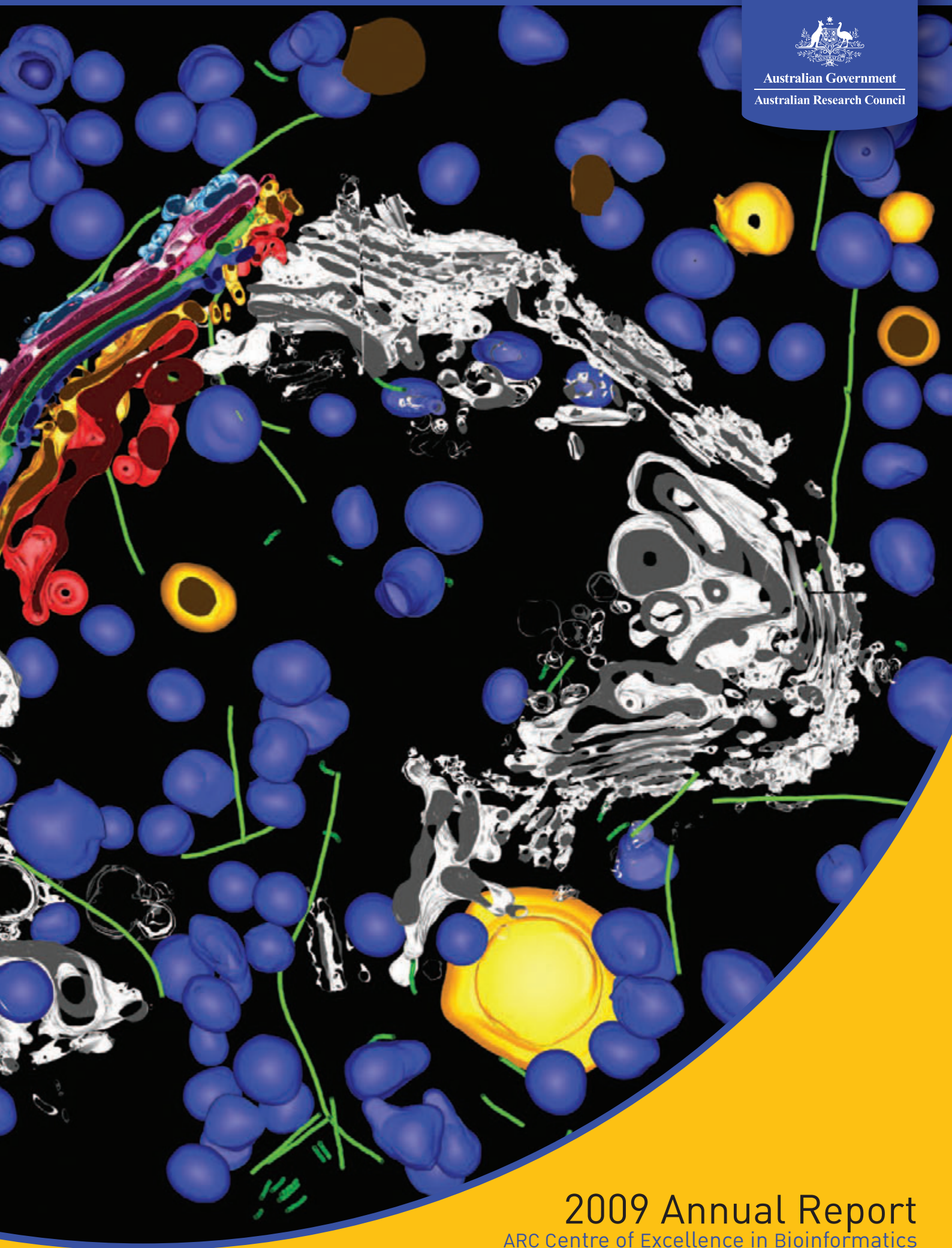
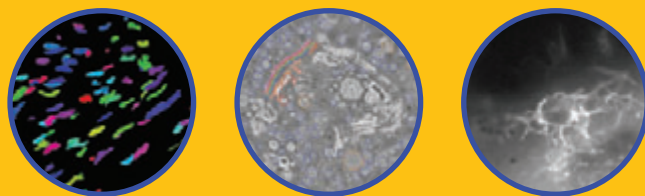




Australian Government
Australian Research Council



2009 Annual Report
ARC Centre of Excellence in Bioinformatics



The Australian Research Council (ARC) Centre of Excellence in Bioinformatics (ACB) is a multi-nodal interdisciplinary Centre that uniquely brings together genomic and post-genomic bioinformatics, mathematics, statistics, systems analysis and experimental phenomics to produce a deep understanding of how information in the genome is transformed into structure and function in the mammalian cell.

www.bioinformatics.org.au

Table of Contents

Chair's Foreword	2	Key Performance Indicators	38
Director's Review and Highlights	3	1. Research findings and competitiveness	39
Organisation and Governance	5	Publications	39
Organisational chart	5	Quality of publications	39
Advisory Board	6	Number of publications	39
Research Committee	10	Patents and trademarks	39
Director	10	Invitations to address and participate in conferences	40
Chief Investigators	10	International conferences	40
Partner Investigators	15	National conferences	42
Special advisor	16	Invitations to visit leading international laboratories, major research groups and centres	42
Strategic partnership	16	Commentaries about the Centre's achievements	43
Information infrastructure	16	Evidence of interdisciplinary linkages within the Centre	43
Centre Manager	16	2. Research Training and professional education	44
Research Assistants	16	Recruitment	44
Postdoctoral Fellows / Research Officers	17	Professional/technical training and advanced career development	44
Masters/PhD students	17	Seminar/Symposium hosted and/or sponsored by ACB	44
Honours students	18	Second Australasian High Content User Group Meeting	44
International interns	18	2009 Winter School in Mathematical and Computational Biology (6–10 July 2009)	44
Undergraduate research trainees and volunteers	19	2009 ACB Annual All-Hands Meeting (18–19 November 2009)	45
Visiting scholars, associates	19	Other research and training and professional education	45
Strategic Direction (2008-2010)	20	Postgraduate and undergraduate courses in the Centre's area	45
Vision	20	Outreach	46
Mission	20	3. International, national and regional links and networks	47
Aims	20	Visitors	47
Objectives	20	International visitors	47
Capabilities — core technologies and infrastructure	20	National visitors to one or more ACB nodes	47
Research Programs	21	Collaborative national and international workshops and exchanges	48
Program 1 – The Visible Cell®: linking genome and phenome	22	Other research linkages	49
1.1 Generation of subcellular localisation data in mammalian cells	22	Membership on national and international professional committees	51
1.2 Project and data management for Visible Cell®	23	Research projects with international partners	51
1.3 Data analysis and knowledge discovery in very large biological network databases	25	4. End-user links	53
Program 2 – Phenotype-informed discovery of networks and systems	27	Commercialisation activities	53
2.1 Computational discovery and modelling of gene-regulatory networks	27	Government, industry and business briefings	53
2.2 Differential expression of genes towards pathway discovery	29	Trained/ing in technology transfer and commercialisation	53
2.3 Discovery and modelling of RNA-based regulatory networks	30	Public awareness programs	53
Program 3 – Modelling dynamic cellular processes	31	5. Organisational support	54
3.1 Mathematical modelling of genetic regulatory networks and biochemical pathways	31	New organisations recruited to or involved in the Centre	54
3.2 Modelling and visualising biological processes in complex spatial environments	32	Infrastructure	54
Program 4 – Algorithms for graphs and networks	33	Annual cash contributions from other organisations 2008–2010	55
4.1 Discrete optimisation and graph clustering	33	Annual in-kind contributions: collaborating organisations 2008–2010	55
4.2 Optimisation-based approaches to large systems	34	6. National benefit	56
4.3 External-memory algorithms for analysis of massive graphs	36	Measures of expansion of Australia's capability in the priority area(s)	56
		Appendix 1: Publications	58
		Appendix 2: Financial Statement	66



I am pleased to be able to introduce you to the 2009 Annual Report of the ARC Centre for Bioinformatics ("ACB"). This report outlines the second year of ACB's three-year extension as an ARC Centre of Excellence.

During the year, the ACB Advisory Board welcomed two new members: Professor Maree Gleeson, Director of the Hunter Medical Research Institute, and Professor Max Lu, Deputy Vice-Chancellor (Research) at The University of Queensland. Professor Lu replaced one of the founding members of the Advisory Board, Professor David Siddle, who retired from The University of Queensland early in the year.

2009 was a year of consolidation for ACB. After the Centre was awarded a three-year extension by ARC in 2007 and upgraded to an ARC Centre of Excellence, the Centre has focused on further building its existing research portfolio and on reinforcing the wide-ranging capabilities and interests of its Investigators and their research teams across both existing and new interdisciplinary research programs, as well as between its various geographical nodes, including original Centre members Australian National University, Deakin and Newcastle Universities, and The University of Queensland, as well as new members Macquarie University, The University of Auckland, and the University of Tennessee. Additionally, collaborations with others outside the Centre's membership have grown further, as the co-authorship of grants and research publications, listed later in this annual report, clearly demonstrates.

Research conducted by members of ACB has continued to grow the Centre's international reputation. High-level individual recognition of key Centre members provides highlight examples, including the following:

- Professor Michael Fellows was based in Europe for much of 2009 in support of his Alexander von Humboldt Fellowship.
- Meanwhile, Partner Investigator Professor Allen Rodrigo was appointed Director of the US National Evolutionary Synthesis Centre.
- Professor Kevin Burrage continued his joint appointment at Oxford University as Professor of Computational Systems Biology.
- Professor John Mattick was awarded the Julian Wells Medal at the Lorne Genome Conference. This award was made in recognition of his leadership in the development of genomics in Australia, and of his long association with the conference itself.
- Postdoctoral fellow Dr Shev MacNamara was awarded a 2010 Fulbright Postdoctoral Scholarship, which he will take up at MIT to investigate the application of mathematical and computational principles to single-molecule DNA technologies.

As reported last year, Australia became an associate member of the European Molecular Biology Laboratory (EMBL) in 2008 with the formation of EMBL Australia in which The University of Queensland is a foundation member. In 2009, ACB Director Professor Mark Ragan and his colleagues were able to secure Commonwealth funding for a new National Computational Infrastructure Specialised Facility in Bioinformatics, and for the EMBL Australia EBI Mirror.

ACB is very proud of its continuing high-impact publication record. During the calendar year, ACB members published 113 peer-reviewed papers in category C1 journals. Of the 104 appearing in journals with ISI impact factors, 66% appeared in journals with an impact factor (IF) ≥ 3.0 , while 36% had an IF ≥ 5.0 . Most notably, 8.6% of the total appeared in journals with an IF ≥ 10.0 and impressively, 61% of these 113 articles were co-authored with overseas collaborators.

ACB continued its well-recognised training program and again conducted the Winter School in Mathematical and Computational Biology in 2009, which proved the most successful yet held: 201 registrants attended from 53 institutions based in five countries. Very strong positive feedback was received from Winter School participants.

ACB was able to co-fund the visit of scientific illustrator Graham Johnson (The Scripps Research Institute, La Jolla CA) to Australia to collaborate with Centre researchers Drs Brad Marsh and Nicholas Hamilton. While in Australia, Graham used his visually stunning animations to explain biomolecular and cell biological processes to Year 6 and 7 classes.

Readers should note that the ACB now enters its final year under the current Centres-of-Excellence program. Nonetheless we anticipate that 2010 will be another year of considerable achievement for the Centre as it develops its activities towards a future beyond the current ARC-funded program.



Dr Gregory R. Smith
Chair, Advisory Board
March 2010



2009 was a productive year for the ARC Centre of Excellence in Bioinformatics, and an important one in the development of Australian bioinformatics. I return to the broader Australian developments below.

The ARC Centre in Bioinformatics was proposed in the 2002-2003 Centres of Excellence funding round of the Australian Research Council (ARC). After interview, our bid for an ARC Centre of Excellence for Genome-Phenome Bioinformatics was placed onto a reserve list, and in April 2003 we were invited to revise our application for consideration for funding as a smaller ARC Centre. On 19 August 2003 the then Minister of Education, Science and Training announced funding for our renamed ARC Centre in Bioinformatics, and we began operation in November 2003. On 1 August 2006 we submitted a proposal for the extension of our Centre, and on 16 March 2007 the ARC announced that funding would be extended through 31 December 2010, and upgraded our status to that of an ARC Centre of Excellence.

The year 2008 was thus the first year of our extension, and in my introduction to last year's Annual Report I envisioned that the upcoming 2009 would be a year of consolidation and scaling-up. This has indeed been the case. In 2009 we concluded Project 4.1, built new external collaborations, and recruited key staff. Nine postgraduate theses were submitted. The quality of our research continued to be recognised by acceptance in leading journals including *Bioinformatics* (6), *Biological Reviews*, *Genome Research* (2), *Nature Genetics* (3), *Nature Reviews Genetics*, *Philosophical Transactions of the Royal Society of London B* (2), *PLoS Genetics*, *Proceedings of the National Academy of Sciences USA* (2), *Science*, and *Trends in Genetics*.

The strength of our Centre lies in our personnel. In 2009, Professor John Mattick was awarded the Julian Wells Medal of the Lorne Genome Conference, citing his outstanding contribution to our understanding of the organisation and expression of the genome. Professor Kevin Burrage continued his 50-50 appointment between Oxford University and The University of Queensland. A/Professor Phoebe Chen chaired the 2009 Bioinformatics Conference, held in association with AusBiotech 2009. Dr Nick Hamilton took scientific leadership of our Visible Cell® collaboration with the Institute for Molecular Bioscience, as this project attracted further international attention with papers in *Bioinformatics* (2009) and *Nature Methods* (2010). There was some change as well in our personnel. Professor Maree Gleeson (Director, Hunter Medical Research Institute) and Professor Max Lu (Deputy Vice-Chancellor Research, The University of Queensland) joined our Advisory Board, replacing Professors Barney Glover and David Siddle. Professor Allen Rodrigo was appointed Director of the US National Evolutionary Synthesis Centre, and accepted a joint appointment at Duke University; Allen will remain associated with The University of Auckland and with our ARC Centre of Excellence. Professor Mike Fellows concluded his formal association with our Centre; one of our original Chief Investigators, Mike's collaborations within the Centre resulted in publications with Professors Kevin Burrage, Mike Langston and Mark Ragan and their groups, and a funded grant with A/Professor Pablo Moscato. Mike also contributed to our annual Winter School in Mathematical and Computational Biology. Our 2009 Winter School was the most-successful yet, with registration exceeding 200 for the first time.

We were particularly delighted to see one of our young researchers, Dr Shearl MacNamara, recognised with the award of a Fulbright Postdoctoral Scholarship. For more on Shev's award and plans, please see page 37.

ARC has funded our Centre of Excellence through 2010. Following the advice of our Advisory Board, almost from the beginning of its extension we discussed its future beyond 2010. Taking into consideration the evolution of bioinformatics internationally and the increasing maturity of the field within Australia, we have decided not to apply for extension of our Centre as currently constituted. In a way this recognises our success. Let me draw an analogy: molecular biology emerged in the 1960s and 1970s from perspectives and technologies originating in physical and organic chemistry, biophysics, microbiology, virology and other fields. At first it was critical to bring together researchers from the component disciplines so they could develop common perspectives, language, approaches and technologies; this was accomplished through new centres, funding initiatives, training programs, conferences and other mechanisms. Generic methods were developed, most instruments became simpler to use, reagents and kits became available commercially, and core facilities were established around technologies too complex or expensive for individual researchers. At that point generic molecular biology centres had served their purpose, and their personnel, trainees and facilities nucleated the molecularisation of all areas of biology – from agriculture, veterinary science and resource management, through evolutionary biology, genetics, microbiology, botany and zoology, to cell and developmental biology, pharmacology, biomedical science, clinical medicine, anthropology, forensics and beyond. Without molecular biology there would be no modern biotechnology, genomics, or other "omic" sciences.

I see bioinformatics evolving along a similar path, albeit with some important differences. The informatisation of biology will have consequences no less-fundamental or far-reaching. The omic sciences in particular depend on high-throughput data capture and management, bioinformatic analysis, workflows and visualisation; bioinformatics will be part of personalised healthcare, management of every herd of livestock and every fish farm, monitoring of every endangered river and reef, real-time control of every wastewater treatment plant, and unimaginably more. Already bioinformaticians, including former students and postdocs from our ARC Centre of Excellence, are employed across the life-sciences sector in Australia.

Director's Review and Highlights



From left:
Dr Greg Smith, Prof. Marc Wilkins, Prof. Maree Gleeson, Prof. Mark Ragan, Prof. Ross Coppel, Prof. Peter Donnelly and Prof. Simon Eastaugh at ACB Advisory Board meeting on 24 July 2009.

As I promised in these pages last year, we are now finding out how robust and scalable our bioinformatics really is. The differences, as I see them, come about because molecular biology grew entirely out of the hard sciences, whereas bioinformatics is a synthesis among hard science (mostly bioscience), mathematics (including statistics), computer science and information technology (*i.e.* engineering), with a bit of logic (ontology) thrown in for good measure. It's a higher bar, a harder ask, and core bioinformatics groups may have a longer life expectancy than did their core molecular-biology counterparts a couple of decades ago.

Yet other key areas remain virgin territory for bioinformatics, most notably bio-imaging. Modern imaging technologies including high-throughput multi-photon fluorescence microscopy and electron tomography, and the coupling of imaging with robotic screening platforms has begun to deliver a flood of data not only comparable in magnitude to that from omic technologies, but of greater dynamic complexity and semantic richness. Unlike genomics (or even proteomics), imaging can provide a direct readout of phenotype: genomic and the other omic technologies are genome-out, imaging is phenome-in. Recall that we started as the ARC Centre of Excellence for Genome-Phenome Bioinformatics: our name is now shorter, but we haven't lost sight of our original *raison d'être*, and our research projects and Winter School sessions on scalable algorithms, bioinformatic workflows, advanced data integration, computational modelling and the Visible Cell® have positioned us (and more broadly, Australia) well. During 2009 some of our Investigators developed a proposal for a new, integrative ARC Centre of Excellence at the interface between bioinformatics and eukaryotic cell biology. I'm confident that our achievements will nucleate much else across the life sciences in Australia and beyond.

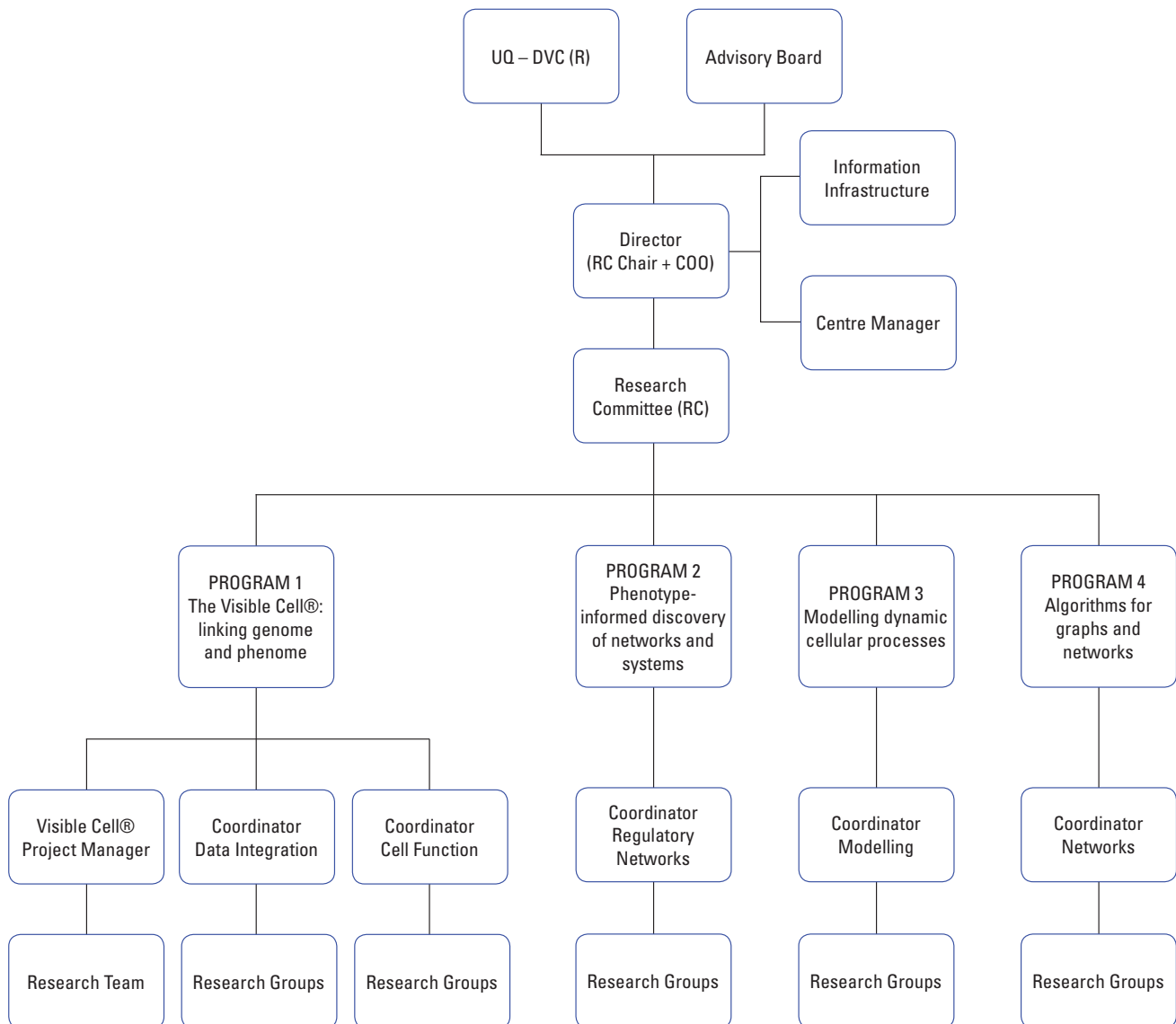
Indeed, 2009 was a year for recognition of bioinformatics more-widely across the research and innovation sector in Australia. Senior and junior positions were filled in the tertiary-education sector and in CSIRO. Australia announced its contribution to the International Cancer Genome Consortium, a project that would be inconceivable without scalable bioinformatics software and infrastructure. National Computational Infrastructure (NCI), the NCRIS/EIF successor to APAC, funded a Specialised Facility in Bioinformatics as one of (currently) two shoulder facilities complementing the National Supercomputing Facility. The Commonwealth Government, through Bioplatforms Australia and the Australian National Data Service, made initial funding available to establish the EMBL Australia EBI Mirror, a world-first initiative in conjunction with EMBL and EBI. The Victorian Life Science Computing Initiative proceeded toward implementation. At least four State Governments are supporting R&D initiatives with significant bioinformatic content. Challenges remain, but Australian governments and our R&D community have taken significant steps down the path.

On behalf of my colleagues in the ARC Centre of Excellence in Bioinformatics, I encourage you to peruse this report of our 2009 activities, and invite your comments.

Professor Mark Ragan
Director
ARC Centre of Excellence in Bioinformatics
March 2010

Organisation and Governance

Organisational Chart



Organisation and Governance

Advisory Board

The 9th Advisory Board meeting was held on Friday 24 July 2009. In 2009 due to the retirement of Prof. David Siddle from The University of Queensland and the departure of Prof. Barney Glover from the University of Newcastle, Prof. Max Lu, Deputy Vice-Chancellor (Research), The University of Queensland and Prof. Maree Gleeson, Director, Hunter Medical Research Institute (HMRI) were invited to be on the Advisory Board.

The members of the Advisory Board are:



Dr Gregory R. Smith (Chair)
Director
SciVentures Investments Pty Ltd
Melbourne VIC, Australia

Dr Greg Smith is a cofounder and director of SciVentures Investments Pty Ltd, the manager of the SciVentures Pre-Seed Fund. He also is a director or chair of four start-up companies into which SciVentures has invested. Greg has been a member of the Commonwealth Government's Industrial Research & Development Board and of its Advisory Council for Intellectual Property. He is the Board Chair for the Australian Microscopy and Microanalysis Research Facility, and an executive committee member of the Australasian Industrial Research Group. Greg was awarded the Maurice Holland award of Industrial Research Institute (Washington DC, USA) in 2000 for his "front-end innovation" at AlliedSignal (now Honeywell) and at Alcoa.



Prof. Ross Coppel
Director, Victorian Bioinformatics Consortium
Department of Microbiology
Monash University
Melbourne VIC, Australia

Prof. Ross Coppel is a recipient of the Glaxo Award for Advanced Research in Infectious Diseases and of an International Investigator award from the Howard Hughes Medical Institute. He is a named inventor on ten patents for inventions in malaria, primary biliary cirrhosis and novel antibiotics, and is internationally recognised for his work in these fields and in malaria genomics. Ross is Professor of Microbiology at Monash University, Director of the Victorian Bioinformatics Consortium, and co-founder of the biotechnology company Glykoz.

Organisation and Governance



Prof. Peter Donnelly FRS FMedSci

Director, Wellcome Trust Centre for Human Genetics
Professor of Statistical Science
University of Oxford, UK

Prof. Donnelly is Director of the Wellcome Trust Centre for Human Genetics and Professor of Statistical Science at the University of Oxford. Peter is a Fellow of both the Royal Society and Academy of Medical Sciences. He has been awarded the Mitchell Prize of the ASA and International Society for Bayesian Analysis, the Guy Medal in Silver of the Royal Statistical Society, and the Weldon Memorial Prize. His early work was in applied probability, particularly stochastic models in genetics, but for some years his research has focused on genetics. He played a major role in the HapMap project, an international collaboration that followed the Human Genome Project in studying genetic diversity in worldwide populations. He currently chairs the Wellcome Trust Case Control Consortium (WTCCC), a collaboration of over 200 UK scientists studying the genetics of 12 common human diseases, and its successor (WTCCC2). Other research interests include human population structure and histories, bacterial variation, human recombination, and the development of statistical methodology for modern genetics.



Prof. Simon Eastaer

Deputy Director
John Curtin School of Medical Research
The Australian National University
Canberra ACT, Australia

Prof. Simon Eastaer is Deputy Director of The John Curtin School of Medical Research at the Australian National University. His research is focused on how the evolutionary dynamic between humans and their environments has shaped the complexity of human biology, given rise to human diversity, and left a lasting impact on human health. Simon was founding co-Director of ANU's Centre for Bioinformation Science, Director of the Genetic Epidemiology Unit at the Menzies Centre for Population Health Research in Hobart, and Editor-in-Chief of *Molecular Biology and Evolution*. His work as a Trusted Intermediary in the Australian Industry Group's InnovationXchange Network involved business intermediation, innovation management and advising on R&D commercialisation. He has served on numerous committees and boards in both private and public sectors.



Prof. Maree Gleeson

Director
Hunter Medical Research Institute (HMRI)
New Lambton, NSW, Australia

Prof. Gleeson is the Director of the Hunter Medical Research Institute (HMRI), responsible for developing and implementing strategies to enhance health and medical research in the Hunter region and promoting the research undertaken by HMRI. HMRI is a partnership between the University of Newcastle, Hunter New England Health, and the Hunter community.

Prof. Gleeson was previously the Inaugural Director of Medical Research in the NSW Ministry for Science and Medical Research and has held a number of leadership roles within the Hunter's health sector, including Director of Immunology, Hunter Area Pathology Service.

Prof. Gleeson is an immunologist and conducts research with the University of Newcastle and the Australian Institute of Sport on the impact of respiratory infections in elite athletes. Other research focuses on the development of asthma and allergy in children and on Sudden Infant Death Syndrome.

In addition to serving on a number of Federal and State Government scientific advisory committees, Prof. Gleeson is a member of the Board of Directors of Alzheimer's Australia NSW and Research Australia, and is President of the International Society for Exercise Immunology.

Organisation and Governance



Prof. G.Q. Max Lu FTSE FIChemE

Deputy Vice-Chancellor (Research)
The University of Queensland
Brisbane QLD, Australia

Prof. Max Lu was appointed Deputy Vice-Chancellor (Research) in June 2009. Previously, he was Acting Deputy Vice-Chancellor (Research) from April 2009 and Pro-Vice-Chancellor (Research Linkages) from October 2008 in a 50 percent capacity while retaining his role as Director of the ARC Centre of Excellence for Functional Nanomaterials – a role he has held since 2003.

After completing his PhD, Prof. Lu spent three years in Singapore as Lecturer at Nanyang Technological University. Upon his return to The University of Queensland in 1994, he held the positions of Senior Lecturer, Associate Professor, Professor and Chair of Nanotechnology in Chemical Engineering. He was awarded his first ARC Federation Fellowship in 2003, and his second ARC Federation Fellowship in 2008.

Prof. Lu's research expertise is in nanoparticles and nanoporous materials for clean energy and environmental technologies. With over 390 journal publications in high-impact journals including *Nature*, *JACS*, *Angewandte Chemie-International Edition* and *Advanced Materials*, he is also co-inventor of 18 international patents. Prof. Lu is a highly cited researcher in chemical engineering and materials science with over 6600 citations (with h-index of 44). He has received numerous prestigious awards nationally and internationally including the Orica Award, RK Murphy Medal, Le Fevre Prize, ExxonMobil Award, IUMRS Young Scientist Award, Top 100 Most Influential Engineers in Australia (2004) and Top 50 Most Inspiring Chinese in the World (2006). He is an elected Fellow of the Australian Academy of Technological Sciences and Engineering, and a Fellow of IChemE.



Prof. Mark Ragan FLS

Director, ARC Centre of Excellence in Bioinformatics (*ex officio*)
Institute for Molecular Bioscience
The University of Queensland
Brisbane QLD, Australia

Prof. Lu formerly served as the DEST Research Quality Framework Chair of Engineering and Technology Panel 2007, on Expert Advisory Groups of the Prime Minister's Science, Engineering and Innovation Council (2004, 2005), and as ARC College of Experts Panel member (2002-2004). He has recently been appointed as Chair of the PMSEIC Thematic Cluster on Science as Engine for Innovation. He also serves as the current Chairman of IChemE Australia Board, and Director of the Board of the Australian Academy of Technological Sciences and Engineering. His other committee memberships include the Research and Investment Committee, Centre for Low Emission Technology, Advisory Board of CSIRO Flagship for Future Manufacturing, Uniseed Management Board of Directors, Management Board of the ARC Nanotechnology Network, and the Queensland China Council.

Prof. Mark Ragan joined IMB in 2000 after 28 years with National Research Council Canada, where he co-founded and developed programs in bioactive compounds, molecular biology, genomics and bioinformatics, including Canadian Bioinformatics Resource. With Prof. W. Ford Doolittle and Dr Robert Charlebois he received the largest single grant under the first Canadian genome program (CGAT) and sequenced *Sulfolobus solfataricus*. Since 2000, Mark has been actively involved in Australian bioinformatics including community-building, research, partnerships among institutions and across sectors, advanced training, awareness-raising with state and national government bodies, international partnerships and national infrastructure. He has served as Chair of the Executive group of the Association of Asian Societies of Bioinformatics (2008), and is a member of the Committee on Global Collaborations, European Life Sciences Infrastructure for Biological Information (ELIXIR) and the Steering Committee of Australian National Data Service. Under the overall theme of comparative and computational genomics, research in his group includes projects on the inference, cellular localisation and analysis of biomolecular-interaction networks, and applications of advanced bioinformatic and semantic web technologies to large-scale biomolecular, chemical and structural data especially in complex disease. His 150-plus peer-reviewed publications have attracted more than 4000 citations.

