



# sparqling-genomics

---

<https://github.com/UMCUGenetics/sparqling-genomics>  
v0.99.7 , August 22, 2018

# Contents

<b>1</b>	<b>Getting started</b>	<b>1</b>
1.1	Prerequisites . . . . .	1
1.2	Setting up a build environment . . . . .	1
1.2.1	Debian . . . . .	1
1.2.2	CentOS . . . . .	2
1.2.3	GNU Guix . . . . .	2
1.2.4	MacOS . . . . .	2
1.3	Obtaining the source code . . . . .	2
1.4	Installation instructions . . . . .	2
<b>2</b>	<b>The knowledge graph</b>	<b>4</b>
2.1	Knowledge expressed by SPARQLing genomics tools . . . . .	4
<b>3</b>	<b>Command-line programs</b>	<b>5</b>
3.1	Preparing variant call data with <code>vcf2rdf</code> . . . . .	5
3.1.1	Knowledge extracted by <code>vcf2rdf</code> . . . . .	5
3.1.2	Example usage . . . . .	6
3.1.3	Run-time properties . . . . .	6
3.2	Preparing tabular data with <code>table2rdf</code> . . . . .	6
3.2.1	Transformers . . . . .	6
3.2.2	Delimiters . . . . .	7
3.2.3	Knowledge extracted by <code>table2rdf</code> . . . . .	9
3.2.4	Example usage . . . . .	9
3.3	Converting MySQL data to RDF with <code>table2rdf</code> . . . . .	10
3.4	Importing data with <code>curl</code> . . . . .	10
3.4.1	Example usage . . . . .	10
<b>4</b>	<b>Web interface</b>	<b>12</b>
4.1	Configuring the web interface . . . . .	12
4.1.1	To fork or not to fork . . . . .	12
4.1.2	Bind address and port . . . . .	12
4.1.3	Authentication . . . . .	12
4.2	Running the web interface . . . . .	13
4.3	Configuring connections . . . . .	13
4.4	Managing projects . . . . .	14
4.5	Executing queries . . . . .	14
4.5.1	Query history . . . . .	15
<b>5</b>	<b>Information retrieval with SPARQL</b>	<b>16</b>
5.1	Local querying . . . . .	16
5.1.1	Listing non-empty graphs . . . . .	16

5.1.2	Querying a specific graph . . . . .	17
5.1.3	Exploring the structure of knowledge in a graph . . . . .	17
5.1.4	Listing samples and their originating files . . . . .	18
5.1.5	Listing samples, originated files, and number of variants . . . . .	19
5.1.6	Retrieving all variants . . . . .	20
5.1.7	Retrieving variants with a specific mutation . . . . .	20
5.1.8	Comparing two datasets on specific properties . . . . .	21
5.2	Federated querying . . . . .	22
5.2.1	Get an overview of Biomodels (from ENSEMBL) . . . . .	22
<b>6</b>	<b>Using SPARQL with other programming languages</b>	<b>24</b>
6.1	Using SPARQL with R . . . . .	24
6.1.1	Querying with authentication . . . . .	25
6.2	Using SPARQL with GNU Guile . . . . .	25

# Chapter 1

## Getting started

### 1.1 Prerequisites

In addition to the tools provided by this project, a RDF store is required. In the manual we use [Virtuoso](#), but [4store](#), [BlazeGraph](#), or [AllegroGraph](#) may also be used.

Before we can use the programs provided by this project, we need to build them first.

The build system needs [GNU Autoconf](#), [GNU Automake](#), [GNU Make](#) and [pkg-config](#). Additionally, for building the documentation, a working  $\LaTeX$  distribution is required including the `pdflatex` program. Because  $\LaTeX$  distributions are rather large, this is optional.

Each component in the repository has its own dependencies. Table 1.1 provides an overview for each tool.

<b>vcf2rdf</b>	<b>table2rdf</b>	<b>Web interface</b>	<b>Documentation</b>
GNU C compiler	GNU C compiler	GNU Guile	$\LaTeX$ distribution
libgcrypt	libgcrypt	Fibers	
raptor2	raptor2		
HTSLib			

Table 1.1: External tools required to build and run the programs this project provides.

The manual provides example commands to import RDF using [cURL](#).

### 1.2 Setting up a build environment

#### 1.2.1 Debian

Debian includes all tools, so use this command to install the build dependencies:

```
apt-get install autoconf automake gcc make pkg-config libgcrypt-dev \
                zlib-dev guile-2.0 guile-2.0-dev libraptor2-dev texlive \
                curl
```

The command has been tested on Debian 9.

### 1.2.2 CentOS

CentOS 7 does not include `htslib`. All other dependencies can be installed using the following command:

```
yum install autoconf automake gcc make pkgconfig libgcrypt-devel \
    guile guile-devel raptor2-devel texlive curl
```

### 1.2.3 GNU Guix

If **GNU Guix** is available on your system, an environment that contains all external tools required to build the programs in this project can be obtained running the following command from the project's repository root:

```
guix environment -l environment.scm
```

### 1.2.4 MacOS

The necessary dependencies to build `sparqling-genomics` can be installed using **homebrew**:

```
brew install autoconf automake gcc make pkg-config libgcrypt guile \
    htslib curl raptor
```

The only missing dependency is a  $\text{\LaTeX}$  distribution. But this is only needed to build this documentation.

Building on MacOS has not been tested. If you've tried it, please let us know, so we can attempt to support it in the future.

## 1.3 Obtaining the source code

The source code can be downloaded at the **Releases**<sup>1</sup> page. Make sure to download the `sparqling-genomics-0.99.7.tar.gz` file.

