



## Poster Session 1

Wednesday 27<sup>th</sup> October, 18:00 – 19:30

### Algorithms for computational biology (and HPC)

- **Beyond sequencing and Future Trends. #57**  
Saadia Karbou
- **Search and Validation of Microsatellite Markers in Olive Tree for the Analysis of Agronomical Traits. #78**  
Antonio Muñoz-Mérida, Juan J. González-Plaza, Inmaculada Ortiz-Martín, María C. Domínguez-García, Nieves Martín-Urdiroz, Conchi Díez-Muñoz, José F. Sánchez-Sevilla, Luis Rallo, Angelina Belaj, Raúl De la Rosa, Oswaldo Trelles, Victoriano Valpuesta, Carmen R Beuzón.
- **A genome browser for NGSmethDB, a database for high throughput, single cytosine resolution methylation data. #29**  
Guillermo Barturen, Michael Hackenberg and José L. Oliver

### Sequence analysis, phylogenetics and evolution, 16 posters

- **An evolutionary view of the DNA Damage Response. #23**  
Aida Arcas, Ildefonso Cases and Ana M Rojas
- **HTML5 highly interactive web application for dynamic representation of results of alignments. #87**  
Ángela Paolino, Juan Falgueras
- **Cis-HOUND: a tool for searching conserved regulatory sequences. #94**  
Antonio J. Pérez Pulido, Carla Sofía Lopes, Fernando Casares
- **Strand bias in the clustering of DNA words in the human genome. #31**  
Antonio Rueda, Francisco Dios, Ricardo Lebrón, Michael Hackenberg and José L. Oliver
- **An Evolutionary Conserved Membrane Receptor Notch-4 is Expressed in Estrogen Receptor Negative but not in Estrogen Receptor Positive Breast Cancer Cells. #1**  
Ayten Sever, Ayse Kevser Ozden-Piskin, Emine Kilic and Duygu Uckan
- **Bioinformatic analysis of survival motor neuron (SMN) gene isoforms. #79**  
Carlos M. Guevara, Manuel M. Corredera, Pablo Mier Muñoz and Antonio J. Perez Pulido
- **Highly conserved genomic regions of Lymphocytic Choriomeningitis Virus during lethal mutagenesis. #26**  
Daniel Aguilar, David Becerra Alonso and Ana Grande Perez
- **Detection of divergent regions in aligned conserved sequences with AlignMiner. #6**  
Darío Guerrero, Rocío Bautista, David P. Villalobos, Francisco R. Cantón and M. Gonzalo Claros
- **Comparative Genome Analysis of Mycobacterium sp(Mycobacterium Tuberculosis and other non tuberculosis Mycobacteria). #39**  
Fathiah Zakhm, Lamiae Belayachi, Mohammed Akrim, Abdelaziz Benjouad, Dave Ussery, Rajae El Aouad and My Mustapha Ennaji
- **A Plant Architecture Study in Olive Tree. #84**  
Juan J. González-Plaza, Inmaculada Ortiz-Martín, Antonio Muñoz-Mérida, Oswaldo Trelles, Eduardo R. Bejarano, Victoriano Valpuesta and Carmen R Beuzón.
- **mtocDB: a community resource to study the evolution of microtubule organizing centers. #68**  
Marc R. Gouw, Zita Santos, Renato Alves, Filipe Tavares-Cadete, Joana Pinto, Neuza Matias, Juliette Azimzadeh, Keith Gull, Michel Bornens, Mónica Bettencourt-Dias and Jose B. Pereira-Leal
- **Phylogenomics and the Evolution of Duplicated Genes in Drosophila species. #73**  
François Serra, Jaime Huerta-Cepas, Toni Gabaldón and Hernan Dopazo
- **SporeDB – an evolutionary systems biology platform for functional and evolutionary studies of bacterial sporulation. #37**  
Renato J. Alves, Ana Abecassis, Mónica Serrano, Catarina Fernandes, Anabela L. Isidro, Adriano O. Henriques and Jose B. Pereira-Leal
- **Phylogenetics in the genomics era: resources for phylome reconstruction and analysis. #89**