Organisation and Governance



Prof. Brandon Wainwright

Director
Institute for Molecular Bioscience
The University of Queensland
Brisbane QLD, Australia

In 2006 Prof. Wainwright was appointed Director of the Institute for Molecular Bioscience (IMB) at the University of Queensland, and before that was IMB's Deputy Director (Research). IMB, recognised nationally and internationally as one of Australia's leading centres for molecular bioscience research, has around 500 research staff and research students with an annual budget in the order of \$40M. Prof. Wainwright currently serves on a number of boards including those of the Australian Genome Research Facility, the Australian Phenomics Facility, and the Health and Medical Research Council of Queensland. In 2007 he was Chair of the DEST Research Quality Framework Panel 6.

Prof. Wainwright's major research focus is the use of genomic approaches to dissect the basis of common genetic disease. He led the team responsible for finding the origins of the often-fatal brain tumour, medulloblastoma, and he is also studying cystic fibrosis and basal cell carcinomas of the skin. Through the mapping and isolation of the genes which are responsible for these diseases, he has continued to follow-through on each to understand how the genetic defects lead to the disease. The ultimate aim of his work is to discover the genes which, when altered, cause the tumour cell to grow in an uncontrolled fashion. Ultimately this will provide validated targets against which potential therapeutics can be developed.



Prof. Marc Wilkins

Department of Biotechnology and
Biomolecular Sciences
University of New South Wales
Sydney NSW, Australia

Prof. Marc Wilkins developed the concept of the proteome and coined the term. He is author of more than 90 publications, and co-editor of two books. He is the Director of the NSW Systems Biology Initiative, a member of the Advisory Board of the Australian Proteomics Computational Facility (APCF) and the Management Committee of the Ramaciotti Centre for Gene Function Analysis. Marc is a Senior Editor of the journal *Proteomics*, and serves on the Editorial Boards of *Clinical Proteomics*, *Bioinformatics and Biology Insights* and *Practical Proteomics*. He has six years' experience in industry and has co-founded two biotechnology companies, one of which, Proteome Systems, employs ~30 staff and is listed on the Australian Securities Exchange. His current research interests are in the dynamics of the interactome and the role that protein post-translational modifications play in the control of protein-protein interactions.

Organisation and Governance

Research Committee

The Research Committee met ten times during 2009. Members of the ARC Centre of Excellence in Bioinformatics Research Committee for 2009 were:

Chair – Prof. Mark Ragan
Program 1 – A/Prof. Rohan Teasdale
Program 1 – Dr Nicholas Hamilton
Program 1 – Prof. Shoba Ranganathan
Program 2 – Dr Timothy Bailey
Program 2 – A/Prof. Phoebe Chen
Program 2 – Prof. Geoff McLachlan
Program 2 – Prof. John Mattick
Program 3 – Prof. Kevin Burrage
Program 4 – A/Prof. Pablo Moscato
Secretary – Ms Lanna Wong

Director



Prof. Mark Ragan FLS
Institute for Molecular Bioscience
The University of Queensland

Please refer to page 8 for profile.

Chief Investigators



Dr Timothy L. Bailey
Institute for Molecular Bioscience
The University of Queensland

Dr Timothy Bailey has been active in bioinformatics and computational biology since the early 1990s, and since 2004 he has been a senior research fellow at the Institute for Molecular Bioscience. He is well-known as an expert in pattern recognition in biological sequences, and as the author of several important bioinformatics software programs, most notably MEME, one of the most heavily used tools in sequence analysis. The sequence analysis tools included in the MEME Suite are currently used by thousands of biologists each month. Tim's research applies state-of-the-art modelling approaches to understanding how the genome controls the development and functioning of cells and organisms. His current focus is on deciphering how the cell controls the transcription of genes. To achieve this, he is developing detailed models of the interactions of transcription factors and chromatin marks (non-mutational chemical modifications of genes) to regulate gene transcription.

Organisation and Governance



Prof. Kevin Burrage

Institute for Molecular Bioscience
The University of Queensland; and
Professor of Computational Systems Biology
COMLAB, Oxford University, UK

Prof. Kevin Burrage was founding CEO of the Queensland Parallel Supercomputer Foundation (now Queensland Cyber Infrastructure Foundation), Director of the Advanced Computational Modelling Centre (ACMC) at UQ, and Director of the ViSAC visualisation laboratory. In 2003 he was awarded a prestigious Federation Fellowship by the Australian Research Council. Kevin has co-authored more than 180 papers in the fields of computational science, computational biology, mathematical modelling and complex systems. This *oeuvre* consists of fundamental work on the numerical solution of both ordinary differential equations and stochastic differential equations, and algorithms for linear systems. He is author of a monograph on parallel and sequential methods for ordinary differential equations. In a computational biological context he is interested in the modelling and simulation of complex cellular processes, and the role of noise in molecular systems. In 2007 Kevin accepted a joint appointment as Professor of Computational Systems Biology at Oxford University.



A/Prof. Yi-Ping Phoebe Chen

School of Engineering and Information
Technology
Deakin University

A/Prof. (Reader) Yi-Ping Phoebe Chen is director of the bioinformatics group at the School of Information Technology, Deakin University. Phoebe has been working in bioinformatics since 1997. Prior to that, she conducted significant research in knowledge discovery, information retrieval, database query languages, data visualisation, and data integration systems. She is the author of some 140 refereed journal articles and international conference papers including papers in *Nucleic Acids Research*, *Briefings in Bioinformatics*, *BMC Genomics* and *BMC Bioinformatics*, and serves on the editorial boards of *IEEE Transactions on Multimedia*, *Current Bioinformatics*, *Journal of Research and Practice in Information Technology*, *International Journal of Intelligent Computing in Medical Sciences*, and *Image Processing*. A/Prof. Chen founded Asia-Pacific Bioinformatics Conference and continues to chair its Steering Committee. From 2007-2009 she also served on the national steering committee of Bioinformatics Australia.



Prof. Michael R. Fellows

Parameterised Complexity Research Unit
Office of the Deputy Vice-Chancellor
(Research)
The University of Newcastle

Prof. Mike Fellows is internationally recognised for his foundational work on parameterised complexity, for which he and collaborator Prof. Rod Downey (Victoria University, New Zealand) were nominated for the Gödel Prize in 2005. They co-authored the foundational papers and the first comprehensive monograph for the field, now considered one of the main branches of theoretical computer science concerned with algorithms and complexity. For more than a decade, this area has had strong applications in bioinformatics and computational biology. Mike is also recognised for significant contributions to cryptography, algebraic graph theory, computational social choice and popular communication of the mathematical sciences. He was a recipient in 2006 of an Alexander von Humboldt Research Award, and in 2007 of an Inaugural Fellowship to the Durham University Institute for Advanced Studies. He is an Associate Editor of *Journal of Computer and System Sciences*, and of *ACM Transactions on Algorithms*. In 2010 he will begin a five-year appointment as an ARC Professorial Fellow.

Organisation and Governance



Dr Markus Hegland

Centre for Mathematics and its Applications
Mathematical Sciences Institute
The Australian National University

Dr Markus Hegland is a member of the Computational Mathematics Program at the ANU's Centre for Mathematics and Its Applications. He is known internationally for his work on ill-posed problems, parallel solution of linear systems of equations and fast Fourier transforms and, most recently, in high-dimensional approximation. He has pioneered the application of numerical techniques, in particular sparse grids in data mining applications. He has also developed chemical master equation solvers which have been shown to work for up to 100 different chemical species. He was co-initiator of the Australasian Data Mining Conference and of the High-Dimensional Approximation Workshop, which annually attract some of the most prominent researchers of the field world-wide to Australia.



Prof. Geoffrey J. McLachlan

Australian Professorial Fellow
Professor and Head, Mathematics
The University of Queensland

Prof. Geoff McLachlan is internationally known for his research in statistics applied in the fields of classification, cluster and discriminant analysis, image analysis, intelligent systems, machine learning, neural networks, pattern recognition, and statistical inference. The focus in the latter has been on the theory and applications of finite mixture models, and on estimation via the EM (expectation-maximisation) algorithm. A common theme has been statistical computation, with particular attention to computational aspects of statistical methodology. This computational theme extends to the field of data mining. In 1994, he was awarded a Doctor of Science by the University of Queensland for his research contributions in these areas. More recently, Geoff has been actively involved in bioinformatics, focussing on the statistical analysis of microarray gene expression data. A joint Wiley monograph on the analysis of microarray data was published in 2004. In 2006 he was awarded a Professorial Research Fellowship for the period 2007-2011 by the Australian Research Council, and in 2007 was appointed to the ARC College of Experts. He is also a Fellow of the American Statistical Association, the Australian Mathematical Society, and the Royal Statistical Society, and is the current President (2010-2011) of the International Federation of Classification Societies. He is an associate editor of several journals in statistics and bioinformatics, including *Biology Direct* and *BMC Bioinformatics*.



Dr Brad Marsh

Senior Research Fellow and Group Leader
Institute for Molecular Bioscience
The University of Queensland

Research in Dr Brad Marsh's group at the Institute for Molecular Bioscience is centered on high-resolution 3D structure-function studies of mammalian cells, with a particular focus on the insulin-secreting beta cells of the pancreas. Brad is recognised internationally for his group's pioneering work developing novel approaches for 3D imaging and detailed computational analysis of large cellular volumes by electron tomography (ET) to map the spatial/structural organisation of beta cells at the nanometer scale in 3D. His work has been featured on the covers of *Proceedings of the National Academy of Sciences USA*, *Proceedings of Microscopy & Microanalysis*, *Materials Today*, *Traffic*, *BBA Molecular Cell Research*, *Nucleic Acids Research* and the *Journal of Structural Biology*, and has been highlighted in high-impact publications including *La Recherche*, *Nature Reviews Molecular Cell Biology*, *Journal of Cell Biology*, *Current Opinion in Structural Biology*, *Current Opinion in Cell Biology*, *Molecular Cell Biology* 5th Edition, *Essential Cell Biology* 2nd Edition, *Genome Biology*, *Australian Life Scientist*, *Nature Chemical Biology* and the 150th anniversary edition of *Gray's Anatomy*. His inaugural *PNAS* article (2001) has been lauded as a landmark by seminal leaders across a range of disciplines including structural biology, microscopy, chemistry, molecular biology, cell biology, diabetes research, and systems biology.

Organisation and Governance



Prof. John Mattick AO

Professor of Molecular Biology and ARC Federation Fellow
Institute for Molecular Bioscience
The University of Queensland

He recently played a major role drafting a 'position' paper on the current state of Golgi research [Emr *et al.* (2009) *Journal of Cell Biology*] and has just completed a book chapter for a new series in *Systems Biology* (to be published by Springer). Early this year, Dr Marsh was selected as an expert in 'Beta Cell Therapies & Bioimaging in Diabetes Research' and invited by the CEO of the Juvenile Diabetes Research Foundation (JDRF) to contribute to the development of a "National Type 1 Diabetes Agenda" policy document, which will serve as a framework for guiding future initiatives in Type 1 diabetes research in Australia for key government authorities and funding bodies (to be officially launched at a special sitting of the Australian Federal Parliament on March 18, 2010).

Prof. John Mattick stepped down as Director of the Institute for Molecular Bioscience at the end of 2005 to take up an ARC Federation Fellowship, after serving as Foundation Co-Director (together with Prof. Peter Andrews) from 2000-2002, and as Director from 2003-2005. He was Foundation Director of the Centre for Molecular and Cellular Biology (previously the Centre for Molecular Biology and Biotechnology) from 1988-1999, Foundation Director of the Australian Genome Research Facility from 1996-2002, and Foundation Director of the ARC Special Research Centre for Functional and Applied Genomics from 2000-2002. His main research interest is the role of non-protein-coding RNA in the evolution and development of humans and other complex organisms. He has been awarded the Pharmacia-LKB Biotechnology Medal from the Australian Biochemical Society, an Honorary Fellowship of the Royal College of Pathologists of Australasia, the Centenary Medal by the Australian Government, the CSIRO Eureka Prize for Leadership in Science and the Julian Wells Medal of the Lorne Genome Society. He was appointed an Officer in the Order of Australia (AO) in 2001 for service to molecular biology and biotechnology, and elected as an Associate Member of the European Molecular Biology Organisation in 2007 and a Fellow of The Australian Academy of Science in 2008. Prof. Mattick serves on the advisory boards of several institutes in Australia and abroad. Prof. Mattick receives no direct funding from the Centre.



A/Prof. Pablo Moscato

Priority Research Centre for Bioinformatics, Biomarker Discovery and Information-Based Medicine
The University of Newcastle; and
Information-based Medicine Program
Hunter Medical Research Institute

A/Prof. Pablo Moscato is Co-Director and Founder of the Priority Research Centre for Bioinformatics, Biomarker Discovery and Information-based Medicine of The University of Newcastle, Australia. He also founded the Newcastle Bioinformatics Initiative in 2002. He is also one of the four members of the Strategic Research Advisory Panel of the Hunter Medical Research Institute. He is founding member of the Australian-New Zealand Multiple Sclerosis Genetic Consortium and the Pharmacogenomics Research for Individualised Medicine Consortium, and a Chief Investigator of the Australian Stroke Genetics Collaborative.

Pablo is a pioneer in the introduction of metaheuristic methods in high-performance computation and his applications. He introduced memetic algorithms in 1989 when he was a member of the Caltech Concurrent Computation Program, and has championed this field for two decades. He is a member of the editorial boards of *Journal of Mathematical Modelling and Algorithms*, *Journal of Heuristics*, and in 2008 *Memetic Computing*. He has shown how successful the application of these hybrid computing methodologies to large-scale problems in combinatorial optimization and bioinformatics can be. Pablo has served on program committees of numerous international conferences in bioinformatics, heuristics and optimisation and is currently leading research programs in data analysis from high-throughput technologies as applied to the study of samples from Alzheimer disease, multiple sclerosis, age-related macular degeneration, melanoma, and breast and prostate cancer.

Organisation and Governance



Prof. Shoba Ranganathan

Department of Chemistry and Biomolecular Sciences
Macquarie University

Prof. Shoba Ranganathan holds the first Chair in Bioinformatics in Australia, at Macquarie University. She holds an Adjunct Professor position at the National University of Singapore (since 2004). Her research interests include genome annotation, transcriptome analysis, structural bioinformatics, immunoinformatics and genome-phenome analysis. Shoba's achievements include the development of graph-theoretical methods for alternative splicing analysis, a rapid and accurate docking protocol for vaccine design, software tools for the analysis of protein sequence and for modelling protein structure, and the development of boutique databases. She pursues collaborations with research groups at the National University of Singapore and the Institute for Infocomm Research, Singapore. Shoba serves on the editorial boards of several bioinformatics journals including *Briefings in Bioinformatics* and *BMC Bioinformatics*, and contributes to the organisation and scientific program of several international bioinformatics conferences. She was re-elected as President of the Asia-Pacific Bioinformatics Network (2008-2011).



A/Prof. Rohan D. Teasdale

Institute for Molecular Bioscience
The University of Queensland

A/Prof. Rohan Teasdale holds a Senior Research Fellowship A from the National Health & Medical Research Council. He leads a multidisciplinary research group at IMB that applies both cellular and computational techniques to investigate how subcellular compartments are generated and how proteins are trafficked within the mammalian cell. Rohan played a key role in the formation of Bioinformatics Australia and is a member of its steering committee. Rohan is author of 65 research publications, many in high-profile and leading bioinformatics and cell biology journals. These publications have focused on how individual proteins are compartmentalised within the cell and defining the protein trafficking machinery responsible for this process. In addition he has numerous publications outlining novel bioinformatics methodologies, database resources and collaborative projects.



Prof. Xiaofang Zhou

School of Information Technology & Electrical Engineering
The University of Queensland

Prof. Xiaofang Zhou is Professor of Computer Science at the University of Queensland, and Head of the Data and Knowledge Engineering program in the School of Information Technology & Electrical Engineering (ITEE). He is also Convenor of the ARC Research Network in Enterprise Information Infrastructure (EII), and Chair of the Steering Committee of the Asia-Pacific Web Conferences. Until 1999, Xiaofang was Principal Researcher and Head of Spatial Information Systems within the Commonwealth Scientific and Industrial Research Organisation (CSIRO). Xiaofang is author of over 100 publications in spatial databases and information systems, Grid computing, and bioinformatics.

Organisation and Governance

Partner Investigators



Dr Isidore Rigoutsos

IBM Thomas J. Watson Research Center
Yorktown Heights, New York USA

Dr Isidore Rigoutsos manages the Bioinformatics and Pattern Discovery group at IBM's Thomas J. Watson Research Center, and has been a visiting lecturer at MIT since 2000, where he teaches a Spring semester course and a Summer professional class in bioinformatics. Isidore is a Fulbright Scholar, and in 2003 was elected a Fellow of the American Institute for Medical and Biological Engineering. He serves on editorial boards of several journals in bioinformatics, and is a member of the Advisory Board for the Master's program in bioinformatics of Oxford University. He recently edited a two-volume book on Systems Biology (Oxford University Press, September 2006). His research activities currently focus on the computational study of RNA interference (RNAi) and its application to regenerative medicine and therapy, the study of cancer as a disruption of normal regulatory processes, the analysis of "junk" DNA in animal and plant genomes, and meta-phylogenomics.



Prof. Michael Langston

Department of Computer Science
University of Tennessee, USA

Prof. Mike Langston's research interests include computational biology, graph theory, discrete optimization and high-performance computation. He is currently Professor of Electrical Engineering and Computer Science at the University of Tennessee, and Collaborating Scientist in the Biosciences Division at Oak Ridge National Laboratory. Mike is lead investigator on a variety of research projects focused on the design and synthesis of combinatorial algorithms used to process high-throughput biological data. His collaborations extend across the US and to research groups in Australia, Canada, Europe and the Middle East. He has worked closely for over twenty years with Prof. Mike Fellows, and has authored over 200 refereed journal articles, conference papers, book chapters and other reports. Beginning in 2007, Mike led the development of the Bertinoro Systems Biology series of workshops. His work has been funded in the US by the National Science Foundation, the National Institutes of Health, the Department of Defence and the Department of Energy, and internationally by the Australian Research Council and the European Commission.



Prof. Allen Rodrigo

Director, National Evolutionary Synthesis Center (NESCent); and
Professor of Biology, Duke University
Durham, North Carolina, USA

Prof. Allen Rodrigo is the Director of the US National Evolutionary Synthesis Center and Professor of Biology at Duke University. He is also an Adjunct Professor at the University of Auckland. He is author of over 90 international publications on bioinformatics and computational biology, phylogenetics, and evolutionary genetics, and the molecular evolution of viruses. Allen is an Associate Editor of *Evolutionary Bioinformatics* and on the Editorial Board of *Mathematical Biosciences*. He also sits on the Scientific Advisory Board of two bioinformatics companies, and is involved in national and international collaborative projects on genomics and bioinformatics. His major research contributions are in the area of virus evolutionary genetics, where he has spearheaded the development of new methods to analyse time-series genetic data from viral populations.

Organisation and Governance

Special advisor



Prof. Gene Myers

Janelia Farms Research Campus
Howard Hughes Medical Institutes
Asburn, Virginia USA

Dr Gene Myers was a foundation group leader at Janelia Farms Research Campus of the Howard Hughes Medical Institutes, near Washington DC. Gene has made fundamental contributions to computational molecular biology and bioinformatics, notably the BLAST algorithm (1990) and whole-genome assembly (1999). He designed and led computer-based assembly of large genome sequences including those of fruit fly (2000), human (2001) and mosquito (2002). His research is now focusing on algorithms for fast image searching and comparison. Gene's numerous awards include the ACM Kannellakis Theory and Practice Award, membership in the US National Academy of Engineering, the Max Planck Research Prize for International Cooperation, induction into Leopoldina, the German National Academy, and most recently an honorary doctorate from ETH Zürich. Gene has been an Honorary Professor in the Institute for Molecular Bioscience at UQ since 2003.

Strategic partnership



Dr Nicholas Hamilton

Institute for Molecular Bioscience
The University of Queensland

Dr Hamilton joined ACB in 2004 as a postdoctoral fellow, and in 2008 was appointed Group Leader at the Institute for Molecular Bioscience. He has wide research interests, having published in bioinformatics, information technology, and mathematics, and in 2000 his research in mathematics was recognised with the award of the Kirkman Medal. Current research focuses on bio-image classification, clustering and visualisation, and utilises and develops techniques in areas such as machine learning, data clustering, graph algorithms, image segmentation, statistical testing and mathematical modelling. He has developed and released a wide range of bioinformatic methods and software – most recently iCluster, a visualisation and clustering tool for high-throughput subcellular imaging which is used in labs in Australia, Europe and USA. Dr Hamilton continues to collaborate closely with many groups in ACB and is currently leading research in the Visible Cell® project.

Information infrastructure

Mr Matthew Bryant
System Administrator,
High-performance computing

Mr Oliver Cairncross
Project Manager, Visible Cell®

Ms Mhairi Marshall
Grid & Database Developer

Mr Matthew Moores
Application Developer, Visible Cell®

Dr Andrew Newman
Application Developer, Visible Cell®

Mr David Wood
Database Administrator/Developer

Centre Manager

Ms Lanna Wong, MBA

Research Assistants

Ms Denis Bauer

Mr Reuben Fletcher-Costin

Ms Janette Galea

Ms Seetha Karunarathne

Mr John Marsden

Ms Ranjeeta Menon

Mr Garry Morgan

Ms Kelin Ru

Organisation and Governance

Postdoctoral Fellows / Research Officers

Dr Marjan Asakarian-Amiri
Dr John Belward (part-time)
Dr Mikael Bodén
Dr Pamela Burrage
Dr Qingfeng Chen
Dr Adrian Cootes
Dr Melissa Davis (QFAB)
Dr Marcel Dinger
Dr J. Lynn Fink
Dr Gabriel Fung
Dr Martin Gómez-Ravetti
Dr John Hawkins
Dr Karin Kassahn
Dr Kim-Anh Lê Cao
Dr Fawang Liu (part-time)
Dr Shev MacNamara
Dr Philip Machanick
Dr Stefan Maetschke
Dr Lorenzo Malquori
Dr Mythily Mariasegaram
Dr Daniel Marshall
Dr Timothy Mercer
Dr Massimo Micaroni
Dr Isabel Morrow
Dr Michael Pheasant
Dr Neelima Pottekkat Sidharthan
Dr Fran Rosamond
Dr Ryan Taft
Dr Johanna Vendelin
Dr Zheng Yuan

Masters/PhD students

Supervision/Associate supervision (principal advisor in ACB):

Paulo Amaral (due to complete in 2010)
Advisor: Prof. John Mattick

Ahmed Shamsul Arefin
(due to complete 2010)
Advisor: A/Prof. Pablo Moscato
Associate Advisor: Dr Regina Berretta

Isye Arieshanti
(MPhil thesis submitted, 2009)
Advisor: Dr Mikael Bodén
Associate Advisors: Dr Timothy Bailey &
Dr Stefan Maetschke

Denis Bauer (PhD thesis submitted, 2009)
Advisor: Dr Timothy Bailey

Fabian Buske (due to complete in 2012)
Advisor: Dr Timothy Bailey
Associate Advisor: Prof. John Mattick

Alhadi Bustamam (due to complete in 2010)
Advisor: Prof. Kevin Burrage
Associate Advisor: Dr Nicholas Hamilton

Pierre Cattenoz (due to complete in 2011)
Advisors: Prof. John Mattick
Co-Advisor: Prof. Eric Westhof (University of
Strasbourg, France)

Elsa Chacko (due to complete in 2011)
Advisor: Prof. Shoba Ranganathan

Feng Chen (due to complete in 2010)
Advisor: A/Prof. Phoebe Chen

Yan Chen (due to complete in 2010)
Advisor: A/Prof. Phoebe Chen

Eun Jung Chin (due to complete in 2012)
Advisor: Prof. Xiaofang Zhou

Joo-Young Choi
(MPhil thesis submitted, January 2010)
Advisor: Prof. Mark Ragan
Associate Advisor: Dr Melissa Davis

Khar Heng Choo (PhD awarded, 2009)
Advisor: Prof. Shoba Ranganathan
Associate Advisor: A/Prof. Tan Tin Wee

Michael Clark (due to complete in 2011)
Advisor: Prof. John Mattick
Associate Advisor: A/Prof. Rohan Teasdale

Adam Costin (due to complete in 2011)
Advisor: Dr Brad Marsh
Associate Advisor: Dr Helen Thomas

Yuan Fang (due to complete in 2011)
Advisor: Dr Markus Hegland

Alex Foo (due to complete in 2011)
Advisor: Dr Brad Marsh
Associate Advisors: A/Prof. Ben Hankamer
& Prof. Boris Martinac

Jitendra Gaikwad (due to complete in 2010)
Advisor: Prof. Shoba Ranganathan

Gagan Garg (due to complete in 2013)
Advisor: Prof. Shoba Ranganathan

Dennis Gascoigne (due to complete in 2012)
Advisor: Prof. John Mattick
Associate Advisor: Dr Marcel Dinger

Mohammad Islam (due to complete in 2010)
Advisor: Prof. Shoba Ranganathan
Associate Advisor: Dr Abhaya Nayak

Chol Hee Jung (due to complete in 2010)
Advisor: Prof. John Mattick
Associate Advisor: Dr Igor Makunin

Mario Inostroza-Ponta (PhD awarded, 2009)
Advisor: A/Prof. Pablo Moscato
Associate Advisor: Dr Regina Berretta

Javed M. Khan (due to complete in 2011)
Advisor: Prof. Shoba Ranganathan

Varun Khanna (due to complete in 2011)
Advisor: Prof. Shoba Ranganathan

Keith Knapp (PhD awarded, 2009)
Advisor: A/Prof. Phoebe Chen

Chin Foon Khoo (due to complete in 2010)
Advisor: Dr Markus Hegland

Darren Korbie (due to complete in 2010)
Advisor: Prof. John Mattick

Gaurav Kumar (due to complete in 2011)
Advisor: Prof. Shoba Ranganathan

Robert McLeay (due to complete in 2011)
Advisor: Dr Timothy Bailey

Piyush Madhamshettiwar
(due to complete in 2012)
Advisor: Prof. Mark Ragan

Scott Mann (PhD thesis submitted, 2009)
Advisor: A/Prof. Phoebe Chen

Ahmed Mehdi (due to complete in 2012)
Advisor: Dr Mikael Bodén
Associate Advisor: Dr Timothy Bailey

Ranjeeta Menon (due to complete in 2011)
Advisor: Prof. Shoba Ranganathan

Tim Mercer (PhD awarded, 2009)
Advisor: Prof. John Mattick

Nurul Mohamad (due to complete in 2010)
Advisor: Dr Mikael Bodén
Associate Advisor: A/Prof. Rohan Teasdale

Satu Nahkuri (due to complete in 2010)
Advisor: Prof. John Mattick

Organisation and Governance

Andrew Noske
(PhD thesis submitted, February 2010)
Advisor: Dr Brad Marsh
Associate Advisors: Prof. Mark Ragan &
Prof. Kevin Burrage

Timothy Pan (due to complete in 2011)
Advisor: Dr Brad Marsh
Associate Advisor: Prof. Rob Capon

Vikram Ratnu (due to complete in 2012)
Advisor: Prof. John Mattick

Mateus Rocha de Paula
(due to complete in 2012)
Advisor: A/Prof. Pablo Moscato
Associate Advisor: Dr Regina Berretta

Nur Intan Ruhaiyem
(due to complete in 2011)
Advisor: Dr Brad Marsh
Associate Advisor: Dr Nicholas Hamilton

Chang Jin Shin (due to complete in 2010)
Advisor: Prof. Mark Ragan
Associate Advisors: Dr Simon Wong (to
2007) & Dr Melissa Davis

Elizabeth Skippington
(due to complete in 2011)
Advisor: Prof. Mark Ragan
Associate Advisor: Dr Thomas Huber

Martin Smith (due to complete in 2011)
Advisor: Prof. John Mattick
Co-Advisor: Prof. Peter Stadler (University
of Leipzig, Germany)

Josefine Sprenger (due to complete in 2010)
Advisor: A/Prof. Rohan Teasdale
Associate Advisor: Dr Nicholas Hamilton

Chinnu Subramaniam
(due to complete in 2012)
Advisor: A/Prof. Phoebe Chen

Vikram Sunkara (due to complete in 2011)
Advisor: Dr Markus Hegland

Sharnsheer Syed
(part-time, due to complete in 2012)
Advisor: Prof. Xiaofang Zhou

Ryan Taft (PhD awarded, 2009)
Advisor: Prof. John Mattick

Selene Fernandez Valverde
(due to complete in 2011)
Advisor: Prof. John Mattick
Associate Advisor: Dr Ryan Taft

Peter van der Heide
(due to complete in 2010)
Advisor: Dr Brad Marsh
Associate Advisor: A/Prof. Niels Volkmann

Renato Vimiero (due to complete 2012)
Advisor: A/Prof. Pablo Moscato
Associate Advisor: Dr Regina Berretta

Lawrence Wee (PhD awarded, 2009)
Advisor: Prof. Shoba Ranganathan
Associate Advisor: A/Prof. Tan Tin Wee

Tom Whittington (due to complete in 2011)
Advisor: Dr Timothy Bailey

Kevin Zheng (due to complete in 2012)
Advisor: Prof. Xiaofang Zhou

Jia Zhu (part-time, due to complete in 2011)
Advisor: Prof. Xiaofang Zhou

Justin Xi Zhu (PhD awarded 2009)
Advisor: Prof. Geoff McLachlan
Associate Advisor: Dr Angus Ng

Co-supervision (principal advisor not an ACB investigator)

Sandy Pineda Gonzalez
(due to complete in 2011)
Associate Advisor: Prof. John Mattick
Advisor: Prof. Glenn King

Weiliang Huang (due to complete in 2011)
Associate Advisor: Dr Mikael Bodén
Advisor: Prof. Elizabeth Gillam

Daniel Johnstone (due to complete in 2010)
Associate Advisors: A/Prof. Pablo Moscato &
Prof. Rodney Scott
Advisor: Dr Liz Millward

Emily Knauth (due to complete 2011)
Associate Advisor: Dr Brad Marsh
Advisor: A/Prof. Ben Hankamer

Duncan Mortimer (PhD awarded 2009)
Associate Advisor: Prof. Kevin Burrage
Advisor: Dr Geoffrey Goodhill

Mitchell Stanton-Cook
(due to complete in 2011)
Associate Advisor: Dr Nicholas Hamilton
Advisor: Prof. Thomas Huber

Honours students

Eva Curley
*Examining the expression and orthology
relationships of the HIN-200 gene family*
Advisors: Dr Katryn Stacey &
Dr Karin Kassahn

Reuben Fletcher-Costin
*Machine learning with gradient penalties
and finite elements*
Advisor: Dr Markus Hegland

Andrew Fitzpatrick
Spectral sharpening: theory and practice
Advisor: Dr Markus Hegland

Tor Lattimore
*Prediction of selected bits by Solomonoff
induction*
Advisors: A/Prof. Marcus Hutter and
Dr Markus Hegland

