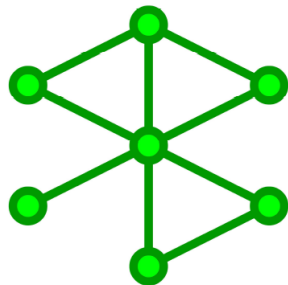


THE NEW SOUTH WALES SYSTEMS BIOLOGY INITIATIVE

Annual Report 2009 / 2010



SYSTEMS BIOLOGY
INITIATIVE



UNSW
THE UNIVERSITY OF NEW SOUTH WALES
SYDNEY • AUSTRALIA

NSW Systems Biology Initiative – Report 2009 / 2010

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NSW SYSTEMS BIOLOGY INITIATIVE ANNUAL REPORT JUNE 2009 TO NOVEMBER 2010



1. Executive Summary

It is approaching 2½ years since the establishment of the Systems Biology Initiative. It has been a very busy time, and one with many successes. Highlights on the last 18 months of operations are summarised here.

We have engaged in numerous collaborative bioinformatic projects. Major projects have included the complete assembly and annotation of the genome of a strain of *Campylobacter* associated with Crohn's disease, the RNA-seq analysis of normal and Alzheimer's brain tissue and the network modeling and analysis of mice that have cardioprotective overexpressor mutations. Our software and databases for network construction and analysis have been improved and new releases made publicly available.

In association with the Ramaciotti Centre for Gene Function Analysis, we have built expertise in the storage and analysis of next-generation sequence data, in particular that from the Illumina Genome Analyser. Pipelines for the analysis of these data have been established and are being maintained on NSW and national supercomputers. These are now available for other research groups to use and for the 'first pass' analysis of information generated by the next-gen sequencers at the Ramaciotti Centre. The hardware for which funds were raised previously, a \$60k computer cluster for the School of Biotechnology and Biomolecular Sciences and a \$1M supercomputer as part of an ARC LIEF consortium, have been installed and commissioned.

We have been successful in raising funds for projects and for our continuing activities. Projects include those funded by Intersect, by the Australian National Data Service (2 projects) and the Anzac Institute; a total of \$450,000. Funds for our continuing activities have been raised through the EIF Super Science Scheme, in association with Bioplatforms Australia and the University of New South Wales. A total of \$2,000,000 has been secured to fund our activities until the end of 2013. Two ARC Discovery Projects with a focus on Systems Biology, have also been funded to a total of \$585,000.

We have organised workshops and large conferences. At UNSW, we delivered a 1 day workshop in Advanced Data Analysis in Proteomics. We also collaborated with the Institute of Systems Biology (Seattle, USA) to host a 4 day hands-on workshop in Proteomic Bioinformatics. Five experts from the Institute visited UNSW to deliver this workshop. It was the first time this workshop had been presented anywhere outside of the Seattle Institute. We co-convoked and were responsible for the program of the HUPO International Proteomics Congress. This attracted 1,100 attendees from around the globe. In addition to the above, the SBI has been an active participant in many other conferences and workshops, both nationally and internationally.

Our research output continues to be strong, having published 12 peer-reviewed papers in 2009 and 2010 and edited a special edition of PROTEOMICS on protein-protein interactions. Our work was featured in the Australian Life Scientist, the Australian Biochemist and in Bio-IT World. Major papers that report on our first projects in genomics and RNA-seq

analysis have been submitted, and other papers describing important progress in the analysis of networks are under revision.

The hard work, above, has been done by an outstanding team. I warmly thank Dr. Nandan Deshpande, Dr. David Fung, Ms Simone Li and Ms Natalie Twine for their hard work and ongoing enthusiasm. I also thank our fantastic collaborators for trusting us with their precious data. I also would like to thank Prof. Ian Dawes for his strategic advice, unfailing wisdom and continuous support. We look forward to further successes and new challenges in the coming 3 years of our Initiative.

Professor Marc Wilkins
Director

2. Staffing

We have continued to employ 4 full time bioinformatics staff.

Simone Li, a UNSW bioinformatics honours graduate, was appointed full-time in May 2008. Simone has an excellent mix of skills in biology and information technology and has continued to make outstanding contributions to the SBI in its second year. Simone has spearheaded our developments in the analysis of protein interaction networks, especially with the GEOMI platform and has been responsible for the organization of workshops.

Dr David Fung commenced in April 2009. David has worked previously at the Westmead Millennium Institute, and has now completed his PhD at the University of Sydney. He has a strong background in human genetics, information technology and bioinformatics. The focus of his PhD was integrative systems-level analysis of liver cancer and visualization of multi-functional protein interaction networks. David has applied this knowledge to the construction of actor-semiotic networks, which have been used in the collaborative projects on the analysis of mammalian gene and protein expression data.

Natalie Twine joined the SBI in June 2009. Natalie has a B.Sc. in molecular biology, a research Masters in Bioinformatics and worked in the Leukaemia Sciences group at Kings College London in microarray and genomic data analysis. In November 2009, Natalie was seconded to Intersect as part of the Genomic Data Storage (GDS) Project. She has since returned full-time to the Systems Biology Initiative and has been responsible for RNA-seq collaborations as well as those involving analysis of microarray data.

