

7th Next Generation Sequencing Symposium

Wednesday 17th May, 2017

Faculty of Medicine Lecture Theatre 2, University Hospital Southampton

8.45 - 9.15	Registration & Coffee	
SESSION 1. (20')		
9.15 - 9.20	Welcome	Sarah Ennis - FoM
9.20 - 9.40	Primary ciliary dyskinesia diagnostics in the genomic era	Jane Lucas - FoM
9.40 - 10.00	Cryptic genetic abnormalities in leukaemia	Nick Cross - WRGL
10.00 - 10.10	A forensic look at the deep past: "Metabarcoding" of ancient DNA	Mary Edwards - Geog
10.10 - 10.20	Prehistoric life on an artificial island; An ancient DNA perspective on crannogs	Thierry Fonville - Geog
10.20 - 10.40	PacBio's long read SMRT Sequencing - Clinical Applications	Nicola Cahill - PacBio
10.40 - 11.00	Networking & Exhibitor Stands with Coffee	
SESSION 2. (6')		
11.00 - 12.00	 <i>Snapshots of local NGS Applications</i> 	
	Investigating the origin and diversification of Canary Islands daisies	Oliver White - FNES
	Storing NGS data: the good, the bad and the oligo	Matthew Addis - Arkivum
	Longitudinal, multi-omic data in Paediatric Inflammatory Bowel Disease (IBD)	James Ashton - FoM
	Translational impacts of next generation sequencing in primary immunodeficiency	Will Rae - UHS
	NovaSeq: a new era of sequencing	Neil Ward - Illumina
	Machine learning modelling of exome and clinical data in IBD	Enrico Mossotto - FoM
	Reconstructing environmental changes since the Last Ice Age in Arctic Russia using ancient DNA: A mammoth task	Charlotte Clarke - Geog
12.00 - 1.00	Lunch & Exhibitor stands	
1.00 - 2.00	Professor Saheer Gharbia Head of Genomics Research, Public Health England - National Infection Service The Human Microbiome: lessons and challenges in deciphering the gut microbiota and its role in disease	
2.00 - 2.10	Comfort break	
SESSION 3. (20')		
2.10 - 2.30	NGS methylation analysis in motor neurone disease	Andrew Douglas - WCGS
2.30 - 2.50	NGS to explore the global distribution and adaptation of marine invasive species	Steve Bourne - NOC
2.50 - 3.10	There and back again, modelling immune response regulation in human skin	Marta Polak - FoM
3.10 - 3.30	Interpretation of variants returned from the 100,000 Genomes Project	Simon Thomas - WRGL
3.30 - 3.50	Droplet-barcoding single-cell RNA sequencing in cancer	Mat Rose-Zerilli - FoM
3.50 - 4.00	Networking & Exhibitor Stands with Coffee	

Thanks to our sponsors:



Organised by Sarah Ennis, S. Hodgson, E. Mossotto, R. Pengelly