Jules Olleon
Models of protein-DNA binding
Advisors: Dr Mikael Bodén &
Dr Timothy Bailey

Anais Painchaud
Aligning protein-protein binding residues
Advisors: Dr Mikael Bodén &
Dr Timothy Bailey

International interns

Christina Fröstl
Upper Austria University of Applied Sciences
(Austria)
Advisor: A/Prof. Pablo Moscato

Phil Gemmell
Oxford University (UK)
Advisor: Prof. Kevin Burrage
Associate Advisor: Dr Nicholas Hamilton

Eoin Hyde
Oxford University (UK)
Advisor: Dr Nicholas Hamilton
Associate Advisor: Prof. Kevin Burrage

Tamas Szekely
Oxford University (UK)
Advisor: Prof. Kevin Burrage
Associate Advisor: Dr Nicholas Hamilton

John Walmsley
Oxford University (UK)
Advisor: Prof. Kevin Burrage
Associate Advisor: Dr Nicholas Hamilton

Organisation and Governance

Undergraduate research trainees and volunteers

Ralph Patrick
Research Trainee
Computational model of protein degradation
Advisor: Dr Mikael Bodén

Ms Chikako Ragan
Volunteer
Computational prediction of miRNA-binding sites
Advisor: Prof. Mark Ragan

Visiting scholars, associates

Visiting scholars

Mr Graham Johnson, Scientific Illustrator,
The Scripps Research Institute (USA)

Mr Vikram Sunkara, Australian National
University (at UQ node)

Associates

Prof. David Abramson, ARC Professorial
Fellow, Monash e-Research Centre (MERC),
Monash University

Dr Jonathan Arthur, Sesqui Lecturer in
Bioinformatics, The University of Sydney

A/Prof. Ian Atkinson, Information
Technology, James Cook University

Prof. Kaye Basford, Head, School of
Land & Food Sciences, The University of
Queensland

Dr Robert Beiko, Faculty of Computer
Science, Dalhousie University (Canada)

Prof. Lindsay Botten, Director, National
Computational Infrastructure, Australian
National University

Prof. Vladimir Brusic, Director of
Bioinformatics, Dana Farber Cancer
Institute, Boston (USA)

Prof. Gillian Bushell, Dean (Research),
Science, Environment, Engineering and
Technology, Griffith University

Dr Robert Charlebois, Sanofi Pasteur Ltd
(Canada)

Dr Brian Dalrymple, CSIRO Livestock
Industries

Prof. Werner Dubitzky, Head, Bioinformatics
and Systems Biology, University of Ulster
(Northern Ireland)

Dr Dave Edwards, Australian Centre for
Plant Functional Genomics

Dr David Green, High Performance
Computing Group, Information Technology
Services, The University of Queensland

Prof. Michael Gribskov, Purdue University
(USA)

Dr Ben Hankamer, Institute for Molecular
Bioscience, The University of Queensland

Dr David Hansen, e-Health Research
Centre, CSIRO

A/Prof. James Hogan, School of Software
Engineering & Data Communications,
Queensland University of Technology

Dr Lindsay Hood, Cray Inc., Canberra

Dr Thomas Huber, School of Molecular
& Microbial Sciences, The University of
Queensland

Prof. Philip Hugenholtz, DOE Joint Genome
Institute (USA)

Prof. Jane Hunter, School of Information
Technology & Electrical Engineering,
The University of Queensland

Dr Lars Jermiin, Office of the Chief
Executive (OCE) Science Leader for the
Bioinformatics team at CSIRO Entomology

Prof. Simon Kaplan, Executive Dean,
Faculty of Information Technology,
Queensland University of Technology

Dr Jonathan Keith, Faculty of Science,
Queensland University of Technology

Prof. Do Han Kim, Department of Life
Science, Seoul National University (Korea)

Mr Krzysztof Kurowski, Director,
Application Department, Poznań
Supercomputing and Networking Center
(Poland)

Prof. Sang Yup Lee, Director, Bioinformatics
Research Center, KAIST (Korea)

Prof. Peter Lindsay, School of Information
Technology & Electrical Engineering,
The University of Queensland

Prof. Satoru Miyano, Institute of Medical
Science, University of Tokyo (Japan)

Prof. Mark Morrison, Science Leader
Metagenomics, CSIRO Livestock Industries

Prof. George Muscat, Molecular Genetics
& Development, Institute for Molecular
Bioscience, The University of Queensland

Prof. Colleen Nelson, Director, Australian
Prostate Cancer Research Centre,
Queensland University of Technology

Prof. Lars Nielsen, Australian Institute
for Bioengineering & Nanotechnology,
The University of Queensland

A/Prof. William Noble, Department of
Genome Sciences, School of Medicine,
University of Washington, USA

Prof. Bernard Pailthorpe, CEO, Queensland
Cyber Infrastructure Foundation

Dr Antonio Reverter-Gomez, CSIRO
Livestock Industries

Prof. Jenny Stow, Institute for Molecular
Bioscience, The University of Queensland

Dr Anne Trefethen, Executive Director,
Oxford e-Research Centre (UK)

Prof. Ah Chung Tsoi, Vice-President,
Research & Institutional Advancement,
Hong Kong Baptist University (Hong Kong)

Dr Alfred Uhlherr, Senior Manager,
Advanced Scientific Computing CSIRO
Information Management & Technology

Dr Mark Wilkinson, Department of Medical
Genetics, University of British Columbia and
St Paul's Hospital Vancouver (Canada)

Prof. Michael Zuker, Rensselaer Polytechnic
Institute (USA)

Vision

The ARC Centre of Excellence in Bioinformatics is a multi-nodal interdisciplinary Centre that applies genome-scale bioinformatics, computational science and advanced data technologies to empirical data on cellular structure and function, yielding a deep understanding of the mammalian cell as an information system.

Mission

The ARC Centre of Excellence in Bioinformatics is committed to research excellence, advanced education and training, interdisciplinarity, improved access to skills, tools and facilities, and building critical mass and national focus for cellular and 'omic' bioinformatics in Australia.

Aims

Within this mission, we aim to:

- Build a powerful new bioinformatics that integrates insights and key developments in mathematics, statistics, computing science, information technology, genomics and molecular cell biology.
- Mutually enrich biomolecular research, mathematics, computer science and IT.
- Apply this new bioinformatics to make innovative use of advanced biomolecular technologies, with the result of illuminating the development and differentiation of the mammalian cell.
- Play a leading role in the national and international bioinformatics agenda and in the generation of human capital, enhancing critical mass and national focus in bioinformatics.

Objectives

More specifically, our objectives for the extension period will be to:

- Build on the capabilities and interdisciplinary perspectives we have developed in the first phase of the Centre (2003-2007).
- Use empirical data from advanced microarray, tomographic and microscopic technologies to construct quantitative dynamic models of selected cellular regulatory networks and subcellular systems.
- Develop advanced algorithmic, statistical and computational methods and knowledge engineering systems, and apply them to extend, refine and inter-relate these models.
- Deliver advanced prototypes of our integrated data and visual framework for hypothesis-testing, validation and discovery, the Visible Cell®, and use them to understand more fundamentally the mammalian cell as an information system.

Capabilities — core technologies and infrastructure

The integrated research programs of the ARC Centre of Excellence in Bioinformatics are underpinned by established strengths in mathematics, computing science, information technologies, cell and structural biology, and molecular and genomic biosciences.

Key capabilities include:

- Algorithmics and computational complexity
- Statistics, including expression microarray statistics
- Pattern discovery, machine learning and adaptive optimisation
- Advanced database architectures, including distributed and visual databases
- Specialised mark-up languages, ontologies and semantic web technologies
- Computational modelling, including stochastic, deterministic, and agent-based approaches
- Computational simulation using high-performance parallel and distributed architectures
- Automated discovery pipelines and workflows in bioinformatics
- Advanced scientific visualisation
- Advanced microscopic, tomographic and imaging technologies in cell biology
- High-throughput microarray-based genomic technologies
- Multiple interfaces to empirical "wet" biology

Research Programs

Research programs highlights for 2009:

The Centre's research in 2009 was delivered through four programs, each of which was further organized as two or three projects. The following pages describe the aims of each of these projects, the Centre and other personnel involved, and the main achievements during 2009.

In **Program 1**, we develop an integrative data and visualisation framework, the Visible Cell®, that allows biologists and modellers to interact with mammalian cells reconstructed from 3D electron tomographic or fluorescence confocal images, annotate cell structures using federated data (sequences, structures, pathways, networks, literature), and conduct quantitative analyses. We also develop tools and an interface to manage the analysis and integration of very large biomolecular data.

Information flows from genome to phenome through complex molecular networks and systems, and in **Program 2** we examine the signals, pathways and regulatory mechanisms by which these networks operate and interconnect. Algorithmic and statistical approaches are being focused on understanding which pathways and networks are up- or down-regulated in complex disease including cancer, and on the discovery of new pathways and sub-networks. This Program includes innovative approaches to the discovery and modelling of RNA-based regulatory networks in mammalian cells.

Computational modelling and simulation allow us to describe the operation of these networks in dynamic, quantitative terms. Key biomolecules often occur transiently, in extremely small numbers and/or in highly restricted locations. Cellular structures move too, driven by mechanical or thermodynamic forces that are highly susceptible to mathematical modelling. In **Program 3** we construct computational models of molecular networks and of the subcellular structures through which they transduce information to the cellular phenome. One of the main goals of our extended Centre will be to embed these models in the Visible Cell®, making it a dynamic environment for hypothesis-generation and -testing.

Representing molecular networks and systems mathematically requires us to work with large numbers of graphs, and **Program 4** develops powerful algorithmic and combinatorial approaches that will make our models computationally tractable. These include data-reduction strategies, implementation of scalable algorithms for problems on very large graphs, and novel computational techniques to make very large problems computable on actual hardware.

Research programs 2008-2010

Program 1

The Visible Cell®: linking genome and phenome

- 1.1 Generation of subcellular localisation data in mammalian cells
- 1.2 Project and data management for Visible Cell®
- 1.3 Data analysis and knowledge discovery in very large biological network databases

Program 2

Phenotype-informed discovery of networks and systems

- 2.1 Computational discovery and modelling of gene-regulatory networks
- 2.2 Differential expression of genes towards pathway discovery
- 2.3 Discovery and modelling of RNA-based regulatory networks

Program 3

Modelling dynamic cellular processes

- 3.1 Mathematical modelling of genetic regulatory networks and biochemical pathways
- 3.2 Modelling and visualising biological processes in complex spatial environments

Program 4

Algorithms for graphs and networks

- 4.1 Discrete optimization and graph clustering
- 4.2 Optimisation-based approaches to large systems
- 4.3 External-memory algorithms for analysis of massive graphs

Research Programs

Program 1 –The Visible Cell®: linking genome and phenome

1.1 Generation of subcellular localisation data in mammalian cells

Investigator:

A/Prof. Rohan Teasdale
(The University of Queensland)

In collaboration with:

Prof. Kevin Burrage
(The University of Queensland)

Dr Melissa Davis
(Queensland Facility for Advanced
Bioinformatics)

Dr Nicholas Hamilton
(The University of Queensland)

Prof. John Mattick
(The University of Queensland)

Prof. Mark Ragan
(The University of Queensland)

Researchers:**Research Associates:**

Ms Seetha Karunaratne
(The University of Queensland)

Dr Karin Kassahn
(The University of Queensland)

Dr Zheng Yuan
(The University of Queensland)

PhD student:

Ms Josefine Sprenger
(The University of Queensland)

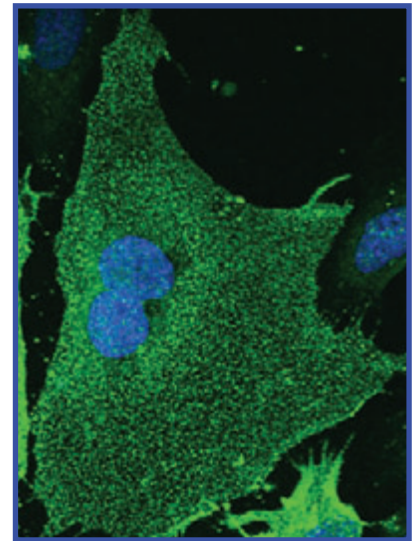
Aims:

Because eukaryotic cells are highly compartmentalised, a protein's function is tightly enmeshed with its location (more precisely, the distribution of its location). Knowing the latter can greatly improve prediction of its function, while conversely, a comprehensive protein inventory is critical to understanding the function of cellular compartments. This project aims to generate unique primary data on subcellular localisation of proteins in mammalian cells, and make these data available *via* value-added data resources for further integration, analysis, computational modelling, simulation and visualisation.

Achievements (2009):

We have:

- (a) Prepared experimental protocols for the subcellular localisation of ncRNAs. Controls ncRNAs known to associate with distinct subcellular domains and structures were identified (Mattick, Teasdale).
- (b) Maintained the LOCATE database and managed its relocation to a new server environment (Sprenger, Teasdale)
- (c) Integrated the Mammalian Endosome System (MESS) protein set with other information. This will include expression data, co-regulation with transcriptional regulators and phenotype annotations (Sprenger, Teasdale)
- (d) Developed a series of phenotype screens directed at endosome physiology. These will be utilised by the LISA facility for shRNA knockdown screens (Karunaratne, Teasdale).
- (e) Developed of a series of endosome protein reporters and lipid sensing reporters for generation of cell lines suitable for live cell imaging (Karunaratne, Teasdale).



Research Programs

1.2 Project and data management for Visible Cell®

Research Leader:

Dr Nicholas Hamilton
(The University of Queensland)

Investigators:

Dr Brad Marsh
(The University of Queensland)

Prof. Mark Ragan
(The University of Queensland)

Prof. Shoba Ranganathan
(Macquarie University)

Prof. Xiaofang Zhou
(The University of Queensland)

Project Manager:

Mr Oliver Cairncross
(ARC Centre of Excellence in Bioinformatics)

In collaboration with:

Dr Melissa Davis
(Queensland Facility for Advanced Bioinformatics)

A/Prof. Niels Volkman
(Burnham Institute for Medical Research)

Researchers:

Research Associates:

Dr Daniel Marshall
(ARC Centre of Excellence in Bioinformatics)

Dr Neelima Sidharthan
(The University of Queensland)

Research staff:

Mr Matthew Moores
(ARC Centre of Excellence in Bioinformatics)

Dr Andrew Newman
(ARC Centre of Excellence in Bioinformatics)

Mr David Wood
(Queensland Facility for Advanced Bioinformatics)

PhD students:

Mr Andrew Noske
(The University of Queensland)

Mr Timothy Pan
(The University of Queensland)

Ms Nur Intan Ruhaiyem
(The University of Queensland)

Mr Peter van der Heide
(The University of Queensland)

Aims:

A defining characteristic of our Visible Cell® is its foundation upon precise 3D spatial matrices for the structural organization of the mammalian cell at nanometer resolution. This ambitious goal will be accomplished by combining high-resolution (<5 nm) 3D spatial information regarding compartmental, cytoskeletal and macromolecular organization derived by electron tomographic (ET) imaging of a significant (~10%) volume of a mammalian (insulin-secreting) pancreatic beta cell, supplemented/guided by whole cell tomograms of multiple islet beta cells imaged/reconstructed in 3D at intermediate (~10-20 nm) resolution under different physiological conditions, using the advanced cryo-electron microscopy facility housed within IMB-UQ. Since each 3D matrix for an entire cell can range up to 10 TB in size, in the first phase of our Centre we designed, constructed and implemented a computational and data infrastructure framework capable of handling TB-sized image data files that links to scaleable data grid environments.

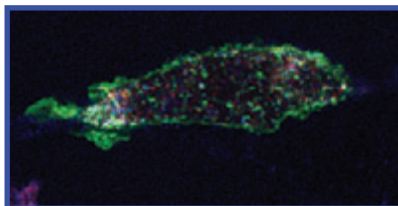
This Project aims to integrate 3D cellular image reconstruction and analyses with more-advanced bioinformatic methods for 3D data query/annotation by incorporating a specific ontology and novel methods for processing semantic data which we have named Illoura™, to yield a world-first Visible Cell® prototype environment. This environment will streamline querying, analysis and visualisation of cellular reconstructions enriched with external sequence, structure, pathway, network and functional data. It will provide data and parameters to drive simulations based on the enriched data, support semantic querying and other applications in systems biology (Project 1.1), and utilise national e-research and other infrastructure initiatives.

Achievements (2009):

- (a) The first publication describing the core Visible Cell® visualisation environment appeared, with Oliver Cairncross and Tim McComb as joint first authors (McComb, Cairncross, Noske, Wood, Marsh & Ragan, *Bioinformatics*). The project's international profile continued to grow, with the Visible Cell® included in an EMBO Workshop "Visualizing Biological Data" scheduled to be held in Heidelberg in March 2010, and in a *Nature Methods* review to appear at the same time (Hamilton, Ragan).
- (b) We completed primary data collection and now continue to process and assemble ET data encompassing a cellular volume equivalent to approximately 10% of a mammalian (insulin-secreting) cell to provide proof-of-concept for imaging and reconstructing an entire mammalian cell in 3D at high resolution (<5 nm). Such data will underpin the primary Visible Cell atlas dataset and provide a precise spatial framework for *in silico* studies to query of mammalian cell form and function (van der Heide, Marsh).
- (c) We continued to develop, test and implement new algorithmic methods for pre- and post-processing high-resolution ET image data to provide a comprehensive set of mathematical tools that can expedite 3D segmentation, quantitative analysis and computational simulation of large scale cellular tomograms (Ruhaiyem, van der Heide, Marsh).
- (d) We developed and continue to optimise automated approaches for the identification and docking of macromolecular complexes using the eukaryotic ribosome as an archetypical macromolecular machine (van der Heide, Volkman, Marsh).
- (e) We completed 3D reconstruction and quantitative/comparative analysis of four whole-cell tomograms of islet beta cells imaged at intermediate (~10-20 nm) resolution (two glucose-stimulated, two steady-state/unstimulated). Two manuscripts detailing our methodology were submitted for publication (Noske, Marsh).
- (f) We consolidated Illoura™ and related prototyped methods into a single robust software package suitable for use and extension by the wider biology community (Cairncross, Moores).

Research Programs

- (g) We further extended the Illoura methodologies in application to data from fluorescence confocal microscopy, with particular emphasis during 2009 on developing the Visible Cell ontology to describe protein localisation in whole cells, and on integrating Illoura with data-management tools for light microscopic (LM) data including OMERO (Cairncross, Moores).
- (h) We developed more-extensive methodologies for the query, visualisation and quantification of LM data in 2D, 3D and 4D using Illoura, including integration with the image-analysis packages ImageJ, CellProfiler, iCluster and OBCOL, and interoperation with data generated therein (Cairncross, Moores, Hamilton, Marshall).
- (i) We extended the semantic data framework underlying the Visible Cell® to include contexts for visualisation. This will permit seamless migration of image data between multiple contexts, modes and visualisations, thereby enabling multiple simultaneous views and comparisons of data (Hamilton, Marshall, Cairncross, Moores).



Research Programs

1.3 Data analysis and knowledge discovery in very large biological network databases

Investigators:

Prof. Shoba Ranganathan
(Macquarie University)

Prof. Xiaofang Zhou
(The University of Queensland)

In collaboration with:

Dr Melissa Davis
(Queensland Facility for Advanced Bioinformatics)

Prof. Alon Halevy
(University of Washington)

Dr Brad Marsh
(The University of Queensland)

Prof. John Mattick
(The University of Queensland)

Prof. Mark Ragan
(The University of Queensland)

A/Prof. Rohan Teasdale
(The University of Queensland)

A/Prof. Wei Wang
(University of North Carolina)

Researchers:

Research Associates:

Dr Adrian Cootes
(Macquarie University)

Dr Gabriel Fung
(The University of Queensland)

Dr Michael Pheasant
(The University of Queensland and Queensland Facility for Advanced Bioinformatics)

PhD students:

Ms. Eun Jung Chin
(The University of Queensland)

Mr Gaurav Kumar
(Macquarie University)

Mr Chang Jin Shin
(The University of Queensland)

Mr Kai Zheng
(The University of Queensland)

Aims:

The Visible Cell® project typifies the data-analysis and knowledge-discovery challenges of omic bioinformatics, including demands for efficiency with very large data, complex data types and relationships, and multiplicity of sources and formats – problems exacerbated by the explorative nature of data analysis in biology. This project addresses these issues by (1) development of a portal that will investigate a new “pay-as-you-go” approach to data integration, allowing biologists to specify just-enough data mappings for a task. It thereby offers low upfront overhead and the ability to evolve with changes in data sources. The key to this incremental, collaborative approach will be a tool that supports online community annotation, automatic consistency enforcement for data mappings, dataset and resource discovery, dynamic dataset membership, data uncertainty and lineage analysis; and (2) data mining that models data and metadata as graphs, and automates the detection of frequent sub-graphs. Initial application will be to RDF diagrams, to sub-structures of protein surfaces indexed by frequency of geometric graphs, and to semi-automatic data linking (where topological structure similarity among annotations labelled differently due to semantic heterogeneity can be automatically detected and reported for the human user to verify). These tools will allow users of our Visible Cell® to specify only the biological data needed to address each question, without our having to incur the upfront cost of fully inter-relating all data across the hundreds of data sources we are mirroring.

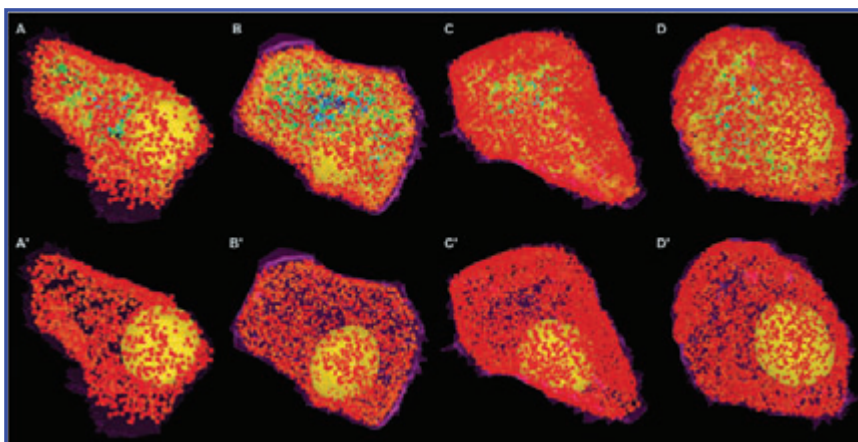
Achievements (2009):

We have:

- (a) Recruited two Ph.D. students (Mr Kai Zheng and Ms Eun Jung Chin) to work jointly with this project (Zhou).
- (b) Proposed how to quantify the distance between two fuzzy objects, which is the first mover in this area. In addition, according to the proposed distance function, we have derived an efficient algorithm for identifying K fuzzy objects that are the nearest neighbours of a given fuzzy object. These achievements effectively aid in the identification of protein-protein interaction in a very large biological network and image analysis (Zhou, Fung, Zheng).
- (c) Demonstrated how we can improve the searching effectiveness of Pubmed *via* a well-presented and informative user interface. This can help bioinformaticians locate useful information effectively from a very large, messy and information-rich database (Pubmed) (Zhou, Fung).
- (d) Investigated some feasible and effective ways to improve the quality of a PPI network by combining and comparing multiple PPI networks, so that we can remove some false positive links and insert some missing links (Zhou, Fung, Chin).
- (e) Reviewed network approaches to solving biological problems in a chapter: “Untangling Biological Networks Using Bioinformatics” in *Algorithms in Computational Molecular Biology: Techniques, Approaches and Application* (Kumar, Cootes, Ranganathan).
- (f) Created an integrated protein interaction, metabolic and subcellular localisation (SCL) network database for human using literature-curated SCL data taken from LOCATE. Protein interaction data were collated from HPRD, MINT, IntAct, BioGrid and DIP. Metabolic data were taken from the KEGG and HUMANCYC databases (Ranganathan).
- (g) Completed a detailed statistical analysis of SCL in human metabolic and interaction networks. We compared and contrasted the tendency of metabolic (indirect) and physical (direct) interactions to occur between proteins in specific cellular compartments. The connectivity properties of human metabolic and interaction networks were also analysed and compared. A manuscript has been prepared for submission (Ranganathan).

Research Programs

- (h) Completed a detailed statistical analysis of protein function in the yeast protein interaction network. We demonstrated that the overall connectivity of the shortest path between proteins strongly determines whether those proteins have the same function. We also demonstrated the effect of removing hubs on functional relationships in the network. In addition, we showed that the significance of a given network path in determining functional similarity depends on the level of detail at which one is studying function. A manuscript has been prepared for submission (Ranganathan).
- (i) Demonstrated that knowledge of high-quality protein-protein interactions can improve the computational prediction of subcellular localisation of proteins in mammalian cells (Shin, Wong, Davis, Ragan), and that protein-protein interactions in human can be used to infer a core mammalian interaction set in mouse (Shin, Davis, Ragan). This work appeared *BMC Systems Biology* and *Proteomics* respectively in 2009.
- (j) In collaboration with QFAB, investigated a new genome browser architecture combining advanced knowledge discovery algorithms, very large amounts of genomic data, and new methods of visualisation to assist researchers to discover new relationships between datasets. Progress in 2009 included development of software code to index and summarise large genomic datasets, and investigation of methods to organise associated metadata and to visualise results (Pheasant, Mattick).



Research Programs

Program 2 – Phenotype-informed discovery of networks and systems

2.1 Computational discovery and modelling of gene-regulatory networks

Investigators:

Dr Timothy Bailey
(The University of Queensland)

Prof. Geoff McLachlan
(The University of Queensland)

Prof. John Mattick
(The University of Queensland)

Prof. Mark Ragan
(The University of Queensland)

In collaboration with:

Dr Paul Horton
(Computational Biology Research Center, Japan)

Dr Colleen Nelson
(Translational Research Institute, QUT / Princess Alexandra Hospital)

Researchers:

Research Associates:

Dr Mikael Bodén
(The University of Queensland)

Dr Melissa Davis
(Queensland Facility for Advanced Bioinformatics)

Dr John Hawkins
(The University of Queensland)

Dr Philip Machanick
(The University of Queensland)

Dr Stefan Maetschke
(The University of Queensland)

PhD students:

Ms Denis Bauer
(The University of Queensland)

Mr Fabian Buske
(The University of Queensland)

Mr Piyush Madhamshettiwar
(The University of Queensland)

Mr Robert McLeay
(The University of Queensland)

Ms Nurul Mohammad
(The University of Queensland)

Mr Thomas Whittington
(The University of Queensland)

Aims:

This project aims to:

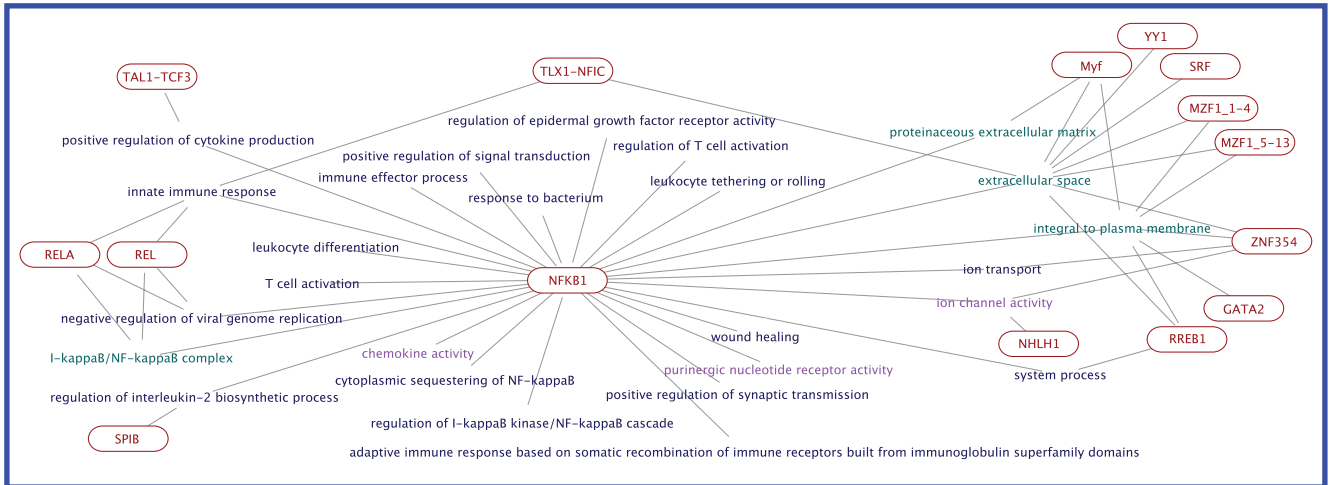
- (a) Develop and integrate scalable methods to infer and analyse genetic regulatory networks incorporating regulation by transcription factors (TFs), non-coding RNAs (ncRNAs) and other elements in mammalian cells.
- (b) In collaboration with researchers outside the ARC Centre of Excellence, generate genome-scale genotype (single-nucleotide polymorphism, copy-number variation) and expression data based on multiple samples of human cells expressing a complex disease state (e.g. cancer), and matched normal controls.
- (c) Apply the above methods to reconstruct, identify and analyse the genetic regulatory networks involved in this complex disease state.
- (d) Build static computational models of the transcriptional output of a gene under the control of TFs and ncRNAs.
- (e) Develop useful software tools implementing the above prediction and modelling tasks, and make them available to the international research community.

Achievements (2009):

- (a) Dr Lynn Fink was recruited back to Australia in July 2009 to manage this Project. Lynn consolidated our preparatory work and established the data environments needed for this project.
- (b) We had intended to analyse data from the National Breast Cancer Foundation project "Nuclear Receptors in Breast Cancer", and had invested personnel and resources to that end. However the NRBC project, under the direction of Prof. Christine Clarke (Westmead Institute for Cancer Research), did not proceed to generate genome-scale data as we had anticipated. A new alliance with Prof. Colleen Nelson (Translational Research Institute, Queensland University of Technology and Princess Alexandra Hospital) was forged, and a research plan involving multi-focal prostate tumours was developed. At year's end, ethics approvals were being reviewed and samples were being sourced. A postdoctoral research position was advertised, candidates were short-listed and interviewed, and an offer was made and accepted to begin in early 2010.

- (c) A computational workflow for reverse-engineering of network topology based on expression data was implemented and tested on public breast-cancer data (Madhamshettiwar, Davis, Ragan).
- (d) Thomas Whittington continued work on the role of chromatin modifications in transcriptional regulation. In collaboration with Paul Horton (Computational Biology Research Center, Tokyo) we showed that advanced machine-learning algorithms can predict which TF binding sites are functional in a given tissue. This work will be published in 2010 in *Proceedings of the Computational Intelligence in Bioinformatics and Computational Biology* (Whittington, Bailey).
- (e) Robert McLeay completed a study of motif enrichment analysis methods for determining which TFs regulate a set of genes. He created an improved algorithm for analysing data from chromatin immunoprecipitation experiments (ChIP), the most popular technology for detecting where transcription factors bind in the genome. A manuscript was accepted for publication in *BMC Bioinformatics* (McLeay, Bailey).
- (f) Fabian Buske created an improved method for predicting the roles of TFs. The new method uses sequence conservation to computationally predict the involvement of more TFs (via their DNA-binding motifs) in biological processes, functions and cellular compartments. The new method, GOMO, has been made freely available for use by biologists via the website of the MEME Suite of Motif-based sequence analysis tools and a manuscript was accepted for publication in *Bioinformatics* (Buske, Bauer, Bodén, Bailey). We also drafted a review of the role of RNA-DNA triplexes in transcriptional regulation (Buske, Bailey, Mattick).
- (g) Denis Bauer developed computational models of transcription and algorithms for optimising them; her paper appeared in *Bioinformatics* in 2009. We developed models to predict sumoylation sites in TFs (the cell is believed to use sumoylation to change the action of transcription factors); this work will appear in *Neurocomputing* in 2010 (Bauer, Buske, Bodén, Bailey).

