Mutations in Time and Space 2026 Conference

13-15 April 2026

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 landscape of human nephrons *Seishi Ogawa, Kyoto University, Japan*
11:00	11:30	Refreshment break and networking
11:15	*11:30*	*Briefing for Session 1 speakers - Auditorium*
11:30	12:00	Somatic methylation changes in blood over the human lifespan *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, Welcome 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 by histone H1-mediated DNA repair restriction *Siyao Wang, Institute of Molecular Biology, Germany*
16:00	16:30	Refreshment break and networking
16:15	*16:30*	*Briefing for session 2 speakers - Auditorium*
16:30	17:00	Using near-complete human genomes to understand mutational processes. *Evan Eichler, Universityv of Washington, USA*
17:00	17:15	Heritability of germline mutagenesis in 40 large three- and four-generation pedigrees *Alexis Garretson, University of Utah, USA*
17:15	17:30	The mutational processes in primate spermatogenesis inferred from HiFi long read sequencing *Mikkel Heide Schierup, Aarhus University, Denmark*
17:30	17:45	Systemic mutagen exposures reported by normal kidney cell genomes *Yichen Wang, Wellcome Sanger Institute, UK*
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

08:45	*09:00*	*Briefing for Session 3 speakers, chair & moderator - Auditorium*
09:00	**12:15**	**Session 3: Mutations across the Tree of Life** *Chair: Michelle Trenkmann, Nature, Germany* *Moderator: Grey Monroe, University of California Davis, USA*
09:00	09:30	Consequences of intragenomic conflict: meiotic drive and satellite DNA in Drosophila *Amanda Larracuente, University of Rochester, USA*
09:30	09:45	Plant somatic disease caused by genome instability *Matthew Davis, UC Davis, USA*
09:45	10:00	Somatic mutation sequencing reveals environmental and genetic modulation of Arabidopsis mutation rates *Chandler Sutherland, University of California, Berkeley, USA*
10:00	10:30	What single molecule PacBio HiFi reads can tell us about somatic mutations and gene conversions *Richard Durbin, University of Cambridge, UK*
10:30	11:00	Refreshment break and networking
10:45	*11:00*	*Briefing for Session 3 speakers - Auditorium*
11:00	11:30	Transmissible cancer: when cancer cells become infectious agents *Elizabeth Murchison, University of Cambridge, UK*
11:30	11:45	DNA methylation erodes CTCF motifs in mammalian genome evolution *Duncan Odom, DKFZ, Germany*
11:45	12:00	Evolution of Mutational Susceptibility to Disease *Maria Kelly, Centre For Genomic Regulation, Spain*
12:00	12:15	Computational inference of somatic variant allele-frequency spectra in plants *Frank Johannes, Technical University Of Munich, Germany*
12:15	13:45	Lunch and networking
12:25	12:55	Wetlands Tour - Group 1 (sign up via the app)
12:55	13:40	Campus Tour (sign up via the app)
13:05	13:35	Wetlands Tour - Group 2 (sign up via the app)
13:30	*13:45*	*Briefing for session 4 speakers, chair & moderator - Auditorium*

13:45	**17:30**	**Session 4: Somatic mutations and disease** *Chair: Tim Coorens, EBI, UK* *Moderator: Kristin Ardlie, Broad Institute of MIT & Harvard, USA*
13:45	14:15	Temporal Evolution and Selection of Somatic Mutations in Human Brain *Christopher Walsh, Harvard University, USA*
14:15	14:30	Somatic Driver Mutations in Rheumatoid Arthritis and Osteoarthritis *Luke Harvey, Wellcome Sanger Institute, UK*
14:30	14:45	Inference of Subclonal Heterogeneity and Phenotypic Trajectories Associated with Therapeutic Resistance in Breast Cancers from Full-Length Single-Cell Transcriptomes *Ghamdan Al-Eryani, The Broad Institute of MIT and Harvard, USA*
14:45	15:15	Investigating acral melanoma in Mexico *Daniela Robles-Espinoza, Universidad Nacional Autónoma de México, Mexico*
15:15	15:45	Refreshment break and networking
15:30	*15:45*	*Briefing for session 4 speakers - Auditorium*
15:45	16:15	Mapping selection against mitochondrial mutations to improve disease variant interpretation *Nicole Lake, Yale, USA*
16:15	16:30	Widespread TP53 second hits in normal tissues in Li-Fraumeni syndrome *Joseph Christopher, Wellcome Sanger Institute, UK*
16:30	16:45	Somatic mutation landscapes in healthy tissues of individuals with inherited BRCA-mediated DNA repair deficiency *Stephanie Gardiner, University of Utah, USA*
16:45	17:00	Genome-wide detection and characterization of de novo loss of heterozygosity events using single-cell haplotype-resolved sequencing *Dmitrii Olisov, European Molecular Biology Laboratory, Germany*
17:00	17:30	Somatic mutation in autoimmune disease *Inigo Martincorena, Wellcome Sanger Institute, UK*
17:30	18:10	Free time
18:10		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	**12:45**	**Session 5: Synthetic genomics/New technologies to study mutations** *Chair: Craig Anderson, DKTK/DKFZ, Germany* *Moderator: TBC*
09:30	10:00	Scalable methods to determine the function of noncoding DNA and RNA *Neville Sanjana, New York Genome Center, USA*
10:00	10:15	Topographical archetypes of somatic mutagenesis in cancer *Peter Park, Harvard Medical School, USA*
10:15	10:30	Slide-tags DNA: Spatially mapped whole genome and transcriptome profiling of single nuclei in human tissues *Claudia Chu, Broad Institute, USA*
10:30	11:00	Talk title TBC *Isidro Cortes-Ciriano, EBI, UK*
11:00	11:30	Refreshment break and networking
11:15	*11:30*	*Briefing for Session 5 speakers - Auditorium*
11:30	12:00	Modeling the evolution of gene regulatory complexity and its role in complex disease *Carl DeBoer, The University of British Columbia, Canada*
12:00	12:15	Experimental evolution of oncogene amplifications following DNA double-strand breaks *Marc Williams, MSKCC, USA*
12:15	12:30	A framework for indel classification reveals alternate mutagenic paths to UV damage tolerance *Jan Verburg, MRC Laboratory Of Molecular Biology, UK*
12:30	12:45	Experimental Modeling Somatic Clonal Expansion During Embryonic Brain Development *Pei-chi Wei, German Cancer Research Center, Germany*
12:45	**13:00**	**Closing remarks and prizes** ***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*
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