

## Virtual Conference Agenda

Monday, 14 September		
13:00	13:05	<b>Welcome</b>  <i>Scientific Programme Committee:</i> <i>Joanna Kelley, Washington State University, USA</i> <i>Nick Loman, University of Birmingham, UK</i> <i>Alicia Oshlack, Murdoch Children's Research Institute, Australia</i> <i>Oliver Stegle, German Cancer Research Center &amp; EMBL Heidelberg, Germany</i>
13:05	13:35	<b>Keynote 1</b>  13:05   13:25   20 years of Genome Informatics <i>Ewan Birney, EMBL-EBI, UK</i>  13:25   13:35   Q&A <i>Chair: Oliver Stegle, German Cancer Research Center &amp; EMBL Heidelberg, Germany</i> <i>Moderator: Nick Loman, University of Birmingham, UK</i>
13:35	14:35	<b>Session 1: Transcriptomics</b>  Introduction to the session <i>Chair: Pall Melsted, University of Iceland, Iceland</i>  13:35   13:50   Deep representation learning for problems in biology <i>Smita Krishnaswamy, Yale University, USA</i>  13:50   14:05   AtacWorks: A deep neural network toolkit to enhance epigenomic data <i>Avantika Lal, Nvidia, USA</i>  14:05   14:20   Uncovering the transcriptomic landscape of SARS-Cov-2 infection using nanopore direct RNA sequencing and npTranscript <i>Lachlan Coin, University of Melbourne, Australia</i>  14:20   14:35   Q&A <i>Chair: Pall Melsted, University of Iceland, Iceland</i> <i>Moderator: Oliver Stegle, German Cancer Research Center &amp; EMBL Heidelberg, Germany</i>
14:35	14:50	Break
14:50	15:50	<b>Session 1: Transcriptomics</b>  Introduction to the session <i>Chair: Smita Krishnaswamy, Yale University, USA</i>  14:50   15:05   Fast and modular processing of single cell RNA-seq datasets with kallisto and bustools <i>Pall Melsted, University of Iceland, Iceland</i>  15:05   15:20   Measuring isoform co-expression in single-cell RNAseq successfully decodes splicing coordination as a key determinant of neural cell <i>Angeles Arzalluz-Luque, Polytechnical University of Valencia, Spain</i>  15:20   15:35   Assessment of chromatin accessibility cell-type annotation using a reference mouse cortex atlas <i>Risa Kawaguchi, Cold Spring Harbor Laboratory, USA</i>  15:35   15:50   Q&A <i>Chair: Smita Krishnaswamy, Yale University, USA</i> <i>Moderator: Oliver Stegle, German Cancer Research Center &amp; EMBL Heidelberg, Germany</i>
15:50	16:05	Break
16:05	16:30	Poster lightning talks
16:30	17:00	Poster session

# Genome Informatics

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Tuesday, 15 September		
<b>13:00 14:00 Session 2: Evolution, Complex Traits and Phylogenetics</b>		
Introduction to the session <i>Chair: Oliver Pybus, University of Oxford, UK</i>		
13:00	13:15	Charting mutation spectrum variation across the genome and the tree of life <i>Kelley Harris, University of Washington, USA</i>
13:15	13:30	Purifying selection acts on germline methylation to modify the CpG mutation rate at promoters <i>Leandros Boukas, Johns Hopkins University, USA</i>
13:30	13:45	Investigating the genetics of social behavior in wolf-dog hybrids <i>Xue Li, University of Massachusetts Medical School, USA</i>
13:45	14:00	Q&A <i>Chair: Oliver Pybus, University of Oxford, UK</i> <i>Moderator: Oliver Stegle, German Cancer Research Center &amp; EMBL Heidelberg, Germany</i>
14:00	14:15	Break
<b>14:15 16:00 Session 2: Evolution, Complex Traits and Phylogenetics</b>		
Introduction to the session <i>Chair: Kelley Harris, University of Washington, USA</i>		
14:15	14:30	National and international dynamics of SARS-CoV-2 evolution and transmission <i>Oliver Pybus, University of Oxford, UK</i>
14:30	14:45	Identifying Regulatory Mechanisms Affected by Hydrogen Sulfide in an Extremophile Fish <i>Kerry McGowan, Washington State University, USA</i>
14:45	15:00	Whole genome sequencing to study the contribution of structural variation to human complex traits <i>Brittany Howell, Wellcome Sanger Institute, UK</i>
15:00	15:15	Q&A <i>Chair: Kelley Harris, University of Washington, USA</i> <i>Moderator: Oliver Stegle, German Cancer Research Center &amp; EMBL Heidelberg, Germany</i>
15:15	15:30	Poster lightning talks
15:30	16:00	Poster session
16:00	16:30	Break
<b>16:30 17:30 Session 3: Sequencing Algorithms, Variant Discovery and Genome Assembly</b>		
Introduction to the session <i>Chair: C. Titus Brown, University of California, Davis, USA</i>		
16:30	16:45	Genetic and epigenetic maps of human centromeric regions <i>Karen Miga, University of California, Santa Cruz, USA</i>
16:45	17:00	Haplotype-resolved de novo assembly with phased assembly graphs <i>Haoyu Cheng, Dana-Farber Cancer Institute, Harvard Medical School, USA</i>
17:00	17:15	Varlociraptor: towards a unified theory of variant calling <i>Johannes Koester, University of Duisburg-Essen, Germany</i>
17:15	17:30	Q&A <i>Chair: C. Titus Brown, University of California, Davis, USA</i> <i>Moderator: Joanna Kelley, Washington State University, USA</i>
17:30	18:00	Break

