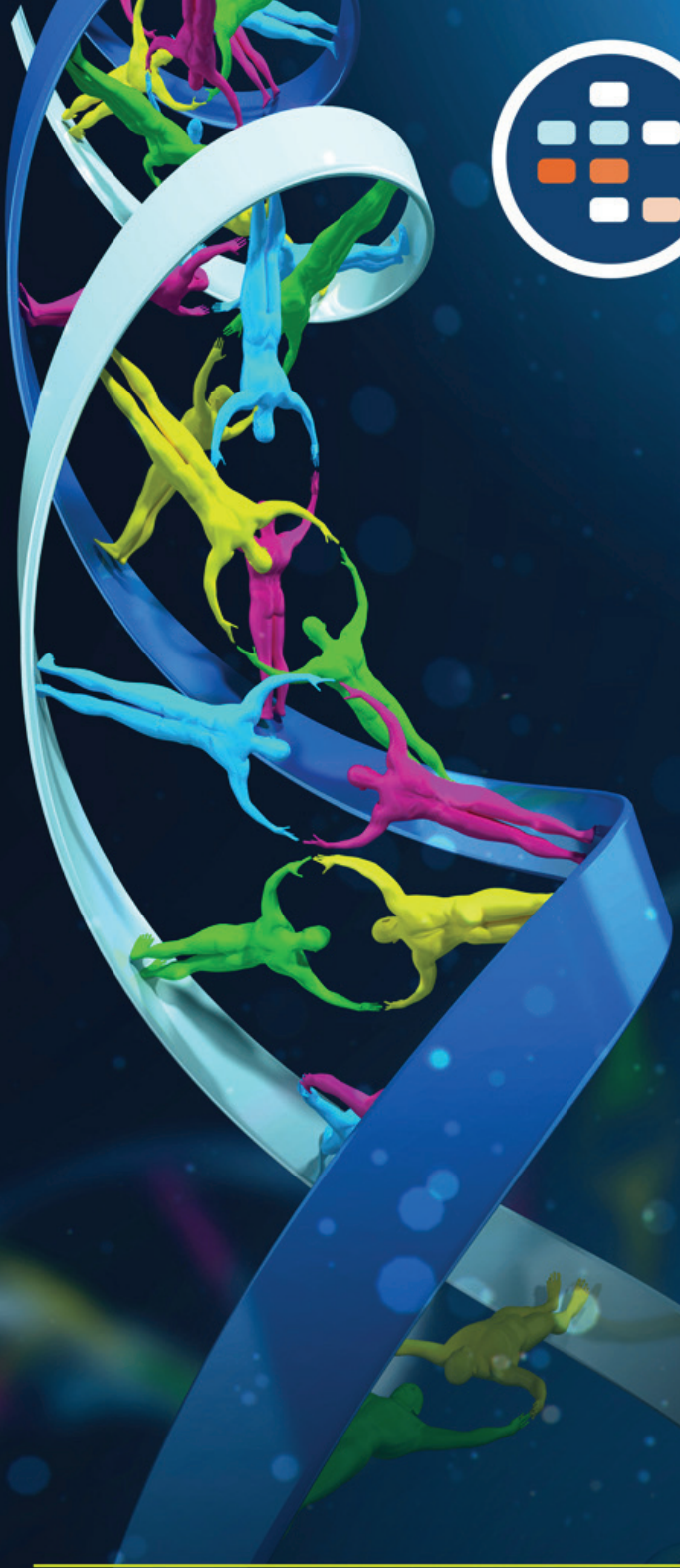

BARCELONA NGS'17:
Structural Variation and Population Genomics

APRIL 3-5, 2017
BARCELONA, SPAIN

MARK YOUR CALENDARS FOR THE NGS 2017!

New sequencing technologies have opened up the possibility to sequence genomes at a previously unprecedented scale.
The sequencing of whole genomes from large number of individuals representing multiple populations allows the extent of genetic diversity, of both at the single nucleotide level, and of larger structural variants, to be catalogued. Using such data the genetic basis of evolutionary and disease processes can be explored.
The meeting will draw together researchers from diverse backgrounds who develop and apply novel tools to sequencing data. Topics covered will include, but are not limited to, genome assembly, variant characterization and analysis, gene expression, population history, disease, and more!

CONFERENCE TOPICS

- Copy number variation in population genomics and translational applications
- Software and algorithms for high-throughput sequencing technologies
- NGS data management and visualisation
- Applications of NGS in:
  Population genomics / Metagenomics / Single cell analysis
  Clinical and translational biology

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

Submission closes
21 January 2017

CONFERENCE CHAIRS

- **Janet Kelso**
  Max Planck Institute for Evolutionary Anthropology DE
- **Cedric Notredame**
  Centre for Genomic Regulation ES
- **Stephan Ossowski**
  Centre for Genomic Regulation ES

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