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12:00 13:30 Registration, Lunch and Networking 13:30 14:30 Keynotes Chair: Nick Lom 13:30 14:00 Lucy Burkitt-Gray (UK Biobank) Massive-scale who 14:00 14:30 Richard Durbin (University of Cambridge) Insights from high 14:30 16:00 Evolving Technologies 1 Chair: Michael of Ch	ole genome sequencing: Insights from the UK Biobank quality genome sequencing across the tree of life Quail, Wellcome Sanger Institute and Product Roadmap Update Quail, Wellcome Sanger Institute Quail, Wellcome Sanger Institute UG100: A flexible, low-cost, scalable sequencing solution
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08:30 09:30 Coffee and Pastries	
nrallel Session A - LT2 rt (GMT) Finish (GMT) Presenter Presentation Detail	ile.
-	, University of Liverpool
09:30 09:55 Alex Cagan (University of Cambridge) TBC	
09:55 10:20 Gary Barker (University of Bristol) Unlocking hidden g	genetic diversity in hexaploid bread wheat
10:20 10:35 Francisco Rodriguez-Algarra (Queen Mary, University of Ribosomal DNA Co	ppy 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 de	etect chromosomal reciprocal translocations using long-read sequencing
10:50 11:00 Silver Sponsor Talk New England Biola	bs
11:05 11:30 Coffee Break	
	Coxhead, Newcastle University
	•
	ality NGS clinical service
11:55 12:20 Mike Hubank (Institute of Cancer Research, London) TBC	and the second s
	sequencing approaches to detect structural variants of clinical significance
childhood cancer	
	ential of FFPE cancer specimens in predicting response and effect of cytoto
Cambridge) therapy	
	g of UK Birth Cohorts
13:00 14:00 Lunch and Poster Session II	
14:00 15:30 Epigenetics/Human & Clinical Genomics Chair: Ania Pisk	orz, CRUK Cambridge Institute University of Cambridge
14:00 14:25 Areeba Patel (University of Heidelberg) Methylation based	l classification of diagnostically relevant tumour classes
	karyotic DNA Methylation Pathways
	mics can resolve pathogens to strain-level identification direct from stool
	unding in rare variant genome wide association studies
15:20 15:30 Silver Sponsor Talk Pacific Biosciences	
15:35 16:00 Coffee Break	
	se, University of Nottingham
16:00 16:25 Rhydian Windsor (Oxford Nanopore) TBC	
16:25 Leonid Chindelevitch (Imperial College London) Insights into AMR	from large-scale genotypic and phenotypic data analysis
16:50 17:05 Tim Downing (Pirbright Institute) Pangenome variati	ion graph analysis reveals insights into livestock poxviruses
17:05 17:20 Rory Munro (University of Nottingham) Adaptive Sampling	on PromethION: Soaring Close to the Sun with Icarust and Readfish
17:20 17:30 Silver Sponsor Talk Opentrons	

Darallel Coo	cion P. ITA		
	sion B - LT2	Dracontor	Presentation Details
	Finish (GMT)		Chair: Jordi Paps Montserrat (University of Bristol)
09:30 09:30		Evolutionary Genomics I	. , , , ,
09.50		Peter WH Holland (University of Oxford) Filipe Castro (CIIMAR/FCUP)	Darwin Tree of Life project: Evolutionary applications 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
10:10		Tom Jenkins (Exeter)	Plastic versus adaptive responses to climate in barbastelle bats
10:40		Gold Sponsor Talk	Element Biosciences
11:05		Coffee Break	Liement biosciences
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		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	14:50		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		Sandra Álvarez Carretero (University College London)	Bayesian methods to infer evolutionary timelines when deep divergences are present and larg genomic datasets used
16:25	16:50	Jialin Wei (Bristol)	Convergent Genome Evolution In The Conquest Of Land By Animals
16:50	17:05	Chris Clarkson (QMUL/UCL)	Characterising structural variation in known pathogenic STRs across genetic ancestries, germ-li instability events and diseased cohorts
17:05		Sarah Quigley (Kent)	Investigating mechanisms of genomic rearrangement in the human genome
17:20	17:35		TBC
onference	Dinner - Bri	stol Harbour Hotel, The Sanisovo Room, Weds	17th [TICKETED]
	Finish (GMT)		
18:30		Arrival Drinks	
19:30	00:00	Banquetting Menu Dinner	
hursdav 1	8th Julv 202	4 - LT1 (Morning)	
	Finish (GMT)	` ",	Presentation Details
08:30		Coffee and Pastries	
09:30		Single Cell Genomics	Chair: Lia Chappell, University of Cambridge
09:30		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	11:05	Sponsor Talk	Parse Biosciences
11:05	11:30	Coffee Break	
11:30	12:30	Keynotes	Chair: Michael Quail, Wellcome Sanger Institute
11:30		Deborah Williamson (UK Health Security Agency)	TBC
11.50			
12:00		Matt Brown (Genomics England)	Improving Diagnostic Rates for Rare Diseases – the Genomics England program