

Web Presence: The Bad, the Ugly, the Good

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Introduction

What we have, and why it's a problem.

Condition

- Static HTML
 - Controlled by timed SCM trigger
 - Who will climb into the lion's den?
- Dynamic HTML
 - Complicated code for common actions
- Knowledge gaps
- Hard to keep organized and up to date

Cohesion

- Too much all over the place
 - Conversation all over the internet
 - No single point of entry for users
 - Where does any community go? Where do you go?
- What happens when new stuff comes along?
- Who knows how to edit the site? Post news? Find online GO conversations?

Cohesion

the Gene Ontology

Search

Downloads Tools Documentation Projects About Contact

Welcome to the Gene Ontology website!

The Gene Ontology project is a major bioinformatics initiative with the aim of standardizing the representation of gene and gene product attributes across species and databases. The project provides a controlled vocabulary of terms for describing gene product characteristics and gene product annotation data from GO Consortium members, as well as tools to access and process this data. [Read more about the Gene Ontology...](#)

Search the Gene Ontology Database

Search for genes, proteins or GO terms using **AmiGO** :

● gene or protein name ○ GO term or ID

AmiGO is the official GO browser and search engine. [Browse the Gene Ontology with AmiGO.](#)

The Gene Ontology project very much encourages input from the community into both the content of the GO and annotation using GO. We are very happy to work with others to ensure that the GO is both complete and accurate, and we also very much encourage contributors to submit GO annotations for inclusion in the GO database. [Please contact us.](#)

The Gene Ontology Consortium is supported by a grant from the National Human Genome Research Institute (NHGRI) grant [5R01HG001717-08](#). [See the full list of funding sources.](#) The Gene Ontology Consortium would like to acknowledge the assistance of many more people than can be listed here. Please visit the [acknowledgements page](#) for the full list.

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 Helpdesk • [Site](#) • [Terms of use](#) • [News](#) • [RSS](#)
 Member of the [Open Biological and Biomedical Ontologies](#)

Quick Links

- Tools
- AmiGO browser
- Submit GO annotations
- OBO-Edit ontology editor
- Ontology downloads
- Annotation downloads
- Database downloads
- Documentation
- GO FAQ
- GO on Bioinformatics
- Central GO

News

- GO on Twitter
- Finding updates...
- GO releases
- GO news RSS feed
- GO on Facebook

Cohesion

The screenshot displays the Gene Ontology website interface. At the top, there is a search bar with the placeholder text "gene or protein name" and a "GO" button. Below the search bar, the main heading reads "Welcome to the Gene Ontology website!".

The page is divided into several sections:

- Search the Gene Ontology Database:** A section with a search input field and a "GO" button, labeled "Search for genes, proteins or GO terms using AmiGO".
- Navigation Menu:** A horizontal menu with links for "page", "discussion", "view source", and "history".
- Main Page:** A section titled "Welcome to the Gene Ontology Consortium Wiki" containing:
 - Contexts [new]:** A list of links including "GOC Public Resources", "GO Frequently Asked Questions", "Community Annotation Pages", "Web Pages", and "Database Query Pages".
 - GO Public Resources:** A section with a link to "GO Frequently Asked Questions".
 - Community Annotation Pages:** A section with links for "Cardiovascular Genes", "Immunology", "Lung Development", "Muscle Biology", and "Reference Genome Genes".
 - Web Pages:** A section with links for "GO Home", "GO Documentation", and "GO Downloads".
 - Database Query Pages:** A section with a link for "AmiGO".
 - GO Working Group Wiki:** A section with a note: "These pages are limited to use by members of the GOC." and a link for "User Advocacy".
- Left Sidebar:** A vertical navigation menu with links for "Main Page", "Gene Practices", "User Advocacy", "Annotation", "Reference Genome", "Software and Utilities", "GO Leadership", "GO Managers", "Consortium Meetings", "Working Groups", "Progress Reports", "Publications", "Calendar", and "BioCantor Forum".
- Right Sidebar:** A section titled "Quick Links" with a list of links including "AmiGO browser", "Search GO annotations", "OBO-Edit ontology editor", "Ontology downloads", "Annotation downloads", "Database downloads", "Documentation", "GO HQ", "GO on SourceForge", and "Contact GO".

