

# Aplicaciones web en docencia estadística y análisis de datos genómicos



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# Introducción

- **Cambios tecnológicos** y demanda de herramientas estadísticas
- **Nuevo paradigma en Genómica: del gen al genoma**
  - Gran volumen de datos
  - Nuevos métodos de análisis
  - Necesidad de formación estadística específica

# Objetivos

- **Búsqueda de recursos** que faciliten el acceso y comprensión de la Estadística
- **Desarrollo de una herramienta web** para el análisis de datos genómicos

# Material y métodos

# Babelomics



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## BABELOMICS<sup>4</sup>

gene expression and functional profiling analysis suite

Babelomics is an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. This new version of Babelomics integrates primary (normalization, calls, etc.) and secondary (signatures, predictors, associations, TDTs, clustering, etc.) analysis tools within an environment that allows relating genomic data and/or interpreting them by means of different functional enrichment or gene set methods. Such interpretation is made not only using functional definitions (GO, KEGG, Biocarta, etc.) but also regulatory information (from Transfac, Jaspas, etc.) and other levels of regulation such as miRNA-mediated interference, protein-protein interactions, fact-mining module definitions and the possibility of producing de novo annotations through the Blast2GO system.

Babelomics has been extensively re-engineered and now it includes the use of web services and Web 2.0 technology features, a new user interface with persistent sessions and a new extended database of gene identifiers. Babelomics is available at <http://babelomics.biocit.ujf.es>

**Sign in**

e-mail:

password:

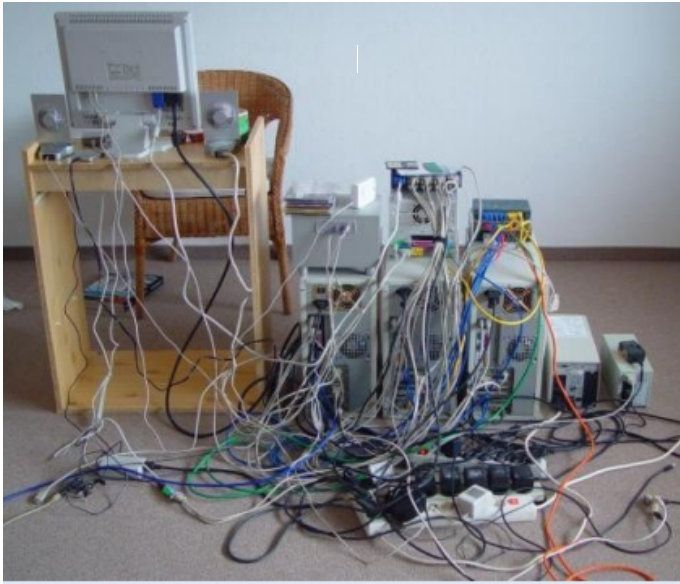
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## Estructura computacional



50 workshops y cursos (2004-2012)



<http://bioinfo.cipf.es/courses>

## BABELOMICS<sup>4</sup> gene expression and functional profiling analysis suite

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password:

