



OBI: The Ontology for Biomedical Investigations

Mélanie Courtot and James Malone on behalf of The OBI Consortium*

<http://obi.sourceforge.net>

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 recognize 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 analyses 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 might have seemed irreconcilable before, 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 developing an integrated ontology that can be applied to the description of biological 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 to structure and guide the ontology's design. As a consequence, OBI is developed following 3 main axes; process (subclass of bfo:occurent) 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 axis. 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 available in Web Ontology Language (OWL) format, which is the specification used for development and an OBO format conversion is also available.

OBI Communities

The OBI project is an international, collaborative effort to build an ontology to be used for annotation of Biomedical Investigations.

It comprises more than 40 scientists representing 18 biological communities, such as Flow Cytometry, Immunology, Transcriptomics and Metabolomics.

Coordinating Committee

Community Representatives

The representatives of the communities participating in the development of OBI.

Core Developers

Core Developers are considered key to the evolution of the ontology, but may or may not be members of any single community.

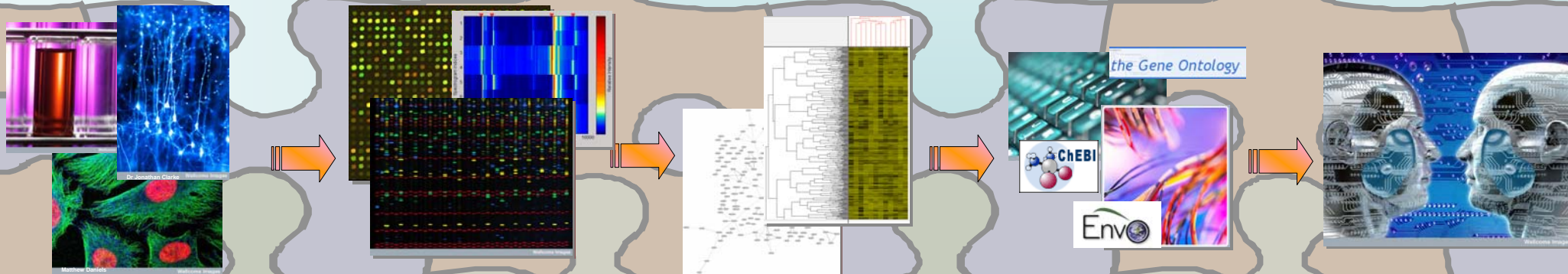
Developers Working Group

The Developers Working Group consists of all developers within the communities collaborating in the development of OBI.

Advisory Group

The Advisory Group consists of individuals invited by the Coordination Committee to provide expert advice in areas such as ontology best practices and technical implementation issues.

OBI: Connecting the pieces...



Design & Inputs:
OBI covers inputs to experiments such as your materials, your 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
material transformation
assays

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, Disease Ontology
OWL

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

*OBI Consortium (in alphabetical order): Ryan Brinkman, Bill Bug, Helen Causton, Kevin Clancy, Christian Cocos, Mélanie Courtot, Eric Deutsch, Liju Fan, Dawn Field, Jennifer Fostel, Gilberto Fragoso, Frank Gibson, Tanya Gray, Jason Greenbaum, Pierre Grenon, Jeff Grethe, Mervi Heiskanen, Tina Hernandez-Boussard, Allyson Lister, James Malone, Elisabetta Manduchi, Luisa Montecchi, Norman Morrison, Chris Mungall, Helen Parkinson, Björn Peters, Matthew Pocock, Philippe Rocca-Serra, Daniel Rubin, Alan Ruttenberg, Susanna-Assunta Sansone, Richard Scheuermann, Daniel Schober, Barry Smith, Holger Stenzhorn, Chris Stoeckert, Chris Taylor, John Westbrook, Joe White, Trish Whetzel, Stefan Wiemann

Funding: This work is partially supported by grant funding from the National Institute of Biomedical Imaging and Bioengineering, National Institutes of Health (R01EB005034, NIH P41 HG003619) and EC EMERALD project (LSHG-CT-2006-037686).

<http://obi.sourceforge.net>
Join our mailing list
obi-users@googlegroups.com

