

# BioinfoGP TOOLS: SMALL UTILITIES FOR BIG RESEARCH

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## Introduction

Our service, BioinfoGP, was recently created at the Spanish National Center of Biotechnology (CNB-CSIC, Madrid, Spain) to provide research groups with analytical tools and expertise in Bioinformatics focused in Genomics and Proteomics, mainly DNA microarrays.

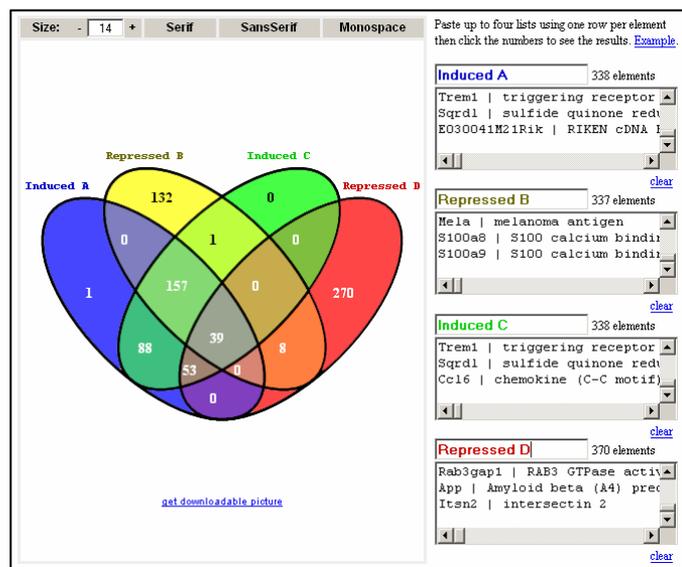
Amongst our starting developments are these two small bioinformatic tools that have demonstrated to be extremely useful for people working in the microarrays field. They are web-based and are available to the scientific community in our web page:

<http://bioinfofp.cnb.csic.es/tools>

## "Venny": An interactive tool for comparing lists using Venn Diagrams with support for up to 4 sets

Interactive Venn diagrams are used to show the relationships between several gene lists and to answer questions like: "Which genes are induced in experiment A and also in experiment B but are repressed in experiment C and experiment D?" (Up to four gene sets can be compared).

Full gene annotations (complete sentences) can be compared, making easy the interpretation of the biological meaning of the results without the need of searching for additional information in external databases.



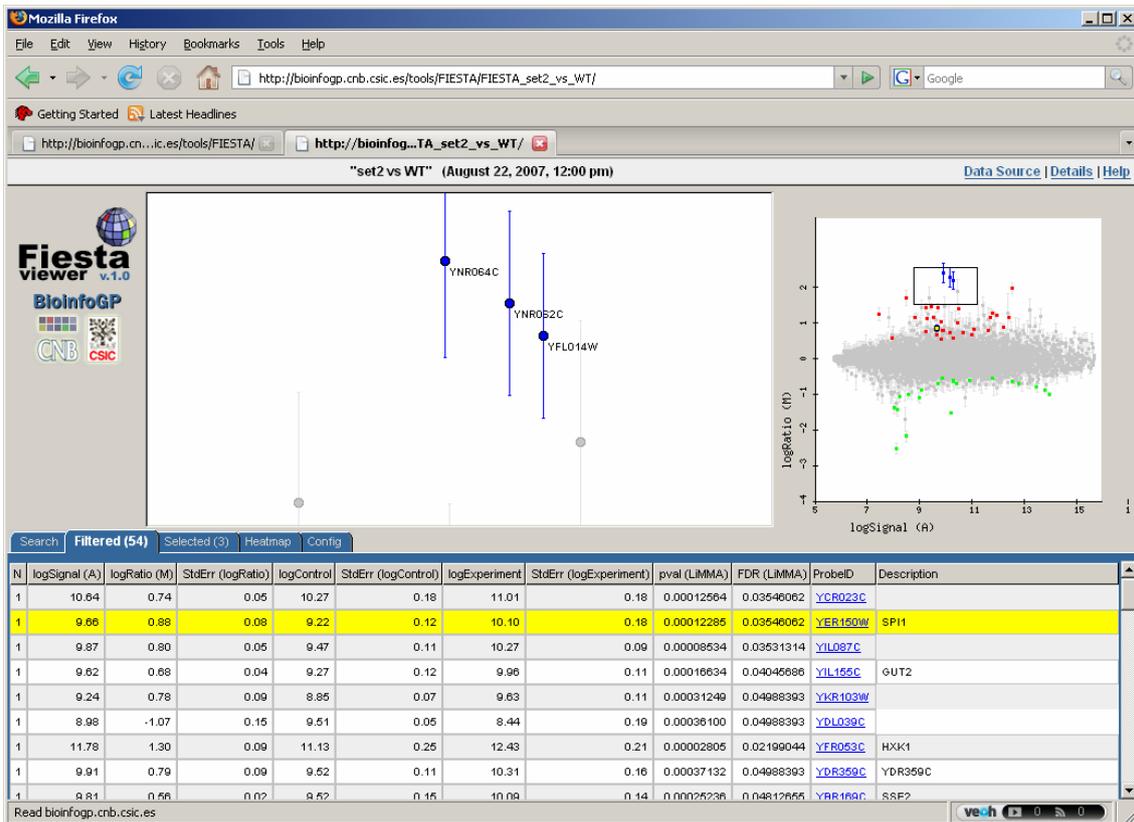
Although Venny is an on-line tool, it runs locally in the user's computer so the number of genes that can be analyzed is not limited by the amount of users accessing simultaneously to our server (in a typical PC with 256 Mb of RAM memory, four lists containing several hundred of genes each can be compared in a second or less).

Venny is accessible at: <http://bioinfofp.cnb.csic.es/tools/venny>

## "FIESTA viewer": An intuitive way of visualizing gene expression results obtained from replicated microarray experiments

Comparative microarray results are usually presented in the form of huge tables containing many pieces of information about each probe: Gene IDs, Gene Descriptions, Ratios, Intensities, p values, etc.

FIESTA converts these expression tables into interactive web pages:



Using a simple table as input, FIESTA generates several web pages containing: interactive plots where individual spots can be selected; direct links to sequence databases where consult the most updated information about any gene; heatmaps showing the logRatios or logIntensities of every single spot in each replicate; and a powerful search engine to make complex queries to filter out the most relevant genes. The result of applying a filter is updated in the plots in real-time.

The results pages are based on HTML-JavaScript web pages compatible with the most popular web browsers, including Mozilla Firefox and Microsoft Internet Explorer, so researchers can use FIESTA viewer to directly publish their results on Internet.

Visit FIESTA at: <http://bioinfogp.cnb.csic.es/tools/FIESTA>