

Poster K-1

OAT - Shows the complementarity of MeSH and GO in interpretation of gene lists



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Short Abstract: OAT is built to represent, condense and summarize the knowledge associated with a gene list. OAT uses MeSH and GO and we show that the two ontologies complement each other with surprisingly low overlap by mapping annotations to UMLS. OAT calculates test statistics and includes novel annotation sets for MeSH.

Long Abstract:

Background:

Gene expression and proteomics analysis let us analyze thousands of biomolecules in parallel, resulting in a list of interesting genes or proteins in the order of dozens or more and a list of annotation terms in the order of thousands. It is not a trivial task to understand the gene list and it would require extensive efforts to mine the overwhelming amounts of associated information from literature and databases. Thus, it is evident that we need ways of condensing and filtering the information. An excellent way to represent knowledge is to use ontologies for which it is possible to group genes or terms with overlapping context, rather than studying one-dimensional lists of keywords.

Results:

We have built the Ontology Annotation Treebrowser (OAT) to represent, condense, filter and summarize the knowledge associated with a list of genes or proteins. OAT is dynamically browsable so that a scientist can interact with the data and govern the outcome. In OAT we have harmonized the two ontologies MeSH and GO to be able to use knowledge both from the literature and the annotation projects in the same tool. We also show that the two ontologies complement each other with surprisingly low overlap by mapping annotations to Unified Medical Language System (UMLS). OAT calculates test statistics for annotation enriched branches. Furthermore, OAT includes novel annotation sets for MeSH that can not be found elsewhere.

Conclusions:

We have developed a novel annotation browser that is the first to incorporate both MeSH and GO for improved interpretation of gene lists. It is available as a public web service <http://www.ifm.liu.se/bioinfo/oat>.