

20TH ANNIVERSARY CONFERENCE 30 October – 2 November 2022 Novotel Twin Waters Sunshine Coast, Queensland

Sunday 30 O	ctober	Minyama 1	
0830-1800	Conference Registration Opens	Arrivals Lounge	
0900-1600	Pre-conference workshop (Registration requi	red) Minyama 1	
	Viral Metagenomics with Hecatomb		
1700-1800	0-1800 Opening Oration Panel		
	20 years of Australasian Genomics and where to from here?		
	Mederator		
	Moderator Associate Prof Ruby C Y Lin, The Westmead Institute for Medical Research		
	Panellists		
	Prof Sean Grimmond, The University of Melbo	ourne	
	Prof Vanessa Hayes, University of Sydney		
	Prof John Mattick, University of New South W	ales	
1800-2000	Welcome Reception & Exhibition	Wandiny Room	
	Welcome to Country		
	Kerry Neill, Director, Tribalink		
Monday 31 C	October	Minyama 1	
0730-1730	Registration desk opens	Arrivals Lounge	
	With thanks to our Name Badge and	\propto IDT	
	Lanyard sponsor	ATED DNA TECHNOLOGIES	
	Exhibition opens	Wandiny Room	
0800-1535	Enjoy barista made coffee with thanks to	umina	
0830-0845	Official Welcome, Conference Opening and A	cknowledgment to Country	
	Conference Convenors		
	Associate Prof Ruby C Y Lin Dr Nic Waddell		
	Professor Marcel Dinger (AGTA President)		
Session 1	The solution of the solution o		
	Aedical Genomics		
	nair A/Prof Mark Cowley & Ashton Curry-hyde		
0845-0925	Keynote Presenter		
	Ending diagnostic, prognostic, and treatment odysseys: Transforming data into		
	clinically actionable knowledge		
	Dr Elizabeth Worthey, The University of Alaba	ma at Birmingham	
0925-0950	National Speaker		
	Pan-cancer proteomic map of 949 human cell lines		
	Dr Qing Zhong, The University of Sydney		

0950-	Platinum Sponsor Presentation		
1010	Illumina technology improvements driving genomic insights		
	Dr. Anthony Beckhouse, Illumina		
	illumin	a°	
1010 -	Morning refreshments & exhibition	Wandiny Room	
1040	With thanks to our Morning Australian Biomolecular		
	Refreshments sponsor National Resource Facility		
1040-	National Speaker		
1105	Genomic basis for prostate cancer health disparities		
	Professor Vanessa Hayes, University of Sydney		
1105-	The Q-IMPROvE (Queensland- IMplementation of PRecision Oncolo	gy in brEast	
1120	cancer) pilot study		
	Dr Amy Mccart Reed, The University of Queensland.		
1120-	Evolving genomic complexity unveiled in ctDNA analysis of melano	ma patients	
1135	Dr Sandra Fitzgerald, University of Auckland		
Lightning	Presentations Session 1	Minyama 1	
Chair & Co	o-chair Dr Tamsin Robb & Huiwen Zheng		
1135-	Identifying Metabolic Shift Gene Signature Pattern in The Wnt-Asso	ciated	
1138	Epithelial-Mesenchymal Plasticity Of The PMC42 Breast Cancer Mo		
	Prof Erik Thompson, Queensland University of Technology		
1138-	Having our Cake and Eating it Too: Building Speculative Research in	to Clinical	
1141	Genomics Studies		
	Dr Mark Pinese, Children's Cancer Institute		
1141-	Application of Long read sequencing (LRS) in cancer genomics		
1144	Lingchen Liu, QIMR Berghofer Medical Research Institute		
1144-	Predicting cell-type specific combinatorial binding of neuronal trans	scription factor	
1147	network by Deep Learning		
	Gunjan Dixit, Australian National University		
1147-	Value of RNA-sequencing in precision medicine expands beyond fu	sion detection	
1150	Chelsea Mayoh, Children's Cancer Institute		
1150-	A novel reference architecture for multi-party federation: enabling	ioint analysis of	
1153	large-scale clinical-genomic data across distributed Trusted Researc	• •	
	Kent Zaitlik, Lifebit Biotech Limited		
1153-	Flexible and efficient handling of nanopore sequencing signal data	with slow5tools	
1156	Hiruna Samarakoon, Garvan Institute of Medical Research		
1156-	Shotgun microbial profiling reveals geo-ethnic disparities in aggressive prostate		
1159	cancer		
	Dr Kaitao Lai, The University of Sydney		
1159-	Sequencing By Binding (SBB) Shows Superior Sensitivity and Specifi	city of Detection	
1202	of Low Frequency Variants from ctDNA		
	Dr James Miller, PacBio		
1205-	Lunch & Exhibition	Wandiny Room	
1305			
1303	National Resource		
	sponsor University Facility		
Cassier 2		N 41	
Session 2	Animal Conomias	Minyama 1	
	Animal Genomics		
chair & Co	o-chair A/Prof Mirana Ramialison & Jillian Hammond		

