

Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details	Location
Monday 8 June 2024			
09:00	10:00	Registration, arrival refreshments and networking	Event space
09:45		Briefing for keynote speaker, microphone runners, chair, moderator and committee	Auditorium
10:00	10:25	Welcome and introductions Wellcome Connecting Science Michelle Bishop, Associate Director, Learning and Training Wellcome Genome Campus Science and Tech Advisory Group Nicole Mather, Chair, Wellcome Genome Campus Science and Tech Advisory Group, United Kingdom Scientific programme committee: Ben Lehner, Wellcome Sanger Institute, United Kingdom Mo Lofollahi, Wellcome Sanger Institute, United Kingdom Deborah Marks, Harvard University, United States Noelia Fernuz, Centre for Genomic Regulation, Spain Jussi Taipale, Wellcome Sanger Institute / Karolinska Institute, United Kingdom / Sweden Jun Cheng, Google DeepMind, United Kingdom	Auditorium
10:25	11:15	Opening keynote Chair: Noelia Fernuz Moderator: Jun Cheng 10:25 11:15 Leveraging AI to advance biology Pushmeet Kohli, Google DeepMind, United Kingdom 11:15 11:45 Coffee break and networking	Auditorium
11:30	11:45	Briefing for Session 1 speakers, chair and moderator	Auditorium
11:45	13:00	Session 1: Solving the Gene Regulatory Code (DNA) Chair: Jussi Taipale Moderator: Constance Ferrau 11:45 12:15 Improving Genomic Deep Learning with Perturbation Data Peter Koo, Cold Spring Harbor Laboratory, United States 12:15 12:45 Solving the genome regulatory code with AI-first synthetic genomic data generation and machine learning Carl de Boer, University of British Columbia, Canada 12:45 13:00 Deciphering gene regulation with a whole-organism sequence-to-expression model Cas Blauw, VIB-KU Leuven, Belgium	Auditorium
13:00	14:10	Lunch and networking	Event Space

13:55	14:10	Briefing for Session 2 speakers, chair and moderator	Auditorium
14:10	15:40	Session 2: Solving the Gene Regulatory Code (RNA)	Auditorium
		Chair: Jun Chenq	
		Moderator: Mo Loffolahi	
14:10	14:40	From protein-RNA interactions to their functional models Jemel Ule, <i>Kino's College London, United Kingdom</i> Charlotte Capitanich, <i>The Francis Crick Institute, United Kingdom</i>	
14:40	15:10	Deep screening of biomolecular repertoires Phil Hollister, <i>MRC Laboratory of Molecular Biology, United Kingdom</i>	
15:10	15:40	Model-guided sequence design for mRNA and gene therapy applications Georg Szeitz, <i>Boehr Institute Of Immune Engineering, United States</i>	
15:40	16:20	Refreshment break and networking	Event Space
16:05	16:20	Briefing for Session 3 speakers, chair and moderator	Auditorium
16:20	17:50	Session 3: Solving Proteins (data)	Auditorium
		Chair: Ben Lehner	
		Moderator: Noelia Fernandez	
16:20	16:50	Large-scale discovery of protein stability and dynamics Gabriel Rocklin, <i>Northwestern, United States</i>	
16:50	17:20	Decoding the protein dance Paola Picotti, <i>ETH Zurich, Switzerland</i>	
17:20	17:35	Scaling data generation for chemical biology Simon d'Oelsnitz, <i>Harvard Medical School, United States</i>	
17:35	17:50	Beyond Substitutions: Generating Protein Variants with Insertions and Deletions Constance Ferragu, <i>Cradle, Switzerland</i>	
17:50	18:30	Poster pitch talks for odd number posters	Auditorium
		Chair: Jun Chenq	
18:30	19:45	Poster session 1 - odd number posters	Event Space
19:45	21:00	Dinner	Hinxton Hall Restaurant
19:45		Bar open (card payments only)	Graham Cameron Bar

