

Applications of the YarcData Urika in Drug Discovery and Healthcare

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Contents

- Motivation and Introduction
- Use Case
- Hardware and Software
- Methodology and Results
- Conclusion



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Acknowledgements

- Jim Maltby and Matt Gianni at YarcData
- Mario Vale at CSCS



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Motivation and Introduction

- I am not a Urika or Semantic Web expert
- Learn more about the Urika
 - Other than marketing material
 - How can the machine be used
- Great partners
 - CCRG for a use case
 - YarcData and CSCS for testing



Motivation and Introduction

- Forget all about writing your own programs and get used to formulating your questions in SPARQL
- Data must be available in RDF triple form
- This is not a relational database, joins are not a problem
- Think of the Urika as an accelerator for SPARQL



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Motivation and Introduction

- Semantic Web technologies
 - RDF
 - SPARQL
 - RDFS and OWL



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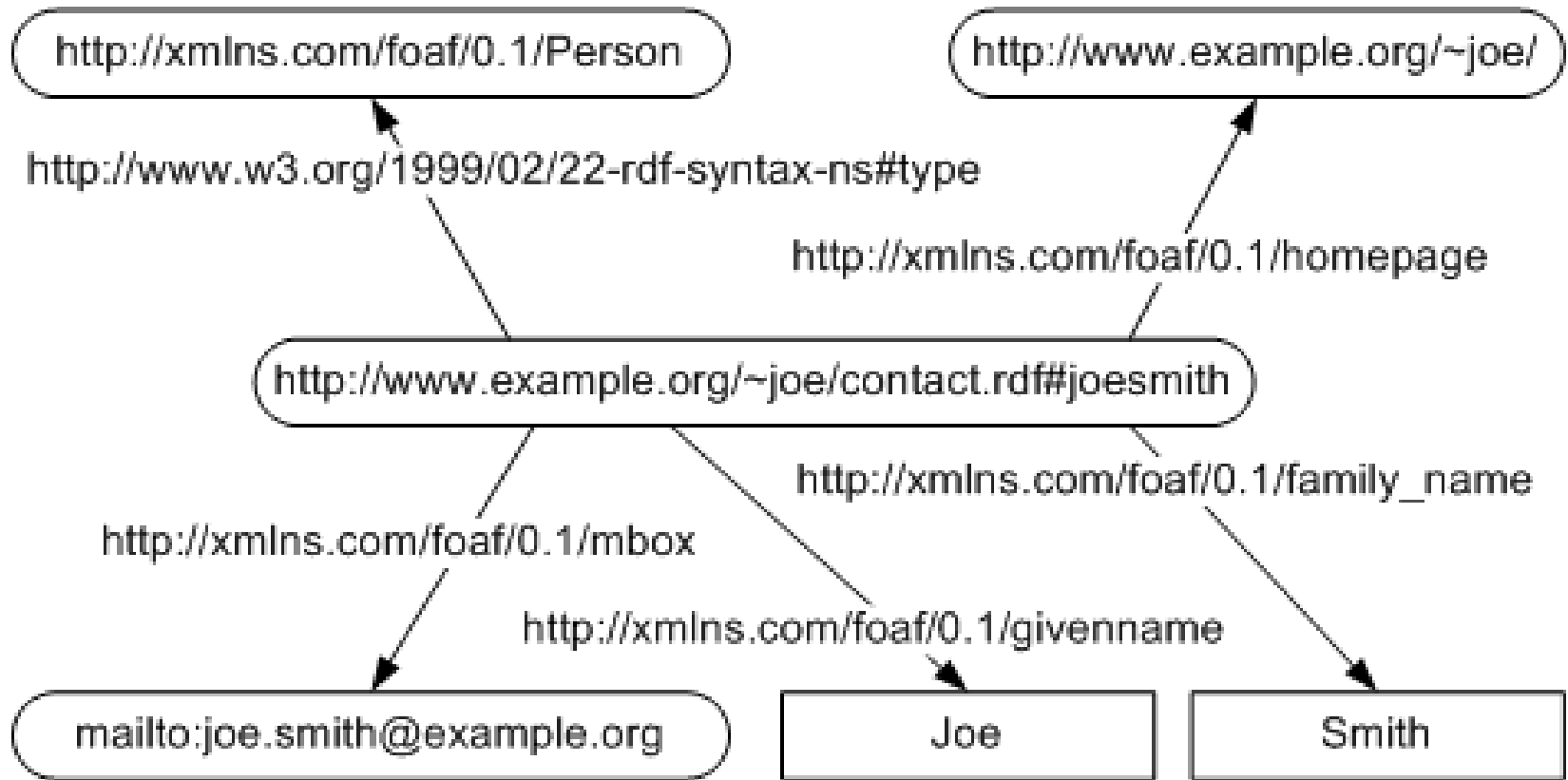