Or, directly download the tarball using the command-line:

```
curl -O https://github.com/UMCUGenetics/sparqling-genomics/releases/\
download/0.99.7/sparqling-genomics-0.99.7.tar.gz
```

After obtaining the tarball, it can be unpacked using the following commands:

```
tar zxvf sparqling-genomics-0.99.7.tar.gz
cd sparqling-genomics-0.99.7
```

## 1.4 Installation instructions

After installing the required tools (see section 1.1 'Prerequisites'), and obtaining the source code (see section 1.3 'Obtaining the source code'), building involves running the following commands:

```
autoreconf -vif # Only needed if the "./configure" step does not work.
./configure
make
```

---

<sup>1</sup><https://github.com/UMCUGenetics/sparqling-genomics/releases>

```
make install
```

To run the `make install` command, super user privileges are possibly required. This step can be ignored, but will keep the tools in the project's directory. So, invoking `vcf2rdf` must be done using `tools/vcf2rdf/vcf2rdf` when inside the project's root directory, instead of "just" `vcf2rdf`.

Alternatively, the individual components can be built by replacing `make && make install` with `make -C <component-directory>`. So, to only build `vcf2rdf`, the following command could be used:

```
make -C tools/vcf2rdf
```

## Chapter 2

# The knowledge graph

The tools provided by `sparqling-genomics` are designed to build a common format to express genomic information. Each program reads data in a domain-specific format, and translates it into a common format; the Resource Description Framework (RDF).

Programs can be categorized in layers. A program belongs to the first layer (layer 0) when it translates a non-RDF format into RDF. In the second layer (layer 1), we find programs that read RDF and generate more RDF. Higher-level layers depend on the knowledge added by programs from the previous layer.

In `sparqling-genomics`, the knowledge graph created by the programs is more important than the programs themselves. When designing and implementing new programs, we should consider the added knowledge first.

Furthermore, programs should not depend on programs, but on the knowledge produced by programs. For example, the `vcf2rdf` program always writes genomic positions by using the *FALDO* ontology. An annotation program needs not to know about the existence of `vcf2rdf`, but it needs to know about the *FALDO* ontology. Therefore, the common interface between programs dealing with genomic positions is the *FALDO* ontology. This enables developers of the knowledge graph to understand the bigger picture without needing to understand the details of each program, or each individual data format.

The next challenge is to describe knowledge in an integrative manner. Again, *FALDO* serves a good example: it describes a way of expressing knowledge that multiple programs can use; locations in a genome. Developing effective ontologies means extracting common patterns in how information is described. This is an ever-ongoing process of refinement that changes over time with the knowledge that is most valuable to the researcher.

With `sparqling-genomics`, we attempt to design a knowledge graph and provide the tools to practically implement it. When improving `sparqling-genomics`, please always keep an eye out for the knowledge graph.

### 2.1 Knowledge expressed by SPARQLing genomics tools

The `vcf2rdf` and `table2rdf` programs express knowledge using a unified pattern. This overlap between the programs defines the *ontology* for SPARQLing genomics. We wrote the ontology in the Terse RDF Triple Language (Turtle) format, and it can be found in the release tarball in `'ontologies/sparqling-genomics.ttl'`.

## Chapter 3

# Command-line programs

The project provides programs to create a complete pipeline including data conversion, data importing and data exploration. The tasks we can perform with the command-line programs are:

- Extract triples from VCF files;
- Extract triples from tabular data files;
- Push data to a SPARQL endpoint.

### 3.1 Preparing variant call data with `vcf2rdf`

Obtaining variants from sequenced data is a task of so called *variant callers*. These programs often output the variants they found in the *Variant Call Format* (VCF). Before we can use the data described in this format, we need to extract *knowledge* (in the form of triples) from it.

The `vcf2rdf` program does exactly this, by converting a VCF file into an RDF format. In section 3.4 ‘Importing data with `curl`’ we describe how to import the data produced by `vcf2rdf` in the database.

#### 3.1.1 Knowledge extracted by `vcf2rdf`

The program treats the VCF as its own ontology. It uses the VCF header as a guide. All fields described in the header of the VCF file will be translated into triples.

In addition to the knowledge from the VCF file, `vcf2rdf` stores the following metadata:

Subject	Predicate	Object	Description
:Origin	rdf:type	owl:Class	:Origin is used to identify a data origin (which is usually a file).
:Sample	rdf:type	owl:Class	:Sample is used to identify a sample name.
:filename	rdf:type	xsd:string	:filename contains the path to the file that :Origin represents.
:convertedBy	rdf:type	owl:AnnotationProperty	:convertedBy is used to identify the program that performed the VCF->RDF conversion.
:foundIn	rdf:type	owl:AnnotationProperty	:foundIn relates the :Origin to a :Sample.

Table 3.1: The additional triple patterns described by `vcf2rdf`.



The following snippet is an example of the extra data in Turtle-format:

```
<http://sparqling-genomics/vcf2rdf/14f2b609b>
  :convertedBy :vcf2rdf ;
  :filename "clone_ref_tumor.vcf.gz"^^xsd:string ;
  a :Origin .

sample:CLONE_REF
  :foundIn <http://sparqling-genomics/vcf2rdf/14f2b609b3> ;
  a :Sample .

sample:CLONE_TUMOR
  :foundIn <http://sparqling-genomics/vcf2rdf/14f2b609b3> ;
  a :Sample .
```

### 3.1.2 Example usage

```
vcf2rdf -i /path/to/my/variants.vcf > /path/to/my/variants.ttl
```

### 3.1.3 Run-time properties

Depending on the serialization format, the program typically uses from two megabytes (in ntriples mode), to multiple times the size of the input VCF (in turtle mode).

