Tuesday, April 21		
Start Time	**End Time**	
8:30 AM	6:00 PM	Registration
ISCB-UK Student Symposium		
8:45 AM	**9:00 AM**	**Student Symposium Welcome**
9:00 AM	**9:15 AM**	34: PISTACHIO: Proteomics-Constrained Negative Binomial Matrix Factorisation for Spatial Transcriptomics Deconvolution (Esra Büşra Işık)
9:15 AM	**9:30 AM**	137: MultiCOCor: identifying multiple clustering structures in high-dimensional data (Jack Hodgkinson)
9:30 AM	**9:45 AM**	125: DeepPathway: Predicting Pathway Expression from Histopathology Images (Muhammad Ahtazaz Ahsan)
9:45 AM	**10:00 AM**	175: Leveraging open-access data in ChEMBL to explore emerging drug modalities (Emma Manners)
10:00 AM	**10:15 AM**	18: Predicting drug resistance across cancer types using multi-omics transfer learning (Semih Alpsoy)
10:15 AM	**10:30 AM**	110: Cell-specific rewiring of GPCR signalling networks: A systems pharmacology perspective (Shanlin Rao)
10:30 AM	**10:45 AM**	152: multiDEGGs: single or multi-omic differential networkanalysis for biomarker discovery and feature engineering for predictive modelling (Elisabetta Sciacca)
10:45 AM	**11:00 AM**	2: Detection of recombination in Arabidopsis centromeres (Jacob González Isa)
11:00 AM	**11:30 AM**	**COFFEE BREAK**
11:30 AM	**11:45 AM**	53: Pushing the limits of AlphaFold3: detecting DNA-binding domains at scale (Francesco Costa)
11:45 AM	**12:00 PM**	62: Identification and characterization of Polyurethane-Degrading Enzymes from MGnify Metagenomes (Joel Roca-Martinez)
12:00 PM	**12:15 PM**	61: Metagenomic analysis identifies co-occurrance of Desulfovibrio and curli genes in Parkinson´s patients (Fang Chi)
12:15 PM	**12:30 PM**	179: Exploring Feature Representations for Cancer-Associated sORF Prediction in Non-coding RNA (Fabiana Rodrigues de Goes)
12:30 PM	**12:40 PM**	**Student Symposium Closing Remarks**
		Tuesday, April 21
12:00 PM	**1:30 PM**	**NETWORKING LUNCH**
1:30 PM	**1:45 PM**	**Conference Welcome (including BBSRC)**
1:45 PM	**2:30 PM**	**Keynote #1: Rob Finn**
2:30 PM	**2:45 PM**	107: ImmunoMatch learns and predicts cognate pairing of heavy and light immunoglobulin chains (Dongjun Guo)
2:45 PM	**3:00 PM**	148: DNA Language Models for Efficient Non-Coding Variant Effect Prediction (Megha Hegde)
3:00 PM	**3:15 PM**	6: ESMRank: A ranking-based AI framework for interpretableprediction of protein variant effects Topic (Riccardo Arnese)
3:15 PM	**4:30 PM**	**CAFFEINATE & CONNECT WITH POSTERS**
4:30 PM	**4:45 PM**	167: Leveraging protein language models and a scoring function for indel characterisation and transfer learning (Oriol Gracia I Carmona)
4:45 PM	**5:00 PM**	98: Mapping the space of protein binding sites by integrating sequence-based protein language models with pocket-context (Jim Horne)
5:00 PM	**5:15 PM**	101: Are We Teaching Computational Biology Backwards? A Call for a Renaissance of Critical Thinking in the GenAI Era (Eva Caamano Gutierrez)
5:15 PM	**6:00 PM**	**Panel: AI Roundtable Discussions**

Wednesday, April 22		
Start Time	**End Time**	
8:30 AM	6:00 PM	Registration
9:00 AM	**9:20 AM**	**Panel: AI Roundtable Discussion Outcomes and Highlights**
9:20 AM	**9:35 AM**	121: Integrating Predicted and Experimental Structures: The Role of AlphaFold DB in Modern Structural Biology (Joseph Ellaway)
