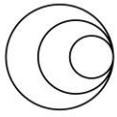


Hybrid Conference Programme

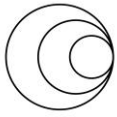
Start (BST)	Finish (BST)	Presenter details
Wednesday, 21 September 2022		
11:30	12:30	Registration, lunch and networking
12:10	12:25	Briefing for Keynote & Session 1 speakers, chair, moderator & committee - Auditorium
12:30	12:40	Welcome Scientific Programme Committee: Joanna Kelley, Washington State 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 Chair: Oliver Stegle, German Cancer Research Center & EMBL Heidelberg, Germany Moderator: Joanna 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 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 refreshments
17:20	17:35	Briefing for Session 2 speakers, chair & moderator - Auditorium



17:40	19:40	Session 2: Functional genomics
		<i>Chair: Heejung Shim, University of Melbourne, Australia & Irene Papatheodorou, European Bioinformatics Institute (EMBL-EBI), UK</i> <i>Moderator: Páll Melsted</i>
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 <i>Brian Clarke, German Cancer Research Center (DKFZ), Germany</i>
18:20	18:40	IRIS: Big data-informed discovery of cancer immunotherapy targets arising from pre-mRNA alternative splicing <i>Yi Xing, Children's Hospital of Philadelphia, USA</i>
18:40	19:00	Computational analysis of single cell atlases across species Irene Papatheodorou, European Bioinformatics Institute (EMBL-EBI), UK
19:00	19:20	Atlas of transcribed non-coding regions from RNA Pol II integration <i>Benoit Ballester, INSERM DR2, France</i>
19:20	19:40	Longitudinal change in alternative splicing in the MultiMuTHER project <i>Dongmeng Wang, King's College London, UK</i>
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
		<i>Chair: Bjarni Halldorsson, Reykjavik University, Iceland & Ryan Layer, University of Colorado, USA</i> <i>Moderator: Páll Melsted</i>
09:30	09:50	The sequences of 150,119 genomes in 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 <i>Marc Antoine Guery, Centre national de la recherche scientifique (CNRS), France</i>
10:10	10:30	Efficient DNA sample contamination metric estimation using a novel variant representation and algorithm <i>Wenhan Lu, Broad Institute of MIT and Harvard, USA</i>
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 <i>Dmitrii Meleshko, Weill Cornell Medical College, USA</i>
11:10	11:30	Variant calling in low-copy repeats <i>Timofey Prodanov, University of California San Diego, USA</i>
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
		<i>Chair: Helder Nakaya, University of Sao Paulo, Brazil & Sarah Teichmann, Wellcome Sanger Institute, UK</i> <i>Moderator: Oliver Stegle</i>
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 <i>Robert Wang, Children's Hospital of Philadelphia, USA</i>
13:40	14:00	Phiclust: a clusterability measure for single-cell transcriptomics reveals phenotypic subpopulations <i>Stefan Semrau, Leiden University, Netherlands</i>
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 <i>Yupei You, University of Melbourne, Australia</i>
14:40	15:00	Artifacts created by batch correction methods of single cell RNA-seq data <i>Sindri Antonsson, University of Iceland, Iceland</i>
15:00	15:30	Lightning talks
15:30	17:00	Poster session II with refreshments
16:40	16:55	Briefing for Session 5 speakers, chair & moderator - Auditorium



17:00 19:00 Session 5: Microbial and metagenomics

Chair: Daniel Wilson, University of Oxford, UK & Joanna Kelley, Washington State University, USA
Moderator: Oliver Stegle

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| 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
<i>Jacqueline Waweru, ICIPE, Kenya</i> |
| 17:40 | 18:00 | Emergence and patho-adaptation of epidemic Pseudomonas aeruginosa
<i>Aaron Weimann, University of Cambridge, UK</i> |
| 18:00 | 18:20 | Untangling the taxonomically complex genus Streptomyces to improve pangenomic analyses
<i>Angelika Kiepas, University of Strathclyde, UK</i> |
| 18:20 | 18:40 | Vertical: efficient and versatile recombination-free phylogenies
<i>Ryan Wick, Monash University, Australia</i> |

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 <i>Chair: Christina Boucher, University of Florida, USA & Nicola Prezza, University of Venice, Italy</i> <i>Moderator: Oliver Stegle</i>
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 <i>Mohab Helmy, European Bioinformatics Institute (EMBL-EBI), UK</i>
10:10	10:30	Graph Gene Caller: a novel approach to bacterial gene calling and gene discovery <i>Samuel Horsfield, Imperial College London, UK</i>
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 <i>Likhitha Surapaneni, European Bioinformatics Institute (EMBL-EBI), UK</i>
11:10	11:30	Assembling hundreds of diverse eukaryotic genomes from across the tree of life <i>Shane McCarthy, Wellcome Sanger Institute, UK</i>
11:30	12:00	Refreshments
12:00	13:00	Keynote 2 <i>Chair: Joanna Kelley, Washington State University, USA</i> <i>Moderator: Páll Melsted</i> Metagenomic analysis of the microbes on our planet Peer Bork, EMBL Heidelberg, Germany
13:00	13:10	Closing remarks and prize presentation Scientific Programme Committee: <i>Joanna Kelley, Washington State University, USA</i> <i>Oliver Stegle, German Cancer Research Center & EMBL Heidelberg, Germany</i> <i>Páll Melsted, University of Iceland, Iceland</i> <i>Nicky Mulder, University of Cape Town, South Africa</i>
13:10	14:00	Lunch & departures
13:50		Coach departures for Stansted and Heathrow airports
14:00		Coach departures for Cambridge city centre and train station