QUERYING WITH TERMINOLOGICAL ONTOLOGIES AND THEIR ANNOTATIONS

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Abstract

Today, with the increasing development of computational biology, various large databases are built to describe genomic information and the used experimental data. To guarantee the consistency of biological concepts used in different databases, the Gene Ontology (GO) has been developed by the Gene Ontology Consortium to describe biological concepts and their relationships in a species-independent manner. Biologists have started to use GO terms to annotate genes in various databases. These annotations create a mapping between GO and gene products. Numerous research groups are focusing on terminological ontologies and the objects annotated using their terms to develop queries that explore the mappings between the objects and ontology and between the objects themselves. Much of this research has centered on the Gene Ontology. An investigation of the prior work serves as the basis for this thesis research which consists of integrating several queries into one software tool and extending and enriching the query techniques by examining how semantic similarity measures and user preference selection for coverage and specificity affect query results. An emphasis throughout the implementation process is that the software should be useable on other terminological ontologies with their associated annotated objects, i.e., the software querying tool should be applicable in a variety of knowledge domains.

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