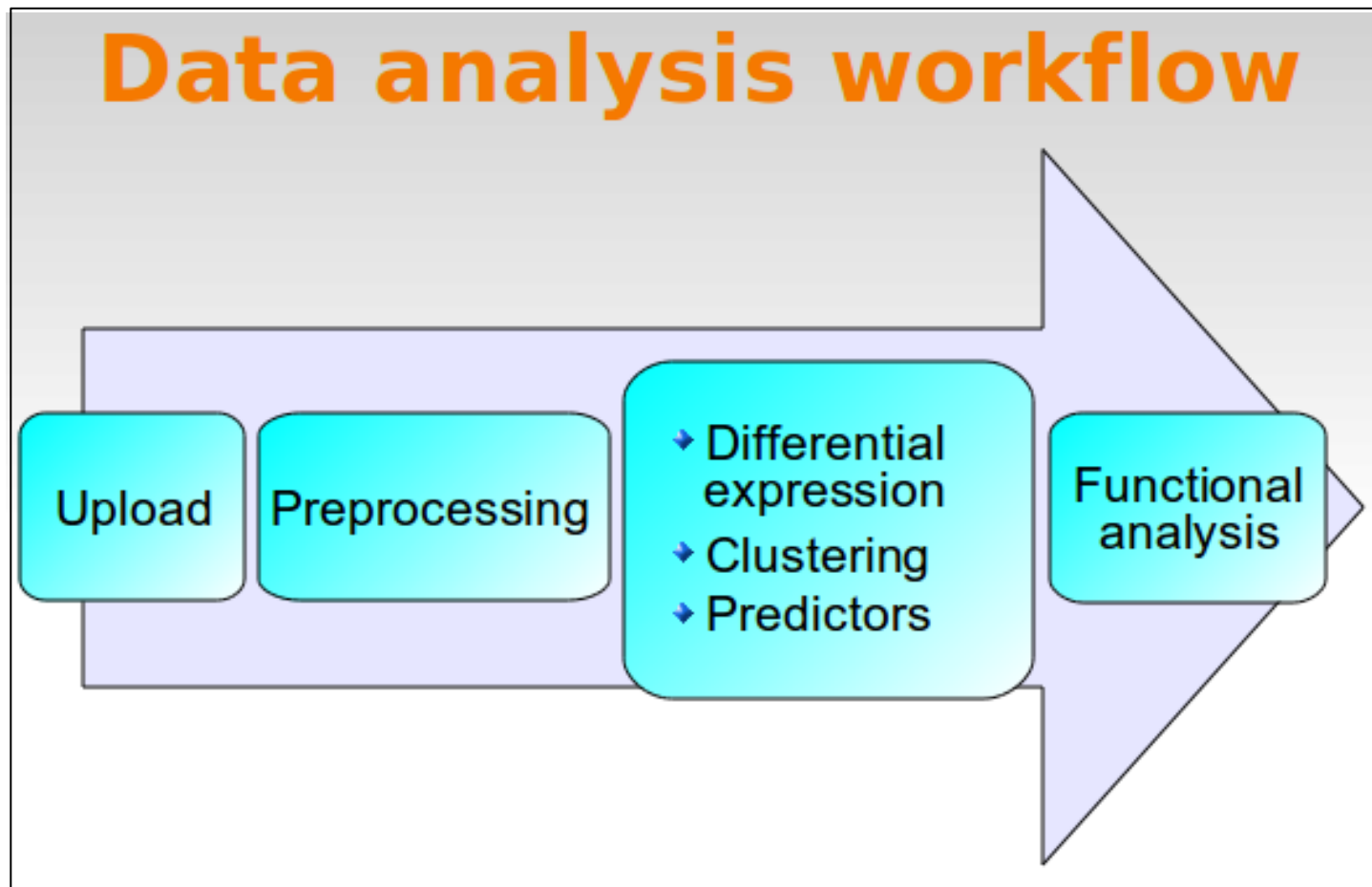
[Forgot you password?](#)

► or start as anonymous user

*(your work will be lost after logout session)*

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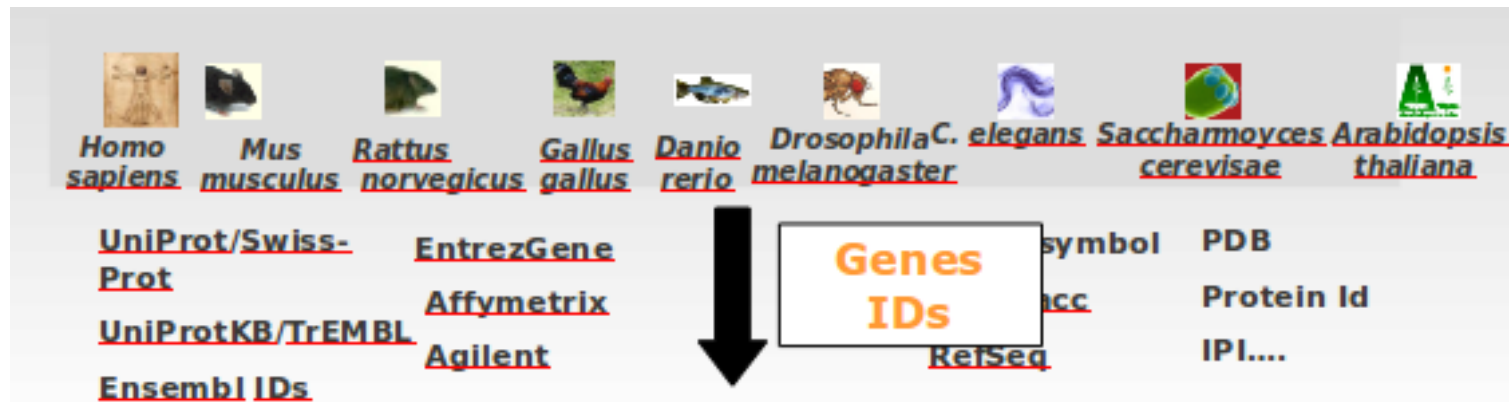
<http://babelomics.bioinfo.cipf.es/>



