

## Practical Course

# BIOINFORMATICS and FUNCTIONAL GENOMICS: from genes to functions and networks

18,19,20 - June - 2008

Centro de Investigación del Cáncer (CIC-IBMCC, CSIC/USAL), Salamanca, Spain

<http://bioinfocourses.cicancer.org>

**Practical course on bioinformatics** tools and methods for **functional genomics** studies. It will be focus on methods and strategies applied to robust **analysis of microarrays data** (mainly transcriptomic data derived from gene expression microarrays from *Affymetrix*) and the critical steps to identify **significant genes**, to reach appropriate **functional annotation and assignment**, to unravel the biological information enclosed in selected **gene lists** and to explore the **biological networks** derived.

### PROGRAM scheme

**Day 1 – 18.June.2008** (Wednesday)

→ **Genomics and transcriptomics: microarray data analysis (focus on *Affymetrix*)**  
(Bioconductor-R, GEO, GeneAtlas, GATE, VisualGenomics, SNP arrays)

**Day 2 – 19.June.2008** (Thursday)

→ **Bioinformatic tools for functional-biological assignment of selected genes and text mining**  
(Babelomics, iHOP, CARGO)

**Day 3 – 20.June.2008** (Friday)

→ **Exploring gene and protein networks and pathways using bioinformatic tools**  
(INGENUITY, GeneCodis, APID, APID2NET, Cytoscape)

### Organized by:

**Dr. Javier De Las Rivas** (Centro de Investigación de Cáncer CIC, CSIC / USAL, Salamanca)

**Dr. Alfonso Valencia** (Instituto Nacional de Bioinformática INB, Centro Nacional Investig. Oncológicas CNIO, Madrid)

**Dr. Federico Moran** (Instituto Nacional de Bioinformática INB, Universidad Complutense, Madrid)

Example links of **some applications** to be studied:

**APID & APID2NET** (CIC) – <http://bioinfow.dep.usal.es/apid/> **Babelomics** (INB) – <http://babelomics.bioinfo.cipf.es/> **CARGO** (INB) – <http://cargo.bioinfo.cnio.es/> **GATE** (CIC) – <http://bioinfow.dep.usal.es/gate/> **iHop** (INB) – <http://www.ihop-net.org/UniPub/iHOP/> **Visual Genomics** (INB) – <http://bioweb.cnb.uam.es/VisualGenomics/>

**Registration:** The price is **280 Euros** (before 31.May). It includes registration, documentation, full practicals and meals.

If you are **interested** please sent as soon as possible an **e-mail** as **pre-registration** to: [jrivas@usal.es](mailto:jrivas@usal.es)  
Bioinformatics and Functional Genomics Research Group, Centro de Investigación del Cáncer (CIC) Salamanca.

**Note:** Bring **your personal computer** (laptop) for the practicals. **Wi-Fi internet connection** will be available.

### PROGRAM

**Day 1 – 18.June.2008** → **Genomics and transcriptomics: microarray data analysis (focus on *Affymetrix*)**

09:00 – 09:30 .- Registration and documentation

**09:30 – 09:45 .- Welcome address to the Course.** *Javier De Las Rivas* (course director, CIC, CSIC / USAL).

**09:45 – 10:00 .- Presentation of the Spanish National Bioinformatics Institute (INB).**

*Federico Morán* (Central Node INB, CNIO, Madrid) (nº 1 - Presentation, 30 min)

**10:00 – 11:00 .- Bioinformatics key tool for Functional Genomics, current overview of needs and tools.**

**Installation of programs, tools and documentation in the computer laptops of the alumni: R, BioC, datasets, etc.**

*Javier De Las Rivas & course team* (Bioinformatics, CIC) (nº 2 - Lecture + Practical session, 60 min)

**11:00 – 12:00 .- Use of R and BioConductor programs for gene expression data analysis.**

*Diego Alonso & Celia Fontanillo* (Bioinformatics, CIC) (nº 3 - Practical session, 60 min)

12:00 – 12:30 .- Coffee break

**12:30 – 13:30 .- 1° Critical analysis of microarray genome-wide expression data: experimental design, normalization, signal calculation, profiling. 2° Databases on gene expression: GEO, GeneAtlas, EMAGE, GDX.**  
Javier De Las Rivas (Bioinformatics, CIC) (n° 4 - Lecture + Practical session, 60 min)

