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**

**BioSemantic**

Rich internet application

**WebSmatch**

- 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

**Web service calls**

[NCBO platform](https://www.ncbi.nlm.nih.gov)

**Ontologies database**