Salvador Capella-Gutiérrez, Jaime Huerta-Cepas, Marina Marcet-Houben, Leszek P. Pryszcz, Ivan Denisov, Diego Kormes and Toni Gabaldón

- **The mode of the distance between two leaves in a phylogenetic tree. #9**  
Arnau Mir and Francesc A. Rosselló
- **MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score. #97**  
Leszek P. Pryszcz, Jaime Huerta-Cepas and Toni Gabaldón

### Structural Bioinformatics

- **FTSZ and The Division of Prokaryotic Cells. #45**  
Almudena Perona, Coderch Claire, Chacón Pablo, Martín Galiano Antonio Javier, Oliva María Ángela, Schaffner Claudia, Andreu Jose Manuel, Gago Federico and Morreale Antonio
- **Setting up a lipid bilayer for Molecular Dynamics simulations. #51**  
Almudena Pino-Ángeles, Aurelio A. Moya-García, Francisca Sánchez-Jiménez
- **The relation between amino-acid substitutions in the interface of transcription factors and their recognized DNA motifs. #47**  
Alvaro Sebastian, Carlos P. Cantalapiedra and Bruno Contreras-Moreira
- **Search for predisposed genes to breast cancer in the Moroccan population. A BRCA1 AND BRCA2 molecular genetic study. #92**  
Benaicha Soumia and Bouali Abderrahim
- **101DNA: a set of tools for Protein-DNA interface analysis. #48**  
Carlos Cantalapiedra, Álvaro Sebastián and Bruno Contreras-Moreira
- **Virtual screening to discover synthetic inhibitors against Phospholipase A2 of Apis mellifera. #3**  
Daniel Macedo de Melo Jorge, Vinicius Barreto da Silva, Carlos Henrique Tomich de Paula da Silva, Silvana Giuliatti
- **New drugs for new targets: Inhibiting the translation machinery of Plasmodium falciparum. #75**  
Eva Maria Novoa, Laia Cubells, Noelia Camacho, Alfred Cortés, Rob Hoen, Alba López, Miriam Royo, Lluís Ribas de Pouplana
- **Docking studies for interactions of the antiangiogenic compound aeroplysinin-1 with key components of survival and proliferation biosignaling pathways. #59**  
María Jesús García Godoy, María Victoria Ruíz Pérez, Francisca Sánchez Jiménez, Ana R. Quesada and Miguel Ángel Medina
- **An Automated Clustering Method to Detect Blocks of Amino-acid Used in the Structure of Protein Correlated by Function. #32**  
Milton Faria Jr.
- **Virtual screenings and molecular properties calculations of new biologically active sulfonamide derivatives: POM as New Guide in Drug Design. #91**  
Zahid H. Chohan, Hazoor A. Shad, Moulay H. Youssoufi and Taibi Ben Hadda
- **Synthesis of bioactive pyridazines. #85**  
Rafik Saddik, Zouheir Ghazi, Ouahiba Fadel and Nour-eddine Benchat
- **Computational Evaluation of Experimental in vitro anti-HIV bioactivity by using a New POM Bioinformatic Model: Petra/ Osiris and Molinspiration. #83**  
Ibrahim El Mounsi, Mostafa Mimouni, Javed Sheikh, Ali Parvez and Taibi Ben Hadda
- **Study of the involvement of GAPDH in the pathogenicity of Pseudomonas syringae: Biotechnological implications. #82**  
Bouchra Elkhalfi, Abdelaziz Soukri and Aurelio Serrano
- **Structural and Physicochemical Peptide Properties and Dimensionality Reduction Representation in Binding Prediction. #55**  
Fadi A. Chakik, Ahmad M. Shahin, Walid H. Moudani and Zena Mida

### Databases, Tools and technologies for computational biology

- **Computational analysis and modeling of cleavage by the immunoproteasome and the constitutive proteasome. #90**  
Carmen M. Diez-Rivero, Esther M. Lafuente and Pedro A. Reche

