The Gene Ontology Newsletter

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The Reference Genome Project

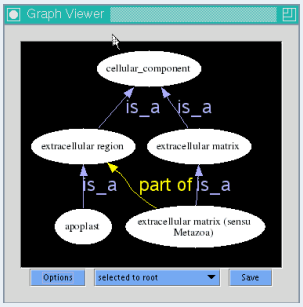
In early 2006, the GO consortium initiated the reference genome project to provide GO annotations for a set of model organisms. Representatives from twelve model organism databases, for the organisms - *A. thaliana* (thale cress), *C. elegans* (nematode), *D. rerio* (zebrafish), *D. discoideum* (slime mold), *D. melanogaster* (fruit fly), *E. coli*, *G. gallus* (chicken), *H. sapiens* (human), *M. musculus* (mouse), *R. rattus* (rat), *S. cerevisiae* (baker's yeast) and *S. pombe* (fission yeast), are working as a team to annotate human disease genes and their orthologs or similar genes in the other genomes. Special effort will be taken to capture the experimental evidence that describes the gene's biological role in these organisms, as this information can also be used for functional assignments of genes in newly sequenced genomes. Annotations related to this project are included in the files that can be downloaded from the FTP site (ftp://ftp.geneontology.org/pub/go/gene-associations).

Paper Highlight: Human Breast and Colorectal Cancers

Sjoblom *et al*. (Science 2006 314:268-274), as part of the Cancer Genome Atlas Project (http://cancergenome.nih.gov/index.asp), identified 189 genes that were mutated at significant frequencies in the genomes of human breast and colorectal cancer tumors. The authors use GO annotations, InterPro domains and literature sources to show that the mutated genes in both cancers are enriched for roles in cellular adhesion and motility, signal transduction and transcription regulation. Publicly available GO annotations and ontologies have been widely used for analyzing data clusters of genes generated by microarray expression studies. Sjoblom *et al*. extend the use of GO into mutational studies to query underlying mechanisms of pathology.

OBO-EDIT Tip: Graph Viewer

The OBO-Edit Graph Viewer Plugin is a new way of visualising the GO tree. It uses the open source GraphViz package to draw parts of an OBO-Edit ontology as a user-configurable graph, as opposed to the standard tree view. Full instructions for setting up the Graph Viewer Plugin can be found in the OBO-Edit user guide, which is available from the 'Help' menu in OBO-Edit.



Improvements to Representing Immunology

We have implemented improvements to the representation of immunology in the biological process ontology. These aim to provide a comprehensive representation of immunological processes, improve the organization of immunology-related terms, and revise poorly formulated terms already present. Sets of new terms have been created to cover areas like mucosal immunity, tolerance induction, and B cell differentiation (see http://www.godatabase.org/cgi-bin/amigo/go.cgi?view=details&search_constraint=terms&depth=0&query=GO:0002376). Discussion at the GO Content Meeting in November 2005 led to a consensus regarding a better high-level structure for immune system process terms, including the existing immune response hierarchy, and modifications in the relationship of the immune and inflammatory response terms to the defense response terms. We hope that with these improvements, the GO will better reflect current literature and knowledge in the area of immunology.

'Gene of the Quarter'

A gene from the reference genome project's current annotation list will be highlighted in the next issue.

Upcoming Meetings

Plant and Animal Genome XV Conference
January 13-17, 2007
http://www.intl-pag.org

GO and PAMGO workshop
January 14, 2007
http://www.intl-pag.org/15/15-gene-ontology.html
Town and Country Convention Center, San Diego, California

Developing the Sequence Ontology (SO)

The SO group held a workshop in September to develop areas of the ontology relating to mobile elements and kinds of replicons. Domain experts with microbiological and viral backgrounds attended and provided much-needed insight into the terms and structure they required to be able to annotate sequence from non-eukaryotic domains of life. Several important changes were made to the ontology. For example, the definition of chromosome was broadened and subtypes added that are differentiated by the following criteria: RNA or DNA, single- or double-stranded, and linear or circular transposable elements and regulatory regions. As an aside from the main proceedings, RNA editing in Trypanosomes and the kinetoplast structure were also discussed. The workshop has proved to be a successful first step towards building collaborations with these communities.