

Bioqueries: a collaborative environment to create, explore and share SPARQL queries in Life Sciences

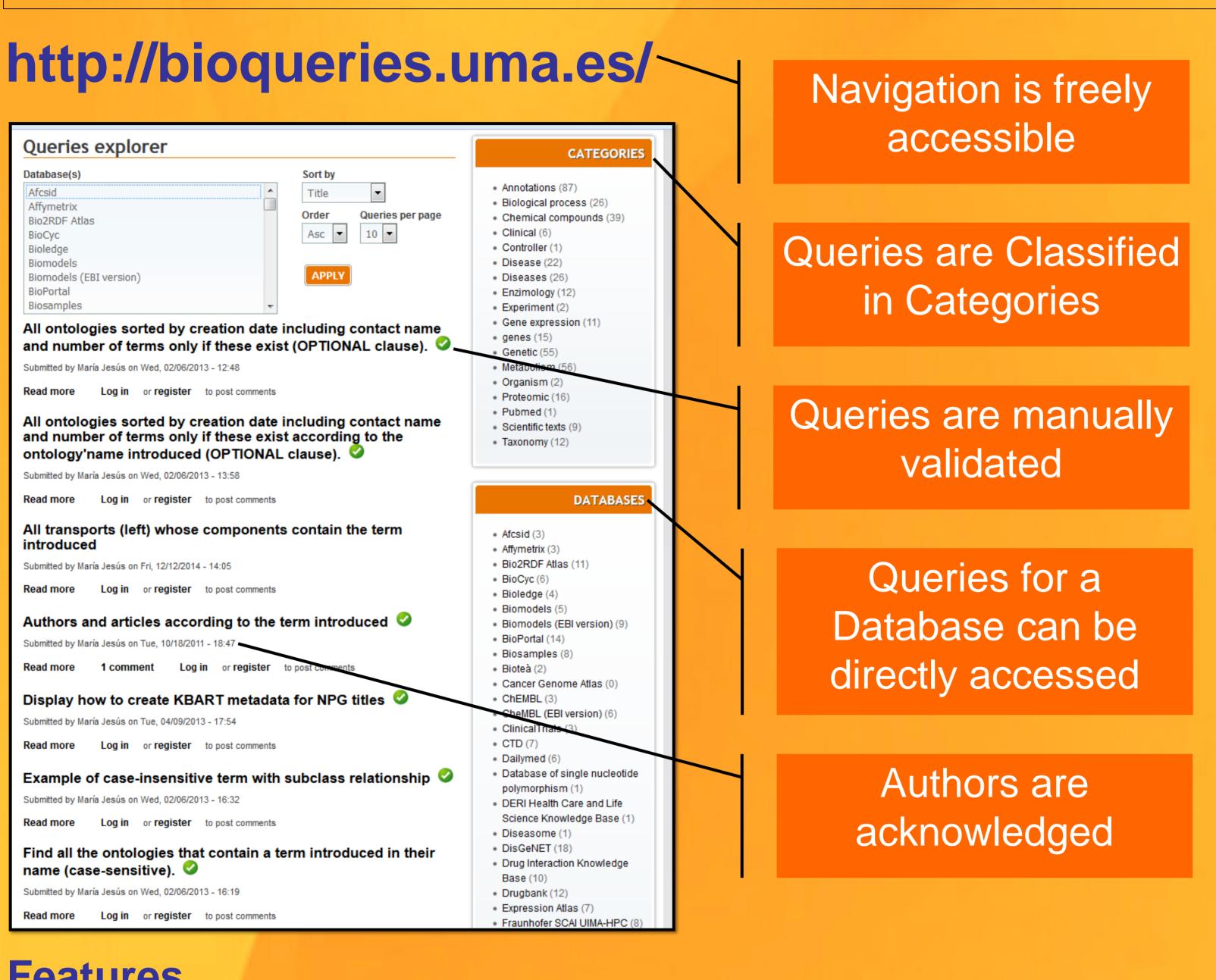


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Bioqueries as a collaborative environment

http://sparql.es/

Bioqueries provides a collaborative environment to create, explore, execute, clone and share SPARQL queries (including Federated Queries). Federated SPARQL queries can retrieve information from more than one data source.



Features

- Tools to create, clone test and execute SPARQL queries.
- Complementary software tools like a visualization tool to preview the data structure of the endpoint to make easier the construction of new queries.
- The retrieved information can be downloaded in formats such as RDF and N3 (N-triples)
- Visualization of query results

