ImmPort Gene Ontology

Gene Ontology

The Gene Ontology (GO) consists of three structured, controlled vocabularies that describe gene products in terms of their associated biological processes, cellular components, and molecular functions in a species-independent manner. GO is being developed by the GO Consortium (http://www.geneontology.org). The use of GO terms by several collaborating databases facilitates uniform queries across them. The controlled vocabularies are structured so that you can query them at different levels. For example, you can use GO to find all the gene products in the mouse genome that are involved in signal transduction, or you can zoom in on all the receptor tyrosine kinases.

Java Runtime Environment Program Needed

To view the ontology, you need a Java Runtime Environment program on your local computer. This program is freely available for download. If your local computer does not have this program installed, the ImmPort system will automatically ask if you would like to download the program. Click "Yes." The download will proceed automatically to a wizard installation, after which the ontology tree view will appear (see Figure 1). The tree view display will enable you to browse the ontology.

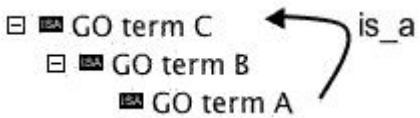
Figure 1. Ontology Browser Tree View

Gene Ontology, Continued

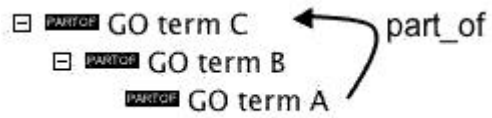
Lineage(s)

The GO ontologies are structured as a directed acyclic graph (DAG), which means that a child (more specialized) term can have multiple parents (less specialized terms). A child term can have one of two different relationships to its parent(s): is_a or part_of. The same term can have different relationships to different parents. For example, the child 'GO term 3' may be an is_a of its parent 'GO term 1' and a part_of its other parent, 'GO term 2':

The is_a relationship means that the term is a subclass of its parent. For example, mitotic cell cycle *is_a* cell cycle. The is_a relationship is transitive, which means that if 'GO term A' is a subclass of 'GO term B', and 'GO term B' is a subclass of 'GO term C', 'GO term A' is also a subclass of 'GO term C':



The part_of relationship used in GO is usually type 'necessarily is_part', which means that wherever the child exists, it is as part of the parent. Like is_a, part_of is transitive, so that if 'GO term A' is part_of 'GO term B', and 'GO term B' is part_of 'GO term C', 'GO term A' is part_of 'GO term C':



Gene Ontology, Continued

Annotations

Specific information about a class. The following provides more details on annotation information presented in this section. At a minimum, annotation information consists of a definition, namespace, and label. Other information (e.g., synonyms) is not provided for all records.

alt_id: Defines an alternate ID for this term. A term may have any number of alternate IDs.

def: Provides a definition of the GO term.

synonym: The synonym relationship types are-

exact_synonym: The term is an exact synonym (e.g., *ornithine cycle* is an exact synonym of *urea cycle*).

narrow_synonym: The synonym is narrower or more precise than the term name (e.g., *pyrimidine-dimer repair by photolyase* is a narrow synonym of *photoreactive repair*).

broad_synonym: The synonym is broader than the term name (e.g., *cell division* is a broad synonym of *cytokinesis*).

related_synonym: The terms are related (e.g., *cytochrome bc1 complex* is a related synonym *of ubiquinol-cytochrome-c reductase activity).*

namespace: The namespace to which terms are assigned. The six namespaces are:

Molecular Function
Cellular Component
Biological Process
Obsolete Molecular Function
Obsolete Cellular Component
Obsolete Biological Process

subset: Indicates a term subset to which the term belongs (e.g., subset: goslim_yeast). A term may belong to any number of subsets. GO Consortium has prepared GO slims, 'slimmed down' versions of the ontologies that allow annotating genomes or sets of gene products to gain a high-level view of gene functions.

xref_analog: A dbxref that describes an analogous object in another vocabulary.

label: Provides the name of the concept.

comments: Provides more information about the term and its usage.

Obsolete Terms

A term that is no longer used is not deleted but is tagged "obsolete." A term can become obsolete when it is removed or redefined. Obsolete terms can have up to three top nodes: Obsolete Molecular Function, Obsolete Cellular Component, and Obsolete Biological Process.

Relationships (Object Properties)

Relationships are properties by which one class is related to another class in the ontology. The GO has two types of relationships: is_a and part_of. However, the Relationships (Object Properties) section makes note of only part_of relationships. Furthermore, this section may be empty if no relationship has been used for modeling.