Semantic Annotation Workflow using Bio-Ontologies

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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

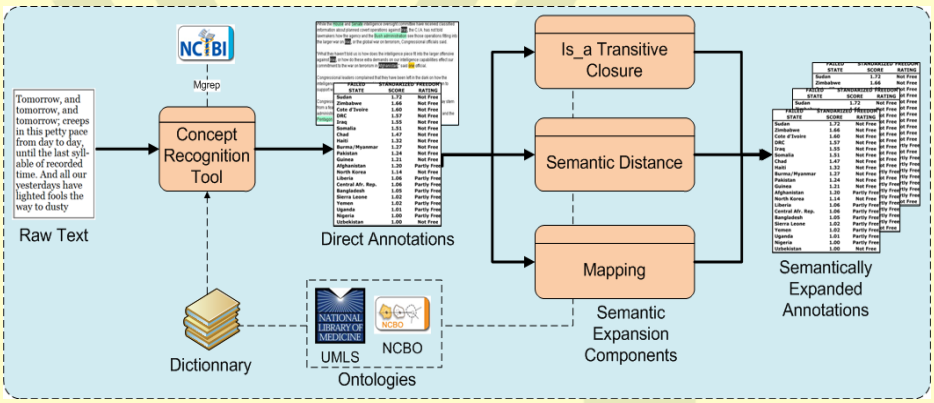
But **off-the-shelf solutions for the biologist** to use ontologies are rare (versions, format, availability, license, overlap, etc.)

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

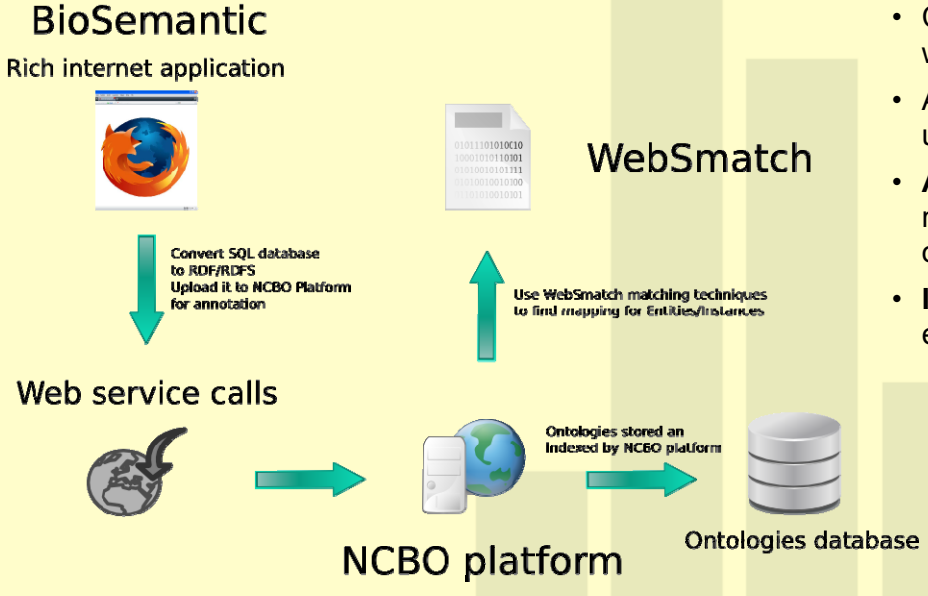
There have been **success stories to reproduce**: GO annotations, PubMed indexing, etc.

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

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