QuickGO - Gene ontology annotation

George Georghiou [1]

- Ontologies
- Proteins
- Beginner
- 0.5 hour

The Gene Ontology Annotation (GOA) project provides high-quality functional annotations to gene products, such as proteins, protein complexes and non-coding RNAs. Currently our database contains over 390 million annotations to 60 million distinct gene products from almost 725,000 taxa. It is therefore critical to be able to easily and quickly mine and visualise the available information.

Our team is happy to announce the release of a new version of our popular web-based tool for browsing and interpreting the GO and associated annotations, QuickGO [2].

This webinar will show you how to retrieve the annotations provided for your genes or gene products and download the corresponding data set using the QuickGO browser. We will also cover where the annotations come from and the features available to help you find the right dataset for your work.

This webinar was recorded on 2nd August 2017 to coincide with the release of the new QuickGo website. The slides from the webinar can be downloaded from the materials section below. This video is best viewed using Google Chrome and in full-screen mode.

For a full list of upcoming webinars from this series, please visit our training pages [3].

Learning objectives:

- Understand the basics of gene ontology
- Evaluate the features of QuickGo and know where to get help

Your feedback

Please tell us what you thought about this webinar. Your feedback is invaluable and helps us to improve our courses and thus enhance your learning experience.

Contributors
George Georghiou [1]

EMBL-EBI
Scientific Database - Protein Function Content

George Georghiou is a scientific database curator [4] for the Gene Ontology [5] Annotation [6] (GOA [7]) project at EMBL-EBI. His work focuses on the CAFA project, co-funded by the BBSRC and NSF. Prior to joining GOA, George obtained his PhD at Stony Brook University for his research on the characterisation of small molecule inhibitors of protein kinases using X-ray crystallography [8]. He went on to conduct his postdoctoral research at the University of Dundee, where he studied the Wnk signaling pathway using CRISPR/Cas9 gene editing technology.

Alice Shypitsyna [9]

EMBL-EBI
Scientific Database Curator (Uniprot) - O'Donovan team: Protein Function Content

Alice Shypitsyna is a scientific database curator in Gene Ontology Annotation (GOA) project at EMBL-EBI. She is passionate about neurobiology, immunology and human evolution, and contributes to GO outreach by helping users through training and documentation. In her role as curator, she manually integrates recently published experimental data on human proteins and other gene products to the GOA database, and helps keep it well organised. Alice obtained her PhD in Developmental Neurobiology from the University of Constance in Germany, combining neurobiology, phylogenetics and bioinformatics, and holds a BSc/MSc in Molecular Biology from the Institute of Protein Research in Russia.

Source URL: https://www.ebi.ac.uk/training/online/course/quickgo-gene-ontology-annotation

Links
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