



BA2009 **AusBiotech**
BIOINFORMATICS AUSTRALIA 2009

National Conference: 29–30 October, 2009. Melbourne Convention and Exhibition Centre
www.ausbiotech2009.com.au/bioinformaticsaustralia2009

PROGRAM*

Wednesday, 28 October 2009	
2:00-6:00pm	WORKSHOP Generic Model Organism Database (GMOD) Speaker: Dave Clements, US National Evolutionary Synthesis Center (NESCent)
Thursday, 29 October 2009	
8:00-9:00am	Registration
9:00-9:10am	Bioinformatics Australia 2009 Conference Opening, Conference Chair: Phoebe Chen
9:10-10:00am	Title: Bioinformatics for personalized onco-genomics. Keynote Speaker: Steve Jones, Canada's Michael Smith Genome Sciences Centre
10:00-10:30am	Title: Getting more from RNA-seq Invited Speaker: Matthew Wakefield, WEHI
Symposium One: Systems Biology, Medical and Agricultural Applications	
10:30-10:50am	The combination of clinical factors and genetic markers can improve cancer prognosis <u>Kim-Anh Le Cao</u> , Emmanuelle Meugnier and <u>Geoffrey J. McLachlan</u>
10:50-11:10am	Genomic scale prioritisation of drug targets: the TDR Targets database <u>Maria A. Doyle</u> , Fernan Agüero, Matthew Berriman, Santiago Carmona, Gregory J. Crowther, Christiane Hertz-Fowler, Solomon Nwaka, Stuart A. Ralph, David S. Roos, Dhanasekaran Shanmugam and Wesley C. Van Voorhis
11:10-11:30am	Break and Poster Sections

Symposium Two: Emerging Areas, including Metabolomics and Immunoinformatics	
11:30-11:50am	Informatics challenges for high-throughput mass spectrometry based protein identification and quantification <u>Eugene Kapp</u>
11:50-12:10pm	Meta-analysis of gene expression microarrays with unique genes <u>Fan Shi</u> , Christopher Leckie and Adam Kowalczyk
12:10-12:30pm	Correlation measures in gene regulatory network discovery: a different perspective <u>Armita Zarnegar</u> , Peter Vamplew and Andrew Stranieri
12:30-12:50pm	Developing strategies for using high-throughput sequencing for viral agent discovery <u>Dieter Bulach</u> and David Boyle
13:00-14:00pm	Lunch and Poster Sections
Symposium Three: Computation, Methods and Tools in Bioinformatics	
14:00-14:20pm	Biobase knowledge library TM - an integrated interface for the combined analysis of gene expression data and gene regulatory knowledgebase to identify upstream biomarkers in the biological networks <u>Jesintha Maniraja</u> , Edgar Wingender, Olga Kel-Margoulis, Jennifer Hogan and Alexander Kel
14:20-14:40pm	PyMS: a python toolkit for processing gas chromatography-mass spectrometry metabolic data <u>Andrew Isaac</u> , Lewis Lee, Woon Wai Keen, Tim Erwin, Qiao Wang, David P De Souza, Ute Roessner, James Pyke, Luke Hodkinson, Bill Appelbe, Ramamohanarao Kotagiri, Richard E. H. Wettenhall, Robert Trengove, Malcolm J. McConville, Antony Bacic and Vladimir A. Likić
14:40-15:10am	Network construction and functional enrichment toolbox <u>David Wood</u> , Dominique Gorse and Melissa Davis
15:10-15:30pm	Web-based Cross -omics Platform Analysis Environment <u>Matthew Bellgard</u>
15:30-16:00pm	Break and Poster Sections
16:00-17:00pm	Forum 1: The impact of next-generation sequencing on bioinformatics in Australia Panel Members: <u>Terry Speed</u> , <u>Steve Jones</u> , <u>Torsten Seemann</u> , <u>Jen Taylor</u>
17:00-17:50pm	Forum 2: New opportunities in bioinformatics career development Panel Members: <u>Tim Littlejohn</u> , <u>Mark Ragan</u> , <u>Matthew Bellgard</u>

