

OBO-Edit 1.1 Officially Released

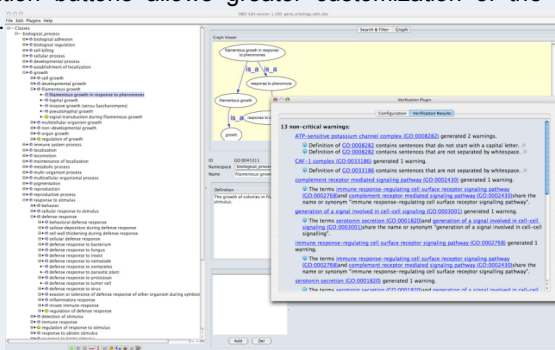
This month OBO-Edit 1.1 becomes the GO Consortium's official editing tool. Bug fixes, small interface improvements, and major new features include:

- * *The Verification System* – This plugin will run quality-control checks on an ontology.
- * *Auto-commit Text Edits* – An "auto-commit" mode is available to complete a text edit.
- * *User-defined customization of OBO-Edit* – The introduction of XML sub-layouts, an OSL scripting language, and Filter Modification buttons allows greater customization of the OBO-Edit data model and user interface.

OBO-Edit can be downloaded from:
<http://www.oboedit.org/>

OBO-Edit tip: OBO-Edit can load files from the disk OR from a URL.

Choose the "File -> Load..." menu option, choose the OBO File Adapter, and type:
"http://www.geneontology.org/ontology/gene_ontology.obo" into the filename box.



Where did the 'unknown' terms go?

Good principles of ontological design state that terms should represent biological entities that actually exist, e.g., functional activities that are catalyzed by enzymes, biological processes that are carried out in cells, specific locations or complexes in cells, etc. To adhere to these principles the Gene Ontology Consortium has removed the terms, "biological process unknown" (GO:0000004), "molecular function unknown" (GO:0005554) and "cellular component unknown" (GO:0008372) from the ontology.

The "unknown" terms violated this principle of sound ontological design because they did not represent actual biological entities but instead represented annotation status. Annotations to "unknown" terms distinguished between genes that were curated when no information was available and genes that were not yet curated (i.e., not annotated). Annotation status is now indicated by annotating to the root nodes, i.e. "biological_process" (GO:0008150), "molecular_function" (GO:0003674), or "cellular_component" (GO:0005575). These annotations continue to signify that a given gene product is expected to have a molecular function, biological process, or cellular component, but that no information was available as of the date of annotation.

Adhering to principles of correct ontology design should allow GO users to take advantage of existing tools and reasoning methods developed by the ontological community.

New AmiGO URLs

The Gene Ontology project has recently moved AmiGO, the web application used to view GO data, to a new hostname: <http://amigo.geneontology.org>. AmiGO is now running on faster servers to enable easy browsing and speedy retrieval of data.

We strongly recommend updating any URLs to point to amigo.geneontology.org, for example:

Old URL for GOID- GO:0004022:
<http://www.godatabase.org/cgi-bin/amigo/go.cgi?view=details&depth=1&query=GO:0004022>

New URL for the same GOID will be:
<http://amigo.geneontology.org/cgi-bin/amigo/go.cgi?view=details&depth=1&query=GO:0004022>

View Expanded Newsletter Online: <http://www.geneontology.org/newsletter/archive/200705.html>

To Receive Future Newsletters: Subscribe to the GO Friends mailing list (gofriends@geneontology.org)

Contact the Gene Ontology Consortium: Please send comments or questions to gohelp@geneontology.org

New electronic GO annotation method using gene orthology data from Ensembl

The GOA group, in collaboration with Ensembl, announces a new electronic method for making GO annotations based on curated gene orthology data obtained from the Ensembl Compara system. This method provides an additional 26,616 annotations for the human, mouse, rat, chicken, cow, fruitfly, and mosquito proteomes (GOA release, 30th April 2007).

Genes that have manually curated GO annotations based on experimental evidence (IDA, IEP, IGI, IMP, or IPI) are used as the source to annotate genes in one or more target species. Only one-to-one and apparent one-to-one orthologies are used in order to transfer the annotations. GO annotations using this technique receive the evidence code IEA and the Ensembl protein identifier of the annotation source is indicated in column 8. In the GOA gene association files these annotations can be distinguished by the GO_REF:0000019 displayed in column 6 (<http://www.geneontology.org/cgi-bin/references.cgi>) and 'Ensembl' is acknowledged in column 15. These annotations have been produced since December 2006 and are updated monthly.

Questions? Contact: goa@ebi.ac.uk

Public GO Database MySQL mirror now available

A public GO MySQL mirror at the EBI now offers a remote connection to a regularly updated mirror of the GO schema including all IEA data. Connection details are:

```
user: go_select
password: amigo
host: mysql.ebi.ac.uk
port: 4085
```

Example connection from command line:
\$ mysql -hmysql.ebi.ac.uk -ugo_select -pamigo -P4085

See :
<http://www.geneontology.org/GO.database.shtml#SQL>

Questions? Contact:
gohelp@geneontology.org