# Genome Informatics

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18:00		19:45		<b>Session 3: Sequencing Algorithms, Variant Discovery and Genome Assembly</b>
				Introduction to the session <i>Chair: Karen Miga, University of California, Santa Cruz, USA</i>
18:00	18:15	Metagenomics is *hard*: the trials and tribulations of graph-based shotgun metagenome analysis <i>C. Titus Brown, University of California, Davis, USA</i>		
18:15	18:30	precisionFDA-GIAB V2 Truth Challenge <i>Nathan Olson, NIST, USA</i>		
18:30	18:45	Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ <i>Iliia Minkin, The Pennsylvania State University, USA</i>		
18:45	19:00	Q&A <i>Chair: Karen Miga, University of California, Santa Cruz, USA</i> <i>Moderator: Joanna Kelley, Washington State University, USA</i>		
19:00	19:15	Poster lightning talks		
19:15	19:45	Poster session		

## Wednesday, 16 September

13:00		14:00		<b>Session 4: Microbial and Metagenomics</b>
				Introduction to the session <i>Chair: Alice McHardy, Helmholtz Centre for Infection, Germany</i>
13:00	13:15	Genomic epidemiology, horizontal gene transfer and evolution of bacterial surface polysaccharides <i>Rafal Mostowy, Jagiellonian University, Poland</i>		
13:15	13:30	A uniformly processed archive of 661K bacterial assemblies <i>Grace Blackwell, EMBL-EBI, Wellcome Sanger Institute, UK</i>		
13:30	13:45	Genome-wide, Mendelian randomization and dietary analysis of gut microbiota in a cohort of ~6,000 individuals with electronic health records <i>Youwen Quin, University of Melbourne, Australia</i>		
13:45	14:00	Q&A <i>Chair: Alice McHardy, Helmholtz Centre for Infection, Germany</i> <i>Moderator: Nick Loman, University of Birmingham, UK</i>		
14:00	14:15	Break		
14:15		16:00		<b>Session 4: Microbial and Metagenomics</b>
				Introduction to the session <i>Chair: Rafal Mostowy, Jagiellonian University, Poland</i>
14:15	14:30	Critical Assessment of Metagenome Interpretation - the Second Round of Challenges <i>Alice McHardy, Helmholtz Centre for Infection, Germany</i>		
14:30	14:45	Hardware-accelerated genome sketching enables real-time genomic epidemiology of pathogens <i>John Lees, Imperial College London, UK</i>		
14:45	15:00	Strain-resolved viral metagenomics of SARS-CoV-2 in sewage <i>Alexander Crits Christoph, University of California, Berkeley, USA</i>		
15:00	15:15	Q&A <i>Chair: Rafal Mostowy, Jagiellonian University, Poland</i> <i>Moderator: Nick Loman, University of Birmingham, UK</i>		
15:15	15:30	Poster lightning talks		
15:30	16:00	Poster session		

# Genome Informatics

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16:00	16:30	Break
<b>16:30</b>	<b>17:30</b>	<b>Session 5: Personal and Medical Genomics</b>
		Introduction to the session <i>Chair: Christoph Bock, CeMM Research Center for Molecular Medicine, Vienna, Austria</i>
16:30	16:45	Data sharing and individual privacy <i>Lucila Ohno-Machado, University of California, San Diego, USA</i>
16:45	17:00	Automatic Tumour Typing Based on Patterns of Somatic Passenger Mutations <i>Gurnit Atwal, University of Toronto, Canada</i>
17:00	17:15	scNOVA: Haplotype-aware single-cell multiomics identifies direct consequences of structural variants in cancer <i>Hyobin Jeong, EMBL, Germany</i>
17:15	17:30	Q&A <i>Chair: Christoph Bock, CeMM Research Center for Molecular Medicine, Vienna, Austria</i> <i>Moderator: Joanna Kelley, Washington State University, USA</i>
17:30	18:00	Break
<b>18:00</b>	<b>19:50</b>	<b>Session 5: Personal and Medical Genomics</b>
		Introduction to the session <i>Chair: Lucila Ohno-Machado, University of California, San Diego, USA</i>
18:00	18:15	Single-cell Analysis of Epigenetic Disease Landscapes and Induced Perturbations <i>Christoph Bock, CeMM Research Center for Molecular Medicine, Vienna, Austria</i>
18:15	18:30	Analyzing adaptive immune system through deep interrogation of antibody repertoires using immunosequencing data <i>Yana Safonova, UCSD, USA</i>
18:30	18:45	Sketching Algorithms for Genomic Data Analysis and Querying in a Secure Enclave <i>Kaiyuan Zhu, Indiana University Bloomington, USA</i>
18:45	19:00	Q&A <i>Chair: Lucila Ohno-Machado, University of California, San Diego, USA</i> <i>Moderator: Joanna Kelley, Washington State University, USA</i>
19:00	19:20	Poster lightning talks
19:20	19:50	Poster session
<b>19:50</b>	<b>19:55</b>	<b>Closing remarks</b>
		<i>Scientific Programme Committee:</i> <i>Joanna Kelley, Washington State University, USA</i> <i>Nick Loman, University of Birmingham, UK</i> <i>Alicia Oshlack, Murdoch Children's Research Institute, Australia</i> <i>Oliver Stegle, German Cancer Research Center &amp; EMBL Heidelberg, Germany</i>