

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: <i>Andy Mains, Wellcome Sanger Institute, Scientific Training and Events</i> Scientific programme committee: Zamin Iqbal, University of Bath, UK Ben Langmead, Johns Hopkins University, USA Camille Marchet, Université de Lille, France
13:10	13:55	Opening keynote
		<i>Chair: TBC</i> <i>Moderator: TBC</i> 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
		<i>Chair: TBC</i> <i>Moderator: TBC</i> 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 Short talk selected from abstracts <i>Short talk speaker</i> 14:45 15:00 Short talk selected from abstracts <i>Short talk speaker</i> 15:00 15:15 Short talk selected from abstracts <i>Short talk speaker</i> 15:15 15:30 Short talk selected from abstracts <i>Short talk speaker</i>
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
		<i>Chair: TBC</i> <i>Moderator: TBC</i> 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 Short talk selected from abstracts <i>Short talk speaker</i> 17:00 17:15 Short talk selected from abstracts <i>Short talk speaker</i> 17:15 17:30 Short talk selected from abstracts <i>Short talk speaker</i> 17:30 17:45 Short talk selected from abstracts

Short talk speaker

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	Short talk selected from abstracts Short talk speaker
10:15	10:30	Short talk selected from abstracts Short talk speaker
10:30	10:45	Short talk selected from abstracts Short talk speaker
10:45	11:00	Short talk selected from abstracts Short talk speaker
11:00	11:45	Refreshment break and networking
11:15		Briefing for Session 4 speakers, chair and moderator
11:45	13:00	Session 4: Single-cell and spatial omics
		Chair: TBC
		Moderator: TBC
11:45	12:00	Title TBC Nikolaus Rajewsky, Max Delbrück Center for Molecular Medicine, Germany
12:00	12:15	The SQANTiverse to unravel the complexity of the full-length transcriptome Ana Conesa, Spanish National Research Council, Spain
12:15	12:30	Short talk selected from abstracts Short talk speaker
12:30	12:45	Short talk selected from abstracts Short talk speaker
12:45	13:00	Short talk selected from abstracts Short talk speaker
13:00	13:15	Short talk selected from abstracts Short talk speaker
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	Short talk selected from abstracts Short talk speaker
15:15	15:30	Short talk selected from abstracts Short talk speaker
15:30	15:45	Short talk selected from abstracts Short talk speaker
15:45	16:00	Short talk selected from abstracts Short talk speaker

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	Short talk selected from abstracts Short talk speaker
10:15	10:30	Short talk selected from abstracts Short talk speaker
10:30	10:45	Short talk selected from abstracts Short talk speaker
10:45	11:00	Short talk selected from abstracts Short talk speaker
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