

Start	End	Event	Speaker	Title
8:00	8:50	COMBINE Registration		
8:50	9:00	Symposium Welcoming Address		
9:00	9:15	Session 1	Andrew H. Buultjens	Comparative genomics suggest <i>Mycobacterium ulcerans</i> migration and expansion is aligned with rise of Buruli ulcer in south-east Australia.
9:15	9:30	Session 1	Jiayuan Huang	Comparative analysis of phosphoethanolamine transferases involved in polymyxin resistance across ten clinically relevant Gram-negative bacteria
9:30	9:45	Session 1	Dharmesh Bhuvu	A dynamical systems simulator to evaluate methods for inferring co-expression networks
9:45	10:00	Session 1	Kirsti Paulsen	Optimising intrinsic protein disorder prediction for short linear motif discovery
10:00	10:15	Session 1	Andrew Pattison	Predicting the outcome of breast cancer using novel RNA-Seq analysis
10:15	10:30	Session 1	Harriet Dashnow	STRetch: detecting and discovering pathogenic short tandem repeat expansions
10:30	11:00	Morning Tea		
11:00	11:15	Session 2	Gustave Severin	Multi-omic Characterisation of a Novel Xylose Metabolising Strain of <i>Saccharomyces cerevisiae</i>
11:15	11:30	Session 2	Eddie Ip	VPOT: a customisable tool for the prioritisation of annotated variants.
11:30	11:45	Session 2	Nhi Hin	Transcriptomic and proteomic characterisation of a zebrafish model of familial Alzheimer's disease
11:45	12:00	Session 2	John Salamon	Visualisation and analysis of spatially-resolved transcript data using InsituNet
12:00	12:15	Session 2	Gabriel Foley	SeqScrub: A web tool for automatic cleaning of FASTA file headers.
12:15	12:35	Session 2	Fast Forward talks	
12:35	13:15	Lunch		
13:15	13:45	Poster Session		
13:45	14:00	Group Photo - Meet out front of SAHMRI		

14:00	14:15	Session 3	Pei Qin Ng	Using genome-wide variants to determine the historical migration of chickens through South East Asia to the Pacific Islands
14:15	14:30	Session 3	Andrian Yang	Cloud-based single-cell transcript reconstruction using Falco
14:30	14:45	Session 3	Yuen Ting Wong	Genome-wide study of 10,539 cancer samples reveals 27 novel associations between mutational processes and somatic driver mutations
14:45	15:00	Session 3	Wei Lu	Genome-wide SNPs modelling improved genetic risk prediction for psoriasis
15:00	15:15	Session 3	Greg Bass	Spatial statistics analysis of super-resolution protein co-localization data
15:15	17:00	Career Panel and Afternoon Tea		
17:00	17:05	Awards and Closing Address		
17:00	18:00	ABACBS Registration		
18:00	19:15	ABACBS Keynote Lecture and award presentations		
19:15	22:00	COMBINE & ABACBS Social Events	COMBINE - The Edinburgh Castle ABACBS ECR - Duke of York ABACBS Professional - Cumberland Arms Hotel	