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

NCBO platform

BioSemantic
Rich internet application

Web service calls

WebSmatch

Use WebSmatch matching techniques to find mappings for relational databases

Ontologies stored an indexed by NCBO platform

Ontologies database

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