



OBI: The Ontology for Biomedical Investigations

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What is an ontology and why do I need one?

Standards for data representation and minimum information enhance the value of experiments. However, even if all researchers and clinicians who generate data agree on what details are required, it is not possible for a computer to analyze this information unless the terms that are used are also standardized. Ontologies, by providing a common vocabulary to annotate data, are essential to facilitate the interchange and analyzes between software packages, investigators and laboratories.

Why is it important for computers to be able to recognize this information?

By using ontologies, scientists will be able to compare results that were previously irreconcilable, by adding the missing biological context to the data file. By tackling the semantics of the information it is possible to integrate and distribute data, therefore allowing complex queries across systems.

The solution

The Ontology for Biomedical Investigations, OBI (formerly known as the Functional Genomics Investigation Ontology, FuGO) is an integrated ontology that can be applied to the description of biomedical and clinical experiments. OBI is an open source, collaborative effort by several international groups representing technological and biological domains from around the globe. It seeks to develop an integrated ontology that provides both a set of universal terms and domain-specific extensions for terms relevant only to a given domain. The purpose of this ontology is to support the consistent annotation of biomedical investigations, regardless of the particular field of study. The ontology will model the design of an investigation, the protocols and instrumentation used, the material used, the data generated and the type of analysis performed on it.

Technical Information

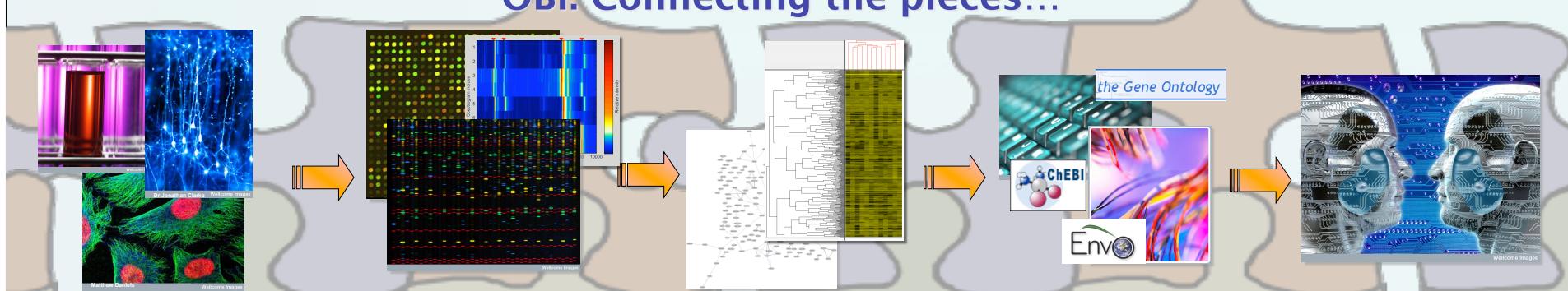
OBI is being developed under the guidance of the OBO Foundry and uses the BFO upper ontology (<http://www.ifomis.org/bfo>) to structure and guide the ontology's design. As a consequence, OBI is developed following 3 main axes; process (subclass of bfo:occurred) covering protocol applications, material (subclass of bfo:independent continuant) encompassing instrument and material entities and bfo:dependent continuant, with subclasses such as quality, role and disposition used to qualify elements of the first two axes. Use cases drive the development of the ontology in order to meet our community needs and all of the development is documented and is openly available for scrutiny. The ontology is developed using the Web Ontology Language (OWL) and is available both in OWL and OBO formats.

In Memoriam - William John Bug, 1961-2008

This work is dedicated to our sadly departed friend and colleague, Bill Bug. Bill was one of the driving forces behind the Ontology for Biomedical Investigations project and his brilliance, warmth and sense of humor are greatly missed.



OBI: Connecting the pieces...



Design & Inputs:
OBI covers inputs to experiments such as materials, plans and protocols

OBI examples:
study design
clinical study design
material
blood serum

Experimental Data:
OBI covers data formats, processing

OBI examples:
digital entity
eMedical record
binary executable
Protocol application
assays
material transformation

Data Analysis:
OBI covers data transformations, analysis methods

OBI examples:
data transformation
similarity calculation
replicate analysis
report figure
dot plot

Data sharing:
OBI aids integration, consistent representation and data sharing

OBI integrates with:
ChEBI, EnvO, Gene Ontology
Cell Ontology, PATO,
Disease Ontology

Integration of databases, cross system queries

Pertinent results: not only a string search but a semantic search.

Different types of resources can be accessed and provide integrated results

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