Semantic Annotation Workflow using Bio-Ontologies

Emmanuel Castanier, Clement Jonquet, Soumia Melzi, Pierre Larmande, Manuel Ruiz, Patrick Valduriez

Semantic Annotation Workflow using Bio-Ontologies

Institut de biologie computationnelle

Castanier E.[1], Jonquet C.[2], Melzi S.[2], Larmande P.[3], Ruiz M.[4], Valduriez P.[1]

1 – Zenith, INRIA-LIRMM
2 – SMILE, UM2-LIRMM
3 – DIADE, IRD
4 – AGAP, CIRAD

Montpellier, France

Introduction

Biologists have adopted ontologies:
- To provide canonical representation of scientific knowledge
- To annotate experimental data to enable interpretation, comparison, and discovery across databases
- To facilitate knowledge-based applications for decision-support, natural language processing, and data integration

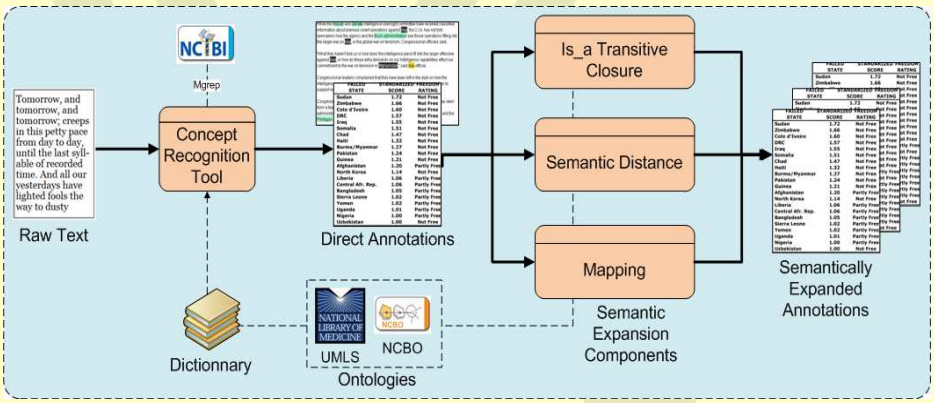
But **off-the-shelf solutions for the biologist** to use ontologies are rare (versions, format, availability, license, overlap, etc.)

The challenge

Automatically process complex biological resources text content and generate annotations :
- Large-scale – to scale up to many resources and ontologies
- Automatic – to keep precision and accuracy
- Easy to use and to access – web service approach
- Customizable – to fit very specific needs
- Smart – to leverage the knowledge contained in ontologies

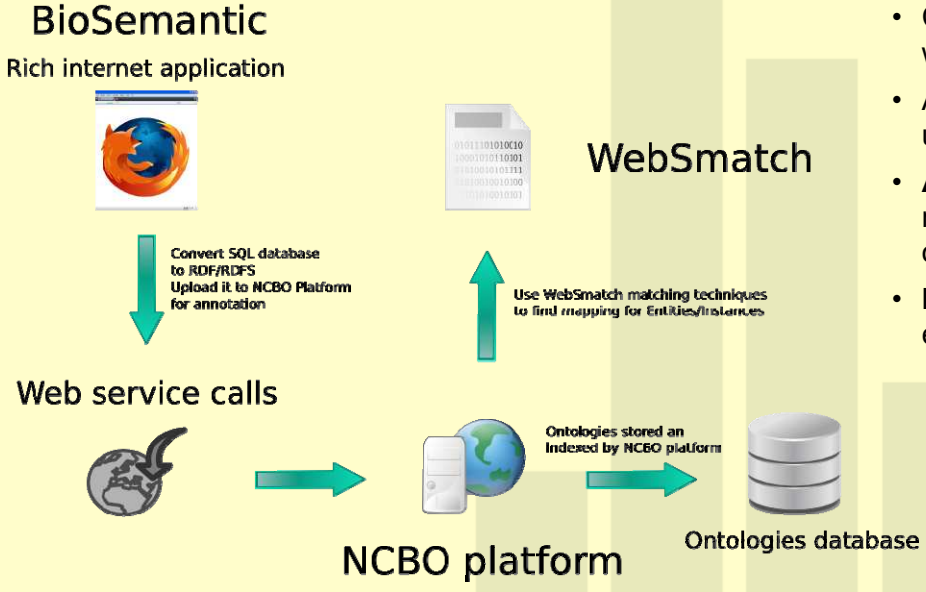
There have been **success stories to reproduce**: GO annotations, PubMed indexing, etc.

NCBO Annotator: Ontology-based annotation workflow



- First, direct annotations are created by **recognizing concepts** in raw text.
- Second, annotations are **semantically expanded** using knowledge of the ontologies.
- Third, all annotations are **aggregated and scored** according to the context in which they have been created.

Customized IBC Annotator for database schemas



- Convert **SQL database schemas to RDF/RDFS** with BioSemantic
- Annotate with NCBO Annotator and WebSmatch using customized NCBO services
- **Annotator relies on WebSmatch** to create mappings between elements of schemas and ontological concepts
- **Indexing IBC related data** with the workflow to enhance semantic search and mining of data

R. Coletta, E. Castanier, P. Valduriez, C. Frisch, D-H. Ngo, Z. Bellahsene: Public data integration with WebSmatch. *Workshop on Open Data*. 2012, pp. 5-12.

C. Jonquet, N. H. Shah, M. A. Musen. **The Open Biomedical Annotator**, In *AMIA Symposium on Translational BioInformatics*. 2009. pp. 56-60.

C. Jonquet, P. LePendu, S. Falconer, A. Coulet, N. F. Noy, M. A. Musen, N. H. Shah. **NCBO Resource Index: Ontology-Based Search and Mining of Biomedical Resources**, *Web Semantics*. 2011. Vol. 9 (3), pp. 316-324.

J. Wollbrett, P. Larmande, F. De Lamotte, M. Ruiz. **Clever generation of rich SPARQL queries from annotated relational schema: application to Semantic Web Service creation for biological databases.** *BMC Bioinformatics*. 2013; 14:126.

In collaboration with
SIFR project
www.lirmm.fr/sifr
THE NATIONAL CENTER FOR BIOMEDICAL ONTOLOGY