Tuesday 9 June 2026			
09:15	09:30	Briefing for Session 4 speakers, chair and moderator	Auditorium
09:30	10:45	Session 4: AI Methods and Development	Auditorium
		<i>Chair: Laura Carlini</i>	
		<i>Moderator: Ben Lehner</i>	
09:30	10:00	How AI Unifies an Ecosystem of Biotechnology <i>Matt Davis, Flaoshia Pioneering, United States</i>	
10:00	10:30	BoltZGen: Toward Universal Binder Design <i>Hannes Stark, Massachusetts Institute of Technology, United States</i>	
10:30	10:45	DeepMechanisticModels: Combining mechanistic models and deep learning to discover drivers of ERK signalling heterogeneity <i>Fabian Frohlich, The Francis Crick Institute, United Kingdom</i>	
10:45	11:30	Refreshment break and networking	Event Space
11:15	11:30	Briefing for Session 5 speakers, chair and moderator	Auditorium
11:30	13:00	Session 5: Solving Chemistry and Therapeutics	Auditorium
		<i>Chair: TBC</i>	
		<i>Moderator: Ben Lehner</i>	
11:30	12:00	Designing Programmable Biologics with Generative Sequence Models <i>Pranam Chatterjee, University of Pennsylvania, United States</i>	
12:00	12:30	Beyond the Funnel: Machine Learning Powered Lab-in-the-Loop for Drug Discovery <i>Richard Bonneau, Genentech / Roche, United States</i>	
12:30	12:45	Learning to predict aptamer sensors for any metabolite or drug target <i>Andrew Fraser, University of Toronto, Canada</i>	
12:45	13:00	Temporally- faithful heterogeneous biomedical knowledge graphs for quasi-prospective clinical advancement prediction <i>Jacky Siu, Queen Mary University of London, United Kingdom</i>	
13:00	14:15	Lunch and networking	Hinxton Hall Restaurant
14:00	14:15	Briefing for Session 6 speakers, chair and moderator	Auditorium
14:15	15:45	Session 6: Solving Proteins (design)	Auditorium
		<i>Chair: Noelia Ferruz</i>	
		<i>Moderator: Mo Loftholm</i>	
14:15	14:45	Natural Language-Guided Protein Mining and Design System <i>Faile Yuan, Westlake University, China</i>	
14:45	15:15	Biohelixes in the age of AI <i>Frank Noe, Microsoft Research, Germany</i>	
15:15	15:30	Capturing transient protein interactions using in-cell photo-crosslinking <i>Santosh Shivakumaraswamy, The Francis Crick Institute, United Kingdom</i>	
15:30	15:45	Protein-Complexes: Atomistic Generative Design of de novo Protein Binders with Experimental Validation <i>Kieran Didi, Oxford University, United Kingdom</i>	
15:45	16:15	Refreshment break and networking	Event Space
16:15	16:55	Poster pitch talks for even number posters	Auditorium
		<i>Chair: Jussi Taipale</i>	
16:55	18:00	Poster session 2 - even number posters	Event Space
18:00	20:00	Dinner	Hinxton Hall Restaurant
18:00		Bar open (card payments only)	Graham Cameron Bar

Wednesday 10 June 2026			
08:45	09:00	Briefing for Session 7 speakers, chair and moderator	Auditorium
09:00	10:30	Session 7: Solving Cells, Tissues and Organs	Auditorium
		Chair: Mo Lotfollahi	
		Moderator: Charlotte Casatlanchik	
09:00	09:30	Modeling cellular migration and differentiation with spatial transcriptomic data Joshua Welch, University of Michigan, United States	
09:30	10:00	Towards Multimodal Foundation Modeling in Pathology Guillaume Jaume, University of Lausanne, Switzerland	
10:00	10:15	Universal model-free cell annotation for high definition spatial transcriptomics data from Visium HD 11mm arrays Prevas Shah, 10x Genomics, United States	
10:15	10:30	Stress-testing drug response prediction: a modular framework, dataset-suitability benchmark, and a functionally aware embedding model Nico Trummer, Oakl Oncology, France	
10:30	11:10	Refreshment break and networking	Event Space
10:55	11:10	Briefing for session 7 (continued), chair, moderator and committee	Auditorium
11:10	12:10	Session 7: Solving Cells, Tissues and Organs (continued)	Auditorium
		Chair: Mo Lotfollahi	
		Moderator: TBC	
11:10	11:40	Multimodal learning for single-cell multi-omics data integration Laura Cantini, Institut Pasteur, France	
11:40	11:55	InterScale reveals multi-scale cellular interaction programs in spatial transcriptomics Francesca Drummer, EBI-EMBL, United Kingdom	
11:55	12:10	Mapping the AI x Bio Capabilities Landscape Nelly Mak, SecureBio, United States	
12:10	12:20	Closing remarks	Auditorium
		Scientific Programme Committee:	
		Ben Lehner, Wellcome Sanger Institute, United Kingdom	
		Mo Lotfollahi, Wellcome Sanger Institute, United Kingdom	
		Debora Marks, Harvard University, United States	
		Noelia Ferris, Centre for Genomic Regulation, Spain	
		Jussi Taipale, Wellcome Sanger Institute / Karolinska Institute, United Kingdom / Sweden	
		Jun Cheng, Google DeepMind, United Kingdom	
12:20	13:30	Lunch	Hinxton Hall Restaurant
13:30		Coach departures for Stansted and Heathrow airports	Main entrance
13:45		Coach departures for Cambridge train station and city centre	Main entrance