9:35 AM	**9:50 AM**	25: Phyre2.2: Predicting protein structure and protein/ligandinteractions prediction in the AlphaFold era Michael J E Sternberg)
9:50 AM	**10:05 AM**	51: FAIRDOM-SEEK: Platform for FAIR data and research assetmanagement (Munazah Andrabi)
10:05 AM	**10:20 AM**	**Royal Society Journals & Open Access Publishing** **(Jessica Miller)**
10:20 AM	**10:25 AM**	193: A foundation model to study the molecular principles of codon usage in eukaryotes (Susanne Bornelöv)
10:25 AM	**10:30 AM**	145: A Sneaky Peek at the CRUK Data Hub (Frances Pearl)
10:30 AM	**10:35 AM**	158: Pandemic-scale phylogenetics (Nicola De Maio)
10:35 AM	**11:40 AM**	**CAFFEINATE & CONNECT WITH POSTERS**
11:40 AM	**11:55 AM**	117: Federated Learning Approaches to Biomedical Knowledge Discovery (Gamze Gursoy)
11:55 AM	**12:10 PM**	4: Mind your own binding: computational prediction ofparatope-epitope interfaces (Montader Ali)
12:10 PM	**12:25 PM**	43: Chemistry Aware AI Model for Interpretable siRNAEngineering and Activity Prediction (Aparajita Karmakar)
12:25 PM	**12:30 PM**	73: Training a force field for proteins and small molecules from scratch (Joe Greener)
12:30 PM	**12:35 PM**	12: Allosteric Communication and Kinetic Regulation in Membrane Protein (Hossein Batebi)
12:35 PM	**12:40 PM**	17: Integrating protein structure and population genomic data to detect diversifying selection related to immunity (Leonie J. Lorenz)
12:40 PM	**1:05 PM**	**BioFAIR: Building a Digital Research Infrastructure for UK Life Sciences**
1:05 PM	**2:15 PM**	**NETWORKING LUNCH WITH POSTERS**
2:15 PM	**2:30 PM**	118: REMAG: recovery of eukaryotic genomes from metagenomes using contrastive learning (Daniel Gómez Pérez)
2:30 PM	**2:45 PM**	174: Protal: Ultra-fast metagenomic profiling and strain-resolved analysis (Joachim Fritscher)
2:45 PM	**3:00 PM**	157: Detecting signatures underlying the composition of biological data (Anthony Duncan)
3:00 PM	**3:05 PM**	146: COTAN: scRNA-seq comprehensive workflow based on gene correlations (Silvia Giulia Galfre')
3:05 PM	**3:10 PM**	139: Fine-tuning Oxford Nanopore basecalling models for high-accuracy repeat expansion calling (Rugare Maruzani)
3:10 PM	**3:15 PM**	160: ProQuest: A Large Language Model Application on the Uniprot Protein Sequence and Annotation Database (Melike Akkaya)
3:15 PM	**3:35 PM**	**COFFEE BREAK**
3:35 PM	**3:50 PM**	27: NetREm: Network Regression Embeddings reveal cell-type transcription factor coordination for gene regulation (Saniya Khullar)
3:50 PM	**4:05 PM**	30: Evolutionary conservation and rewiring of enhancer-promoterconnectivity across mammals (Stephen Rong)
4:05 PM	**4:20 PM**	159: FlowSign – A NextFlow Workflow for Network Orientation andRegulatory Sign Prediction Using Prior Knowledge and Omics Data (Benjamin Dominik Maier)
4:20 PM	**4:35 PM**	68: Phylogenetically structured machine learning allows forinterpretable virus-host prediction models (James Herzig)
4:35 PM	**4:40 PM**	111: InterProScan 6: a modern large-scale protein functionannotation pipeline (Matthias Blum)
4:40 PM	**4:45 PM**	A Sneaky Peek at the CRUK Data Hub (Frances Pearl)
4:45 PM	**5:30 PM**	**Keynote #2: Syma Khalid**
5:30 PM	**6:00 PM**	**Conference Closing Remarks**