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RDF



(<http://www.example.org/~joe/contact.rdf#joesmith>,
http://xmlns.com/foaf/0.1/family_name, "Smith")



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SPARQL

Query:

```
PREFIX foaf: <http://xmlns.com/foaf/0.1/>
SELECT *
WHERE {
    ?person foaf:family_name ?name .
}
```

Result:

```
http://www.example.org/~joe/contact.rdf#joesmith Smith
```



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Use Case

- Drug – Drug interaction and side effects
- Chem2Bio2RDF
- Using public data sets



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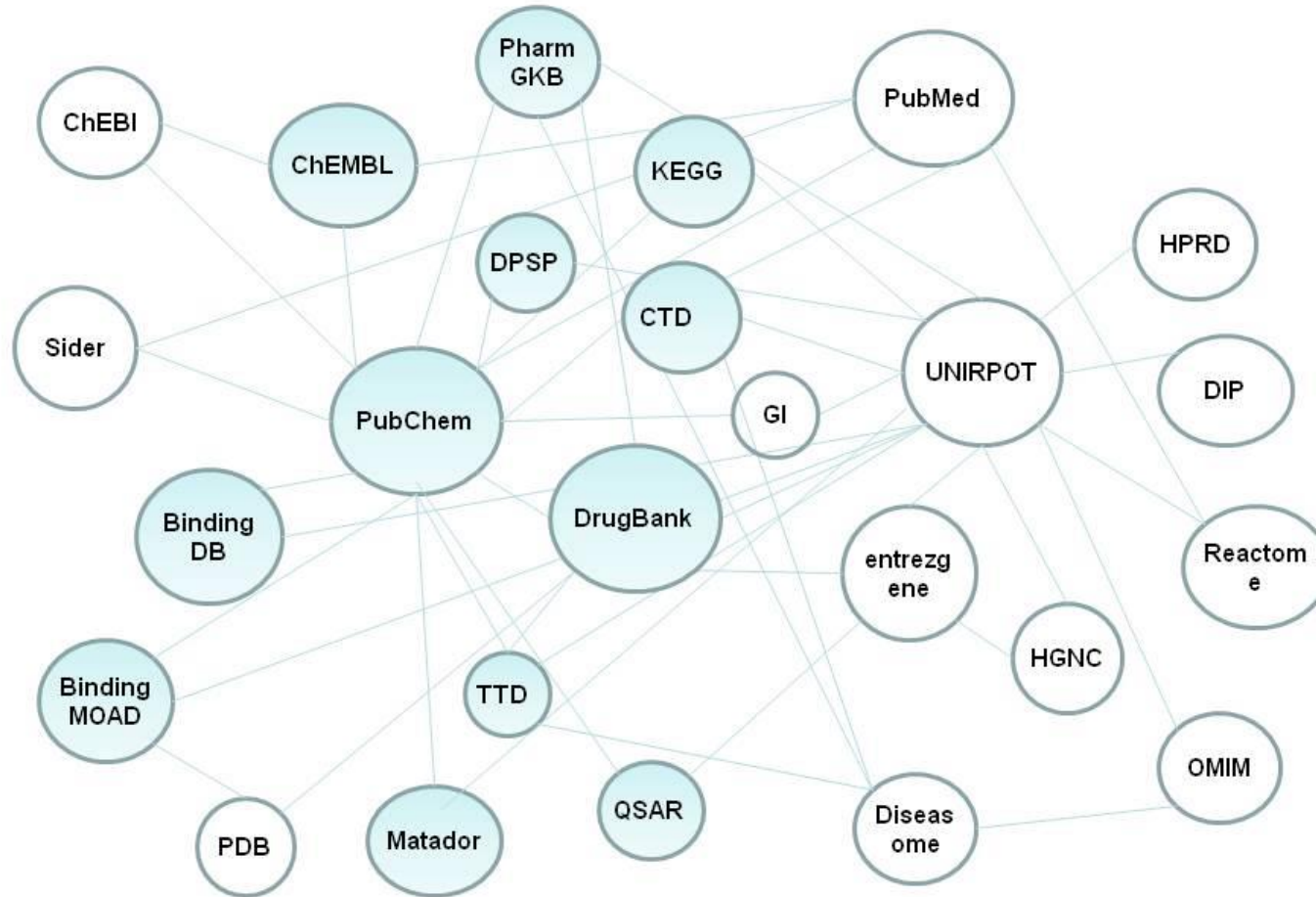


