

X CRG SYMPOSIUM

10-11 November 2011

COMPUTATIONAL BIOLOGY OF MOLECULAR SEQUENCES

Organizers: R.Guigó, C.Notredame, T.Gabaldón, F.Kondrashov, G.G.Tartaglia



Friday 11 November

Session 3: Genome Regulation (II)

Chair: Cédric Notredame

- 09:00 – 09:45 Gary STORMO
Department of Genetics, Washington University School of Medicine, St. Louis (MO) USA
“Modeling Protein-DNA interactions”
- 09:45 – 10:30 Ron SHAMIR
School of Computer Science, Tel Aviv University, Tel Aviv IL
“Gene regulation, protein interaction and disease - a computational perspective”
- 10:30 – 11:30 Coffee Break

Session 4: RNA Analysis

Chair: Cédric Notredame

- 11:30 – 12:15 Ana TRAMONTANO
Department of Physics, Sapienza University of Rome, Rome IT
“More surprises from the RNA world”
- 12:15 – 13:00 Peter STADLER
Bioinformatics Group, Department of Computer Science, University of Leipzig, Leipzig DE
“Structural Evolution of Long Non-Coding RNAs”
- 13:00 – 14:30 Lunch

Session 5: Genome Annotation

Chair: Roderic Guigó

- 14:30 – 15:15 Tim HUBBARD
Wellcome Trust Sanger Institute, Hinxton, Cambridge UK
“From reference genomes to genome medicine”
- 15:15 – 16:00 Søren BRUNAK
Technical University of Denmark & University of Copenhagen, Copenhagen DK
“Interfacing sequencing and network biology data to personal healthcare sector information”
- 16:00 – 16:45 Brendan FREY
Department of Electrical and Computer Engineering, and Banting and Best Department of Medical Research, and Department of Computer Science, Univ. of Toronto, Ontario CA
“The new and improved splicing code”
- 16:45 – 17:15 Coffee Break
- 17:15 – 18:00 Terry SPEED
Bioinformatics Division, Walter & Eliza Hall Institute of Medical Research, Parkville Victoria AU
“Dealing with the GC-content bias in second-generation DNA sequence data”
- 18:00 – 18:45 Mark GERSTEIN
Department of Molecular Biophysics and Biochemistry, and Department of Computer Science, Yale University, New Haven (CT) USA
“Annotating non-coding regions of the genome”
- 18:45 – 19:00 Conclusions