### Last minute submission

- **Locmine: Automatic retrieval of protein localization descriptions using literature mining approaches**  
Martin Krallinger and Alfonso Valencia

- **RNA-seq data analysis provides evidence for a new molecular mechanism generating antisense transcripts in human cells**  
Virginia Gonzalez
- **A pipeline for identifying contaminants in assembling projects**  
José Luis Mosquera, Alex Sanchez Pla

## Poster Session 2

Thursday 28th October, 18:15 – 19:45

### System and synthetic biology

- **Gene Regulatory Network Dynamics of Mus Musculus Mouse Eye Development Applying Hybrid Evolutionary Algorithm. #27**  
Daniel Aguilar, Antonio Córdoba and Ma Carmen Lemos
- **A Flux Balance Approach to study the metabolic capability of endosymbiont bacteria. #80**  
Federico Morán, Miguel Ponce de León, Sara Vázquez, Daniela Xavier and Francisco Montero
- **Synergistic effect of erythromycin on polymorphonuclear cell antibacterial activity against erythromycin-resistant phenotypes of Streptococcus pyogenes. #95**  
Giuliana Banche, Vivian Tullio, Valeria Allizond, Narcisa Mandras, Janira Roana, Daniela Scalas, Fadwa El Fassi, Sergio D'Antico, Anna Maria Cuffini and Nicola Carlone
- **gSNOW: A set-enrichment based methodology to extract protein-protein interaction networks associated to specific phenotypes. #41**  
Luz Garcia-Alonso, Ignacio Medina, Alicia Amadoz, Roberto Alonso, Pablo Minguez and Joaquin Dopazo
- **Dissecting signaling pathways to understand the consequences of gene expression changes. #5**  
Patricia Sebastian-Leon, Enrique Vidal, Ana Conesa, Sonia Tarazona, David Montaner and Joaquín Dopazo
- **Effects of oxidative and nitrosative stress on the protozoan Tetrahymena thermophila. #81**  
Nadia. Errafiy and Abdelaziz. Soukri

### Bioinformatics in Transcriptomics and proteomics

- **Evolution of human transcriptome mapping and its influence in the expression signals detected by microarrays. #15**  
Alberto Risueño and Javier De Las Rivas
- **Transcriptomic analysis of two strawberry (Fragaria x ananassa) cultivars determines key genes in response to Colletotrichum acutatum infection. #88**  
Amil-Ruiz F., Muñoz-Mérida A., Trelles O., Muñoz-Blanco J. and Caballero J L.
- **Meta-analysis of transcriptomic profiles from mesenchymal stem cells and other related cell types. #16**  
Beatriz Rosón, Alberto Risueño, Consuelo del Cañizo, Fermín Sánchez-Guijo and Javier De Las Rivas
- **Multidimensional Gene Set Analysis of Genomic Data. #8**  
David Montaner and Joaquín Dopazo
- **Analysis of Microsatellites in Medicago truncatula Unigenes. #93**  
Fatima Gaboun, Sripada M.Udupa, Fouad Abbad Andaloussi, M. Ibriz and A. Soulaymani
- **Possible sources of wrongly performing probes on Affymetrix GeneChipR Platforms. #76**  
Noura Chelbat, Ulrich Bodenhofer and Sepp Hochreiter
- **Ranking Affymetrix microarray-based pre-processing methods. #10**  
J.P.Florido, M.G.Claros, H.Pomares and I.Rojas
- **An extension of the Minimum Distance Probability Algorithm for Kernel-based Pattern Analysis. #44**  
Ferran Reverter, Esteban Vegas, Josep M. Oller and Martin Ríos

### Databases, Tools and technologies for computational biology

- **Integration and grouping of structural experimental data of RAS family in signaling pathways targeted in a database: SignaProt. #96**  
Ahmed El Amrani, Amina El Gonnouni, Amal Maurady, Jamal Brigui, Nabil Miled Faker Frikha
- **BioData-SF: Step beyond integration. #13**  
Alfredo Martínez, Paul M.K. Gordon, Christoph W. Sensen and Oswaldo Trelles
- **jsDAS: a javascript DAS client library. #62**  
Bernat Gel Moreno, Jose Villaveces and Rafael C. Jimenez
- **A Bioinformatics Platform for the Cork oak (Quercus suber) EST project. #56**

