Hybrid Conference Programme

Start (GMT)	Finish (GMT)	Presenter details
Wednesday 13 November 2024		
12:00	**13:00**	**Registration, lunch and networking**
12:45	*13:00*	*Briefing for Keynote & Session 1 speakers, microphone runners, chair, moderator & committee - Auditorium*
13:00	**13:10**	**Welcome** ***Wellcome Connecting Science:*** *Jane Murphy, Wellcome Connecting Science, UK* ***Scientific Programme Committee:*** *Zamin Iqbal, University of Bath, UK* *Páll Melsted, University of Iceland, Iceland* *Nicola Mulder, University of Cape Town, South Africa*
13:10	**13:55**	**Keynote**
		The de Bruijn graph, a computational structure useful beyond assembly *Camille Marchet, Lille Computer Science, Signal and Automation Research Center (CRIStAL - CNRS), France*
13:55	14:00	Comfort break
14:00	**15:30**	**Session 1: PanGenome** *Session chairs: Jana Ebler and Pierre Peterlongo*
14:00	14:15	Pangenome-based genome inference *Jana Ebler, Heinrich-Heine University Düsseldorf, Germany*
14:15	14:30	Producing reference gene annotation for the human pangenome *Jonathan Mudge, EMBL-EBI, UK*
14:30	14:45	Detecting recurrent inversion polymorphisms in human pangenomes *Hufsah Ashraf, Heinrich Heine University Düsseldorf Germany*
14:45	15:00	Molecular clocks in the accessory genome?: Investigating rates of gene gain, loss, and selection *Caitlin Collins, University Of Cambridge, UK*
15:00	15:15	Genotyping and structural variant characterization in 1,019 samples from the 1000 Genomes Project *Samarendra Pani, Heinrich Heine University, Germany*
15:15	15:30	Index the planet: index SRA unitigs with kmindex. Results, joys and sorrows *Pierre Peterlongo, Inria, France*
15:30	16:15	Refreshment break and networking
16:00	*16:15*	*Briefing for Session 2 speakers, microphone runners, chair & moderator - Auditorium*
16:15	**17:45**	**Session 2: Genome Assembly and Sequencing Algorithms** *Session chairs: Can Alkan and Jasmijn Baaijens*
16:15	16:30	Acceleration of read mapping through hardware/algorithm co-design *Can Alkan, Bilkent University, Turkey*
16:30	16:45	A new sketching method for metagenome assembly from accurate long reads *Roland Faure, Université De Rennes, France*
16:45	17:00	Reconstructing extrachromosomal DNA structural heterogeneity from long-read sequencing data using Decoil *Madalina Giurgiu, Charite Universitaetsmedizin Berlin, Germany*
17:00	17:15	MUSET: Set of utilities for the construction of abundance unitig matrices from sequencing data *Camila Duitama, Institut Pasteur, France*
17:15	17:30	Dynamic Adaptive Sampling for Human Trio Sequencing *Isabel Marleen Poetzsch, EMBL-EBI, UK*
17:30	17:45	Local viral haplotype reconstruction from long reads *Jasmijn Baaijens, TU Delft, Netherlands*
17:45	**18:15**	**Poster pitch talks for odd number posters**
18:15	**19:15**	**Poster session 1 - odd number posters**
19:15	21:00	Dinner
19:15		Bar open (card payments only)

