

A data mining platform for systems biology and biomarker discovery



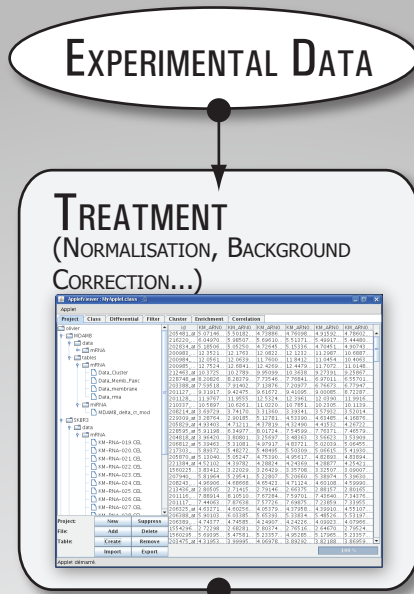
Olivier Stern¹, Raphaël Marée², Christophe Van Huffel³, Jean-François Laes⁴, Carine Michiels⁵, Lionel Flamant⁵, Véronique Mainfroid⁶, Daisy Flamez⁷, Louis Wehenkel¹, Pierre Geurts¹

(1) Department of Electrical Engineering and Computer Science, GIGA-Research, ULg, (2) GIGA Management, Bioinformatics Platform, ULg, (3) KeyMarker project - BioWin, Namur, (4) DNAvision SA, Gosselies, (5) Unité de Recherche en Biologie Cellulaire, FUNDP, Namur, (6) Eppendorf Array Technologies SA, Namur, (7) Laboratory of Experimental Medicine, ULB

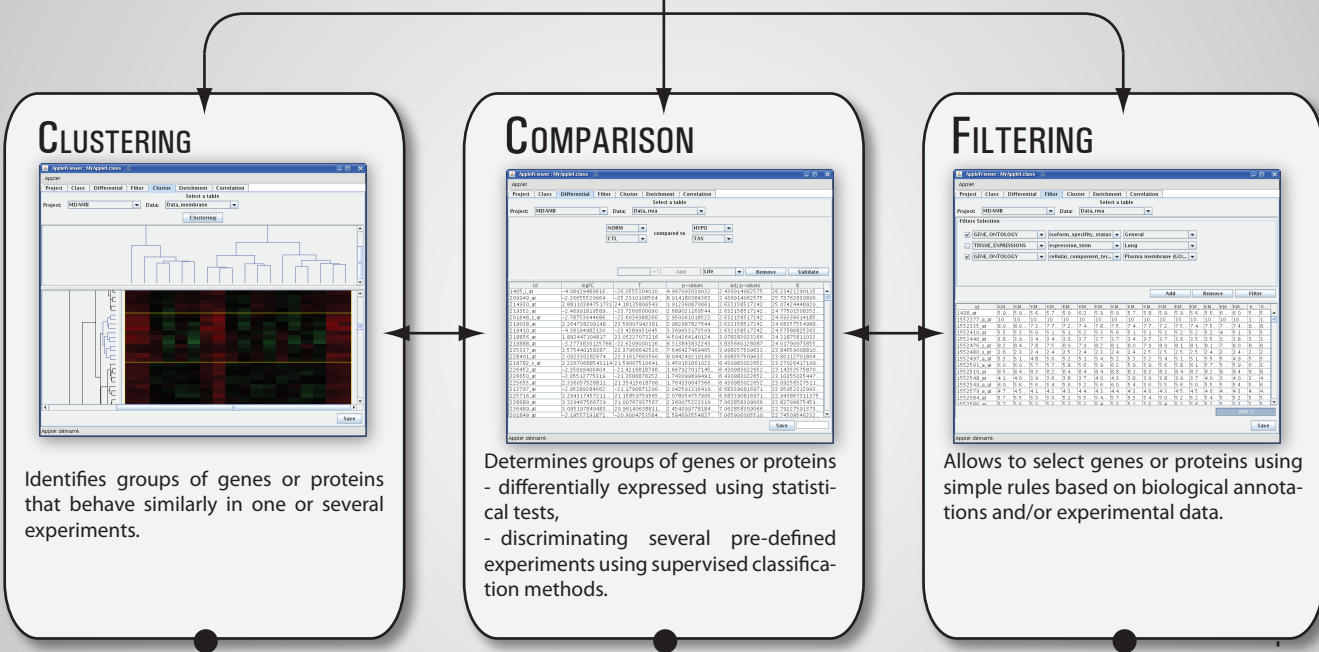


Motivation

The general goal of this research is to develop a bioinformatic strategy to discover new candidate biomarkers for some specific disease, by integrating biological knowledge available in public databases and experimental data related to this disease obtained from high-throughput instrumentations, such as transcriptomic (microarray), proteomic (mass spectrometry), and genomic (SNP) data. The resulting strategy will be implemented in a generic and flexible software platform that will allow biologists to easily instantiate this strategy on their own datasets. This research is part of the Keymarker project (Biowin), whose general goal is to identify biomarkers for molecular imagery.



A key aspect of the software is that it integrates all the steps of the analysis in a common platform, making easier the interactions between them. The platform is accessible as a web service as well as a standalone application. Future modules will be added to allow the integration of different experimental data sources (transcriptomic, proteomic, and genomic).



CLUSTERING

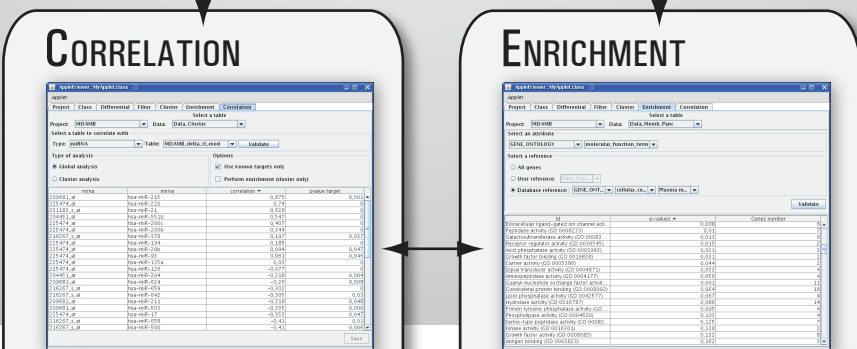
Identifies groups of genes or proteins that behave similarly in one or several experiments.

COMPARISON

Determines groups of genes or proteins - differentially expressed using statistical tests, - discriminating several pre-defined experiments using supervised classification methods.

FILTERING

Allows to select genes or proteins using simple rules based on biological annotations and/or experimental data.



CORRELATION

Analyses jointly mRNA data with other biological data such as transcription factors or micro-RNA. The method determines, from expression patterns, whether there is a link between two particular elements.

ENRICHMENT

Characterizes the groups of relevant biomarkers highlighted by the other modules (by exploiting existing annotations of the corresponding genes or proteins in biological databases).

BIOLOGICAL DATABASES

Acknowledgements
This work is supported by "Pôles de compétitivité de la région Wallonne" as part of the KeyMarker - BioWin project

