Thursday 10 November

08:00 – 09:00   Registration
09:00 – 09:05   Welcome by Luis Serrano
09:05 – 09:15   Introduction by Roderic Guigó

Session 1: Protein Analysis
Chair: Gian Gaetano Tartaglia

09:15 – 10:00   Temple F. SMITH
Department of Biomedical Engineering, Boston University, Boston US
"A Unique Mammalian Apoptosis Regulatory Gene, Lfg5, and a Homo sapiens Neanderthal Mystery"

10:00 – 10:45   Michele VENDRUSCOLO
Department of Chemistry, University of Cambridge, Cambridge UK
"Life on the edge: Proteins are close to their solubility limits"

10:45 – 11:30   Amos BAIROCH
Swiss Institute of Bioinformatics, and Department of Structural Biology and Bioinformatics, Faculty of Medicine, University of Geneva, Geneva CH
"Organising human protein-centric knowledge: the challenge of neXtProt"

11:30 – 12:00   Coffee break

Session 2: Genome Evolution
Chair: Fyodor Kondrashov

12:00 – 12:45   Eugene V. KOONIN
National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda (MD) USA
"Are there laws in evolutionary genomics?"

12:45 – 13:30   Nick GOLDMAN
EMBL - European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton UK
"Adventures in Evolutionary Alignment"

13:30 – 15:00   Lunch

15:00 – 15:45   Mathieu BLANCHETTE
School of Computer Science, McGill University, Montreal CA
"Ancestral Mammalian Genome Reconstruction and its Uses toward Annotating the Human Genome"

15:45 – 16:30   David SANKOFF
Department of Mathematics and Statistics, University of Ottawa, Ottawa CA
"The ancestral rosid, fabid and malvid gene orders after the eudicot hexaploidization event but before widespread whole genome duplication events"

16:30 – 17:00   Coffee break

Session 3: Genome Regulation (I)
Chair: Toni Gabaldón

17:00 – 17:45   Martin VINGRON
Max Planck Institute for Molecular Genetics, Berlin DE
"Transcription factor binding sites, histone modifications, and two promoter classes"

17:45 – 18:30   Philipp BUCHER
Swiss Institute of Bioinformatics (SIB) & Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne CH
"Computational Promoter Analysis in the Era of Ultra-High-Throughput Sequencing"

18:30 – 19:15   Gene MYERS
Janelia Farm Research Campus, Howard Hughes Medical Institute, Ashburn (VA) USA
"Decoding Genomes with Light Microcopy"

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 – 11:00   Coffee Break

Session 4: RNA Analysis
Chair: Cédric Notredame

11:00 – 11:45   Ana TRAMONTANO
Department of Physics, Sapienza University of Rome, Rome IT
"More surprises from the RNA world"

11:45 – 12:30   Peter STADLER
Bioinformatics Group, Department of Computer Science, University of Leipzig, Leipzig DE
"Structural Evolution of Long Non-Coding RNAs"

12:30 – 13:15   Chris PONTING
MRC Functional Genomics Unit, University of Oxford, Oxford UK
"Rapid turnover of long noncoding RNAs and the evolution of gene expression"

13:15 – 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, Copenhaguen 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