

# Practical Course on Gene/Protein Functional Networks and Interactomes

This will be a short practical course on **Bioinformatics** for biologists, molecular biologists or young researchers working in the field of biomedical or biological sciences who are interested in learning, in a practical way, how to build and explore gene and protein networks and how to place in a relational context (i.e. in a network-based context) the lists of genes or proteins, often derived from genomic or proteomic analyses. The course will be held for two days in Cape Town (South Africa) at the University of Cape Town Medical School, hosted by the Computational Biology Group (CBIO). It will be given by Professor Dr. Javier De Las Rivas, from the University of Salamanca and the Spanish National Research Council (USAL/CSIC, Spain).

The course will be divided in **four sessions** with the following topics:

- (1) Bioinformatics tools for functional enrichment analysis;
- (2) Construction of gene functional networks;
- (3) Protein interaction networks;
- (4) Construction and analysis of gene/protein networks.

The students attending do not need to know programming, but should be familiar with working on computers and keen to learn how to use Bioinformatics tools and concepts.

Dates: Monday 23rd and Tuesday 24th of November 2015
Place: Cape Town, South Africa
Venue: Health Teaching Labs 1-2, Basement of Anatomy Building, UCT Medical School, Anzio Rd, Observatory
Time: 9:30 to 16:30

Lecturer: Dr. Javier De Las Rivas Bioinformatics and Functional Genomics Group Cancer Research Center (CiC-IBMCC, CSIC/USAL) University of Salamanca, Spain See scientific profile at: http://scholar.google.com/citations?user=VY2k-EQAAAAJ&hl=en https://www.linkedin.com/profile/view?id=68956567 jrivas@usal.es

**Course fee:** R500 per person. Please note, catering will NOT be provided, however 2 cafeterias are available on the campus. The course fee is to cover the lecturer's travel costs.

To apply please complete the form at:

https://docs.google.com/forms/d/1d5EsrmB7sZLYvU9ehg2CWcMuElt-xEXcrkLSpugFIno/viewform by Monday the 9th November.

### PROGRAM

### DAY 1 - 23 November 2015

### Session 1 (9:30 - 12:30, 3h)

Bioinformatics tools for functional Enrichment Analysis: annotation of selected gene lists.

- Functional biological information and annotation: GO, KEGG, Interpro (orthogonal databases).
- Functional Enrichment Analysis (EA): from single to modular methods.



- Using EA tools to annotate gene lists: DAVID (single), GSEA (gene sets), GeneCodis (modular)
- The problems of redundant and general terms: post-enrichment tool GeneTermLinker (postEA)

## Session 2 (13:30 - 16:30, 3h)

### Construction of gene functional networks: linking genes that share common functions.

- From co-annotation and enrichment to the construction of functional networks:
- Using an R-Bioconductor tool to build functional networks: FGNet.
- Analysis of functional modules and groups: distances calculations.

## DAY 2 - 24 November 2015

## Session 3 (9:30 - 12:30, 3h)

## Protein interaction networks: definition, databases, tools.

- Definition and properties of protein interaction networks
- Protein interaction networks compared to coexpression networks and biological pathways
- Using on-line tools to build protein interaction networks: APID, STRING, GeneMANIA, PSICQUIC
- Binary networks: proteins and drugs interactions (STITCH)

### Session 4 (13:30 - 16:30, 3h)

## Construction and analysis of gene/protein networks using Cytoscape

- Import biomolecular networks in Cytoscape
- Visualize and explore biomolecular networks in Cytoscape
- Topological analysis of biomolecular networks: nodes centrality and modules finding
- From networks to pathways: a human functional protein interaction network

Overview of the Sessions: Session 1 (9:30 - 12:30, 3h) Bioinformatics tools for functional Enrichment Analysis Session 2 (13:30 - 16:30, 3h) Construction of gene functional networks Session 3 (9:30 - 12:30, 3h) Protein interaction networks Session 4 (13:30 - 16:30, 3h) Construction and analysis of gene/protein networks