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Hierarchy-based 3D Visualization of Gene Expression Data*

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Abstract

We present a new approach to visualize complex datasets representing gene expression and pathway models from different data sources in 3D hierarchical view space using the Starlight information visualization system. With the explosive growth of proteomic and expression data of homologous genes, it becomes necessary to explore new methods to visualize and analyze related metabolic pathways to explore inherent similarities and differences of different organisms. This will enable molecular biologists to achieve a better understanding of the evolutionary relationships among species. In our project, a novel, flexible and generalizable, bioinformatics, multi-agent system, called BioMAS, is used to retrieve and integrate genomic and expression information from various databases or web sources to generate knowledge databases for organisms of interest. With chicken and human as model organisms, we describe our approach to visualize genomic data of different organisms in a hierarchical structure. The Gallus knowledge base (GallusKB) has been built up with BioMAS, by gathering and processing data from KEGG, GenBank, ProDomain, SwissPro, PSort, etc. In our visualization approach, not only the text-based data but also diagrams of pathways and chromosome of both organisms, are visualized within the 3D hierarchical view space such that data of different organisms can be compared visually. Our approach is an innovative application for comparative genomics using the Starlight system to conduct a visual analysis of pathway and gene expression data of homologous genes of different organisms.

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