

# Conference Schedule – VIBE/ICBG 2024



Time	Thursday, 5 December 2024	
10:00-10:30	<b>Registration &amp; Coffee/Tea</b>	
10:30-11:00	<b>Registration &amp; Opening Address</b>	
11:00-12:00	<b>Keynote</b>	
11:00-12:00	<b>Dr Davide Cirillo</b>	<i>Synthetic Data in Biomedical Research: From Knowledge Discovery to Knowledge Generation</i>
<b>Session 1: Methods &amp; Algorithms</b>		
12:00-13:00	Michael Lynch	<i>Supervised multimodal demultiplexing outperforms conventional demultiplexing of scRNAseq</i>
12:00-13:00	Seyed Aghil Hooshmand	<i>Advancing Cancer Research through Integration of Liquid Biopsy Data in cBioPortal: Insights from the All-Ireland Cancer Liquid Biopsies Consortium (CLuB)</i>
12:00-13:00	Yezhao Zhong	<i>Adverse Drug Reaction Profile Prediction: Denoising, Signal Enhancement and Missing Row Imputation</i>
13:00-14:00	<b>Lunch &amp; Coffee/Tea</b>	
<b>Session 2: Cancer Genomics</b>		
14:00-15:00	Roofiya Koya	<i>Mechanistic insights into long noncoding RNAs through high resolution analysis of tumour mutations.</i>
14:00-15:00	Aideen McCabe	<i>Understanding Ovarian Cancer: Lessons Learned from Cells, Apps and Patients</i>
14:00-15:00	Hannah Nyarko	<i>Assessing the spatial patterns of immune and stromal cells for prognosis in early-stage ER+/HER2- Breast Cancer</i>
14:00-15:00	Micheál Ó Dálaigh	<i>Kinnex Long-Read Resequencing of Acute Myeloid Leukaemia Single-Cell RNA Samples for Improved Detection of Malignant Genomic Alterations</i>
15:00-16:00	<b>Keynote</b>	
15:00-16:00	<b>Dr Elisabeth Bik</b>	<i>Errors and Misconduct in Biomedical Research</i>
<b>Lightning Talks &amp; Gold Sponsor</b>		
16:00-16:30	Ahmad Alkhan	<i>Deep Learning approach for detecting and segmenting Perineural Invasion in Colon, Prostate, and Pancreatic cancers</i>
16:00-16:30	Stefanus Bernard	<i>Bioinformatics Refinement of CRISPR-Cas9 Knockout Screens Reveals Additional Genes Modulating Cellular Responses to CDC7 Inhibitors</i>
16:00-16:30	Catherine Higgins	<i>Clustering imbalanced functional data - enhancing the clustering accuracy of time-course gene expression data</i>
16:00-16:30	Pouya Motienoparvar	<i>A genetic network integrates regulation of the vegetative-reproductive phase transition in Arabidopsis thaliana</i>
<b>Poster Session &amp; Sponsors</b>		
16:30-17:30	Presenting: Odd Posters	
17:30	<b>Social Event</b>	

Time	Friday, 6 December 2024	
09:30-10:30	<b>Keynote</b>	
	<b>Prof Karen Miga</b>	<i>The Human Pangenome Project: Creating a Reference that Better Represents Human Global Genetic Diversity</i>
10:30-11:00	<b>Lightning Talks</b>	
	Elle Loughran	<i>Factors in the Development of Extreme Ploidy States in Cancer</i>
	Mariagiovanna Pais	<i>Exploring endocrine disrupting pathways using knowledge graph and network biology.</i>
	Anna Großbach	<i>Mapping Genetic Determinants of DNA Methylation Across Early Development</i>
	Emma Corley	<i>Associating Mood Symptom Severity with Subcortical Brain Volumes in Bipolar Disorder and Major Depressive Disorder using an Item Response Theory Model</i>
	Metin Yazar	<i>Unravelling Resistance Mechanisms to Synthetic Lethal Therapies in Cancer Through Protein-Protein Interaction Networks</i>
11:00-12:00	<b>Poster Session &amp; Sponsors</b>	
	Presenting: Even Posters	
12:00-13:00	<b>Session 3: Population Genetics &amp; Molecular Evolution</b>	
	Olivier Dennler	<i>Evaluating Sequence and Structural Similarity Metrics for Predicting Shared Paralog Functions</i>
	Sophie Matthews	<i>Variable gene copy number in cancer-related pathways is associated with cancer prevalence across mammals</i>
	Maria Eleonora Rossi	<i>Independent origins of spicules reconcile the evolutionary history of sponges (Porifera)</i>
	James McInerney	<i>panGPT: An AI transformer for generating large pangenome models.</i>
13:00-14:00	<b>Lunch &amp; Coffee/Tea</b>	
14:00-15:00	<b>Session 4: Metagenomics &amp; Pathogen Surveillance</b>	
	Kate Ryan	<i>Genomic identification and characterisation of novel bacterial species from Space Craft Assembly Clean Rooms</i>
	Emmet Campbell	<i>In silico phage-bacteria infection networks (PBINs) of Streptococcus suis reveal co-evolution patterns between host and prophage</i>
	Anna Tumeo	<i>Validation of a field-deployable automated DNA extraction system as a tool for assessment of microbial diversity in marine ecosystems</i>
	John Paul Wilkins	<i>Secrets in the Sewers - Revealing the hidden diversity of SARS-CoV-2 in Northern Irish wastewater</i>
15:00-15:30	<b>Coffee/Tea Break</b>	
15:30-16:30	<b>Session 5: Genomics of Health &amp; Disease</b>	
	Javier Villegas Salmerón	<i>Characterization of the mouse intra-amygdala kainic acid model at single-cell resolution reveals cell-type specific contributions to epilepsy phenotype</i>
	Sophia Heneghan	<i>The impact of copy number variants in diagnosis and severity of autosomal dominant polycystic kidney disease</i>
	Nicole Glendinning	<i>DNA Methylation in Vulnerability to Opioid Use Disorder</i>
	Karen Guerrero Vazquez	<i>Predicting Age and Identifying Aging-Related Genes from Muscle Gene Expression Data</i>
16:30-17:00	<b>Awards &amp; Close of Conference</b>	