# Gene Ontology

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- Problems with biological databases
- The answer to the problems

### 2 Database structure

- General decisions and techniques
- The three domains

### 3 Tools

- General information
- A small selection of tools

# Why Gene Ontology?

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- $\Rightarrow$  No way to perform an **automated search**
- ⇒ Unification of terms needed to allow simultaneous searches on many databases
- $\Rightarrow$  Ontologies

Introduction 0●0 Database structure 0000000

Problems with biological databases

## Why Gene Ontology? (2)

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- Genetical knowledge **spread** over lots of different projects
- There are genes and proteins shared by most or even all living cells
- Knowing a protein's function in one organism helps to understand its function in other organisms
- Interoperability of databases should be ensured to enable automatic transfer of annotations
- Search queries covering **several** databases while applying **filters** concerning i.e. a biological function needed

The answer to the problems

# What is Gene Ontology?

- Founded in 1998 as collaboration of:
  - Flybase
  - Saccharomyces Genome Database
  - Mouse Genome Database
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## What is Gene Ontology?

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- Tries to build a **set of ontologies** providing unified terminologies for a set of domains
- Since its foundation **13 projects** joined the consortium and another **4 are contributing associates**
- On March 25th, 2009 GO contained 27009 terms

### Three domains

 GO covers three different domains to describe gene products:



- Cellular component
- 2 Molecular function
- Biological process

## Three domains

 GO covers three different domains to describe gene products:



- Cellular component
- 2 Molecular function
- Biological process
- Every gene product can be annotated with one or more terms from each of these ontologies
- Not meant to provide a complete cover of biology, but consensus terminologies used by all participating projects

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("cell part" part of "cell")

regulates: in a biological process the former has an influence on the latter

("translational frameshifting" regulates
"translation")

• There are transitive relations between these relationships

## Screenshot: Term "translation"

### translation

	Term information 🖡 Term lineage 🖡 External references 🖡 6399 gene product associations 🌩				
Term Information					
Accession	GO:0006412				
Ontology	biological process				
Synonyms	exact: protein anabolism exact: protein biosynthesis exact: protein synthesis exact: protein synthesis exact: protein translation alt_id: G0:0006416 alt_id: G0:006453 alt_id: G0:0064337				
Definition	The chemical reactions and pathways resulting in the formation of a protein. This is a ribosome-mediated process in which the information in messenger RNA (mRNA) is used to specify the sequence of amino acids in the protein. [source: GOC:go_curators]				
Comment	None				
Subset	goslim_generic goslim_pir goslim_plant goslim_yeast				
	Back to top				

## Screenshot: Term "translation"

Term Lineage					
Switch to viewing term ancestors					
▼ Filter tree view ℓ       Filter Gene Product Counts       Data source       All       CGD       Analissma phagocy       dictyBase       Bacillus anthraci					
GO:0034961 : cellular biopolymer biosynthetic process [19483 gene products]     Actions     GO:003692 : cellular polysaccharide biosynthetic process [779 gene products]     GO:006260 : DNA replication [1817 gene products]     GO:0006260 : poly-gamma-glutamate biosynthetic process [0 gene products]     GO:0006350 : transcription [10789 gene products]     GO:0006412 : translation [6399 gene products]     GO:0006412 : translation [6399 gene products]	i: Reset View ie browser				
Image: Construction of the second	5				
<ul> <li>G0:0006413 : translational initiation [455 gene products]</li> <li>G0:0006415 : translational termination [93 gene products]</li> <li>G0:0006418 : tRNA aminoacylation for protein translation [810 gene products]</li> <li>G0:0006414 : translational elongation [1654 gene products]</li> <li>G0:0044267 : cellular protein metabolic process [17264 gene products]</li> </ul>					

# GO: Cellular component

- Describes **locations** on the level of subcellular structures and macromolecular complexes
- Multicellular (or anatomical) locations and individual proteins are **not included**
- Root node: cell (GO:0005623)
- Locations are clearly seperated into classes like "Intracellular" or "Plasma membrane"

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### Example

```
sarcoplasmic reticulum
```

- [p] sarcoplasmic reticulum membrane
- ---[i] free sarcoplasmic reticulum membrane
- ---[i] junctional sarcoplasmic reticulum membrane
- [p] sarcoplasmic reticulum lumen

# GO: Molecular function

- Covers abilities a gene product has, i.e. transport or binding
- Are often named "activity" to clearly seperate them from the gene product itself
- There are **no terms** describing more than one function at the same time

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### Example

```
regulation of transcription
[i] regulation of transcription factor activity
---[i] positive reg. of transcription factor activity
---[i] negative reg. of transcription factor activity
[i] regulation of transcription, start site selection
```

## GO: Biological process

- Contains terms that describe series of events or molecular functions
- Terms describe processes or represent a collection of processes
- Processes might be summarized in a single "development node" to prevent a proliferation
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### Example

```
cell cycle
[p] cell cycle process
---[i] cell cycle phase
-----[i] anaphase
----[i] centromere seperation
```

# Standard definitions

- For all three ontologies there are defined standards
- They set rules for:
  - the choice of term names
  - the creation of **new subclasses**
  - tests to ensure consistency and correctness
  - **ontology specific things** like terms for start and end of a process
- These standards are especially relevant if you want to **contribute** to GO

General information

# Working with GO

- There is a **huge amount of tools** (over 100) that either use GO or can be used to work with GO
- Only **two official tools** are maintained by the GO consortium
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- The remaining ones were created by the community for many different tasks
- On the GO homepage there is a complete list available: http://www.geneontology.org/GO.tools.shtml
- $\Rightarrow$  I will only provide a very short overview

Official tools

### AmiGO

- Web-based **browsing and searching** tool to access the GO database
- Searches GO for terms or gene products
- Shows the **position** of terms in the ontology (parents, siblings)
- Gene products are shown with their GO term **annotations**

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### OBO-Edit

- Graph-based tool to view and edit OBO format ontologies
- Easy user interface focussing on the display of the ontology structure

## Unofficial tools

Tasks performed by these tools:

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- Analyzation of data sets
   e.g. BiNGO, EasyGO, FatiGO, GOArray, MultiGO, ...
- Analysis of the GO database itself and other things e.g. CateGOrizer, FunSpec, GOChase, WEGO, Whatizit, ...

Introd		

## The last slide

### Thank you for listening.

### References



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Gene Ontology Consortium.

Homepage: www.genetontology.org.