# Jobim 2019

## AskOmics, a collaborative user-friendly interface for integrating datasets with references resources using semantic web technologies

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1. Inria, Univ Rennes, CNRS, IRISA

# Outline

1. The nightmare of data: how to integrate project data with reference datasets
2. AskOmics as a solution
3. Demo
4. What's next?

# The nightmare of data

# The nightmare of data

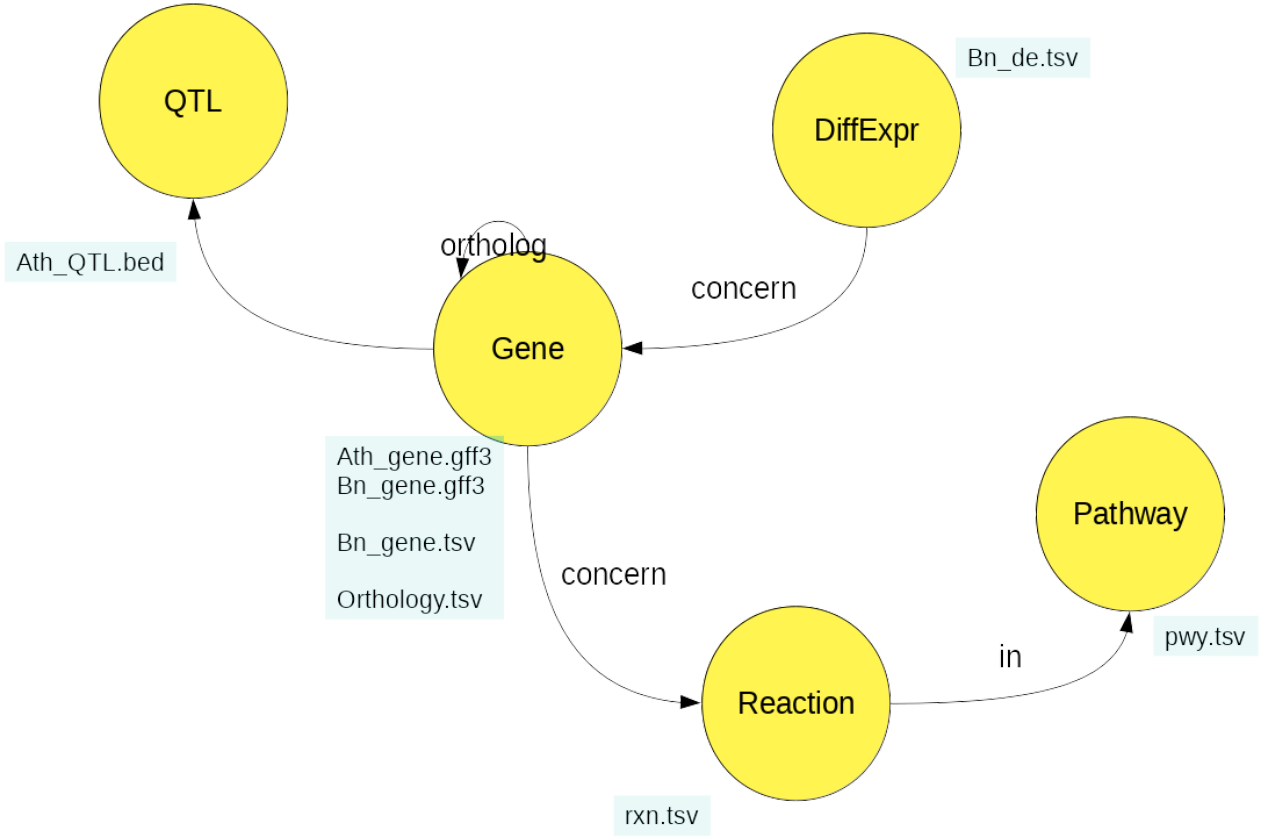
Big Data: Datasets so **large** or **complex** that traditional data processing is inadequate.

- More than 1500 databases, lack of interoperability, multiple file format
- Need to integrate public data and project specific data
- Integration and query require technical skills and time