*Conference Program as at 20 October – Subject to change

17:50-19:00pm	Poster Presentations Sections
19:00pm	Conference Dinner
Friday, 30 October 2009	
9:00-10:00am	Title: Analysis of ChIP-Seq data Keynote Speaker: Terry Speed, University of California, Berkeley and WEHI,
10:00-10:30am	Title: PyCogent: an integrated framework for computational genomics Invited Speaker: Gavin Huttley, ANU
Symposium Four: Comparative Genomics and Evolution	
10:30-10:50am	An integrative bioinformatics predictor of protein sub-cellular localisation in malaria <u>Ben J. Woodcroft</u> , Kristie-Lee Scanlon, Maria A. Doyle, James Bailey, Terry P. Speed and Stuart A. Ralph
10:50-11:10am	Comparative bioinformatics of the lactation system <u>Christophe Lefèvre</u> , Philip Church, Adam Wong, Karensa Menzies, Julie Sharp and Kevin Nicholas
11:10-11:30am	Break and Poster Sections
Symposium Five: Proteomics and Structural Bioinformatics	
11:30-11:50am	A statistical study of protein function and subcellular localisation in interaction in and metabolic networks <u>Adrian Cootes</u> , Gaurav Kumar and <u>Shoba Ranganathan</u>
11:50-12:10pm	Inference of phylogenetic trees from protein structural information <u>Yuslina Zakaria</u> , Merridee Wouters, Bret Church and <u>Bruno Gaeta</u>
12:10-12:30pm	An Integrated Approach to iTRAQ Analysis <u>Penghao Wang</u> , Yee Hwa, Jean Yang and Jonathan Arthur
12:30-12:50pm	Conformational transitions associated with different redox states of di-thiol pairs Samuel W. Fan, Richard A. George, Naomi L. Haworth, <u>Jason Y. Liu</u> and <u>Merridee A. Wouters</u>
12:50-12:55pm	Conference Closing
13:00-14:00pm	Lunch

Posters Presentations:

- P1. RELATING UNKNOWN AND KNOWN METABOLITES IN THE METABOLOMIC ANALYSIS OF LEISHMANIA PARASITES. Amsha Nahid, Eleanor Saunders, David De Souza, Antony Bacic, Malcolm McConville and Vladimir Likic.
- P2. CLUSTERING-BASED IDENTIFICATION OF CLONALLY-RELATED IMMUNOGLOBULIN GENE SEQUENCE SETS. Zhiliang Chen, Andrew M. Collins and Bruno A. Gaëta.
- P3. TRANSPORTDB V2.0 - TO GENOMICS AND BEYOND! Liam Elbourne, Qinghu Ren, Daniel Johnson, Karl Hassan, Sasha Tetu and Ian Paulsen.
- P4. NOVEL DNA CHARACTERISTICS FOR THE PRELIMINARY BINNING OF A METAGENOME. Isaam Saeed, Saman Halgamuge, Arthur Hsu and Sen-Lin Tang.
- P5. SYSTEMS LEVEL ANALYSIS OF THE Wnt/ β -CATENIN PATHWAY IN MAMMALIAN CELLS. Chin Wee Tan, Bruce Gardiner, Antony Burgess and David Smith.
- P6. COMPARISON OF USING FULL SCAN VERSUS CENTROID DATA IN LC-MS ANALYSIS. Moshe Olshansky, Thusitha Rupasinghe, Damien Callahan, Ute Roessner, Malcolm McConville, Antony Bacic and Vladimir Likic.
- P7. SUPERVISED LEARNING FOR THE DETECTION OF TRANSCRIPTION FACTOR BINDING SITES. Justin Bedo, Geoff Macintyre, Izhak Haviv and Adam Kowalczyk.
- P8. EXP-PAC: A WEB BASED PACKAGE FOR THE COMPARATIVE ANALYSIS OF MICROARRAY DATA. Philip Church, Andrzej Goscinski, Adam Wong and Christophe Lefèvre.
- P9. AN OPTIMISER OF SHORT READ SEQUENCE ASSEMBLY BASED ON THE VELVET ASSEMBLER. Simon Gladman.
- P10. An R tool for the statistical analysis of label-free shotgun proteomics data. Dana Pascovici, Tim Keighley, Mehdi Mirzaei, Gayani Gammula, Paul Haynes and Brett Cooke.
- P11. DE-NOVO SEQUENCE ASSEMBLY AND CHARACTERIZATION OF THE COMPLEX GENOME OF FIVE BACS FROM RHIPICEPHALUS MICROPLUS. Paula Moolhuijzen, Rudi Appels, Ala Lew-Tabor, Manuel Rodriguez Valle, Jessica Morgan, Felix Guerrero, Adam Hunter, David Schibeci and Matthew Bellgard.
- P12. ANALYSING THE STABILITY OF GENE-SET SIGNATURES. Gad Abraham, Adam Kowalczyk, Izhak Haviv and Justin Zobel.
- P13. Taking a Sequence Homology Perspective in Identifying Recurrent Copy Number Aberrations in SNP Array Data. Gerard Wong, Christopher Leckie and Adam Kowalczyk.
- P14. COMPARATIVE ANALYSIS OF REGULAR AND ALTERNATIVE SPLICE SITE STRENGTH IN SEVERAL EUKARYOTIC SPECIES. A K M Abdul Baten, Matthew Bellgard and Saman Halgamuge.
- P15. From high-throughput sequencing read alignments to confident, biologically relevant conclusions with Nsoni. Paul Harrison and Torsten Seemann.
- P16. METABOLITE MASS SPECTRAL DATABASE OF METABOLOMICS AUSTRALIA. Saravanan Dayalan, David De Souza, James Pyke, Jeremy Hack, Meagan Mercurio, Ricarda Fenske, Shana Jacob, Robert Trengove, Brad Power, Tamas Szabo, Nick Takayama, Adam Hunter, Matthew Bellgard, Marcus Herderich, Lars Nielsen, Matthew Timmins, Ute Roessner, Malcolm J McConville, Antony Bacic and Vladimir Likic.
- P17. CRITICAL ISSUES FOR AN AUTOMATED ANNOTATION PIPELINE FOR PROKARYOTIC GENOMES. Karon Ryan, Paula Moolhuijzen, Byron Hammond, David Schibeci, Mark O'Shea, Roberto Barrero, Adam Hunter and Matthew Bellgard.