The ntriples mode can output triples as soon as they are formed, while the turtle mode waits until all triples are known, so that it can output them efficiently, producing compact output at the cost of using more memory.

We recommend using the ntriples format for large input files, and turtle for small input files.

## 3.2 Preparing tabular data with table2rdf

Data that can be represented as a table, like comma-separated values (CSV) or BED files, can be imported using table2rdf. The column headers are used as predicates, and each row gets a unique row ID. Non-alphanumeric characters in the header line are replaced by underscores, and all characters are replaced by their lowercase equivalent to make a consistent scheme for predicates.

When the file does not contain a header line, one can be specified using the `--header-line` argument. When using this command-line argument, the delimiter must be a semicolon (;).

### 3.2.1 Transformers

Furthermore, table2rdf knows nothing about ontologies. So when the input table has a column “Chromosome”, by default table2rdf will treat these cells as literal values. A *transformer* can be used to express a column as an *individual* in RDF. An example follows.

Take the following input file:

```
$ cat test.tsv
Chromosome      Position
chr1            1500000
chrMT           11000
```

Running `table2rdf` with its default settings will produce:

```
$ table2rdf -i test.tsv
...
<http://sparqling-genomics/table2rdf/Row/...-R0000000000>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome "chr1"^^xsd:string ;
  col:position 1500000 ;
  a :Row .

<http://sparqling-genomics/table2rdf/Row/...-R0000000001>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome "chrMT"^^xsd:string ;
  col:position 11000 ;
  a :Row .
...
```

When we know that the data in a column refers to items in an ontology, like chromosomes defined in <http://rdf.biosemantics.org/data/genomeassemblies/hg19>, `table2rdf` can be told to use that ontology to describe that column.

To do so, we can use the `--transform` option, or `-t` for short:

```
$ table2rdf \
  -i test.tsv \
  -t Chromosome=http://rdf.biosemantics.org/data/genomeassemblies/hg19#
...
@prefix p00000: <http://rdf.biosemantics.org/data/genomeassemblies/hg19#> .
...
<http://sparqling-genomics/table2rdf/Row/...-R0000000000>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome p00000:chr1 ;
  col:position 1500000 ;
  a :Row .

<http://sparqling-genomics/table2rdf/Row/...-R0000000001>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome p00000:chrMT ;
  col:position 11000 ;
  a :Row .
...
```

After the transformation, the output produced by `table2rdf` uses URIs pointing to the ontology instead of literal values for chromosomes.

### 3.2.2 Delimiters

Tabular data consists of rows and columns. A field is a specific place in a table, having a column-coordinate, and a row-coordinate. To distinguish fields from one another we use a delimiter. Which delimiter to use (a tab, a comma, or a semicolon are common ones) is up to the dataset. The delimiter can be chosen using the `--delimiter` option, or `-d` for short.

Sometimes a single field can consist of multiple “subfields”. To distinguish subfields, we use a secondary delimiter. In RDF, we can split those subfields by using the same predicate as we would use for the entire field. Using the `--secondary-delimiter` option, we can invoke this behavior.

The following example demonstrates the usage of `--delimiter` and `--secondary-delimiter`.

Take the following input file:

```
$ cat multi.tsv
Chromosome Position Filter
1 10000 A;B;C;D
1 10010 A
1 11000
```

Without using the secondary delimiter, we get:

```
$ table2rdf -i multi.tsv
...
<http://sparqling-genomics/table2rdf/Row/...-R0000000000>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome 1 ;
  col:filter "A;B;C;D"^^xsd:string ;
  col:position 10000 ;
  a :Row .

<http://sparqling-genomics/table2rdf/Row/...-R0000000001>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome 1 ;
  col:filter "A"^^xsd:string ;
  col:position 10010 ;
  a :Row .

<http://sparqling-genomics/table2rdf/Row/...-R0000000002>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome 1 ;
  col:position 11000 ;
  a :Row .
...
```

Using the secondary delimiter, we get:

```
$ table2rdf -i multi.tsv -D ":"
...
<http://sparqling-genomics/table2rdf/Row/...-R0000000000>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome 1 ;
  col:filter "A"^^xsd:string, "B"^^xsd:string, "C"^^xsd:string,
            "D"^^xsd:string ;
  col:position 10000 ;
  a :Row .
```

```

<http://sparqling-genomics/table2rdf/Row/...-R0000000001>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome 1 ;
  col:filter "A"^^xsd:string ;
  col:position 10010 ;
  a :Row .

<http://sparqling-genomics/table2rdf/Row/...-R0000000002>
  sg:originatedFrom <http://sparqling-genomics/...> ;
  col:chromosome 1 ;
  col:position 11000 ;
  a :Row .

...

```

Notice how the `col:filter` predicate now describes a connection to four objects instead of one.

### 3.2.3 Knowledge extracted by table2rdf

The `table2rdf` program extracts all fields in the table. In addition to the knowledge from the table file, `table2rdf` stores the following metadata:

Subject	Predicate	Object	Description
:Origin	rdf:type	owl:Class	:Origin is used to identify a data origin (which is usually a file).
:Sample	rdf:type	owl:Class	:Sample is used to identify a sample name.
:filename	rdf:type	xsd:string	:filename contains the path to the file that :Origin represents.
:convertedBy	rdf:type	owl:AnnotationProperty	:convertedBy is used to identify the program that performed the VCF->RDF conversion.
:foundIn	rdf:type	owl:AnnotationProperty	:foundIn relates the :Origin to a :Sample.

