

# Guest Editorial for Special Section on Semantic-Based Approaches for Analysis of Biological Data

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THE systematic integration of biological (e.g., *omics*) data with biological knowledge is a recent trend in bioinformatics. Current biological information is spread among multiple sources and encoded in different ontologies (e.g., gene ontology, as well as in many others hosted by the Open Biomedical Ontologies Foundry). Biological information is associated to biological concepts in a process known as annotation. The annotation of biological data with this additional information enable the use (and the development) of algorithms that use biological ontologies as a framework to mine annotated data based on the use of semantics.

The use of such annotations for the analysis of protein data is a relatively novel research area that is becoming more and more important in the field. Indeed, as shown in literature, there is a positive trend in the use of biological information in the analysis of protein data.

This special section presents some recent developments in this field. The article “Extracting Cross-Ontology Weighted Association Rules from Gene Ontology Annotations” by Giuseppe Agapito, Marianna Milano, Pietro Hiram Guzzi, and Mario Cannataro discusses the application of association rules to mine annotated data. Marco Masseroli, Arif Canakoglu, and Stefano Ceri present the application of Gene Ontology to search genomic data in “Integration and Querying of Genomic and Proteomic Semantic Annotations for Biomedical Knowledge Extraction”. Guoxian Yu, Guangyuan Fu, Jun Wang, and Hailong Zhu discuss the application of semantic and network based methods to predict protein function in “Predicting Protein Function via Semantic Integration of Multiple Networks”. The fourth paper “Ontology-Based Search of Genomic Metadata” by Javier D. Fernández, Maurizio Lenzerini, Marco Masseroli, Francesco Venco, and Stefano Ceri demonstrate the integration of different data sources by using ontologies. Finally, “Ontology-Based Prediction and Prioritization of Gene Functional Annotations” the work by Davide Chicco and Marco Masseroli highlights the use of ontologies to rank genes extracted from in silico experiments.

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