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## ABSTRACT

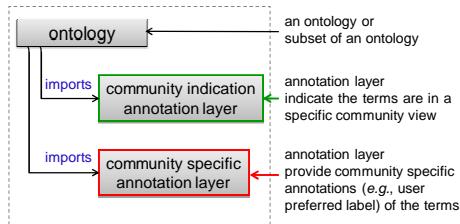
Reference ontologies are often very large and complex. When applied to a specific application, generally a subset of one reference ontology is needed. Moreover, the labels of ontology terms that were given in the perspective of ontology developers might not be preferred labels to the end users. Therefore, it is desirable to have a community view of a reference ontology that is a subset of the ontology including the terms needed for a particular application or community with user-preferred labels. Ontodog is a web-based system to support generation of ontology community views. Ontodog allows users to provide terms of interest in a source ontology and customized annotation information, such as user-preferred label. With these inputs, Ontodog can extract a subset of the source ontology containing all the terms of interest and generate user specified annotations in RDF/XML format (i.e., OWL files) which can be used to build an ontology community view. Currently over 100 ontologies including all OBO Foundry ontologies are available in Ontodog to generate views for a specific application or community. We demonstrate the application of Ontodog in generating ontology community views using the Ontology for Biomedical Investigations (OBI)<sup>[1]</sup> as the source ontology.

Ontodog website: <http://ontodog.hegroup.org/>

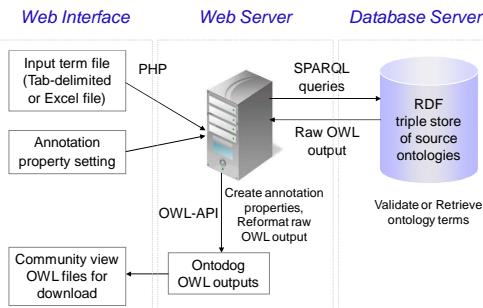
## Ontology Community View

- a subset of the whole ontology or tagged subset of terms in the whole ontology to meet users' specific need
- contains user specified annotations (e.g., user preferred label) where needed

### Ontology Community View



## System Architecture



### Ontodog workflow

- The input data is processed using PHP.
- SPARQL queries are issued against an RDF triple store to validate whether terms exist in the source ontology or retrieve terms from the source ontology.
- OWL-API is used to create annotation properties and reformat the files in RDF/XML format as output files.
- Then the RDF/XML format output files are provided to the users for download.

## References:

- Brinkman RR, et al (2010) Modeling biomedical experimental processes with OBI. *J. Biomed. Semantics*. 1(Suppl. 1), S7.
- Xiang Z, et al (2010) OntoFox: web-based support for ontology reuse. *BMC Res Notes*. 3:175.

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## Features and Usage

### Ontodog

<http://ontodog.hegroup.org/>

Ontodog data input:

(1) Provide Ontodog input term file (Microsoft Excel file or tab-delimited text file. see [help](#) or use [tool to generate template file](#)):

Upload: [lobireleases2012-01-18mergedOBI\\_FGED.xlsx](#)  \* Required

(2) Select one source ontology: \* Required

Ontology for biomedical investigations (OBI)

Or enter your own source ontology and SPARQL endpoint: [Example](#)

Input term file:

A list of terms in a source ontology with required information to generate the view

Settings for Ontodog output files: \* Please check at least one file

(1) Output File 1: InSubSet annotation ontology ([help](#))

(1) URI of owl file (e.g.: [http://purl.obolibrary.org/obo/FGED\\_inSubset.owl](http://purl.obolibrary.org/obo/FGED_inSubset.owl), optional):

InSubSet annotation layer OWL file

(2) Annotation Property URI (default: <http://www.geneontology.org/formats/obol#inSubset>).

(3) Annotation Value (e.g.: SLIM, FGED, IEED ...):

\* Required for output file 1

User preferred label annotation layer OWL file

(4) Output File 2: User preferred annotation ontology ([help](#))

NOTE: This file includes user-preferred label defined in Ontodog input term file (e.g., OBI term 'selective maintained organism'= FGED term 'strain').

(1) URI of owl file (e.g.: [http://purl.obolibrary.org/obo/FGED\\_annotation.owl](http://purl.obolibrary.org/obo/FGED_annotation.owl)):

(2) \* Required for output file 2

Annotation Property URI (one child term of IAO: alternative term, e.g.: [http://purl.obolibrary.org/obo/OBI\\_9991119](http://purl.obolibrary.org/obo/OBI_9991119))

or label of the Annotation Property if not defined. A new term will be generated.

Subset of source ontology OWL file

Retrieved using OntoFox SPARQL related term retrieval approach [2]

(3) Language of annotation values used: English

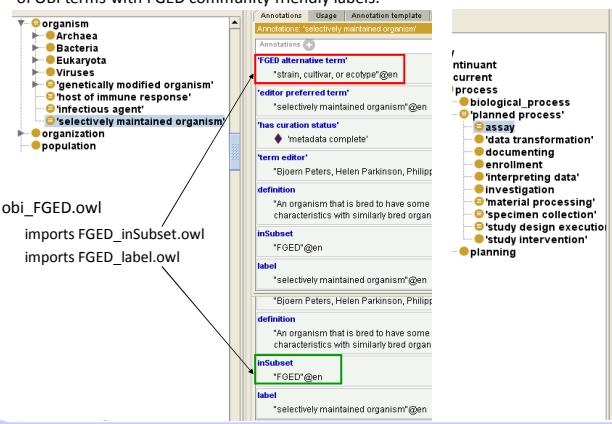
Reset

Input term file (tab-delimited or Excel file, template file can be generated by Ontodog)

A	B	C	D	E
Source ontology term IRI	Source ontology term label	Include in View	User-preferred label	Include all children
<a href="http://purl.obolibrary.org/obo/OBI_0001182">http://purl.obolibrary.org/obo/OBI_0001182</a>	negative binding datum	<input checked="" type="checkbox"/>		
<a href="http://purl.obolibrary.org/obo/OBI_0001183">http://purl.obolibrary.org/obo/OBI_0001183</a>	epitope protection from tumor challenge experiment	<input checked="" type="checkbox"/>		
<a href="http://purl.obolibrary.org/obo/OBI_0001184">http://purl.obolibrary.org/obo/OBI_0001184</a>	epitope protection experiment	<input checked="" type="checkbox"/>		
<a href="http://purl.obolibrary.org/obo/OBI_0001185">http://purl.obolibrary.org/obo/OBI_0001185</a>	selectively maintained organism	<input checked="" type="checkbox"/>		
		<input checked="" type="checkbox"/>	yes	strain, cultivar, or ecotype
			indicate terms are chosen for inclusion in the view	indicate all children of the chosen term will be included in the view

## Use Cases: OBI FGED View, OBI Core

**OBI FGED view:** a view generated for the Functional Genomics Data (FGED) community, a simplified set of OBI terms with FGED community friendly labels.



**OBI core:** a view contains all OBI core terms with labels in different languages



## Summary

- A web system that generates ontology community views with customized annotations
- Easy to use with minimal ontology knowledge and no installation required
- Currently only supports ontologies in OWL format

\* Authors contribute equivalently