Rare Disease Ontology & Search Tool: Demonstration and Discussion

John Bellamy

Indiana University

Agenda:

- Part I: A discussion of the problem and an exploration of the steps completed to arrive at final model and tool.
- Part II: A demonstration of the Rare Disease Ontology and
 Search Tool.
- Part III: Closing remarks.
- Conclusion.

Introduction:

- As highlighted in the report *Improving Rare Disease Information Retrieval with Semantic Web Technology* this tool is built on keywords that appear frequently in two datasets.
- An ontology was created to improve information retrieval,
 through semantic reasoning.
- An ontology and model were then persisted and stored for serving in a Fuseki Sparql endpoint.

- Part I: A discussion of the problem and an exploration of the steps completed to arrive at final model and tool.
- PubMed does a great job of indexing articles, in order to improve article retrieval, but doesn't index all or even most articles about rare diseases. Furthermore, many medical research databases do not index rare diseases at all, thus one is left to search only by disease name or title.
- Can we beat PubMed's results using just the "title" field?

About the data:

Accessing http://www.ncbi.nlm.nih.gov/pubmed/ (PubMed) I searched for common names for two rare diseases: Hunter's

Syndrome and Spinal Bulbar Muscular Atrophy. The results were then combined into two datasets, one for each disease.

- Cluster analysis was then performed on the two datasets in Python. The most popular terms (disease names) were taken out to discover the other terms (pathophysiological) that make up the rest of the results.
- Finally, once a set of significant keywords were obtained for both datasets, *one* keyword/phrase was assigned as a tuple and the output further analyzed in Jena. A keyword was found for 72% of SBMA articles (545) and 71% of Hunter's Syndrome articles.

Protege/Jena

Using Protege, I developed an ontology for both datasets.
The ontologies were mostly identical, except the URI's and

named instances (keywords) were different so that when the two datasets were combined, two prefixes could be used to query. Disease names and pathophysiological terms that referred to the same thing were assigned owl:sameAs.

Once I had the datasets and ontologies, I used the great library CSVReader to parse the files into .rdf format, in cooperation with Jena. The two datasets were then reasoned separately and output as .ttl files.

Model Persistence

Finally, the two .ttl files were combined and stored in a Jena TDB database, and the combined model output as a single .ttl file.

The TDB database and the output file were then loaded into a Fuseki Server.

Part II: A demonstration of the Rare Disease Ontology and Search Tool.

- The demo follows after the model has been created. Because the database alone is 128MB, and because you must include Fuseki, I recommend you use an IDE. I used the latest version of Fuseki and Jena 3.0.1. If you load the .jar file as it stands now, you will need to follow directions in the package's "readme."
- > The demo will follow from the creation of the model, which generates everything needed in the fuseki folder.

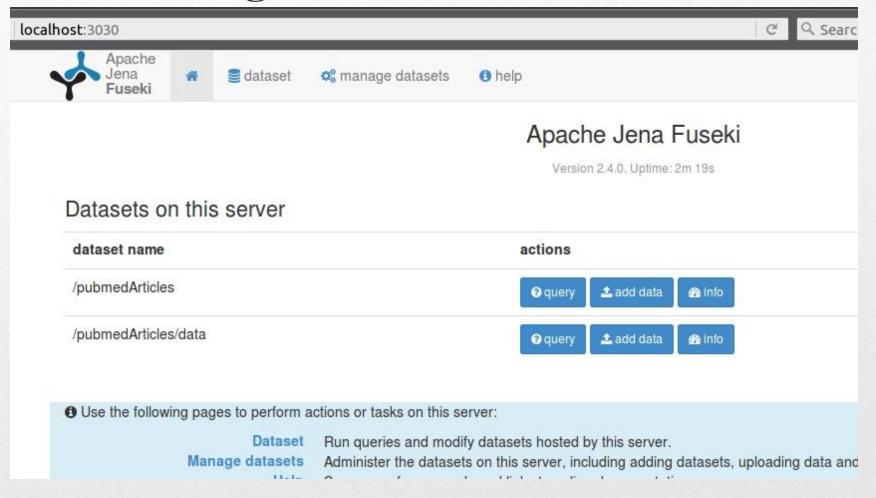
Navigate to fuseki folder:

