

**Hybrid Conference Programme**

**Start**      **Finish (BST)**   **Presenter details**  
**(BST)**

**Monday, 6 June 2022**

11:30	12:50	Registration, lunch and networking
<b>12:50</b>	<b>13:00</b>	<b>Welcome</b>
		<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>
<b>13:00</b>	<b>14:00</b>	<b>Keynote 1</b>
		From Cell Atlases to Tissue Biology in Health and Disease <i>Aviv Regev, Genentech, USA</i>
14:00	14:10	Comfort Break
<b>14:15</b>	<b>15:40</b>	<b>Session 1: How is a cell's state influenced by its microenvironment?</b>
14:10	14:40	Love thy neighbor – Identifying structure in the tumor microenvironment by multiplexed imaging <i>Leeat Keren, Weizmann, Israel</i>
14:40	15:10	Comparative analysis of the tumor microenvironment across different cancer types - VIRTUAL <i>Zemin Zhang, Peking University, China</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	16:15	Lightning talks
16:15	17:45	Poster session I with afternoon tea
<b>17:45</b>	<b>19:45</b>	<b>Session 2: How does a cell's lineage influence its fate?</b>
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>Leïla 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
<b>09:30</b>	<b>11:00</b>	<b>Networking/posters - free flow coffee</b>
<b>11:00</b>	<b>12:30</b>	<b>Session 3: How does cell identity create morphology?</b>
11:00	11:30	Self-organization and symmetry breaking in intestinal organoids <i>Prisca Liberali, The Friedrich Miescher Institute, Switzerland</i>
11:30	12:00	Stem cell ecology in the germ line <i>Ben Simons, University of Cambridge, UK</i>
12:00	12:15	Spatial transcriptome mapping of mouse and human brain with high throughput by electrophoretic capture of RNA <i>Lars Borm, 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
<b>14:00</b>	<b>15:30</b>	<b>Session 4: How is cell identity regulated?</b>
14:00	14:30	Tracking cellular identities through micro- and macroevolution <i>Detlev Arendt, EMBL, Germany</i>
14:30	15:00	Illumination of transcription factor mechanisms in T-cell development at the single-cell level <i>Ellen Rothenburg, California Institute of Technology, USA</i>
15:00	15:15	Biologically informed deep learning to infer gene program activity in single cells <i>Mohammad Lotfollahi, Helmholtz Zentrum München Deutsches Forschungszentrum für Gesundheit und Umwelt (GmbH), 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>
15:30	16:05	Lightning talks
16:05	17:35	Poster session II with afternoon tea
<b>17:35</b>	<b>19:05</b>	<b>Session 5: What are the mechanisms of molecular memory?</b>
17:35	18:05	The single cell epigenomic landscape in the bone marrow post-vaccination <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/posters - Free flow coffee**

**10:30 12:30 Session 6: What are the dynamics of cell transitions?**

10:30 11:00 Computational strategies to decipher gene regulatory programs from single-cell multi-omics data  
*Stein Aerts, KU Leuven, Belgium*

11:00 11:30 Chasing recurrent cell state dynamics using omics data  
*Gioele La Manno, Swiss Federal Institute of Technology Lausanne (EPFL), Switzerland*

11:30 12:00 Probing nervous system structure and function with contextual genomics  
*Evan Macosko, MIT, USA*

12:00 12:15 Mapping lineage-traced single-cells across time-points using Optimal Transport  
*Zoe Piran, The Hebrew University of Jerusalem, Israel*

12:15 12:30 The bacterial cell cycle transcriptome at single cell resolution  
*Andrew Pountain, NYU Langone Health, USA*

**12:30 12:45 Closing remarks and prize presentation**

**Scientific Programme Committee:**

*Ellen Rothenberg, California Institute of Technology, USA*

*Fabian Theis, Helmholtz Zentrum München GmbH, Germany*

*Roser Vento, Wellcome Sanger Institute, UK*

*Itai Yanai, NYU Langone Health, USA*

12:50 13:50 Lunch & departures

13:50 Coach departures for Cambridge train station and Stansted and Heathrow airports