Tuesday 16	th July 2024	- LT1 (Afternoon)	
	Finish (GMT)		Presentation Details
12:00			i resentation petalis
		Registration, Lunch and Networking	
13:30		Keynotes	Chair: Nick Loman, University of Bristol
13:30	14:00	Lucy Burkitt-Gray (UK Biobank)	Massive-scale whole genome sequencing: Insights from the UK Biobank
14:00	14:30	Richard Durbin (University of Cambridge)	Insights from high quality genome sequencing across the tree of life
14:30	16:00	Evolving Technologies 1	Chair: Michael Quail, Wellcome Sanger Institute
14:30		Shawn Levy (Element)	Integrated Multiomic and Genomic Profiling for Precision Biology on the AVITI24 platform
15:00		Jason Betley (Illumina)	Illumina Technical and Product Roadmap Update
15:30		Neil Ward (PacBio)	Platinum Genomes
16:00	16:30	Coffee Break	
16:30	18:00	Evolving Technologies 2	Chair: Michael Quail, Wellcome Sanger Institute
16:30	17:00	Andy Larrea (Ultima)	Ultima Genomics UG100: A flexible, low-cost, scalable sequencing solution
17:00	17:30	Graham Hall (Oxford Nanopore)	ONT Technology Update
17:30	18:00	Nicola Cahill (10x Genomics)	The application of single cell & spatial technologies to study the tumor microenvironment
18:00	19:30	Drinks Reception and Poster Session 1	
ednesday	y 17th July 2	024	
art (GMT)	Finish (GMT)		
08:30	09:30	Coffee and Pastries	
	sion A - LT2 Finish (GMT)	Presenter	Presentation Details
09:30		Plant and Animal Genomics	Chair: Al Darby, University of Liverpool
09:30	09:55	Alex Cagan (University of Cambridge)	Somatic evolution across the tree of life
09:55	10:20	Gary Barker (University of Bristol)	Unlocking hidden genetic diversity in hexaploid bread wheat
10:20		Francisco Rodriguez-Algarra (Queen Mary, University of	Ribosomal DNA Copy Number Variation Associates with Hematological Profiles and Renal
		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: UltraExpress™: Streamlined library prep for RNA and DNA samples fro
11:00	11.20	Coffee Break	New England Biolabs
11:30		Human & Clinical Genomics	Chair: Jonathan Coxhead, Newcastle University
11:30	11:55	Sandi Deans (University of Edinburgh)	Ensuring a high quality NGS clinical service
11:55	12:20	Mike Hubank (Institute of Cancer Research, London)	Circulating tumour DNA diagnostics in the NHS
12:20	12:35	Steven Hair (Newcastle University)	Utilising long-read sequencing approaches to detect structural variants of clinical significance
			childhood cancer
12:35	12:50	Ania Piskorz (CRUK Cambridge Institute, University of Cambridge)	Unlocking the potential of FFPE cancer specimens in predicting response and effect of cytoto therapy
12:50	13.05	Nicholas Timpson (University of Bristol)	Exome Sequencing of UK Birth Cohorts
13:05		Photo, Lunch and Poster Session II	Exame sequencing of on birth control
14:00		Epigenetics/Human & Clinical Genomics	Chair: Ania Piskorz, CRUK Cambridge Institute University of Cambridge
14:00		Areeba Patel (University of Heidelberg)	Methylation based classification of diagnostically relevant tumour classes
14:25	14:50	Alex de Mendoza (Queen Mary University of London)	Early Origins of Eukaryotic DNA Methylation Pathways
14:50	15:05	Hannah Trivett (University of Liverpool)	Clinical metagenomics can resolve pathogens to strain-level identification direct from stool
15:05	15:20	Aimee Hanson (University of Bristol)	Considering confounding in rare variant genome wide association studies
15:20		Silver Sponsor Talk	Pacific Biosciences: The power of high accuracy sequencing. Game-changing sequencing
15:20	10.00	Coffee Break	capabilities
15:30			Chair Mark Land Habrary Children
16:00		Bioinformatics & Machine Learning in Genomics	Chair: Matt Loose, University of Nottingham
16:00	16:25	Rhydian Windsor (Oxford Nanopore)	Generative Modelling of Nanopore Signals
16:25	16:50	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 Readfish
17:20		Silver Sponsor Talk	Opentrons: Accessible, touch-screen enabled automation for hands-off NGS library preparati

