Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details
Wednesday, 21 September 2022		
11:15	**12:30**	**Registration, lunch and networking**
12:10	*12:25*	*Briefing for Keynote & Session 1 speakers, chair, moderator & committee - Auditorium*
12:30	**12:40**	**Welcome** ***Scientific Programme Committee:*** *Joanna Kelley, Washington State University, USA* *Oliver Stegle, German Cancer Research Center & EMBL Heidelberg, Germany* *Páll Melsted, University of Iceland, Iceland* *Nicola Mulder, University of Cape Town, South Africa*
12:40	**13:40**	**Keynote 1** Introduction to the session *Chair: Oliver Stegle, German Cancer Research Center & EMBL Heidelberg, Germany* *Moderator: Joanne Kelley* Going from Maps to Mechanisms, to Medicines in Obesity *Cecilia Lindgren, University of Oxford, UK*
13:40	13:50	Comfort Break
13:50	**17:40**	**Session 1: Genome assembly & Sequence algorithms** Introduction to the session *Chair: Chirag Jain, Indian Institute of Science, India & Camille Marchet, Centre national de la recherche scientifique (CNRS), France* *Moderator: Joanna Kelley*
13:50	14:10	Repeat-aware long read mapping algorithms *Chirag Jain, Indian Institute of Science, India*
14:10	14:30	The Tree of Life Genome Engine – generating high quality reference genome assemblies at scale *Kerstin Howe, Wellcome Sanger Institute, UK*
14:30	14:50	Identifying and correcting repeat-calling errors in nanopore sequencing of telomeres *Kar-Tong Tan, Broad Institute of MIT and Harvard, USA*
14:50	15:10	Scalable sequence database search using Partitioned Aggregated Bloom Comb-Trees *Camille Marchet, Centre national de la recherche scientifique (CNRS), France*
15:10	15:30	steppingStone – A pipeline to identify chromothripsis breakpoints and trace cancer rearrangements using Euler path *Zemin Ning, Wellcome Sanger Institute, UK*
15:30	15:50	Strobealign: ultrafast and accurate short-read alignment *Kristoffer Sahlin, Stockholm University, Sweden*
15:50	**16:20**	**Lightning talks**
16:20	17:40	Poster session I with tea break
17:20	*17:35*	*Briefing for Session 2 speakers, chair & moderator - Auditorium*
17:40	**19:40**	**Session 2: Functional genomics** Introduction to the session *Chair: Heejung Skim, University of Melbourne, Australia & Irene Papatheodorou, European Bioinformatics Institute (EMBL-EBI), UK* *Moderator: Páll Melsted*
17:40	18:00	Alternative splicing analysis using nanopore data *Heejung Shim, University of Melbourne, Australia*
18:00	18:20	DeepRVAT - Joint modeling of rare variant genetic effects using deep learning and data-driven burden scores *Eva Holtkamp, Technical University of Munich, Germany*

18:20	18:40	IRIS: Big data-informed discovery of cancer immunotherapy targets arising from pre-mRNA alternative splicing *Yi Xing, Children's Hospital of Philadelphia, USA*
18:40	19:00	Computational analysis of single cell atlases across species *Irene Papatheodorou, European Bioinformatics Institute (EMBL-EBI), UK*
19:00	19:20	DeepRVAT - Joint modeling of rare variant genetic effects using deep learning and data-driven burden scores *Benoit Ballester, INSERM DR2, France*
19:20	19:40	Longitudinal change in alternative splicing in the MultiMuTHER project *Dongmeng Wang, King's College London, UK*
19:40	21:40	Dinner
		Bar open (card payments only)

