

# BARCELONA NGS'17: Structural Variation and Population Genomics



APRIL 3-5, 2017 BARCELONA, SPAIN

## Keynote Speakers:

Jaume Bertranpetit, Pompeu Fabra University, Barcelona ES  
Deanna Church, Applications at 10x Genomics, Pleasanton USA  
Jan Korbel, European Molecular Biology Laboratory, Heidelberg DE  
Nicole Soranzo, University of Cambridge UK

## Key dates:

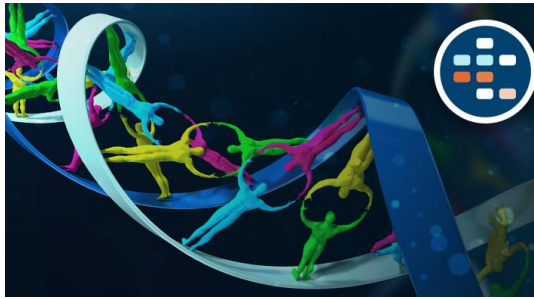
Early registration deadline 10 March 2017  
Online registration deadline 24 March 2017



## Schedule

### Monday, April 3

- 08:00-08:30 Registration
- 08:30-09:00 Opening by **Alfonso VALENCIA** (ISCB)
- 09:00-09:45 **Keynote: Deanna CHURCH**, 10x Genomics California, USA  
“Advancing genomics drop by drop”
- Session 1: Methods** (chair: Stephan Ossowski)
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- 09:45-10:03 **OP1 - “Mapping and phasing of structural variation in patient genomes using nanopore sequencing”**  
**Wigard KLOOSTERMAN**, UMC Utrecht NL
- 10:03-10:21 **OP2 - “GemBS – fast and efficient WGBS data processing pipeline”**  
**Angelika MERKEL**, Centro Nacional de Análisis Genómico (CNAG-CRG), Barcelona ES
- 10:21-10:50 Coffee break
- 10:50-11:08 **OP3 - “High-Throughput Data Analysis Workflow for Large Scale Epigenome Profiling”**  
**Povilas GIBAS**, Department of Biological DNA Modification, Institute of Biotechnology, Vilnius University LT
- 11:08-11:26 **OP4 - “GRIDSS: sensitive and specific genomic rearrangement detection using positional de Bruijn graph assembly”**  
**Daniel CAMERON**, Walter and Eliza Hall Institute of Medical Research, Victoria AU
- 11:26-11:44 **OP5 - “Count-based Probabilistic PCA for single-cell data analysis”**  
**Ghislain DURIF**, CNRS, FR
- 11:44-12:02 **OP6 - “Approaches to building spatio-temporal models of splicing regulation that include RNA structure”**  
**Dmitri PERVOUCHINE**, Center for Genomic Regulation, Barcelona ES
- 12:02-12:20 **OP7 - “OrthoFiller — identifying missing annotations for evolutionarily conserved genes”**  
**Michael DUNNE**, University of Oxford UK
- 12:20-12:38 **OP8 - “Bi-CoPaM: an automated method to identify clusters of consistently co-expressed genes from multiple heterogeneous transcriptomic datasets”**  
**Basel ABU-JAMOUS**, University of Oxford UK
- 12:38-14:00 Lunch and Poster viewing
- 14:00-14:05 Introduction by **Cedric NOTREDAME** (CRG)
- 14:05-14:50 **Keynote: Jan KORBEL**, European Molecular Biology Laboratory (EMBL) Heidelberg DE  
“From genomic variation to molecular mechanism”
- Session 2: Population Genomics** (chair: Mario Cáceres)
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- 14:50-15:08 **OP09 - “Genetic variants of 1,011 natural yeast genomes provide a deep insight into the multiplicity of the genetic basis of phenotypic diversity”**  
**Anne FRIEDRICH**, University of Strasbourg FR
- 15:08-15:26 **OP10 - “Population Genomics of Transposable Elements in Drosophila”**  
**Maite G. BARRÓN ADURIZ**, Institut de Biologia Evolutiva, Barcelona ES
- 15:26-15:44 **OP11 - “Genome-wide scans between two geographically isolated honeybee subpopulations reveal putative signatures of human-mediated selection”**  
**Melanie PAREJO**, Swiss Bee Research Center, Agroscope and Institute of Bee Health, University of Bern CH



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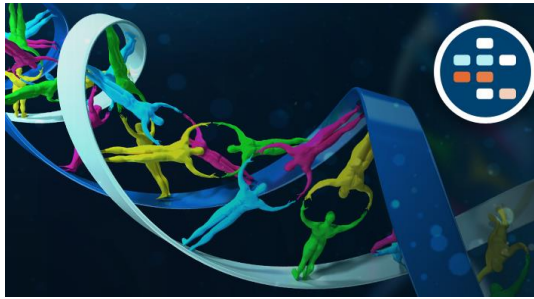


