

Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details
Monday, 6 June 2022		
11:30	12:50	Registration, lunch and networking
12:25	12:40	<i>Briefing for Keynote & Session 1 speakers, chair & moderator - Auditorium</i>
12:50	13:00	Welcome <i>Scientific Programme Committee:</i> <i>Ellen Rothenberg, California Institute of Technology, USA</i> <i>Fabian Theis, Helmholtz Zentrum München GmbH, Germany</i> <i>Roser Vento, Wellcome Sanger Institute, UK</i> <i>Itai Yanai, NYU Langone Health, USA</i>
13:00	14:00	Keynote Introduction to the session <i>Chair: Itai Yanai, NYU Langone Health, USA</i> <i>Moderator: Ellen Rothenberg, California Institute of Technology, USA</i> From Cell Atlases to Tissue Biology in Health and Disease <i>Aviv Regev, Genentech, USA</i>
14:00	14:10	Comfort Break
14:10	15:40	Session 1: How is a cell's state influenced by its microenvironment? <i>Chair: Ellen Rothenberg, California Institute of Technology, USA</i> <i>Moderator: Itai Yanai, NYU Langone Health, USA</i>
14:10	14:40	Comparative analysis of the tumor microenvironment across different cancer types - VIRTUAL <i>Zemin Zhang, Peking University, China</i>
14:40	15:10	Stem cell ecology in the germ line <i>Ben Simons, University of Cambridge, UK</i>
15:10	15:25	Stromal and Oncogenic Regulation of Colonic Stem Cells revealed by single-cell analysis of heterocellular organoids <i>Ferran Cardoso Rodriguez, University College London, UK</i>
15:25	15:40	Integrated single cell and spatial multi-omics reveals the regional organisation of the glioblastoma tumour microenvironment <i>Omer Bayraktar, Wellcome Sanger Institute, UK</i>
15:40	17:45	Poster session 1
15:40	16:15	Lightning talks for poster session 1
16:15	17:45	Poster session 1 with afternoon tea
17:20	17:35	<i>Briefing for Session 2 speakers, chair & moderator - Auditorium</i>
17:45	19:45	Session 2: How does a cell's lineage influence its fate? <i>Chair: Omer Bayraktar, Wellcome Sanger Institute, UK</i> <i>Moderator: Ellen Rothenberg, California Institute of Technology, USA</i>
17:45	18:15	Massively multiplexed, whole-embryo developmental genetics at single-cell resolution <i>Cole Trapnell, University of Washington, USA</i>
18:15	18:45	A quantitative gaze at blood cell production <i>Leila Perié, Institut Curie, France</i>
18:45	19:15	Human haematopoiesis through a single cell lens <i>Elisa Laurenti, University of Cambridge, UK</i>
19:15	19:30	Investigating how the genome directs development - mother to daughter cell regulation of chromatin and gene expression across developmental trajectories in <i>C. elegans</i> <i>Julie Ahringer, University of Cambridge, UK</i>
19:30	19:45	Lineage (in)decisions in the enteric nervous system <i>Anna Laddach, The Francis Crick Institute, UK</i>
19:45	21:30	Dinner

