



AGENDA

DAY before- Tuesday 26 October 2010

- 08:30 – 10:30** **Registration and information desk**
- 11:00 – 14:30** **National Institute of Bioinformatics, Spain**
Internal session: INB-technicians
Chairs: Allan Orozco, José María Fernández, Victoria Martín-Requena and Max García
- 13:00 – 19:30** **I Spain, Portugal and North Africa Bioinformatics Student Symposium (NPS3Bio)**
Chairs: Pedro Lopez, Noura Chelbat, Lorena Pantano, Manuel Corpas, Allan Orozco
- 15:00 – 17:30** **Registration and information desk**

DAY 1- Wednesday 27 October 2010

- 08:00 – 09:00** **Registration and information desk**
- 08:30 – 09:00** **Welcome and Opening**
Dra. Adelaida de la calle Martín
Chancellor of the University of Malaga
Sr. D. Francisco de la Torre
Major of Málaga, Spain
Sr. D. Pedro Fernández Montes
Major of Torremolinos, Spain
Dr. Alfonso Valencia
INB Director
- 09:00 – 10:00** **Main lecture: Ivo GUT. Director National Genome Analysis Center Barcelona.**
Presentation: Dr. Alfonso Valencia. CNIO.
- 10:00 – 10:30** **Coffee break**
- 10:30 – 12:00** **Session 1.1: Analysis of HT-NGS data**
Chair: Ana Conesa. Centro de Investigación Príncipe Felipe.
- 10:30 Multivariate Methods for Genomic Data Integration and Visualization.
Alex Sánchez, Ferrán Reverter, José Fernández-Real, Esteban Vegas, Francesc Carmona, Jacques Amar, Remy Burcelin, Matteo Serino, Francisco Tinahones, Eduardo García Fuentes, Antonio Miñarro and M. Carmen Ruíz de Villa.
 - 10:50 Pyicos: A flexible tool library for analyzing Protein-Nucleotide interactions with mapped reads from deep sequencing.
Juan González-Vallinas, Sonja Althammer and Eduardo Eyras
 - 11:10 Genome-wide Association Studies Pipeline (GWASpi): a desktop application for genome-wide SNP analysis and management.
Fernando Muñiz Fernández, Ángel Carreño Torres, Carlos Morcillo-Suarez and Arcadi Navarro
 - 11:30 Differential expression in RNA-seq: a matter of depth. *Sonia Sonia Tarazona, Fernando García-Alcalde, Joaquín Dopazo and Ana Conesa.*
- 12:00 – 14:00** **Session 1.2: Genomic projects design: success cases**
Chair: Victoriano Valpuesta. University of Málaga.
- The need of going fast in a complex genome.
Carmen Beuzón
 - Getting Deeper into Primate Genomes.
Tomás Marqués
 - One stop shop for tomato genomics: the value of centralization.
Toni Granell,
 - Brazilian Genomics activities in a nutshell
Ana Tereza Vasconcelos
 - How to sequence a plant genome with next generation sequencing technologies: the melon genome project
Jordi García Mas,
 - Genomes and Genomics in Aquaculture.
Antonio Figueras
 - International Cancer Genome Consortium
Ivo Gut
- 14:00 – 15:00** **Lunch**

- 15:00 – 16:30** **Session 1.3: Highlights of the year 1**
Chair: Alberto Pascual. National Center for Biotechnology-CSIC.
- 15:00 Quantifying the relationship between sequence and three-dimensional structure conservation in RNA.
Emidio Capriotti and Marc A. Marti-Renom
 - 15:25 3D-footprint: a database for the structural analysis of protein-DNA complexes
Bruno Contreras-Moreira
 - 15:50 Optimization of multi-classifiers for computational biology: application to gene finding and expression
Rocio Romero-Zaliz, Cristina Rubio-Escudero, Coral del Val Muñoz and Igor Zwir
- 16:30-17:00** **Coffee break**
- 17:00 – 18:30** **Session 1.4: Open discussion on the bioinformatics challenges in personalized medicine**
Presentation: Alfonso Valencia. CNIO.
Chairs: Jose Pereira-Instituto Gulbenkian de Ciencia, Fernando Martín- National Institute of Health "Carlos III".
- 18:30 – 20:00** **Poster Session (1)**
- 15:00 – 17:30** **Parallel Session 1: Bioinformatics Software Developments in Spain and beyond**
Chairs: Jose María Fernández, J.R. Valverde, Victoria Martín-Requena , Max García and Allan Orozco.
- 19:00 – 19:30** **Parallel Session 2: Status of the ELIXIR project**
Chairs: Alfonso Valencia and José Leal
- 20:00 – 23:00** **Social event (TBC)**