Thursday 14 November 2024

09:15	*09:30*	*Briefing for Session 3 speakers, microphone runners, chair & moderator - Auditorium*
09:30	**11:00**	**Session 3: Variant Discovery**
		Session chairs: Birte Kehr and Ananyo Choudhury
09:30	09:45	Structural variant detection in many genomes: From human populations to cell populations *Birte Kehr, Leibniz Institute for Immunotherapy, Germany*
09:45	10:00	Platform-independent, uncertainty-aware joint variant and methylation calling *Adrian Prinz, Ikim – Institut Für Künstliche Intelligenz In Der Medizin, Germany*
10:00	10:15	Genomic LLMs uncover constrained regions in the genome *Alexandrina Pancheva, CRUK Scotland Institute, UK*
10:15	10:30	Exploiting pleiotropy to enhance variant discovery in genome-wide association studies with functional false discovery rates *Andrew Bass, University of Cambridge, UK*
10:30	10:45	Manual and automatic image-derived phenotypes to discover genetic variants associated with skeletal development in medaka (Oryzias latipes) *Esther Yoo, EMBL-EBI, UK*
10:45	11:00	Impact of history and ancestry on variant discovery: the African paradigm *Ananyo Choudhury, University of the Witwatersrand, South Africa*
11:00	11:45	Refreshment break and networking
11:30	*11:45*	*Briefing for Session 4 speakers, microphone runners, chair & moderator - Auditorium*
11:45	**13:00**	**Session 4: Single Cell and Spatial Omics**
		Session chairs:Wolfgang Huber and Maria Brbic, EPFL, Switzerland
11:45	12:00	Analysing multi-condition single-cell data without discrete cell type categorisation *Wolfgang Huber, EMBL, Germany*
12:00	12:15	Milo2.0 unlocks cohort-level genetic analyses of cell state abundance using a counts-based mixed model *Mike Morgan, University Of Aberdeen, UK*
12:15	12:30	Haplotype-resolved full-length transcriptome analysis in single cells *Yi Xing, Children's Hospital of Philadelphia, USA*
12:30	12:45	Universal preprocessing of genomics reads with seqspec *Ali Sina Booeshaghi, UC Berkeley, USA*
12:45	13:00	Towards AI-driven discoveries in Spatial Biology *Maria Brbic, EPFL, Switzerland*
13:00	14:30	Lunch and networking
14:15	*14:30*	*Briefing for Session 5 speakers, microphone runners, chair & moderator - Auditorium*
14:30	**16:00**	**Session 5: Microbial and Metagenomics**
		Session chairs: Gang Fang and Gaëtan Benoit
14:30	14:45	Illuminating the bacterial epigenome in human pathogens and microbiome *Gang Fang, Icahn School of Medicine at Mount Sinai, USA*
14:45	15:00	Machine learning prediction of antimicrobial resistance in Escherichia coli *Roxana Zamudio Zea, UK Health Security Agency, UK*
15:00	15:15	Applying rearrangement distances to enable plasmid epidemiology with pling *Daria Frolova, EMBL-EBI, UK*
15:15	15:30	Assessing assembly quality in metagenomes of increasing complexity sequenced with HiFi long reads *Nicolas Maurice, Inria de Rennes, France*
15:30	15:45	Using Amira to detect multi-copy antimicrobial resistance genes in long-read sequencing data *Daniel Anderson, EMBL-EBI, UK*
15:45	16:00	Fast correction and assembly of long metagenomics reads in minimizer-space *Gaëtan Benoit, Pasteur Institute, France*
16:00	**16:30**	**Poster pitch talks for even number posters**
16:30	17:15	Refreshment break and networking
17:15	**18:15**	**Poster session 2 - even number posters**
18:15	20:30	Dinner
18:15		Bar open (card payments only)

Friday 15 November 2024

09:15	*09:30*	*Briefing for Session 6 speakers, microphone runners, chair & moderator - Auditorium*
09:30	**11:00**	**Session 6: Functional Genomics**
		Session chairs: Valentina Boeva and Lude Franke
09:30	09:45	Predicting chromatin interactions in unseen and rare cell types *Valentina Boeva, ETH Zurich, Switzerland*
09:45	10:00	One third of the human genes contain translated small open reading frames in the 3' untranslated region *Victor Daniel Aldas Bulos, Stowers Institute For Medical Research, USA*
10:00	10:15	Recalibrating differential gene expression by genetic dosage variance prioritizes functionally relevant genes *Philipp Rentzsch, KTH-Scilifelab, Stockholm, Sweden*
10:15	10:30	BigBrain: Decoding the trans-regulatory architecture of expression and splicing using >13k postmortem human brain transcriptomes *Kailash Babu Panneerselvam, Icahn School of Medicine at Mount Sinai, USA*
10:30	10:45	Computational Prediction of interactions between TE-derived enhancers and genes *Yizhi Yan, Mcgill University, Canada*
10:45	11:00	Linking common and rare diseases using gene regulatory networks *Lude Franke, University Medical Centre Groningen, Netherlands*
11:00	11:45	Refreshment break and networking
11:30	*11:45*	*Briefing for Keynote, microphone runners, chair, moderator & committee - Auditorium*
11:45	**12:30**	**Keynote**
		Generative AI for modeling single-cell state and response *Fabian Theis, Technical University of Munich, Germany*
12:30	**12:45**	**Closing remarks and prize presentation**
		Scientific Programme Committee: *Zamin Iqbal, University of Bath, UK* *Páll Melsted, University of Iceland, Iceland* *Nicola Mulder, University of Cape Town, South Africa*
12:45	13:45	Lunch and departures
13:45		Coach departures for Stansted and Heathrow airports
13:55		Coach departures for Cambridge train station and city centre