2026 Cancer Bioinformatics Australia Symposium

8:00am	**Registrations Open**
8:45 - 9:00am	**Welcome & Acknowledgement of Country**
Session One - Cancer Genomics	
9:00 - 9:45am	**International Speaker: Wei Dai (University of Hong Kong)** "Elucidation of 3D Genome in Epstein-Barr Virus-associated Nasopharyngeal Carcinoma"
9:45 - 10:00am	**Siddharth Pruthi** "Whole-genome insights into KRAS-driven lung adenocarcinoma"
10:00 - 10:05am	**Kesong Wu** "A Transformer-Based Foundation Model for Large-Scale Representation Learning on Inferred Single-Cell CNV Profiles"
10:05 - 10:10am	**Jue Jiang** "Under-represented populations and geographies reveal new signatures of somatic mutations"
10:10 - 10:25am	Lightning Talks
10:25 - 10:55am	**MORNING TEA**
Session Two - Clinical Bioinformatics	
10:55 - 11:25am	**National Speaker: Roxane Legaie (Children's Cancer Institute)** "The Translational Last Mile: Taking Bioinformatics from Bench to Bedside"
11:25 - 11:40am	**David Goode** "Tumour fitness as an evolutionarily-informed biomarker for more effective stratification of patients by clinical outcomes in solid cancers"
11:40 - 11:55am	**Montana Spiteri** "Unravelling the cellular landscape of response and resistance in glioma"
11:55am - 12:00pm	**Kiran Gnana** "Tumour antigen landscape of Paediatric brain cancer"
12:00 - 12:05pm	**Navya Shukla** "Investigating the landscape of enhancer hijacking in paediatric cancer"
12:05 - 12:20pm	Lightning Talks
12:20 - 1:45pm	**LUNCH & POSTERS**
Session Three - Spatial and Multi-omics	
1:45 - 2:30pm	**International Speaker: Shyam Prabhakar (A*STAR, Singapore)** "Spatial omics reveals intra-tumor malignant cell diversity shaped by microenvironmental cues in colorectal cancer"
2:30 - 2:45pm	**Xiao Tan** "STimage: A Robust and Interpretable Deep Learning Framework for Predicting Spatial Gene Expression and Cell Types from Histology Images to Advance Digital Pathology"
2:45 - 3:00pm	**Zhaoxiang Cai** "Augmenting the Childhood Cancer Cell Map through Multi-Omic Data Synthesis and Predictive Modelling"
3:00 - 3:15pm	**Hao Nguyen** "Adaptive Integration of Heterogeneous Foundation Models to Find Histologically Predictable Genes in Breast Cancer"
3:15 - 3:45pm	**AFTERNOON TEA**
Session Four - Long-Read Sequencing & Transcriptomics	
3:45 - 4:15pm	**National Speaker: Quentin Gouil (Olivia Newton-John Cancer Research Institute)** "Long-read transcriptomics in cancer research: promise, pitfalls, and practical applications"
4:15 - 4:30pm	**Jia Wei Tan** "LINDTIE: Identify Aberrant Transcripts in Long-Read RNA Sequencing"
4:30 - 4:45pm	**Fayrouz Hammal** "Decoding Transposable Element-Driven Regulatory Programs in Melanoma Using Long-Read Sequencing"
4:45 - 5:00pm	**Sean Burnard** "Single-read metrics resolve cell-to-cell methylation heterogeneity from bulk nanopore data"
5:00 - 5:05pm	**Lijun Xu** "Long read sequencing reveals in cis genomic alterations associated with BRCA1 promoter methylation instability in high grade serous ovarian carcinoma"
5:05 - 5:10pm	**Diya Prabhuram** "Quantifying transcriptomic fidelity of cancer cell models from Latent Embeddings extracted from Variational Autoencoders (LEVAE)"
5:10 - 5:15pm	**Kirill Orlov** "RAIN: AI-based software for pathway activity prediction and analysis"
5:15 - 5:30pm	**Closing Remarks and Prizes**
5:30pm - Late	**DRINKS & NETWORKING**