

SemScape: Visualizing Semantic Web Data Landscapes with Cytoscape 3.0

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What ?

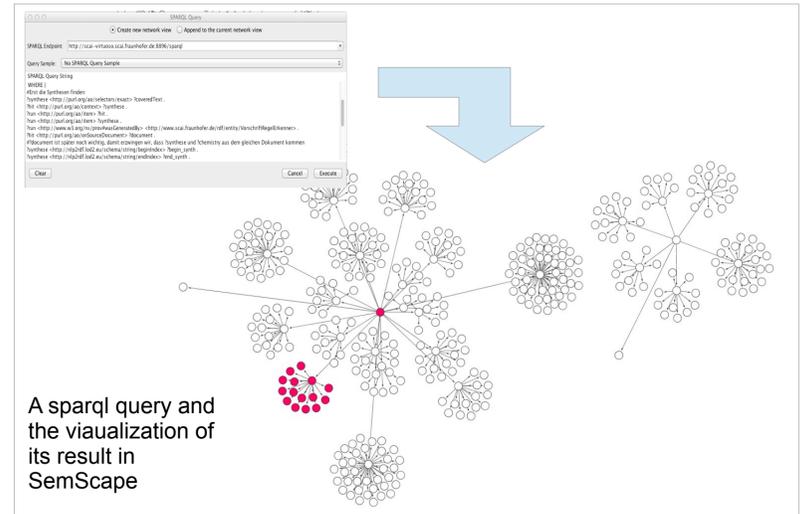
SemScape is a plugin for the popular network biology software Cytoscape [1] that allows user interaction and queries over remote sparql endpoints.

In particular it allows visualization of sparql queries' results, interactive navigation of RDF graphs and reconstruction of semantic data landscapes.

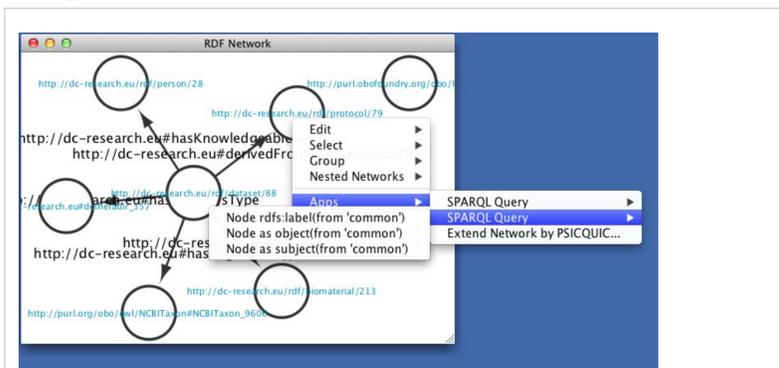
Cytoscape is a network visualization and analysis tool that, while inherently domain independent, provides links and shortcuts to typical biomedical datasets and manipulations. It offers a plugin architecture and it has a very active community both of developers and users. SemScape is developed as plugin for the latest version of Cytoscape, 3.0, which is released in beta at the time of this writing and presents a completely new architecture from previous versions.

SemScape offers a range of functionalities, which are derived from what was implemented in RDFscape [2] and AGUIA [3]. However this system provides a newer, more efficient and up to date implementation.

SemScape is available at <http://code.google.com/p/vsdic3/> and released under the **Apache License 2.0**.



A sparql query and the visualization of its result in SemScape



Top: a contextual menu showing possible actions for a node. Left: subscription mechanism for queries. Below: example of a parametric query

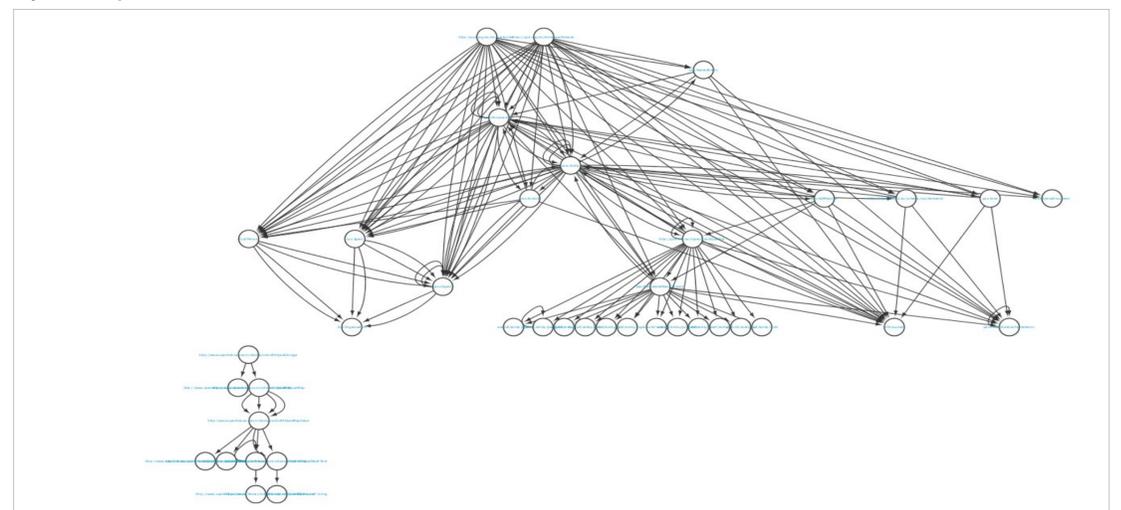
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How ?

The functionalities of SemScape can be categorized essentially in discovery and navigation of linked data landscapes.

Discovery functions are based on the automatic extraction of a data map (typically types and relations from a given endpoint).

Navigation functions are based on contextual menus that can be configured by users and data publishers: when right-selecting a node, the system uses attributes of the node (e.g. its type) to look into a query library for queries that can be applied to the node. E.g.: if the node is a protein, the system may find queries for interacting proteins. In general for each resource simple queries such as all statements including the resource as object or subject are provided. Once a selection is performed, results are used to expand the graph, and provenance information is kept for each new element visualized (which in turns allow new contextual queries to the original endpoint). In particular, queries are written as parametric queries, and can be provided by data publisher as a package to which the user can subscribe. For instance a pathway resource provider may provide, together with an endpoint, a set of preconfigured queries to drive user interaction on its knowledge base. The user can keep track of such preconfigured packages and update them if newer versions are proposed by the data publisher. Together with the possibility to execute and visualize generic SPARQL queries, SemScape allow the possibility to extract and define data landscapes, which are graphs visualizing the semantic links between data sets in a given context (e.g. Cancer). These graphs can be restructured using the visualization layouts provided by Cytoscape.



A Semantic Data Landscape Example

We need you!

If you own a dataset and wish to publish queries that can help its exploration via SemScape, or if you want to explore semantic knowledge bases with Cytoscape, please get in touch!

Acknowledgements

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References

1. Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T: Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Research*. 13(11) (2003) 2498–504 .
2. Splendiani A: RDFscape: Semantic Web meets Systems Biology *BMC Bioinformatics* 9(Suppl 4) (2008) S6
3. Correa MC, Deus HF, Vasconcelos AT, Hayashi Y, Ajani JA, Patnana SV, Almeida JS: AGUIA: autonomous graphical user interface assembly for clinical trials semantic data services. *BMC Medical Informatics and Decision Making*. 10:65 (2010) .