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Chem2Bio2RDF Data Set



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Example SPARQL Query

```
PREFIX sider:<http://chem2bio2rdf.org/sider/resource/>
SELECT * FROM <http://chem2bio2rdf.org/sider>
WHERE
{
?sider sider:drug_name ?drug_name .
FILTER
regex(?drug_name,"Fenofibrate|Aspirin|Rosuvastatin|Levot
hyroxine|Valsartan","i" ).
?sider sider:side_effect ?side_effect .
}
```



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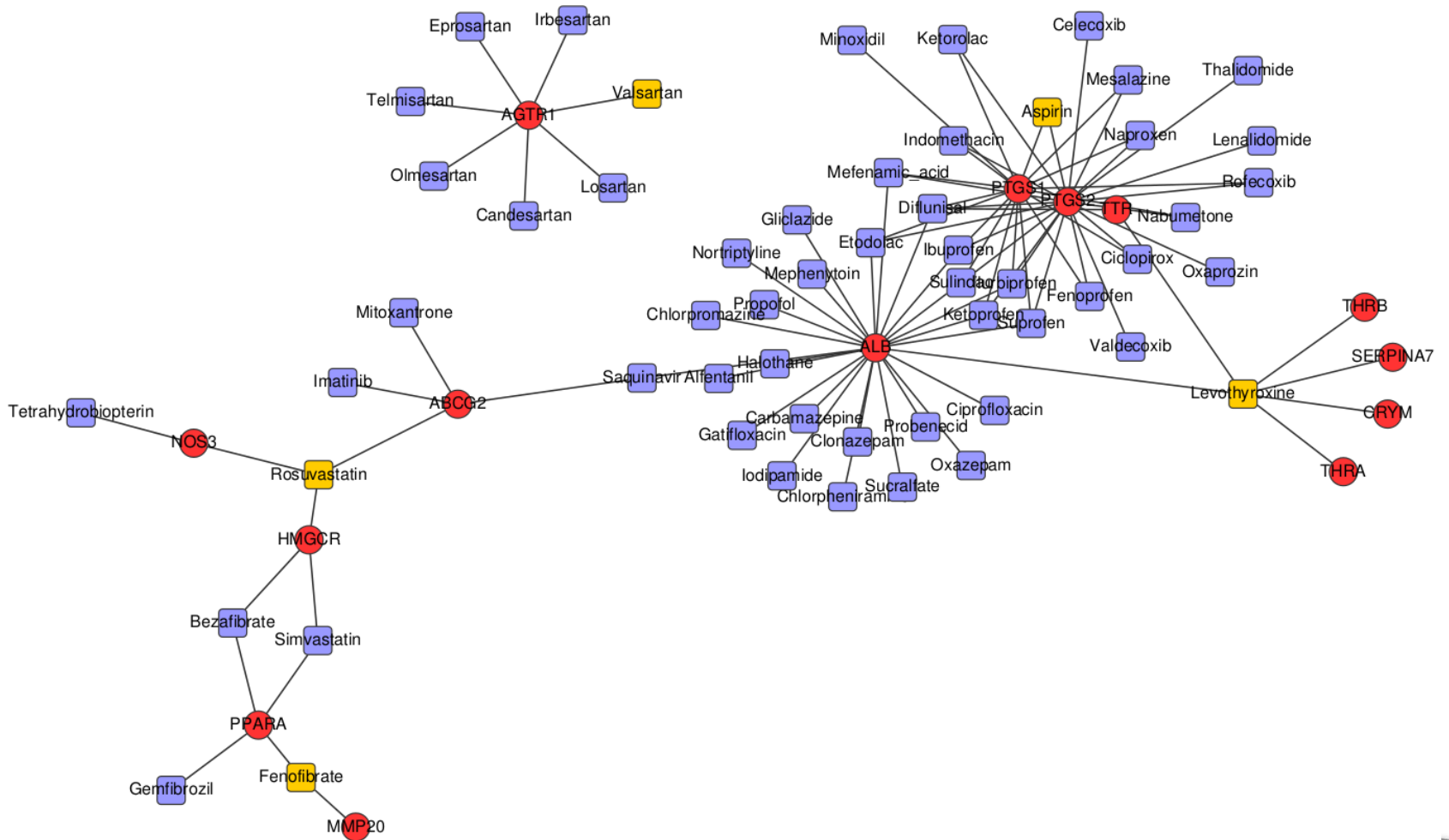