Research Programs



- (h) Mikael Bodén developed a method for modelling the localisation of proteins to promyelocytic (PML) nuclear bodies. This work is aimed at understanding how TFs and related proteins are trafficked in and out of these nuclear structures. This work was accepted for publication in *Journal of Computational Biology*.
- (i) Stefan Maetschke developed a scalable algorithm and software (MOSAIC) to discover, visualise and analyse related but highly divergent areas of protein sequence. The method, which uses shared n -grams and spectral analysis, is much faster than multiple sequence alignment and phylogenetic analysis. A manuscript was accepted in *Bioinformatics* for publication in 2010 (Maetschke, Kassahn, Ragan and collaborators).

Research Programs

2.2 Differential expression of genes towards pathway discovery

Investigator:

Prof. Geoff McLachlan
(The University of Queensland)

In collaboration with:

Dr Regina Berretta
(The University of Newcastle)

A/Prof. Phoebe Chen
(Deakin University)

A/Prof. Pablo Moscato
(The University of Newcastle)

Researchers:

Research Associate:

Dr Kim-Anh Lê Cao
(The University of Queensland)

PhD Students:

Mr Mateus Rocha de Paula
(The University of Newcastle)

Mr Renato Vimieiro
(The University of Newcastle)

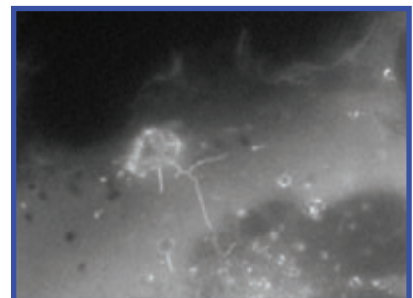
Aims:

This project aims to:

- (a) Develop further methodology for the problem of the detection of genes that are differentially expressed in a given number of classes. It is proposed that more-powerful methods can be obtained by modelling directly the gene-expression profiles rather than working with the P -values obtained by summary statistics of the differences between the classes.
- (b) Complete the development of user-friendly software to implement the methodology in (a) for use by biologists.
- (c) Continue work on the development of a fast and general method of factorisation which is based on decomposition by parts that can reduce the dimension of gene-expression data from thousands of genes to several factors. The proposed method is to be applied to data under analysis by this Program.
- (d) Continue with the development of powerful methods for the clustering of short time-series applicable for the clustering of gene profiles in an attempt to find genes that are co-expressed over time from data collected in time course experiments.

Achievements (2009):

- (a) Encouraging results have been obtained for statistical methods and software for the problem of the detection of differential expression, using models that allow for correlations between the gene profiles. These methods are based on the EMMIX-FDR and EMMIX-WIRE procedures. The improvement in power from this approach based on stronger distributional assumptions has been demonstrated in several data sets
- (b) We have extended the EMMIX-WIRE procedure for the clustering of gene profiles including time-course data by specifying the fixed effects as a function of time via the leading terms in a Fourier series in which the period is allowed to differ in each cluster. Our result from the use of this approach has been demonstrated to be superior to existing procedures proposed up to now in the literature.
- (c) Using mixtures of experts methodology for tackling complex nonlinear problems, we have developed an approach to the supervised classification of tissue samples that is based on both clinical factors and gene markers. A manuscript has been prepared on this work.



Research Programs

2.3 Discovery and modelling of RNA-based regulatory networks

Investigators:

Prof. John Mattick
(The University of Queensland)

A/Prof. Phoebe Chen
(Deakin University)

A/Prof. Pablo Moscato
(The University of Newcastle)

In collaboration with:

Dr Tim Bailey
(The University of Queensland)

Dr Regina Berretta
(The University of Newcastle)

Dr Colleen Nelson
(Translational Research Institute,
QUT / Princess Alexandra Hospital)

Dr Carlos Riveros
(The University of Newcastle)

Researchers:

Research Associates:

Dr Qingfeng Chen
(Deakin University)

Dr Marcel Dinger
(The University of Queensland)

Dr Mario Inostroza-Ponta
(The University of Newcastle)

Research staff:

Dr Lynn Fink
(ARC Centre of Excellence in Bioinformatics)

Mr David Wood
(Queensland Facility for Advanced
Bioinformatics)

PhD student:

Mr Feng Chen
(Deakin University)

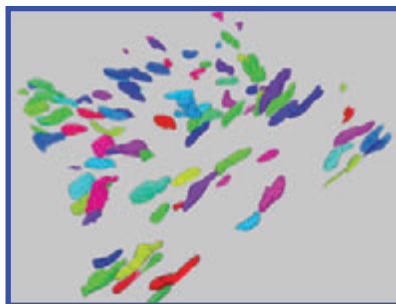
Aims:

Apply microarray technologies to discover novel non-protein-coding RNAs (ncRNAs) involved in the control of in mammalian systems under selected conditions of development, health and disease.

Infer and characterise RNA-based regulatory networks involved in these systems, and identify the molecular interactions by which this control is transduced.

Characterise candidate ncRNAs transcripts in human, and identify their homologs in other mammalian and vertebrate genomes and transcriptomes.

Identify evolutionarily conserved secondary structures in ncRNAs and construct hypotheses concerning their function.



Achievements (2009):

- (a) We have expanded the databases of ncRNAs and their expression patterns (RNAdb2.0 and NRED) (Mattick).
- (b) We have developed a system for cross-referencing expression data with different transcript relationships, such as genomic context, clustering and three-dimensional proximity (using hi-C) (Mattick).
- (c) We have developed algorithms and programs to identify evolutionarily conserved secondary structures in ncRNAs (Mattick).
- (d) We have developed a standardised nomenclature for naming ncRNAs, in conjunction with HUGO's Gene Nomenclature Committee and the European Bioinformatics Institute (Mattick).
- (e) We have improved the learned candidate models by combining expanded data from RNAdb, NONCODE and other relevant databases (Chen).
- (f) We have investigated discovering sequence and structural features of ncRNA patterns in specific ncRNAs, including tRNA (Chen).
- (g) We have started to plan to develop filtering algorithms to search for non-coding RNAs in genomes by proposing novel similarity functions (Chen).
- (h) We developed a clustering algorithm and are using it to identify clusters of ncRNAs of high sequence similarity across species (Moscato, Berretta, Inostroza-Ponta).

Research Programs

Program 3 – Modelling dynamic cellular processes

3.1 Mathematical modelling of genetic regulatory networks and biochemical pathways

Investigators:

Prof. Kevin Burrage
(The University of Queensland)

Dr Markus Hegland
(Australian National University)

In collaboration with:

Prof. Manuel Barrio
(Valladolid University, Spain)

Dr Mikael Bodén
(The University of Queensland)

Prof. Simon Davis
(Oxford University, UK)

Dr Nicholas Hamilton
(The University of Queensland)

Prof. Des Higham
(University of Strathclyde, UK)

Dr André Leier
(ETH, Switzerland)

Dr Grant Lythe
(University of Leeds, UK)

Dr Tatiana Marquez Lago
(ETH, Switzerland)

Dr Carmen Molina-Paris
(University of Leeds, UK)

Dr Martin Swain
(Edinburgh University)

Prof. Jordi Villa
(University of Barcelona, Spain)

Researchers:

Research Associates:

Dr John Belward
(The University of Queensland)

Dr Pamela Burrage
(The University of Queensland)

Dr Fawang Liu
(The University of Queensland)

Dr Shev MacNamara
(The University of Queensland)

Research Assistant:

Ms Denis Bauer
(The University of Queensland)

PhD students:

Mr Alhadi Bustamam
(The University of Queensland)

Ms Chin Foon Khoo
(Australian National University)

Mr Vikram Sunkara
(Australian National University)

Aims:

When viewed in isolation, a genome-wide data set seldom reflects the dynamic nature of cellular processes. Likewise, static biological networks such as molecular interaction and regulatory networks do not adequately represent the true complexity of biological systems.

We aim to generate mechanistic explanations for emergent system properties by:

- (a) integrating multiple complementary data sources (that on their own fail to reflect the dynamic nature of components); and
- (b) utilising a dynamic representation (introducing a notion of time).

We will utilise recent dynamic data in the context of static data, to build representations of components that are spatially and temporally constrained. This can involve building semi-dynamic network representations based on snapshots of system states at particular times or in particular tissues. Alternatively, by representing (temporal) transitions between states the model can also *predict* the state of the process.

Achievements (2009):

We have:

- (a) Developed new, efficient methods for the simulation of large-scale stochastic biochemical kinetic models based on discrete, stochastic simulation methods (Barrio, Burrage, Higham, MacNamara, Villa – manuscript accepted in *Journal of Chemical Physics*).
- (b) Developed new models that incorporate both extrinsic and intrinsic noise effects, including models of molecular clocks involving Hes1 and Her1/7, and used these models to evaluate the robustness of these clocks (Burrage, MacNamara, Swain – manuscript in preparation).
- (c) Investigated different methods for integrating data sources, and explored different representations of dynamic system properties. We have tested integrative methods and representations on systems biology problems for which data are available and where time plays an important role, including as the integration of a proposed gene regulatory network for yeast, and cell-cycle expression data (Bodén, Burrage, Bailey – manuscript accepted in *BMC Bioinformatics*).
- (d) Developed new methods for fitting interaction data (for proteins or genes) to dynamic mathematical models represented as differential equations, based on the Picard method and through the use of the Chemical Master Equation (Burrage, MacNamara).
- (e) Developed new stochastic methods for exploring anomalous diffusion in a variety of biological settings including that of T cell receptor immunology (Burrage, Lythe, MacNamara, Molina-Paris – book chapter accepted).
- (f) Continued with the development and analysis of Chemical Master Equation solvers for reaction networks and multiscale systems (Hegland, Khoo, Sunkara).

Research Programs

3.2 Modelling and visualising biological processes in complex spatial environments

Investigators:

Prof. Kevin Burrage
(The University of Queensland)

Dr Markus Hegland
(Australian National University)

In collaboration with:

Dr Mikael Bodén
(The University of Queensland)

Dr Nicholas Hamilton
(The University of Queensland)

Prof. John Hancock
(University of Texas, Houston)

Dr André Leier
(ETH, Switzerland)

Dr Tatiana Marquez Lago
(ETH, Switzerland)

Mr Dan Nicolau Jr
(Oxford University)

A/Prof. Rohan Teasdale
(The University of Queensland)

Researchers:

Research Associates:

Dr John Belward
(The University of Queensland)

Dr Pamela Burrage
(The University of Queensland)

Dr Fawang Liu
(The University of Queensland)

Dr Shev MacNamara
(The University of Queensland)

PhD students:

Mr Alhadi Bustamam
(The University of Queensland)

Ms ChinFoon Koo
(Australian National University)

Mr Vikram Sunkara
(Australian National University)

Aims:

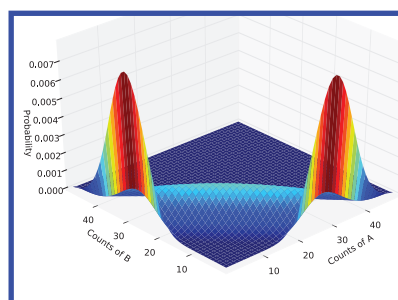
The core goal of this project is to develop novel methodologies for geometric, stochastic and statistical modelling of cellular processes based, where possible, on live cell imaging data in order to deepen our understanding of the processes being observed, and to extend the range of inference.

Some biological processes map readily to familiar mathematical formalisms (*e.g.* genetic regulatory networks as graphs). It is often less obvious how to model dynamic processes that involve complex cellular structures and spatial relationships. Within ACB we have established collaborations of experimentalists and mathematicians that have yielded new modelling techniques, new mathematics for generating experimentally verifiable hypotheses, and models for the kinetics of lipid raft mobility, tubular-vesicle formation from endosomes, macropinosome biogenesis and vesicle recycling. These models are parameterised using live cell imaging, high-resolution confocal and EM data.

- We will analyse 3D movies of processes such as macropinocytosis and Golgi events that are currently being captured in the laboratory of A/Prof. Rohan Teasdale, with the aim of getting deeper insights into the nature of the complex spatial and temporal dynamics of these cellular processes.
- We will extend this work to whole beta-cell tomograms (Program 1) and to 4D live images, producing and applying novel protocols, automated image-analysis and visualisation tools, and voxel-based stochastic simulators.
- We will extend our virtual membrane models so that simulations can be run on larger problems and over more-appropriate (longer) time scales.

Achievements (2009):

- We developed new parameter-fitting techniques and applied them to important genetic regulatory models (Burrage, Hamilton, Liu – manuscript submitted to *SIAM Journal on Scientific Computing*).
- We continued our work on parallelising chemical kinetic processes on the plasma membrane, putting more-realistic chemistry into the simulations. Implementations have been carried out on heterogeneous networks of computers (Burrage and Burrage – paper presented at HiBi 2009 and manuscript accepted).
- We built and are refining models of phosphoinositide transformations in endocytosis. These models give detailed information on the rates and relationships between phosphoinositides based on quantification from experimental imaging. These are the first mathematical models created of this important system that has been implicated in a number of major disease pathways including *Salmonella* infection (Hamilton, Burrage, Teasdale, Hyde).
- We further refined our virtual membrane models by considering more-sophisticated models of lipid raft formation and breakup (Burrage, Hancock, Nicolau Jr -- manuscript in preparation).
- We developed new numerical techniques for simulating anomalous diffusion (Burrage and Liu – paper in *Journal of Computational and Applied Mathematics*).
- We developed new Bayesian techniques for modelling the responses of axons to molecular gradients (Mortimer, Goodhill, Burrage – paper in *Proceedings of the National Academy of Sciences USA*).



Research Programs

Program 4 – Algorithms for graphs and networks

4.1 Discrete optimisation and graph clustering

Investigator:

Prof. Michael Fellows
(The University of Newcastle)

In collaboration with:

Mr Daniel Hermelin
(University of Haifa)
Prof. Mike Langston
(University of Tennessee and ORNL)

Researcher:**Research Associate:**

Dr Frances Rosamond
(The University of Newcastle)

Aims:

- (a) Develop and implement algorithms for discrete clustering problems related to the VERTEX COVER problem, especially FPT algorithms that can be applied to very large datasets due to effective data-reduction subroutines.
- (b) Integrate discrete clustering models with problems concerning motif identification for sequence-based datasets.
- (c) Develop general algorithmic approaches to classes of discrete clustering problems, such as MINIMUM EDGE DELETION EDITING to a graph of maximum degree d (the VERTEX COVER problem is the special case $d = 0$).
- (d) Develop algorithms for problems on coloured graphs, such as the graph-based Biochemical Motif Identification problem (a relaxed form of coloured subgraph isomorphism), and problems on convex recolouring of trees applicable in phylogenetic modelling and analysis.
- (e) Integrate novel algorithmic strategies for identifying key nodes in networks, with broader strategies for experimentally verifying interpretations of the data suggested by the algorithmic outputs.
- (f) Develop algorithms for multiple-interval graph-based analysis of sequence data.
- (g) Develop new algorithms for realistic discrete graph-based modelling of haplotype data in the presence of errors.

Achievements (2009):

We have:

- (a) Continued to work on the parameterised complexity of clustering and ranking algorithms. To facilitate collaborations, we visited Friedrich-Schiller University (Jena, Germany) for three weeks in April 2009. Several manuscripts were completed and submitted to conferences and journals.
- (b) Developed plans for implementation of further FPT algorithms, particularly in collaboration with PI Prof. Mike Langston. We visited Prof. Mike Langston in Tennessee in July 2009, and began to organise a Dagstuhl workshop on implementation of FPT algorithms.
- (c) Presented two invited lectures in the seminar series at the City University of Hong Kong in April, 2009.
- (d) Presented extensive lectures at a Summer School on FPT in Montpellier (France), and worked on kernelisation problems during a visit to Le Laboratoire d'Informatique de Robotique et de Microélectronique de Montpellier (LIRMM) in May and June, 2009.
- (e) Revised a collaborative manuscript on convex recolouring. In early 2010 the revised manuscript was accepted for publication in the journal *Algorithmica*. We completed a number of other projects about highly structured graph problems.
- (f) Completed two projects addressing intellectual workflow issues.
- (g) Revised and resubmitted a manuscript on multiple-interval graph problems.
- (h) Revised and resubmitted a manuscript on haplotyping problems in genomics.
- (i) Project 4.1 was concluded on 31 December 2009, with the resignation of Prof. Fellows from the ARC Centre of Excellence in Bioinformatics. Prof. Fellows will take up an ARC Professorial Fellowship from 1 January 2010. Project 4.1 has been successful in extending the FPT framework to problems motivated by genome-scale bioinformatics, developing and implementing scalable FPT algorithms, and in transferring knowledge and expertise to other Programs and Projects.

Research Programs

4.2 Optimisation-based approaches to large systems

Investigator:

A/Prof. Pablo Moscato
(The University of Newcastle)

In collaboration with:

Dr Timothy Bailey
(The University of Queensland)

Dr Regina Berretta
(The University of Newcastle)

A/Prof. Phoebe Chen
(Deakin University)

Prof. Hugh Craig
(The University of Newcastle)

A/Prof. Mick Hunter
(The University of Newcastle)

Prof. Mike Langston
(University of Tennessee and ORNL)

Prof. Geoff McLachlan
(The University of Queensland)

Dr Alexandre Mendes
(The University of Newcastle)

Dr Carlos Riveros
(The University of Newcastle)

Prof. John Rostas
(The University of Newcastle)

Dr Osvaldo Rosso
(The University of Newcastle)

Researchers:

Research Associates:

Dr Marcel Dinger
(The University of Queensland)

Dr Martin Gómez-Ravetti
(The University of Newcastle)

Dr Mario Inostroza-Ponta
(The University of Newcastle)

Research Assistant:

Mr Daniel Johnstone
(The University of Newcastle)

PhD students:

Mr Mateus Rocha de Paula
(University of Newcastle)

Mr Renato Vimieiro
(University of Newcastle)

Intern:

Ms Christina Fröstl
(Upper Austria University of Applied Sciences)

Aims:

- (a) Develop a comprehensive methodology based on combinatorial optimisation approaches for the identification of “oncosystems”, networks of highly correlated gene expression patterns in cancer samples as measured from microarray and miRNA datasets.
- (b) Address open problems including the development of powerful semi-supervised methods that identify subgroups representing potentially under-sampled phenotypes.
- (c) Develop more-robust pattern recognition methods that allow platform-independent recognition of molecular profiles characterising phenome subtypes, and will combine unsupervised and semi-supervised approaches to identify pathways that are differentially expressed according to disease state.

Achievements (2009):

- (a) In 2009, Moscato and Berretta tested a new metaheuristic-based method, based on evolutionary algorithms, for identification of large molecular signatures in microarray datasets. In 2010 we aim to identify networks of associated transcription factors that may be related to differential expression. Mathematical models to produce such inference will be developed and the results analysed (Berretta, Moscato).
- (b) In 2009 we completed a manuscript that presents a novel methodology for identifying, from gene-expression data, the gene expression patterns that correlate with disease progression. Three datasets have been studied. The method uses Shannon entropies, and the generalised statistical complexity quantifiers based on Jensen-Shannon divergence. Berretta and Moscato have been working in this project since late 2007 with datasets in melanoma and prostate cancer. A manuscript covering methodology, implementation and results was finalised and submitted for publication in December 2009. The combined method complements the capabilities of this group in support of Projects 2.2 and 2.3.
- (c) Mario Inostroza-Ponta was awarded a PhD in April 2009. A manuscript based on Mario’s work was submitted for publication (Inostroza-Ponta, Berretta, Moscato). Mario’s thesis set a foundation for a highly scalable clustering algorithm that was used to study microarray datasets in melanoma and prostate cancer. In addition, manuscripts related to the thesis covered aspects of the application of this technique in other types of datasets (*e.g.* time series analysis, functional genomics of yeast). Mario accepted a faculty position at the Universidad de Santiago de Chile.
- (d) In 2009, we started the investigation on the use of combinatorial optimisation mathematical models based on generalisations of problems related to weighted cliques and biclique identification, to obtain better biomarkers of putative gene expression deregulation in prostate cancer (Langston, Moscato).

Research Programs

- (e) In a collaboration of Prof. Hugh Craig, in 2008 we studied a large corpus of English Renaissance literature: 185 texts (136 plays and 49 poems between 1580-1640) including 30 texts unquestionably written by Shakespeare. This constituted an excellent dataset to provide an insight on the information that can be obtained by using statistical complexity quantifiers. We have used the probability distribution function of observed word-use frequencies. We have shown that, for a given entropy, poems display higher complexity than plays, and that Shakespeare's works fall into two distinct entropy clusters. A manuscript (Rosso, Craig, Moscato) was accepted and appeared in *Physica A* (2009). We explored variants of the traditional entropy function definition that masks words with frequent but ubiquitous use. We will explore the use of these ideas in the area of high-throughput technologies datasets (Moscato, Rosso, Berretta, Riveros). Later in 2009, we used a larger dataset with the aim of finding a novel methodology for authorship in spite of the highly different profiles of plays and poems. A novel non-parametric statistic has been established, and initial tests give an indication of its usefulness. During 2010 a new manuscript describing the method and the results will be completed and submitted for publication.
- (f) In 2008, we analysed background electroencephalograms (EEG), recorded with scalp electrodes, in children with childhood absence epilepsy (CAE) and in control individuals, and developed a method that showed clear differences between CAE and healthy control background EEG. A paper (Rosso *et al.*) was submitted and published in *Journal of Neuroscience Methods* (2009). Later in 2009, a follow-up study was conducted to explore the use of (α, β) -*k*-FEATURE SET to identify a smaller, yet more predictive, sets of electrode pairs that discriminate cases from controls (Moscato, Mendes, Rosso, Rostas, Hunter); this manuscript was published in *Journal of Neuroscience Methods* (2009).
- (g) In December 2009, we submitted the results of a new method to identify biomarkers for the progression of Alzheimer's disease (Moscato, Ravetti, Rosso, Berretta).
- (g) We have studied a dataset to identify differentially expressed genes that may be useful in building classifiers that predict recurrence of estrogen positive breast cancer tumors after tamoxifen treatment (Fröstl, Moscato, Berretta).
- (h) With PhD student Renato Vimieiro, we examined novel algorithms for computing frequent itemsets in databases. Initially, the method was applied to a large database from a genome-wide association study (Vimieiro, Moscato).
- (g) Moscato and PhD student Mateus Rocha de Paula develop a new methodology to identify pairs of proteins that can predict the onset of clinical symptoms of Alzheimer's disease five years before they manifest. A manuscript is being prepared and will be submitted in 2010 (Moscato, Rocha de Paula, Berretta).

Research Programs

4.3 External-memory algorithms for analysis of massive graphs

Investigator:

A/Prof. Pablo Moscato
(The University of Newcastle)

In collaboration with:

Dr Tim Bailey
(The University of Queensland)

Dr Luciana Briol
(Universidade Federal de Rio Grande do Sul, Brazil)

Prof. Mike Langston
(University of Tennessee and ORNL)

Prof. Mark Ragan
(The University of Queensland)

Dr Marcus Ritt
(Universidade Federal de Rio Grande do Sul, Brazil)

Dr Carlos Riveros
(The University of Newcastle)

Researchers:

Research Associate:

Dr Mario Inostroza-Ponta
(The University of Newcastle)

PhD student:

Mr Ahmed Shamsul Arefin
(The University of Newcastle)

MSc student:

Mr Leomar Costa
(Universidade Federal de Rio Grande do Sul, Brazil)

Aims:

Since 2003, the meaning of *large graph* has changed by several orders of magnitude. The gene co-expression graphs analysed by Mike Langston and Pablo Moscato typically have 25K-200K nodes and ~1M edges, while problems in protein-protein interaction graphs and MACHOS (Wong & Ragan) can be 1-2 orders of magnitude larger yet.

At least initially, this project will constitute a watching brief on technologies potentially useful for the analysis of graphs of this order. We will study the feasibility of translating to bioinformatics new algorithmic advances in advanced telecommunications, including external memory algorithms and novel data structures now being implemented by AT&T for clique and quasi-clique computations in multi-digraphs of ~200M edges, and biclique partitioning in massive weighted bipartite graphs as potentially applied to multiple microarray datasets.

Achievements (2009):

During 2009 we continued the collaboration with Drs Luciana Briol and Marcus Ritt at Universidade Federal de Rio Grande do Sul, Brazil. MSc Student Leomar Costa developed an external-memory algorithm version of the clustering method developed by Moscato and Inostroza-Ponta (2005-2008) and tested it on shared datasets to compare results and validate the implementation of the algorithm. We studied the feasibility of applying this algorithm for problems involving genome-wide association studies and microarray data analysis. A manuscript explaining the method and preliminary results was prepared. PhD student Ahmed Shamsul Arefin joined the Newcastle node in May 2009 and has begun to investigate the extension of this project to GPU-based computing systems. The existing software uses STXXL, a free, open-source library available under the Boost Software License 1.0. We are starting to investigate the use of the algorithm in some datasets in Alzheimer and/or multiple sclerosis.

“Recent advances in single-molecule technologies will soon make DNA sequencing more personal and more affordable than ever. But exploring the masses of data these technologies generate is a challenge we have to face if we are to realise their true potential to transform medicine and our understanding of health and disease. It’s a great challenge, and mathematics can help.”

Dr Shevarl Macnamara, a Postdoctoral Research Assistant with the ARC Centre of Excellence in Bioinformatics based at the Institute for Molecular Bioscience at The University of Queensland, has won a 2010 Fulbright Postdoctoral Scholarship to Massachusetts Institute of Technology (MIT) in USA. Shev’s research will look at the application of mathematical and computational principles to biology.

“The potential of computational mathematics to make contributions is sometimes underestimated, but if you look just a little beneath the surface, you may find it in unexpected places. Even in the seemingly ordinary, curious minds have discovered interesting mathematics to help us understand. From things as commonplace as the way a piece of paper crumples, to the grander scales of climate modelling, computational approaches sometimes reveal surprises.

“My research involves bringing together two different fields, as well as a new technology, which is a bit like looking at chemistry one molecule at a time.

“Previously we could study chemistry only by ensemble, averaging of billions of molecules. Now, emerging technologies such as quantum dots are now allowing us to see important processes, such as the way a single molecule can bind to our DNA to turn a nearby gene on or off, or the way our immune system can detect a single molecule of a virus’s fingerprint.

“Master equations are perhaps better known in statistical physics, but the same mathematical theory can be applied to certain aspects of biology. It is especially well-suited to the purpose of modelling single molecules and thus also to enhancing related technologies, for example to make DNA sequencing faster, more accurate or cheaper.”

Professor Gil Strang at the MIT Department of Mathematics will be the mentor for this project. As a computational mathematician, his pedagogy is world-renowned.

“Continuing my studies in that department will be both humbling and inspiring, and I’m grateful to have been entrusted with this fantastic opportunity.”

Shev holds a PhD in Mathematics from The University of Queensland, and a BSc First Class Honours in Mathematics from The Australian National University. He has recently completed a postdoc at Oxford. In addition to his academic qualifications, Shev plays indoor cricket, enjoys cycling the Green Bridge over the Brisbane River, bushwalking, and exploring Australia’s natural landscapes.

The prestigious Fulbright program is the largest educational scholarship of its kind, created by US Senator J. William Fulbright and the US Government in 1946. Aimed at promoting mutual understanding through educational exchange, it operates between the U.S. and 150 countries. In Australia, the scholarships are funded by the Australian and US Governments and corporate partners, and are administered by the Australian-American Fulbright Commission in Canberra.

Incorporating material from the Australian-American Fulbright Commission press release

Key Performance Indicators

ACB's Key Performance Indicators (KPIs) encompass the following areas:

1. Research findings and competitiveness
2. Research training and professional education
3. International, national and regional links and networks
4. End-user links
5. Organisational support
6. National benefit

Highlights for 2009:

The ARC Centre of Excellence in Bioinformatics again organised and sponsored our annual national Winter School in Mathematical and Computational Biology. The 2009 Winter School was our sixth and most-successful yet, attracting 201 registrants (including 23 speakers) from 53 institutions in five countries. Winter School is designed to introduce topics in mathematical and computational biology to postgraduate and advanced undergraduate students, postdoctoral researchers, and others working in mathematics, statistics, computer science, information technology, and biological, chemical or medical sciences and engineering.

In 2009 our Investigators, research staff and students published 113 C1 journal articles and 38 E1 full conference papers, of which 69 articles and 22 papers were co-authored with overseas collaborators, an increase over the last year. A paper by Professor Kevin Burrage was mentioned on the cover of *Proceedings of the National Academy of Sciences USA*. Professor Mark Ragan was lead editor of a theme issue of *Philosophical Transactions of the Royal Society of London B: Biological Sciences*. An image from a paper by Dr Nick Hamilton graced the cover of *Traffic*.

Professor John Mattick was awarded the 2009 Julian Wells Medal of the Lorne Genome Conference. The Julian Wells Medal may be awarded annually to an Australian scientist who has made an outstanding contribution to our understanding of the organisation and expression of the genome; has contributed to the development of genomics in Australia; and has had some association with and contributed to the Lorne Genome Conference.

Partner Investigator Professor Allen Rodrigo was appointed Director of the US National Evolutionary Synthesis Centre, and accepted a joint appointment at Duke University. Allen will remain associated with The University of Auckland and with our ARC Centre of Excellence.

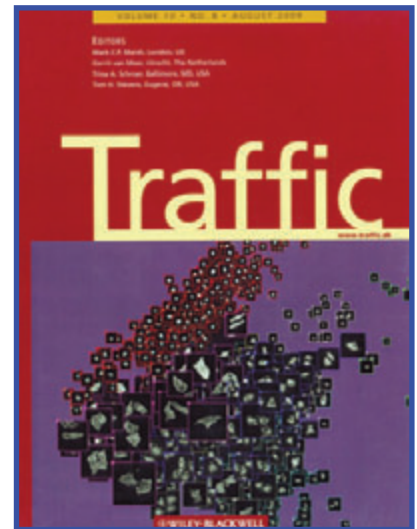
A/Professor Phoebe Chen chaired the 2009 Bioinformatics Australia conference, held in association with AusBiotech2009 in Melbourne.

ACB postdoc Dr Shev MacNamara was awarded the 2010 Fulbright Postdoctoral Scholarship, which he will take up at the Massachusetts Institute of Technology to study the application of mathematical and computational principles to single-molecule DNA technologies. Shev studied for his PhD with Dr Markus Hegland (through September 2005) and Professor Kevin Burrage, receiving his PhD in 2008 and staying on as a postdoc first at UQ, then at Oxford University. Shev was featured in our 2006 Annual Report, page 57.

