Programme

Programme for Genome Science 2019

Tuesday 3rd September 2019

Start	End	Who	Title
11:30	**12:20**	***Registration and lunch***	
12:20	12:30	Mick Watson	Introduction and Welcome
12:30	13:20	**Keynote:** Wendy Bickmore	Understanding function in the non-coding genome
13:20	14:10	**Keynote:** Sarah Teichmann	Immunogenomics one cell at a time
14:10	14:40	*Coffee*	
14:40	**16:00**	***Evolving Technologies 1***	
14:40	15:00	Clive Brown (Oxford Nanopore)	The latest from Nanopore sequencing
15:00	15:20	Vince Smith (Illumina)	Advances in sequencing technology that are transforming genomics
15:20	15:35	Louise Williams (New England BioLabs)	New England BioLabs
15:35	15:50	Matt Loose	Long Read Club - the future is very long reads indeed
15:50	16:00	Yannick Delpu (BioNano)	Next-Generation Cytogenomics: High-throughput Mapping of Structural Variation in Genetic Disease and Clinical Oncology
16:00	16:25	*Coffee*	
16:25	**18:10**	***Evolving Technologies 2***	
16:25	16:50	Omer Bayraktar	The Rise of Spatial Genomics

Start	End	Who	Title
16:50	17:10	Rade Drmanac (BGI/Complete):	A new generation of NGS: PCR free DNBseq + CoolNGS chemistry with unlabeled nucleotides + Single-tube unique cobarcoding (stLFR).
17:10	17:25	Marie Just Mikkelsen (Samplix)	Xdrop™ - Targeted Sequencing into the Dark and Unknown
17:25	17:45	Tuval Ben Yehezkel (LoopSeq):	LoopSeq Synthetic Long Read Sequencing and Its Applications: from Microbiome to Transcriptome and Beyond
17:45	17:55	Klaus Hentrich (TTP LabTech)	Cost-effective miniaturised NGS library preparation using positive-displacement liquid handling technology
17:55	18:10	Mike Quail	PacBio comes of age
18:10	**19:30**	***Wine, snacks, and posters***	

Wednesday 4th September 2019

Parallel sessions

Time	A	B
09:00 - 10:40	*Plant and Animal Genomics*	*Evolutionary Genomics*
11:15 - 13:15	*Clinical Genomics*	*Microbes I*
14:15 - 16:00	*Developmental Biology*	*Microbes II*
16:20 - 18:00	*Bioinformatics and software*	*Genome Engineering*

Session A

Start	End	Who	Title
09:00	**10:40**	***Plant and animal genomics***	
09:00	09:25	Emily Humble	Scimitar-horned oryx conservation genomics
09:25	09:50	Rachel Gilroy	The broiler chicken intestinal microbiome: interventions to improve health and welfare
09:50	10:05	Jon Rock (Lexogen)	Improving the quality of your RNA Next Generation Sequencing with Lexogen
10:05	10:20	Matthew Parker	Direct RNA Sequencing of the Arabidopsis transcriptome with Nanopores

Start	End	Who	Title
10:20	10:35	Miriam Schreiber	Increasing recombination in the barley (Hordeum vulgare) by manipulating meiotic genes
10:40	11:15	*Coffee*	
11:15	**13:15**	***Clinical Genomics***	
11:15	11:40	Sian Ellard	Application of genomic sequencing technology to the diagnosis of rare diseases: from the 100,000 Genomes Project to a nationally commissioned Genomic Medicine Service
11:40	11:55	Ben Harvey (Agilent)	Agilent's workflow solutions for the clinical genomics laboratory
11:55	12:20	Mike Inouye	The utility of polygenic risk scores for cardiovascular disease
12:20	12:35	Nick Jordan (Fluidigm)	The Juno System: Automated and cost-effective NGS workflows leveraging Fluidigm microfluidic technology
12:35	12:50	Sergey Koren	Telomere-to-telomere assembly of complete human chromosomes
12:50	13:05	Giordano Bottà	Integration of Polygenic Risk Score in CAD risk models for clinical use
13:05	13:15	Alexandra Martin (Stilla)	Crystal digital PCR™ – The next generation
13:15	14:15	*Lunch*	
14:15	**16:00**	***Developmental Biology***	
14:15	14:40	Alistair McGregor	Investigating the developmental consequences of whole genome duplication in arachnids
14:40	15:05	Mansi Srivastava	Acoel genome reveals the regulatory landscape for whole-body regeneration
15:05	15:15	Brennan Martin (Qiagen)	QIAGEN Solutions for Developmental Biology
15:15	15:35	Tamir Chandra	Mouse embryonic stem cells switch from naïve to formative state during transition through G2M
15:35	15:55	Laura Mincarelli	Combined short and long read single-cell sequencing identify aging related transcriptional profile and splicing landscape in hematopoietic stem cells and progenitors

