```
    ?allergy_episode sphn:hasSubstance ?substance .
```



Patients allergic to Peanuts

```
PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
```

```
SELECT distinct ?patient
```

```
WHERE {
```

```
  ?patient a sphn:SubjectPseudoidentifier .
```

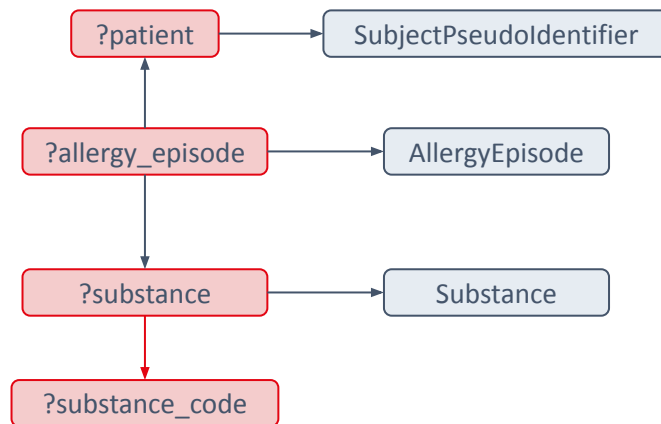
```
  ?allergy_episode a sphn:AllergyEpisode .
```

```
  ?substance a sphn:Substance .
```

```
  ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
```

```
  ?allergy_episode sphn:hasSubstance ?substance .
```

```
  ?substance sphn:hasSubstanceCode ?substance_code .
```

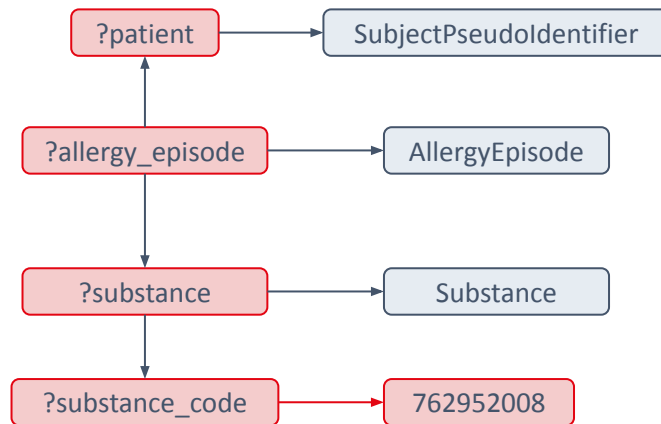


Patients allergic to Peanuts

```

PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
SELECT distinct ?patient
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
    ?allergy_episode a sphn:AllergyEpisode .
    ?substance a sphn:Substance .
    ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
    ?allergy_episode sphn:hasSubstance ?substance .
    ?substance sphn:hasSubstanceCode ?substance_code .
    ?substance_code a snomed:762952008 .
}

```



Patients allergic to Peanuts

```

SELECT (COUNT (distinct ?patient) AS ?patients) ?snomed_code ?label
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
    ?allergy_episode a sphn:AllergyEpisode .
    ?substance a sphn:Substance .

    ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
    ?allergy_episode sphn:hasSubstance ?substance .
    ?substance sphn:hasSubstanceCode ?substance_code .

    ?substance_code a snomed:762952008 .
    ?substance_code rdf:type ?snomed_code .
    ?snomed_code rdfs:label ?label .

    FILTER(strStarts(str(?snomed_code), "http://snomed.info/id/"))
} GROUP BY ?snomed_code ?label

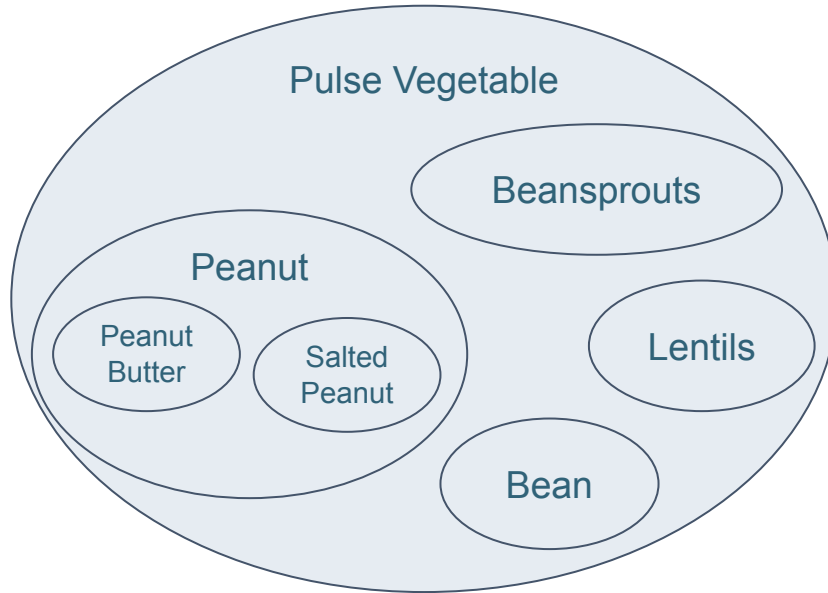
```