ACB hosted four students from the computational systems biology program at Oxford University, UK.

The first paper describing the core Visible Cell® environment appeared (*Bioinformatics*), and was featured among other forefront technologies for visualising spatial bioscience data in a major review submitted in 2009 to *Nature Methods* (published March 2010 to coincide with the EMBO Workshop "Visualizing Biological Data"). Dr Nick Hamilton demonstrated our Visible Cell® software to a delegation led by the Minister of Science, Technology and Innovation, Malaysia, Datuk Dr Maximus Ongkili.

The article "Automated organelle-based colocalization in whole-cell imaging" (Ben Woodcroft, Luke Hammond, Jenny Stow and Nick Hamilton, *Cytometry* 75A:941-950, 2009) was featured in the journal's highlights section ("In this issue" for Issue 11, 2009).



Key Performance Indicators

1. Research findings and competitiveness

Publications

Quality of publications

ACB researchers continue to perform well in peer-reviewed publication. Our Investigators and their research groups were authors of 113 Category C1 journal articles in 2009. Of the 104 published in journals with ISI impact factors, 69 (66%) appeared in journals with an impact factor (IF) ≥ 3.0 , 37 (36%) with IF ≥ 5.0 , and 9 (8.6%) with an IF ≥ 10.0 . Of the 113 articles, 69 (61%) were co-authored with overseas collaborators.

Our Investigators demonstrated strong research performance in bioinformatics by publications in the top two specialist journals by impact factor, *Bioinformatics* (6 papers) and *BMC Bioinformatics* (7 papers). Our impact beyond bioinformatics *per se* is reflected by publications in prestigious journals including *Biological Reviews*, *Genome Research* (2), *Journal of Cell Biology*, *Nature Genetics* (3), *Nature Cell Biology*, *Nature Reviews Genetics*, *Philosophical Transactions of the Royal Society B* (2), *PLoS Computational Biology* (2), *PLoS Genetics*, *Proceedings of the National Academy of Sciences USA* (2), *Science*, *Systematic Biology*, and *Trends in Genetics*. Of our 102 C1 publications in journals assigned an ERA ranking, 36 appeared in A* journals and 43 in A journals, an increase over last year (98 C1 publications in ERA-ranked journals: 33 in A* journals and 36 in A journals).

Number of publications

The table below summarises the published output by our investigators and research groups that appeared with a 2009 publication date. We do not count papers that at the end of December 2009 were available only electronically in advance of print publication, or were in press, under review, submitted or in preparation. For details, please refer to Appendix 1: Publications and Papers.

Category	Quantity
A1 Book – authored research	1
B Book chapter	9
C1 Journal articles – articles in scholarly refereed journal	113
E1 Conference – full written paper – refereed proceedings	38
E2 Conference – full written paper – non-refereed proceedings	1
E4i Conference – edited volume of conference proceedings	5
E4 Conference – unpublished presentations	3
Other academic outputs	
– Demos	3
– Editorship of journal issue	1
– Posters	3
– Postgraduate theses	9
TOTAL	186

Patents and trademarks

No patents were awarded to our investigators during 2009.

Visible Cell® is now owned by The University of Queensland. This has been registered in Europe, USA, Australia and New Zealand. Trademark application is pending in China.

In December 2009 we filed an application for registration of trademark for Illoura™.

Centre student Feng Chen from our Deakin University node attended the BioBusiness Retreat (1–3 April 2009) held by IMBcom Pty Ltd. The BioBusiness Retreat exposes third-year students to issues in commercialisation, and to the diversity of career options. Several months prior to the retreat, students are assigned to groups and prepare, with the help of an IMBcom mentor, a business plan for presentation at the retreat.

Key Performance Indicators

Invitations to address and participate in conferences

International conferences

Chief and Partner Investigators

Dr Timothy Bailey

- Intelligent Systems for Molecular Biology (ISMB2009), Stockholm, UK (July)
- Australasian Conference on Statistical Methods for Genomic Data Analysis (SMGD), Brisbane (October)

Prof. Kevin Burrage

- Numerical Analysis and Scientific Computing with Applications (NASCA09), Agadir, Morocco (May)

A/Prof. Phoebe Chen

- Chair, Steering Committee and Program Committee, 7th Asia-Pacific Bioinformatics Conference (APBC2009), Beijing, China (January)
- Chair, Steering Committee, 15th International Multimedia Modeling Conference (MMM 2009), Sophia-Antipolis, France (January)
- Program Committee, 14th International Conference on Database Systems for Advanced Applications (DASFAA 2009), Brisbane (April)
- Program Committee, 3rd International Conference on Complex, Intelligent and Software Intensive Systems (CISIS 2009), Fukuoka, Japan (March)
- Program Committee, 13th Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD2009), Bangkok, Thailand (April)
- Program Committee, 11th IEEE International Conference on High Performance Computing and Communications (HPCC-09), Seoul, Korea (June)
- Program Committee, 2009 IEEE International Conference on Multimedia and Expo (ICME 2009), Cancun, Mexico (June-July)
- Tutorial speaker, First International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing (IJCBS 2009), Shanghai, China (August)
- Program Committee, 20th International Conference on Database and Expert Systems Applications (DEXA 2009), Linz, Austria (August-September)
- Program Committee, 1st Asian Conference on Machine Learning (ACML'09), Nanjing, China (November)

- Program Committee, 10th International Symposium on Pervasive Systems, Algorithms and Networks (I-SPAN'09), Kaoshiung, Taiwan (December)

Prof. Michael Fellows

- 26th International Symposium on Theoretical Aspects of Computer Science (STACS 2009), Freiburg, Germany (February)
- Eighth International Conference on Autonomous Agents and Multiagent Systems (AAMAS 2009), Budapest, Hungary (May)
- 20th Annual Symposium of Combinatorial Pattern Matching (CPM 2009), Lille, France (June)
- Fifth Conference on Computability in Europe (CiE 2009) on Mathematical Theory and Computational Practice, Heidelberg, Germany (July)
- 36th International Colloquium on Automata Languages and Programming (ICALP 2009), Rhodes, Greece (July)
- International Joint Conference on Artificial Intelligence (IJCAI 2009), Pasadena, California, USA (July)
- 15th Annual International Conference on Computing and Combinatorics (COCOON 2009), Niagara Falls, USA (July)
- 34th International Symposium on Mathematical Foundations of Computer Science (MFCS 2009), Novy Smokovec, Slovakia (August)

Dr Markus Hegland

- Program Committee, Fourth International Conference on High Performance Scientific Computing, Hanoi, Vietnam (March)
- Invited speaker, International Conference on Engineering and Computational Mathematics (ECM 2009), Hong Kong (May)
- Stream co-organizer, International Congress on Modelling and Simulation (MODSIM 2009), Cairns (July)

Prof. Geoff McLachlan

- 11th Conference of the International Federation of the Classification Societies (IFCS 2009), Dresden, Germany (March)
- The Classification Society and Interface Society Annual 2009 Meetings, Missouri, USA (June)
- Fourth International Conference on Rough Sets and Knowledge Technology (RSKT 2009), Gold Coast (July)
- Royal Statistical Society Conference 2009, Edinburgh, UK (September)

- CIBB 2009 – Sixth International Meeting on Computational Intelligence for Bioinformatics & Biostatistics, Genoa, Italy (October)
- Australasian Conference on Statistical Methods for Genomic Data Analysis, Brisbane (October)

Dr Brad Marsh

- Principal Organiser/Conference Chair, Asia-Pacific Congress on Electron Tomography (APCET), Brisbane. Officially supported through the 'Sir Mark Oliphant Conferences - International Frontiers of Science and Technology' program managed by the Australian Academy of Science and the Australian Academy of Technological Sciences & Engineering (January)
- Bioimage Informatics Conference, Janelia Farm Research Campus, Howard Hughes Medical Institute, Virginia, USA (April)
- Opening plenary, 26th Biennial Conference of the Society of Crystallographers in Australia and New Zealand, Barossa Valley, South Australia (April)
- American Society for Cell Biology Annual Meeting, San Diego, USA (December)

Prof. John Mattick

- Plenary, 7th Asia-Pacific Bioinformatics Conference (APBC2009), Beijing China (January)
- Plenary, Miami 2009 Winter Symposium: Interpreting the Human Genome, Miami, USA (January)
- The New World of RNAs, Biovision: 6th World Life Sciences Forum, Lyon, France (March)
- Plenary, 2009 Cologne Spring Meeting: The Variable Genome, Cologne, Germany (March)
- 74th Cold Spring Harbor Symposium on Quantitative Biology - Evolution: The Molecular Landscape, Cold Spring Harbor, New York, USA (May)
- Plenary, Keystone Symposium on MicroRNA and Cancer, Colorado, USA (June)
- Plenary, 4th European Society for Neurochemistry Conference on Advances in Molecular Mechanisms of Neurological Disorders, Leipzig, Germany (July)
- Plenary, Wellcome Trust Conference on the Evolution of Brain, Behaviour & Intelligence, Hinxton, UK (September)
- Opening Plenary, Chromatin: Structure & Function Conference 2009, Golfo de Papagayo, Costa Rica (November)

Key Performance Indicators

A/Prof. Pablo Moscato

- Seventh European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO 2009), Tübingen, Germany (April)
- Ninth European Conference on Evolutionary Computation in Combinatorial Optimization (EVOCOP 2009), Tübingen, Germany (April)
- IEEE Congress on Evolutionary Computation (CEC), Trondheim, Norway (May)
- Co-organiser, 2009 IEEE Congress on Evolutionary Computation, Special Session on Memetic Algorithms for Hard to Solve Problems, Trondheim, Norway (May)
- Eighth Metaheuristic International Conference (MIC 2009), Hamburg, Germany (July)

Prof. Mark Ragan

- Society for Molecular Biology and Evolution (SMBE) 2009, Iowa City, USA (June)
- Invited speaker, International Society for the History, Philosophy and Social Studies of Biology, Brisbane (July)
- Invited speaker, Visualising Science: Create World 2009, Brisbane (November)
- Keynote, 20th International Conference on Genome Informatics (GIW-2009), Yokohama, Japan (December)

Prof. Shoba Ranganathan

- Program Committee Member, 6th International Symposium on Bioinformatics Research and Applications (ISBRA'09), Storres, CT, USA (May)
- Invited speaker, 18th Malaysian Society for Molecular Biology and Biotechnology (MSMBB) Annual Conference, Kuala Lumpur, Malaysia (August)
- Invited speaker, MSMBB Post-conference Agri-genomics Data Management Symposium, Kuala Lumpur, Malaysia (August)
- Chair, Program Committee, 8th International Conference on Bioinformatics, Singapore (September)
- Program Committee, IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2009, Washington DC, USA (November)
- Program Committee, 20th International Conference on Genome Informatics (GIW-2009), Yokohama, Japan (December)

A/Prof. Rohan Teasdale

- Cell Organisation and Morphogenesis Conference, Singapore (June)
- RNAi For Screening Cellular Pathways and Targets, Boston, USA (November)
- RNAi for Developing Targeted Therapeutics, Boston, USA (November)
- ComBio 2009, Christchurch, NZ (December)

Prof. Xiaofang Zhou

- Vice Chair, Program Committee, 25th International Conference on Data Engineering (ICDE 2009), Shanghai, China (March)
- General Chair, Joint Asia Pacific Web Conference (APWeb) and Web Age Information Management (WAIM) Conference, Suzhou, China (April)
- Program Committee, 26th International Conference on Data Engineering (ICDE 2010), Los Angeles, USA (April)
- Chair, Program Committee, 4th International Conference on Database Systems for Advanced Applications (DASFAA 2009), Brisbane, Australia (April)
- Program Committee, 18th International World Wide Web Conference (WWW 2009), Madrid, Spain (April)
- Program Committee, 29th ACM SIGMOD International Conference on Management of Data (SIGMOD 2009), Rhode Island, USA (June)
- Program Committee, 35th International Conference on Very Large Databases (VLDB 2009), Lyons, France (August)

Postdoctoral fellows, Research Officers and students

Dr Adrian Cootes

- Bioinformatics Australia 2009, Melbourne, Australia (October)

Dr Adrian Cootes, Ms Elsa Chacko, Mr Khar Heng Choo, Mr Mohammad Islam, Mr Javed Khan, Mr Varun Khanna, Mr Gaurav Kumar, Ms Ranjeeta Menon & Mr Lawrence Wee

- Eighth International Conference on Bioinformatics, Singapore (September)

Dr Marcel Dinger & Dr Timothy Mercer

- MCGARD Marie Curie Genome Architecture in Relation to Disease, Third Conference – Higher Order Genome Architecture, Edinburgh, UK (April)

Dr Marcel Dinger, Dr Timothy Mercer, Dr Ryan Taft & Mr Paulo Amaral

- 74th Cold Spring Harbor Symposium on Quantitative Biology - Evolution: The Molecular Landscape, Cold Spring Harbor, New York, USA (May)

Dr Marcel Dinger, Dr Timothy Mercer, Dr Ryan Taft, Mr Paulo Amaral & Ms Satu Nahkuri

- Chromatin: Structure & Function Conference 2009, Costa Rica (November)

Mr. Jitendra Gaikwad

- e-Biosphere 09 International Conference on Biodiversity Informatics, London, UK (June)

Dr Nicholas Hamilton

- Janelia Biolmage Informatics Conference, Howard Hughes Medical Institute, Janelia Farm, Virginia, USA, (April)

Dr Karin Kassahn

- Genetics Society of Australasia, Brisbane (July)

Ms Chin Foon Khoo & Mr Vikram Sunkara

- Stream co-organizer, International Congress on Modelling and Simulation (MODSIM 2009), Cairns (July)

Dr Kim-Anh Lê Cao

- 41èmes Journées de Statistique (SfdS), invited presentation for the Marie-Jeanne Laurent-Duhamel prize 2009, Bordeaux, France (May)

Dr Isabel Morrow, Mr Garry Morgan, Mr Alex Foo, Mr Andrew Noske & Mr Peter van der Heide

- Asia-Pacific Congress on Electron Tomography, Brisbane, Australia (January)

Mr Vikram Sunkara

- 18th World IMACS and MODSIM 09 International Congress on Modelling and Simulation, Cairns (July)

Key Performance Indicators

National conferences

Chief Investigators

Dr Timothy Bailey

- Annual Conference of the Australasian Microarray and Associated Technologies Association (AMATA), Katoomba (October)

A/Prof. Phoebe Chen

- Conference Chair, Bioinformatics Australia 2009 (BA2009), Melbourne (October)

Dr Markus Hegland

- Australian Mathematical Society Annual Meeting, Adelaide (October)

Prof. Geoff McLachlan

- 53rd Annual Meeting of the Australian Mathematical Society, Adelaide (September-October)
- Bioinformatics Australia 2009 Conference (BA2009), Melbourne (October)
- Statistical Methods in Genetics and Bioinformatics, Brisbane (November)

Dr Brad Marsh

- Organising Committee, Australian Islet Study Group, Melbourne (August)
- Banyu (Merck) Endocrinology Educational Forum, Baker IDI Heart & Diabetes Institute, Melbourne, Australia (October)

Prof. John Mattick

- Plenary, Evolution - The Experience Conference, Melbourne (February)
- Plenary, The 2009 Lorne Genome Conference, Lorne (February)
- Opening Plenary, Mater Medical Research Institute 2009 Annual Stem Cell Symposium, Brisbane (May)
- Invited speaker, The Adelaide Festival of Ideas, Adelaide (February)
- Plenary, Charles Darwin Symposium 2009 (Charles Darwin: Shaping our Science, Society and Future), Darwin (September)
- Opening Plenary, Comparative Genomics Workshop, 30th Anniversary Conference of the Association for the Advancement of Animal Breeding and Genetics (AAABG), Barossa Valley (September)
- AMATA 2009 (9th Annual Australian Microarray and Associated Technologies Association) Conference, Katoomba (October)
- Epigenetics Annual Scientific Conference 2009, Melbourne (December)

A/Prof. Pablo Moscato

- GeneMappers 2009 conference, Blue Mountains (April)

Prof. Mark Ragan

- Bioinformatics Australia 2009 Conference, Melbourne (October)

A/Prof. Rohan Teasdale

- 29th Annual Meeting of the Australian Neuroscience (ANS 2009), Canberra (February)
- Seventh Hunter Cellular Biology Meeting, Pokolbin, NSW (March)
- TLROZ 2009, Pattern Recognition Receptors in Health and Disease, Gold Coast (October)

Postdoctoral fellows, Research Officers and students

Dr Marcel Dinger & Dr Timothy Mercer

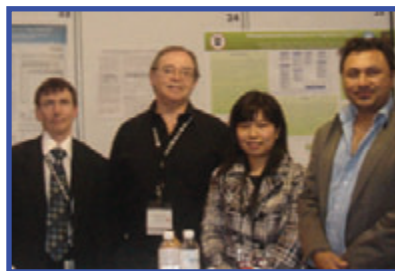
- Epigenetics Annual Scientific Conference 2009, Melbourne (December)

Dr Nick Hamilton

- Ninth Hunter Meeting, Hunter Valley, NSW (March)

Dr Kim-Anh Lê Cao

- Bioinformatics Australia 2009 Conference (BA2009), Melbourne (October)



From left: Dr Tim Littlejohn (IBM Corporation), Prof. Mark Ragan, A/Prof. Phoebe Chen and Prof. Matthew Bellgard (Murdoch University) at Bioinformatics Australia 2009 Conference, Melbourne, 30 October 2009.

Invitations to visit leading international laboratories, major research groups and centres

Chief Investigators

Dr Timothy Bailey

- Genome Sciences COMBI Seminar Series, University of Washington, USA (February)

Prof. Kevin Burrage

- Mathematics Department, University of Uppsala, Sweden (May)
- Systems Biology and Mathematics Departments, Technische Universität Braunschweig, Germany (May)
- Microsoft Computational Biology Centre, Trento, Italy (October)
- Systems Biology Centre, ETH, Zürich (October)

Prof. Michael Fellows

- Prof. Rolf Niedermeier, Friedrich-Schiller University, Jena, Germany (April, December)
- Prof. Michael Langston, University of Tennessee and Oak Ridge National Laboratory, USA (July, December)
- Le Laboratoire d'Informatique, de Robotique et de Microélectronique de Montpellier, France (May, June)
- Prof. Jan Arne Telle & Prof. Pinar Heggernes, University of Bergen, Norway (September & October)

Dr Markus Hegland

- Bungartz group, Technische Universität Munich, Germany (July)
- Hohage group, Universität Göttingen, Germany (July)
- Griebel group, Universität Bonn, Germany (August)
- Universität Marburg, Germany (September)
- Computational Science and Engineering, ETH Zürich (September)

Dr Brad Marsh

- Naomi Berrie Diabetes Center, Columbia University College of Physicians & Surgeons, New York, USA (April)
- Subcellular Structure and Cellular Dynamics unit, Curie Institute, Paris, France (June)
- Department of Biochemistry & Molecular Biology, Universitat Autònoma de Barcelona, Barcelona, Spain (June)
- Children's Medical Research Institute, Sydney (August)
- California Institute of Technology, Pasadena, USA (October)

Key Performance Indicators

- Burnham Institute for Medical Research, La Jolla, USA (October)
- Amylin Pharmaceuticals, Inc., San Diego, USA (October)
- Baker IDI Heart & Diabetes Institute, Melbourne (October)
- Lawrence Berkeley National Laboratory, Berkeley, USA (December)
- University of California San Diego, La Jolla, USA (December)
- Gatan Inc., Pleasanton, CA, USA (December)

Prof. John Mattick

- German Cancer Research Centre (DKFZ), Heidelberg, Germany (March)
- Institute for Biomedicine, University of Bergen, Norway (March)
- Rinn / Lander group, Broad Institute, MIT, Cambridge, Massachusetts, USA (June)
- Monsanto Corporation, St. Louis, Missouri, USA (June)
- Pääbo group, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany (July)
- John Curtin School of Medical Research, Australian National University, Canberra (July)
- Kouzarides group, Gurdon Institute, Cambridge, UK (September)
- National University of Singapore, Singapore (November)

Prof. Mark Ragan

- ELIXIR WP3 Global Committee Meeting, European Bioinformatics Institute, Hinxton, UK (April)
- QoS/GRID Final Review Meeting, Leibniz Supercomputing Centre, Munich, Germany (June)
- Massey University, Auckland, NZ (August)

Prof. Shoba Ranganathan

- Seminar Series, Institute of Systems Biology, Universiti Kebangsaan Malaysia (February)
- Universiti Malaya, Malaysia (August)
- Bioinformatics Institute, Singapore (September)

Prof. Xiaofang Zhou

- Fudan and Shanghai Jiaotong Universities, Shanghai (November)
- Milan Polytechnics, Italy (November-December)
- Nanjing University (December)

Postdoctoral fellows, Research Officers and students

Dr Miakel Bodén

- Dr Peter Tino, School of Computer Science, The University of Birmingham, UK (June)

Mr. Jitendra Gaikwad

- Global Biodiversity Information Facility, Copenhagen, Denmark (June)
- Royal Botanic Gardens, Kew, London, UK (June)

Dr Frances Rosamond

- Invited speaker, Chinese University, Hong Kong (April)

Commentaries about the Centre's achievements

Prof. Geoff McLachlan appeared in a commentary "Going with the skewed flow" in *Nature Methods* 6:482-483 (2009) on his joint article with Prof. Jill Mesirov, Broad Institute of MIT and Harvard entitled "Automated high-dimensional flow cytometric data analysis" in *Proceedings of the National Academy of Sciences USA* 106:8519-8524 (2009).

Prof. John Mattick was an invited speaker at the Adelaide Festival of Ideas.

Prof. Mark Ragan was an invited speaker at CreateWorld 2009 in a session with nature photographer and publisher Steve Parish.

A/Prof. Pablo Moscato appeared in:

- Hunter researchers contribute to MS discovery, HMRI media release (<http://www.hmri.net.au/pages/news/index.php?id=283>)
- Gene discovery offers hope to MS sufferers, ABC News (<http://www.abc.net.au/news/stories/2009/06/15/2597821.htm?section=justin>)
- Two gene locations linked to multiple sclerosis discovered, ScienceDaily (<http://www.sciencedaily.com/releases/2009/06/090614153259.htm>)
- Aussie and Kiwi researchers make double MS genetic discovery, Medical News Today (<http://www.medicalnewstoday.com/articles/153933.php>)
- Researchers pin down suspect MS genes, Brisbane Times (<http://news.brisbanetimes.com.au/breaking-news-world/researchers-pin-down-suspect-ms-genes-20090614-c7h5.html>)

- New hope for a multiple sclerosis cure, Newcastle Herald (<http://www.theherald.com.au/news/local/news/general/new-hope-for-a-multiple-sclerosis-cure/1541582.aspx>)

Evidence of interdisciplinary linkages within the Centre

Much of ACB's research is conducted by interdisciplinary teams within which many of our postgraduate and postdoctoral researchers are co-supervised or mentored by researchers from different fields, *e.g.* bioscience and mathematics, or bioscience and ICT. In this way we prepare the next generation of researchers to recognise and appreciate problems in systems biology to think laterally into other fields, leverage insights and methods from multiple disciplines, and work in and lead multi-disciplinary teams.

Interdisciplinary linkages among bioinformaticians, mathematicians and cell biologists (both within and external to our Centre of Excellence) deepened during 2009. One specific outcome was an Expression of Interest for a new ARC Centre of Excellence in Integrative Bioinformatics involving investigators within the Centre, and at The University of Melbourne, Monash University, and overseas universities and research institutes.

Of our 11 projects and sub-projects active during 2009, 10 (91%) included personnel with advanced degrees in different disciplines; 22 of our 30 PDFs (73%), 21 of our 60 postgraduate students (35%) worked in these 11 projects. Of our 47 C1 papers during 2009 with at least two Centre personnel as co-authors, 23 (49%) of those co-authors hold (or are working toward) advanced degrees in different disciplines. Our Winter School is intentionally interdisciplinary, and all ACB students and postdoctoral researchers are strongly encouraged to attend.

Key Performance Indicators

2. Research Training and professional education

Recruitment

In 2009, ACB recruited:

- Dr Daniel Marshall, Research Officer into Project 1.2 (Project and data management for Visible Cell® with Dr Nicholas Hamilton.
- Mr Matthew Moores, Application Developer into Project 1.2 (Project and data management for the Visible Cell®) with Dr Nicholas Hamilton.
- Ms Denis Bauer, Research Assistant into Project 2.1 (Computational discovery and modelling of gene-regulatory networks) with Dr Mikael Bodén.
- Dr Philip Machanick, Research Officer into Project 2.1 (Computational discovery and modelling of gene-regulatory networks) with Dr Timothy Bailey.
- Dr Stefan Maetschke, Research Officer into Project 2.1 (Computational discovery and modelling of gene-regulatory networks) with Prof. Mark Ragan.
- Dr Lynn Fink, Senior Research Officer into Project 2.3 (Discovery and modelling of RNA-based regulatory networks) with Prof. John Mattick.
- Dr Michael Pheasant, Software Engineer into a limited-term strategic project in collaboration with Prof. John Mattick and QFAB.

Professional/technical training and advanced career development

Seminar/Symposium hosted and/or sponsored by ACB

Second Australasian High Content User Group Meeting

ACB co-sponsored the Second Australasian High Content User Group Meeting at the University of Queensland's Institute for Molecular Bioscience (IMB) on 14 August 2009. This one-day meeting was hosted by IMB's Facility for Life Science Automation (LISA), included 10 oral presentations and a discussion forum. It attracted 30 participants from 11 top research institutions from across Australia and New Zealand. The Australasian High-Content User Group comprises scientists from Australia and New Zealand with a main interest in high-content screening and life Science automation. The group was founded in February 2009 to promote collaboration and the exchange of automation-specific knowledge, and meets bi-annually.

2009 Winter School in Mathematical and Computational Biology (6–10 July 2009)

The 2009 Winter School in Mathematical and Computational Biology featured 23 speakers (3 international, 20 national), and attracted 178 other participants from 47 institutions across Australia and from New Zealand, Malaysia, Korea and USA. Of these 93.8% were researchers or postgraduate students, and 6.2% advanced undergraduates; 44% identified a biological background, with most others from mathematics, statistics, computer science or IT. About 96% represented Australian universities. Again, we received highly positive written feedback from the participants about the topics and quality of presentations.

Each of the five days focused on a specific theme:

- Days 1 & 2: Next-Generation DNA Sequencing and Bioinformatics
- Day 3: Genome-wide Association Studies
- Day 4: Biomolecular Networks: Analysis and Inference
- Day 5: Computational Neurobiology

For the first time Winter School introduced a two-hour practical session as part of Day 3 (Genome-wide Association Studies). The format of the day included an introduction and "live" demonstration session on PLINK, followed by lectures on extensions to the standard analyses covered in the practical session. This practical session was well received.

Our distinguished invited speakers were:

- Prof. Mark Ragan
ARC Centre of Excellence in Bioinformatics,
Institute for Molecular Bioscience,
The University of Queensland
What are genomes, why sequence them, and why is genome sequencing a mathematically and computationally interesting problem?
- Mr David Miller
Australian Genome Research Facility Ltd
Classic and next-gen technologies
- Dr Annette McGrath
Bioinformatics Unit Manager
Australian Genome Research Facility Ltd
Classic and next-gen assembly strategies
- Mr Michael Imelfort
Australian Centre for Plant Functional Genomics – Bioinformatics Group
De novo assembly approaches for second-generation sequence data
- Mr Daniel Marshall
Australian Centre for Plant Functional Genomics – Bioinformatics Group
Issues of coverage with next-generation sequencing, and several applications
- Miss Lauren Bragg
Australian Centre for Plant Functional Genomics – Bioinformatics Group
Development of bioinformatics approaches to extract information from metagenomic data produced by next-generation sequencing technologies
- Prof. Sean Grimmond
Institute for Molecular Bioscience,
The University of Queensland
Next-generation assembly challenges The future of next-gen
- Dr Nicole Cloonan
Institute for Molecular Bioscience,
The University of Queensland
Transcriptomes 101 (including paired ends, mate pairs, and SNPs)

Key Performance Indicators

- Dr Lesley Collins
Institute of Molecular Biosciences,
Massey University, New Zealand
Transcriptomics and other impossible things that can be done with orphan species
- Dr Roberto Barrero
Centre for Comparative Genomics,
Murdoch University; and
Australian Bioinformatics Facility
Development of computational pipelines for microRNA profiling, chromatin modification (ChIP-Seq) and DNA methylation analysis (BI-Seq)
- Dr Gene Tyson
Advanced Water Management Centre,
The University of Queensland
Metagenomics characterisation of microbial communities
- Dr Grant W. Montgomery
Molecular Epidemiology Laboratory,
Queensland Institute of Medical Research
Genomic technologies and gene discovery in complex disease
- Dr Jim Stankovich
Menzies Research Institute,
University of Tasmania
Statistical analysis of genome-wide association study (GWAS) data
- Prof. Peter M. Visscher
Queensland Statistical Genetics,
Queensland Institute of Medical Research
GWAS for quantitative traits
- A/Prof. Pablo Moscato
ARC Centre of Excellence in Bioinformatics,
Priority Research Centre for Bioinformatics,
Biomarker Discovery and Information-Based Medicine; and
The University of Newcastle
Combinatorial optimisation models and algorithms for GWAS
- Dr Allan McRae
Queensland Statistical Genetics,
Queensland Institute of Medical Research
Gene mapping with sequence data
- A/Prof. Seiya Imoto
Human Genome Center,
Institute of Medical Science,
University of Tokyo
Statistical inference of gene networks for computational drug-target pathway discovery

- A/Prof. Seokhee Hong
School of Information Technologies,
University of Sydney
Visualisation and analysis of biological networks
- Prof. Lars Nielsen
Australian Institute for Bioengineering & Nanotechnology,
The University of Queensland
Network reconstruction, topology and feasible solution space
- Dr Melissa Davis
Queensland Facility for Advanced Bioinformatics; and
Institute for Molecular Bioscience,
The University of Queensland
An introduction to and demonstration of the Cytoscape application
- A/Prof. Geoffrey Goodhill
Queensland Brain Institute,
The University of Queensland
Brains and computers
- Prof. Thomas Albright
The Salk Institute,
La Jolla, CA, USA
Contextual influences on perception [tutorial]
- A/Prof. Michael Breakspear
Queensland Institute of Medical Research
Computational models of the brain

2009 ACB Annual All-Hands Meeting (18–19 November 2009)

ACB Chief Investigators, staff and students participated in the Annual All-Hands Meeting. On the first day, Centre's Chief Investigators and postdoctoral fellows presented a brief status of major outcomes of their respective research programs. On Day 2, Chief Investigators made plans for their research programs for 2010 and beyond.