At the bottom of the page, there are navigation icons for back, forward, and search.

Cohesion

The screenshot displays the Gene Ontology website, which is characterized by a highly cluttered and overlapping layout. The main content area is filled with multiple text blocks, search bars, and navigation menus that do not clearly separate different sections of the site. Key elements include:

- Top Navigation:** A blue header with the Gene Ontology logo, navigation links (Downloads, Tools, Documentation, Projects, About, Contact), and a search bar.
- Main Content Area:** A large text block titled "Welcome to the Gene Ontology website!" followed by a detailed paragraph about the project's goals. Below this is a search bar for the Gene Ontology Database and a section for "New Links" with a list of external resources.
- Right-Side Sidebar:** A section titled "GO News" with a sub-header "What's Going on?" and a search bar. Below this is a "root" section with a list of links and a "Main GO Site" section with a list of links.
- Bottom Section:** A "Main Page" section titled "Welcome to the Gene Ontology Consortium" with a list of links to various resources. Below this is a "GO Public Resources" section with a list of links to frequently asked questions, community annotation pages, web pages, and database query pages.
- Overlapping Elements:** A "Cardiovascular GO Annotation Initiative Newsletter" section is overlaid on the right side, and a "Final Renal GO Annotation Newsletter" section is overlaid at the bottom right. A "GO Working Group Wiki" section is also visible at the bottom.

The overall design is a dense collection of text and links, with little visual hierarchy or clear separation between different types of content, leading to a confusing user experience.

Cohesion

The image shows three distinct digital touchpoints for the Gene Ontology (GO) project, illustrating a lack of cohesion:

- Gene Ontology Website (Left):** A functional website with a search bar, navigation tabs (Downloads, Tools, Documents), and a main heading "Welcome to the Gene Ontology". It includes a search section for genes, proteins, or GO terms, and a sidebar with a search box and a list of links.
- Facebook Page (Middle):** A Facebook profile for "Gene Ontology" featuring a group photo of project members. The page includes a bio, a "Like" button (271 likes), and a "Recent Posts" section with a post from April 2012.
- Gene Ontology Newsletters (Right):** Two newsletter headers: "Annotation Initiative Newsletter June 12" and "Annotation Newsletter (April 2012)".

The overall layout is fragmented, with no clear visual or functional integration between these three elements, which is the "Bad" and "Ugly" aspects of the design.

Cohesion

The image displays three overlapping screenshots from the Gene Ontology (GO) ecosystem, illustrating a lack of cohesion:

- Top Left (GO Website):** Shows the main homepage with a navigation bar (Downloads, Tools, Documents) and a search bar. The text reads: "Welcome to the Gene Ontology project. The Gene Ontology project is a major bioinformatics initiative of genes and gene product attributes across species and database vocabularies of terms for describing gene product characteristics. Consortium members, as well as tools to access and process GO Ontology..."
- Top Right (Facebook Page):** Shows the GO Facebook page with a large group photo and a post titled "Gene Ontology is on Facebook." The post says: "To connect with Gene Ontology, sign up for Facebook today." It includes "Sign Up" and "Log In" buttons.
- Bottom Left (Twitter Feed):** Shows a Twitter feed for GO News. The header says "GO News @news4go". The bio states: "The Gene Ontology project provides a controlled vocabulary to describe gene and gene product attributes in any organism. <http://www.geneontology.org>". The feed lists several tweets, including:
 - "Cardiovascular GO Annotation Initiative Newsletter June 12" (27 Jun)
 - "Open post for collaborations with human phenotype ontology" (18 May)
 - "First Renal GO Annotation Newsletter (April 2012)" (20 Apr)
 - "Cardiovascular GO Annotation Initiative Newsletter April 12" (11 Apr)
 - "Fluorescent GO News, GOOSE, Berkeley mirror, and AmiGO Labs outage (3/9-3/11)" (7 Mar)
 - "New January 2012 Renal GO Annotation Newsletter" (10 Jan)
- Bottom Right (GO Website - Newsletter Section):** Shows a search bar and a section titled "Annotation Initiative Newsletter June 12". The text reads: "Issued by the Cardiovascular Gene Ontology Annotation Initiative is now available at www.geneontology.org/Newsletters/Issue18. Annotation Initiative represents a collaboration between University College London and the European led by the British Heart Foundation (grant SP/07/007/23674). [ggo.org](http://www.ggo.org)"