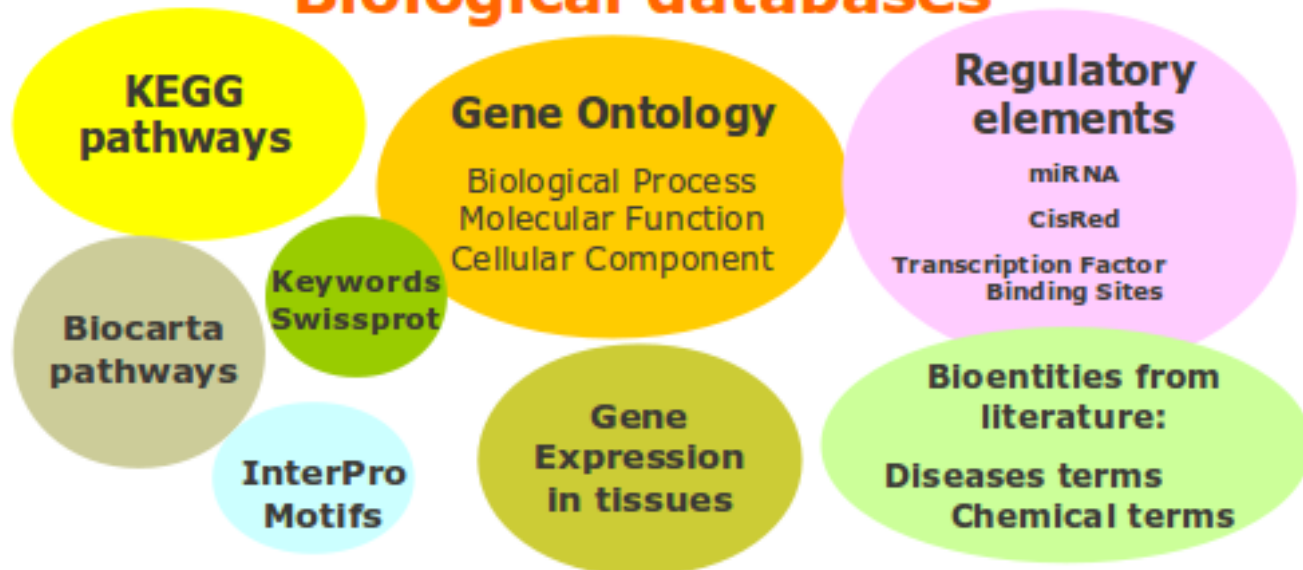


# Material y métodos

# Babelomics



## Biological databases



# Material y métodos

# Babelomics

Limma, t-test:

$$H_0: \mu_1 = \mu_2$$

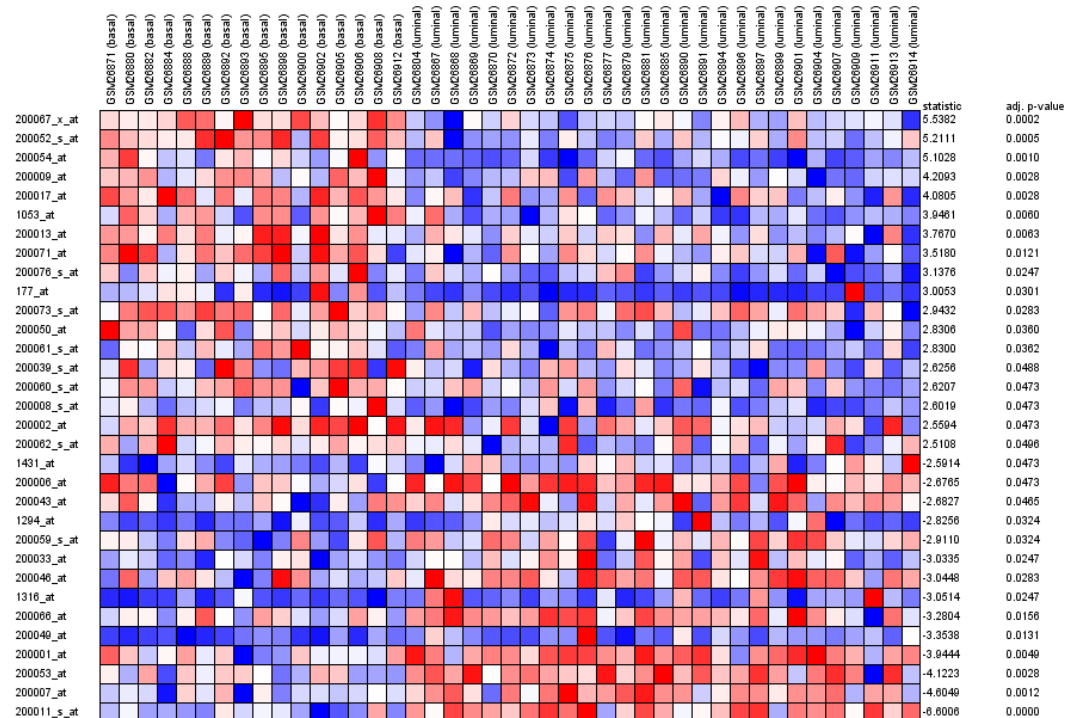
$$H_a: \mu_1 \neq \mu_2$$

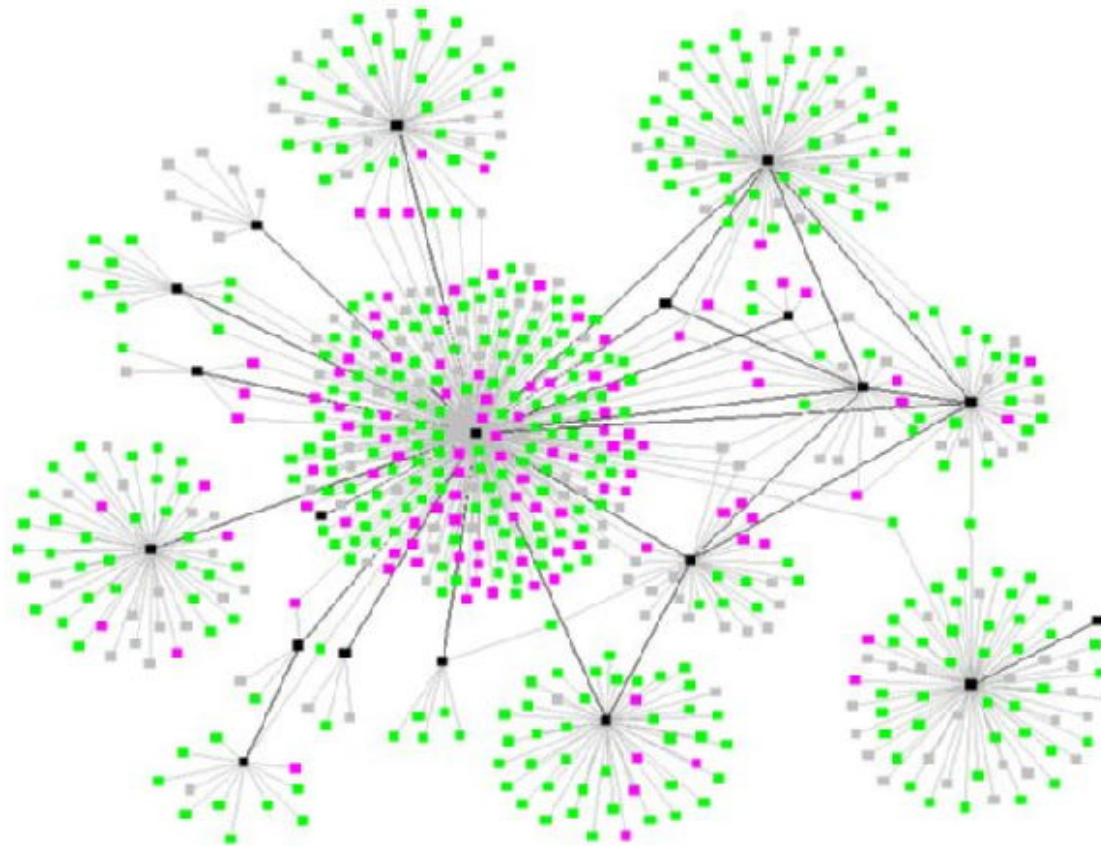
| #NAMES      | statistic          | p-value               | adj. p-value          |
|-------------|--------------------|-----------------------|-----------------------|
| 200067_x_at | 5.538204986516149  | 4.974604961551534E-6  | 2.4375564311602516E-4 |
| 200052_s_at | 5.2110706353314535 | 1.4519552681244469E-5 | 4.743053875873193E-4  |
| 200054_at   | 5.102797363044661  | 4.263454480923057E-5  | 0.001044546347826149  |
| 200009_at   | 4.209329258084638  | 1.9598818661190837E-4 | 0.002755732412247896  |
| 200017_at   | 4.0805286865632855 | 2.2495774793860376E-4 | 0.002755732412247896  |
| 1053_at     | 3.9460740578057503 | 6.082189146003286E-4  | 0.005960545363083221  |
| 200013_at   | 3.767033234598989  | 7.042746674112254E-4  | 0.006274447036936371  |