Table 3.2: The additional triple patterns described by `table2rdf`.

The following snippet is an example of the extra data in Turtle-format:

```

<http://sparqling-genomics/table2rdf/1jka8923i4>
  :convertedBy :table2rdf ;
  :filename "grch37.bed"^^xsd:string ;
  a :Origin .

sample:grch37
  :foundIn <http://sparqling-genomics/table2rdf/1jka8923i4> ;
  a :Sample .

```

### 3.2.4 Example usage

```
table2rdf -i /path/to/my/table.tsv > /path/to/my/table.ttl
```

### 3.3 Converting MySQL data to RDF with table2rdf

Relational databases store data in tables. With `table2rdf` we can oftentimes convert the data in a single go to RDF triples. The following example extracts the `regions` table from a MySQL server in a database called `example`.

```
mysql --host=127.0.0.1 -e "SELECT * FROM example.regions" \
  --batch | table2rdf --stdin -0 ntriples > regions.n3
```

The `mysql` command outputs the table in tab-delimited form when using the `--batch` argument, which is the default input type for `table2rdf`. To accept input from a UNIX pipe `table2rdf` must be invoked with the `--stdin` argument.

### 3.4 Importing data with curl

To load RDF data into a triple store (our database), we can use `curl`.

The triple stores typically store data in *graphs*. One triple store can host multiple graphs, so we must tell the triple store which graph we would like to add the data to.

#### 3.4.1 Example usage

```
curl -X POST \
  -H "Content-Type: text/turtle" \
  -T /path/to/variants.ttl \
  -G <endpoint URL> \
  --digest -u <username>:<password> \
  --data-urlencode graph=http://example/graph
```

#### Virtuoso example

The following example inserts the file `vcf2rdf-variants.ttl` into a graph called `http://example/graph` in a Virtuoso endpoint at `http://127.0.0.1:8890` with the username `dba` and password `qwerty`.

```
curl -X POST \
  -H "Content-Type: text/turtle" \
  -T vcf2rdf-variants.ttl \
  -G http://127.0.0.1:8890/sparql-graph-crud-auth \
  --digest -u dba:qwerty \
  --data-urlencode graph=http://example/graph
```

#### 4store example

Similar to the Virtuoso example, for 4store the command looks like this:

```
curl -X POST \
  -H "Content-Type: text/turtle" \
  -T vcf2rdf-variants.ttl \
  -G http://127.0.0.1:8080/data/http://example/graph
```

Notice that 4store does not provide an authentication mechanism.

### **Sending gzip-compressed data**

When the RDF file is compressed with gzip, extra HTTP headers must be added to the `curl` command:

```
curl -X POST \
  -H "Content-Type: text/turtle" \
  -H "Transfer-Encoding: chunked" \
  -H "Content-Encoding: gzip" \
  ...
```

# Chapter 4

## Web interface

In addition to the command-line programs, the project provides a web interface for prototyping queries, and quick data reporting. With the web interface you can:

- Write and execute SPARQL queries;
- Combine multiple SPARQL endpoints;
- Configure “projects” to subset data.

### 4.1 Configuring the web interface

Before the web interface can be started, a few parameters have to be configured. This is done through an XML file. The following example displays all options, except for the authentication part, which is discussed separately in section 4.1.3 ‘Authentication’.

```
<?xml version="1.0" encoding="utf-8"?>
<web-interface>
  <fork>0</fork>
  <bind-address>127.0.0.1</bind-address>
  <port>8080</port>
  <authentication>
    <!-- Either LDAP settings, or single-user authentication -->
  </authentication>
</web-interface>
```

#### 4.1.1 To fork or not to fork

The fork property can be either 0 to keep the sg-web process in the foreground of your shell, or 1 to run the sg-web process as a daemon.

#### 4.1.2 Bind address and port

Because web services are popular these days, sg-web can be configured to bind on an arbitrary address and an arbitrary port.

#### 4.1.3 Authentication

There are two ways to configure authentication. For single-user deployments or environments that lack an LDAP service, a preconfigured username and password can be set. For a multi-user deployment, the web interface can be configured to use an LDAP server.

### Single-user configuration

The simplest form of authentication is the “single-user configuration”. Make sure the configuration file is only readable by yourself, as the credentials are stored in plain text. The following example shows how to configure “single-user authentication”:

```
<?xml version="1.0" encoding="utf-8"?>
<web-interface>
  ...
  <authentication>
    <single-user>
      <username>user</username>
      <password>test</password>
    </single-user>
  </authentication>
</web-interface>
```

### LDAP authentication example

To configure LDAP, three parameters must be specified: the URI to the LDAP service (1), the “organizational unit” (2), and the “domain” (3). The username is used as the “common name”.

The following example shows how to configure LDAP authentication:

```
<?xml version="1.0" encoding="utf-8"?>
<web-interface>
  ...
  <authentication>
    <ldap>
      <uri>ldap://example.local</uri>
      <organizational-unit>People</organizational-unit>
      <domain>department.organization.tld</domain>
    </ldap>
  </authentication>
</web-interface>
```

## 4.2 Running the web interface

The web interface can be started using the `sg-web` command:

```
sg-web --configuration-file=file.xml
```

... where `file.xml` is a configuration file as discussed in section 4.1 ‘Configuring the web interface’.

## 4.3 Configuring connections

The first useful step is to configure a connection to a SPARQL endpoint.

When providing a username and password for a connection, it will attempt to connect using *digest authentication*.