1305- 1308	Welcome from Platinum Sponsor		
	Dr. Anthony Beckhouse, Illumina	nina®	
	IIIUII	ша	
1308-	Keynote Presenter		
1348	Animal Genomics Enables Selection and Dissemination of Improved Livestock		
	Prof Alison van Eenennaam, University of California, Davis		
1348-	Multi-omics analysis of O. corymbosa reveals the biosynthesis of anti-cancer		
1403	metabolites		
	Dr Irene Julca, Nanyang Technological University		
1403-	The Australian Dingo is an Early Offshoot of Modern Breed Dogs		
1418	A/Prof Matt Field, James Cook University		
PhD runne			
1418-	Assessing the effects of date and sequence data in phylodynamics		
1425	Leo Featherstone, University of Melbourne		
1425-	A novel non-invasive method to infer fetal genotype in pregnancy		
1432	Carol Wang, University of Newcastle		
1435-	Afternoon refreshments & Exhibition & Poster Session	Wandiny Room	
1535	With thanks to our Afternoon Australian Biomolecular		
	Refreshments sponsor National Resource Facility		
Session 3		Minyama 1	
Computati	onal Biology, Bioinformatics, Statistical Genetics		
Chair & Co	-chair Dr Mark Pinese & Lochlan Fennell		
1525	National Speaker		
1535-	National Speaker		
1535- 1600	Viral extraction, sequencing, and identification with hecatomb		
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1600	Viral extraction, sequencing, and identification with hecatombProfessor Rob Edwards, Flinders UniversityKeynote PresenterThe Origin and Evolution of COVID-19: A Genomic Perspective		
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1600 1600- 1640 1640- 1655	 Viral extraction, sequencing, and identification with hecatomb Professor Rob Edwards, Flinders University Keynote Presenter The Origin and Evolution of COVID-19: A Genomic Perspective Professor Eddie Holmes, The University of Sydney Machine learning to predict BRCA1 and BRCA2 variant pathogenicit world cancer genomic profiling data Dr Olga Kondrashova, QIMR Berghofer Medical Research Institute Mining the Cancer Contaminome for MAGs – Intra-tumoural Microl Signatures are associated with Patient Mortality in Head and Neck S 	biome	
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1600 1600- 1640 1655 1655- 1710 1800- 2000	 Viral extraction, sequencing, and identification with hecatomb Professor Rob Edwards, Flinders University Keynote Presenter The Origin and Evolution of COVID-19: A Genomic Perspective Professor Eddie Holmes, The University of Sydney Machine learning to predict BRCA1 and BRCA2 variant pathogenicit world cancer genomic profiling data Dr Olga Kondrashova, QIMR Berghofer Medical Research Institute Mining the Cancer Contaminome for MAGs – Intra-tumoural Microl Signatures are associated with Patient Mortality in Head and Neck S Carcinomas George Bouras, The University of Adelaide Student Night – Registered Students Only 	biome Squamous Cell Sola Restaurant Deck	
1600 1600- 1640 1655 1655- 1710 1800-	 Viral extraction, sequencing, and identification with hecatomb Professor Rob Edwards, Flinders University Keynote Presenter The Origin and Evolution of COVID-19: A Genomic Perspective Professor Eddie Holmes, The University of Sydney Machine learning to predict BRCA1 and BRCA2 variant pathogenicit world cancer genomic profiling data Dr Olga Kondrashova, QIMR Berghofer Medical Research Institute Mining the Cancer Contaminome for MAGs – Intra-tumoural Microl Signatures are associated with Patient Mortality in Head and Neck S Carcinomas George Bouras, The University of Adelaide 	biome Squamous Cell Sola Restaurant	

