

Hybrid Conference Programme

Start (GMT)	Finish (GMT)	Presenter details
Wednesday 16 November 2022		
12:00	12:50	Registration, lunch and networking
12:35	12:50	Briefing for Keynote & Session 1 speakers, microphone runners, chair, moderator & committee - Auditorium
12:50	13:00	Welcome
		<p>Scientific Programme Committee: Daniele Fallin, Emory University, USA Bas Heijmans, Leiden University Medical Center, Netherlands Charlotte Ling, Lund University, Sweden Jon Mill, University of Exeter, UK</p>
13:00	14:00	Keynote
		<p>Chair: Charlotte Ling, Lund University, Sweden Moderator: Jon Mill, University of Exeter, UK</p> <p>Finding your place: transcription factors as sensors and modifiers of the epigenome Dirk Schübeler, Friedrich Miescher Institute for Biomedical Research, Switzerland</p>
14:00	14:05	Comfort break
14:05	15:35	Session 1: Evolution, inheritance and development
		<p>Chair: Jon Mill, University of Exeter, UK Moderator: Charlotte Ling, Lund University, Sweden</p>
14:05	14:35	Paleo-epigenetics: Using ancient bones to peek into the Neanderthal brain Liran Carmel, The Hebrew University of Jerusalem, Israel
14:35	15:05	Epigenetic changes induced by environmental exposures Mathew Van de Pette, University of Cambridge
15:05	15:20	Lifestyle intervention during pregnancy alters DNA methylation in offspring cord blood Josefine Jönsson, Lund University, Sweden
15:20	15:35	Developmental trajectories of DNA methylation across human brain development Alice Franklin, University of Exeter, UK
15:35	16:20	Refreshment break and networking
16:05	16:20	Briefing for Session 2 speakers, chair & moderator - Auditorium
16:20	17:55	Session 2: Translational epigenomics
		<p>Chair: Bas Heijmans, Leiden University Medical Center, Netherlands Moderator: Jon Mill, University of Exeter, UK</p>
16:20	16:50	Cerebral organoids and prenatal stress Elizabeth Binder, Max Planck Institute of Psychiatry, Germany
16:50	17:20	Spatial and single cell multi-omic analysis of human heart disease Christoph Kuppe, Aachen University, Germany
17:20	17:35	Cell-free DNA methylome analysis enables early preeclampsia prediction Marie De Borre, KU Leuven, Belgium
17:35	17:50	Novel subgroups of type 2 diabetes reveal different DNA methylation patterns Sonia Garcia-Calzon, University of Navarra, Spain
17:50	18:20	Lightning talks for odd number posters
18:20	19:20	Poster session 1 - odd number posters, with drinks reception
19:20	21:00	Dinner
		Bar open (card payments only)