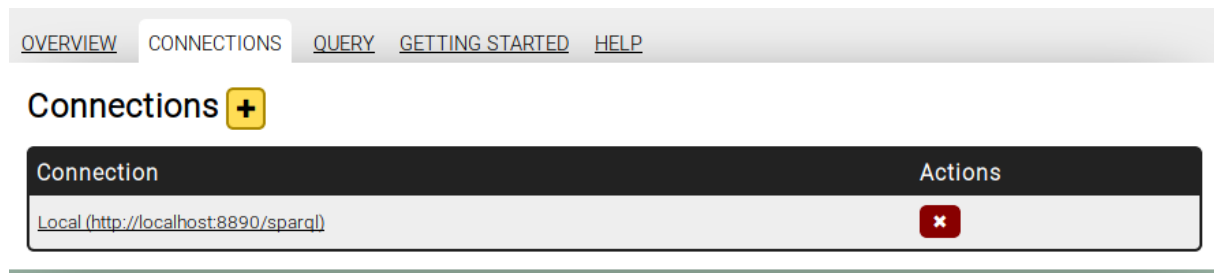


Figure 4.1: The *connections* page enables users to configure accessible SPARQL endpoints. Adding a connection here will provide an option to query it on the *query* page.

## 4.4 Managing projects

When interacting with large datasets, it may be useful to confine queries to a subset of the dataset. On the *projects* page, subsets can be made based on *sample names*. These sample names are automatically extracted from VCF files, and can also be extracted from tabular data.

Marking a project as “active” indicates that queries executed using the web interface relate to that project. See also section 4.5.1 ‘Query history’.

## 4.5 Executing queries

After configuring at least one endpoint, it can be chosen on the *query* page to execute a query against it.

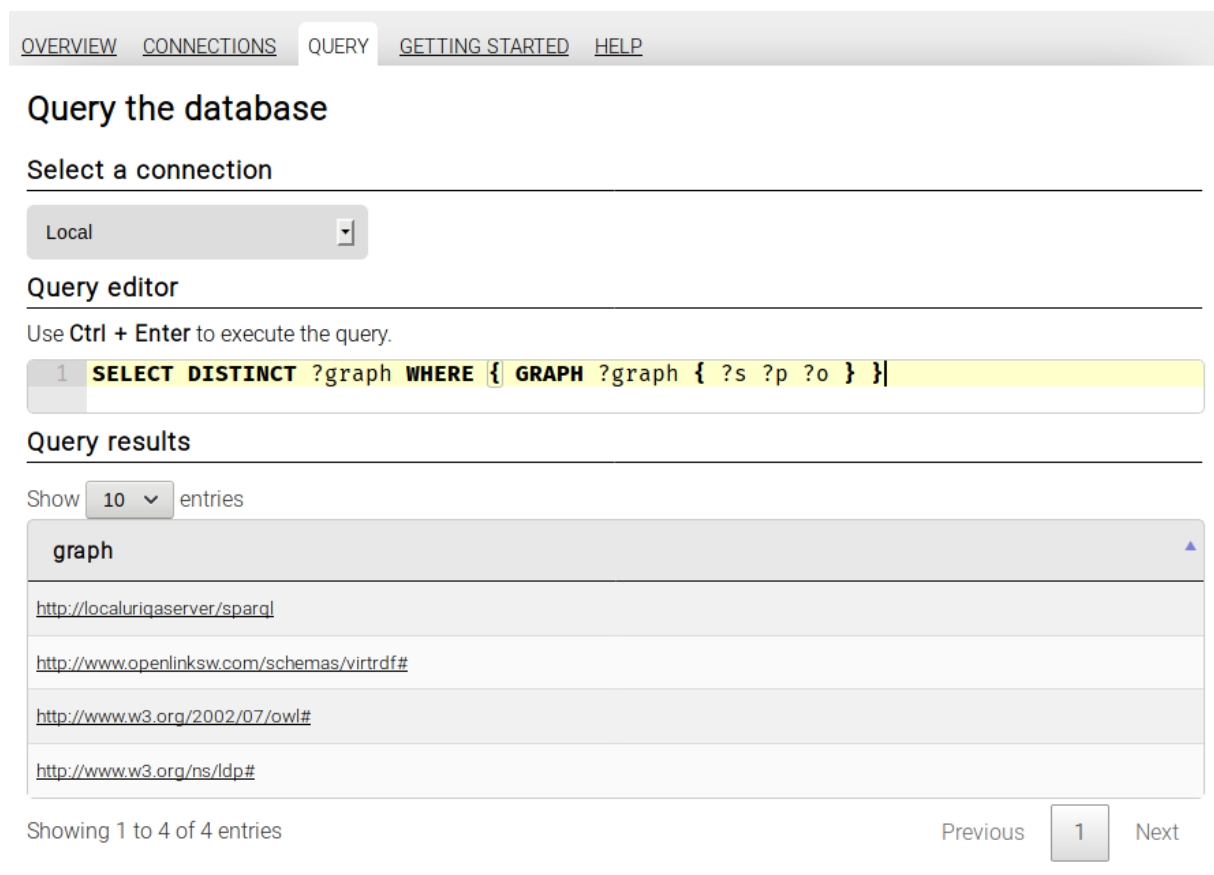


Figure 4.2: The *query* page enables users to execute a query against a SPARQL endpoint. The connections configured at the *connections* page can be chosen from the drop-down menu.

### 4.5.1 Query history

When prototyping SPARQL queries, better known as “SPARQLing around”, it’s good to know that all queries that yielded a result are stored in the *query history*. The history is shown on the *query* page below the query editor.

Each *project* has its own query history, and newly executed queries are added to the current *active* project.

