

Time	Topic	Presenter
1:30 - 1:35	Welcome and introduction	Nigel Laing – Centre for Medical Research, University of Western Australia and Harry Perkins Institute of Medical Research Hamish Scott – Genetic and Molecular Pathology, Centre for Cancer Biology
SESSION 1: Chair - Nigel Laing		
1:35 – 1:50	Diagnostic RNA-seq pipelines.	Karin Kassahn – Technology Advancement Unit, SA Pathology
1:50 – 2:05	RNA studies extend diagnostic yield by 20% in a paediatric neuromuscular cohort of 220 families.	Sandra Cooper – Kids Neuroscience Centre, University of Sydney
2:05 – 2:25	Using RNA-seq to determine treatment, monitor disease and classify risk in childhood leukaemia.	Alicia Oshlack – Bioinformatics, Murdoch Children's Research Institute
2:25 – 2:45	Incorporation of RNA-seq with whole exome sequencing and copy number variation reveals a higher yield of clinically relevant variants than whole exome sequencing alone.	Susan Branford – Genetic and Molecular Pathology, Centre for Cancer Biology
2:45 – 3:05	Transcriptome sequencing-based genetic testing of cardiomyocytes derived from patients with hypertrophic cardiomyopathy.	Richard Bagnall - Bioinformatics and Molecular Genetics, Centenary Institute
3:05 – 3:20 Afternoon Tea		
SESSION 2: Chair - Hamish Scott		
3:20 - 3:35	RNA-sequencing: understanding the data.	Fathin Faiz – Neurogenetics, Diagnostic Genomics, PathWest
3:35 - 3:55	RNA-seq data analysis in the context of ALL.	Jacqueline Rehn – South Australian Health and Medical Research Institute
3:55 - 4:10	Machine learning and cloud computing is empowering RNA-seq analysis.	Natalie Twine – Cloud-Computing Bioinformatics, CSIRO
4:10 - 4:25	Implementation in clinical laboratories.	Natalie Thorne – Bioinformatics, Melbourne Genomics Health Alliance
4:25 - 5:00	Discussion & action plans.	Nigel Laing Hamish Scott
5:00 Workshop close		