NGS 2018
Next Generation Sequencing Conference 2018
April 9 – 11, 2018 | Barcelona, Spain
Submission closes: Monday, 29 January 2018
Early registration deadline: Monday, March 12, 2018
Online registration deadline: Monday, April 2, 2018

Program

Monday, April 9

08:30-09:00	Registration
09:00-09:15	Welcome by Alfonso Valencia, BSC, Barcelona, ES and ISCB past president
09:15-09:20	Opening by Núria López-Bigas, IRB, Barcelona, ES
09:20-10:05	**Keynote: Francesca D. Ciccarelli,** King's College London, UK **“Systems biology to rebuild cancer evolution and identify new cancer genes”**
10:05	**Session 1: Cancer Genomics** (chair: Núria López-Bigas)
	OP01 “A 10.000 sample overview of cancer driver events” **Eduard Porta**, Barcelona Supercomputing Centre, Barcelona, ES
	OP02 “Systematic pan-cancer analysis of somatic allele frequency” **Anelia Horvath**, George Washington University, USA
10:45-11:15	Coffee break
	OP03 “Sweepstake evolution revealed by population-genetic analysis of copy-number alterations in single genomes of breast cancer” **Daniel A Vasco**, Centre for Systems Biomedicine, LU
	OP04 “Mutated Tumor Suppressors Follow Oncogenes Profile by the Gene Hypermethylation of Partners in the Protein Interaction Networks” **Somnath Tagore**, Bar-Ilan University, IL
	OP05 “Network-based smoothing of somatic mutations improves patient classification from sparse genetic data” **Rosalba Giugno**, Department of Computer Science, University of Verona, IT
	OP06 “Racial/Ethnic Disparities in Cancer Research: a Never-ending Battle” **Santiago Guerrero**, Centro de Investigación Genética y Genómica, EC
12:35-14:00	Lunch and Poster viewing
14:00-14:05	Introduction by Cedric Notredame, Centre for Genomic Regulation, Barcelona, ES
14:05-14:50	**Keynote: Nicholas Luscombe,** The Francis Crick Institute, UK
14:50	**Session 2 Genetics & Transcriptomics** (chair: Cedric Notredame)
	OP07 “Predicting disease-causing variant combinations accurately” **Tom Lenaerts**, Universite Libre de Bruxelles, BE -
	OP08 “Comprehensive sequencing of the myocilin gene in a selected cohort of primary open-angle glaucoma patients” **Luke O'Gorman**, University of Southampton, UK
	OP09 “GenePy: a gene score for next generation sequencing data modelling” **Enrico Mossotto**, University of Southampton, UK
	OP10 “Phenotype-driven variant prioritization significantly improves over impact and prevalence scores in a large-scale analysis of 1,963 cases of Mendelian disease diagnostics by whole-genome sequencing” **Francisco De La Vega**, Stanford University, USA
	OP11 “Dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues” **Serghei Mangul**, University of California, Los Angeles, USA

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16:30-17:00 Coffee break

OP12 "Identification and validation of novel and annotated LncRNAs in canine B-cell lymphoma by RNA-Seq"
Rosalba Giugno, Department of Computer Science, University of Verona, IT

OP13 "Towards novel signalling functions of mobile mRNAs"
Federico Apelt, Max Planck Institute of Molecular Plant Physiology, DE

OP14 "Understanding regulation of alternative splicing through RNA binding proteins"
Dmitri Pervouchine, Skolkovo Institute of Science and Technology, RU

OP15 "Stratified co-morbidity networks: Inferring patient-specific comorbidities from transcriptomic data"
Jon Sánchez, Barcelona Supercomputing Centre, Barcelona, ES

OP16 "bigSCale: An Analytical Framework for Big-Scale Single-Cell Data"
Giovanni Iacono, CRG-CNAG, Barcelona, ES

18:40 Poster Session

20:00 Conference Dinner. Xiroi Ca la Nuri. Address: Passeig Marítim de la Nova Icària, 38.

Tuesday, April 10

08:45-09:00 Morning welcome and Introduction

09:00-09:05 Introduction by Alfonso Valencia, BSC, Barcelona, ES

09:05-09:50 **Keynote: Nick Loman,** University of Birmingham, UK

"A sequencing singularity for infectious disease?"

09:50 **Session 3: Transcriptomics (II) and Model Organisms** (Chair: Alfonso Valencia)

OP17 "Reference-free reconstruction and error correction of transcriptomes from Nanopore long-read sequencing"
Eduardo Eyras, Pompeu Fabra University, Barcelona, ES

OP18 "3D determinants of gene expression variability"
Vera Pancaldi, Barcelona Supercomputing Centre, Barcelona, Spain

10:30-11:00 Coffee break

OP19 "Study of genome evolution among traditional bakery yeasts in relation to domestication"
Colin Tinsley, Inra, France

OP20 "Weighted correlation network analysis and transcriptome dynamics during early gonadal differentiation of the European sea bass (*Dicentrarchus labrax*)"
Núria Sánchez-Baizán, Institute of Marine Sciences, Barcelona, ES

OP21 "NGS-based resequencing and reannotation of the Trypanosoma congolense genome and trancriptome"
Marcin Jąkalski, Department of Plant Taxonomy and Nature Conservation, University of Gdańsk, PL

OP22 "High quality genome of a Norwegian reindeer using 10X Genomics"
Montserrat Torres-Oliva, Institute of Clinical Molecular Biology, Christian-Albrechts-University, Kiel, DE

OP23 "Genomic characterisation and vulnerabilities of two transmissible cancers in Tasmanian devils"
Maximilian Stammnitz, University of Cambridge, UK

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OP24 “Genome diversity and evolution in a transmissible cancer”
Adrian Baez-Ortega, Transmissible Cancer Group, University of Cambridge, UK

13:00-14:00 Lunch and Poster viewing

Session 4: Multi-Omics, & Metagenomics (Chair: Francisco De La Vega)

OP25 “Single cell systems immunology of viral specific B cells and CD8+ T cells”
Simone Rizzetto, School of Medical Science, UNSW, AU

OP26 “Toward decoding complete human immunome. Assemble recombined T and B cell receptor sequences across 50,000 individuals”
Serghei Mangul, University of California, Los Angeles, USA

OP27 “Detection of radiation-Induced alterations in the transcriptome and Exome of human gingiva fibroblasts”
Neetika Nath, University Medicine Greifswald, DE

OP28 “Corrections for asymmetry in high-throughput sequencing datasets applied to a meta-transcriptome dataset”
Greg Gloor, U. Western Ontario, CA

OP29 “Fast and sensitive protein sequence search, clustering and assembly tools for the analysis of massive metagenomics datasets”
Martin Steinegger, Max-Planck-Institute, DE

15:40-16:00 Coffee Break

OP30 “Characterizing the microbiome in factory ingredient samples using metatranscriptome deep sequencing data”
Kristen Beck, IBM, USA

OP31 “The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of Antimicrobial Resistance determinants using next generation sequencing technologies”
Alexandre Angers, Joint Research Centre, European Commission, IT

16:40 Introduction by Francisco De La Vega, Stanford University, USA

16:40-17:25 **Keynote: Ami Bhatt**, Stanford University, USA.
“Translating metagenomics”

17:25 Awards and closing remarks