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- 15:44-16:00 **Tech Talk 1 –“BaseSpace Sequence Hub: Software suite for high throughput sequencing technology and NGS data management”**  
**Kevin MIRANDA**, EMEA Bioinformatics Specialist, Illumina
- 16:00-16:30 Coffee break
- 16:30-16:48 **OP12 – “Exploiting NGS data to quantify within-host viral evolution”**  
**Christopher ILLINGWORTH**, University of Cambridge UK
- 16:48-17:06 **OP13 - “Studying miRNA and isomiR populations in Norwegian rheumatoid arthritis patients”**  
**Fatima HEINICKE and XiangFu ZHONG**, Department of Medical Genetics, University of Oslo University Hospital NO
- 17:06-17:24 **OP14 – “Insights into gorilla speciation and current genetic health with structural variant analysis”**  
**Andrey GRIGORIEV**, Rutgers University USA
- 17:24-17:39 **Tech Talk 2: "A One-stop Shop for Finding and Accessing Genomics Data"**  
**Manuel CORPAS**, Scientific Lead at Repositive
- 17:39-19:30 Poster Session
- 20:00 Conference Dinner will be held at the Marina Bay restaurant (Calle Marina, 19-21) – Ticket required

### Tuesday, April 4

- 08:45-09:00 Morning welcome and Introduction
- 09:00-09:05 Introduction by **Janet KELSO** (Max Planck Institute for Evolutionary Anthropology)
- 09:05-09:50 **Keynote: Jaume BERTRANPETIT**, Pompeu Fabra University Barcelona, Spain  
**“Unveiling the information in the variation in the human genome: from ancestry to adaptation”**
- Session 3: Human Variation** (chair: Janet Kelso)
- 09:50-10:08 **OP15 - “Evolutionarily ancient genes accumulate intronic deletions in human populations”**  
**Maria RIGAU**, Institute of Cellular Medicine, Newcastle University UK
- 10:08-10:26 **OP16 – “Life beyond NGS: Overcoming current limitations in the study of human inversions with new high-throughput methods to validate and genotype them in multiple individuals”**  
**Mario CACERES**, ICREA and Institut de Biociencia i de Biomedicina, Universitat Autònoma de Barcelona ES
- 10:26-11:00 Coffee break
- 11:00-11:18 **OP17 – “eDGAR: a webserver for analysing the relationship among genes and polygenic diseases”**  
**Giulia BABBI**, University of Bologna IT
- 11:18-11:36 **OP18 – “Where did you come from, where did you go: Integrating SV Detection Methods for Horizontal Gene Transfer Detection from NGS Data”**  
**Kathrin TRAPPE**, Robert Koch Institute DE
- 11:36-11:54 **OP19 – “RNA editing heterogeneity in human brain revealed by Single Cell RNAseq”**  
**Ernesto PICARDI**, University of Bari & IBBE-CNR, IT



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- 11:54-12:12 **OP20 – “A Real-time Approach for Privacy Protection in Next Generation Sequencing”**  
**Tobias P. LOKA**, Robert Koch Insitute, DE
- 12:12-12:30 **OP21 – “Analysis of copy-number variations from whole-exome sequencing data using the CANOES software reveals rare genomic rearrangements involved in neuropsychiatric disorders”**  
**Olivier QUENEZ**, Normandie Univ, UNIROUEN, Inserm U1245, Normandy Centre for Genomic and Personalized Medicine, CNR-MAJ, Rouen FR
- 12:30-12:48 **OP22 – “Genetic stratification in a cohort of patients with familiar dilated cardiomyopathy”**  
**Lenka PIHEROVA**, Institute of Inherited Metabolic Disorders, 1st Faculty of Medicine, Charles University CZ
- 12:48-13:03 **Tech Talk 3: “End-2-End Infrastructure for NGS”**  
**Wolfgang MERTZ**, CTO Life Sciences and Healthcare, Dell EMC Isilon
- 13:03-14:30 Lunch and Poster viewing
- Session 4: Genomics** (chair: Cedric Notredame)
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- 14:30-14:48 **OP23 – “Characterization of Vaccinium vitis-idaea genetic diversity and its association with environmental and biochemical variables”**  
**Lourdes PENA-CASTILLO**, Memorial University of Newfoundland CA
- 14:48-15:06 **OP24 – “Findings from the Fourth Critical Assessment of Genome Interpretation, a community experiment to evaluate phenotype prediction”**  
**Gaia ANDREOLETTI**, University of California, Berkeley USA pending
- 15:06-15:24 **OP25 – “Genome variation in the emerging fungal pathogen Candida glabrata”**  
**Laija CARRETÉ**, Centre for Genomic Regulation, Barcelona ES
- 15:24-15:42 **OP26 – “Integrative analysis of genetic, transcriptomic and epigenetic data to decipher and model gene regulatory networks in drosophila embryos”**  
**Swann FLOC’HLAY**, IBEns (UMR CNRS 8197 - INSERM 1024), FR
- 15:42-16:10 Coffee Break
- 16:10-16:28 **OP27 – “Evolution of Proboscidea genomes illustrated by variant analysis”**  
**Andrey GRIGORIEV**, Rutgers University USA
- 16:28-16:46 **OP28 – “Real time pathogen identification from metagenomic Illumina datasets”**  
**Simon H. TAUSCH**, Robert Koch Institute DE
- 16:46-16:50 Introduction by **Stephan OSSOWSKI** (CRG)
- 16:50-17:35 **Keynote: Nicole SORANZO**, Wellcome Trust Sanger Institute, Cambridge UK  
**“Genetic and epigenetic variation in population-based cohorts informs cardiometabolic and immune disease risk”**
- 17:35 Awards and closing remarks