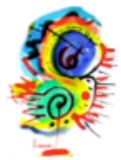
NGS2009

Conference on Next Generation Sequencing: Challenges and Opportunities



PROGRAM

THURSDAY 1st OCTOBER

9h30 – 9h45: Presentation (M. Pérez-Enciso)
9h45 – 10h30: Inaugural speech (Chair: D. Torrents)
- **R.K. Wilson:** Sequencing the Cancer Genome.

10h30 – 11h00: General Genomics
- **G. Marth:** Informatics Tools for Next-Generation Sequencing Analysis.

11h00-11h30 Coffee break

11h30 – 13h00 Technology section (Chair: M. Pérez-Enciso)
- **11h30 – J. Knight (Roche).** Sequencing Solutions for Small and Large Genomes.
- **12h00 – M.T. Ross (Illumina)**: Sequencing Human Genomes Using Genome Analyzer.
- **12h30 – R. Dixon (Applied Biosystems):** Introducing BioScopeT for SOLID System Data Analisis.

13h00 – 15h00 LUNCH AND POSTER VIEWING

15h00 – 16h30: General Genomics (Chair: J. García)
- **15h00 – G. McVean:** The 1000 Genomes project.
- **15h30 – H. Himmelbauer:** Plant Genomics in the Era of High-Throughput Sequencing: the Case of the Sugar Beet.
- **16h00 – N.J. van Orsouw:** Whole Genome Profiling: a New Method for Sequence Based Whole Genome Physical Mapping.
- **16h15 – C.H. Cannon:** Comparative Genomics of Tropical Evergreen Fagaceae.

16h30 – 17h00 Coffee break

17h00 – 18h45: Computational challenges (Chair: A. Ruiz)
- **17h00 –. C. Notredame:** Upcoming Challenges for Multiple Sequence Alignment Methods.
- **17h30 – P. Green**: Next-Generation Data Analysis.
- **18h00 – M. Brudno:** Discovering INDEL and Copy Number Genomic Variation from Short Reads
- **18h30 – H. Corrada Bravo:** Model-Based Quality Assessment and Base-Calling for Second-Generation Sequencing Data
- **18h45 – Bicheng Yang:** Sequencing, sequencing and sequencing.

19h00 – GROUP PICTURE

19h15 – WELCOME COCKTAIL AND POSTER VIEWING

FRIDAY 2nd OCTOBER MORNING

9h30 – 11h00 - Population Genomics (Chair: A. Navarro)

- **09h30 – M. Lynch:** Maximum-Likelihood Estimation of Population-Genetic Parameters from High-Throughput Sequencing Data.
- **10h00 – M. Groenen:** SNP Discovery and Analysis of Selective Sweeps Using Massive Parallel Short-Read Sequencing.
- **10h30 – L. Ferretti:** Population Genomics from Individual and Pool Sequencing.
- **10h45 – I. Ortega-Serrano:** A Pipeline for Studying Minor Variants in Complex Genetic Populations Using Long Reads from High-Throughput Sequencing Technologies. .

11h00-11h30 Coffee break

11h30 – 13h00 Population genomics (Chair: S. Ramos-Onsins/De Lorenzo)

- **11h30 – C. Bustamante:** Population Genomics in the Personal Genome Era.
- **12h00 – F. de la Vega:** Understanding Human Genetic Variation at the Personal and Population Level through Massively-Parallel Whole-Genome Sequencing.
- **12h30 – J. Satkoski:** Combining Reduced Representation Libraries and Short-Read Sequencing for High-Throughput SNP Discovery in the Absence of Sequenced Genomes.
- **12h45 – L. Mularoni:** High-Resolution Genome-Wide Mapping of Hermes Transposon Insertion Sites in *S. cerevisiae*.

13h00 – 15h00 LUNCH AND POSTER VIEWING

15h00 - 16h30 Functional genomics (**Chair: J. Betranpetit)**

- **15h00 – R. Guigó:** The Transcriptional Complexity of the Human Genome: Insights from Next Generation Technologies.
- **15h30 – A. Clark:** Using Short-Read Sequencing to Dissect Allele-Specific Expression.
- **16h00 – N. Naouar**: Quantification of Allele-specific Expression Patterns by GS FLX 454 Technology.
- **16h15 – V. Boeva:** Peak Selection Coupled with de Novo Motif Identification Improves the Accuracy of Transcription Factor Binding Site Prediction in ChIP-Seq Data Analysis.

