Técnicas de lA para Biologia

9 - OBO Language and Gene Ontology

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OBO Language and Gene Ontology

OBO Language

Overview

- Open Biomedical Ontologies (OBO) Language
- Developed by the Gene Ontology (GO) Consortium
- Main target the GO
- Adopted by numerous bio-ontologies
- Subset of the semantics of OWL 2 language

OBO Ontologies

- Composed of
- A header
- Provides information about the ontology
- A set of stanzas
- Correspond to the content of the ontology

OBO header

- Information about
- Format
- Version date
- Subsetdef indications Slims
- top-level terms
- Synonyms
- Name
- Metaproperties

OBO header Example

Gene Ontology

```
format-version: 1.2
data-version: releases/2023-04-01
subsetdef: chebi ph7 3 "Rhea list of ChEBI terms representing the major species
     at pH 7.3."
subsetdef: gocheck do not annotate "Term not to be used for direct annotation"
subsetdef: goslim yeast "Yeast GO slim"
synonymtypedef: syngo official label "label approved by the SynGO project"
synonymtypedef: systematic synonym "Systematic synonym" EXACT
default-namespace: gene ontology
ontology: go
property value: http://purl.org/dc/elements/1.1/description "The Gene Ontology
     (GO) provides a framework and set of concepts for describing the functions
     of gene products from all organisms." xsd:string
property value: http://purl.org/dc/elements/1.1/title "Gene Ontology" xsd:string
property value: http://purl.org/dc/terms/license http://creativecommons.org/
     licenses/by/4.0/
property value: owl:versionInfo "2023-04-01" xsd:string
```

OBO stanzas

- Contain key-value lines
- Refer to
- Universal types classes/concepts ([Term])
- Type definitions properties/roles ([TypeDef])
- Instances objects/individuals ([Instance])
- Classified into namespaces
- For GO:
- Molecular function
- Biological process
- Cellular component

OBO stanzas

- Alternative identifiers
- Definition of the item
- with reference to the source(s)/author(s)
- Subsets to which this item belongs
- Different semantic links
- Synonyms
- External references
- Relations between terms
- Logical definitions
- Comments indicated with !

OBO stanzas - Example

```
[Term]
id: GO:0000003
name: reproduction
namespace: biological process
alt id: GO:0019952
alt id: GO:0050876
def: "The production of new individuals that contain some portion of genetic
     material inherited from one or more parent organisms." [GOC:go_curators,
     GOC:isa complete, GOC:jl, ISBN:0198506732]
subset: goslim agr
subset: goslim chembl
subset: goslim flybase ribbon
subset: goslim pir
subset: goslim plant
synonym: "reproductive physiological process" EXACT []
xref: Wikipedia:Reproduction
is a: GO:0008150 ! biological process
disjoint from: GO:0044848 ! biological phase
```

OBO stanzas - Example

Also definitions of relations

```
[Typedef]
id: part_of
name: part of
namespace: external
xref: BFO:0000050
is_transitive: true
inverse_of: has_part ! has part
```

OBO stanzas - Example

Such definitions can be used in other stanzas

```
[Term]
id: GO:0000139
name: Golgi membrane
namespace: cellular_component
def: "The lipid bilayer surrounding any of the compartments of the Golgi
    apparatus." [GOC:mah]
is_a: GO:0098588 ! bounding membrane of organelle
relationship: part_of GO:0005794 ! Golgi apparatus
```

Logical relations

- Subclasses is_a
- Class Disjointness disjoint_from
- Property characteristics
- Transitivity is_transitive
- Inverse properties inverse_of
- Logical definitions
- Set of lines starting with intersection_of
- Equivalent to the conjunction of these terms/representations

OBO stanzas - Example

Logical definition

```
[Term]
id: GO:0000019
name: regulation of mitotic recombination
namespace: biological_process
def: "Any process that modulates the frequency, rate or extent of DNA
        recombination during mitosis." [GOC:go_curators]
synonym: "regulation of recombination within rDNA repeats" NARROW []
is_a: GO:0000018 ! regulation of DNA recombination
intersection_of: GO:0065007 ! biological regulation
intersection_of: regulates GO:0006312 ! mitotic recombination
relationship: regulates GO:0006312 ! mitotic recombination
```

OBO Language and Gene Ontology

Gene Ontology

Overview

- Comprehensive model of biological systems
- From the molecular level to larger pathways, cellular and organism-level systems
- Computational representation of scientific knowledge about the function of genes
- Taking into considerations all possible organisms
- Widely used to support scientific research
- Cited in tens of thousands of publications
- Linked to many other biomedical ontologies

Main Idea

- Understanding gene function is one of the primary aims of biomedical research
- Experimental knowledge obtained in one organism often applicable in others
- If Organisms share relevant genes inherited from common ancestors
- Gene Ontology consortium appeared in 1998 with genom studies of three model organisms
- Drosophila melanogaster (fruit fly)
- Mus musculus (mouse)
- Saccharomyces cerevisiae (baker's yeast)
- Create collaborative classification schema for gene function
- Today extended to thousands of organisms

Usage Overview

- Cross-species comparisons
- Gene-expression profiling experiments
- Automatic annotation of expression sequence tags (EST) and genomes
- Comparative genomics
- Network modeling
- Analysis of semantic similarity

Three Subontologies

- Molecular Function
- Biochemical activity of a gene product
- On a molecular level of granularity
- No indication when or where event occurs (or purpose)