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Use Case



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Hardware and Software

- Standard Server
- Urika-64



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Standard Server – Hardware

- Dell PowerEdge R510
- Two quad-core Intel Xeon X5550, at 2.6 GHz
- 26 GB of memory



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Standard Server – Software

- RHEL 5.1
- Virtuoso 06.01.3127-pthreads



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Urika-64 – Hardware



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Urika-64 – Hardware

- Cray XT-5 architecture
 - Blade architecture
 - SeaStar2 interconnect
- Opteron based service nodes
- Compute nodes with Cray Threadstorm 4.0 ASIC
 - 64 processors with 128 streams per processor
 - 32 GB of memory per processor

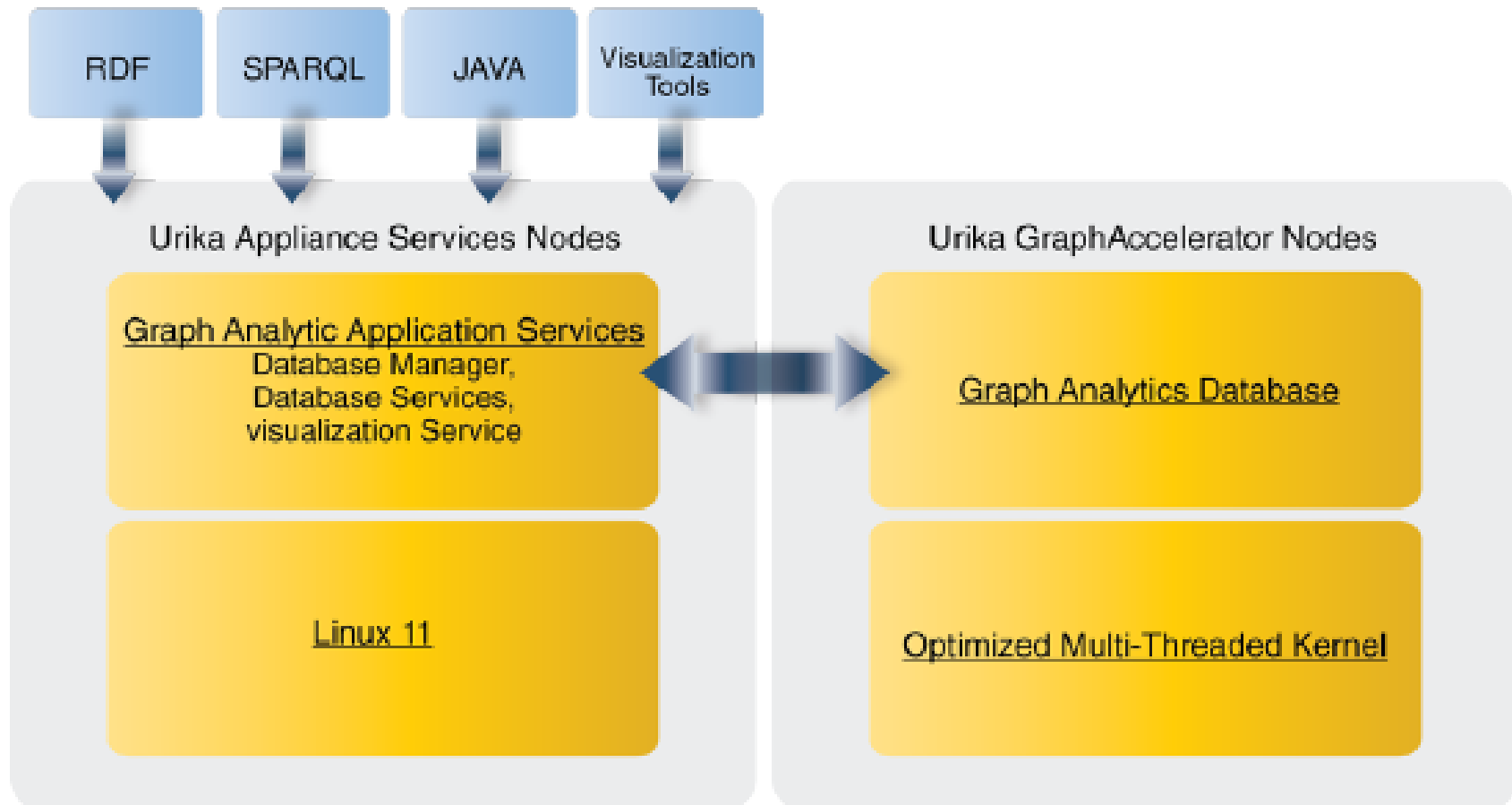


Urika-64 – Software

- Not at all like a Cray XT-5
- Linux, unified view of memory and processors
 - 2 TByte of memory, 64 processors, 8192 streams
- Cray proprietary RDF triple store, exposed via an Apache Jena interface
- Large data import via Lustre possible
- Web interface for running queries



Urika-64 – Software



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Data Set

Dataset

<http://chem2bio2rdf.org/omim>
<http://chem2bio2rdf.org/kegg>
<http://chem2bio2rdf.org/reactome>
<http://chem2bio2rdf.org/ctd>