Centre's Chief Investigators, postdoctoral fellows, students and staff at the 2009 Annual All-Hands Meeting (18-19 November 2009)

Other research and training and professional education

Apart from our Winter School, our CIs and researchers participated in:

- Prof. Michael Fellows
- French Summer School on Parameterized Algorithms, Corscia (May)
- Prof. Xiaofang Zhou
- 2nd Sino-Australia IT Research and Education Summit, Beijing (November)

Postgraduate and undergraduate courses in the Centre's area

Our investigators and researchers participated in the following for-credit courses and programs in 2009:

- Dr Timothy Bailey
- BIOL3014 Advanced Bioinformatics (lecturer and co-convener)
- Dr Mikael Bodén
- BSc Bioinformatics dual major (convener)
 - BInfTech Bioinformatics dual major (convener)
 - BIOL3014 Advanced Bioinformatics (lecturer/coordinator)
- A/Prof. Phoebe Chen
- SIT781 Introduction to Bioinformatics (lecturer)
 - SIT772 Database and Information Retrieval (lecturer)

- Dr Gabriel Fung
- INFS4203/7203 Data Mining

- Dr Markus Hegland
- 3352 Topics in Computational Mathematics

- Dr Karin Kassahn
- BIOL3010 Evolutionary and Ecological Genetics (guest lecturer)

Key Performance Indicators

Dr Stefan Maetschke

- BIOL3014 Advanced Bioinformatics: Python tutorial
- CSSE2002 Programming in the Large (lecturer)
- CSSE7023 Advanced Software Engineering (lecturer)

Prof. John Mattick

- BIOC3002 DNA and Protein Technology (lecturer)

Dr Kim-Anh Lê Cao

- STAT2004 Statistical modelling and analysis (lecturer)

Dr Brad Marsh

- BIOL3006 Molecular Cell Biology (lecturer)
- BIOC3004 Structural Biology: Macromolecular Structure (lecturer)

A/Prof. Pablo Moscato

- COMP4120 Knowledge Discovery and Data Mining (lecturer/coordinator)
- COMP2270, COMP6270 Formal Languages and Automata (lecturer and coordinator)
- SENG4800, Final Year Project (instructor)

Prof. Mark Ragan

- BIOL3004 Genomics and Bioinformatics (introductory lecture)

Prof. Shoba Ranganathan

- CBMS223 Biochemistry and Molecular Biology I (Unit coordinator and lecturer)
- CBMS880 Selected Topics in Biotechnology (lecturer)

A/Prof. Rohan Teasdale

- BIOL3004 Genomics and Bioinformatics (lecturer)

Prof. Xiaofang Zhou

- INFS4205/7205 Spatial and Multimedia Databases (lecturer)
- INFS2202/7903 Relational Database Systems (lecturer)

Outreach

The 'Scientists in Schools' program promotes science education in primary and secondary schools, helps to engage and motivate students in their learning of science, and broadens awareness of the types and variety of exciting careers available in the sciences. The project is funded under the Quality Outcomes Program administered by the Australian Government Department of Education, Employment and Workplace Relations and is managed by CSIRO. More recently, the program has been expanded to include the sub-program 'Mathematicians in Schools' supporting long-term, professional partnerships between practising mathematicians and teachers across Australia.

Over the past three years, researchers from ACB participating in the Scientists in Schools program have visited local primary schools, assisted with classroom experiments (providing both basic equipment and scientific guidance) and organised visits on-site at The University of Queensland by students, teachers and parents. In 2009, classroom visits by leading scientific animator/illustrator Mr Graham Johnson from The Scripps Research Institute were a highlight for local Year 6/7 students.

Through the CSIRO Scientists in Schools Program, Dr Melissa Davis continued her three-year partnership with Ironside State School teacher Ms Andrea O'Brien. Dr Davis presented four workshops at the annual ISS science day, and attended meetings of the School's Double Helix Club (September).

Dr Davis also participated in the Queensland State Government Talking Scientists Program. She was guest speaker at a dinner of the Toowoomba North Rotary Group, where she presented her systems biology research in breast cancer. Melissa also presented four workshops at the University of Central Queensland's Girls in Mathematics, ICT, Science and Technology day, introducing high-school students to computational biology (October).

In 2009 Prof. Kevin Burrage continued his 50-50 appointment between the Institute for Molecular Bioscience and Oxford University. Four students from Oxford's systems biology program were based at IMB for 1-2 months each.

Key Performance Indicators

3. International, national and regional links and networks

Visitors

International visitors

- Prof. Thomas Albright, The Salk Institute, USA
- Prof. Arif Anwar, General Manager, Synamatix Sdn Bhd, Malaysia
- Dr Cindy Bell, Genome Canada, Canada
- Dr Ewan Birney, European Bioinformatics Institute, EMBL, Hinxton, Cambridge, UK
- Prof. Janusz M. Bujnicki, International Institute of Molecular and Cell Biology, Poland
- Prof. Benny Chor, School of Computer Science, Tel-Aviv University, Israel
- Dr Lesley Collins, Institute of Molecular BioSciences, Massey University, New Zealand
- Prof. Peter Donnelly, Director, Wellcome Trust Centre for Human Genetics, University of Oxford, UK
- Prof. Werner Dubitzky, Professor of Bioinformatics, University of Ulster, UK
- Dr. Alejandra Figliola, Universidad de Buenos Aires, Argentina
- Prof. David Galas, Senior Vice President, Institute for Systems Biology, USA
- Dr Stephen Goldson, AgResearch, New Zealand
- Prof. Martyn Goulding, Molecular Neurobiology Laboratory, The Salk Institute, USA
- Prof. Daniel Hermelin, Department of Computer Science, Haifa University, Israel
- Prof. Philip Hugenholtz, Head, Microbial Ecology and Metagenomics Program, DOE Joint Genome Institute, USA
- Dr Steven Jones, Head of Bioinformatics, Michael Smith Genome Sciences Centre, Vancouver, Canada
- Dr Rodrigo Lopez, European Bioinformatics Institute, EMBL, Hinxton, Cambridge, UK
- Dr Kevin Morris, The Scripps Institute, La Jolla, USA
- Prof. Nor Muhammad Mahadi, Director General, Malaysia Genome Institute, Ministry of Science, Technology and Innovation, Malaysia
- Dr Maria Martín, European Bioinformatics Institute, EMBL, Hinxton, Cambridge, UK
- Prof. Jill Mesirov, Associate Director and Chief Informatics Officer, Broad Institute of MIT and Harvard University, USA

- Dr Pierre Meulien, Chief Scientific Officer, Genome British Columbia, Canada
- Dr Seán O' Donoghue, EMBL Heidelberg, Germany
- Datuk Dr Maximus Ongkili, Minister of Science, Technology and Innovation, Malaysia
- A/Prof. Seiya Imoto, Human Genome Center, Institute of Medical Science, University of Tokyo, Japan
- Dr Scott Tebbutt, UBC James Hogg Research Laboratories, and Providence Heart & Lung Institute, St Paul's Hospital, Vancouver, Canada
- Dr Claes Wahlestedt, The Scripps Institute Florida, USA
- Dr Andrew West, AgResearch, New Zealand

National visitors to one or more ACB nodes

- Dr Roberto Barrero, Centre for Comparative Genomics, Murdoch University and Australian Bioinformatics Facility
- Ms Carole Branton, Team Leader, Innovative Projects Fund, Innovation Investment Programs, Queensland Department of Employment, Industry Development and Innovation
- Mr Nick Conomo, SGI
- Dr Rhys Francis, Executive Director, Australian eResearch Infrastructure Council
- Prof. Andrew Gilbert, General Manager, Bioplatforms Australia Limited, Macquarie University
- A/Prof. Jim Hogan, Microsoft QUT eResearch Centre, Queensland University of Technology
- A/Prof. Seokhee Hong, School of Information Technologies, University of Sydney
- Prof. Richard Jefferson, Director, Initiative for Open Innovation (IOI), Chief Executive, Cambia Ltd, and Professor of Science, Technology & Law, Queensland University of Technology
- Prof. Simon Kaplan, Executive Dean, Faculty of Science and Technology, Queensland University of Technology
- Dr Gavin Kennedy, Australian Phenomics Network, Canberra
- A/Prof. Christophe Lefèvre, BioDeakin, Deakin University
- Prof. Doug McEachern, Deputy Vice-Chancellor (Research), The University of Western Australia
- Prof. Geoff McFadden, School of Botany, University of Melbourne

- Mr Benjamin Nordland, Senior Agreement Officer, Commercial Advisory Services, Queensland Department of Employment, Industry Development and Innovation
- Prof. John O'Callaghan, Director of Planning, Victorian Life Sciences Computation Initiative (VLSCI), University of Melbourne
- Dr Uwe Roehm, School of Information Technologies, University of Sydney
- Ms Elizabeth Shannon, Manager, Industry Development, Information Industries Bureau, Queensland Department of Employment, Industry Development and Innovation
- Dr Jim Stankovich, Menzies Research Institute, University of Tasmania
- Dr Anthony van Herwaarden, State Relationship Manager, Queensland CSIRO Business Development and Commercialisation
- Mr Paul Vint, Project Manager, Program and Agreement Services, Queensland Department of Employment, Industry Development and Innovation
- Dr Ross Wilkinson, Executive Director, Australian National Data Service

Key Performance Indicators

Collaborative national and international workshops and exchanges

In addition to the 2009 Winter School and Student Symposium, our CIs, PDFs, PhDs presented at or participated in workshops as follows:

Chief Investigators

Prof. Kevin Burrage

- Signal Processing Workshop for Cardiac Modelling, Zaragoza, Spain (May)
- Invited participant, The Cardiac Physiome: Multi-scale and Multi-physics Mathematical Modelling Applied to the Heart. Newton Institute for Mathematical Sciences, Cambridge University, UK (June)
- Invited speaker, Keith Worsley Workshop "Neuroimaging: Anatomical, Methodological and Statistical Constraints on Neural Mass Modeling", Banff, Canada (June)
- Cardiac Modelling Workshop '09, Monash University, Melbourne (October)
- Plenary, International Workshop on High Performance Computational Systems Biology (HiBi 2009), Trento, Italy (October)
- Cardiac Modelling and Simulation Workshop, Valencia, Spain (November)
- Stochastic Modelling Workshop, COMLAB, Oxford University, UK (November)

Prof. Michael Fellows

- 3rd International Workshop WALCOM: Algorithms and Computation (WALCOM 2009), Kolkata, India (February)
- Keynote, 20th International Workshop on Combinatorial Algorithms (IWOCA 2009), Hradec and Moravici, Czech Republic (June)
- 35th International Workshop on Graph-Theoretic Concepts in Computer Science (WG 2009), Montpellier, France (June)
- 4th International Workshop on Parameterized and Exact Computation (IWPEC 2009), Copenhagen, Denmark (September)
- Keynote, 2009 Annual Doctoral Workshop on Mathematical and Engineering Methods in Computer Science (MEMICS), Znojmo, Czechia (November)

Dr Markus Hegland

- Fifth International Workshop on Meshfree Methods for Partial Differential Equations, Bonn (August)
- Invited speaker, Dagstuhl Workshop on Algorithms and Complexity for Continuous Problems, Schloss Dagstuhl, Germany (September-October)
- Invited speaker, 2009 Fourth Trilateral Meeting on Analysis and Applications "Australia-Italy-Taiwan", Academia Sinica, Taipei (December)

Prof. Geoff McLachlan

- Workshop of the Young Statisticians Section (YSS) of the Royal Statistical Society, Edinburgh, UK (September)

Dr Brad Marsh

- Panel of Experts, Islet Biology section, JDRF Australian Type 1 Diabetes Research & Capacity Workshop, Melbourne (March)
- 2009 NIH Workshop on Imaging the Pancreatic Beta Cell, Washington DC, USA (April)
- 2009 EMBO Practical Workshop on Electron Tomography in Life Science, Leiden, The Netherlands (June)
- Panel of Experts, Workshop on Structure & Function of the Golgi Complex, Centre for Genomic Regulation (CRG), Barcelona, Spain (June)

Prof. Shoba Ranganathan

- Introductory workshop on automated EST analysis, Institute of Systems Biology, Universiti Kebangsaan Malaysia (February)
- Workshop on Education in Bioinformatics and Computational Biology (WEBCB) 2009, Singapore (September)

A/Prof. Rohan Teasdale

- Organiser, Annual High Content User Group Meeting, Brisbane (August)
- Workshop on Strategies for Effective RNAi Screens (CHI) 2009, Boston, USA (November)
- Workshop on Strategies for Optimizing RNAi Delivery (CHI) 2009, Boston, USA (November)

Prof. Xiaofang Zhou

- General Chair, International Workshop on Location Based Social Networks (LBSN'09), in conjunction with the 17th ACM SIGSPATIAL International Conference on Advances in Geographic Information Systems, Seattle, USA (November)
- Frontiers of Data Management Workshop, Shanghai (November)
- UQ-ISCAS Joint Lab steering committee annual meeting and workshop, Beijing (December)
- Microsoft Location-based Services Workshop, Beijing (December)

Postdoctoral fellows, Research Officers and students

Dr Nicholas Hamilton

- Techfest 09: The Analysis of High Dimensional and Large Data, CSIRO, Brisbane (June)
- Program Committee, ICML-UAI-COLT 2009 Workshop on Automated Interpretation and Modelling of Cell Images, Canada (July)
- Annual High Content User Group Meeting, Brisbane (August)

Key Performance Indicators

Other research linkages

Our investigators and senior members of their research groups maintain active research linkages in Australia with essentially every research-active university, many other research institutions, several Divisions within CSIRO, and with companies. In addition we have active research linkages with numerous institutions as follows. Please see also page 42, *Invitations to visit leading international laboratories*.

National collaborating institutions:

Agilent Technologies
ARC Centre of Excellence for Integrative Legume Research
Australian Centre for Plant Functional Genomics
Australian Institute of Marine Science
Australian Neuromuscular Research Institute, West Australia
Barwon Health, Victoria
Box Hill Hospital, Victoria
Calvary Mater Newcastle, Newcastle
Centre for Clinical Research, University of Queensland
Centre for Neuroscience, University of Melbourne
Centre for Statistics, University of Queensland
CRC for Chronic Inflammatory Disease
Diamantina Institute of Cancer, Immunology and Metabolic Medicine
Elizabeth Macarthur Agricultural Institute
Energy Edge Pty Ltd., Brisbane
Flinders Medical Centre, Flinders University
Genomics Research Centre, Griffith University
Gold Coast Hospital
Hunter Medical Research Institute, Newcastle
ICT Centre, CSIRO
John Hunter Hospital, Newcastle
Ludwig Institute for Cancer Research, Austin Hospital, Melbourne
Menzies Research Institute, University of Tasmania
Museum Victoria
Nepean Hospital, New South Wales
Peter MacCallum Cancer Institute
Premion, Tugun, Queensland
Queensland Institute of Medical Research
Royal Brisbane and Women's Hospital, Brisbane
Royal Melbourne Hospital, Melbourne
Sir Charles Gairdner Hospital, Western Australia
Southern Zone Radiation Oncology, Mater Centre

The Eskitis Institute for Cell and Molecular Therapies, Griffith University
The Howard Florey Institute, University of Melbourne
The Walter and Eliza Hall Institute of Medical Research, Melbourne
The Westmead Millenium Institute, Sydney

International collaborating institutions:

Academia Sinica, Taiwan
Alfred-Wegener Institute, Germany
Allen Institute for Brain Science, Seattle, WA, USA
Auckland District Health Board, New Zealand
Auckland Hospital, New Zealand
Bergen Center for Computational Science, Bergen, Norway
Bioinformatics Centre, University of Copenhagen, Denmark
Biozentrum, University of Basel, Switzerland
Botnar Research Centre, University of Oxford, UK
Broad Institute of MIT and Harvard, Cambridge, MA, USA
Caesaria Rothschild Institute, University of Haifa, Israel
California Institute of Technology, USA
Canterbury District Health Board, New Zealand
Center for Neurologic Diseases, Brigham and Women's Hospital, Harvard Medical School, Boston, USA
Chinese University of Hong Kong, China
Christchurch Hospital, New Zealand
City University of Hong Kong, Hong Kong
Cold Spring Harbour Laboratory, New York, USA
College of Animal Science and Technology, Yunnan Agricultural University, Kunming, China
College of Automation Engineering, Nanjing University of Aeronautics and Astronautics, Nanjing, China
Computational Biology Research Center, Institute for Advanced Industrial Science and Technology, Tokyo, Japan
CRG-Centre de Regulació Genòmica, Institut Catalana de Recerca – Estudis Avancats, Spain
Cuidad Universitaria, Argentina
Dalhousie University, Halifax, NS, Canada
Dana-Farber Cancer Institute, Harvard Medical School, Boston, USA
DePaul University, Chicago, IL, USA
Discovery and Research Institute, RIKEN Wako Institute, Saitama, Japan
Dunedin Hospital, New Zealand
Durham University, UK
EMBL European Bioinformatics Institute, Hinxton, Cambridge, UK
European Brain Research Institute, Rome, Italy

European Institute of Oncology, Milan, Italy
Fudan University, Shanghai, China
George Washington University Medical Center, Washington, DC, USA
Georgetown University, Washington, DC, USA
Google, Israel
Gunma University, Gunma, Japan
Halmstad University, Sweden
Harbin Institute of Technology, Harbin, China
Harvard School of Public Health, Boston, MA, USA
Hitachi Ltd, Tokyo, Japan
Hohai University, Nanjing, China
Hong Kong University of Science and Technology, Hong Kong
Huazhong University of Science & Technology, Wuhan, China
Human Genome Sequencing Center, Baylor College of Medicine, Houston, USA
Imperial College London, UK
Institut de Mathématiques de Toulouse, Université de Toulouse et CNRS, France
Institut für Informatik, Friedrich-Schiller-Universität Jena, Germany
Institut für Mathematik, Technische Universität Berlin, Germany
Institut National des Sciences Appliquées, Toulouse, France
Institut Pasteur, Paris, France
Institute of Advanced Energy, Kyoto University, Japan
Institute for Brain Disorders and Neural Regeneration, New York, USA
Institute for Infocomm Research, Singapore
Institute for Theoretical Computer Science, Charles University, Prague, Czech Republic
Institute of Biomedical Technologies, National Research Council, Milan, Italy
Institute of Genetics and Biophysics, Consiglio Nazionale delle Ricerche, Naples, Italy
Institute of Infectious Disease and Molecular Medicine, University of Cape Town, South Africa
Institute of Information and Computing Sciences, Utrecht University, Netherlands
Institute of Mathematical Sciences, India
Instituto Nacional de Salud Pública en México
International Institute of Information Technology, Chennai, India
Irish Centre for High End Computing, Dublin, Ireland
Istituto di Ricovero e Cura a Carattere Scientifico MultiMedica, Milan, Italy
Istituto Nazionale Tumori, Milan, Italy
Karolinska Institutet, Stockholm, Sweden
Kazusa DNA Research Institute, Chiba, Japan
Keio University, Kanagawa, Japan

Key Performance Indicators

Key Laboratories of Data Engineering and Knowledge Engineering, Ministry of Education, Beijing, China
Key Laboratory of High Confidence Software Technologies (Ministry of Education), Peking University, China
Kyoto University, Kyoto, Japan
Linköping University, Sweden
Lund University, Sweden
McGill University, Québec, Canada
Medical University of Gdansk, Poland
Moredun Research Institute, UK
MRC Laboratory of Molecular Biology, Cambridge, UK
Nanyang Technological University, Singapore
National and Kapodistrian University of Athens, Greece
National Biomedical Computation Resource, University of California, USA
National Chung Hsing University, Taichung, Taiwan
National Research Institute for Child Health and Development, Tokyo, Japan
National University of Defense Technology, Changsha, China
National University of Ireland, Ireland
National University of Singapore, Singapore
National Yang-Ming University, Taiwan
Netanya Academic College, Netanya, Israel
Osaka University of Pharmaceutical Sciences, Osaka, Japan
Osaka University, Osaka, Japan
Oxford University, UK
Parahyangan Catholic University, Bandung, Indonesia
Partners Center for Personalized Genetic Medicine, Boston, USA
Peking University, Beijing, China
Poznań Supercomputing and Networking Center, Poland
Purdue University, West Lafayette, IN, USA
Renmin University of China, Beijing, China
Rensselaer Polytechnic Institute, Troy, NY, USA
Research Organization of Information and Systems, Center for Information Biology and DNA Data Bank of Japan (DDBJ), National Institute of Genetics, Shizuoka, Japan
RIKEN Omics Science Center, RIKEN Yokohama Institute, Japan
Saitama Medical School, Saitama, Japan
Shanghai Key Laboratory of Intelligent Information Processing, Fudan University, Shanghai, China
South African National Bioinformatics Institute, University of the Western Cape, Bellville, South Africa
St. Vincent's University Hospital, Dublin, Republic of Ireland
Stanford University, USA
State Key Lab for Advanced Optical Communication Systems & Networks, Peking University, China
State University of New York at Stony Brook, USA
Swiss Institute of Bioinformatics, Switzerland
Systems Biology Institute, Tokyo, Japan
Technical University of Catalonia, Barcelona, Spain
Technical University of Eindhoven, Netherlands
Temasek Life Sciences Laboratory, Singapore
The Scripps Research Institute, Florida, USA
The University of Edinburgh, UK
Tokyo Institute of Technology, Japan
Tokyo Institute of Technology, Tokyo, Japan
Tokyo University of Science, Japan
Tottori University, Japan
Tsinghua University, Beijing, China
Universidad de Buenos Aires, Argentina
Universidade Federal de Minas Gerais, Brasil
University College London, UK
University of Auckland, New Zealand
University of Bari, Italy
University of Bergen, Norway
University of Bristol, UK
University of California, Davis, USA
University of California, Los Angeles, USA
University of California, San Diego, USA
University of Central Florida, Orlando, FL, USA
University of Freiburg, Germany
University of Haifa, Israel
University of Iceland, Reykjavik, Iceland
University of Leeds, UK
University of Milan, Italy
University of Otago, New Zealand
University of Puerto Rico, San Juan, PR, USA
University of Regensburg, Germany
University of Science and Technology, Beijing, China
University of Tokyo, Japan
University of Ulster, UK
University of Washington, Seattle, USA
UPMC University, Paris, France
Utrecht University, Netherlands
Victoria University of Wellington, New Zealand
Wellington Cancer Centre, New Zealand
Western General Hospital, Edinburgh, UK
Xiamen University, Xiamen, China
Yale University, New Haven, CT, USA

Key Performance Indicators

Membership on national and international professional committees

In addition to participation on organising or program committees for specific conferences or workshops, ACB Chief Investigators were actively engaged in 2009 with executive, management and professional committees, advisory and review committees, and similar continuing bodies (excludes fellowships, journal editorial boards and learned societies):

Prof. Kevin Burrage

- Research Committee, Oxford Centre for Integrative Systems Biology

A/Prof. Phoebe Chen

- Management Committee, Bioinformatics Australia (AusBiotech)

Prof. Michael Fellows

- Steering Committee, International Workshop on Parameterized and Exact Computation (IWPEC)

Prof. Geoff McLachlan

- President-Elect, International Federation of Classification Societies
- College of Experts, Australian Research Council

Dr Brad Marsh

- Chair, Communications & Program Awareness Sub-committee, Network for Pancreatic Organ Donors with Diabetes (Juvenile Diabetes Research Foundation, USA)
- Biology Faculty Member (Invited), Faculty of 1000 Cell Biology (Membranes & Sorting)

Prof. John Mattick

- Chair, Scientific Advisory Committee, Lorne Genome Conference
- Research Advisory Committee, Peter Macallum Cancer Centre
- Scientific Advisory Committee, Bioplatforms Australia

A/Prof. Pablo Moscato

- Research Council Member, Hunter Medical Research Institute
- Strategic Research Advisory Panel, Hunter Medical Research Institute

Prof. Mark Ragan

- Vice-president, Bioinformatics Australia (AusBiotech)
- Committee on Global Collaborations, European Life Sciences Infrastructure for Biological Information (ELIXIR)
- Steering Committee, Australian National Data Service
- National Working Group and Queensland Coordinator, EMBL Australia
- Chair, Management Committee, and Member, Industrial Research Advisory Panel, Queensland Facility for Advanced Bioinformatics
- Advisory Board, QosCosGRID (Quasi-Opportunistic Supercomputing for Complex Systems in Grid Environments) project, European Sixth Framework
- External Examiner, Masters of Biotechnology Programme, Universiti Malaya (2005-2010)

Prof. Shoba Ranganathan

- President, Asia-Pacific Bioinformatics Network
- Chair, International Conference in Bioinformatics Executive Committee
- Chair, S* Life Science Informatics Alliance
- Steering Committee, Bioinformatics Australia (AusBiotech)
- Council, International Immunomics Society

Prof. Xiaofang Zhou

- Executive Committee, Web Information Systems Engineering Society (WISE Society)
- Expert Consultant, Mid and Long Term Strategic Planning for Science and Technology Development, Ministry of Science and Technology of the People's Republic of China
- Academic Board, State Ministry of Education Key Lab in Data Engineering and Knowledge Engineering, China

Research projects with international partners

Listed below are research projects with international partners that were underway in 2009:

Dr Timothy Bailey

- A/Prof. William Noble, Department of Genome Sciences, University of Washington (USA)
Development of computational biology software tools
- Dr Paul Horton, Computational Biology Research Center (CBRC), Tokyo (Japan)
Investigation of chromatin modifications and transcriptional regulation

Prof. Kevin Burrage

- Professor Simon Davis, John Radcliffe Hospital, Oxford (UK)
Computational Immunology
- Prof. John Hancock (University of Texas Health Sciences Center, Houston) & Dr Dan Nicolau Jr, University of California at Berkeley (USA)
Stochastic simulations for modelling anomalous diffusion and exploring the role of lipid rafts in the plasma membrane
- Dr André Leier & Dr Tatiana Marquez Lago, ETH Zürich (Switzerland)
Dynamics of the Her1 and Her 7 complex in somite formation in zebrafish
- Dr Grant Lythe, University of Leeds (UK)
New numerical methods for second-order stochastic equations
- Dr Tatiana Marquez Lago, ETH Zürich (Switzerland)
Multiscale algorithms for the spatial modelling of discrete chemical kinetics in a cell
- Dr Blanca Rodriguez, Oxford (UK)
Cardiac modelling and simulation
- Professor Jordi Villa, Universitat Pompeu Fabra (Spain)
Multiscale simulation of cellular processes

Prof. Michael Fellows

- Prof. Jan Arne Telle & Prof. Pinar Heggernes, University of Bergen (Norway)
PARALGO: Parameterized Algorithms and FPT Kernelization
- Prof. Rolf Niedermeier, Friedrich-Schiller-Universität Jena (Germany)
Parameterized graph clustering algorithms for bioinformatics applications

Key Performance Indicators

- Prof. Daniel Hermelin, Haifa University (Israel)
Algorithms for problems that model sequence evolution based on multiple interval graphs and haplotype problems
 - Prof. Michael Langston, University of Tennessee and Oak Ridge National Laboratory (USA)
Integrating new algorithmic results concerning motif identification
- Dr Karin Kassahn
- Dr Stéphane Guindon, University of Auckland (New Zealand)
Positive selection and rates of evolution in duplicated gene loci
- Prof. Geoff McLachlan
- Dr Jill Mesirov, Broad Institute of MIT and Harvard (USA)
Automated high-dimensional flow cytometric data analysis
- Prof. Brad Marsh
- A/Prof. Niels Volkmann, The Burnham Institute of Medical Research, La Jolla (USA)
Automated methods for macromolecular identification in situ in electron tomograms
 - Prof. Brian Storrie, University of Arkansas for Medical Sciences (USA)
Correlative structure-function studies of cis- and trans-Golgi membrane traffic in mammalian cells
 - Mr Graham Johnson, The Scripps Research Institute (USA)
Novel computational approaches for the rapid quantitative visualization of cellular tomograms
- Prof. John Mattick
- Prof. Thomas Arendt, University of Leipzig, Leipzig (Germany)
Analysis of noncoding RNA expression and in Alzheimer's disease
 - Piero Carninci, RIKEN Omics Science Center, Yokohama (Japan)
Identification and expression of noncoding RNA in mouse and human cells
 - Dr Davide Gabellini, San Raffaele Scientific Institute, Milan (Italy)
Noncoding RNA expression in facioscapulohumeral muscular dystrophy (FSHD)
 - Prof. Yoshihide Hayashizaki, RIKEN Omics Science Center, Yokohama (Japan)
Characterization of the mouse transcriptome
- Dr Friedemann Horn, University of Leipzig, Leipzig (Germany)
Analysis of noncoding RNA expression and function in the cell cycle
 - Dr Craig Hunter, Harvard University, Boston (USA)
Analysis of RNA transport in sidT1 and sidT2 mutants
 - Dr Craig Kaplan, Stanford University, Stanford (USA)
Analysis of nucleosome positioning and the biogenesis of tiRNAs
 - Dr Juan Larrain, Pontificia Universidad Católica de Chile, Santiago (Chile)
Deep sequencing of the transcriptome during early Xenopus development
 - Prof. Mark Mehler, Albert Einstein College of Medicine, New York (USA)
Functional analysis of noncoding RNA expression in brain and neural differentiation
 - Dr Gunter Meister, Max Planck Institute for Biochemistry, Martinsreid (Germany)
Deep sequencing of small RNAs associated with Argonaute proteins
 - Dr Kevin Morris, The Scripps Institute, San Diego (USA)
Functional analysis of tiRNAs
 - Dr Chuck Perou, University of North Carolina, Durham (USA)
Noncoding RNAs in breast cancer
 - Dr John Rinn, Broad Institute of MIT and Harvard (USA)
Functional analysis of enhancer-derived noncoding RNAs
 - Prof. Jeff Rosen, Baylor College of Medicine, Houston (USA)
Noncoding RNAs in breast development
 - Prof. David Spector, Cold Spring Harbor Laboratory, New York (USA)
Noncoding RNA expression and function in muscle development, breast cancer, paraspeckles and other nuclear compartments
 - Prof. Peter Stadler, University of Leipzig, Leipzig (Germany)
Prediction of RNA structures encoded in the mammalian genome
 - Professor Eric Westhof, IMCB, University of Strasbourg (France)
RNA structural parsing of the mammalian genome
 - Dr Matt Wright, European Bioinformatics Institute, Cambridge (UK)
Classification and nomenclature of long noncoding RNAs
- Prof. Mark Ragan
- Dr Cheong-Xin Chan, Rutgers University (USA) & Dr Robert Beiko, Dalhousie University (Canada)
Lateral genetic transfer in Staphylococcus genomes
 - Dr Cheong-Xin Chan, Rutgers University (USA) & Dr Aaron Darling, Genome Centre, University of California at Davis (USA)
Protein domains as units of lateral genetic transfer
 - Dr Shoaib Sehgal, Microsoft (USA)
Automatic, context-specific generation of Gene Ontology slims
 - Prof. Michael Zuker, Rensselaer Polytechnic Institute (USA)
Quantitative computational prediction of miRNA target sites
- Prof. Shoba Ranganathan
- US National Institutes of Health (USA)
Large-scale antibody and T-cell epitope discovery program
- A/Prof. Rohan Teasdale
- Dr Harukazu Suzuki & Prof. Yoshihide Hayashizaki, RIKEN Genomic Sciences Center (Japan)
Systematic determination of the subcellular localisation of transcriptional regulators

Key Performance Indicators

4. End-user links

Commercialisation activities

Licensing agreements were reached between The University of Queensland, University of Washington and University of California, San Diego (UCSD) regarding jointly developed computational biology software partly developed by Dr Timothy Bailey.

Government, industry and business briefings

The events below are in addition to the numerous meetings, teleconferences and interactions with colleagues in government, industry and business implicit in the above collaborations and links.