0815-1800	Registration desk opens	
		Arrivals Lounge
	Exhibition opens	Wandiny Room
0830-1535	Enjoy barista made coffee with thanks to	
Session 4		
Indigenous an	d Population Genomics	
Chair & Co-cha	air Prof Vanessa Hayes & Dr Andrew Lonsdale	
0855-0900	Welcome to Day 2	Minyama 1
0900-0925	National Speaker	
	Empowering Indigenous Australians in Genomic Medicine	
	Professor Alex Brown, Australian National University	
0925-0950	National Speaker	
	Indigenous Australian genomic variation reveals deep populatio	n structure
	Professor Stephen Leslie, The University of Melbourne	
0950-1005	Influence of geographical variations on the structure of human g	gut microbiome
	Gauraw Kumar, Indian Institute of Science Education and Researc	h Kolkata, India
1005-1020	A long-read nanopore sequencing platform for Indigenous genor	mics
	Dr Andre Reis, Garvan Institute of Medical Research	
1020-1035	A Population Genomics Approach to Prostate Cancer in Diverse	Geo-ethnic
	Samples	
	Dr Weerachai Jaratlerdsiri, The University of Sydney	
1035-1105	Morning Refreshments and Exhibition	Wandiny Room
	With thanks to our Morning Refreshments sponsor	
Session 5		Minyama 1
Functional and	d Clinical Genomics	· ·
Chair & Co-cha	air Prof Robert Edwards & Dr Berenice Talamantes Becerra	
1105-1145	Keynote Presenter	
	Long-read sequencing in cancer and rare disease genomics – the	Genomics
	England experience	
	Prof Matt Brown, Genomics England	
1145-1210	National Speaker	
	Human Cardiac Organoids for Functional Genomics	
	Professor James Hudson, QIMR Berghofer	
1210-1225	Genome Wide Mapping of Physiologically Relevant i-Motifs Usir	ng an i-Motif
	Specific Nanobody	
	Dr Samuel Ross, University of New South Wales	
1225-1240	Tracking transcriptional evolution in cancer using circulating tumour DNA Dr Dineika Chandrananda, Peter MacCallum Cancer Centre	
1240-1255	Identifying integrations of a clinical gene therapy vector with isling Dr Suzanne Scott, Children's Medical Research Institute	
1255-1355	Lunch & exhibition	Wandiny Room
	With thanks to our Lunch sponsor	

Session 6 Microbial Met	agenomics nair Dr Nouri Ben Zakour & George Bouras	Minyama 1
1355 – 1358	Welcome from Platinum Sponsor	
1000 1000	Dr Bicheng Yang, BGI Australia	华大BGI
1358-1438	Keynote Presenter The Use of Targeted Microbial Therapeutics to Improve Health – Are We There Yet? Professor Georgina Hold, University of New South Wales	
1438-1443	Beer Presentation Jack Black, Your Mates Brewing Co.	
1443-1458	Screening high-risk paediatric cancer for microbial DNA using whole-genome- sequencing data Sam El-kamand, Children's Cancer Institute	
1458-1513	Drug resistance prediction with reference graphs Dr Michael Hall, University of Melbourne	
1513-1528	The importance of deciphering the bacterial epitranscriptome and utilising native long-read RNA sequencing Dr Miranda Pitt, University of Melbourne	
1528-1623	Exhibition Viewing, Poster Session & Afternoon refreshments With thanks to our Afternoon Refreshments sponsor LIFE SCIENCES	Wandiny Room
Session 7 Viral Genomic Chair & Co-ch	s air Dr Nic Waddell & Dr Jessica Mar	Minyama 1
1625-1645	Platinum Sponsor Presentation WGS for newborn screening of an unselected 10k children co Dr. Mingyan Fang, BGI Research Asia-Pacific 华大BC	
1645-1700	Improving gene therapy delivery by optimizing the capsid and DNA packaging of AAVs Dr Anne Klein, CSIRO	
1700-1715	What can we learn from the human panvirome? Dr Michael Roach, Flinders University	
1715-1745	AGTA Annual General Meeting	
1830-2200	Conference Dinner Dress Code: Casual Proudly sponsored by	Arrivals Lounge

