Everybody a Translational Data Scientist

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Abstract. A lot of companies are facing the challenge of linking and characterizing biomedical data of human studies, biological specimen, cell lines, microarrays and other research data to enhance resource sharing which ultimately speeds experimentation and encourages interdisciplinary collaboration. DISQOVER uses an ontology-centric architecture to organize and visualize internal data in conjunction with third party and public data. It builds semantically linked data repositories allowing users to 'hop' from one data type to another. We will zoom on the architecture and ontologies used.

The core search engine has been optimized and is now more powerful, more scalable and faster compared to traditional semantic web architectures. Users can search in different data types, follow links between data concepts while the data is being harnessed from many different heterogeneous data sources in a federated way.

The intuitive visualization engine allows everybody to easily build complex semantic queries across healthcare and life sciences data from many different data sources. Results are stored in a reusable information network and can be visualized using lists, tables, tree-views, world maps, timelines, etc. depending on the data type or property. At the end of the executed search, all search steps can be stored, exported, re-used or shared in multiple formats resulting in true collaboration across harmonized data fueling translational science. A short demo will be given where real life scientific questions will be solved.