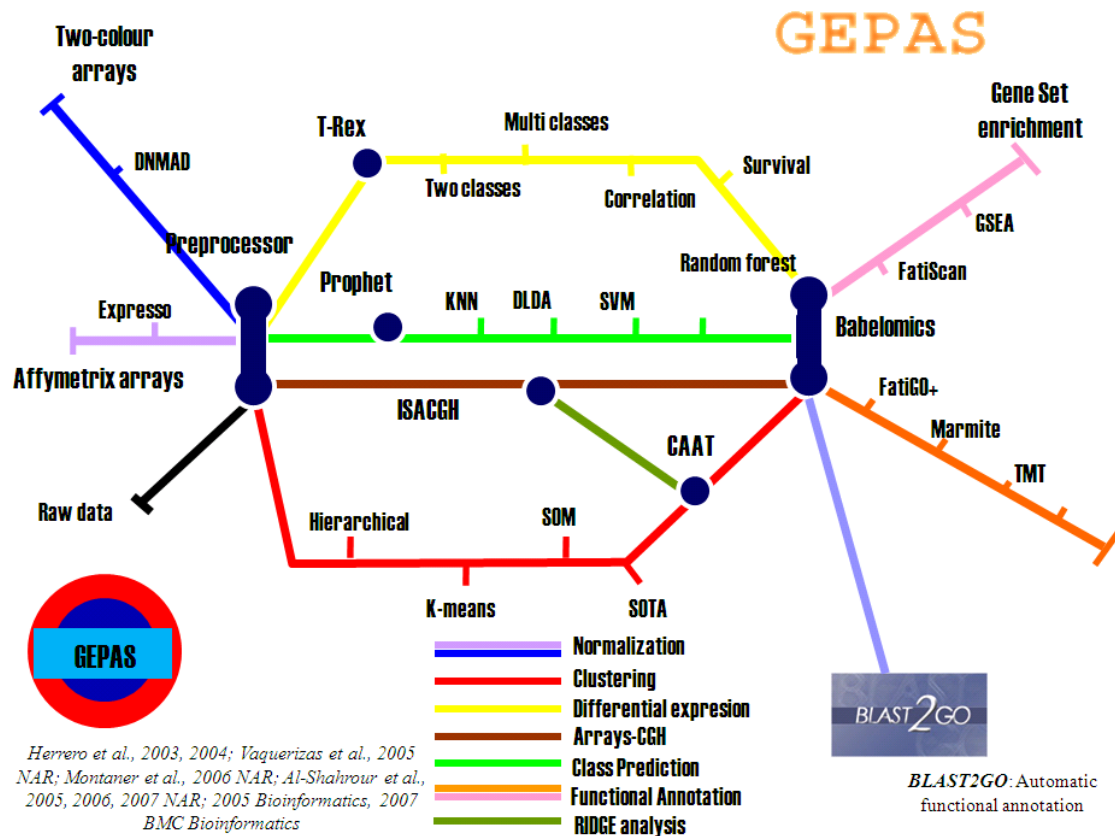# The GEPAS: a web-based suite for microarray data analysis

David Montaner, Joaquín Tárraga, Ignacio Medina, Jaime Huerta-Cepas, Pablo Minguez, Eva Alloza, Fátima Al-Shahrour and Joaquín Dopazo

Bioinformatics Department, Centro de Investigación Príncipe Felipe (CIPF), Autopista del Saler 16, E46013, Valencia, Spain

The Gene Expression Profile Analysis Suite (GEPAS) has been running for more than five years. During this time it has evolved to keep pace with the new interests and trends in the ever changing world of microarray data analysis [1-10]. GEPAS has been designed to provide an intuitive although powerful web-based interface that offers diverse analysis options from the early step of preprocessing (normalization of Affymetrix and two-colour microarray experiments and other preprocessing options), to the final step of the functional profiling of the experiment (using Gene Ontology, pathways, PubMed abstracts, etc.), and include different possibilities for clustering, gene selection, class prediction and array-CGH management. GEPAS is extensively used by researchers of many countries and its records indicate an average usage rate of more than 500 experiments per day from worldwide users (see http://bioinfo.cipf.es/access_map/map.html). The web-based pipeline for microarray gene expression data, GEPAS, is available at http://www.gepas.org

The figure shows the schematic representation of the program with all their facilities. In the last version, a new module, the Blast2GO [11], has been included. This module allows for the automatic annotation of large number of sequences to be further used with functional profiling purposes.

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