Tuesday 16	ith July 2024	- LT1 (Afternoon)	
	Finish (GMT)		Presentation Details
12:00		Registration, Lunch and Networking	
13:30		Keynotes	Chair: Nick Loman, University of Bristol
13:30		Lucy Burkitt-Gray (UK Biobank)	Silan Hill Zonian, Gintalon, G. Zhata.
14:00		Richard Durbin (University of Cambridge)	Insights from high quality genome sequencing across the tree of life
14:30		Evolving Technologies 1	Chair: Michael Quail, Wellcome Sanger Institute
14:30		Shawn Levy (Element)	Chair. Wichael Quali, Wellcome Sanger Histitute
15:00		Jason Betley (Illumina)	Illumina Technical and Product Roadmap Update
15:30		Neil Ward (PacBio)	marinia recimicararia rroduce noduriup opuate
16:00		Coffee Break	
16:30		Evolving Technologies 2	Chair: Michael Quail Wellcome Sanger Institute
16:30		Andy Larrea (Ultima)	Chair: Michael Quail, Wellcome Sanger Institute
17:00			Ultima Genomics UG100: A flexible, low-cost, scalable sequencing solution
17:30		Graham Hall (Oxford Nanopore) Speaker TBC (10X)	
18:00		Drinks Reception and Poster Session 1	
18.00	19.30	Diffixs Reception and Poster Session 1	
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	Finish (GMT)		
08:30		Coffee and Pastries	
00.30	05.30	2325 00 . 0.000	
arallel Ses	sion A - LT2		
	Finish (GMT)	Presenter	Presentation Details
09:30		Plant and Animal Genomics	Chair: Al Darby, University of Liverpool
09:30		Alex Cagan (University of Cambridge)	TBC
09:30			
10:20		Gary Barker (University of Bristol) Francisco Rodriguez-Algarra (Queen Mary, University of	Unlocking hidden genetic diversity in hexaploid bread wheat Ribosomal DNA Copy Number Variation Associates with Hematological Profiles and Renal
10.20	10.55	London)	Function in the UK Biobank
10:35	10.50	Carla Canedo-Ribeiro (University of Kent)	New method to detect chromosomal reciprocal translocations using long-read sequencing
10:50		Silver Sponsor Talk	New England Biolabs
11:05		Coffee Break	New Eligiatio biolabs
			Chaire Innathan Cauhand Nausantla University
11:30		Human & Clinical Genomics	Chair: Jonathan Coxhead, Newcastle University
11:30		Sandi Deans (University of Edinburgh)	Ensuring a high quality NGS clinical service
11:55		Mike Hubank (Institute of Cancer Research, London)	TBC
12:20	12:35	Steven Hair (Newcastle University)	Utilising long-read sequencing approaches to detect structural variants of clinical significance
12:35	12.50	Ania Bickers (CBLIK Cambridge Institute University of	childhood cancer
12.55	12.50	Ania Piskorz (CRUK Cambridge Institute, University of Cambridge)	Unlocking the potential of FFPE cancer specimens in predicting response and effect of cytotoxi therapy
12:50	13:05	Nicholas Timpson (University of Bristol)	Exome Sequencing of UK Birth Cohorts
13:00		Lunch and Poster Session II	Exome sequenting of on sixth control
14:00		Epigenetics/Human & Clinical Genomics	Chair: Ania Piskorz, CRUK Cambridge Institute University of Cambridge
14:00		Areeba Patel (University of Heidelberg)	TBC
14:00		Alex de Mendoza (Queen Mary University of London)	Early Origins of Eukaryotic DNA Methylation Pathways
14:50		Hannah Trivett (University of Liverpool)	Clinical metagenomics can resolve pathogens to strain-level identification direct from stool
15:05		. , , ,	
15:05		Aimee Hanson (University of Bristol) Silver Sponsor Talk	Considering confounding in rare variant genome wide association studies PacBio
15:35		Coffee Break	racbio
16:00		Bioinformatics & Machine Learning in Genomics	Chair: Matt Loose, University of Nottingham
16:00		Rhydian Windsor (Oxford Nanopore)	TBC
16:00		Leonid Chindelevitch (Imperial College London)	
			Insights into AMR from large-scale genotypic and phenotypic data analysis
16:50		Tim Downing (Pirbright Institute)	Pangenome variation graph analysis reveals insights into livestock poxviruses
17:05		Rory Munro (University of Nottingham)	Adaptive Sampling on PromethION: Soaring Close to the Sun with Icarust and Readfin
17:20	17:30	Silver Sponsor Talk	Opentrons

Parallel Ses	sion B - LT2		
	Finish (GMT)	Presenter	Presentation Details
09:30		Evolutionary Genomics I	Chair: Jordi Paps Montserrat (University of Bristol)