Dr Brad Marsh

- Amylin Pharmaceuticals Inc., San Diego, USA (October)
- Direct Electron LP, San Diego, USA (October)
- Gatan Inc., San Francisco, USA (December)

Prof. Mark Ragan

- NICTA Board, Brisbane (June)
- Pfizer Delegation, Brisbane (August)
- CSIRO Science Day, Brisbane (August)
- UQ Research Week 2009 – Industry and Business meeting, Brisbane (September)
- Committee for Economic Development of Australia, Brisbane (September)
- “Health Innovation: A Key Driver for Economic Development”, Innovation Series (Queensland), Brisbane (November)

Trained/ing in technology transfer and commercialisation

Prof. John Mattick and Dr Marcel Dinger worked with Invitrogen Life Technologies (USA) in the development and commercialisation of mouse and human noncoding RNA arrays (“NCode”) – see <http://www.invitrogen.com/site/us/en/home/Products-and-Services/Applications/RNAi-Epigenetics-and-Gene-Regulation/miRNA-Profiling-/NCode-miRNA-and-ncRNA-Research/NCode-Noncoding-RNA-Arrays.html>.

Public awareness programs

Dr Nicholas Hamilton met and presented ACB research to:

- Delegation from Malaysia (April)
 - Datuk Dr Maximus Ongkili, Minister of Science, Technology and Innovation
 - Prof Nor Muhammad Mahadi, Director General of Malaysia Genome Institute, Ministry of Science, Technology and Innovation.
- Delegation from British Columbia (October)
 - Dr Steven Jones, Head of Bioinformatics, Michael Smith Genome Sciences Centre, Canada
 - Dr Pierre Meulien, Chief Scientific Officer, Genome British Columbia.

Dr Brad Marsh and Dr Melissa Davis participated in the CISRO Scientists in Schools program.

Dr Davis also participated in the “Talking Scientists” public outreach programs sponsored by Queensland Government, and in workshops at the University of Central Queensland’s Girls in Mathematics, ICT, Science and Technology day, introducing high-school students to computational biology.

Key Performance Indicators

5. Organisational support

New organisations recruited to or involved in the Centre

No new organisation formally joined the Centre during 2009.

Infrastructure

World-class expertise:

Bioinformatics is a key research technology underpinning almost areas of life sciences and biotechnology. ACB researchers, students and collaborators have access to top Australian and international experts in genomics, bioinformatics, statistics, machine learning, high-performance computing, and data management and integration. This expertise is aggregated further through research collaborations, research travel and interaction support, QFAB, EMBL Australia and other initiatives.

Computing:

The ARC Centre of Excellence in Bioinformatics is headquartered on Level 6-West of the Queensland Bioscience Precinct (QBP) on the St Lucia campus of The University of Queensland. QBP-6W has been purpose-built for bioinformatics, with space for more than 75 researchers and students. All ACB researchers access some of the best computing facilities in Australia, including more than 660 research-dedicated compute cores and nearly 200 TB research-dedicated storage at IMB, new compute and storage infrastructure at UQ/QCIF, a new cluster at Newcastle Bioinformatics Initiative, and (via merit allocation) the 2200-processor NCI National supercomputing Facility. In 2009, initial funding was secured to establish the NCI Specialised computing Facility in Bioinformatics at UQ. Partners in the NCI SF are the Commonwealth Government through NCI, CSIRO, UQ, QCIF and QFAB. Our Centre of Excellence was a partner in the European Union Sixth Framework project Quasi-Opportunistic Supercomputing for Complex Systems in GRID Environments (www.qoscosgrid.eu) and in early 2008, the UQ node of ACB was physically connected to the European grid-computing testbed.

Data infrastructure:

ACB has built significant data environments, database mirrors and specialised software, some of which are exposed on our research website. Others have been partnered-into QFAB, which is further developing this infrastructure with commercial bioinformatics software (e.g. SRS) and data sources. In 2009, initial funding was secured to establish a world-first dynamic mirror of the European Bioinformatics Institute (EBI) data facilities, based in part in the NCI SF hardware at UQ. Partners in the Australian EBI Mirror are the Commonwealth Government through Bioplatforms Australia and ANDS, CSIRO, Queensland Government and UQ.

Microscopy:

The \$1.4M ACRF/IMB Dynamic Imaging Facility and the High-Content Screening Facility were established with active involvement of CI Rohan Teasdale. The former includes two state-of-the-art Zeiss Meta 510 confocal microscope systems with two-photon and motorised stage capabilities. This live-cell imaging facility complements the Advanced Cryo-Electron Microscopy Laboratory housed within the IMB, a peak node of the NCRIS-funded Australian Microscopy & Microanalysis Research Facility (AMMRF) that provides instruments and expertise for high-resolution 3D reconstruction and analysis of molecules, cells and tissues. Major equipment and infrastructure includes Tecnai 300 keV and 120 keV scopes (FEI Company), 4Kx4K fiber optic (FEI Company) and 4Kx4K lens-coupled (Direct Electron, LP) CCD cameras, as well as BalTec HPM010 and EMPact2 high-pressure freezers, automated freeze-substitution units and cryo-ultra-microtomes (Leica Microsystems). Dr Brad Marsh has a key role in providing strategic advice on facility management and personnel, new major instrument acquisition and future R&D directions – including collaborations with industry – to ensure that these facilities remain internationally competitive at the highest levels.

Next-generation DNA sequencing:

Queensland Centre for Medical Genomics was established at IMB in 2009 through the leadership of Professor Sean Grimmond, an Investigator in the first phase of ACB. Partners include Queensland Government, Applied Biosystems division of Life Technologies Corporation, SGI, and UQ. The facility is currently built around 12 ABI SOLiD next-generation sequencing platforms, making it the highest-capacity DNA sequencing facility in the Southern Hemisphere. The Australian node of the International Cancer Genome Consortium (ICGC) is based at IMB, and includes partners in the Garvan Institute (Sydney), the Peter MacCallum Institute (Melbourne), the Walter and Eliza Hall Institute (Melbourne), and in the USA. The Australian ICGC project is funded by NHMRC, Cancer Council New South Wales, Queensland Government, and UQ.

Microarrays and other wet-lab technologies:

Queensland Bioscience Precinct has state-of-the-art facilities and infrastructure to undertake a wide range of experimental phenomic research, including the Affymetrix, Agilent, Illumina and spotted-array platforms, protein expression and crystallisation, Rigaku FR-E and HU-2R x-ray sources, eight advanced mass spectrometry platforms with capillary separation front-ends and robotics, single-particle analysis, robotic high-content chemical screening, transgenic animals, and the zebrafish model system.

Network analysis for systems biology:

In 2009 the ARC LIEF Systems Biology Platform became functional. This facility enables the interoperation and systematic analysis of data from high-throughput biomolecular platforms, *in silico* exploration of network models, and experimental validation leading to a deeper understanding of the biological mechanisms in health, biotechnology and environmental processes. The platform provides a state-of-the-art, scalable computational environment to analyse, model and infer biomolecular networks. Partners in this facility include The University of Queensland, Griffith University and the Australian Stem Cell Centre. Further, our node at the University of Newcastle has purchased two individual licences of Pathway Studio for three years, to help develop the program on pathway-aware investigation of differential patterns of gene expression in microarray data. QFAB has signed an agreement to become the Australasian reference site and distributor for GeneGo.

Key Performance Indicators

Annual cash contributions from other organisations 2008–2010

	2008	2009	2010
ARC	1,144,719	1,167,900.00	1,192,134
The University of Queensland**	525,000	525,000	525,000
Australian National University	10,000	10,000	10,000
Deakin University	30,000	30,000	30,000
Macquarie University	70,000	70,000	70,000
University of Newcastle	80,000	80,000	80,000
TOTAL	1,859,719	1,882,900	1,907,134

** In addition to the cash support identified here, the Centre will benefit from IGS generated by the core ARC grant funds at UQ distributed *via* IMB.

Annual in-kind contributions: collaborating organisations 2008–2010

		2008	2009	2010*
The University of Queensland	Personnel	551,499	570,220	598,731
	Equipment	20,000	25,000	25,000
	Other	227,970	213,799	73,000
	Total	799,469	809,019	696,731
Australian National University	Personnel	22,988	29,412	30,883
	Equipment	0	0	0
	Other	8,800	9,600	0
	Total	31,788	39,012	30,883
Deakin University	Personnel	22,052	22,052	23,155
	Equipment	0	0	0
	Other	12,750	12,750	0
	Total	34,802	34,802	23,155
Macquarie University	Personnel	34,420	44,334	46,551
	Equipment	0	0	0
	Other	48,618	41,050	10,000
	Total	83,038	85,384	56,551
University of Newcastle	Personnel	74,796	67,350	31,308
	Equipment	0	0	0
	Other	21,738	29,225	0
	Total	96,534	96,575	31,308
University of Auckland	Personnel	6,985	7,334	7,700
	Equipment	0	0	0
	Other	0	0	0
	Total	6,985	7,334	7,700
University of Tennessee	Personnel	32,416	33,389	34,391
	Equipment	0	0	0
	Other		0	0
	Total	32,416	33,389	34,391
IBM	Personnel	20,000	20,000	20,000
	Equipment	0	0	0
	Other	133,353	163,353	163,353
	Total	153,353	183,353	183,353
TOTAL		1,238,386	1,288,868	1,064,071
TOTAL (annual cash + annual in-kind contributions)		3,098,105	3,171,768	2,971,205

* The numbers shown in 2010 assume indexing at 5% for the personnel component only, in addition to probable salary increments where known.

Key Performance Indicators

6. National benefit

Measures of expansion of Australia's capability in the priority area(s)

National Collaborative Research Infrastructure Scheme (NCRIS) and Education Investment Fund (EIF)

The strategic role of bioinformatics in genome-scale biology was explicitly recognised in the scoping of NCRIS capability area 5.1 (Emerging Biomolecular Platforms and Informatics) and in the entity that arose from NCRIS 5.1, Bioplatforms Australia (BPA). Core bioinformatic capabilities within and among the NCRIS/EIF-supported national genomics, proteomics and metabolomics platforms are managed by Australian Bioinformatics Facility, headquartered at Murdoch University in Perth, under contract to BPA. The strategic importance of bioinformatics has also been recognised, explicitly or implicitly, in the business plans and investments of several activities within capability area 5.16 (Platforms for Collaboration). In 2009 National Computational Infrastructure (NCI), the successor to Australian Partnership in Advanced Computing (APAC), awarded one of its two Specialised Facilities to serve national bioinformatics needs; partners in this new facility are The University of Queensland, CSIRO, Queensland Cyber Infrastructure Foundation, and Queensland Facility for Advanced Bioinformatics. Other Platforms for Collaboration bodies are investing in bioinformatics (see next paragraph).

EMBL Australia

In conjunction with the NCRIS process, Australia became an Associate Member of the European Molecular Biology Laboratory (EMBL) on 1 March 2008. Monash University was proactive in the process that led to formalisation of a new body, EMBL Australia. The founding members of EMBL Australia are CSIRO, Monash University, The University of Queensland, The University of Sydney and The University of Western Australia, as well as DIISR. The National Health and Medical Research Council (NHMRC) and the Australian Research Council (ARC) have committed support for an initiative under Australia's associate membership. Bioinformatics has a high profile within EMBL Australia. From its core Super Science funding, EMBL Australia will co-fund bioinformatics positions in several States to facilitate and coordinate uptake of genome-scale bioinformatics. Further, in 2009 funding was secured to mirror substantial components of the European Bioinformatics Institute (EBI) data facility in Australia. This EMBL Australia EBI Mirror will be co-localised with the NCI Specialised Facility in Bioinformatics (see above) and will constitute the technology core of the Queensland node of the EMBL Australia Partner Laboratory Network. Partners in the Mirror include Platforms for Collaboration bodies BPA and Australian National Data Service (ANDS), CSIRO, UQ and Queensland Government.

Bioinformatics Australia

Bioinformatics Australia, our national bioinformatics society, has been constituted within AusBiotech, Australia's peak body in biotechnology. ACB Chief Investigators Phoebe Chen, Mark Ragan (Vice-President) and Shoba Ranganathan served on the BA Committee during 2007-2009, and Rohan Teasdale was earlier instrumental in establishing BA. Mark and Shoba stood for re-election in January 2010 and both were re-elected. Bioinformatics Australia hosted the 2008 International Conference on Genome Informatics (GIW-2008), with the 2008 annual BA conference combined into GIW-2008.

Queensland Facility for Advanced Bioinformatics

As described in our 2006 Annual Report, QFAB was established to provide advanced infrastructure and service to partners and clients. ACB has supported this start-up by seconding certain infrastructure staff into QFAB on a term basis; in return QFAB manages components of our infrastructure requirements, originally focusing on the Visible Cell® project but during 2008-2009 emphasising support of ACB's Research Program 2 (Phenotype-informed discovery of networks and systems). The QFAB partners are currently The University of Queensland, Griffith University, Queensland University of Technology, Queensland Primary Industries and Fisheries, Australian e-Health Research Centre (CSIRO) and QCIF. There are indications that one or more new partners may join during 2010. In addition to its core business, during 2009 QFAB hosted advanced training sessions and was a sponsor of the BA-2009 conference in Melbourne. Several ACB alumni and alumnae now have research and/or high-end service-oriented positions in QFAB.

ACB–Oxford postgraduate student exchange

Brisbane – home away from home

Akin to the many people who have travelled to Australia before me, I arrived in Brisbane full of hope and excitement. As a postgraduate student from the Life Science Interface Doctoral Training Centre at the University of Oxford, we are afforded the opportunity to undertake two short research projects of twelve weeks' duration each, the purpose of which is to gain hands-on insight into the current state of the chosen research field before commencing a PhD degree.

Fortunately I was offered the chance to spend one such research period working with ARC Centre of Excellence in Bioinformatics researchers Prof. Kevin Burrage and Dr Nick Hamilton at the Institute for Molecular Bioscience within the beautiful sandstone campus that is St Lucia. It proved to be a fruitful partnership for all involved, during which time a mathematical model was developed in order to test a hypothesis about the mechanism utilised by Salmonellae to avoid entry into the lysosomal pathway. This work had a refreshing blend of mathematical analysis, *in silico* implementation, and cutting-edge 4D videomicroscopy data provided to us by our experimentalist colleagues at the IMB.

The deep-founded respect amongst theoreticians and experimentalists at the IMB was plain for all to see, and it created an exhilarating, focussed research environment which I enjoyed immensely. This was no more apparent than at the weekly Friday seminars where a wide range of topics was deftly discussed.

Of course, one the reasons that UQ is so internationally renowned is surely the driving force provided by the healthy level of national competition amongst many top universities in Australia. I was delighted to have been able to accompany Prof. Burrage to a conference at Monash University in relation to stochastic effects on cardiac electrophysiology.

One cannot work all the time, and nor would one want to when residing in a city such as Brisbane, where there is an abundance of activities – whether it's spending an afternoon admiring the aboriginal artwork housed at the Queensland Museum, or simply cheering on the Brisbane Lions at the 'Gabba'. Indeed it is impossible to be complacent in a region with such a wide spectrum of activities. My favoured memories include the times spent feeding elephants, snorkelling the reef, hiking in the rainforest, and even sand tobogganing.

It was an invaluable experience for me, both academically and culturally. I can only hope to return at some future stage, in whatever capacity life will allow me. I miss the people, the place, the atmosphere... and a little sunshine wouldn't be unwelcome either!

I sincerely thank the National University of Ireland, the Engineering and Physical Sciences Research Council UK, the ARC Centre of Excellence in Bioinformatics and the Institute for Molecular Biosciences for financial support throughout my time in Queensland.

Eoin Hyde
Oxford University

Names of ACB investigators, postdoctoral researchers and students are shown in boldface. We do not list papers that at the end of December 2009 were available only electronically in advance of print publication, or were in press, under review, submitted or in preparation.

A. BOOKS

A1. Books – Authored Research

Maetschke, S. (2009) *Computational protein localization prediction: Topological models of transmembrane proteins for localization prediction*. VDM Verlag. ISBN: 3639137418

B. BOOK CHAPTERS

Beiko, R.G. & Ragan, M.A. (2009) Untangling hybrid phylogenetic signals – HGT and artifacts of phylogenetic reconstruction. *In: Horizontal Gene Transfer – Genomes in Flux* (M.B. Gogarten, L.C. Olendzenski & J.P. Gogarten, Eds), Humana Press – Springer. Methods in Molecular Biology Series 532, Chapter 14, pp. 241-256. ISBN: 978-1603278522.

Chen, Y.-P.P., Rong, J. & Li, G. (2009) Advanced graph mining methods for protein analysis. *In: Biological Data Mining* (J.Y. Chen & S. Lonardi, Eds), Chapman & Hall. Chapter 6, pp. 111-136. ISBN: 978-1420086843.

Eblen, J.D., Gerling, I.C., Saxton, A.M., Wu, J., Snoddy, J.R. & **Langston, M.A.** (2009) Graph algorithms for integrated biological analysis, with applications to type 1 diabetes data. *In: Clustering Challenges in Biological Networks* (S. Butenko, W. A. Chaovalitwongse & P. Pardalos, Eds), World Scientific. Chapter 10, pp. 207-222. ISBN: 978-981-277-165-0.

Flack, L.K. & McLachlan, G.J. (2009) Clustering methods for gene-expression data. *In: Handbook of Research on Systems Biology Applications in Medicine* (A. Daskalaki, Ed.), Medical Information Science Reference. Chapter XI, pp. 209-220. ISBN: 978-1-60566-076-9.

Gomez-Ravetti, M., Berretta R. & Moscato, P. (2009) Novel biomarkers for prostate cancer revealed by (α, β) -*k*-feature sets. *In: Foundations of Computational Intelligence, Volume 5: Function Approximation and Classifications*. Series: Studies in Computational Intelligence, Vol. 205 (A. Abraham, A.-E. Hassanien, V. Snášel, Eds), Springer. Chapter 3, pp. 149-175. ISBN: 978-3-642-01535-9.

Lê Cao, K.-A., McLachlan, G.J. (2009) Statistical analysis of microarray data: selection of gene prognosis signature. *In: Computational Biology: Issues and Applications in Oncology* (T. Pham, Ed.), Springer. Chapter 3, pp. 55-76. ISBN: 978-1-4419-0812-4.

McLachlan, G.J. & Ng, S.K. (2009). The EM algorithm. *In: The Top-Ten Algorithms in Data Mining* (X. Wu & V. Kumar, Eds), Chapman & Hall. Chapter 5, pp. 93-115. ISBN: 978-1-42008-964-6.

McLachlan, G.J. (2009) Unsupervised data mining: statistical model-based clustering. *In: Comprehensive Chemometrics: Chemical and Biochemical Data Analysis. Vol. 2* (S. Brown, R. Tauler & R. Walczak, Eds), Elsevier Science. pp. 655-681. IBN: 978-044452-702-8.

Ng, S.K. & **McLachlan, G.J.** (2009). Expert networks with mixed continuous and categorical feature variables: a location modeling approach. *In: Machine Learning Research Progress* (H. Peters & M. Vogel, Eds), Hauppauge, New York: Novinka Books. Chapter 1, pp. 1-14. ISBN: 989-1-60456-646-8.

C. JOURNAL ARTICLES

C1. Journal articles in scholarly refereed publications

Abbott, W.G., Tsai, P., Leung, E., Trevarton, A., Ofanoa, M., Hornell, J., Gane, E.J., Munn, S.R. & **Rodrigo, A.G.** (2009) Associations between HLA class I alleles and escape mutations in the hepatitis B virus core gene in New Zealand-resident Tongans. *Journal of Virology* 84:621-629.

Amaral, P.P., Neyt, C., Wilkins, S.J., Askarian-Amiri, M.E., Sunkin, S.M., Perkins, A.C. & Mattick, J.S. (2009) Complex architecture and regulated expression of the *Sox2ot* locus during vertebrate development. *RNA* 15:2013-2027.

An, J. & Chen, Y.-P.P. (2009) Finding coverage using incremental attribute combinations. *International Journal of Innovative Computing, Information and Control* 5:1419-1428.

An, J. & Chen, Y.-P.P. (2009) Finding rule groups to classify high dimensional gene expression datasets. *Computational Biology and Chemistry* 33:108-113.

Asadi, S., **Zhou X. & Yang, G.** (2009) Using local popularity of web resources for geo-ranking of search engine results. *World Wide Web Journal* 12:149-170.

Bahlo, M., Booth, D.R., Broadley, S.A., Brown, M.A., Foote, S.J., Griffiths, L.R., Kilpatrick, T.J., Lechner-Scott, J., **Moscato, P.**, Perreau, V.M., Rubio, J.P., Scott, R., Stankovich, J., Stewart, G.J., Taylor, B.V., Wiley, J., Clarke, G., Cox, M.B., Csurhes, P.A., Danoy, P., Drysdale, K., Field, J., Greer, J.M., Guru, P., Hadler, J., McMorran, B.J., Jensen, C.J., Johnson, L.J., McCallum, R., Merriman, M., Merriman, T., Pryce, K., Tajouri, L., Wilkins, E.J., Browning, B.L., Browning, S.R., Perera, D., Broadley, S., Butzkueven, H., Carroll, W.M., Chapman, C., Kermod, A.G., Marriott, M., Mason, D., Heard, R.N., Pender, M.P., Slee, M., Tubridy, N. & Willoughby, E. (2009) Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. *Nature Genetics* 41:824-828.

Bailey, T.L., Bodén, M., Buske, F.A., Frith, M., Grant, C.E., Clementi, L., Ren, J., Li, W.W. & Noble, W.S. (2009) MEME Suite: tools for motif discovery and searching. *Nucleic Acids Research* 37:W202-W208.

Baker, E.J., Jay, J.J., Philip, V.M., Zhang, Y., Li, Z., Kirova, R., **Langston, M.A. & Chesler, E.J.** (2009) Ontological Discovery Environment: a system for integrating gene-phenotype associations. *Genomics* 94:377-387.

Bauer, D.C. & Bailey, T.L. (2009) Optimizing static thermodynamic models of transcriptional regulation. *Bioinformatics* 25:1640-1646.

Bodlaender, H.L., Downey, R.G., **Fellows, M.R. & Hermelin, D.** (2009) On problems without polynomial kernels. *Journal of Computer and System Sciences* 75:423-434.

Bodlaender, H.L., **Fellows, M.R. & Thilikos, D.M.** (2009) Derivation of algorithms for cutwidth and related graph layout parameters. *Journal of Computer and System Sciences* 75:231-244.

Appendix 1: Publications

- Borate, B.R., Chesler, E.J., **Langston, M.A.**, Saxton, A.M. & Voy, B.H. (2009) Comparison of threshold selection methods for microarray gene co-expression matrices. *BMC Research Notes* 2:240.
- Bordewich, M., **Rodrigo, A.G.** & Semple, C. (2009) Selecting taxa to save or sequence: desirable criteria and a greedy solution. *Systematic Biology* 57:825-834.
- Bovine Genome Sequencing and Analysis Consortium, Elsik, C.G., Tellam, R.L., Worley, K.C., Gibbs, R.A., Muzny, D.M., Weinstock, G.M., Adelson, Nogueira, M.F., Olsaker, I., Pant, S.D., Panzitta, F., Pastor, R.C., Poli, M.A., Poslusny, N., Rachagani, S., **Ranganathan, S.**, Razpet, A., Riggs, P.K., Wunderlich, K.R., Yang, J., Zhao, F.Q. (2009) The genome sequence of taurine cattle: a window to ruminant biology and evolution. *Science* 324:522-528.
- Burrage, K.** & Lythe, G. (2009) Accurate stationary densities with partitioned numerical methods for stochastic differential equations. *SIAM Journal on Numerical Analysis* 47:1601-1618.
- Buske, F.A.**, **Maetschke, S.** & **Bodén, M.** (2009) It's about time: signal recognition in staged models of protein translocation. *Pattern Recognition* 42:567-574.
- Buske, F.A.**, Thier, R., Gillam, E.M.J. & **Bodén, M.** (2009) *In silico* characterisation of protein chimeras: relating sequence and function within the same fold. *Proteins – Structure, Function and Bioinformatics* 77:111-120.
- Cantacessi, C., Zou, F.C., Hall, R.S., Zhong, W., Jex, A.R., Campbell, B.E., **Ranganathan, S.**, Sternberg, P.W., Zhu, X.Q. & Gasser, R.B. (2009) Bioinformatic analysis of abundant, gender-enriched transcripts of adult *Ascaris suum* (Nematoda) using a semi-automated workflow platform. *Molecular and Cellular Probes* 23:205-217.
- Capp, A., **Inostroza-Ponta, M.**, Bill, D., **Moscato, P.**, Lai, C., Christie, D., Lamb, D., Turner, S., Joseph, D., Matthews, J., Atkinson, C., North, J., Poulsen, M., Spry, N.A., Tai, K.H., Wynne, C., Duchesne, G., Steigler, A. & Denham, J.W. (2009) Is there more than one proctitis syndrome? A revisit using data from the TROG 96.01 trial. *Radiotherapy and Oncology* 90:400-407.
- Chacko, E.**, & **Ranganathan, S.** (2009) Comprehensive splicing graph analysis of alternative splicing patterns in chicken, compared to human and mouse. *BMC Genomics* 10 (Suppl. 1):S5.
- Chacko, E.**, & **Ranganathan, S.** (2009) Genome-wide analysis of alternative splicing in cow: implications in bovine as a model for human diseases. *BMC Genomics* 10 (Suppl. 3):S11.
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- Chan, C.X.**, **Darling, A.E.**, **Beiko, R.G.** & **Ragan, M.A.** (2009) Are protein domains modules of lateral genetic transfer? *PLoS ONE* 4:e4524.
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- Clermont, G., Auffray, C., Moreau, Y., Rocke, D.M., Dalevi, D., Dubhashi, D., Marshall, D.R., Raasch, P., Dehne, F., Provero, P., Tegner, J., Aronow, B.J., **Langston, M.A.** & Benson, M. (2009) Bridging the gap between systems biology and medicine. *Genome Medicine* 1:88.
- Deng, K., **Zhou, X.**, Shen, H. T., Sadiq, S. & Li X. (2009) Instance optimal query processing in spatial networks. *The VLDB Journal* 18:675-693.
- Detering, F., Blackwell, B.D., **Hegland, M.**, Pretty, D.G., Nagasaki, K. & Yamamoto, S. (2009) Reduction of magnetic confinement fusion data for data mining applications. *ANZIAM Journal* 50:C729-C743.
- Dinger, M.E.**, **Amaral, P.P.**, **Mercer, T.R.** & **Mattick, J.S.** (2009) Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. *Briefings in Functional Genomics & Proteomics* 8:407-423.
- Dinger, M.E.**, Pang, K.C., **Mercer, T.R.**, Crowe, M.L., Grimmond, S.M. & **Mattick, J.S.** (2009) NRED: a database of long noncoding RNA expression. *Nucleic Acids Research* 37:D122-D126.
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- Esteban-Marcos, A., **Darling, A.E.** & **Ragan, M.A.** (2009) Seevolution: visualizing chromosome evolution. *Bioinformatics* 25:960-961.
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- Fellows, M.**, Hermelin D. & **Rosamond, F.** (2009) On the fixed-parameter intractability and tractability of multiple-interval graph problems. *Theoretical Computer Science* 410:53–61.
- Fellows, M.**, Lokshtanov, D., Misra, N., Mnich, M., **Rosamond, F.** & Saurabh, S. (2009) Complexity ecology of parameters: an illustration using bounded max leaf number. *Theory of Computing Systems* 45:822–848.
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- Garcke, J & **Hegland, M.** (2009) Fitting multidimensional data using gradient penalties and the sparse grid combination technique. *Computing* 84:1-25.
- Guffanti, A., Iacono, M., Pelucchi, P., Kim, N., Soldà, G., Croft, L.J., **Taft, R.J.**, Rizzi, E., Askarian-Amiri, M., Bonnal, R.J., Callari, M., Mignone, F., Pesole, G., Bertalot, G., Bernardi, L.R., Albertini, A., Lee, C., **Mattick, J.S.**, Zucchi, I., De Bellis, G. (2009) A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. *BMC Genomics* 10:163.
- Hamilton, N.** (2009) Quantification and its applications in fluorescent microscopy imaging. *Traffic* 10:951-961.
- Hamilton, N.**, Wang, J.T., Kerr, M.C. & **Teasdale, R.D.** (2009). Statistical and visual differentiation of high throughput subcellular imaging. *BMC Bioinformatics* 10:94.