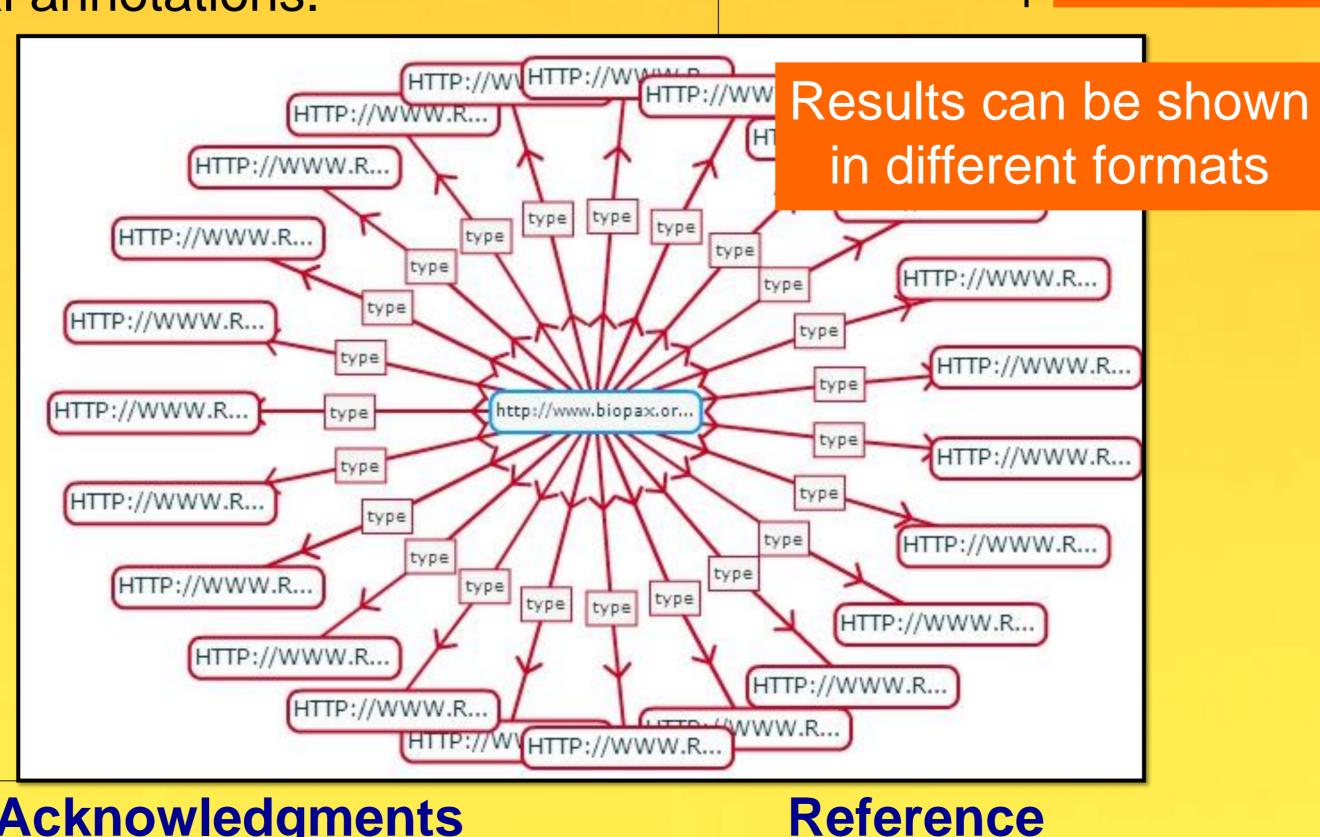
Bioqueries' evolution

Bioqueries was initially populated with a seed of 100 SPARQL queries. Since then, Bioqueries has grown up to 373 SPARQL queries (59 federated queries) which have been classified into different groups according to manual annotations.

250 users have registered in Bioqueries and have collaborated to create new SPARQL queries. the last years, we also implemented new functionalities to improve Bioqueries. Some of these improvements are manual curation to validate queries, improved administration support additional formats and download the query results.

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Acknowledgments

Introduction

Linked Data (http://linkeddata.org/) technology has emerged as a set of good practices based on the W3C's specifications whose main goal is to publish data in standards formats like RDF (Resource Description Framework).

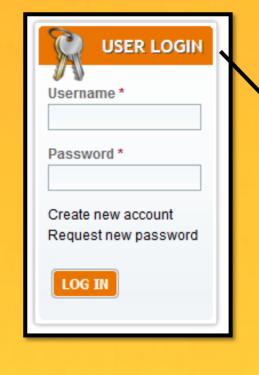
RDF Databases are accessible by means of SPARQL queries. Bioqueries aims to bring either biologists or bioinformaticians closer to this emerging technology by accessing to this information.

VIEW EXECUTE

Users can read the documentation of a query

Users can explore the SPARQL query (helping learning this language)

User can introduce values for the query parameters, and execute the it



Registration is optional, but only registered users can post new queries

Protein by organism ID 2 ubmitted by María Jesús on Thu, 03/21/2013 - 13:08 Database: Uniprot (Official Endpoint) 🧶 SHOW QUERY CODE This query access official Uniprot SPARQL Endpoint to retrieve all those UniProt entries that are associated with a given organism Select UniProt entries, given a taxon ID \$taxon\$ (e.g. 83333). The result is the proteins and their amino acid sequences. You should ntroduce a maximun number of results to be retrieved \$number\$ (e.g.10) Protein by organism ID 🕗 Submitted by María Jesús on Thu, 03/21/2013 - 13:08 Database: Uniprot (Official Endpoint) IIDE QUERY CODE This query access official Uniprot SPARQL Endpoint to retrieve all those UniProt entries that are associated with a given organism (using as input their organism identifier). The results shown is a sequence variant that leads to an aminoacid to another aminoaci Select UniProt entries, given a taxon ID \$taxon\$ (e.g. 83333). The result is the proteins and their amino acid sequences. You should introduce a maximun number of results to be retrieved \$number\$ (e.g. 10) PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#> ?protein up:organism ?organism ?protein up:organism ?organism VIEW EXECUT Execute guery (e.g. 83333). The result is the proteins and their amino You should introduce a maximun number of results to be retrieved 50 ▼ EXECUTE QUERY HTML (Show) Graph RelFinder (Show) RDF/XML (Download) NTriples (Download)

http://purl.uniprot.org http://purl.uniprot.org

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