kpath: An example of metabolic pathway data integration using Linked Data

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INTRODUCTION

The main databases related to metabolic pathways, such as Kegg, Brenda, Reactome and Biocyc, provide partially interlinked data on metabolic pathways. This limitation only allows independent searches to retrieve cross-database information on metabolism and restricts the use of more complex searches to discover new knowledge or relationships.

SYSTEM AND METHODS

Kpath integrates information on metabolic pathways from different sources:

- Bio2RDF's Kegg (core data)
- NCBI Taxonomy (organism data)
- SwissProt (protein data)
- Bio2RDF's Reactome (related pathway data).

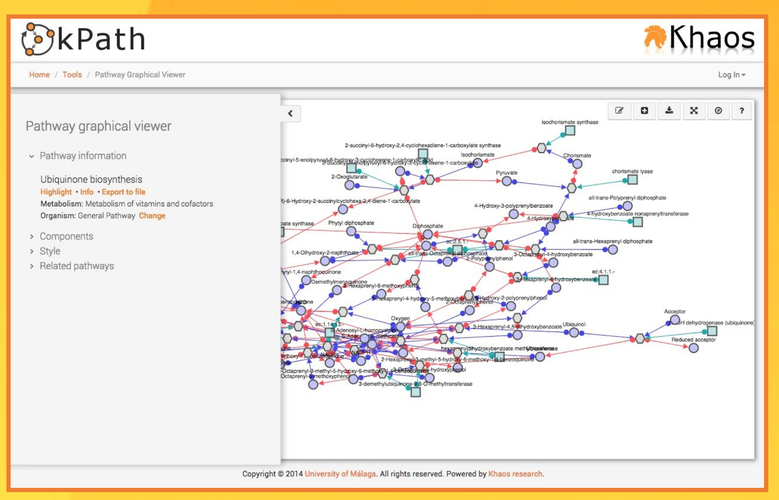
KPATH USER INTERFACE

http://browser.kpath.khaos.uma.es

Kpath provides a navigational interface to ease the use of the integrated data by end users.
It includes three different applications:
1.Pathway Graphical Viewer
2.Pathway Graphical Editor
3.Relationship Search

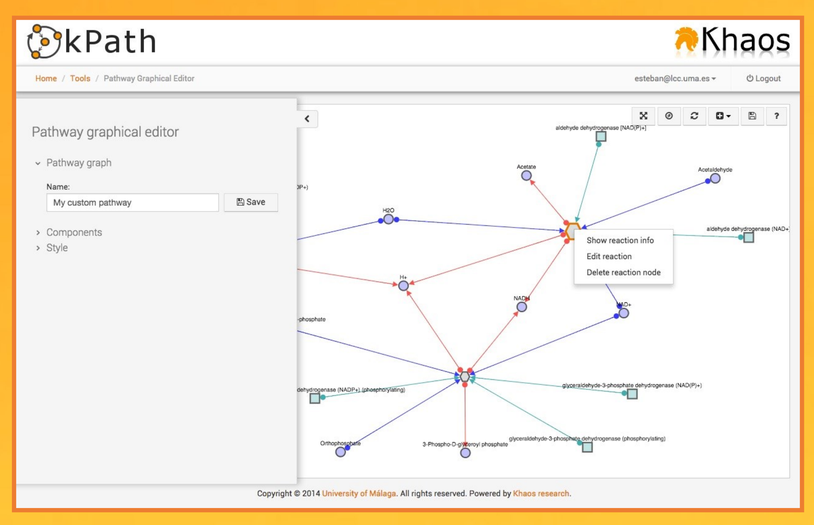
Pathway Graphical Viewer

Graphs with the participating biochemical reactions (i.e. metabolites, enzymes and genes) in a given pathway. Components related to other pathways are also shown allowing comparative analyses between pathways.

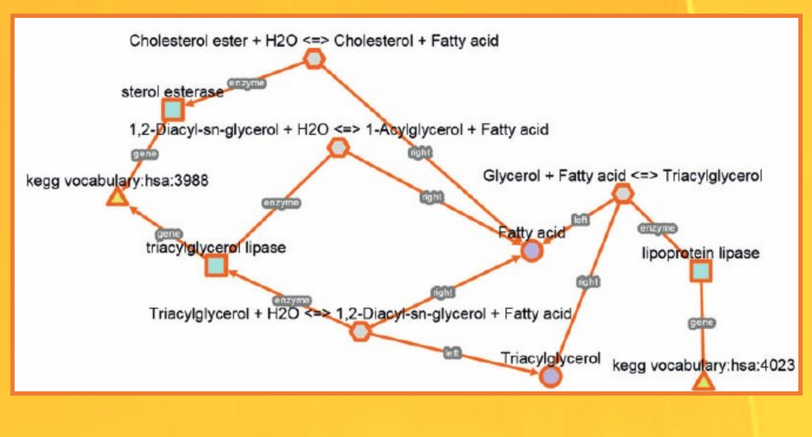


Pathway Graphical Editor

Edition functionality, enabling users to customize pathways and save a local copy of their version.