Cohesion

The collage consists of several overlapping screenshots:

- Gene Ontology Website:** Shows the homepage with a 'Welcome to the Gene Ontology' message, a search bar, and a 'Search for genes, proteins or GO IDs' input field.
- Facebook Page:** Displays the 'Gene Ontology is on Facebook' announcement, a group photo of team members, and a 'Sign Up' button. It also shows a post from 'Arul Pong' asking 'Hello! How to cite GO in the paper?'.
- GO News:** A sidebar section with the GO logo and a red flower icon, containing a 'Follow GO News' form and a 'Tweets' section with recent updates.
- BioStar Forum:** A screenshot of a forum post titled 'Question: 'HOW TO' on gene ontology analysis'. The post asks for help with ontology analysis and lists six specific questions. A user named 'Sheela' has responded with a detailed list of steps.
- Announcement Initiative Newsletter:** A snippet of a newsletter titled 'Annotation Initiative Newsletter June 12'.
- Collaboration with human phenotype ontology:** A snippet of a page discussing collaboration with HPO.
- Team at the European Bioinformatics Institute:** A snippet of a page mentioning the team at EMBL-EBI.
- Annotation Newsletter (April 2012):** A snippet of a newsletter titled 'Annotation Newsletter (April 2012)'.

Question: 'HOW TO' on gene ontology analysis

Hi All,

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I am trying to make a 'HOW TO' on gene ontology analysis. If you know answer of these questions please help. I hope it will be very useful to all people who are new to gene ontology analysis and bioinformatic (like me :). Please post answers in one specific tool/language (preferable in R/Python/perl)

Give a GO ID (e.g. GO:0095342) How to:

- find all its children up-to a specific depth. For example first up-to 4th level
- find all its parents and grand parents up-to a specific height. For example up-to 4th level
- the name (prefix) of the GO ID
- draw the tree (with name (definition) & GO ID)
- find all the directly associated gene/protein with specific GO ID
- find all gene/protein associated with specific GO ID and its children (up-to level n)

Given a gene/protein ID/name (e.g. UniProtKB ID) How to:

- find all the associated GO IDs with specific type (e.g. all GO IDs associated with UniProtKB ID which are related to 'biological process')
- remove all over-represented GO IDs (from the result of last query). (e.g. GO:0090342 and GO:0050793 both are associated with p03 but as GO:0050793 is child of GO:0090342 so I want to remove GO:0090342 from the data and want to keep only GO:0050793)
- find whether a specific GO ID is associated with a given UniProtKB ID or not?



Cohesion

The collage consists of several overlapping screenshots:

- Gene Ontology (top left):** Shows the homepage with a navigation bar, a search box, and a large group photo of the team. A Facebook sign-up button is visible.
- Facebook (top center):** A Facebook post from Gene Ontology with a group photo and a sign-up button.
- JIRA Bug Tracker (top right):** A screenshot of a JIRA issue page for 'GO Helpdesk' with various filters and a 'Project Summary' bar chart.
- GO News (middle left):** A news article from GO News with a red flower logo and a 'Follow' button.
- BioStar (bottom center):** A forum post titled 'Question: HOW TO on gene ontology analysis' with a list of steps for ontology analysis.