] To retrieve only labels
 from SNOMED CT

Results:

➤ 134 patients

Patients allergic to Pulse Vegetable



Patients can have information annotated at different levels of granularity.

You **DO NOT** need to query individually for all levels in order to get all patients that are allergic to Pulse Vegetable

thanks to the RDF graph structure and the hierarchy of SNOMED CT.

Figure: Hierarchical structure from SNOMED CT

Patients allergic to Pulse Vegetable

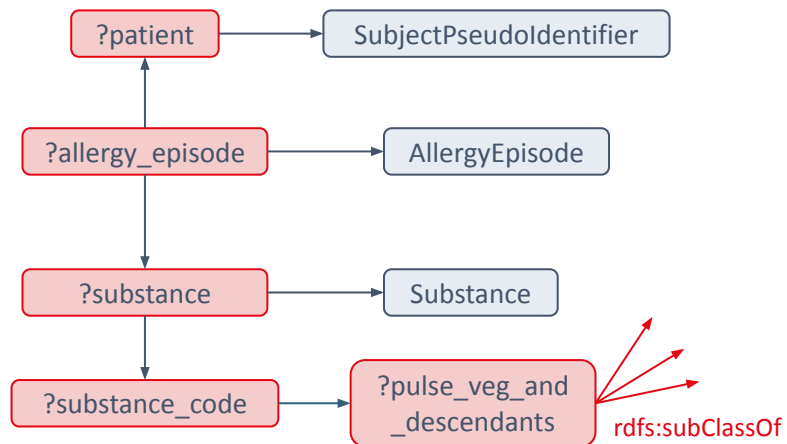
Query Option 1: REASONING WITH QUERY (NO INFERENCE TURNED ON)

Patients allergic to Pulse Vegetable

```

PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
SELECT distinct ?patient
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
    ?allergy_episode a sphn:AllergyEpisode .
    ?substance a sphn:Substance .
    ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
    ?allergy_episode sphn:hasSubstance ?substance .
    ?substance sphn:hasSubstanceCode ?substance_code .
    ?substance_code a ?pulse_veg_and_descendants .
    ?pulse_veg_and_descendants rdfs:subClassOf* snomed:227313005 .
}

```



Patients allergic to Pulse Vegetable

```

SELECT (COUNT (distinct ?patient) AS ?patients) ?snomed_code?label
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
    ?allergy_episode a sphn:AllergyEpisode .
    ?substance a sphn:Substance .
    ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
    ?allergy_episode sphn:hasSubstance ?substance .
    ?substance sphn:hasSubstanceCode ?substance_code .
    ?substance_code a ?pulse_veg_and_descendants .
    ?pulse_veg_and_descendants rdfs:subClassOf* snomed:227313005 .
    ?substance_code rdf:type ?snomed_code .
    ?snomed_code rdfs:label ?label .
    FILTER(strStarts(str(?snomed_code), "http://snomed.info/id/"))
} GROUP BY ?snomed_code ?label
  
```

Results:

- 134 patients Peanuts
- 123 patients Pulse Vegetable
- 123 patients Beansprouts

Patients allergic to Pulse Vegetable

Option 2: INFERENCE TURNED ON → use the possibilities offered by the graph structure



The screenshot shows a settings menu on the left with 'My Settings' highlighted. The main content area displays 'SPARQL editor settings' with several options:

- Unset password
- Expand results over owl:SameAs is **OFF** by default
- Inference is **ON** by default (highlighted with a red box)
- Count total results
- Ignore shared saved queries

RDF Reasoning



Class vs Subclass

Measurement

- HeartRate
- BodyHeight

X is a HeartRate

X is a Measurement

Property vs Subproperty

hasBodySite

- hasInsertionSite
- hasInfectionSite

X hasInsertionSite Arm

X hasBodySite Arm

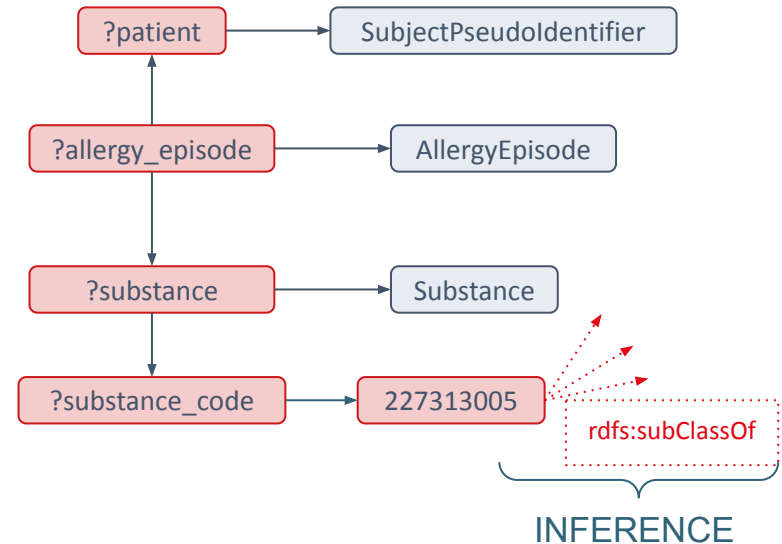
Patients allergic to Pulse Vegetable



```

PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
PREFIX snomed: <http://snomed.info/id/>
SELECT distinct ?patient
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
    ?allergy_episode a sphn:AllergyEpisode .
    ?substance a sphn:Substance .
    ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
    ?allergy_episode sphn:hasSubstance ?substance .
    ?substance sphn:hasSubstanceCode ?substance_code .
    ?substance_code a snomed:227313005 .
}

```



Patients allergic to Pulse Vegetable

```

SELECT (COUNT (distinct ?patient) as ?patients) ?snomed_code ?label
WHERE {
    ?patient a sphn:SubjectPseudoidentifier .
    ?allergy_episode a sphn:AllergyEpisode .
    ?substance a sphn:Substance .
    ?allergy_episode sphn:hasSubjectPseudoidentifier ?patient .
    ?allergy_episode sphn:hasSubstance ?substance .
    ?substance sphn:hasSubstanceCode ?substance_code .
    ?substance_code a snomed:227313005 .
    ?substance_code rdf:type ?snomed_code .
    ?snomed_code rdfs:label ?label .
    FILTER(strStarts(str(?snomed_code), "http://snomed.info/id/"))
} GROUP BY ?snomed_code ?label

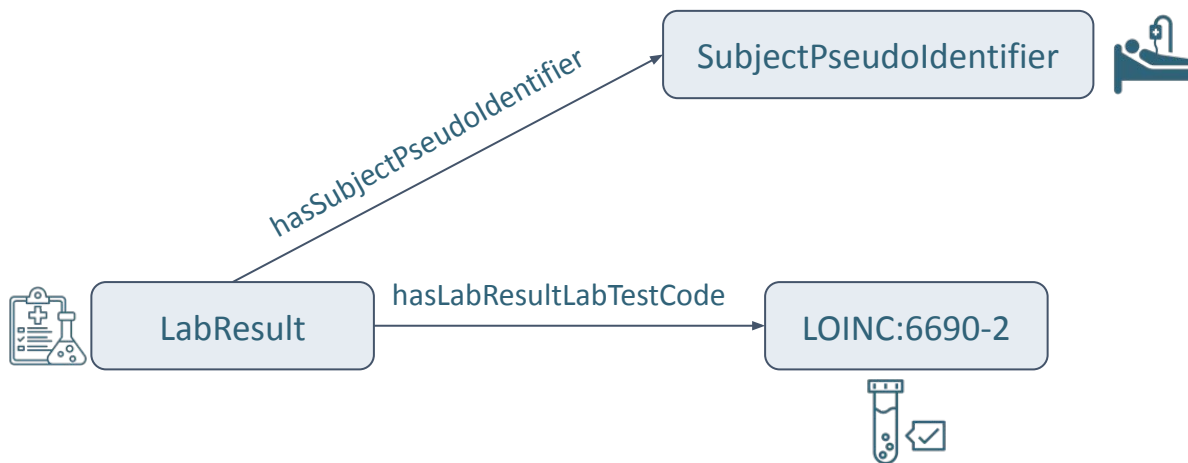
```