17h00 – 18h30 General and functional Genomics - II (Chair: M. Bink)

- **17h00 – B. Timmermann:** Advanced Data Analysis in Targeted Resequencing Projects.
- **17h30 – J.M. Rosa-Rosa:** High Throughput Sequencing Analysis of Linkage Assay-Identified Candidate Regions in Familial Breast Cancer: Methods, Analysis Pipeline and Troubleshooting.
- **17h45 – R.B. Parmigiani:** Surfing on the Surface: Mutation Detection in Human Genes Coding for Cell Surface Trans-Membrane Proteins.
- **18h00 – A. G. Perera:** Identification of EMS-Induced Mutations by Whole-Genome Sequencing.
- **18h15 – C. Pérez-Llamas:** IntOGen: A Novel Framework for Integration and Data-Mining of Multidimensional Oncogenomic Data.

20h30 – CONGRESS DINNER

SATURDAY 3rd OCTOBER

9h30 – 10h45 Metagenomics: (Chair: Kua CS)

- **09h30 – F.O. Gloeckner:** Next Generation Sequencing in Marine Ecological Genomics: Tools and Applications.
- **10h00 – D. Rusch:** Metagenomics versus Next Generation Sequencing Technologies.
- **10h30 – M. Hajibabaei:** Large-scale Biodiversity Analysis through Next-Generation Sequencing.

10h45-11h15 Coffee break

11h15 – 12h15 Epigenomics: (Chair: J. Cruz Cigudosa)

- **11h15 – H. Stunnenberg:** A Systems Biology View at Transcription Regulation Networks.
- **11h45 – S. Beck:** Reverse Phenotyping: Towards an Integrated (Epi)Genomic Approach to Complex Phenotypes and Common Disease.

12h15 – 13h15 Round table (Chair A. Navarro)

13h30: FAREWELL COCKTAIL

POSTER LIST

(Only shown the Corresponding Author)
Please place your poster in the panel with assigned number

General genomics

P1. **Garcia-Mas, J.** Towards the Whole Sequence of the Melon Genome.
P2. **Bergero, R.** Using 454 Sequencing of ESTs for Linkage Analyses in a Dioecious Plant Species.
P3. **Kua, CS.** Using a 'Framework Species' Concept for Ecological and Evolutionary Studies in Comparative Genomics.
P4. **Esteve, A.** Partial Short-Read Resequencing of a Highly Inbred Iberian Pig..
P5. **Lin, Y-C.** Genome Sequence of the Recombinant Protein Production Host Pichia pastoris.
P6. **Tobes, R.** Mutant HIV Minority Variants Detected by Ultradeep Sequencing do Not Condition Virological Failure in Patients Starting ARV Therapy Including Low Genetic Barrier Drugs.

Bioinformatics and Population Genomics

P7. **Amaral, A.J.** Finding Selection Footprints in the Swine Genome Using Massive Parallel Sequencing.
P8. **Balzer, S.** Novel Tools and Methods for Exploring Pyrosequencing Data Including Quality Assessment and Simulation.
P9. **Bink, M.** StatSeq : Statistical Challenges on the 1000 Genome Sequences in Plants (EU COST Action TD0801).
P10. **Megens, H.-J.** Genome-Wide Assessment of Nucleotide Diversity and Signatures of Selection in Chicken Using Massive Parallel Sequencing.
P11. **Tobes, R.** Cloud Computing and NGS: Massively Parallel Computing for Massively Parallel Sequencing.
P12. **Barbadilla, A.** Genome Browser of Genetic Diversity in Drosophila.
P13. **Toro, M.A.** Including Dominance Effects in Genomic Selection.
P14. Unterländer, M. Using Next Generation Sequencing on Ancient DNA – Preamplified Via a New Muliplex Approach – to Detect Migration and Population Structure.

Transcriptomics and metagenomics

P15. **Cancio, I.** Pyrosequencing of Non-Model Sentinel Species for Gene Transcription Profiling Studies in Environmental Pollution Monitoring.
P16. **Gosalbes M.J.** High-Throughput Sequencing Technologies Applied to Human Gut Microbiota Research and Genomics of Pathogens.
P17. **Piferrer, F.** Analysis of the Gonadal Transcriptome During Sex Determination, Sex Differentiation and Gonadal Maturation in the Sea Bass (Dicentrarchus labrax) and Turbot (Scophthalmus maximus) by 454 Sequencing and Two Specific Oligo-Based Microarrays.
P18. **Schönfeld, B. I. K**. Rhopalodia gibba and its Spheroid Body - Sequencing Endosymbiosis.
P19. **Stuglik, M.** Investigating Molecular Basis of Response to Selection in Bank Vole with Next Generation Sequencing.
P20. **Haase, B.** Selection of Cancer-Related Gene Exons for Targeted Resequencing with a Flexible and Fully Automated Microarray Platform.