The overall layout is cluttered and lacks a unified design, illustrating the 'The Bad' and 'The Ugly' aspects of the current state.

Cohesion

The collage consists of several overlapping screenshots from Gene Ontology (GO) related websites:

- Top Left:** The main Gene Ontology website homepage, featuring a navigation bar with 'Downloads', 'Tools', and 'Documents'. The main content area says 'Welcome to the Gene Ontology' and provides information about the project as a major bioinformatics initiative.
- Top Center:** A Facebook page for Gene Ontology, showing a group photo of the team and a sign-up button for the Facebook page.
- Top Right:** An 'Annotation Initiative Newsletter June 12' page, dated 05.06, with a search bar and a 'Search' button.
- Middle Left:** A 'GO News' page with a red flower logo and a sidebar for 'Follow GO News' with fields for name, email, and password.
- Middle Center:** A 'Biology beta' forum page titled 'Main methods used to predict functional annotations in GO'. It shows a question about inferring electronic annotations and several answers, including one from 'Sheela'.
- Middle Right:** A 'Project Summary' page with a progress bar showing 27% completion and a 'Project Summary' section with 'Open Issues' and 'By Assignee'.
- Bottom:** A detailed list of instructions for creating a gene/protein ID tree, such as '1. find all its children up-to a specific depth. For example first up-to 4th level'.

Cohesion

The image is a collage of several screenshots from the SourceForge and Gene Ontology (GO) websites, illustrating various interface elements and content. The top left shows the SourceForge logo and navigation links. The top right shows a search bar and a 'Log In' button. The middle left shows the Gene Ontology project page, including a 'Download' button and a 'Recommended Projects' section. The middle right shows a 'Gene Ontology is on Facebook' banner with a photo of people. The bottom left shows a 'Tweets' sidebar with a list of tweets. The bottom middle shows a 'What else?' section with a list of questions and answers. The bottom right shows a 'Project Summary' section with a progress bar and a 'Project Information' section.

SourceForge

Home | Science & Engineering | Bioinformatics | Gene Ontology

Summary | Files | Reviews | Support | Deviate | Installed Apps | Tracker | Mailing Lists | Code

Gene Ontology

bioinformatics | 123 Downloads (this week) | Last Update: 2012-08-12

Description

The focus of the Gene Ontology project on SourceForge, including ontology requests, software downloads, bug trackers, and much, much, more.

Gene Ontology Web Site >

Update Notifications

100% **RECOMMENDED**

User Ratings

Tweets

Open post to Disqus

Recent

Question

What else?

1. This is an interesting question but I'm not sure I can answer it. I'll leave it to the experts.

2. Thank you for the suggestion, it's by them, if I obtain answers I will report them.

3. I believe the most common source of electronic annotations comes from analysis of peptide sequences. A collection of UniProt to GO mappings were created manually and can generate GO annotations. DNA binding domains of transcription factors would be given "DNA binding" GO annotations.

4. This method has its flaws - if the domain detected has evolved away from the function used for the Interpro to GO linking, there is a potential for error in this method.

5. Update: Improve this answer

1. find all its children up-to a specific depth. For example first up-to 4th level

2. find all its parents and grand parents up-to a specific height. For example up to 4th level

3. the name (prefix) of the GO ID

4. draw the tree (with name (definition) & GO ID)

5. find all the directly associated genes/protein with specific GO ID

6. find all gene/protein associated with specific GO ID and its children (up-to level n)

Given a gene/protein ID/name (e.g. UniProtKB ID) How to:

1. find all the associated GO IDs with specific type (e.g. all GO IDs associated with UniProtKB ID which are related to 'biological process')

2. remove all over-represented GO IDs (from the result of last query). (e.g. GO:000342 and GO:0050793 both are associated with p53 but as GO:0050793 is child of GO:000342 so I want to remove GO:000342 from the data and want to keep only GO:0050793).