Thursday 17 November 2022		
07:30	09:30	Breakfast
09:15	09:30	Briefing for Session 3 speakers, chair & moderator - Auditorium
09:30	11:00	Session 3: Epigenomics mechanisms of complex diseases <i>Chair: Charlotte Ling, Lund University, Sweden</i> <i>Moderator: Bas Heijmans, Leiden University Medical Center, Netherlands</i>
09:30	10:00	Applied epigenetics: deciphering the mechanisms of Multiple Sclerosis development and progression Maja Jagodic, Karolinska Institute, Sweden
10:00	10:30	Epigenetics and noncoding RNAs in diabetic complications and metabolic memory Rama Natarajan, City of Hope, USA
10:30	10:45	High-resolution transcriptomic and epigenetic profiling across disease stages identifies novel regulators of COPD <i>Renata Jurkowska, Cardiff University, UK</i>
10:45	11:00	The epigenome of liver sinusoidal endothelial cells in fatty liver disease <i>Hannah Maude, Imperial College London, UK</i>
11:00	11:45	Refreshment break and networking
11:30	11:45	Briefing for Session 4 speakers, microphone runners, chair & moderator - Auditorium
11:45	13:15	Session 4: Computational epigenomics <i>Chair: Bas Heijmans, Leiden University Medical Center, Netherlands</i> <i>Moderator: Jon Mill, University of Exeter, UK</i>
11:45	12:15	EpiATLAS – a reference for human epigenomic research Martin Hirst, University of British Columbia, Canada
12:15	12:45	Cell-type deconvolution of solid tissue DNA methylomes at cell-type resolution Andrew Teschendorff, Shanghai Institute for Nutrition & Health, China
12:45	13:00	Detecting rare epigenetic dysregulation in common psychiatric disorder <i>Christine Hansen, Mount Sinai, USA</i>
13:00	13:15	Discontinuities aging: artificial intelligence for identifying switch points in DNA methylation <i>Elad Segev, Holon Institute of Technology, Israel</i>
13:15	14:45	Lunch
14:30	14:45	Briefing for Session 5 speakers, chair & moderator - Auditorium
14:45	16:15	Session 5: Epigenetic epidemiology <i>Chair: Jon Mill, University of Exeter, UK</i> <i>Moderator: Charlotte Ling, Lund University, Sweden</i>
14:45	15:15	The immune factors driving DNA methylation variation in human blood Jacob Bergstedt, Karolinska Institute, Sweden
15:15	15:45	Epigenetics and human genetic diversity Nora Franceschini, University of North Carolina, USA
15:45	16:00	Nucleated red blood cells explain most of the association between DNA methylation and gestational age <i>Kristine Løkås Haftorn, Norwegian Institute of Public Health, Norway</i>
16:00	16:15	Circulating interleukin-6 levels are associated with DNA methylation in regulatory regions of key inflammatory genes <i>Lucy Sinke, Leiden University Medical Centre, Netherlands</i>
16:15	16:45	Refreshment break
16:45	17:30	Special Guest Interview <i>Chair: Daniele Fallin, Emory University, USA</i> <i>Moderator: Bas Heijmans, Leiden University Medical Center, Netherlands</i> Francis Collins, Acting Science Advisor to the President of the United States and Former Director of the National Institutes of Health
17:30	18:00	Lightning talks for odd number posters
18:00	18:10	Sponsored talk by Illumina
18:10	19:10	Poster session 2 - even number posters, with drinks reception sponsored by Illumina
19:10	21:00	Dinner
		Bar open (card payments only)

Friday 18 November 2022		
07:30	09:30	Breakfast
09:15	09:30	Briefing for Session 6 speakers, chair & moderator - Auditorium
09:30	11:00	Session 6: New frontiers in epigenomic technologies <i>Chair: Jon Mill, University of Exeter, UK</i> <i>Moderator: Bas Heijmans, Leiden University Medical Center, Netherlands</i>
09:30	10:00	Spatial epigenomics tissue profiling at the cellular level Rong Fan, Yale University, USA
10:00	10:30	Epigenetic patterns in a complete human genome Ariel Gershman, Johns Hopkins University, USA
10:30	10:45	Genome-wide analysis of single-molecule DNA methylation using long reads reveals heterogenous patterns in heterochromatin <i>Duncan Sproul, MRC Human Genetics Unit, Edinburgh, UK</i>
10:45	11:00	Investigating epigenetic regulation of microglia in a human-mouse chimera model of Alzheimer's disease <i>Sarah Marzi, Imperial College London, UK</i>
11:00	11:45	Refreshment break and networking
11:30	11:45	Briefing for Keynote, chair, moderator & committee
11:45	12:45	Keynote <i>Chair: Bas Heijmans, Leiden University Medical Center, Netherlands</i> <i>Moderator: Charlotte Ling, Lund University, Sweden</i> Single germline aminoacid substitution in H3.3 alters recruitment of Dnmt3a to cause neurodegeneration Nada Jabado, McGill University, Canada
12:45	13:00	Closing remarks and prize presentation Scientific Programme Committee: <i>Daniele Fallin, Emory University, USA</i> <i>Bas Heijmans, Leiden University Medical Center, Netherlands</i> <i>Charlotte Ling, Lund University, Sweden</i> <i>Jon Mill, University of Exeter, UK</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