## Chapter 5

# Information retrieval with SPARQL

In section 3.1 ‘Preparing variant call data with `vcf2rdf`’ we discussed how to extract triples from common data formats. In section 3.4 ‘Importing data with `curl`’ we discussed how we could insert those triples into a SPARQL endpoint.

In this section, we will start exploring the inserted data by using a query language called *SPARQL*. Understanding SPARQL will be crucial for the integration in your own programs or scripts — something we will discuss in chapter 6 ‘Using SPARQL with other programming languages’.

The queries in the remainder of this chapter can be readily copy/pasted into the query editor of the web interface (see chapter 4 ‘Web interface’).

### 5.1 Local querying

When we request information from a SPARQL endpoint, we are performing a *local query* because we request data from a single place. In our case, that is most likely to be our own SPARQL endpoint.

In contrast to *local querying*, we can also query multiple SPARQL endpoints in one go, to combine the information from multiple locations. Combining information from multiple SPARQL endpoints is called *federated querying*.

Federated querying is discussed in section 5.2 ‘Federated querying’.

#### 5.1.1 Listing non-empty graphs

Each SPARQL endpoint can host multiple *graphs*. Each graph can contain an independent set of triples. The following query displays the available non-empty graphs in a SPARQL endpoint:

```
SELECT DISTINCT ?graph WHERE { GRAPH ?graph { ?s ?p ?o } }
```

Which may yield the following table:

graph
http://example
http://localuriquaserver/sparql
http://www.openlinksw.com/schemas/virttrdf#
http://www.w3.org/2002/07/owl#
http://www.w3.org/ns/ldp#

Table 5.1: Results of the query to list non-empty graphs.

The graph names usually look like URLs, like we would encounter them on the web. In fact, not only graph names, but any node that has a symbolic meaning, rather than a literal<sup>1</sup> meaning is usually written as a URL. We can go to such a URL with a web browser and might even find more information.

### 5.1.2 Querying a specific graph

The sooner we can reduce the dataset to query over, the faster the query will return with an answer. One easy way to reduce the size of the dataset is to be specific about which graph to query. This can be achieved using the FROM clause in the query.

```
SELECT ?s ?p ?o
FROM <graph-name>
WHERE { ?s ?p ?o }
```

The graph-name must be one of the graphs returned by the query from section 5.1.1 ‘Listing non-empty graphs’.

Without the FROM clause, the RDF store will search in all graphs. We can repeat the FROM clause to query over multiple graphs in the same RDF store.

```
SELECT ?s ?p ?o
FROM <graph-name>
FROM <another-graph-name>
WHERE { ?s ?p ?o }
```

In section 5.2 ‘Federated querying’ we will look at querying over multiple RDF stores.

### 5.1.3 Exploring the structure of knowledge in a graph

Inside the WHERE clause of a SPARQL query we specify a graph pattern. When the information in a graph is structured, there are only few predicates in comparison to the number of subjects and the number of objects.

```
SELECT COUNT(DISTINCT ?s) AS ?subjects
      COUNT(DISTINCT ?p) AS ?predicates
      COUNT(DISTINCT ?o) AS ?objects
FROM <http://example>
WHERE { ?s ?p ?o }
```

<sup>1</sup>Examples of literals are numbers and strings. Symbols are nodes that don’t have a literal value.

On a typical graph with data originating from vcf2rdf, this may yield the following table:

subjects	predicates	objects
3011691	229	4000809

Table 5.2: Results of the query to count the number of subjects, predicates, and objects in a graph.

Therefore, one useful method of finding out which patterns exist in a graph is to look for predicates:

```
SELECT DISTINCT ?predicate
FROM <http://example>
WHERE {
    ?subject ?predicate ?object .
}
```

Which may yield the following table:

predicate
http://biohackathon.org/resource/faldo#position
http://biohackathon.org/resource/faldo#reference
http://sparqling-genomics/vcf2rdf/filename
http://sparqling-genomics/vcf2rdf/foundIn
http://sparqling-genomics/vcf2rdf/sample
http://sparqling-genomics/vcf2rdf/VariantCall/ALT
http://sparqling-genomics/vcf2rdf/VariantCall/FILTER
...

Table 5.3: Results of the query to list predicates.

#### 5.1.4 Listing samples and their originating files

Using the knowledge we gained from exploring the predicates in a graph, we can construct more insightful queries, like finding the names of the samples and their originating filenames from the output of vcf2rdf:

```
PREFIX vcf2rdf: <http://sparqling-genomics/vcf2rdf/>

SELECT DISTINCT STRAFTER(STR(?sample), "Sample/") AS ?sample ?filename
FROM <graph-name>
WHERE {
    ?variant vcf2rdf:sample ?sample .
    ?sample vcf2rdf:foundIn ?origin .
    ?origin vcf2rdf:filename ?filename .
}
```

Which may yield the following table:

sample	filename
REF0047	/data/examples/TUMOR_REF0047.annotated.vcf.gz
TUMOR0047	/data/examples/TUMOR_REF0047.annotated.vcf.gz
...	...

Table 5.4: Results of the query to list samples and their originating filenames.

Notice how most predicates for `vcf2rdf` in table 5.3 start with `http://sparqling-genomics/vcf2rdf/`. In the above query, we used this to shorten the query. We started the query by writing a PREFIX rule for `http://sparqling-genomics/vcf2rdf/`, which we called `vcf2rdf:`. This means that whenever we write `vcf2rdf:F00`, the SPARQL endpoint interprets it as if we would write `<http://sparqling-genomics/vcf2rdf/F00>`.

