Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details
Wednesday 2 December 2026		
12:00	**13:00**	**Registration, lunch and networking**
12:45		*Briefing for keynote speaker, Session 1 speakers, microphone runners, chair, moderator and committee*
13:00	**13:10**	**Welcome and introductions**
		Wellcome Connecting Science: *Andy Mains, Wellcome Sanger Instiute, Scientific Training and Events* **Scientific programme committee:** *Zamin Iqbal, University of Bath, UK* *Ben Langmead, Johns Hopkins University, USA* *Camille Marchet, Universite de Lille, France*
13:10	**13:55**	**Opening keynote**
		Chair: TBC *Moderator: TBC*
13:10	13:55	Algorithms for Variant Representation and Genotyping with Pangenome References *Chirag Jain, Indian Institute of Science, India*
13:55	14:00	Comfort break
14:00	**15:30**	**Session 1: Pangenomes**
		Chair: TBC *Moderator: TBC*
14:00	14:15	Decomposing pangenome graphs via bubbles, 2-separators and SPQR trees *Alexandru I. Tomescu, University of Helsinki, Finland*
14:15	14:30	Scalable and rare-variant aware genome inference *Jana Ebler, Heinrich Heine University Düsseldorf, Germany*
14:30	14:45	LCPan: efficient variation graph construction using locally consistent parsing *Akmuhammet Ashyralyyev, Bilkent University, Turkey*
14:45	15:00	Ask the archive: MetaGraph search for researchers and their AI agents *Andre Kahles, Eth Zurich, Switzerland*
15:00	15:15	Pangenome Assemblies and Annotations Are Not Static and Need Support for Tracking Their Evolution *Amanda Clare, Aberystwyth University, UK*
15:15	15:30	Chromosome-Specific Telomere Length Profiling from Nanopore Telo-seq Reads Using Pangenome-Based Alignment *Lucas Ligtvoet, St Antonius Hospital, Netherlands*
15:30	16:15	Refreshment break and networking
16:00	*16:15*	*Briefing for Session 2 speakers, chair and moderator*
16:15	**17:45**	**Session 2: Genome assembly and sequencing algorithms**
		Chair: TBC *Moderator: TBC*
16:15	16:30	Correctness Guarantees for Sequence Assembly *Leena Salmela, University of Helsinki, Finland*
16:30	16:45	Genomic read alignment with minibwa *Heng Li, Harvard University, USA*
16:45	17:00	Reference-free scaffolding of bacterial genomes using TruPath™ Genome proximity and assembly-graph topology *Ritu Kundu, Illumina, UK*
17:00	17:15	Pandedup: building and applying k-mer spectra of HPRCv2 *Ragnar Groot Koerkamp, Karlsruhe Institute Of Technology, Germany*
17:15	17:30	sufr: fast, low-memory, repeat-robust construction of suffix arrays, with support for spaced seeds *Travis Wheeler, University of Arizona, USA*
17:30	17:45	Masked superstrings: a universal representation of k-mer sets beyond de Bruijn graphs *Karel Brinda, Inria, France*
17:45	**18:15**	**Poster pitch talks for odd number posters**
18:15	**19:30**	**Poster session 1 (odd number posters) and networking reception**
19:30	21:30	Dinner
19:30		Bar open (card payments only)

Thursday 3 December 2026		
09:15		*Briefing for Session 3 speakers, chair and moderator*
09:30	**11:00**	**Session 3: Algorithmic evolutionary biology**
		Chair: TBC *Moderator: TBC*
09:30	09:45	A scalable framework for ancestral genome reconstruction: gene content, order, and function *Christophe Dessimoz, University of Lausanne/SIB Swiss Institute of Bioinformatics, Switzerland*
09:45	10:00	Phasing genome assemblies of non-model animal species in the era of high-accuracy long reads *Nadège Guiglielmoni, Université Libre de Bruxelles, Belgium*
10:00	10:15	glmANI: Benchmarking Genomic Language Models for Evolutionary Distance Estimation *Sina Majidian, Chalmers University of Technology, Sweden*
10:15	10:30	Integrating protein structure and population genomic data to detect diversifying selection in large-scale bacterial datasets and pangenomes *Leonie Lorenz, EMBL-EBI, UK*
10:30	10:45	Unconstrained identification of candidate genome-modifying loci *Kristen Curry, Institut Pasteur, France*
10:45	11:00	Shared Heritability–Selection Patterns across Distinct Genetic Architectures *Stepan Grinek, The Jackson Laboratory, USA*
