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The VANTED software system for transcriptomics, proteomics and metabolomics analysis

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Abstract:

Current research in biology generates data sets of increasing size that are very difficult to manage and analyze manually. Bioinformatics tools are necessary to facilitate statistical analysis and visualization of the data. While multiple tools exist for this purpose, they are often limited to specific kinds of data or allow only certain types of analyses. Recently, we have reported on the development of VANTED, a software system that allows mapping of multi-dimensional data sets onto relevant biological networks. VANTED provides a variety of functions for network editing, data mapping and processing, statistical analysis, and visualization. This review summarizes the main features of VANTED.

Keywords:

genomics, transcriptomics, proteomics, metabolomics, biological networks, data analysis, visualization



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