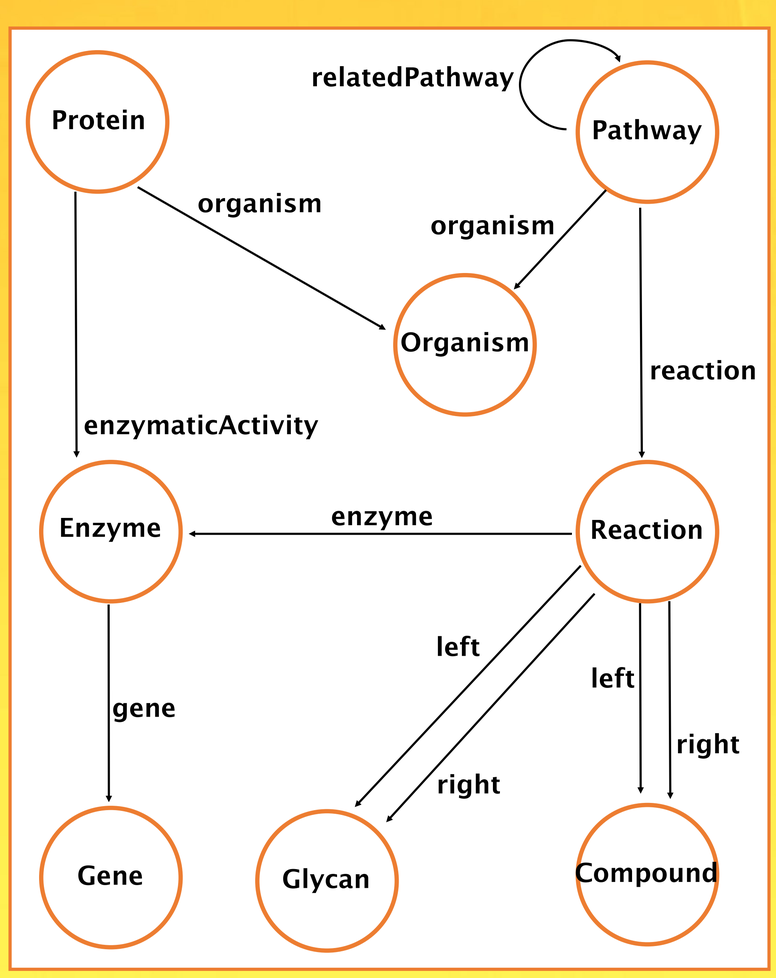


The **Relationship Search** tool enables the graphical browsing of relationships between pathway components (independently of their source).



Integrated data available through a public SPARQL (Virtuoso) endpoint:

http://sparql.kpath.khaos.uma.es



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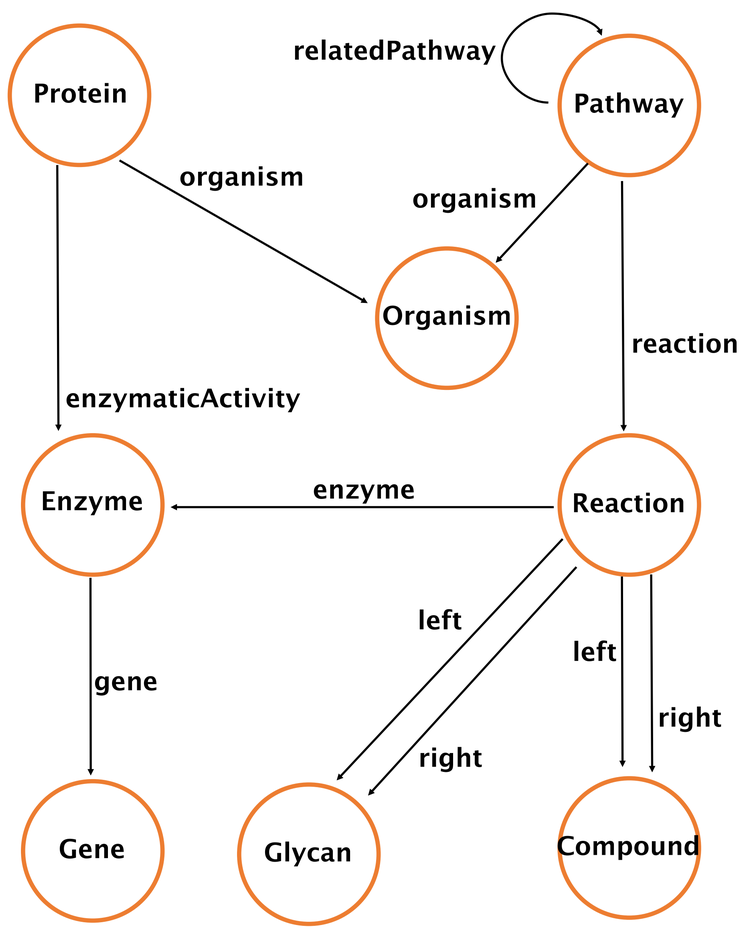
REFERENCE

Navas-Delgado, I., García-Godoy, M.J., López-Camacho, E., Rybinski, M., Reyes-Palomares, A., Medina, M.A., and Aldana-Montes, J.F.
kpath: integration of metabolic pathway linked data. *Database* 2015 1-11.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