

Improving Statistical Methods in Biological Pathway Analysis

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The analysis of genomics data encompasses studying the relevance of genes involved in pathways and underlying reactions. Current statistical methods for the analysis of gene and pathway relationships overlook the complex yet essential biological aspects of the pathways. The methods, often provided as tools in online open-source databases, fail to incorporate the structure and relative size of pathways, location of reactions and multiple inheritance of genes in the calculation of p -values. This talk explores various techniques that address some of these issues in an effort to accurately capture statistical significance in biological pathways.