

Bringing Ontology to the Gene Ontology

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Much work has been devoted to the development of the Gene Ontology (GO). GO's objective is described as "to provide controlled vocabularies"(1); its intended use is to facilitate communication between biologists by standardizing usage of terms found in database annotations. Expanding the utility of such controlled vocabularies to support bioinformatics applications would require formalizing the semantics of the background knowledge that enables human users to interpret the meaning of the vocabulary terms. In the case of GO, the meaning of GO terms would have to be clarified by domain experts, referring to the documentation describing GO itself, and evaluating any systemic issues such as polysemy. Formalization of GO's semantics would involve describing GO concepts in a formal language, constraining the logical semantics of these terms to match as closely as possible the intended interpretations. At least one research project, GONG, is underway to place GO on a firm logical footing. In this paper, we intend to explore other ontological requirements for formalizing the semantics of GO. Taking as our starting point the words used to describe the three GO hierarchies (molecular function, biological process, and cellular component) we investigate the facility with which GO concepts can be formalized using available insights from the philosophical and ontology-engineering literature.

(1)Gene Ontology General Documentation, <http://www.geneontology.org/doc/GO.doc.html>

Biographical notes:

1992, Bachelor of Science degree in Biology, Chemistry minor; Virginia Polytechnic Institute, Blacksburg, Virginia.

1993 – 1998 Molecular biology laboratory technician, departments of Microbiology and Neurology, University of Maryland at Baltimore

1999 Began work as Ontologist (Biology specialization) at Ontology Works, Inc., a company dedicated to applying principles of ontology to improve data integration, maintainability, quality, and flexibility in generated databases and other software artifacts.

Since 1999 Jennifer has participated in projects focusing on the development of ontological models of various domains, including biochemical pathways and electrical power grids.