- P18. “Forbidden” disulfides: their role as redox switches. Merridee A. Wouters, Richard A. George and Naomi L. Haworth.
- P19. Application of the Gentrepid candidate gene prediction system to genome-wide association studies. Sara Ballouz, Jason Liu, Erdahl Teber, Diane Fatkin and Merridee Wouters.
- P20. BENCHMARKING TOOLS FOR MAPPING MILLIONS OF SHORT READS, SNP CALLING AND INDEL DETECTION. Roberto Barrero, Zayed Albertyn, Colin Hercus, Adam Hunter and Matthew Bellgard.
- P21. EST-PACHPC: A WEB BASED PACKAGE FOR EST ANNOTATION AND PROTEIN SEQUENCE PREDICTION IN HIGH PERFORMANCE COMPUTING. Adam Wong, christophe lefèvre, Andrzej Goscinski and Philip Church.
- P22. Freckle: An improved visualisation approach for heuristics dot-matrix genome analysis. Crispin Wellington, Adam Hunter and Matthew Bellgard.
- P23. PBWeb: An information management system for plant breeding. Adam Hunter, Bevan Buirchell, Andrew Macgregor, Robyn McLean, Iain Barclay, Craig Smith, Rudi Appels and Matthew Bellgard.
- P24. Mining Blowout Pattern in Multiple Data Streams in Genomics Context. Tingting Wang and Feng Chen.
- P25. Mining Genomic Databases for Regulatory Signals. Amit Kumar, Pragati Sharma, Mark Tizard, Robert Moore and christophe lefèvre.
- P26. BIOINFORMATICS RESOURCE TO CAPTURE, INTEGRATE AND ANALYSE DIVERSE DATA TYPES. Paula Moolhuijzen, Karon Ryan, Ala Lew-Tabor, Adam Hunter, David Schibeci and Matthew Bellgard.
- P27. Repetition-based Compression of Large DNA Datasets. Shanika Kuruppu, Bryan Beresford-Smith, Thomas Conway and Justin Zobel.
- P28. ARACHNOSERVER: A DATABASE OF PROTEIN TOXINS FROM SPIDERS. David Wood, Tomas Miljenović, Shuzhi Cai, Robert Raven, Quentin Kaas, Pierre Escoubas, Volker Herzig, David Wilson and Glenn King.
- P29. TRANSCRIPTOME WIDE HIGH THROUGHPUT BIOINFORMATICS PIPELINE FOR VACCINE CANDIDATE IDENTIFICATION. Paula Moolhuijzen, Ala Lew-Tabor, Manuel Rodriguez Valle, Felix D. Guerrero, Adam Hunter, David Schibeci and Matthew Bellgard.
- P30. Visualizing Next Generation Sequence Data with GBrowse and SAMtools. Dave Clements, Scott Cain, Nicholas Stiffler, Elizabeth Perry, Paul Hohenlohe, William Cresko, Brendan Bohannon, Heng Li and Lincoln Stein.
- P31. A PIPELINE FOR DESIGNING PCR PRIMERS TO DISTINGUISH BETWEEN SIMILAR GENOMES. Stephen Du, Kashyap Uppuluri and Bruno Gaeta.
- P32. IMPROVING STRUCTURE-BASED PREDICTION OF BINDING AFFINITY IN PEPTIDES BOUND TO THE MHC. Webber W.P. Liao and Jonathan W. Arthur.
- P33. A SNP DETECTION PIPELINE FOR 454 SEQUENCE DATA USING MOSAIK FOR READ MAPPING PLUS 454POLYBAYES FOR SNP CALLING. Charlotte Anderson, Vishal Gupta, Ben Hayes and Keith Savin.

- P34. Caution! Compositions! Can constraints on omics data lead analyses astray? David R Lovell, Warren Müller, Jen Taylor and Alec Zwart.
- P35. HYBRID METHODS FOR THE DETECTION OF SPLICE SITES IN THE HUMAN GENOME. A K M Abdul Baten and Saman Halgamuge.
- P36. Patterns across data sets: finding the cell origin of basal-like breast tumours. Di Wu, Elgene Lim, François Vaillant, Jane E Visvader, Geoffrey J Lindeman, Gordon K Smyth.
- P37. A COMPARISON OF OPEN SOURCE ASSEMBLY TOOLS FOR THE DENOVO ASSEMBLY OF BACTERIAL GENOMES USING ILLUMINA GAII DATA. John Davis, Deniz Koellhofer, Lien Le and Kelly Hanson, Annette McGrath.
- P38. Combinations of High Density Genotyping Microarray and HAPMAP consortia population data can restore missed or verify known ancestry genetic background of individuals used in a case control study. Rust Turakulov, Annette McGrath and Sue Forrest.