- Isabel Queirós Neves, Aleix Badia, Andreas Bohn, José B. Pereira-Leal
- **Conceptual Study of Data Integration in Biomedicine. #58**  
Johan Karlsson, Maximiliano García and Oswaldo Trelles
  - **Friendly and extensible web platform for bioinformatics tools integration. #60**  
Jose Manuel Mateos, Alfredo Martínez and Oswaldo Trelles
  - **PseudomonasDW: an integrated database for Pseudomonas data. #71**  
Kamar Marrakchi, Abdelaali Briache, Amine Kerzazi, Ismael-Navas-Delgado, José F. Aldana-Montes, Khalid Lairini and Badr D. Rossi Hassani
  - **BBMS – Basic Bioinformatics Meta-searcher. #25**  
Márcio S. Carochó and Sérgio Deusdado
  - **Generation of Genomic Tools in Olive Tree for the Analysis of Agronomical Traits. #61**  
Maria C. Dominguez-García, Juan J. González-Plaza, Antonio Muñoz-Mérida, Oswaldo Trelles, Angjelina Belaj, Raúl De la Rosa, Victoriano Valpuesta and Carmen R. Beuzón
  - **Using decision trees in the analysis of the concentration of tannins in Stryphnodendron adstringens. #38**  
Saulo França Amui, Ana Maria Soares Pereira and Silvana Giuliatti
  - **Using R in Tiki for Bioinformatics. #64**  
Xavier de Pedro and Alex Sánchez
  - **easyDAS: Automatic creation of DAS servers. #20**  
Bernat Gel Moreno, Andrew M. Jenkinson, Rafael C. Jimenez, Xavier Messeguer Peypoch and Henning Hermjakob
  - **Analyzing human mutations from a disease perspective. #42**  
Eduard Porta, Ana Maria Rojas and Ildefonso Cases
  - **Multi-objective strategy for the prediction of bacterial sRNAs. #43**  
Javier Arnedo, Rocío Romero-Zalaz, Igor Żwir and Coral del Val

#### Algorithms for computational biology (and HPC)

- **Collaborative action for the promotion of HPC applied to NGS. #77**  
Javier Ríos, Noura Chelbat, Antonio Muñoz-Mérida, Victoria Martín-Requena, Jose Manuel Mateos-Durán, Hicham Benzekri, Günter Klambauer, Ulrich Bodenhofer, Andreas Mayr, Andreas Mitterecker, Sepp Hochreiter and Oswaldo Trelles
- **Defining the Plasticity of Transcription Factor Binding Sites by Deconstructing DNA Consensus Sequences: The PhoP-Binding Sites among Gamma/Enterobacteria. #50**  
Oscar Harari, Luis Miguel Merino and Igor Żwir
- **A metric for galled networks. #22**  
Gabriel Cardona, Mercè Llabrés, and Francesc Rosselló

#### Last minute submission

- **QSTR and POM Studies of Propionic Acid Derivatives as Non Steroidal Anti Inflammatory Drugs information #98**  
Moulay Hfid Youssoufi, Vijay H. Masand, Komalsingh N. Patil and Taibi Ben Hadda
- **PLASMID-MEDIATED QUINOLONE RESISTANCE IN NAL R, CIP R CLINICAL ISOLATES OF ESCHERICHIA COLI FROM CASABLANCA, MOROCCO #99**  
Loubna JAMALI, Fatna Bourjilate, Brahim Bouhrif, Noureddine Dersi, H. Amarouch, S. Nadifi and Mohammed Timinouni
- **TreeKO: a duplication-aware algorithm for the comparison of phylogenetic trees**  
Marina Marcet-Houben and Toni Gabaldón