Results:

- 134 patients Peanuts
- 123 patients Beansprouts
- 380 patients Pulse Vegetable

	patients	snomed_code	label
1	*380**xsd:integer	snomed:227313005	"Pulse vegetable (substance)" ^{en}
2	*134**xsd:integer	snomed:762952008	"Peanut (substance)" ^{en}
3	*500**xsd:integer	snomed:255620007	"Food (substance)" ^{en}
4	*500**xsd:integer	snomed:22836000	"Vegetable (substance)" ^{en}
5	*500**xsd:integer	snomed:138875005	"SNOMED CT Concept (SNOMED RT+CTV3)" ^{en}
6	*500**xsd:integer	snomed:105590001	"Substance (substance)" ^{en}
7	*500**xsd:integer	snomed:762766007	"Edible substance (substance)" ^{en}
8	*500**xsd:integer	snomed:227210005	"Vegetables pulses herbs and spices (substance)" ^{en}
9	*120**xsd:integer	snomed:227920007	"Vegetable risotto (substance)" ^{en}
10	*120**xsd:integer	snomed:227765005	"Vegetable dishes (substance)" ^{en}
11	*120**xsd:integer	snomed:227917004	"Rice dishes (substance)" ^{en}
12	*123**xsd:integer	snomed:227339008	"Beansprouts (substance)" ^{en}

Patient with measurements of Leukocytes in Blood by Automated count (LOINC 6690-2)



Patient with measurements of Leukocytes in Blood by Automated count (LOINC 6690-2)

PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>

PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>

PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>

PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>

PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>

PREFIX loinc: <https://loinc.org/rdf/>

SELECT distinct ?patient

WHERE {

 ?patient a sphn:SubjectPseudIdentifier .

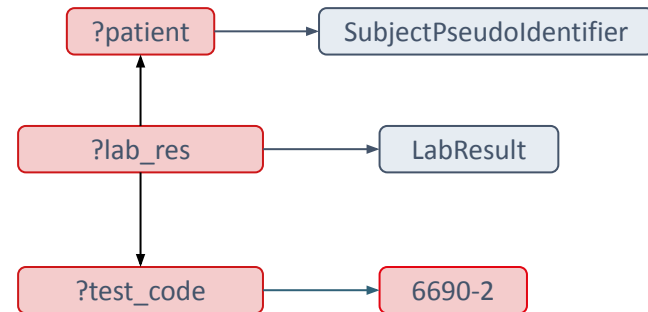
 ?lab_res a sphn:LabResult .

 ?lab_res sphn:hasSubjectPseudIdentifier ?patient .

 ?lab_res sphn:hasLabResultLabTestCode ?test_code .