Thursday, 22 September 2022

07:30	09:00	Breakfast
09:10	*09:25*	*Briefing for Session 3 speakers, chair & moderator - Auditorium*
09:30	**11:30**	**Session 3: Variant Discovery**
		Introduction to the session *Chair: Bjarni Halldorsson, Reykjavik University, Iceland & Ryan Layer, University of Colorado, USA* *Moderator: Páll Melsted*
09:30	09:50	Whole genome sequencing of the UK biobank *Bjarni Halldorsson, Reykjavik University, Iceland*
09:50	10:10	In depth analysis of the indel mutation and recombination rates of five geographically dispersed Plasmodium falciparum parasites *Marc Antione Guery, Centre national de la recherche scientifique (CNRS), France*
10:10	10:30	Efficient DNA sample contamination metric estimation using a novel variant representation and algorithm *Wenham Lu, Broad Institute of MIT and Harvard, USA*
10:30	10:50	Leveraging Populations to Interpret Structural Variants *Ryan Layer, University of Colorado, USA*
10:50	11:10	Blackbird: detection and assembly of structural variants using linked-read and long-read hybrid datasets *Dmitrii Meleshko, Weill Cornell Medical College, USA*
11:10	11:30	Variant calling in low-copy repeats *Timofey Prodanov, University of California San Diego, USA*
11:30	13:00	Lunch and networking
12:40	*12:55*	*Briefing for Session 4 speakers, chair & moderator - Auditorium*
13:00	**15:00**	**Session 4: Single cell and spatial omics**
		Introduction to the session *Chair: Helder Nakaya, University of Sao Paulo, Brazil & Sarah Teichmann, Wellcome Sanger Institute, UK* *Moderator: Joanna Kelley*
13:00	13:20	Assessing inflammation using spatially-resolved transcriptomics *Helder Nakaya, University of Sao Paulo, Brazil*
13:20	13:40	Robust discovery and quantification of transcript isoforms from error-prone long-read RNA sequencing data *Robert Wang, Children's Hospital of Philadelphia, USA*
13:40	14:00	Phiclust: a clusterability measure for single-cell transcriptomics reveals phenotypic subpopulations *Stefan Semrau, Leiden University, Netherlands*
14:00	14:20	Mapping tissue micro environments one cell at a time *Sarah Teichmann, Wellcome Sanger Institute, UK*
14:20	14:40	Identification of cell barcodes from long-read sc-RNAseq with BLAZE *Yupei You, University of Melbourne, Australia*
14:40	15:00	Artifacts created by batch correction methods of single cell RNA-seq data *Sindri Antonsson, University of Iceland, Iceland*
15:00	**15:30**	**Lightning talks**
15:30	17:00	Poster session II with afternoon tea
16:40	*16:55*	*Briefing for Session 5 speakers, chair & moderator - Auditorium*
17:00	**19:00**	**Session 5: Microbial and metagenomics**
		Introduction to the session *Chair: Daniel Wilson, University of Oxford, UK & Joanna Kelley, Washington State University, USA* *Moderator: Oliver Stegle*
17:00	17:20	Oligopeptide-based bacterial genome-wide association studies *Daniel Wilson, University of Oxford, UK*
17:20	17:40	Investigating Symbiont-Based Immunity in Anopheles Mosquitoes against Plasmodium falciparum Infection *Jacqueline Waweru, ICIPE, Kenya*

17:40	18:00	Emergence and patho-adaptation of epidemic Pseudomonas aeruginosa *Aaron Weimann, University of Cambridge, UK*
18:00	18:20	Untangling the taxonomically complex genus Streptomyces to improve pangenomic analyses *Angelika Kiepas, University of Strathclyde, UK*
18:20	18:40	Verticall: efficient and versatile recombination-free phylogenies *Ryan Wick, Monash University, Australia*
18:40	21:00	Dinner
		Bar open (card payments only)

Friday, 23 September 2022

07:30	09:00	Breakfast
09:10	*09:25*	*Briefing for Keynote & Session 6 speakers, chair & moderator - Auditorium*
09:30	**11:30**	**Session 6: Pan genome**
		Introduction to the session *Chair: Christina Boucher, University of Florida, USA & Nicola Prezza, University of Venice, Italy* *Moderator: Oliver Stegle*
09:30	09:50	Building scalable indexes that can be efficiently queried *Christina Boucher, University of Florida, USA*
09:50	10:10	Towards a Mouse pan-genome: maximising the potential of mouse as an animal model *Mohab Helmy, European Bioinformatics Institute (EMBL-EBI), UK*
10:10	10:30	Graph Gene Caller: a novel approach to bacterial gene calling and gene discovery *Samuel Horsfield, Imperial College London, UK*
10:30	10:50	Aligning sequences on pan-genome graphs: lower bounds, algorithms, and data structures *Nicola Prezza, University of Venice, Italy*
10:50	11:10	Enabling variant annotation and displays across multiple human assemblies in Ensembl *Likhitha Surapaneni, European Bioinformatics Institute (EMBL-EBI), UK*
11:10	11:30	Assembling hundreds of diverse eukaryotic genomes from across the tree of life *Shane McCarthy, Wellcome Sanger Institute, UK*
11:30	11:45	Comfort break
11:45	**12:45**	**Keynote 2**
		Introduction to the session *Chair: Joanna Kelley, Washington State University, USA* *Moderator: Páll Melsted* Metagenomic analysis of the microbes on our planet *Peer Bork, EMBL Heidelberg, Germany*
12:45	**13:00**	**Closing remarks and prize presentation**
		Scientific Programme Committee: *Joanna Kelley, Washington State University, USA* *Oliver Stegle, German Cancer Research Center & EMBL Heidelberg, Germany* *Páll Melsted, University of Iceland, Iceland* *Nicky Mulder, University of Cape Town, South Africa*
13:00	14:00	Lunch & departures
13:50		Coach departures for Stansted and Heathrow airports
14:00		Coach departures for Cambridge train station