SERBGO: ALL FOR GO AND ONE FOR ALL

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DNA microarray experiments have become popular during the last decade. The results of these experiments often consist in long lists of genes which require a biological interpretation. A useful resource for this is the Gene Ontology database (GO) and many GO-mining tools have been developed. Some of these programs are intended for functional annotation management. Others are specific for exploring and analyzing gene expression datasets. After a thorough review of GO tools we identified a list of standard functionalities. This allowed to classify the existing programs according to their capabilities. In a first approach this classification suggested that GO tools could be reduced to a few models. Based on this suggestion we performed a multivariate analysis in order to find the main commonalities in the programs features. The results of these analysis show that, whereas certain aspects appear redundantly in many tools, others are missing in most of them or contained in a single one. So, in spite of our initial impression, we concluded that this wide variety of programs is necessary. In order to help researchers to choose the suitable software for their purposes we developed SerbGO (*S*earching the *b*est *GO* tool). It is a web-based application working in two directions: one can ask for some functionalities and get the most appropriate tool for them or one can analyze an existing tool and see which features it implements.