<http://chem2bio2rdf.org/chebi>
<http://chem2bio2rdf.org/dcdb>
<http://chem2bio2rdf.org/bindingdb>
<http://chem2bio2rdf.org/hprd>
<http://chem2bio2rdf.org/hgnc>
<http://chem2bio2rdf.org/medline>
<http://chem2bio2rdf.org/kidb>
<http://chem2bio2rdf.org/pubchem>
<http://chem2bio2rdf.org/qsar>
<http://chem2bio2rdf.org/bindingmoad>
<http://chem2bio2rdf.org/matador>
<http://chem2bio2rdf.org/pharmgkb>
<http://chem2bio2rdf.org/pdb>
<http://chem2bio2rdf.org/ttd>
<http://chem2bio2rdf.org/chembl>
http://chem2bio2rdf.org/medline_lite
<http://chem2bio2rdf.org/dip>
<http://chem2bio2rdf.org/sider>
<http://chem2bio2rdf.org/uniprot>
<http://chem2bio2rdf.org/drugbank>
<http://chem2bio2rdf.org/chemogenomics>

Triple Count

17,251
245,997
15,849
4,933,479
5,812,141
20,780
1,191,201
477,697
1,720,541
480,716,135
744,738
15,439,873
32,206
252,938
269,656
512,361
95,925
116,767
85,156,878
56,212,993
1,113,871
127,755
1,994,607
436,283
7,327,361
664,985,283

Total



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Methodology

- Import all triples into the Urika
- Create database
- Start database
- Run query through the web interface
- Run query using Java application



Overall Results

- Importing the data and running SPARQL queries worked
- Accessing the SPARQL endpoint was easy
- Custom hardware, proprietary software, exposed via standards compliant interfaces
- Performance results are interesting