Need a user-friendly interface for data integration and querying

# The nightmare of data

## How to explore data



# The nightmare of data The semantic web

- RDF (resource description framework) can well describe entities and relations

```
:gene rdf:type owl:Class .
:chromosome rdf:type owl:ObjectProperty .
:chromosome rdfs:domain :Gene .

:AT001 rdf:type :Gene ;
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       :chromosome :AT1 ;
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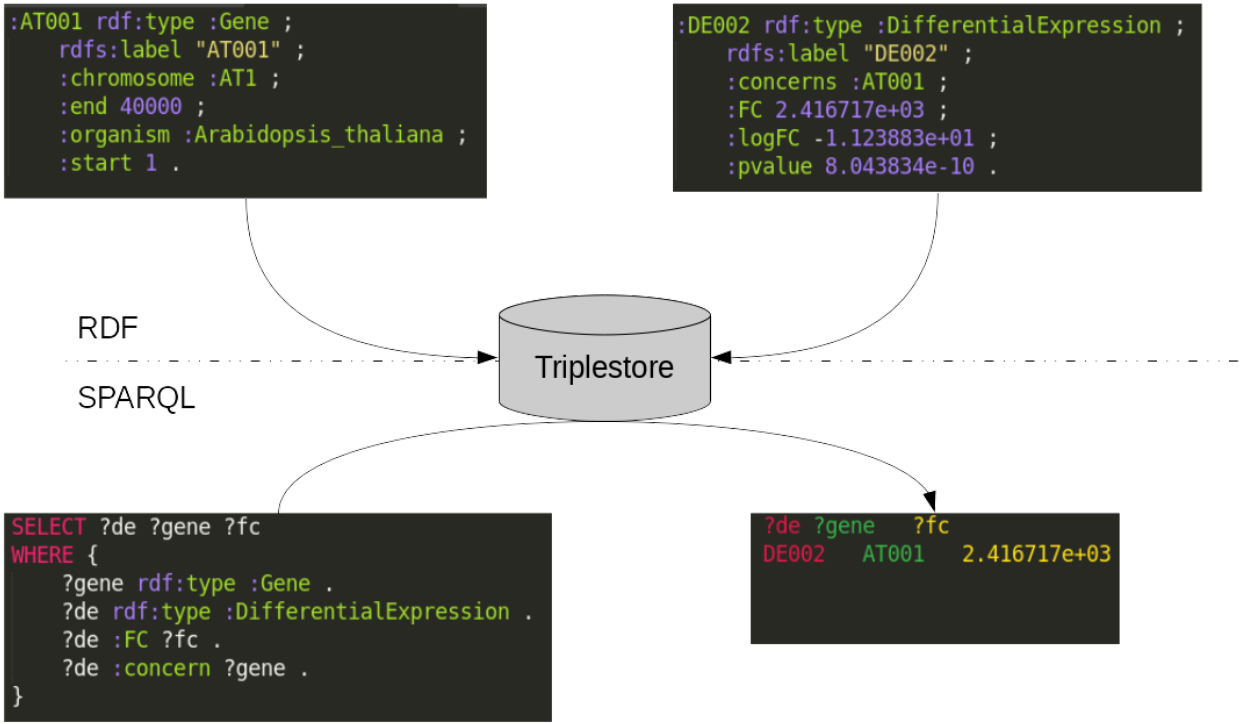
- SPARQL (SPARQL protocol and query language) can be used to extract information