Appendix 1: Publications

- Hawkins, J., Grant, C., Noble, W. & Bailey, T.L.** (2009) Assessing phylogenetic motif models for predicting transcription factor binding sites. *Bioinformatics* 25:12:i339–i347.
- Hayward, J.J. & **Rodrigo, A.G.** (2009) Molecular epidemiology of feline immunodeficiency virus in the domestic cat (*Felis catus*). *Veterinary Immunology and Immunopathology* 134:68–74.
- Huang, Z., Shen, H.T., Shao, J., Zhou X. & Cui, B.** (2009) Bounded coordinate system indexing for real-time video clip search. *ACM Transactions on Information Systems* 27:17.
- Jiang, D., Zhou, S. **Chen, Y.-P.P.** (2009) Compensatory ability to null mutation in metabolic networks. *Biotechnology and Bioengineering* 103:361–369.
- Kassahn, K.S., Crozier, R.H., Pörtner, H.O. & Caley, M.J.** (2009) Animal performance and stress: responses and tolerance limits at different levels of biological organisation. *Biological Reviews* 84:277–292.
- Kassahn, K.S., Dang, V.T., Wilkins, S.J., Perkins, A.C. & Ragan, M.A.** (2009) Evolution of gene function and regulatory control after whole-genome duplication: comparative analyses in vertebrates. *Genome Research* 19:1404–1418.
- Kerr, M.C. & **Teasdale, R.D.** (2009) Defining macropinocytosis. *Traffic* 10:364–371.
- Khan, J. & Ranganathan, S.** (2009) A multi-species comparative structural bioinformatics analysis of inherited mutations in α -d-mannosidase reveals strong genotype-phenotype correlation. *BMC Genomics* 10 (Suppl. 3):S33.
- Khanna, V., & Ranganathan, S.** (2009) Physicochemical property space distribution among human metabolites, drugs and toxins. *BMC Bioinformatics* 10 (Suppl. 15):S10.
- Kirino, Y., Kim, N., de Planell-Saguer, M., Khandros, E., Chiorean, S., Klein, P.S., **Rigoutsos, I., Jongens, T.A. & Mourelatos, Z.** (2009) Arginine methylation of Piwi proteins catalysed by dPRMT5 is required for Ago3 and Aub stability. *Nature Cell Biology* 11:652–658.
- Lê Cao K.-A., González I. & Déjean S** (2009) integrOmics: an R package to unravel relationships between two omics data sets. *Bioinformatics* 25:2855–2856.
- Lesmono, D., Tonkes, E. & **Burrage, K.** (2009) Opportunistic timing and manipulation in Australian Federal Elections. *European Journal of Operational Research* 192:677–691.
- Li, W.L. & **Rodrigo, A.G.** (2009) Covariation of branch lengths in phylogenies of functionally related genes. *PLoS ONE* 4:e8487.
- Liu, F., Yang, C. & Burrage, K.** (2009) Numerical method and analytical technique of the modified anomalous subdiffusion equation with a nonlinear source term. *Journal of Computational and Applied Mathematics* 231:160–176.
- MacNamara, S. & Burrage, K.** (2009) Krylov and steady-state techniques for the solution of the chemical master equation for the mitogen-activated protein kinase cascade. *Numerical Algorithms* 51:281–307.
- Maetschke, S. & Yuan, Z.** (2009) Exploiting structural and topological information to improve prediction of RNA-protein binding sites. *BMC Bioinformatics* 10:341.
- Mattick, J.S.** (2009) Deconstructing the dogma: a new view of the evolution and genetic programming of complex organisms. *Annals of the New York Academy of Sciences* 1178:29–46.
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- Mattick, J.S.** (2009) The genetic signatures of noncoding RNAs. *PLoS Genetics* 5:e1000459.
- Mattick, J.S., Amaral, P.P., Dinger, M.E., Mercer, T.R. & Mehler, M.F.** (2009) RNA regulation of epigenetic processes. *BioEssays* 31:51–59.
- Mattick, J.S., Taft, R.J. & Faulkner, G.J.** (2009) A global view of genomic information – moving beyond the gene and the master regulator. *Trends in Genetics* 26:21–28.
- McComb, T., Cairncross, O., Noske, A.B., Wood, D.L.A., Marsh, B.J. & Ragan, M.A.** (2009) Illoura™: a software tool for analysis, visualization and semantic querying of cellular and other spatial biological data. *Bioinformatics* 25:1208–1210.
- Mercer, T.R., Dinger, M.E. & Mattick, J.S.** (2009) Long non-coding RNAs: insights into functions. *Nature Reviews Genetics* 10:155–159.
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- Mortimer, D., Dayan, P., **Burrage, K. & Goodhill, G.J.** (2009) Optimizing chemotaxis by measuring unbound-bound transitions. *Physica D* 239:477–484.
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- Perkins, A.D. & **Langston, M.A.** (2009) Threshold selection in gene co-expression networks using spectral graph theory techniques. *BMC Bioinformatics* 10 (Suppl.11):S4.
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Appendix 1: Publications

- Ragan, C.,** Cloonan, N., Grimmond, S.M., Zuker, M. & **Ragan, M.A.** (2009) Transcriptome-wide prediction of miRNA targets in human and mouse using FASTH. *PLoS ONE* 29:e5745.
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- Ranganathan, S.,** Eisenhaber, F., Tong, J.C. & Tan, T.W. (2009) Extending Asia Pacific bioinformatics into new realms in the «-omics» era. *BMC Genomics* 10 (Suppl. 3):S1.
- Ranganathan, S., Menon, R. & Gasser, R.B.** (2009) Advanced *in silico* analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance — fundamental insights toward biotechnological outcomes. *Biotechnology Advances* 27:439-448.
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- Shin, C.J., Wong, S., Davis, M.J. & Ragan, M.A.** (2009) Protein-protein interaction as a predictor of subcellular location. *BMC Systems Biology* 3:28.
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- The FANTOM Consortium, Suzuki, H., Forrest, A.R., van Nimwegen, E., Daub, C.O., Balwierz, P.J., Irvine, K.M., Lassmann, T., Ravasi, T., Hasegawa, Y., de Hoon, M.J., Katayama, S., Schroder, K., Carninci, P., Tomaru, Y., Kanamori-Katayama, M., Kubosaki, A., Akalin, A., Ando, Y., Arner, E., Asada, M., Asahara, H., **Bailey, T.,** Bajic, V.B., **Bauer, D.,** Beckhouse, A.G., Cloonan, N., **Fink, J.L.,** Grimmond, S.M., Gustafsson, M., **Mattick J.S.,** Simons, C., **Taft, R.J.,** **Teasdale, R.D.,** Hume, D.A., RIKEN Omics Science Center, Arakawa T, Fukuda S. *et al.* (2009) The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. *Nature Genetics* 41:553-562.

Appendix 1: Publications

Treangen, T.J., **Darling, A.E.**, Achaz, G., **Ragan, M.A.**, Messegueur, X. & Rocha, E.P. (2009) A novel heuristic for local multiple alignment of interspersed DNA repeats. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 6:180-189.

Tsirigos, A. & **Rigoutsos, I.** (2009) Alu and b1 repeats have been selectively retained in the upstream and intronic regions of genes of specific functional classes. *PLoS Computational Biology* 5:e1000610.

Webster, R.J., Giles, K.M., Price, K.J., Zhang, P.M., **Mattick, J.S.** & Leedman, P.J. (2009) Regulation of epidermal growth factor receptor signalling in human cancer cells by microRNA-7. *Journal of Biological Chemistry* 284:5731-5741.

Wee, L.J.K., Tong, J.C., Tan, T.W. & **Ranganathan, S.** (2009) A multi-factor model for caspase degradome prediction. *BMC Genomics* 10 (Suppl. 3):S6.

Woodcroft, B.J., Hammond, L. Stow, J.L. & **Hamilton, N.** (2009) Automated organelle-based colocalization in whole-cell imaging. *Cytometry Part A* 75A:11:941-950.

Wu, S.H., Black, M.A., North, R.A., Atkinson, K.R. & **Rodrigo, A.G.** (2009) A statistical model to identify differentially expressed proteins in 2D PAGE gels. *PLoS Computational Biology* 5:e1000509.

Xi, Y., **Chen, Y.-P.P.**, Cao, M., Wang, W. & Wang, F. (2009) Analysis on relationship between extreme pathways and correlated reaction sets. *BMC Bioinformatics* 10:S58.

Zhang, Y., Gao, J.S., Tang, X., Tucker, L.D., Quesenberry, P., **Rigoutsos, I.** & Ramratnam, B. (2009) MicroRNA 125a and its regulation of the p53 tumor suppressor gene. *FEBS Letters* 583:3725-3730.

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Zhou, X. (2009) Data quality. *Communications of Chinese Computer Federation* (中国计算机协会通讯) 5:49-51.

Zhou, X., **Zhou, X.**, Chen, L. & Bouguettaya, A., Xiao, N. & Taylor, J.A. (2009) An efficient near-duplicate video shot detection method using shot-based interest points. *IEEE Transactions on Multimedia* 11:879-891.

E. CONFERENCE PROCEEDINGS

E1. Conference – full written paper – refereed proceedings

Betzler, N., **Fellows, M.R.**, Guo, J., Niedermeier, R. & **Rosamond, F.A.** (2009) How similarity helps to efficiently compute Kemeny rankings. *In: Proceedings of 8th International Conference on Autonomous Agents and Multiagent Systems (AAMAS 2009)*, Budapest, Hungary, 11-15 May 2009 (K.S. Decker, J.S. Sichman, C. Sierra & C. Castelfranchi, Eds), pp. 657–664. Curran Associates, Inc. ISBN: 978-0-9817381-6-1.

Burrage, P.M., **Burrage, K.**, **Kurowski, K.**, Lorenc, M., Nicolau, D.V. Jr, Swain, M. & **Ragan, M.A.** (2009) A parallel plasma membrane simulation. *In: Proceedings of 1st International Workshop on High Performance Computational Systems Biology (HiBi 2009)*, Trento, Italy, 14-16 October 2009 (J. Guerrero, Ed.), pp. 105-112. IEEE Computer Society. ISBN: 978-0-7695-3809-9

Bustamam, A., **Sehgal, M.S.**, **Hamilton, N.**, **Wong, S.**, **Ragan, M.A.** & **Burrage, K.** (2009). An efficient parallel implementation of Markov clustering algorithm for large-scale protein-protein interaction networks that uses MPI. *In: Proceedings of the 5th IMT-GT International Conference on Mathematics, Statistics and Their Applications (ICMSA-2009)*, Bukittinggi, Indonesia, 9-11 June 2009 (I.M. Arnawa, M. Muhafzan & S. Bahri, Eds), pp. 94-101. Department of Mathematics, Andalas University, Indonesia. ISBN: 978-602-95343-0-6.

Chen, L., Cui, B., Shen, H.T., Lu, W. & **Zhou, X.** (2009) Efficient information retrieval in mobile peer-to-peer networks. *In: Proceedings of the 18th ACM Conference on Information and Knowledge Management (CIKM 2009)*, Hong Kong, 2-6 November 2009 (D.W.-L. Cheung, I.-Y. Song, W.W. Chu, X. Hu & J.J. Lin, Eds), pp. 967-976. ACM. ISBN: 978-1-60558-512-3.

Chen, Z., Shen, H.T., **Zhou, X.** & Yu, J. (2009) Monitoring path nearest neighbor in road networks. *In: Proceedings of ACM SIGMOD International conference on Management of Data (SIGMOD 2009)*, Providence, RI, USA, 29 June-2 July 2009 (U. Çetintemel, S.B. Zdonik, D. Kossmann, & N. Tatbul, Eds), pp. 591-602. ACM. ISBN: 978-1-60558-551-2.

Chen, Z., Shen, H.T., Xu, Q. & **Zhou, X.** (2009) Instant advertising in mobile peer-to-peer networks. *In: Proceedings of 25th International Conference on Data Engineering (ICDE 2009)*, Shanghai, China, 29 March-2 April 2009 (Y. Ioannidis, D. Lee & R. Ng, Eds), pp. 736-737. IEEE. ISBN: 978-0-7695-3545-6.

Deng, K., Xu, H., Sadiq, S., Lu, Y., **Fung, G.**, Shen, H.T. (2009) Processing group nearest group query. *In: Proceedings of the 25th International Conference on Data Engineering (ICDE 2009)*, Shanghai, China, 29 March-2 April 2009 (Y. Ioannidis, D. Lee & R. Ng, Eds), pp. 1144-1147. IEEE. ISBN: 978-0-7695-3545-6.

Dom, M., **Fellows, M.R.** & **Rosamond, F.A.** (2009) Parameterized complexity of stabbing rectangles and squares in the plane. *In: Proceedings of 3rd International Workshop WALCOM: Algorithms and Computation (WALCOM 2009)*, Kolkata, India, 18-20 February 2009. *Lecture Notes in Computer Science* 5431:298–309 (S. Das & R. Uehara, Eds). Springer. ISBN: 978-3-642-00201-4.

Enciso, R., **Fellows, M.R.**, Guo, J., Kanj, I.A., **Rosamond, F.A.** & Suchý (2009) What makes equitable connected partition easy? *In: Proceedings of 4th International Workshop on Parameterized and Exact Computation (IWPEC 2009)*, Copenhagen, Denmark, 10-11 September 2009. *Lecture Notes in Computer Science* 5917:122-133 (J.Chen & F.V. Fomin, Eds). Springer. ISBN: 978-3-642-11268-3.

Fellows, M.R. (2009) The complexity ecology of parameters: some new developments and research directions. *In: Proceedings of 20th International Workshop on Combinatorial Algorithms (IWOCA 2009)*, Hradec and Moravici, Czech Republic, 28 June-2 July 2009. *Lecture Notes in Computer Science* 5874:2-10 (J. Fiala, J. Králóvic & M. Miller, Eds). Springer. ISBN: 978-3-642-10216-5.

Fellows, M.R., Fomin, F.V., Lokshtanov, D., Losievskaja, E., **Rosamond, F.A.** & Saurabh, S. (2009) Distortion is fixed-parameter tractable. *In: Proceedings of 36th International Colloquium on Automata Languages and Programming (ICALP 2009)*, Rhodes, Greece, 5-12 July 2009. *Lecture Notes in Computer Science* 555:463-474 (S. Albers, A. Marchetti-Spaccamela, Y. Matias, S.E. Nikolettseas & W. Thomas, Eds). Springer. ISBN: 978-3-642-02926-4.

Appendix 1: Publications

- Fellows, M.R.**, Guo, J. & Kanj, I.A. (2009) The parameterized complexity of some minimum label problems. *In: Proceedings of 35th International Workshop on Graph-Theoretic Concepts in Computer Science (WG 2009)*, Montpellier, France, 24-26 June 2009. *Lecture Notes in Computer Science* 5911:88-99 (C. Paul & M. Habib, Eds). Springer. ISBN: 978-3-642-11408-3.
- Fellows, M.R.**, Guo, J., Komusiewicz, C., Niedermeier, R. & Uhlmann, J. (2009) Graph-based data clustering with overlaps. *In: Proceedings of 15th Annual International Conference on Computing and Combinatorics (COCOON 2009)*, Niagara Falls, N.Y., USA, 13-15 July 2009. *Lecture Notes in Computer Science* 5609:516-526 (H.Q. Ngo, Ed.) Springer. ISBN: 978-3-642-02881-6.
- Fellows, M.R.**, Guo, J., Moser, H. & Niedermeier, R. (2009) A complexity dichotomy for finding disjoint solutions of vertex deletion problems. *In: Proceedings of 34th International Symposium on Mathematical Foundations of Computer Science (MFCS 2009)*, Novy Smokovec, Slovakia, 24-28 August 2009. *Lecture Notes in Computer Science* 5734:319-330 (R. Královic & D. Niwinski, Eds). Springer. ISBN: 978-3-642-03815-0.
- Fellows, M.R.**, Guo, J., Moser, H. & Niedermeier, R. (2009) A generalization of Nemhauser and Trotter's local optimization algorithm. *In: Proceedings of 26th International Symposium on Theoretical Aspects of Computer Science (STACS 2009)*, Freiburg, Germany, 26-28 February 2009. *LIPICs 09001 Schloss Dagstuhl - Leibniz-Zentrum für Informatik, Germany/ Internationales Begegnungs- und Forschungszentrum für Informatik* (S. Albers, J.-Y. Marion, Eds), pp. 409-420. Schloss Dagstuhl, Germany. ISBN: 978-3-939897-09-5.
- Fellows, M.R.**, Hartman, T., Hermelin, D., Landau, G.M., **Rosamond, F.** & Rozenberg, L. (2009) Haplotype inference constrained by plausible haplotype data. *In: Proceedings of 20th Annual Symposium of Combinatorial Pattern Matching (CPM 2009)*, Lille, France, 22-24 June 2009. *Lecture Notes in Computer Science* 5577:339-352 (G. Kucherov & E. Ukkonen, Eds). Springer. ISBN: 978-3-642-02440-5.
- Fellows, M.R.**, Hermelin, D. & **Rosamond, F.A.** (2009) Well-quasi-ordering bounded treewidth graphs. *In: Proceedings of 4th International Workshop on Parameterized and Exact Computation (IWPEC 2009)*, Copenhagen, Denmark, 10-11 September 2009. *Lecture Notes in Computer Science* 5917:149-160 (J.Chen & F.V. Fomin, Eds). Springer. ISBN: 978-3-642-11268-3.
- Fellows, M.R.**, **Rosamond, F.A.**, Fomin, F.V., Lokshtanov, D., Saurabh, S. & Villanger, Y. (2009) Local search: Is brute force avoidable? *In: Proceedings of International Joint Conference on Artificial Intelligence (IJCAI 2009)*, Pasadena, California, USA, 11-17 July 2009 (C. Boutilier, Ed.) pp. 486-491. AAAI Press. ISBN: 978-1-57735-426-0.
- Fung, G.**, Lu, W., Du, X. (2009) Dominant and K nearest probabilistic skyline. *In: Proceedings of Database Systems for Advanced Applications, 14th International Conference, (DASFAA 2009)*, Brisbane, Australia, 21-23, April 2009. *Lecture Notes in Computer Science* 5463:263-277. (X. Zhou, H. Yokota, K. Deng & Q. Liu, Eds). Springer. ISBN 978-3-642-00886-3.
- Hegland, M.** (2009) Solving the chemical master equation with the aggregation-disaggregation method. *In: Proceedings of 18th World IMACS Congress and MODSIM09 International Congress on Modelling and Simulation*, Cairns, Australia, 13-17 July 2009 (R.S. Anderssen, R.D. Braddock & L.T.H. Newham, Eds), pp. 691-696. ISBN: 978-0-9758400-7-8.
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- Huang, Z.**, Wang, L., Shen, H.T., Shao, J. & **Zhou X.** (2009) Online near-duplicate video clip detection and retrieval: an accurate and fast system. *In: Proceedings of 25th International Conference on Data Engineering (ICDE 2009)*, Shanghai, China, 29 March-2 April 2009 (Y. Ioannidis, D. Lee & R. Ng, Eds), pp. 1511-1514. IEEE. ISBN: 978-0-7695-3545-6.
- Khodabandehloo, N., Sadiq, S., Deng K. & **Zhou, X.** (2009) Data quality aware query processing in collaborative information systems. *In: Proceedings of Advances in Data and Web Management Joint International Conferences (APWeb/WAIM 2009)*, Suzhou, China, 2-4 April 2009. *Lecture Notes in Computer Science* 5446:39-50. Springer, ISBN: 978-3-642-00671-5.
- Li, Z., Du, X., Liu, H., He, J. & **Zhou, X.** (2009) IRankCS: a term-based innovation ranking system for conferences and scholars. *In: Proceedings of Advances in Data and Web Management Joint International Conferences (APWeb/WAIM 2009)*, Suzhou, China, 2-4 April 2009. *Lecture Notes in Computer Science* 5446:126-137. (Q. Li, L. Feng, J. Pei, X.S. Wang, X. Zhou & Q.-M. Zhu, Eds). Springer, ISBN: 978-3-642-00671-5.
- Li, G., **Zhou, X.**, Feng, J. & Wang J. (2009) Progressive $top-k$ keyword search in relational database. *In: Proceedings of 25th International Conference on Data Engineering (ICDE 2009)*, Shanghai, China, 29 March-2 April 2009 (Y. Ioannidis, D. Lee & R. Ng, Eds), pp. 1183-1186. IEEE. ISBN: 978-0-7695-3545-6.
- Liu, Q., **Chen, Y.-P.P.** & Li, J. (2009) High functional coherence in k -partite protein cliques of protein interaction networks. *In: Proceedings of 2009 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2009)*, Washington, DC, USA, 1-4 November 2009 (X. Chen, S. Kim, C. Wu & D. Xu, Eds), pp. 111-117. IEEE Computer Society. ISBN: 978-0-7695-3885-3.
- Nahar, J., Tickle, K.S., Ali, S. & **Chen, Y.-P.P.** (2009) Early breast cancer identification: which way to go? Microarray or image based computer aided diagnosis! *In: Proceedings of 2009 Third International Conference on Network and System Security (NSS 2009)*, Gold Coast, Queensland, Australia, 19-21 October 2009 (Y. Xiang, J. Lopez, H. Wang & W. Zhou, Eds), pp. 456-461. Institute of Electrical and Electronics Engineers (IEEE). ISBN: 978-0-7695-3838-9.
- Nikulin, V. & **McLachlan, G.J.** (2009). Classification of imbalanced marketing data with balanced random sets. *In: Workshop and Conference Proceedings of KDD-CUP 2009*, Paris, France, 28-29 June 2009 (G. Dror, M. Boullé, I. Guyon, V. Lemaire & D. Vogel, Eds), 7:89-100. Proceedings of Journal of Machine Learning Research. ISSN: 1938-7228.

Appendix 1: Publications

- Nikulin, V. & **McLachlan, G.J.** (2009). On a general method for matrix factorisation applied to supervised classification. *In: Proceedings of 2009 IEEE International Conference on Bioinformatics and Biomedicine Workshop*, Washington, DC, USA, 1-4 November 2009 (J. Chen *et al*, Eds), pp. 44-49. IEEE. ISBN: 978-1-4244-5121-0.
- Nikulin, V. & **McLachlan, G.J.** (2009) Regularised k -means clustering for dimension reduction applied to supervised classification. *In: DMI Proceedings Series 3, Proceedings of CIBB 2009, Sixth International Meeting on Computational Intelligence for Bioinformatics and Biostatistics*, Genoa, Italy, 15-17 October 2009 (F. Masulli, L. Peterson & R. Tagliaferri Eds.) pp 1-10. Salerno, Italy: DMI, University of Salerno. ISBN: 978-88-903537-2-7.
- Nikulin, V., **McLachlan, G.J.**, & Ng, S.K. (2009) Ensemble approach for the classification of imbalanced data. *In: Proceedings of 22nd Australasian Joint Conference on Advances in Artificial Intelligence (AI 2009)*, Melbourne, Australia, 1-4 December 2009. *Lecture Notes in Artificial Intelligence* 5866:291-300 (A.E. Nicholson & X. Li, Eds). Springer. ISBN: 978-3-642-10438-1.
- Sajjanhar, A., Lu, G., Zhang, D., Hou, J. & **Chen, Y.-P.P.** (2009) Spherical harmonics and distance transform for image representation and retrieval. *In: Proceedings of 10th International Conference on Intelligent Data Engineering and Automated Learning (IDEAL 2009)*, Burgo, Spain, 23-26 September 2009. *Lecture Notes in Computer Science* 5788:309-316 (E. Corchado & H. Yin, Eds). Springer. ISBN: 978-3-642-04393-2.
- Sunkara, V.** (2009) The chemical master equation with respect to reaction counts. *In: Proceedings of 18th World IMACS and MODSIM 09 International Congress on Modelling and Simulation*, Cairns, Australia, 13-17 July 2009 (R.S. Anderssen, R.D. Braddock & L.T.H. Newham, Eds), pp. 703-707. ISBN: 978-0-9758400-7-8.
- Wang, K., Ng, S.K., & **McLachlan, G.J.** (2009) Multivariate skew t mixture models: applications to fluorescence-activated cell sorting data. *In: Proceedings of Conference on Digital Image Computing: Techniques and Applications (DICTA 2009)* Melbourne, Australia, 1-3 December 2009 (H. Shi, Y. Zhang, M.J. Bottema, B.C. Lovell, & A.J. Maeder, Eds), pp. 526-531. IEEE Computer Society. ISBN: 978-0-7695-3866-2.
- Xie, K., Deng, K. & **Zhou, X.** (2009) From trajectories to activities: a spatio-temporal joint approach. *In: Proceedings of 2009 International Workshop on Location Based Social Network*, Seattle, WA, USA, 3 November 2009 (X. Zhou & X. Xie, Eds), pp. 25-32. ACM. ISBN: 978-1-60558-860-5.
- Xu, Q., Shen, H.T., Chen, Z., Cui, B., **Zhou, X.** & Dai, Y. (2009) Hybrid retrieval mechanisms in vehicle-based P2P networks. *In: Proceedings of 9th International Conference on Computational Science (ICCS 2009)*, Louisiana, USA, 25-27 May 2009. *Lecture Notes in Computer Science* 5544:330-314 (G., Allen, J. Nabrzyski, E. Seidel, G.D. van Albada, J. Dongarra, P.M.A. Sloot, Eds). Springer. ISBN: 978-3-642-01969-2.
- Zhu, J., **Zhou, X.** & **Fung, G.** (2009) A term-based driven clustering approach for name disambiguation. *In: Proceedings of Advances in Data and Web Management Joint International Conferences (APWeb/WAIM 2009)*, Suzhou, China, 2-4 April 2009. *Lecture Notes in Computer Science* 5446:320-331. (Q. Li, L. Feng, J. Pei, X.S. Wang, X. Zhou & Q.-M. Zhu, Eds). Springer, ISBN: 978-3-642-00671-5.
- Zhou, X.M., **Zhou, X.**, Bouguettaya, A. & Taylor, J.A. (2009) A subspace symbolization approach to content-based video search. *In: Proceedings of 25th International Conference on Data Engineering (ICDE 2009)*, Shanghai, China, 29 March-2 April 2009 (Y. Ioannidis, D. Lee & R. Ng, Eds), pp. 1191-1194. IEEE. ISBN: 978-0-7695-3545-6.
- E2. Conference – full conference paper – non-refereed proceedings**
- Ariesanti, I., Bodén, M., Maetschke, S. & Buske, F.A.** (2009) Detecting sequence and structure homology via an integrative kernel: a case study in recognizing enzymes. *In: Proceedings of the 2009 IEEE Computational Intelligence for Bioinformatics and Computational Biology (CIBCB 2009)*, Nashville, TN, U.S.A., 30 March-2 April 2009, pp. 46-52. IEEE. ISBN 978-1-4244-2756-7.
- E4. Conference – unpublished presentation**
- Fellows, M.R., Hromkovi, J., Rosamond, F.A. & Steinová, M.** (2009) Fixed-parameter tractability, relative kernelization and the effectivization of structural connections. 5th Conference on Computability in Europe (CiE 2009): Mathematical Theory and Computational Practice, Heidelberg, Germany, 19-24 July 2009.
- Bailey, T.L.** (2009) The value of position-specific priors in EM-based biological sequence motif discovery. Australasian Conference on Statistical Methods for Genomic Data Analysis, Brisbane, Australia, 5-6 October, 2009.
- Ranganathan, S.** (2009) A career in bioinformatics. Singapore Symposium on Computational Biology (SYMBIO), Singapore, 8 September 2009 (invited).
- E4i. Conference – edited volume of conference proceedings**
- Chan, C.-Y., Chawla, S., Sadiq, S., **Zhou, X.** & Pudi, V., Eds (2009) Proceedings of Data Quality and High-Dimensional Data Analysis Workshops (DASFAA 2008), New Delhi, India, 19-21 March 2008. World Scientific Publishing Company. ISBN: 9814273481.
- Li, Q., Feng, L., Pei, J., Wang, S.X., **Zhou, X.** & Zhu, Q., Eds (2009) Proceedings of Advances in Data and Web Management Joint International Conferences (APWeb/WAIM 2009), Suzhou, China, 2-4 April 2009. *Lecture Notes in Computer Science* 5446. Springer, ISBN: 978-3-642-00671-5.
- Tanka, K., **Zhou, X.** & Jatowt, A., Eds (2009) Proceedings of the 3rd ACM Workshop on Information Credibility on the Web (WICOW 2008), Madrid, Spain, 20 April 2009. ACM. ISBN: 978-1-60558-488-1.
- Zhou, X.** & Xie, X., Eds (2009) Proceedings of the 2009 International Workshop on Location Based Social Networks (LBSN 2009), Seattle, Washington, USA, 3 November 2009. ACM. ISBN: 978-1-60558-860-5.
- Zhou, X., Yokota, H., Deng, K. & Liu, Q.,** Eds (2009) Proceedings of 14th International Conference on Database Systems for Advanced Applications (DASFAA 2009), Brisbane, Australia, 21-23 April 2009. *Lecture Notes in Computer Science* 5463. Springer. ISBN: 978-3-642-00886-3

Appendix 1: Publications

OTHER ACADEMIC OUTPUT

Demos

Cheng, R., Huang, Z., Shen, H.T. & **Zhou, X.** (2009) Interactive near-duplicate video retrieval and detection. 17th ACM International Conference on Multimedia, Beijing, China, 19-23 October 2009.

Huang, Z., Wang, L., Shen, H.T., Shao, J. & **Zhou X.** (2009) Online near-duplicate video clip detection and retrieval: an accurate and fast system. 25th International Conference on Data Engineering (ICDE 2009), Shanghai, China, 29 March-2 April 2009.

Liu, K., Chen, Q., Deng, K., Ding, Z., Li, M. & **Zhou, X.** (2009) MOIR/MT: monitoring large-scale traffic of road network in real time. 35th International Conference on Very Large Data Bases (VLDB09), Lyon, France, 24-28 August 2009.

Editorship of journal issue

Ragan, M.A., McInerney, J.O. & Lake, J.A., Eds (2009) The network of life: genome beginnings and evolution. *Philosophical Transactions of the Royal Society B: Biological Sciences*. 364(1527):2167-2289. ISSN: 0962-8436.

Posters

Cootes, A.P., Kumar, G. & Ranganathan S. (2009) A statistical study of protein function and subcellular localisation in interaction and metabolic networks. Bioinformatics Australia conference, Melbourne, Australia, 19-20 October 2009.

Gaikwad, J., Jamie, J., Vemulpad, S., Kohen, J. & **Ranganathan, S.** (2009) Combating medicinal plant extinction and indigenous culture loss - an Australian model. e-Biosphere 09 International conference on Biodiversity Informatics, 2009, London, UK, 1-3 June 2009.

Kumar, G., Nevalainen, H. & **Ranganathan, S.** (2009) Statistical significance of protein Interaction and metabolic data for SCL prediction. 8th International Conference on Bioinformatics, Singapore, 7-11 September 2009.

Postgraduate theses

Arieshanti, I. (2009) Integrating sequence and structure for annotating proteins in the twilight zone: A Machine Learning Approach. MPhil thesis, The University of Queensland. 100 pp.

Bauer, D.C. (2009) Thermodynamic models for the analysis of quantitative transcriptional regulation. PhD thesis, The University of Queensland. 251 pp.

Choo, K.H. (2009) Bioinformatic analysis of bacterial and eukaryotic amino-terminal signal peptides. PhD thesis, Macquarie University. 192 pp.

Inostroza-Ponta, M. (2009) An integrated and scalable approach based on combinatorial optimization techniques for the analysis of microarray data. PhD thesis, The University of Newcastle. 227 pp.

Mann, S. (2009) Extensible motif and aberrant nucleotide extraction in genomic sequences, PhD thesis, Deakin University. 185 pp.

Mercer, T. (2009) The expression of long non-coding RNAs during mouse development. PhD thesis, The University of Queensland. 183 pp.

Taft, R.J. (2009) Adding gears to the RNA machine: discovery and characterisation of new classes of small RNAs in eukaryotes. PhD thesis, The University of Queensland. 289 pp.

Wee, L.J.K. (2009) *In silico* prediction of the caspase degradome. PhD thesis, Macquarie University. 130 pp.

Zhu, J. (2009) Statistical analysis of high-dimensional gene expression data. PhD thesis, The University of Queensland. 213 pp.

Appendix 2: Financial statement

INCOME

Balance carry forward	784,538.62	
ARC	1,167,900.00	
Host institution support	525,000.00	
TOTAL INCOME		<u>2,477,438.62</u>

EXPENDITURE

Salaries		1,200,835.35
Scholarships		61,306.89
Funds to other nodes (2008, 2009)		
The Australian National University	26,000.00	
Deakin University	103,872.00	
Macquarie University	167,997.80	
University of Newcastle	<u>178,095.00</u>	475,964.80
Workshops/Conferences		8,644.54
Strategic Visitors/Sponsorship Program/Director Strategic Discretionary		
Winter School (2008, 2009)	40,000.00	
Sabbatical visit/overseas speaker	930.89	
2nd Australasian High Content Screening Workshop	285.00	
Staff development	<u>2,489.85</u>	43,705.74
Equipment		12,899.00
Accommodation		1,772.73
Travel		4,470.21
Maintenance/Consumables		
Annual Report	14,842.00	
Consumables		
Computer consumables/Maintenance	1,308.01	
Laboratory consumables	19,162.85	
Photography/Slides/Posters	35.00	
Postage & freight	1,149.68	
Stationery & photocopy	1,331.95	
Transport - Local	<u>894.64</u>	23,882.13
Meetings - Advisory Board & Annual All-Hands Meeting	2,432.90	
Printing - books/journals/reprints	1,292.65	
Relocation	2,195.73	
Recruitment	190.00	
Telephone & Fax	87.37	
Registration: trademark, domain name	<u>80.00</u>	45,002.78
Others: Hospitality, bank charges, payroll tax, FBT, card payments etc		271.76
TOTAL EXPENDITURE		<u>1,854,873.80</u>
BALANCE		<u>622,564.82</u>

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