

Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details
Monday 13 April 2026		
08:30	09:20	Registration, refreshments and networking
09:05	09:20	Briefing for Session 1 speakers, microphone runners, chair, moderator & committee - Auditorium
09:20	09:30	Welcome and introductions
		Wellcome Connecting Science: Michelle Bishop, Wellcome Connecting Science, UK Scientific programme committee: Craig Anderson, DKTK/DKFZ, Germany Tim Coorens, EBI, UK Raheleh Rahbari, Wellcome Sanger Institute, UK Martin Taylor, University of Edinburgh, UK Michelle Trenkmann, Nature, Germany
09:30	12:45	Session 1: Somatic evolution and lineages in development and aging
		Chair: Martin Taylor, University of Edinburgh, UK Moderator: TBC
09:30	10:00	The Evolutionary Road to AML Caroline Watson, Early Cancer Institute, UK
10:00	10:15	Population-scale single-cell multiomics reveals cell type-specific genetic regulation and selection in clonal haematopoiesis Zhen Qiao, Garvan Institute of Medical Research, Australia
10:15	10:30	Epigenetic drift reveals stem cell dynamics, lifespan evolution, and clonal expansion Tamir Chandra, Mayo Clinic, USA
10:30	11:00	Clonal structure of nephron Seishi Ogawa, Kyoto University, Japan
11:00	11:30	Refreshment break and networking
11:30	12:00	Title TBC Jyoti Nangalia, Wellcome Sanger Institute, UK
12:00	12:15	Mosaicism with somatic tissue development and with heterozygosity in meiosis assessed using long-read, whole-genome sequencing Joseph Butler, University of Western Ontario, Canada
12:15	12:30	The repertoire of indel mutational signatures in 6,975 tumors based on three indel classification schemes Steve Rozen, Duke University, USA
12:30	12:45	Diversity in somatic mutation processes in human cerebellar neurons Marta Gronska-Peski, New York University School Of Medicine, USA
12:45	13:00	Poster pitches - Odd numbers
13:00	14:30	Poster session with lunch
14:15	14:30	Briefing for session 2 speakers, chair & moderator - Auditorium
14:30	17:45	Session 2: Mutations in the germline and across populations
		Chair: Raheleh Rahbari, Wellcome Sanger Institute, UK Moderator: TBC
14:30	15:00	Generation of sequence diversity: from one zygote to another Hákon Jónsson, deCODE Genetics, Iceland
15:00	15:15	Sperm sequencing maps positive selection in the human germline at population scale Matthew Neville, Wellcome Sanger Institute, UK
15:15	15:30	Leveraging relatedness in genomic datasets to study variation in germline mutation rates Molly Przeworski, Columbia University, USA
15:30	16:00	Transgenerational inheritance of paternal DNA damage Siyao Wang, Institute of Molecular Biology, Germany

16:00	16:30	Refreshment break and networking
16:30	17:00	Using near-complete human genomes to understand mutational processes. Evan Eichler, University of Washington, USA
17:00	17:15	Heritability of germline mutagenesis in 40 large three- and four-generation pedigrees <i>Alexis Garretson, University of Utah, USA</i>
17:15	17:30	The mutational processes in primate spermatogenesis inferred from HIFI long read sequencing <i>Mikkel Heide Schierup, Aarhus University, Denmark</i>
17:30	17:45	Systemic mutagen exposures reported by normal kidney cell genomes <i>Yichen Wang, Wellcome Sanger Institute, UK</i>
17:45	18:00	Poster pitches - Even numbers
18:00	19:30	Poster session with refreshments
19:30	21:00	Dinner
19:30		Bar open (card payments only)

