Hybrid Conference Programme

Start (GMT)	Finish (GMT)	Presenter details			
Wednesday 15 November 2023					
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			
		Scientific Programme Committee: Bas Heijmans, Leiden University Medical Center, Netherlands Claudia Kleinman, McGill University, Canada Charlotte Ling, Lund University Diabetes Center, Sweden Jon Mill, University of Exeter, UK			
13:00	14:00	Keynote 1			
		Chair: Claudia Kleinman Moderator: Bas Heijmans			
		Laminopathies, heterochromatin and muscle integrity: chromosome structure and disease Susan Gasser, Friedrich Miescher Institute, Switzerland			
14:00	14:05	Comfort break			
14:05	15:35	Session 1: Epigenetics and common disease: establishing causality			
		Chair: Charlotte Ling Moderator: Bas Heijmans			
14:05	14:35	3D chromatin maps of the human pancreas reveal cell type-specific regulatory architecture of T2D risk Klaus Kaestner, University of Pennsylvania, USA			
14:35	15:05	Current practices and challenges in using genetic factors to infer causal relationships between molecular phenotypes and disease risk Gibran Hemani, University of Bristol, UK			
15:05	15:20	DNA methylation is a mechanism leading to aberrant protein N-glycosylation in hepatocellular carcinoma cell line Ana Vujić, University of Zagreb, Faculty of Science, Croatia			
15:20	15:35	Examining Causality between Cigarette Smoking and Peripheral Blood DNA Methylation Using Mendelian Randomization Analyses in Twin Data Madhurbain Singh, Virginia Commonwealth University, USA (VIRTUAL)			
15:35	16:20	Refreshment break and networking			





16:05	16:20	Briefing for Session 2 speakers, microphone runners, chair & moderator - Auditorium
16:20	18:05	Session 2: Technical and methodical advances in epigenomics
		Chair: Claudia Kleinman Moderator: Jon Mill
16:20	16:50	Remodeling of genome-lamina contacts is an early event during random X-chromosome inactivation Jop Kind, Hubrecht Institute, Netherlands
16:50	17:20	Studying DNA methylation using nanopore long-read sequencing approaches Lucia Clemens-Daxinger, Leiden University Medical Center, Netherlands
17:20	17:35	Physiological roles of aberrant DNA methylation in vitro and in vivo Gabi Ficz, Barts Cancer Institute, UK
17:35	17:50	Analytical Approaches for Predicted Blood Cell Counts: an application to DNA methylation age Thomas Jonkman, Leiden University Medical Center, Netherlands
17:50	18:05	Poster pitch talks for odd number posters
18:05	19:15	Poster session 1 - odd number posters
19:15	21:00	Dinner
		Bar open (card payments only)

Thursday	y 16 No	vember 2023
07:30	09:00	Breakfast
09:15	09:30	Briefing for Session 3 speakers, microphone runners, chair & moderator - Auditorium
09:30	11:00	Session 3: Epigenomics: from bench to bedside
		Chair: Bas Heijmans Moderator: Jon Mill
09:30	10:00	Targeted methylation sequencing to transform cancer detection Sir Harpal Kumar, GRAIL Bio UK Ltd, UK
10:00	10:30	Ultra-fast deep-learned pediatric CNS tumor classification during surgery Jeroen de Ridder, University Medical Center Utrecht, Netherlands
10:30	10:45	Detailed DNA methylation characterisation of phyllodes tumours identifies a signature of malignancy and distinguishes phyllodes from metaplastic breast carcinoma Braydon Meyer, Garvan Institute of Medical Research, Australia
10:45	11:00	DNA methylation in cord blood partially mediates the effects of the pre-pregnancy BMI in pregnant women with obesity on offspring's BMI z-score at 36 months of age. Alice Maguolo, Lund University, Sweden
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: Reference data and computational epigenomics
		Chair: Charlotte Ling Moderator: Claudia Kleinman
11:45	12:15	DNA methylation throughout life and aging Tommy Kaplan, The Hebrew University, Israel
12:15	12:45	Gene regulatory networks integrate genetic and non-genetic factors of disease mechanisms <i>Judith Zaugg, EMBL, Germany</i>
12:45	13:00	Cell-specific methylomic variation in neurodevelopment and Schizophrenia Emma Dempster, Exeter University, UK
13:00	13:15	Modeling the genome and prenatal exposome contribution to newborn DNA methylome variability with the RAMEN package Erick Navarro-Delgado, The University of British Columbia, Canada
13:15	14:30	Lunch and networking



14:15	14:30	Briefing for Session 5 speakers, microphone runners, chair & moderator - Auditorium
14:30	16:00	Session 5: Inheritance, development and epigenetic mechanisms
		Chair: Jon Mill Moderator: Claudia Kleinman
14:30	15:00	Transgenerational inheritance of acquired epigenetic signatures at CpG islands in mice Yuta Takahashi, Altos Labs, USA
15:00	15:30	Transgenerational epigenetic inheritance of polycystic ovary syndrome Elisabet Stener-Victorin, Karolinska Institute, Sweden
15:30	15:45	Genetic impacts on DNA methylation variance in monozygotic twins capture gene-environment interactions and cell-specific effects Xiaopu Zhang, King's College London, UK
15:45	16:00	Aberrant EZHIP Expression Drives Tumorigenesis in Osteosarcoma Alva Annett, McGill University, Canada
16:00	16:30	Refreshment break
16:30	17:15	Meet the speakers
16:30 17:15	17:15 17:35	Meet the speakers Poster pitch talks for even number posters
17:15	17:35	Poster pitch talks for even number posters
17:15 17:35	17:35 17:50	Poster pitch talks for even number posters Sponsored talk What You're Missing Matters
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Friday 17	7 Noven	nber 2023
07:30	09:00	Breakfast
09:15	09:30	Briefing for Session 6 speakers, microphone runners, chair & moderator - Auditorium
09:30	11:00	Session 6: Epigenetic epidemiology
		Chair: Bas Heijmans Moderator: Charlotte Ling
09:30	10:00	Lipid metabolism and the human methylome: Meta-analysis of epigenome-wide association studies of blood lipid levels Melanie Waldenberger, Helmholtz Munich, Germany
10:00	10:15	Sex differences in DNA methylation across gestation: a large scale, cross-cohort, multi-tissue analysis Darina Czamara, Max-Planck-Institute of Psychiatry, Germany
10:15	10:30	Meta-analysis of genome-wide DNA methylation in schizophrenia: Does sex stratification improve discovery? Markos Tesfaye Woldeyohannes, University of Oslo, Norway
10:30	10:45	What makes clocks tick? Decomposing adult epigenetic clocks to probe the early origins of accelerated epigenetic ageing Rosa Mulder, Erasmus Medical Center, Netherlands
10:45	11:00	Epigenetic insights into chronic inflammation and brain ageing Eleanor Conole, University of Edinburgh, UK
11:00	11:45	Refreshment break and networking
11:30	11:45	Briefing for Keynote, microphone runners, chair, moderator & committee - Auditorium
11:45	12:45	Keynote lecture
		Chair: Jon Mill Moderator: Claudia Kleinman
		Fundamental equations linking methylation dynamics to maximum lifespan in mammals Steve Horvath, Altos Labs, USA
12:45	13:00	Closing remarks and prize presentation
		Scientific Programme Committee: Bas Heijmans, Leiden University Medical Center, Netherlands Claudia Kleinman, McGill University, Canada Charlotte Ling, Lund University Diabetes Center, Sweden Jon Mill, University of Exeter, UK
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