ANOVA, limma:

$$H_0: \mu_1 = \mu_2 = \dots = \mu_n$$

$$H_a: \text{not } H_0$$



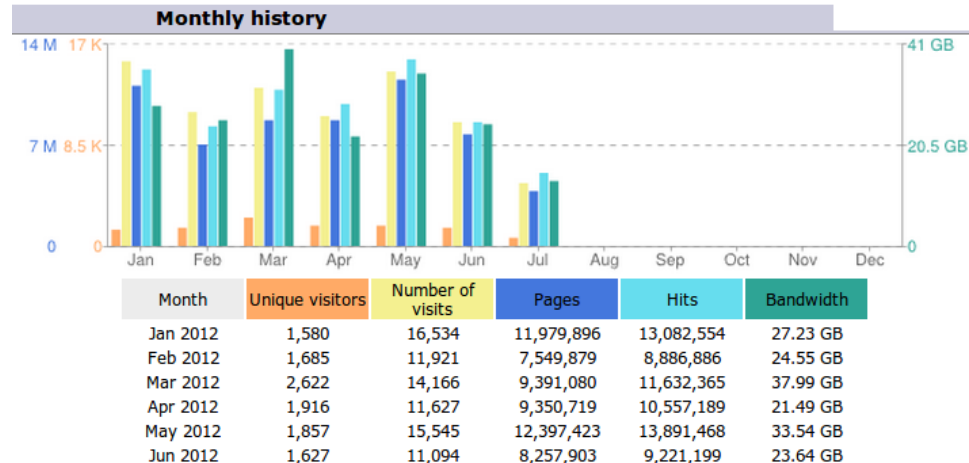


Análisis de networks

# Resultados

# Indicadores de uso

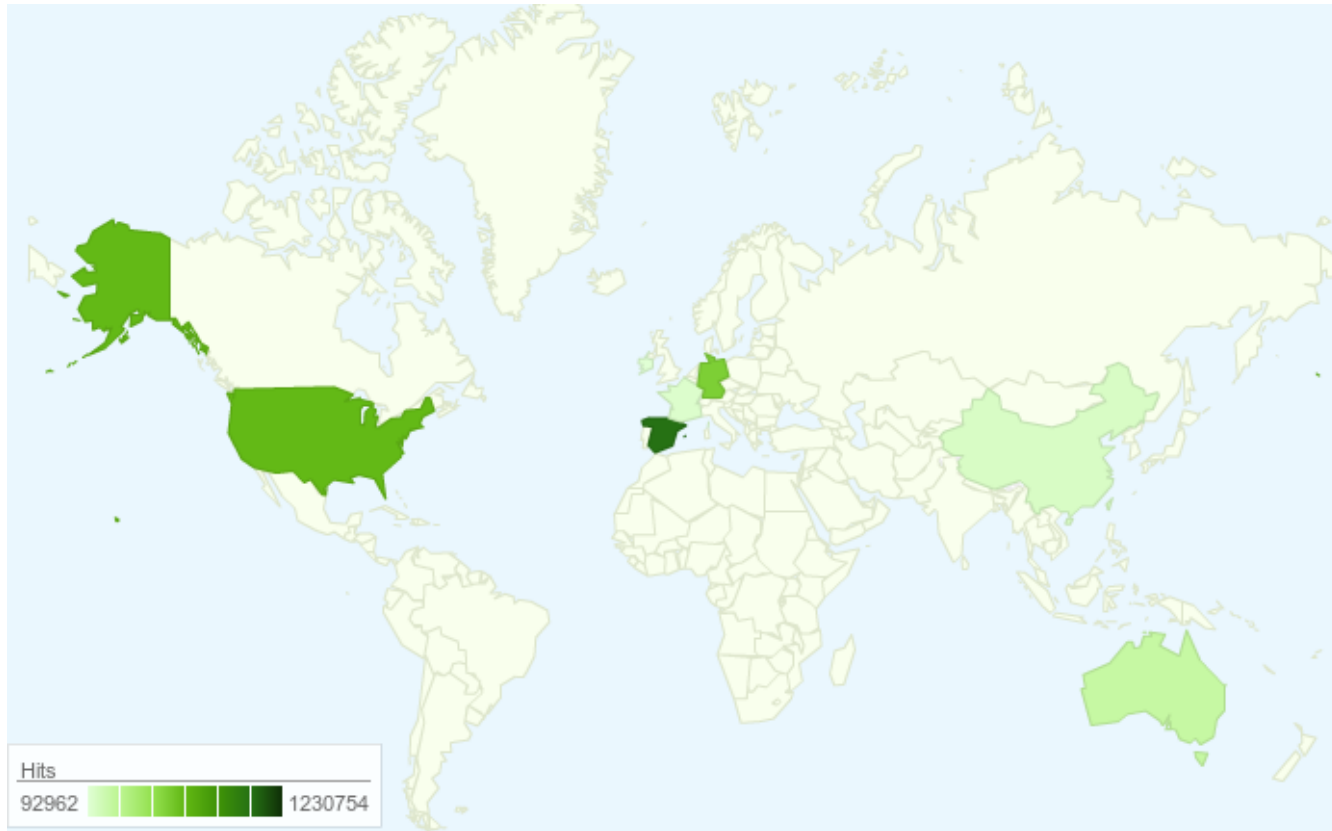
- 1800 visitantes por mes
- 200 experimentos analizados por día
- 5000 usuarios registrados
- 70000 usuarios anónimos



<http://bioinfo.cipf.es/webstats/babelomics/awstats>

# Resultados

# *Indicadores de uso*



<http://bioinfo.cipf.es/webstats/babelomics/awstats>

# Resultados

# Publicaciones



25 publicaciones + 2300 citas  
( 2004-2012)



Medina I, Carbonell J, Pulido L, et al. "Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling." *Nucleic Acids Research*. 2010;38:W210-W213

Nueda MJ, Sebastián P, Tarazona S, et al. "Functional assessment of time course microarray data." *BMC Bioinformatics*. 2009;10 Suppl 6:S9



Al-Shahrour F, Carbonell J, Minguéz P, et al. "Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments." *Nucleic Acids Res*. 2008;

Tarraga J, Medina I, Carbonell J, et al. "GEPAS, a web-based tool for microarray data analysis and interpretation." *Nucleic Acids Res*. 2008;36:W308-14



Montaner D, Tarraga J, Huerta-Cepas J, et al. "Next station in microarray data analysis: GEPAS." *Nucleic Acids Res*. 2006;34:W486-91

<http://babelomics.bioinfo.cipf.es/publications>

# Resultados

# *Docencia universitaria*



Grado de Biotecnología



Grado de Biotecnología, Biología y Matemáticas



Cursos Doctorado Bioinformática



Máster de Medicina Translacional

# Conclusiones

- El uso de herramientas web constituye un **recurso eficiente** en docencia en Estadística
- Permite el **desarrollo de competencias** para mejorar el acceso al mercado laboral



# Agradecimientos



<http://bioinfo.cipf.es/people>