Start	End	Who	Title
15:55	16:20	*Coffee*	
16:20	**18:00**	***Bioinformatics and Software***	
16:20	16:45	Rachel Colquhoun	Nucleotide level analysis of genetic variation in the bacterial pan-genome with Pandora
16:45	17:10	Anton Korobeynikov	Tools for assembly graph analysis and more
17:10	17:35	Apurva Narechania	What do we gain when tolerating loss? The information bottleneck, lossy compression, and detecting horizontal gene transfer
17:35	18:00	Wenbin Guo	3D RNA-seq - a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists

Session B

Start	End	Who	Title
09:00	**10:40**	***Evolutionary genomics***	
09:00	09:25	Reuben Nowell	Genome evolution in the bdelloid rotifers: ancient asexuality and genome structure
09:25	09:50	Alejandro Sanchez-Flores	Omics of the fish-tongue-eating parasitic isopod Cymothoa exigua
09:50	10:15	Max Stammnitz	Tracing the evolution of two transmissible cancers in Tasmanian devils
10:15	10:40	Fiona Jane Whelan	The coincident (co-occurrence and avoidance) relationships of genes in prokaryote genomes
10:40	11:15	*Coffee*	
11:15	**13:15**	***Microbes I***	
11:15	11:45	Anna V. Protasio:	Parasites within parasites: transposable elements in platyhelminthes
11:45	12:15	Julie Segre:	Human skin microbiome: trans-kingdom, host-immune interactions
12:15	12:40	Emma Ainsworth	Long-Read Sequencing Determines Genome Structure in Salmonella Typhi
12:40	13:05	Leigh Monahan	Morphoseq enables closed circle bacterial genome assemblies from short read platforms

Start	End	Who	Title
13:05	13:15	Ralph Vogelsang (PacBio)	PacBio HiFi Long Reads for Metagenomic Discoveries
13:15	14:15	*Lunch*	
14:15	**16:00**	***Microbes II***	
14:15	14:40	David Gally	Prophage-mediated chromosomal rearrangements in Escherichia coli O157
14:40	15:05	Miren Iturriza-Gomara	Rotavirus vaccines and strain diversity
15:05	15:30	Max Stammnitiz	Scrutinising nanopore sequencing for freshwater microbiomes
15:30	15:55	Tania Duarte	Deep Sequencing of Microbial Communities in Cystic Fibrosis Airways
15:55	16:20	*Coffee*	
16:20	**18:00**	***Genome Engineering***	
16:20	16:45	Maria Paz Zafra Martin	Engineering the cancer genome at single base resolution
16:45	17:10	Julian Gruenewald	CRISPR DNA base editors with reduced rna off-target effects
17:10	17:35	Mike McGrew	Genome editing in chickens
17:35	18:00	Spring Tan	Genome Wide CRISPR Knockout Screen Identifies Host Factors Involved in Bovine Herpes Virus Type 1 Infection

Conference Dinner on the evening of Weds 4th - *ticketed*

Thursday 5th September 2019

Start	End	Who	Title
09:00	**11:00**	***Single Cell Genomics***	
09:00	09:25	Iain Macaulay	Isoform Sequencing in Single Cells
09:25	09:40	Stephen Hague (10X Genomics)	From Single Cell Genomics to Multi-Omics
09:40	10:05	Martin Hemberg	Searching large collections of single cell data using scfind

Start	End	Who	Title
10:05	10:20	Daniel Liber (Takara)	What are you missing from your single cell RNA-seq? Go beyond gene expression with the ICELL8 Single-Cell System!
10:20	10:35	Kristina Kirschner	Single cell Sequencing reveals Notch mediated secondary senescence
10:35	10:50	Zhouchun Shang (MGI/BGI)	Dissecting cell heterogeneity using single-cell omics powered by DNBSEQ
10:50	11:05	Daniel Seaton	Mapping the functions of human disease risk alleles during neuronal development using multiplexed differentiation of human induced pluripotent stem cells
11:05	11:30	*Coffee*	
11:30	12:20	**Keynote:** Jane Carlton	Bringing genomics into malaria field studies in India
12:20	13:10	**Keynote:** Kirsten Bos	Genomic reconstructions of ancient pathogens
13:10	**THE END**		***Packed lunch available***