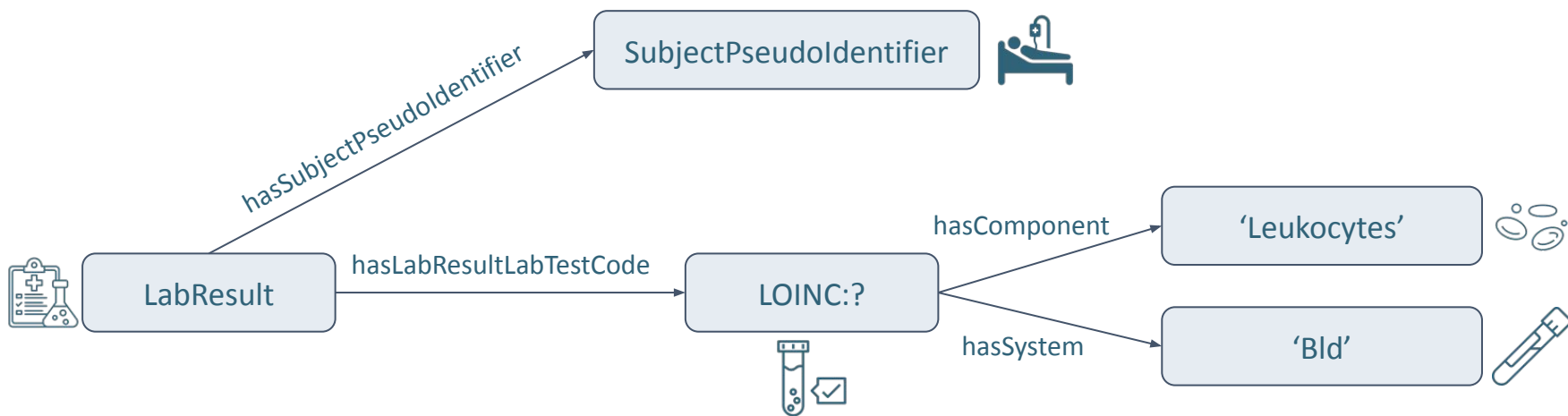
 ?test_code rdf:type loinc:6690-2 .

}



	patients	label
1	"253"^^xsd:integer	"Leukocytes [# /volume] in Blood by Automated count"

Patients with measurements of Leukocytes in Blood



Patients with measurements of Leukocytes in Blood

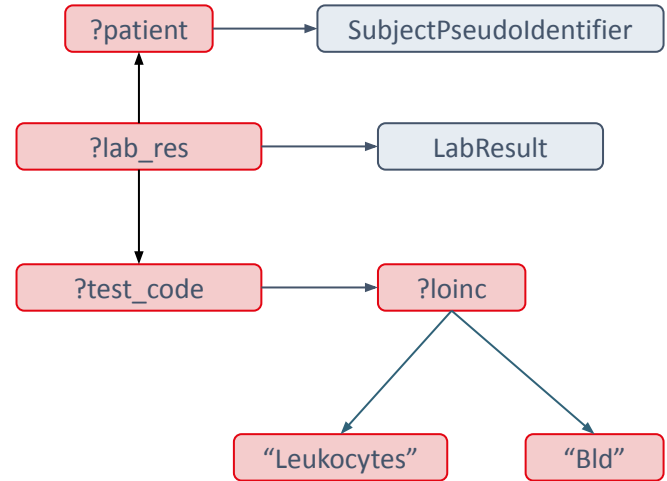
PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
 PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
 PREFIX sphn:<https://biomedit.ch/rdf/sphn-ontology/sphn#>
 PREFIX resource:<https://biomedit.ch/rdf/sphn-resource/>
 PREFIX xsd:<http://www.w3.org/2001/XMLSchema#>
 PREFIX loinc: <https://loinc.org/rdf/>
 PREFIX sphn-loinc: <https://biomedit.ch/rdf/sphn-resource/loinc/>

SELECT distinct ?patient

WHERE {

?patient a sphn:SubjectPseudoidentifier .
 ?lab_res a sphn:LabResult .
 ?lab_res sphn:hasSubjectPseudoidentifier ?patient .
 ?lab_res sphn:hasLabResultLabTestCode ?test_code .
 ?test_code rdf:type ?loinc .
 ?loinc sphn-loinc:hasComponent "Leukocytes" .
 ?loinc sphn-loinc:hasSystem "Bld" .

}



	patients	loinc	label
1	"247"^^xsd:integer	loinc:26464-8	"Leukocytes [# /volume] in Blood"
2	"253"^^xsd:integer	loinc:6690-2	"Leukocytes [# /volume] in Blood by Automated count"

References

SPARQL Documentation: <https://www.w3.org/TR/sparql11-query/>

SPHN Semantic Framework: <https://sphn-semantic-framework.readthedocs.io/>

SPHN LOINC:

https://sphn-semantic-framework.readthedocs.io/en/latest/external_resources/loinc.html

SPHN SNOMED CT:

https://sphn-semantic-framework.readthedocs.io/en/latest/external_resources/snomed-ct.html

Thank you for your attention



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