Term	Term ID	Definition
mannosyltransferase activity	GO:0000030	Catalysis of the transfer of a mannosyl group to an acceptor molecule, typically another carbohydrate or a lipid
zinc binding	GO:0008270	Interacting selectively and noncovalently with zinc (Zn) ions

Three Subontologies

- Biological Process
- Biological objective to which gene (product) contributes
- Assemblies of molecular function, collection of events with beginning and end
- At the level of granularity of the cell or organism

Term	Term ID	Definition
ossification	GO:0001503	The formation of bone or of a bony substance, or the conversion of fibrious tissue or of cartilage into bone or a bony substance
regulation of glial cell proliferation	GO:0060251	Any process that modulates the frequency, rate or extent of glial cell proliferation

Three Subontologies

- Cellular Component
- Location where gene product is active

Term	Term ID	Definition
Golgi apparatus	GO:0005794	A compound membranous cytoplasmic organelle of eukaryotic cells, consisting of flattened, ribosome-free vesicles arranged in a more or less regular stack
viral capsid	GO:0019208	The protein coat that surrounds the infective nucleic acid in some virus particles

Relations

- Subclasses is_a
- Part-whole relations part_of
- E.g. nucleus is part of a cell $nucleus \sqsubseteq \exists part_of.\ cell$
- Relations between processes regulates
- ullet With subrelations $positively_regulates$ and $negatively_regulates$
- Whole-part relations has_part
- Inverse to part_of
- But the established relations are not necessary inverse $nucleus \sqsubseteq \exists has_part.chromosome$
- Does not imply that every chromosome is part of a nucleus

OBO Language and Gene Ontology

Annotations

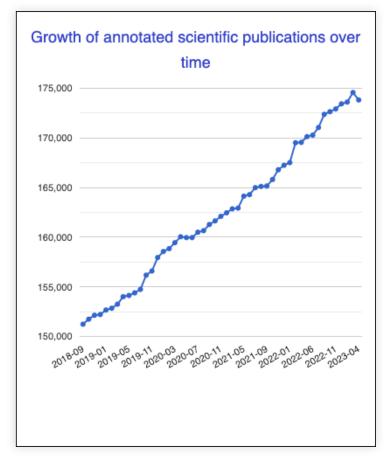
Overview

- Used during curation process
- Terms of GO do not refer to specific genes
- Rather to their characteristics
- Annotation indicates that a GO term applies to a particular gene product
- Biocurators read full-text articles in their area of expertise and add information to a database using structured vocabularies, such as GO

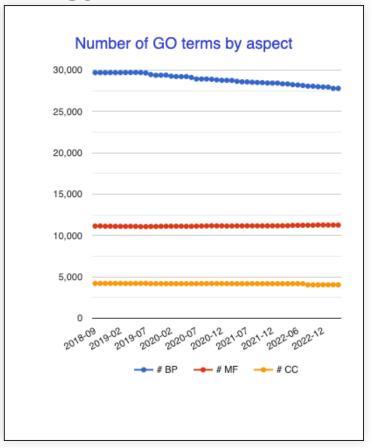
Some Statistics for GO

- Release April 2023
- Number of annotations: 7,442,411
- Number of annotated scientific publications: 173,800
- Annotated gene products: 1,502,221
- Annotated species: 5291

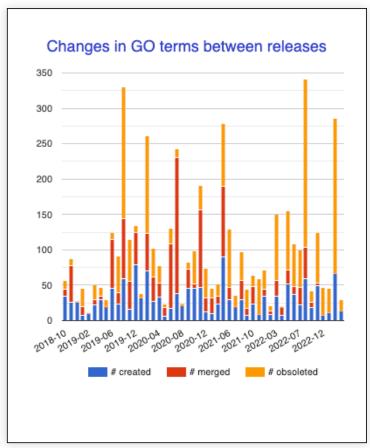
Growth of Annoted Publications



Terms per Subontology



Changes in GO terms



Annotation information

- Gene identifier
- GO term
- Type of evidence to support annotation
- reference to the evidence
- Further complementary data (on database, synonyms, species etc.)

Evidence for Gene Functions

- Tradeoff between coverage and accuracy
- Highest-quality annotations from experiments
- Computational analyis based on in silico analysis
- Sequence orthology genes in two different species have common evolutionary origin
- E.g., because of that location/type of gene in a species can be inferred
- Author statement evidence
- For references to articles that refer to papers with the original research
- Curatorial evidence based on inference by curator from GO annotations
- ND no biological data available

Inferred from Electronic Annotations

- Generated automatically, and not validated (yet)
- Two kinds:
- Map functional data from other databases with different but compatible vocabulary
- E.g. UniProt in molecular biology with different goals (compared to GO)
- MGI map UniProt keywords to GO terms to create GO annotations automatically
- Use common origin of genes to pass annotations from well-studied organisms to less-studied organisms

General Principles (from GO webpage)

- Annotations represent normal functions of gene products
- A gene product annotated to zero or more terms from each ontology
- Each annotation supported by a GO evidence code from the evidence and conclusions ontology and a references
- Gene products annotated to the most granular term in the ontology that is supported by available evidence
- Annotation to a GO term implies annotation to all its parents
- Annotations may change over time and reflect the current view
- Open world assumption lack of annotation role still unknown

OBO Language and Gene Ontology

Summary

- OBO Language
- Gene Ontology
- Annotations

Further reading:

- Robinson and Bauer, Introduction to Bio-Ontologies, Chapters 4.1 and 5
- Dessimoz and Skunca, The Gene Ontology Handbook
- GO webpage http://geneontology.org/