Parallel Ses	sion B - LT2		
Start (GMT)	Finish (GMT)	Presenter	Presentation Details
09:30	11:05	Evolutionary Genomics I	Chair: Jordi Paps Montserrat (University of Bristol)
09:30	09:55	Peter WH Holland (University of Oxford)	Darwin Tree of Life project: Evolutionary applications
09:55	10:10	Filipe Castro (CIIMAR/FCUP)	A Domino Effect? Of loss, duplication and novelty in a transition to the sea
10:10	10:35	Marta Farré-Belmonte (Kent)	The role of 3D chromosome folding in mammalian genome evolution
10:25	10:40	Tom Jenkins (Exeter)	Plastic versus adaptive responses to climate in barbastelle bats
10:40		Gold Sponsor Talk	Element Biosciences
11:00	11:30	Coffee Break	
11:30		Microbes and Microbiomes I	Chair: Kate Baker, University of Cambridge
11:30		Alexandre Almeida (University of Cambridge)	Meta-analysis of the uncultured gut microbiome reveals a novel keystone biomarker of health
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		Winnie Lee (Imperial College London)	Genomic population study of bloodstream Klebsiella spp. in 2020 in Southwest, UK
12:35		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 Birmingham
14:00		Alan Walker (University of Aberdeen)	Questioning the foetal microbiome illustrates pitfalls of low-biomass microbial studies
14:25		Edward Cunningham-Oakes (University of Liverpool)	Metatranscriptomics improves the laboratory diagnosis of infectious intestinal disease from huma
14:50		Alice Nisbett (Quadram Institute, Norwich) Kirsty Sands (University of Oxford)	The genomic switcheroo: characterising genome rearrangements within typhoidal infections
15:05			Providencia in the fly microbiome acting as a reservoir of blaNDM carriage: A threat in the dissemination of antimicrobial resistance and infection?
15:20		Steven Rudder (Quadram Institute, Norwich)	Genomic diversity of non-typhoidal Salmonella found within patients suffering from gastroenteritis in Norfolk, UK
15:35		Coffee Break	
16:00		Evolutionary Genomics II	Chair: Sion Bayliss, University of Bristol
16:00		Sandra Álvarez Carretero (University College London)	Bayesian methods to infer evolutionary timelines when deep divergences are present and large genomic datasets used
16:25		Jialin Wei (Bristol)	Convergent Genome Evolution In The Conquest Of Land By Animals
16:50		Chris Clarkson (QMUL/UCL)	Characterising structural variation in known pathogenic STRs across genetic ancestries, germ-line instability events and diseased cohorts
17:05	17:20	Sarah Quigley (Kent)	Investigating mechanisms of genomic rearrangement in the human genome
	Dinner - Bri Finish (GMT)	stol Harbour Hotel, The Sanisovo Room, Weds Event	17th [TICKETED]
18:30	19:30	Arrival Drinks	
19:30	00:00	Banquetting Menu Dinner	
Thursday 1	8th July 202	4 - LT1 (Morning)	
Start (GMT)	Finish (GMT)	Presenter	Presentation Details
08:30	09:30	Coffee and Pastries	
09:30	11:05	Single Cell Genomics	Chair: Lia Chappell, University of Cambridge
09:30	09:55	Jimmy Lee (Wellcome Trust, Sanger)	Shared molecular vulnerabilities of human cortical neurons in C9ORF72 Amyotrophic Lateral Sclerosis
09:55	10:20	Rebecca Berrens (University of Oxford)	Study transposable elements at single molecule level in single cells to understand their role in gene regulation.
10:20	10:35	Christos Proukakis (UCL)	The somatic CNV landscape of the Parkinson's disease brain at single cell resolution
10:35	10:50	Simon Cockell (Newcastle University)	Geographically weighted methods for spatial transcriptomics data analysis
10:50	11:00	Silver Sponsor Talk	Parse Biosciences: Smash the Limits of Single Cell Sequencing with Parse Biosciences
11:00	11:30	Coffee Break	
11:30		Keynotes	Chair: Michael Quail, Wellcome Sanger Institute
11.30	12:30	Reynotes	Chair. Wilchael Quali, Wellcome Sanger Institute
11:30		Deborah Williamson (UK Health Security Agency)	TBD
	12:00	•	