Tuesday 14 April 2026

09:15	09:30	Briefing for Session 3 speakers, chair & moderator - Auditorium
09:30	12:45	Session 3: Mutations across the Tree of Life <i>Chair: Michelle Trenkmann, Nature, Germany</i> <i>Moderator: Grey Monroe, University of California Davis, USA</i>
09:30	10:00	Transposable element mutation across the Tree of Life Richard Durbin, University of Cambridge, UK
10:00	10:15	Plant somatic disease caused by genome instability <i>Matthew Davis, UC Davis, USA</i>
10:15	10:30	Somatic mutation sequencing reveals environmental and genetic modulation of Arabidopsis mutation rates <i>Chandler Sutherland, University of California, Berkeley, USA</i>
10:30	11:00	Consequences of intragenomic conflict: meiotic drive and satellite DNA in Drosophila Amanda Larracuenta, University of Rochester, USA
11:00	11:30	Refreshment break and networking
11:30	12:00	Transmissible cancer Elizabeth Murchison, University of Cambridge, UK
12:00	12:15	DNA methylation erodes CTCF motifs in mammalian genome evolution <i>Duncan Odum, DKFZ, Germany</i>
12:15	12:30	Evolution of Mutational Susceptibility to Disease <i>Maria Kelly, Centre For Genomic Regulation, Spain</i>
12:30	12:45	Computational inference of somatic variant allele-frequency spectra in plants <i>Frank Johannes, Technical University Of Munich, Germany</i>
12:45	14:15	Lunch and networking
12:55	13:25	Wetlands Tour - Group 1, Campus Tour - Group 1 (sign up via the app)
13:35	14:05	Wetlands Tour - Group 2, Campus Tour - Group 2 (sign up via the app)
14:00	14:15	Briefing for session 4 speakers, chair & moderator - Auditorium
14:15	17:30	Session 4: Somatic mutations and disease <i>Chair: Tim Coorens, EBI, UK</i> <i>Moderator: TBC</i>
14:15	14:45	Somatic Mosaicism in Human Brain Christopher Walsh, Harvard University, USA
14:45	15:00	Somatic Driver Mutations in Rheumatoid Arthritis and Osteoarthritis <i>Luke Harvey, Wellcome Sanger Institute, UK</i>
15:00	15:15	Inference of Subclonal Heterogeneity and Phenotypic Trajectories Associated with Therapeutic Resistance in Breast Cancers from Full-Length Single-Cell Transcriptomes <i>Ghamdan Al-Eryani, The Broad Institute of MIT and Harvard, USA</i>
15:15	15:45	Investigating acral melanoma in Mexico Daniela Robles-Espinoza, Universidad Nacional Autónoma de México, Mexico
15:45	16:15	Refreshment break and networking
16:15	16:45	Title TBC Nicole Lake, Yale, USA
16:45	17:00	Widespread TP53 second hits in normal tissues in Li-Fraumeni syndrome <i>Joseph Christopher, Wellcome Sanger Institute, UK</i>
17:00	17:15	Somatic mutation landscapes in healthy tissues of individuals with inherited BRCA-mediated DNA repair deficiency <i>Stephanie Gardiner, University of Utah, USA</i>
17:15	17:30	Genome-wide detection and characterization of de novo loss of heterozygosity events using single-cell haplotype-resolved sequencing <i>Dmitrii Olssov, European Molecular Biology Laboratory, Germany</i>
17:30	18:15	Free time
18:15		Coaches leave Hinxton Hall for offsite dinner - King's College
18:50		Dinner - King's College
22:30		Coaches depart - King's College for Hinxton Hall

Wednesday 15 April 2026

09:15	09:30	Briefing for Session 5 speakers, chair & moderator - Auditorium
09:30	11:00	Session 5: Synthetic genomics/New technologies to study mutations <i>Chair: Craig Anderson, DTKK/DFZ, Germany</i> <i>Moderator: TBC</i>
09:30	10:00	Modeling the evolution of gene regulatory complexity and its role in complex disease Carl DeBoer, The University of British Columbia, Canada
10:00	10:15	Topographical archetypes of somatic mutagenesis in cancer <i>Peter Park, Harvard Medical School, USA</i>
10:15	10:30	Slide-tags DNA: Spatially mapped whole genome and transcriptome profiling of single nuclei in human tissues <i>Claudia Chu, Broad Institute, USA</i>
10:30	11:00	Mutate Everything! Mapping the energetic and allosteric structures of proteins at scale Ben Lehner, Wellcome Sanger Institute, UK
11:00	11:30	Refreshment break and networking
11:30	12:00	Massively-parallel approaches to understand the human noncoding genome and transcriptome Neville Sanjana, New York Genome Center, USA
12:00	12:15	Experimental evolution of oncogene amplifications following DNA double-strand breaks <i>Marc Williams, MSKCC, USA</i>
12:15	12:30	A framework for indel classification reveals alternate mutagenic paths to UV damage tolerance <i>Jan Verburg, MRC Laboratory Of Molecular Biology, UK</i>
12:30	12:45	Experimental Modeling Somatic Clonal Expansion During Embryonic Brain Development <i>Pei-chi Wei, German Cancer Research Center, Germany</i>
12:45	13:00	Closing remarks and prizes Scientific Programme Committee: <i>Craig Anderson, DTKK/DFZ, Germany</i> <i>Tim Coorens, EBI, UK</i> <i>Raheleh Rahbari, Wellcome Sanger Institute, UK</i> <i>Martin Taylor, University of Edinburgh, UK</i> <i>Michelle Trenkmann, Nature, Germany</i>
13:00	13:50	Lunch and departures
13:50		Coach departures for Stansted and Heathrow airports
14:00		Coach departures for Cambridge train station and city centre