DAY 2- Thursday 28 October 2010

- 08:00 – 09:00** **Registration and information desk**
- 09:00 – 10:00** **Main lecture: Sarah Hunter. Group Leader Inter Pro Team; EMBL-EBI Hinxton**
Classification of uncharacterised sequences; challenges and considerations.
Presentation: Dr. José María Carazo. Centro Nacional de Biotecnología.
- 10:00 – 10:30** **Coffee break**
- 10:30 – 12:00** **Session 2.1: Tools and technologies for computational biology**
Chair: Joao Carriço. Faculdade de Medicina de Lisboa and INESC-ID.
- **10:30. A Holistic Approach for Integrating Genomic Variation Information**
Pedro Lopes and José Luis Oliveira
 - **10:50. Toward an efficient integration of Yeast Data**
Abdelaali Briache, Kamar Marrakchi, Amine Kerzazi, Ismael Navas-Delgado, José F. Aldana Montes, Badr Din Rossi Hassani and Khalid Lairini
 - **11:10. Anatomic Gene Expression Mapping, a Data Integration Platform**
Natalia Jiménez-Lozano, Joan Segura, José Ramón Macías, Juanjo Vega and José María Carazo
 - **11:30. Understanding the plasticity of c-Src tyrosine kinase through mutagenesis and atomically detailed large-scale molecular dynamics simulations.**
Ralitza Boubeva, Andrea Cristiani, Lucile Pernot, Remo Perozzo, Ludovico Sutto, Leonardo Scapozza and Francesco Luigi Gervasio
- 12:00 – 14:00** **Session 2.2: Highlights of the year 2**
Chair: Ana Tereza Vasconcelos. National Laboratory of Scientific Computation.
- **12:00 “Dark Matter” Assessment in Protein Network Prediction and Modelling.**
JAG Ranea, Ian Morilla, Jon G Lees, Adam Reid, Corin Yeats, Andrew B Clegg, Francisca Sanchez-Jiménez and Christine Orengo.
 - **12:25. Torsional Network Model: Normal modes in torsion angle space better correlate with conformation changes in proteins**
Ugo Bastolla and Raul Mendez
 - **12:50. jORCA and Magallanes sailing together towards Web Services Integration**
Victoria Martín-Requena, Javier Ríos and Oswaldo Trelles
 - **13:15. Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling**
Ignacio Medina, Jose Carbonell, Luis Pulido, Sara Madeira, Stefan Goetz, Ana Conesa, Joaquin Tárraga, Alberto Pascual-Montano, Ruben Nogales-Cadenas, Javier Santoyo, Francisco García, Martina Marbà, David Montaner and Joaquin Dopazo
- 14:00 – 15:00** **Lunch**

- 15:00 – 16:45 Session 2.3: Short Oral Presentations (1)**
Chair: Sergio Deusdado. ESA Polytechnic Institute of Bragança.
- 15.00 GeNOTE: a web tool for annotation of non-model, eukaryotic, unfinished sequences
Noé Fernández, Darío Guerrero, Rocio Bautista and M. Gonzalo Claros
 - 15.15 Usefulness and applications of whole genome, single cytosine resolution methylation maps
Michael Hackenberg, Pedro Bernaola, Pedro Carpena, Guillermo Barturen and José L. Oliver
 - 15.30 Bioinformatics Platform for the Characterization of G Protein-Coupled Receptors
David Rodríguez, Xabier Bello and Hugo Gutierrez de Teran
 - 15.45 Combined use of gene networks and classifiers to characterize disease states
Sara Aibar, Celia Fontanillo and Javier de las Rivas
 - 16.00 Benchmarking for 3D Electron Microscopy
Adrián Quintana, Carlos Oscar Sánchez Sorzano, Roberto Marabini and Jose María Carazo
 - 16.15 iHOP web services family
José María Fernández González, Robert Hoffmann and Alfonso Valencia Herrera
- 16:45 – 17:15 Coffee break**
- 17:15 – 18:45 Session 2.4: Options and Priorities in hands-on training in Spain and Portugal**
Chair: Pedro Fernandes. Instituto Gulbenkian de Ciência.
- 18:45 – 20:15 Poster Session 2**
- 21:00 – 23:00 Gala Dinner**

DAY 3- Friday 29 October 2010

- 08:00 – 09:00** **Registration and information desk**
- 09:00 – 10:00** **Main lecture: Julio Saez Rodriguez**
Comparative logical models of signaling networks in normal and transformed hepatocytes.
EMBL Outstation-Hinxton. European Bioinformatics Institute.
Presentation: Dra. Ana Teresa Freitas INESC-ID/IST Portugal.
- 10:00 – 10:30** **Coffee break**
- 10:30 – 12:00** **Session 3.1: Short Oral Presentations (2)**
Chair: Toni Gabaldón. Center for Genomic Regulation (CRG).
- 10:30 PromoterSweep: a tool for identification of transcription factor binding sites
Coral del Val, Oliver Pelz, Karl Heinz Glatting, Endre Barta and Agnes Hotz-Wagenblatt
 - 10:45 Statistical significance for NGS reads similarities
Antonio Muñoz, Javier Ríos, Hicham Benzekri and Oswaldo Trelles A Structural
 - 11:00 Generation of Biopax Instances from Integrated Data
María Jesús García-Godoy, Amine Kerzazi, Ismael Navas-Delgado and José F. Aldana-Montes.
 - 11:15 An Ontology and a REST API for Sequenced Based Microbial Typing Data information
João Almeida, João Tiple, Mário Ramirez, José Melo-Cristino, Cátia Vaz, Alexandre P. Francisco and João A. Carriço
- 12:00 – 12:30** **Closure session**