



Clinical Interpretation of Variants from Next - Generation Sequencing

**Hotel Vincci Maritimo
Barcelona, Spain
20th May 2016**

8.00 – 8.55 Registration
Speakers arrive and hand in presentations

9.00 – 9.10 **Introduction**
William Oetting

Session I **Chair: Peter Taschner**

9.10 – 9.40 **The 100,000 Genomes Project**
Tim Hubbard
Head of Genome Analysis, Genomics England, & Head of Department of Medical & Molecular Genetics Director of Bioinformatics King's Health Partners/King's College London, Faculty of Life Sciences & Medicine, King's College London

9.40 – 10.00 **Comparing WGS to WES in a clinical setting**
Martin Elferink

10.00 – 10.20 **Genetic testing for hereditary cancer: is exome sequencing ready or there is still room for *ad hoc* designed panels?**
Lidia Feliubadalo

10.20 – 10.30 Discussion

10.30 – 11.00 **Coffee Break & Poster Session**

Session 2 **Chair: Anthony Brookes**

11.00 – 11.30 **Are we done with variant calling?**

Ivo Gut
Director, CNAG, Barcelona, Spain

11.30 – 11.50 **Towards formal specification of HGVS nomenclature enabling computational tool development**

Jonathan Vis

11.50 – 12.10 **An efficient and accurate end-to-end solution leveraging network analytics to infer patient syndrome and identify causal mutations in rare disease cases**

Sohela Shah

12.10 – 12.30 **What do public databases of clinical variants really tell us about classification concordance?**

Stephen Lincoln

12.30 – 12.40 **Discussion**

12.40 – 14.00 **Lunch**

Session 3 **Chair: Christophe Beroud**

14.00 – 14.30 **Variants annotation and filtration in NGS context**

David Salgado
NGS Team Manager at UMR_S910 - Aix-Marseille Université, France

14.30 – 14.50 **Improving the annotation of clinically important genes to aid identification of missing causal variants**

Adam Frankish

14.50 – 15.10 **Sitting on the fence: variant interpretation in RASopathies**

Vijaya Ramachandran

15.10 – 15.20 **Discussion**

15.20 – 15.40 **Coffee Break**

15.40 – 16.10 Ethical issues of NGS and diagnosis of human genetics diseases

Heidi Howard

16.10 – 16.20 Congenital haemolytic anaemia study with a targeted NGS panel

Celeste Bento

16.20 – 16.30 Molecular Analysis of Single Nucleotide Polymorphism (SNPs) for β - Globin Gene in Tribes of Madhya-Pradesh, India

Ruchira Chaudhary

16.30 – 16.40 SNPs based Genetic variability in tribes of Madhya-Pradesh (India) in reference to G-6-PD gene

Nitin Pathak

16.40 – 16.50 Characterizing the intrinsic component of disease severity

Oscar Marin

16.50 – 17.00 Meeting Summary & End