09:30		Peter WH Holland (University of Oxford)	Darwin Tree of Life project: Evolutionary applications
09:55		Filipe Castro (CIIMAR/FCUP)	A Domino Effect? Of loss, duplication and novelty in a transition to the sea
10:10		Marta Farré-Belmonte (Kent)	The role of 3D chromosome folding in mammalian genome evolution
10:25		Tom Jenkins (Exeter)	Plastic versus adaptive responses to climate in barbastelle bats
10:40		Gold Sponsor Talk	Element Biosciences
11:05		Coffee Break	Element blosdenees
11:30		Microbes and Microbiomes I	Chair: Kate Baker, University of Cambridge
11:30		Alexandre Almeida (University of Cambridge)	TBC
11:55		Lauren Cowley (University of Bath)	Using phylogeographical signal of Salmonella enterica serovar Enteritidis to train a hierarchical machine learning model to rapidly predict source attribution
12:20	12:35	Winnie Lee (Imperial College London)	Genomic population study of bloodstream Klebsiella spp. in 2020 in Southwest, UK
12:35	12:50	Eleanor Hayles (Quadram Institute, Norwich)	Genomic Epidemiology of SARS-CoV-2 in Norfolk, UK, March 2020- December 2022
12:50		Silver Sponsor Talk	Oxford Nanopore
13:00		Lunch and Poster Session II	
14:00		Microbes and Microbiomes II	Chair: Nick Loman, University of Bristol
14:00		Alan Walker (University of Aberdeen)	Questioning the foetal microbiome illustrates pitfalls of low-biomass microbial studies
14:25			TBC
14:50		Alice Nisbett (Quadram Institute, Norwich)	The genomic switcheroo: characterising genome rearrangements within typhoidal infections
15:05		Kirsty Sands (University of Oxford)	Providencia in the fly microbiome acting as a reservoir of blaNDM carriage: A threat in the dissemination of antimicrobial resistance and infection?
15:20	15:35	Steven Rudder (Quadram Institute, Norwich)	Genomic diversity of non-typhoidal Salmonella found within patients suffering from gastroenteritis in Norfolk, UK
15:35	16:00	Coffee Break	
16:00	17:35	Evolutionary Genomics II	Chair: Sion Bayliss (University of Bristol)
16:00	16:25	Sandra Álvarez Carretero (University College London)	Bayesian methods to infer evolutionary timelines when deep divergences are present and large genomic datasets used
16:25	16:50	Corey Kirkland (Kent)	Insights into population differences and polymorphic chromosome fusions in the waterbuck
16:50		Jialin Wei (Bristol)	Convergent Genome Evolution In The Conquest Of Land By Animals
17:05		Chris Clarkson (QMUL/UCL)	Characterising structural variation in known pathogenic STRs across genetic ancestries, germ-line instability events and diseased cohorts
17:20	17:35	Sarah Quigley (Kent)	Investigating mechanisms of genomic rearrangement in the human genome
		stol Harbour Hotel, The Sanisovo Room, Weds	17th [TICKETED]
	Finish (GMT)		
18:30		Arrival Drinks	
19:30	00:00	Banquetting Menu Dinner	
		4 - LT1 (Morning)	
Start (GMT)	Finish (GMT)	Presenter	Presentation Details
09:30	11:05	Single Cell Genomics	Chair: Lia Chappell, University of Cambridge
09:30		Proceedings (Maller on Transfer Course)	Shared molecular vulnerabilities of human cortical neurons in C9ORF72 Amyotrophic Lateral
		Jimmy Lee (Wellcome Trust, Sanger)	Sclerosis
09:55	10:20	Rebecca Berrens (University of Oxford)	Sclerosis TBC
09:55 10:20	10:20 10:35	Rebecca Berrens (University of Oxford) Christos Proukakis (UCL)	Sclerosis TBC The somatic CNV landscape of the Parkinson's disease brain at single cell resolution
09:55 10:20 10:35	10:20 10:35 10:50	Rebecca Berrens (University of Oxford) Christos Proukakis (UCL) Simon Cockell (Newcastle University)	Sclerosis TBC The somatic CNV landscape of the Parkinson's disease brain at single cell resolution Geographically weighted methods for spatial transcriptomics data analysis
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09:55 10:20 10:35 10:50 11:05	10:20 10:35 10:50 11:05 11:30 12:30	Rebecca Berrens (University of Oxford) Christos Proukakis (UCL) Simon Cockell (Newcastle University) Sponsor Talk Coffee Break Keynotes	Sclerosis TBC The somatic CNV landscape of the Parkinson's disease brain at single cell resolution Geographically weighted methods for spatial transcriptomics data analysis Parse Genomics Chair: Michael Quail, Wellcome Sanger Institute