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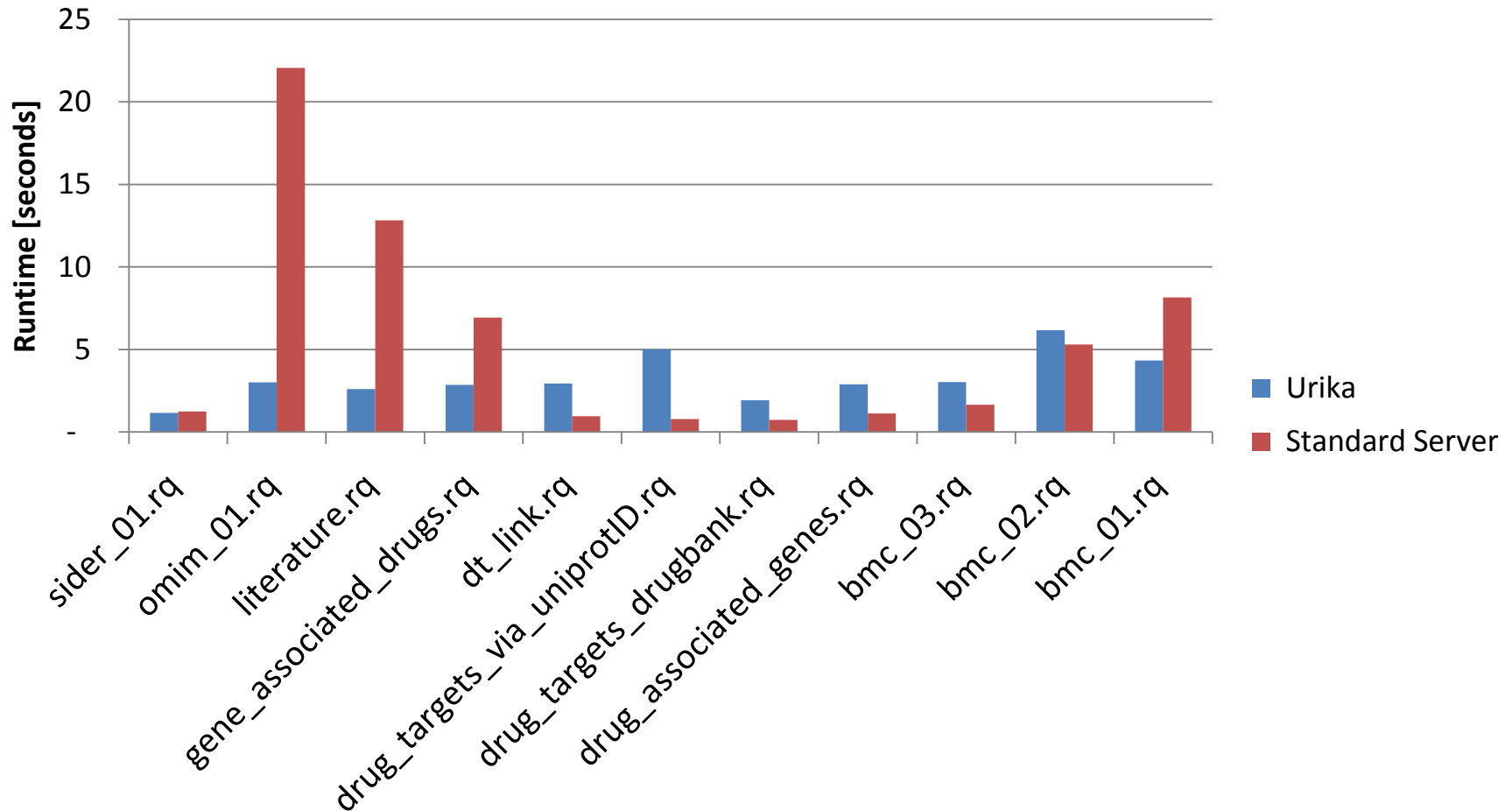


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Performance Results



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Conclusion

- Initial testing of how to use a Urika went fine
- Integrating it into an existing workflow is easy
- Getting researchers to use a Urika could be a challenge
- Not sure about multi user operation
- Our tests do not allow for a performance comparison



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Thank You!

Questions?!



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