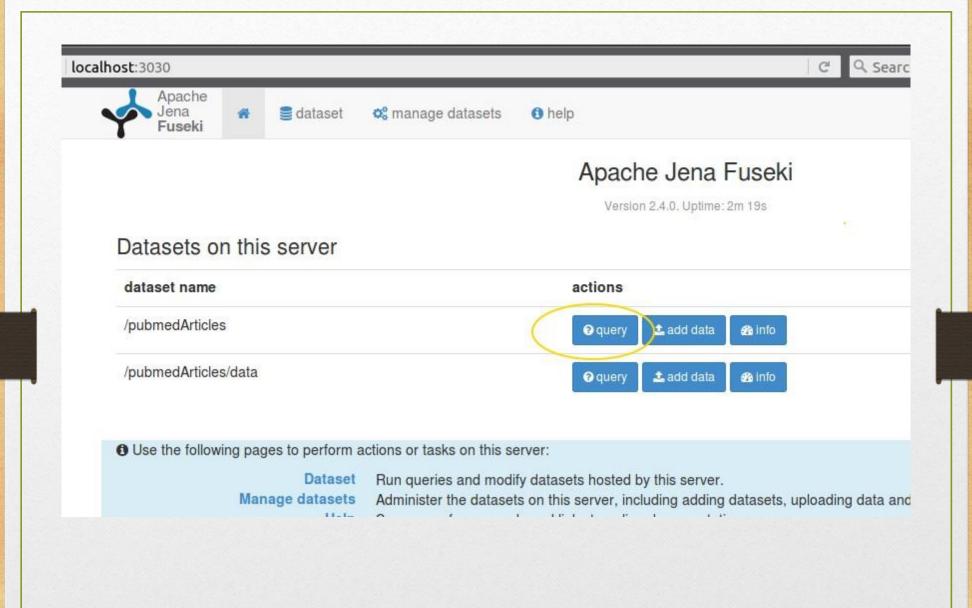
```
john@johnny-pi: ~/fuseki
File Edit View Search Terminal Help
john@johnny-pi:~$ cd fuseki
john@johnny-pi:~/fuseki$ ls
assembler.ttl data
                                 fuseki-server.jar
                                                    Lucene
                                                                      tdb.ttl
                                 fuseki.war
                                                    newAssembler.ttl
                                                                      webapp
ootstrap.sh) fuseki
                                 huntMS.ttl
                                                    NOTICE
                                 javaAssembler.ttl oneClickLoad.ttl
              fuseki-server
confly.ttl
configuration fuseki-server.bat LICENSE
                                                    run
john@johnny-pi:~/fuseki$
```