Tuesday, 7 June 2022

07:30	09:00	Breakfast
09:30	11:00	Networking with morning coffee
09:30	10:30	Meet the editors session - optional session - Auditorium <i>Chair: Itai Yanai, NYU Langone Health, USA</i> Katherine Brown, The Company of Biologists, UK Barbara Cheifet, Springer Nature, Nature Biotechnology, USA - VIRTUAL Stephanie McClelland, Springer Nature - Genome Biology, UK Judith Nicholson, Cell Press, UK
10:35	10:50	Briefing for Session 3 speakers, chair & moderator - Auditorium
11:00	12:30	Session 3: How does cell identity create morphology? <i>Chair: Sarah Teichmann, Wellcome Sanger Institute, UK</i> <i>Moderator: Omer Bayraktar, Wellcome Sanger Institute, UK</i>
11:00	11:30	Self-organization and symmetry breaking in intestinal organoids - VIRTUAL <i>Prisca Liberali, The Friedrich Miescher Institute, Switzerland</i>
11:30	12:00	Love thy neighbor – Identifying structure in the tumor microenvironment by multiplexed imaging <i>Leeat Keren, Weizmann, Israel</i>
12:00	12:15	Spatial transcriptome mapping of mouse and human brain with high throughput by electrophoretic capture of RNA <i>Lars Born, Karolinska institute, Sweden</i>
12:15	12:30	Single-cell roadmap of human gonadal development <i>Luz Garcia Alonso, Wellcome Sanger Institute, UK</i>
12:30	14:00	Lunch
13:35	13:50	Briefing for Session 4 speakers, chair & moderator - Auditorium
14:00	15:30	Session 4: How is cell identity regulated? <i>Chair: Sarah Teichmann, Wellcome Sanger Institute, UK</i> <i>Moderator: Itai Yanai, NYU Langone Health, USA</i>
14:00	14:15	Biologically informed deep learning to infer gene program activity in single cells - VIRTUAL <i>Mohammad Lotfollahi, Helmholtz Zentrum München Deutsches Forschungszentrum für Gesundheit und Umwelt (GmbH), Germany</i>
14:15	14:45	Illumination of transcription factor mechanisms in T-cell development at the single-cell level <i>Ellen Rothenburg, California Institute of Technology, USA</i>
14:45	15:15	Tracking cellular identities through micro- and macroevolution <i>Detlev Arendt, EMBL, Germany</i>
15:15	15:30	TF-seq: a single-cell RNA-seq transcription factor gain of function screen in mesenchymal stem cells <i>Pernille Rainer, EPFL, Switzerland</i>
15:40	17:45	Poster session 2
15:30	16:05	Lightning talks for poster session 2
16:05	17:35	Poster session 2 with afternoon tea

17:10	17:25	Briefing for Session 5 speakers, chair & moderator - Auditorium
17:35	19:05	Session 5: What are the mechanisms of molecular memory?
		<i>Chair: Roser Vento, Wellcome Sanger Institute, UK</i> <i>Moderator: Ellen Rothenberg, California Institute of Technology, USA</i>
17:35	18:05	Integrated single-cell analysis reveals adjuvant mediated epigenomic reprogramming of human innate immune cells and their bone marrow progenitors <i>Musa Mhlanga, University of Cape Town, South Africa</i>
18:05	18:35	Single cell computational epigenomics <i>Maria Colomé-Tatché, Ludwig-Maximilians-Universität, Germany</i>
18:35	18:50	Mapping the developing human immune system across organs <i>Emma Dann, Wellcome Sanger Institute, UK</i>
18:50	19:05	A Machine Learning Optimized Cas12a Lineage Tracing System Reveals Features of Transcriptional Memory <i>Nicholas Hughes, Stanford University, USA</i>
19:05	21:00	Dinner

Wednesday, 8 June 2022

07:30	09:00	Breakfast
09:30	10:30	Networking with morning coffee
10:05	10:20	Briefing for Session 6 speakers, chair & moderator
10:30	12:30	Session 6: What are the dynamics of cell transitions?
		<i>Chair: Itai Yanai, NYU Langone Health, USA</i> <i>Moderator: Roser Vento, Wellcome Sanger Institute, UK</i>
10:30	11:00	Computational strategies to decipher gene regulatory programs from single-cell multi-omics data <i>Stein Aerts, KU Leuven, Belgium</i>
11:00	11:30	Chasing recurrent cell state dynamics using omics data <i>Gioele La Manno, Swiss Federal Institute of Technology Lausanne (EPFL), Switzerland</i>
11:30	12:00	Cell states and differential vulnerabilities in neurodegenerative disease <i>Evan Macosko, MIT, USA</i>
12:00	12:15	Mapping lineage-traced single-cells across time-points using Optimal Transport <i>Zoe Piran, The Hebrew University of Jerusalem, Israel</i>
12:15	12:30	The bacterial cell cycle transcriptome at single cell resolution <i>Andrew Pountain, NYU Langone Health, USA</i>
12:30	12:45	Closing remarks
		Scientific Programme Committee: <i>Ellen Rothenberg, California Institute of Technology, USA</i> <i>Fabian Theis, Helmholtz Zentrum München GmbH, Germany</i> <i>Roser Vento, Wellcome Sanger Institute, UK</i> <i>Itai Yanai, NYU Langone Health, USA</i>
12:50	13:50	Lunch
13:50		Coach departure for Stansted and Heathrow airports
14:00		Coach departure for Cambridge train station & city centre