3. find whether a specific GO ID is associated with a given UniProtKB ID or not?

Gene Ontology is on Facebook

To connect with Gene Ontology, sign up for Facebook today.

Annotation Initiative Newsletter June 12

6/12/12

Created by the Cardiovascular Gene Ontology Annotation Initiative is now available at cardioannotation.org/Newsletters/Issue16.

Annotation Initiative represents a collaboration between University College London and the European led by the British Heart Foundation (grant IP/07/007/21674).

sfg.com

Collaboration with human phenotype ontology

12/04/05

Annotations in GO

in method used to predict the inferred

Webconfer

This is a collaboratively edited question and answer site for biology researchers, students, and students. It's 100% free, no registration required.

Got a question about the site itself? That's the place to talk about things like what questions are appropriate, what tags we should use, etc.

Tagged

Asking 5 Months Ago

Active 5 Months Ago

Community Bulletin

Join the Slack Exchange

Use code for linking for emphasis in questions

Should we (re)write ask for help?

Project Summary

3 Issues 27% Closed 4 74%

Open Issues

My Priority

By Assignee

Assigned Issues 1 33% Unassigned 2 67%

What would be better?

A lot of work to get things together.

- Content users
 - One stop shopping for correct answers
 - Easy to browse
 - No tumbleweeds
- Content creators
 - Easy central interface
 - Easy to interact with users
 - Dont' have to worry about what's under the hood
- Multiple inputs
 - Trackers, wiki, Jira, etc.
- Multiple outputs
 - RSS/Atom, Facebook, Twitter, etc.

A proposal

the Gene Ontology

Home Community Downloads Projects Tools About

Welcome to the Gene Ontology!

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The Gene Ontology project very much encourages input from the community into both the content of the GO and annotation using GO. We are very happy to work with others to ensure that the GO is both complete and accurate, and we also very much encourage communities to [submit GO annotations](#) for inclusion in the GO database. [Please contact us](#).

What's new...

GO Community

root

Cardiovascular GO Annotation Initiative Newsletter June 12

root

Active forum topics

- [Uploading annotations](#)
- [Beta testing](#)

[More](#)

Current sources

Source	Percentage
UniPro...	34.8%
ZFIN	21.9%
Fungi...	11.1%
KEGG	10.1%
RGD	10.1%
GOC	6.0%

GO Internal

- [Manager 03Oct2012](#)
- [\[GOHELP-71\] GO Help query \(from website\)](#)
- [\[GOHELP-70\] GO Help query \(from website\)](#)
- [RE: \[GOHELP-59\] Out-of-date InterPro links from AmiGO](#)
- [\[GOHELP-59\] Out-of-date InterPro links from AmiGO](#)

[More](#)

GO news feed

GO External (forums, social, etc.)

- [Retrieve all genes associated with a GO term](#)
- [Clustering genes in GO categories](#)
GO enrichment for different p values problem
[Hiding/Merging child annotations terms under the parents \[Gene Ontology\]](#)
[How to extract GO terms from a given KEGG ID](#)
[GO visualization from a set of peaks and set of ontology result files](#)
- [Best way to visualize GeneOntology enrichments for multiple datasets?](#)
- [Gene names from GO accessions numbers](#)
- [GO terms Redundancy remover](#)
- [sequences\(without ref genome\) for pathway analysis?](#)

[More](#)

A proposal: switch to Drupal

- Aggregates
 - External (non-GO) sources; internal sources
 - Control what you see in your feed (interest groups)
- Forums
 - Start our own community
 - Drive traffic towards us
- Content push
 - Facebook, Twitter
 - Whatever comes next
- Control
 - Permissions (different kinds of users)
 - Easy content creation
 - Easy day-to-day maintenance
 - Trivial to update, make changes to menus, etc.

Demo Site

Demo site at: `http://fork.lbl.gov/`