11:00	11:45	Refreshment break and networking
11:15		*Briefing for Session 4 speakers, chair and moderator*
11:45	**13:00**	**Session 4: Transcriptomics**
		Chair: TBC *Moderator: TBC*
11:45	12:00	Title TBC *Nikolaus Rajewsky, Max Delbruck Center for Molecular Medicine, Germany*
12:00	12:15	The SQANTIverse to unravel de complexity of the full-length transcriptome *Ana Conesa, Spanish National Research Council, Spain*
12:15	12:30	Common variants influence gene expression in human bone marrow *Thomas Guinan, Menzies Institute For Medical Research, Australia*
12:30	12:45	PanXpress: resolving reference bias in bacterial RNA-seq with a pan-transcriptomic k-mer index *Inês Alves Ferreira, Saarland University, Germany*
12:45	13:00	Discovery and visualisation of rare splice junctions at scale with LemonSplice *Andrew Lonsdale, Peter MacCallum Cancer Centre, Australia*
13:00	13:15	Metappuccino: scalable reconstruction of metadata for systematic exploration of public RNA-seq data *Fiona Hak, Institute Of Integrative Biology Of The Cell (i2bc), France*
13:15	14:30	Lunch and networking
14:15		*Briefing for Session 5 speakers, chair and moderator*
14:30	**16:00**	**Session 5: Microbial genomics**
		Chair: TBC *Moderator: TBC*
14:30	14:45	The Mobility Of The Unknown Mobile Genetic Elements *Eduardo Rocha, Institut Pasteur, France*
14:45	15:00	Advances in Microbial Genome Reconstruction and Analysis Using Graph-Based Approaches *Vijini Mallawaarachchi, Flinders University, Australia*
15:00	15:15	Logan-protein-search: deep homology search across 141 billion proteins *Roland Faure, Institut Pasteur, France*
15:15	15:30	Themisto 2: Composable Indexed Sequence Search at Scale *Lore Depuydt, Université De Lille, Finland*
15:30	15:45	The EDEN family of foundation models: from environmental metagenomes to programmable therapeutics *Daniel Anderson, Basecamp Research, UK*
15:45	16:00	Cleanifier: contamination removal from microbial sequences using spaced seeds of a human pangenome index *Jens Zentgraf, Saarland University, Germany*
16:00	16:45	Refreshment break and networking
16:45	**17:15**	**Poster pitch talks for odd number posters**
17:15	**18:30**	**Poster session 1 (odd number posters) and networking reception**
18:30	20:30	Dinner
18:30		Bar open (card payments only)

Friday 4 December 2026		
09:15		*Briefing for Session 6 speakers, chair and moderator*
09:30	**11:00**	**Session 6: Cancer and other diseases**
		Chair: TBC *Moderator: TBC*
09:30	09:45	Pangenomes for Disease Genomics *Jean Monlong, INSERM IRSD, France*
09:45	10:00	Recovering Clone-Resolved Programs from Routine Bulk Tumor Sequencing *Rachel Karchin, Johns Hopkins University, USA*
10:00	10:15	Roll over, beta value: there's a new alpha in town for DNA methylation analysis *Alicia Oshlack, Peter Maccallum Cancer Centre, Australia*
10:15	10:30	Coupled copy number and fragmentomic signatures in plasma cfDNA distinguish karyotype complexity across sarcoma subtypesw *Myesha Jahin, University Of Heidelberg/DKFZ (German Cancer Research Center), Germany*
10:30	10:45	Phenotype-definition contamination is detectable from summary statistics alone: a genome-wide screen validated against multivariable Mendelian randomisation *Vishnupriya Kannan, Nanyang Technological University, Singapore*
10:45	11:00	Bulk to single cell mapping resolves the multicellular architecture of pancreatic cancer programs *Akhil Dinesan, Shiv Nadar Institute of Eminence, India*
11:00	11:45	Refreshment break and networking
11:30		*Briefing for keynote, chair, moderator and committee*
11:45	**12:30**	**Closing keynote**
		Chair: TBC *Moderator: TBC* New statistical methods for metagenomic analysis *Tandy Warnow, University of Illinois Urbana-Champaign, USA*
12:30	**12:45**	**Closing remarks** **Scientific Programme Committee:** *Zamin Iqbal, University of Bath, UK* *Ben Langmead, Johns Hopkins University, USA* *Camille Marchet, Universite de Lille, France*
12:45	13:50	Lunch
13:50		Coach departures for Stansted and Heathrow airports
14:00		Coach departures for Cambridge train station and city centre