We will use more prefixes in the upcoming queries. We can look up prefixes for common ontologies using <http://prefix.cc>.

### 5.1.5 Listing samples, originated files, and number of variants

Building on the previous query, and by exploring the predicates of a `vcf2rdf:VariantCall`, we can construct the following query to include the number of variants for each sample, in each file.

```
PREFIX vcf2rdf: <http://sparqling-genomics/vcf2rdf/>
PREFIX rdf:    <http://www.w3.org/1999/02/22-rdf-syntax-ns#>

SELECT DISTINCT STRAFTER(STR(?sample), "Sample/") AS ?sample
               ?filename
               COUNT(DISTINCT ?variant) AS ?numberOfVariants

FROM <graph-name>
WHERE
{
    ?variant    rdf:type                vcf2rdf:VariantCall ;
                vcf2rdf:sample          ?sample ;
                vcf2rdf:originatedFrom  ?origin .

    ?origin     vcf2rdf:filename        ?filename .
}
```

Which may yield the following table:

sample	filename	numberOfVariants
REF0047	/data/examples/TUMOR_REF0047.annotated.vcf.gz	1505712
TUMOR0047	/data/examples/TUMOR_REF0047.annotated.vcf.gz	1505712
...	...	...

Table 5.5: Results of the query to list samples, their originated filenames, and the number of variant calls for each sample in a file.

By using `COUNT`, we can get the `DISTINCT` number of matching patterns for a variant call for a sample, originating from a distinct file.

### 5.1.6 Retrieving all variants

When retrieving potentially large amounts of data, the LIMIT clause may come in handy to prototype a query until we are sure enough that the query answers the actual question we would like to answer.

In the next example query, we will retrieve the sample name, chromosome, position, and the corresponding VCF FILTER field(s) from the database.

```
PREFIX vcf2rdf: <http://sparqling-genomics/vcf2rdf/>
PREFIX vc:      <http://sparqling-genomics/vcf2rdf/VariantCall/>
PREFIX rdf:     <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX faldo:   <http://biohackathon.org/resource/faldo#>

SELECT DISTINCT ?variant ?sample ?chromosome ?position ?filter
FROM <graph-name>
WHERE
{
    ?variant    rdf:type                vcf2rdf:VariantCall ;
                vcf2rdf:sample          ?sample ;
                faldo:reference          ?chromosome ;
                faldo:position           ?position ;
                vc:FILTER                 ?filter .
}
LIMIT 100
```

By limiting the result set to the first 100 rows, the query will return with an answer rather quickly. Had we not set a limit to the number of rows, the query could have returned possibly a few million rows, which would obviously take longer to process.

### 5.1.7 Retrieving variants with a specific mutation

Any property can be used to subset the results. For example, we can look for occurrences of a C to T mutation in the positional range 202950000 to 202960000 on chromosome 2, according to the *GRCh37* (*hg19*) reference genome with the following query:

```
PREFIX rdf:      <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs:     <http://www.w3.org/2000/01/rdf-schema#>
PREFIX faldo:    <http://biohackathon.org/resource/faldo#>
PREFIX hg19:     <http://rdf.biosemantics.org/data/genomeassemblies/hg19#>
PREFIX v:        <http://sparqling-genomics/vcf2rdf/>
PREFIX vc:       <http://sparqling-genomics/vcf2rdf/VariantCall/>
PREFIX seq:      <http://sparqling-genomics/vcf2rdf/Sequence/>

SELECT COUNT(DISTINCT ?variant) AS ?occurrences ?sample
FROM <http://example>
WHERE {
    ?variant    rdf:type                v:VariantCall .
    ?variant    rdf:type                ?genotype .
    ?variant    v:sample                ?sample .
    ?variant    vc:REF                   seq:C .
    ?variant    vc:ALT                   seq:T .
    ?variant    faldo:reference          hg19:chr2 .
}
```

```

?variant faldo:position ?position .

FILTER (?position >= 202950000)
FILTER (?position <= 202960000)

# Exclude variants that actually do not deviate from hg19.
FILTER (?genotype != v:HomozygousReferenceGenotype)
}
LIMIT 2

```

Which may yield the following table:

occurrences	sample
5	<a href="http://sparqling-genomics/vcf2rdf/Sample/REF0047">http://sparqling-genomics/vcf2rdf/Sample/REF0047</a>
5	<a href="http://sparqling-genomics/vcf2rdf/Sample/TUMOR0047">http://sparqling-genomics/vcf2rdf/Sample/TUMOR0047</a>

Table 5.6: Query results of the above query.

### 5.1.8 Comparing two datasets on specific properties

Suppose we run variant calling on the same sample with slightly different analysis programs. We expect a large overlap in variants between the datasets, and would like to view the few variants that differ in each dataset.

We imported each dataset in a separate graph (<http://comparison/aaa> and <http://comparison/bbb>).

The properties we are going to compare are the predicates `faldo:reference`, `faldo:position`, `vc:REF`, and `vc:ALT`.

