

Schedule

Monday, June 2

- 08:00-08:30 Registration
- 08:30-09:00 Opening by **Roderic GUIGÓ** (CRG), **Burkhard ROST** (ISCB) and **Cedric NOTREDAME** (CRG)
- 09:00-09:05 Introduction by **Victor DE LA TORRE** (INB) (to be confirmed)
- 09:05-10:00 **Keynote: Thomas GINGERAS**, *Cold Spring Harbor Laboratory (CSHL)*
“**Conservation and Novel Functions of Non-coding RNAs**”

Sanger Memorial Session

- 10:00-10:20 Introduction by **Pere PUIGDOMÈNECH** (Centre for Research in Agricultural Genomics)
- 10:20-10:45 (23) **Heinz Himmelbauer**, Centre for Genomic Regulation (CRG)
“Long sequencing reads: No end in sight?”
- 10:45-11:10 (12) **Amin Ardehshirdavani**, KU Leuven ESAT-STADIUS Center for Dynamical Systems
“NGS logistics: federated analysis of NGS sequence variants across multiple locations”
- 11:10-11:40 coffee break

Session 1: Sequencing and Assembly Methods

- 11:40-12:05 (54) **Fidel Ramirez**, Max Planck Institute of Immunobiology and Epigenetics
“Super scaffolding of de novo assemblies using the three-dimensional folding of the genome”
- 12:05-12:30 (57) **Tyler Alioto**, Centro Nacional de Análisis Genómico, Barcelona, Spain.
“Divide and conquer: strategies for achieving better de novo genome assemblies from NGS data”
- 12:30-12:55 (73) **Olga Nikolayeva**, University of Zurich.
“de novo assembly of PacBio reads and integrative analysis: *Bartonella henselae* case study”
- 12:55-13:15 Tech Talk: **Wolfgang Mertz**, EMC-Isilon
“The Foundation of NGS Data Analysis”
- 13:15-14:30 Lunch

Session 2: Epigenetic Analysis Methods

- 14:30-14:55 (68) **Emanuele Raineri, Marc Dabad**, Centro Nacional de Análisis Genómico, Barcelona, Spain.
“methyldiff : Analysis of differential methylation in paired samples and group of replicates”
- 14:55-15:20 (86) **Rory Stark**, University of Cambridge, Cancer Research UK, Cambridge Institute
“ChIPQC: Computing and reporting quality metrics for assessing ChIP-seq experiments”

Session 3: Population genomics

- 15:20-15:45 (9) **Ofer Isakov**, Tel Aviv University
“Deep sequencing analysis of viral infection and evolution allows rapid and detailed characterization of viral mutant spectrum”
- 15:45-16:10 (59) **Laia Carreté**, Centre for Genomic Regulation (CRG)
“Genome variation across clinical and commensal isolates in the emerging fungal pathogen *Candida glabrata*”
- 16:10-16:35 (93) **Martin Steinegger**, Gene Center Munich, Ludwig-Maximilian University Munich, Germany.
“MMseqs suite for fast and sensitive batch searching and clustering of huge (metagenomic) protein sequence sets”
- 16:35-17:00 coffee break

Schedule

- 17:00-17:05 Introduction by **Roderic GUIGÓ** (CRG) (to be confirmed)
- 17:05-18:00 **Keynote: Kristin ARDLIE**, *The Broad Institute of Harvard and MIT*
"The Genotype-Tissue Expression (GTEx) Project"
- 18:00-20:30 Networking reception + POSTER SESSION 1
- 20:30- Gala Dinner (only for participants who inscribed in Gala Dinner)

Tuesday, June 3

- 08:30-09:00 morning coffee
- 09:00-09:05 Introduction by **Jen HARROW** (Wellcome Trust)
- 09:05-10:00 **Keynote: John MARIONI**, *EMBL-EBI*
"Computational challenges in single-cell transcriptomics – from immune cells to neurons"
- 10:00-10:30 coffee break
- Session 4: Genetics**
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- 10:30-10:55 (70) **Beatriz Bellosillo**, Hospital del Mar-IMIM
"Molecular characterization of acquired resistance to cetuximab-based therapy in colorectal cancer"
- 10:55-11:20 (85) **Konstantinos Alexiou**, IRTA
"In silico detection of recombination breakpoints in an almond x peach interspecific cross"
- 11:20-11:45 Business Meeting by **Burkhard ROST** (ISCB)
- 11:45-12:05 Tech Talk 2: **Erik BONGCAM-RUDLOFF**, SLU-Global Bioinformatics Centre, Uppsala SE
ALLBIO: "Broadening the Bioinformatics Infrastructure to unicellular, animal, and plant science"
- 12:05-12:25 Tech Talk 3: **Ville PARVIAINEN**, MediSapiens Ltd
"Oncogenomics Explorer – Connecting the clinical to molecular in NGS"
- 12:25-14:15 Lunch + POSTER SESSION 2
- Session 5: Gene Expression**
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- 14:15-14:40 (5) **Mette Boyd**, The Bioinformatics Centre, University of Copenhagen, Denmark
"Identification of TNF- α -responsive Promoters and Enhancers in the Intestinal Epithelial Cell Model Caco-2"
- 14:40 -15:05 (46) **Angela Brooks**, Broad Institute
"The landscape of RNA splicing alterations in human cancers"
- 15:05-15:30 (76) **Anna Lorenc**, Biomedical Research Centre, Guy's and St Thomas' NHS FT, King's College L.
"Identification of novel imprinted transcripts in mouse hypothalamus and vomeronasal organ that could contribute to mate choice differences between natural populations"
- 15:30-15:55 (45) **Lourdes Peña-Castillo**, Memorial University of Newfoundland, St. John's, NL, Canada
"Computational identification of small RNAs in *Rhodobacter capsulatus* from RNA-Seq data"
- 15:55-16:20 (82) **Jette Bornholdt Lange**, The Bioinformatics Centre, University of Copenhagen, Denmark.
"Dramatic in vivo responses to carbon nanotubes at promoter level"
- 16:20-17:00 coffee break
- 17:00-17:05 Introduction by **Cedric NOTREDAME** (CRG) (to be confirmed)
- 17:05-18:00 **Keynote: Cornelia M. VAN DUIJN**, *Erasmus MC*
"Finding rare variants for complex genetic disorders combining statistics and bioinformatics"
- 18:00-18:30 Awards and Closing Remarks