



BEATING HEART DISEASE TOGETHER



Cardiovascular GO Annotation Initiative

providing full GO annotation to genes associated with cardiovascular processes

Newsletter April 2010

Gene annotation

GO annotation continues to progress at UCL, and we can now report that we have associated over 12,000 GO terms to 1,600 proteins, the vast majority of which (9895 GO terms) are to human proteins (1,112 human proteins). These figures are based on the statistics available at EBI, '[current composition of UniProt-GOA](#)', released on 4th March 2010. Varsha has compiled a list of 60 genes involved in heart development, which will be annotated as part of the [Reference Genome project](#) in the coming months. This will lead to the annotation of orthologous genes across 12 different species and should not only improve the annotation of these genes but also focus the development of GO terms to describe the processes, functions and specific cellular locations relevant to heart development. Regular [GO annotation jamborees](#) are part of the ongoing GO Consortium (GOC) aim to improve annotation consistency. In February, the BHF-UCL team hosted the UK-based jamboree discussion day, focused on the annotation of [NIPBL](#) and [SLIT2](#). The participating groups in the UK and US then discussed the resulting annotations, any difficulties, inconsistencies and new GO terms. This jamboree led to the comprehensive annotation of these proteins across 12 different species, with 36 unique GO terms now associated with human [NIPBL](#), and 53 unique GO terms associated with human [SLIT2](#).

Meetings attended

Varsha attended the Computational Biology Town Meeting, at UCL, in January. This was a good opportunity to find out how computational sciences are being applied to biological problems across UCL, and led to interesting discussions at the reception about the role of biocuration in this area. At the end of March Ruth and Varsha 'remotely' attended the GOC meeting, Stanford, US. GOC conferences regularly provide WebEx and conference call facilities to maximise attendance at these meetings; however, this did lead to late nights for the UK remote attendees. Key topics included an overview of GOC management structure changes, recent improvements to the GOC browser - AmiGO, extending the evidence codes, creating links between function and process ontologies, cross-product term creation, and cell ontology. There was also a substantial discussion about 'binding' term annotations, and significant progress was made on establishing guidelines in this area. Importing high quality IMEx Consortium protein-protein interaction data was also discussed, and a range of progress reports were presented.

Upcoming meetings

In May Ruth will attend the 2nd RFH International Cardiovascular Diseases Workshop London. Following this, in June, Ruth and Varsha will be attending the GO annotation camp, Geneva. The GO annotation camp provides the opportunity for GO curators to meet to discuss and improve the consistency of GO annotation. GO is used by numerous different Model Organism Databases, therefore, it is important for the GOC to ensure there is a consistent application of GO terms, so that annotations made to one gene can be transferred to orthologous genes in different species. In addition, Varsha will be presenting a poster describing the Heart Development GO Workshop success at this meeting.

Publications

The Gene Ontology in 2010: extensions and refinements. Gene Ontology Consortium. *Nucleic Acids Research* 2010 Jan;38(Database issue):D331-5. PMID: [19920128](#)

www.cardiovasculargeneontology.com
www.ebi.ac.uk/GOA/CVI

Issue 9
Editor: [R Lovering](#)