

GenNav: Visualizing Gene Ontology as a graph

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Most browsers available for visualizing and navigating the Gene Ontology™¹ display its polyhierarchical structure as a list of indented concepts. Figure 1 partially shows, for example, how the AmiGO browser² visualizes the concept *extrinsic plasma membrane protein*. As a result, although all the information needed to transform this representation into a graph structure is present, we argue that the cognitive effort required to do this transformation is probably unnecessary.

Applying the same techniques to the visualization of polyhierarchical structures from Gene Ontology, we developed GenNav. Figure 2 shows an example of the graphs produced by GenNav. In this example, the concepts used to annotate the gene *Dystrophin* include the cellular component *extrinsic plasma membrane protein*, also represented displayed in Figure 1, so the representation of this concept can be compared across the two figures.

In a previous experiment, we developed strategies for visualizing complex, polyhierarchical structures drawn from the Unified Medical Language System® (UMLS®), and found directed acyclic graphs (DAGs) to provide suitable representations. This experiment resulted in the development of an application: the UMLS Semantic Navigator³, based, in part, on the graph visualization package GraphViz⁴.

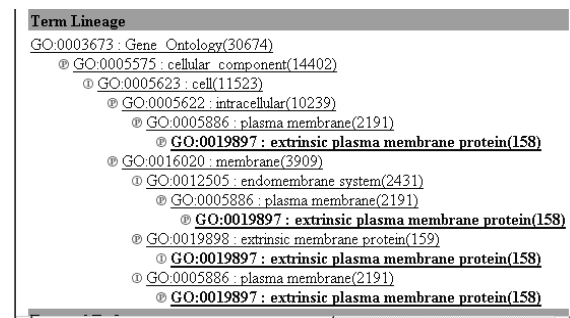


Figure 1 – The AmiGO browser.

¹ www.geneontology.org
² godatabase.org/cgi-bin/go.cgi
³ umlks.nlm.nih.gov → Resources → Semantic Navigator
⁴ www.research.att.com/sw/tools/graphviz/

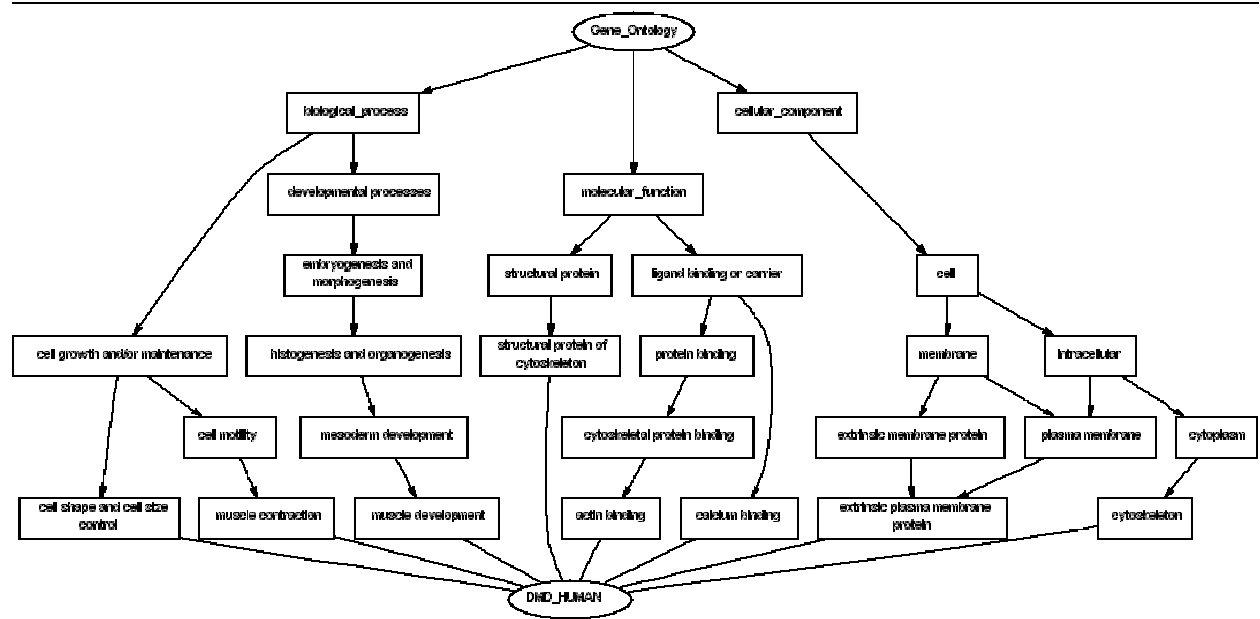


Figure 2 - Graph of the concepts related to “dystrophin” (DMD_HUMAN) in Gene Ontology.