Wednesday 2	November		
0830-1500	Registration desk opens	Arrivals Lounge	
0830-1330 Exhibition opens		Wandiny Room	
	Enjoy barista made coffee with thanks to		
Session 8			
Single Cell and	d Spatial Genomics		
Chair & Co-ch	air Lachlan Coin & Berivan Temiz		
0855-0900	Welcome to Day Three	Minyama 1	
0900-0940	0900-0940 Keynote Presentation		
	Setting up single cell experiments: lots of considerations		
	Associate Professor Luciano Martelotto, University of Adelaide		
0940-1005	National Speaker		
	Designing and analysing complex single cell experiments		
	Professor Alicia Oshlack, Peter MacCallum Cancer Centre		
1005-1020	A single-cell and spatially resolved atlas of human breast cancer	S	
	Dr Daniel Roden, Garvan Institute of Medical Research		
1020-1050	Morning refreshments & Exhibition	Wandiny Room	
1050-1105	Multi-omic machine learning approach for survivability prediction	on in breast	
	cancer		
	Khoa Tran, QIMR Berghofer Medical Research Institute		
1105-1120	MultiGO: A multi sample approach for gene expression pathway	enrichment	
	analysis		
	Dr Devika Ganesamoorthy, The University of Queensland		
1120-1135	Genomics through a HoloLens: Cancer Evolution in Augmented I	Reality	
	Dr Tamsin Robb, University of Auckland		
• •	sentations Session 2	Minyama 1	
1135-1138	air Dr Sandra Fitzgerald & Dr Venkateswar Addala	anatic hasis of	
1135-1138	Assembling high-quality sea snake genomes to investigate the g	enetic basis of	
	aquatic adaptation		
1138-1141	Jillian Hammond, Garvan Institute of Medical Research		
1130-1141			
1141-1144	Dr Kira Xiaohuan Sun, BGI The Spatial Biology Revolution: multi-omic whole-transcriptome GeoMx		
1141-1144	profiling combined with sub-cellular resolved Spatial Molecular		
	Michael Rhodes, NanoString Technologies	inaging	
1144-1147			
1144 1147	cell biology applications with the Singulator™ 100 system		
	Dr Janette Tong, TrendBio		
1147-1150 Spatially Resolved Transcriptomics Exploration in Virtual Reality		,	
	Denis Bienroth, Murdoch Children's Research Institute		
L150-1153 Characterization of Botrylloides diegensis whole body regeneration thro		ion through	
	single-cell RNA-sequencing		
	Berivan Temiz, University of Otago		
1153-1156	Hey Siri, how can I use Deep Learning for Variant Calling in my F	amilial Whole	
Genome Sequencing Studies?			
	Macabe Daley, Children's Cancer Institute		
1156-1159			
	Ashton Curry-hyde, University of New South Wales		
1200-1305	Lunch & Exhibition	Wandiny Room	

Session 9		Minyama 1	
Emerging Tec	hnology		
Chair & Co-ch	air Professor James Hudson & Dr Michael Roach		
1305-1310	Virtual Introduction		
	Dr Chris Mason, Weill Cornell Medicine, and WorldQuant Initiative for Quantitative Prediction Due to unforeseen circumstances Dr Chris Mason will present a short speech virtually.		
1310-1345	Closing Invited Speaker Presentation		
	The Microbial Waypoints on our Path to Mars		
	Dr. Braden Tierney, Cornell University		
1345-1410	National Speaker		
	Spatially Resolved Transcriptomics For Deciphering Gene Regulatory Networks in Heart Development and Disease		
	A/Prof Mirana Ramialison, Murdoch Children's Research Institute		
1410-1425	Identifying candidate circulating RNA biomarkers for coronary artery disease		
	deep RNA-Sequencing in human plasma		
	Dr Anna Pilbrow, University of Otago		
1425-1440	Decode the Stable Cell Communications Based on Neuropeptide-Receptor		
	Network in 36746 Tumor Cells		
	Dr Min Zhao, University of The Sunshine Coast		
1440-1510	Awards Ceremony, 2023 Conference Launch and Conference Clos	e	

The AGTA Conference reserves the right to amend or alter any advertised details relating to dates, program and speakers if necessary and without notice, as a result of circumstances beyond their control. All attempts will be made to keep any changes to an absolute minimum.