```
SELECT ?gene ?label
WHERE {
    ?gene rdf:type :Gene .
    ?gene rdfs:label ?label .
}
```

# The nightmare of data

## The semantic web



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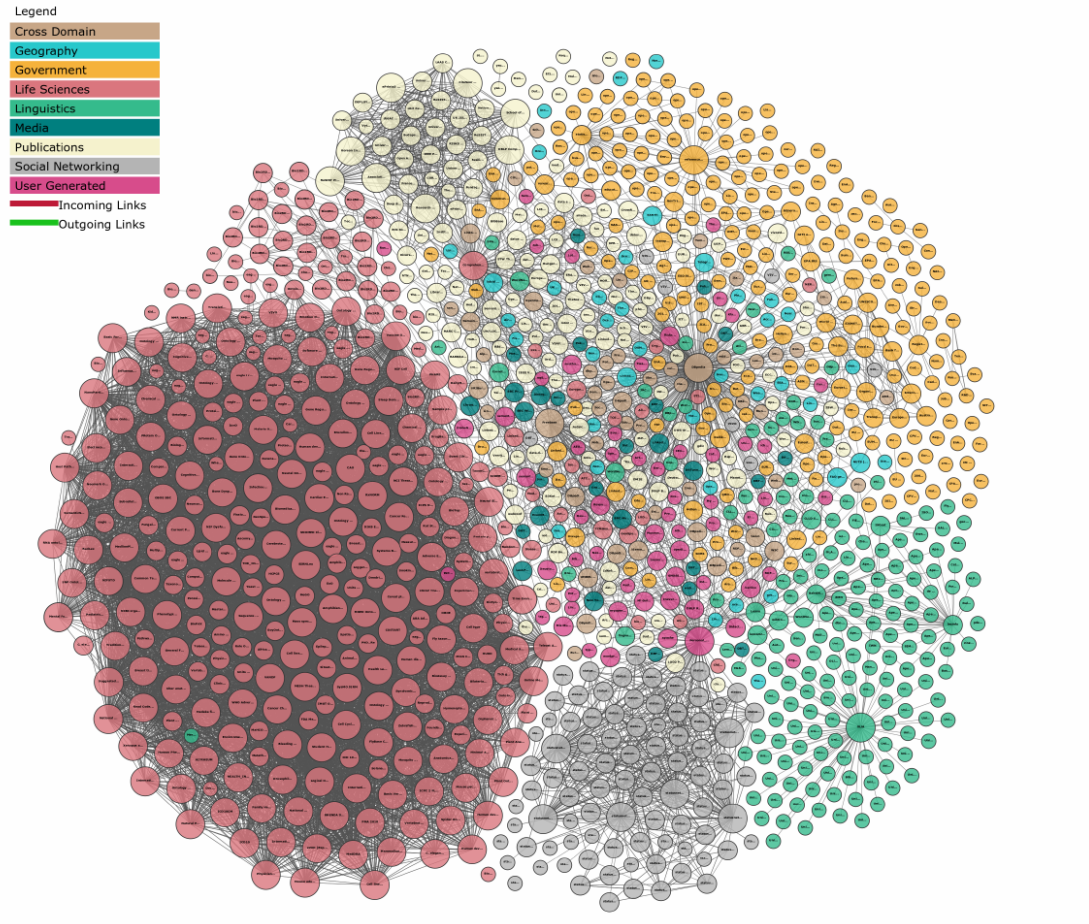


Linked open data cloud, by M. Schmachtenberg, C. Bizer, A. Jentzsch and R. Cyganiak http ://lod-cloud.net/

# AskOmics as a solution

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AskOmics is a web software for data integration (references data and project specific data) and query using semantic web

- Convert multiple data format into rdf triples, and store them into a triplestore
- Query the rdf graph using a user-friendly interface
- Save, relaunch and share queries and results with other users (AskOmics is multi-users)
- AskOmics ecosystem: tools to generate AskOmics compliant files (AskoR, AuReMe), Interoperability with Galaxy

# Demo Input files

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- Genetic files
  - *Arabidopsis thaliana* (GFF, TAIR)
  - *Brassica napus* genes (GFF, BBIP platform)
  - Orthology relation (TSV, Chalhoub *et al*, 2014)
- Differential expression
  - Differential expression of *Brassica napus* genes between roots and leaves (TSV, EdgeR + AskoR)
- Pathway
  - genes reaction and pathway data of *Brassica napus* (TSV, Metacyc + AuReMe)

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- What are their orthologs in *Arabidospis thaliana*? Are they in a QTL?
- In which biological reactions are the genes obtained involved, and in which metabolic pathways are they involved?

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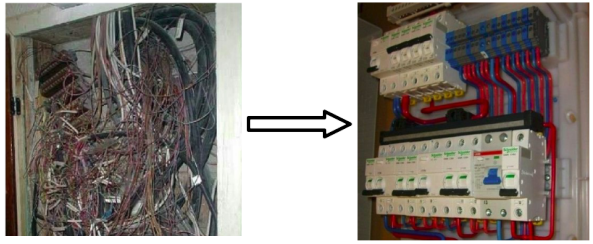

# Collaboration

Thanks to all AskOmics users:

- C Bettembourg – IGEPP aphids (D. Tagu)
- A. Evrard – IGEPP rapeseed (M. Jubault)
- M.Aite/C.Frioux/A.Siegel AUREME
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- IFB project (CIRAD/INRA) - Connecting AskOmics with ”SouthGreen” endpoint
- M. Rousseau/J.Lucas/J.Ferreira de Carvalho/S.Knosp - Rapeseed
- A. Sarniguet,J.Chappat - Rhysophere Colza
- M. Louarn Hematology
- M. Conan Seaweed
- L. Guillot-Cloarec Uniprot/NextProt
- S. Daval (INRA) - Meta-transcriptomics
- BIPAA (Arthropodes)/BBIP (Rapeseed) endpoint in production mode
- M. Wery these CIFRE - Sanofi
- M. Louarn these INSERM-INRIA
- J. Yon - Pegase, INRA
- M. Gonzalez - CGR, Universidad de Chile
- O. Chakoory/E. Forano - INRA
- G. Rabut - IGDR - protein-protein interactions
- P. Baudier/M. Aite - Drugs repositioning
- V. Henry - Neuromarkers

# Usefull links

- Github repos
  - AskOmics: askomics/askomics
  - AskOmics3: xgaia/flaskomics
- Docs:
  - AskOmics: askomics.readthedocs.io
  - AskOmics3: flaskomics.readthedocs.io
- Running instance: askomics.genouest.org
- This slides: xgaia.github.io/askomics/jobim/2019
- Contact me: xavier.garnier@irisa.fr