Launching Fuseki

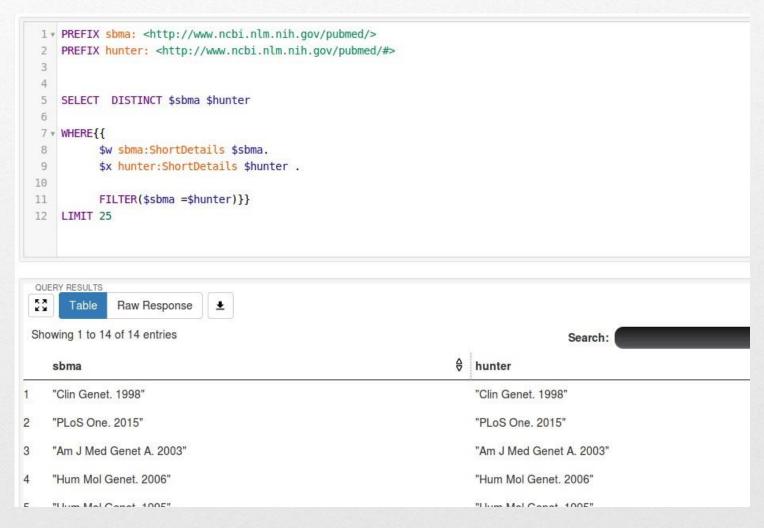
```
iohn@johnny-pi: ~/workspace/Java/SemanticsFinal/fuseki
 File Edit View Search Terminal Help
                                  fuseki.war
                                                     newAssembler.ttl webapp
bin
               DB
bootstrap.sh
               fuseki
                                  huntMS.ttl
                                                     NOTICE
config.ttl
                                  javaAssembler.ttl oneClickLoad.ttl
               fuseki-server
configuration fuseki-server.bat LICENSE
                                                     run
john@johnny-pi:~/workspace/Java/SemanticsFinal/fuseki$ bash bootstrap.sh
[2016-07-15 13:05:58] Server
                                 INFO Running in read-only mode for /pubmedArti
cles/data
[2016-07-15 13:05:58] Server
                                 INFO Fuseki 2.4.0
                                 INFO FUSEKI HOME=/home/john/workspace/Java/Sem
[2016-07-15 13:05:58] Config
anticsFinal/fuseki
[2016-07-15 13:05:58] Config
                                 INFO FUSEKI BASE=/home/john/workspace/Java/Sem
anticsFinal/fuseki/run
[2016-07-15 13:05:58] Servlet
                                 INFO Initializing Shiro environment
                                 INFO Shiro file: file:///home/john/workspace/J
[2016-07-15 13:05:58] Config
ava/SemanticsFinal/fuseki/run/shiro.ini
[2016-07-15 13:05:58] Config
                                 INFO Template file: templates/config-tdb-dir
[2016-07-15 13:05:58] Config
                                 INFO TDB dataset: directory=DB
                                 INFO Load configuration: file:///home/john/wor
[2016-07-15 13:05:59] Config
kspace/Java/SemanticsFinal/fuseki/run/confiquration/huntMS.ttl
[2016-07-15 13:05:59] Config
                                 INFO Register: /pubmedArticles/data
[2016-07-15 13:05:59] Config
                                 INFO Register: /pubmedArticles
[2016-07-15 13:05:59] Server
                                 INFO Started 2016/07/15 13:05:59 MST on port 3
030
```

Navigate to localhost:3030





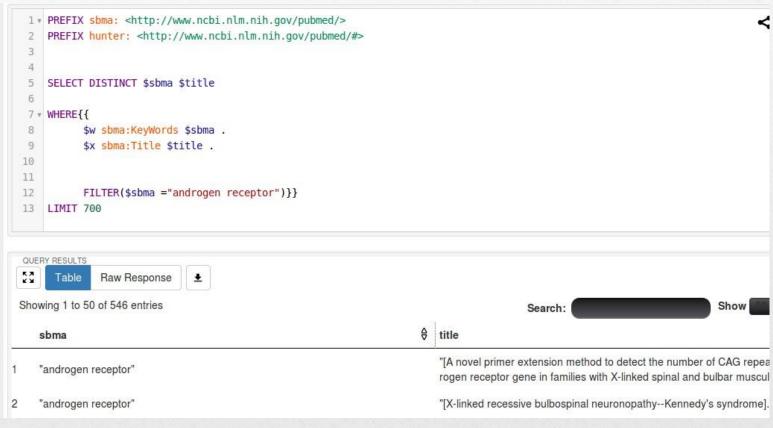
What publishers do the two rare diseases have in common?



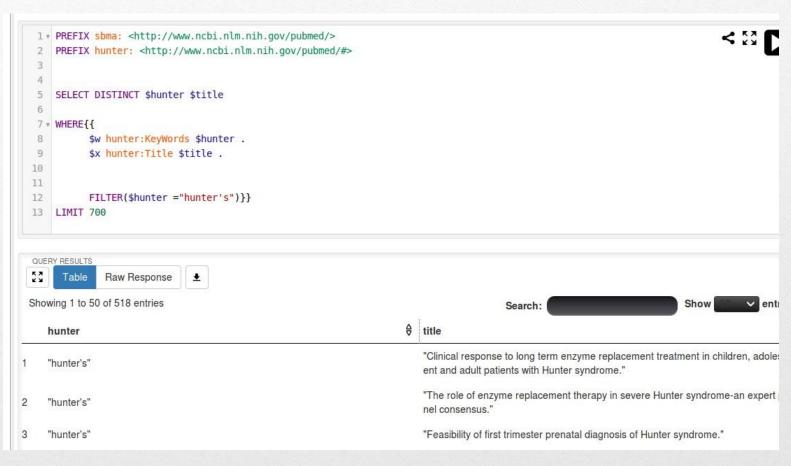
What articles mention both diseases?