13:30 – 14:30 .- Lunch

**15:30 – 16:20 .- Exploring the complexity of the genomes and the transcriptomes of human and mouse: GATE an ENSEMBL-based web tool to analyse a complex biomolecular lanscape.**  
Alberto Risueño (Bioinformatics, CIC) (n° 5 - Practical session, 50 min)

**16:30 – 17:20 .- Visual genomics: finding gene activity *in situ* on tissues and cells (immunohistochemistry, RNA *in situ*, etc). Integration of EMAGE, GDX, GENSAT in a new bioinformatic tool.**  
Natalia Jimenez (Visual Genomics and Proteomics, INB, CNB-CSIC, Madrid) (n° 6 - Lecture + Practical session, 50 min)

**17:30 – 18:20 .- Use of R and BioConductor data analysis programs to find significant gene differential expression (SAM, EBA) and gene altered expression (AlteredExpression).**  
Jose Manuel Sánchez-Santos & Carlos Prieto (Bioinformatics, CIC) (n° 7 - Practical session, 50 min)

---

## Day 2 – 19.June.2008 → Bioinformatic tools for functional assignment of selected genes and text mining

**09:30 – 10:15 .- Human SNP microarrays from Affymetrix: genotyping (BRLMM) and copy number (CNAT).**  
Celia Fontanillo & Diego Alonso (Bioinformatics, CIC) (n° 8 - Practical session, 45 min)

**10:15 – 11:00 .- BABELOMICS: functional analysis of genome-scale experiments.**  
David Montaner (Functional Genomics Bioinformatics, INB, CIPF, Valencia) (n° 9 - Lecture, 45 min)

**11:00 – 12:00 .- Unravelling the biological meaning of selected lists of genes: tools for functional enrichment analysis and gene set enrichment analysis (GSEA).**  
David Montaner & Francisco García (Funct. Genom. Bioinfo., INB, CIPF, Valencia) (n° 10 - Practical session, 60 min)

12:00 – 12:30 .- Coffee break

**12:30 – 13:20 .- Text mining applied to the biomedical literature (introduction, parts of a text mining approach and applications).**  
Osvaldo Graña (INB and Bioinformatics Unit CNIO, Madrid) (n° 11 - Lecture, 50 min)

13:30 – 14:30 .- Lunch

**15:30 – 16:20 .- Web Service architecture: from bioinformatic applications to workflows (tools and service repositories).**  
José Manuel Rodríguez (INB, CNIO, Madrid) (n° 12 - Lecture 50 min)

**16:30 – 17:30 .- Text mining of biomedical literature, iHOP and other tools to find new information about groups of genes or proteins & CARGO (Cancer And Related Genes Online) a configurable biological web portal designed as a tool to facilitate, integrate and visualize results from biological on-line resources**  
José Manuel Rodríguez & Osvaldo Graña (INB, CNIO, Madrid) (n° 13 - Practical session, 60 min)

---

## Day 3 – 20.June.2008 → Exploring gene and protein networks and pathways using bioinformatic tools

**09:30 – 10:15 .- INGENUITY pathways analysis: a platform for quickly search and discover biological and chemical information.**  
Catalina Guerra (Field Application Scientist, Ingenuity Systems, UK) (n° 14 - Lecture, 45 min)

**10:15 – 11:00 .- Functional concurrent annotation using GeneCodis: finding common GOs and pathways.**  
Javier De Las Rivas (Bioinformatics, CIC) (n° 15 - Practical session, 45 min)

**11:00 – 12:00 .- INGENUITY pathways analysis: from a gene list to a biological network revealing functional meaning.**  
Catalina Guerra (Field Application Scientist, Ingenuity Systems, UK) (n° 16 - Practical session, 60 min)

12:00 – 12:30 .- Coffee break

**12:30 – 13:20 .- APID and APID2NET: find, build and explore a protein-protein interaction network using a query subset of proteins.**  
Carlos Prieto (Bioinformatics, CIC) (n° 17 - Practical session, 50 min)

**13:30 – 14:20 .- Cytoscape: open source bioinformatics software platform for visualizing molecular interaction networks and integrating these with other state data.**  
Javier De Las Rivas (Bioinformatics, CIC) (n° 18 - Lecture + Practical session, 50 min)

---