

New AmiGO Release

April 2008 saw a new release of AmiGO, the official GO consortium tool for searching and browsing the GO database. AmiGO 1.5 has a new search engine and incorporates two new tools, Term Enrichment and GO Slimmer. There are also more download options (gene association, RDF/XML, and OBO formats), bar charts to show the distribution of annotations beneath a term, and a slew of improvements and bug fixes to the interface and behind the scenes.

A More Relevant Search

When you search for a gene product or term, AmiGO will now return the results sorted by relevance, bringing more salient hits to the top of the result set. The sort order is now customizable, and users can set their sort parameter of choice. If there are no matches in the fields initially specified, AmiGO will automatically search other fields. Try it out at <http://amigo.geneontology.org/cgi-bin/amigo/search.cgi>

255 results for **transcription** in terms fields **term accession, term name, synonyms**
Filter search results

rel ↓	Accession , Term	Ontology
<input type="checkbox"/>	GO:0006350 : transcription [show def]	10804 gene products view in tree biological process
<input type="checkbox"/>	GO:0009299 : mRNA transcription [show def]	17 gene products view in tree biological process
<input type="checkbox"/>	GO:0009303 : rRNA transcription [show def]	56 gene products view in tree biological process

Screenshot of the results of a search for 'transcription'

Enrich Your AmiGO Experience

The Term Enrichment tool can be used to discover what a set of genes may have in common by examining annotations and finding significant shared GO terms. The algorithm employed by the tool attempts to determine whether an observed level of annotation for a group of genes is significant within the context of annotation for all genes within the genome; examples of studies that have used this algorithm are PMID:15492223 and PMID:14561723. AmiGO's Term Enrichment tool, which is based on the GO-TermFinder perl module by Gavin Sherlock and Shuai Weng at Stanford University, allows users to specify a list of genes, define a background set against which the significance will be calculated and set the *p*-value [significance indicator] cut-off. Term enrichment is a very handy method for analyzing data from large scale experiments, such as gene clusters from microarray expression data. The Term Enrichment tool can be found at http://amigo.geneontology.org/cgi-bin/amigo/term_enrichment

Slim Your GO

Sometimes it can be useful to get an overview of a data set by viewing the high level terms to which gene products are annotated; this is the function of GO Slimmer. GO Slimmer is an adaptation of the map2slim script by Chris Mungall. By mapping the granular annotations of a query set up to a chosen group of broad, high-level parent terms, one can view the distribution of annotations more easily. The GO Slimmer tool simply bins annotations up to high level terms without calculating significance. Slim down your annotation set at <http://amigo.geneontology.org/cgi-bin/amigo/slimmer>

Future Plans for Ontology Development

Having successfully implemented the *regulates* relationships in the biological process (BP) ontology, we now plan to add *regulates* relationships within the molecular function (MF) ontology and between the BP and MF ontologies. Adding these relationships greatly improves the ability of the ontology to represent biology completely and accurately. This allows users to ask more complex questions, such as "which gene products either regulate kinase activity or are kinases?".

We will make the implied relationships between MF terms and the corresponding 'regulation of molecular function' BP terms explicit. For example:

regulation of kinase activity (BP) *regulates* kinase activity (MF)

Similarly, we will make implicit regulatory relationships between terms within the MF ontology explicit. For example:

kinase regulator activity (MF) *regulates* kinase activity (MF)

The former will be the first inter-ontology links in the GO vocabularies and may cause errors with loading or parsing scripts that do not allow inter-ontology links. The addition of these links also has major implications for tools that ignore relationship types when summarizing annotations. For example, if your tool lumps annotations to 'kinase regulator activity' together with the *regulates* parent 'kinase activity', users will retrieve gene products that function as kinase regulators (and not necessarily as kinases!) in a query for kinases.

A test file with the BP-MF links is available at http://www.geneontology.org/scratch/regulates_relations_examples/go_regt_est_noPosNeg_withPF_noXP.obo

We plan to implement these links in the live ontology on November 30th, 2008. Please provide feedback to us regarding this plan.

EXP: Inferred from Experiment

A new evidence code, EXP, has been created for groups contributing high-quality manually-curated GO annotations from published experimental results, but who are unable to apply a specific experimental evidence code to each annotation. The EXP code is the parent code for the IDA, IPI, IMP, IGI and IEP experimental codes and can be used where any of the assays described by these codes is reported; however, we greatly encourage groups who annotate manually to GO to use one of the more specific experimental codes instead of EXP.

Currently EXP annotations are being supplied by the Reactome group, who have released almost 6,000 EXP annotations in the last month. As with all other manual evidence codes, EXP annotations are available via AmiGO and included in all downloadable files.

Further information is available on the GO website at <http://www.geneontology.org/GO.evidence.shtml#exp>

Upcoming Meetings and Workshops

22-27 Jul 2008: Yeast Genetics and Molecular Biology
University of Toronto, Ontario, Canada <http://www.yeast-meet.org/>

View Expanded Newsletter Online: <http://www.geneontology.org/newsletter/archive/200805.html>

To Receive Future Newsletters: Subscribe to the GO Friends list at <http://genome.stanford.edu/mailman/listinfo/gofriends>

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