- > None :(
- > Surprising, because these are both x-linked (affecting mostly the genes in males). These diseases also affect a similar number of males.

How many articles can we return with just the keywords appearing in the title?



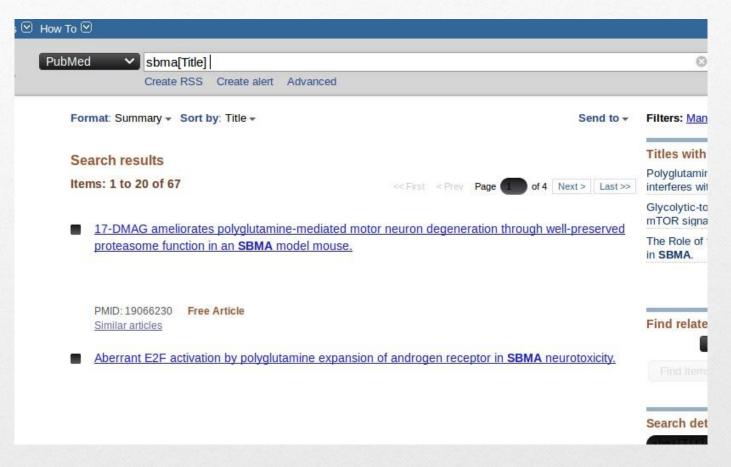
How many articles can we return using just the disease name?



Part III: Closing Remarks

- While I expected the results with the disease name keyword, I was really surprised that the reasoner figured out the non-disease keywords were also related to the disease names. The result: for SBMA, "androgen receptor gene," "androgen receptor cag" and other similar terms were replaced by "androgen receptor." And this single term can return ALL of the articles loaded relating to SBMA. Awesome...
 - What about searching disease names? As we see searching for "hunter's" (I chose Hunter's rather than Hunter's disease or Hunter's syndrome, because we see both.), searching by one of the popular names for the disease returns all of the results. Not 40% or so, as expected. How does this compare to PubMed?

PubMed



Rare Disease Ontology & Search Tool:

```
1 * PREFIX sbma: <http://www.ncbi.nlm.nih.gov/pubmed/>
     PREFIX hunter: <a href="http://www.ncbi.nlm.nih.gov/pubmed/#>">http://www.ncbi.nlm.nih.gov/pubmed/#>">
     SELECT DISTINCT $sbma $title
 7 * WHERE{{
             $w sbma:KeyWords $sbma .
             $x sbma:Title $title .
10
11
12
             FILTER($sbma ="sbma")}}
     LIMIT 700
QUERY RESULTS
                Raw Response
       Table
Showing 1 to 50 of 546 entries
                                                                                                         Search:
                                                                                      title
    sbma
                                                                                       "[A novel primer extension method to detect the numb
    "sbma"
                                                                                       rogen receptor gene in families with X-linked spinal an
    "sbma"
                                                                                       "[X-linked recessive bulbospinal neuronopathy--Kenne
                                                                                       "Testosterone treatment fails to accelerate disease in
    "sbma"
                                                                                       spinal and bulbar muscular atrophy."
```

Remarks:

- The SBMA dataset had many more pathophysiological terms to describe it than the Hunter dataset. Therefore, there was more processing at the reasoner level; i.e. many pathophysiological declared owl:samesAs. Through reasoning, three of them disappeared; the variations on "androgen receptor."
 - For Hunter's "lyosomal storage" disappeared, leaving 10/11 terms. It is interesting to note that the only "owl:sameAs" in this model, were the various disease names.

Conclusion

While the model still needs some fine-tuning, it is abundantly clear that semantic web technology and Jena reasoning delivers a very powerful database that outperforms traditional information retrieval methods based on disease names and indexing.