The query below displays how each variant in <http://comparison/aaa> can be compared to a matching variant in <http://comparison/bbb>. Only those variants in <http://comparison/aaa> that **do not** have an equivalent variant in <http://comparison/bbb> will be returned by the SPARQL endpoint.

```

PREFIX rdf:      <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX faldo:    <http://biohackathon.org/resource/faldo#>
PREFIX vcf2rdf:  <http://sparqling-genomics/vcf2rdf/>
PREFIX vc:       <http://sparqling-genomics/vcf2rdf/VariantCall/>

SELECT DISTINCT
  STRAFTER(STR(?chromosome), "hg19#") AS ?chromosome
  ?position
  STRAFTER(STR(?reference), "Sequence/") AS ?reference
  STRAFTER(STR(?alternative), "Sequence/") AS ?alternative
  STRAFTER(STR(?filter), "vcf2rdf/") AS ?filter
WHERE
{
  GRAPH <http://comparison/aaa>
  {
    ?aaa_variant  rdf:type          vcf2rdf:VariantCall ;
                  vc:REF            ?reference ;
                  vc:ALT            ?alternative ;
                  vc:FILTER         ?filter ;

```



```

        faldo:reference    ?chromosome ;
        faldo:position     ?position .
    }

    MINUS
    {
        GRAPH <http://comparison/bbb>
        {
            ?variant    rdf:type          vcf2rdf:VariantCall ;
                        vc:REF            ?reference ;
                        vc:ALT            ?alternative ;
                        faldo:reference    ?chromosome ;
                        faldo:position     ?position .
        }
    }
}

```

So the MINUS construct in SPARQL can be used to filter overlapping information between multiple graphs.

This query demonstrates how a fine-grained “diff” can be constructed between two datasets.

## 5.2 Federated querying

Now that we’ve seen local queries, there’s only one more construct we need to know to combine this with remote SPARQL endpoints: the SERVICE construct.

For the next example, we will use the [public SPARQL endpoint hosted by EBI](#).

### 5.2.1 Get an overview of Biomodels (from ENSEMBL)

```

PREFIX sbmlrdf: <http://identifiers.org/biomodels.vocabulary#>
PREFIX sbmlldb: <http://identifiers.org/biomodels.db/>

SELECT ?speciesId ?name {
    SERVICE <http://www.ebi.ac.uk/rdf/services/sparql/> {
        sbmlldb:BIOMD0000000001 sbmlrdf:species ?speciesId .
        ?speciesId sbmlrdf:name ?name
    }
}

```

Which may yield the following table:

speciesId	name
<a href="http://identifiers.org/biomodels.db/BIOMD0000000001#_000003">http://identifiers.org/biomodels.db/BIOMD0000000001#_000003</a>	BasalACh2
<a href="http://identifiers.org/biomodels.db/BIOMD0000000001#_000004">http://identifiers.org/biomodels.db/BIOMD0000000001#_000004</a>	IntermediateACh
<a href="http://identifiers.org/biomodels.db/BIOMD0000000001#_000005">http://identifiers.org/biomodels.db/BIOMD0000000001#_000005</a>	ActiveACh
<a href="http://identifiers.org/biomodels.db/BIOMD0000000001#_000006">http://identifiers.org/biomodels.db/BIOMD0000000001#_000006</a>	Active
<a href="http://identifiers.org/biomodels.db/BIOMD0000000001#_000007">http://identifiers.org/biomodels.db/BIOMD0000000001#_000007</a>	BasalACh
...	...

Table 5.7: Query results of the above query.

## Chapter 6

# Using SPARQL with other programming languages

### 6.1 Using SPARQL with R

Before we can start, we need to install the SPARQL package from [CRAN](#).

```
install.packages("SPARQL")
```

Once the package is installed, we can load it:

```
library("SPARQL")
```

Let's define where to send the query to:

```
endpoint <- "http://localhost:8890/sparql"
```

... and the query itself:

```
query <- "PREFIX vcf2rdf: <http://sparqling-genomics/vcf2rdf/>
PREFIX vc:      <http://sparqling-genomics/vcf2rdf/VariantCall/>
PREFIX rdf:     <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX faldo:   <http://biohackathon.org/resource/faldo#>

SELECT DISTINCT ?variant ?sample ?chromosome ?position ?filter
FROM <graph-name>
WHERE
{
    ?variant    rdf:type                vcf2rdf:VariantCall ;
                vcf2rdf:sample          ?sample ;
                faldo:reference          ?chromosome ;
                faldo:position          ?position ;
                vc:FILTER                ?filter .
}
LIMIT 10";
```

To actually execute the query, we can use the SPARQL function:

```
query_data <- SPARQL (endpoint, query)
```

If the query execution went fine, we can gather the resulting dataframe from the `results` index.

```
query_results <- query_data$results
```

### 6.1.1 Querying with authentication

When the SPARQL endpoint we try to reach requires authentication before it accepts a query, we can use the `curl_args` parameter of the `SPARQL` function.

In the following example, we use `dba` as username, and `secret-password` as password.

```
endpoint      <- "http://localhost:8890/sparql-auth"
auth_options  <- curlOptions(userpwd="dba:secret-password")
query         <- "SELECT DISTINCT ?p WHERE { ?s ?p ?o }"
query_data    <- SPARQL (endpoint, query, curl_args=auth_options)
results       <- query_data$results
```

## 6.2 Using SPARQL with GNU Guile

For Schemers using GNU Guile, the [guile-sparql](https://github.com/roelj/guile-sparql)<sup>1</sup> package provides a SPARQL interface.

The package provides a `driver` module that communicates with the SPARQL endpoint, a `lang` module to construct SPARQL queries using S-expressions, and a `util` module containing convenience functions.

After installation, the modules can be loaded using:

```
(use-modules (sparql driver)
             (sparql lang)
             (sparql util))
```

Using the `sparql-query` function, we can execute a query:

```
(let ((endpoint      "http://localhost:8890/sparql-auth")
      (authentication "dba:secret-password")
      (query         "SELECT DISTINCT ?p WHERE { ?s ?p ?o }"))
  (display-query-results-of
   (sparql-query query
                  #:uri      endpoint
                  #:digest authentication)))
```

<sup>1</sup><https://github.com/roelj/guile-sparql>