Dr Nandan Deshpande joined the SBI in November 2009. He graduated with a Masters of Science in Biomedical Engineering from the University of Texas (Southwestern Medical Center) in Dallas, USA, worked as a bioinformatics scientist at the Institute of Bioinformatics (Bangalore, India) and has just completed his PhD at Macquarie University in the systems biology of glycosylation in filamentous fungi. Nandan has been responsible for bacterial genome assembly and annotation, and the establishment of analysis pipelines on supercomputers.

We were joined by Amy Lo, a University Medalist in bioinformatics, for a 6-month part-time project funded by the Anzac Institute.

3. Computer infrastructure

Prof. Wilkins led an application for a research computer cluster via the UNSW ITIP scheme in 2009. This raised funds for a \$60k cluster for bioinformatics research, for use by the NSW Systems Biology Initiative staff and other bioinformatics researchers in the School of Biotechnology and Biomolecular Science. This has now been installed and is in use by many researchers in the school, including the groups of Dr. Tanaka, Dr. Lan and Dr Thomas. We thank the UNSW Faculty IT team for their assistance with the systems administration of this computer.

Prof. Wilkins was a member of a consortium on a 2009 ARC LIEF grant. This raised \$500k towards a \$1M project for a 256 node computer cluster for use by all NSW universities. The awardees of this grant agreed that rather than establishing this relatively small cluster, that greater computer power could be obtained by buying into the Vayu supercomputer in the National Computer Infrastructure (NCI). This Oracle (Sun) Constellation, comprises nearly 12,000 compute cores, 36 terabytes of main memory, and in excess of 800 terabytes of

global storage. It came on-line in September 2009 and has been expanded in 2010 to bring it up to full capacity.

The SBI has been successful in competing for resources on the high performance computers, for use in genome assembly and analysis. In May 2009, the NSW Resource Allocation Committee granted the SBI 162,000 service units of high performance computing. This was one of the largest allocations for that period. In 2010 we were granted 56,000 service units on the new Vayu supercomputer. For 2011, we have been awarded 100,000 service units.

4. Strategic direction and new technology

We have been able to expand the scope and depth of the projects we have undertaken in 2009 / 2010. This has been done with a focus on network biology and the analysis of next-generation sequence data. We have not focused strongly on microarray data analysis, although have been involved in collaborative projects and some training in this area.

Network biology:

In network biology, we have constructed and analysed biological networks (including protein-protein interaction networks and those integrated with gene regulation, signal transduction and metabolic pathways) and further explored how these can be used to interpret gene and protein expression data. A particular interest is how these networks can assist us in understanding the interrelationships of different elements of the cell or the function of specific genes or proteins.

To underpin research in this area, we have continued our developments of the GEOMI platform. A particular focus has been the integration of protein complexes to generate views of the 'complexome'. We have also continued our collaboration with Dr. Tim Lambert and Yose Widjaja (Computer Science and Engineering, UNSW) on the development of the Interactorium. A focus in 2009 and 2010 has been the integration of the KEGG metabolomic pathways. We have adopted the NetMap Analytics platform (Netmap Pty Ltd, Sydney) for the analysis of human gene and protein data. This platform allows us to develop actor-semiotic networks (those that combine physical and descriptive nodes) specific to the biological question of interest. These technology platforms have been central to our collaborative work in systems biology (see projects).

Next-Generation Sequencing:

For next-generation sequencing, we have focused on the development and deployment of infrastructure to underpin genomics and new aspects of transcriptomics.

The Systems Biology Initiative was successful in competing for grants to support two genomics infrastructure projects. The first, Genomic Data Storage, was funded by the Australian National Data Service (ANDS). This has built a web-based system for the storage of the sequence data generated in next-generation sequencing. This has been beta-tested and will be put into production at the Ramaciotti Centre for Gene Function Analysis (UNSW) and the Centre for Plant Conservation Genetics (Southern Cross University) in January 2011.

The second infrastructure project, Genomic Data Analysis, was an Intersect Innovation project. This involved installing and benchmarking most major tools for the assembly and annotation of next-generation sequence data on the NSW and National supercomputers. This project was completed in May 2010. These technology platforms have underpinned our collaborative work in genomics (see projects).

Dissemination of technology:

Many of the outcomes of the technology projects, above, are available to the wider bioinformatics and genomics community. GEOMI and the Interactorium are available for download from the SBI web site and the genomics tools installed on the NSW and national supercomputer can be used by any researcher who is awarded computer time by the Resource Allocation Committee.

5. Collaborative projects

Below is a list of collaborative projects commenced and/or ongoing in 2009 / 2010. It is noteworthy that several of the projects contributed to hypotheses of grants to the ARC and NHMRC in 2010. Other projects laid foundations for funding from other sources, such as with the Australian National Data Service (ANDS) in association with Prof. Nicolle Packer.

Large and Medium-scale Projects:

- Interaction network analysis of oxidative stress-related proteins in *Saccharomyces* (Prof. Ian Dawes, Faculty of Science, UNSW, completed).
- Human proteome peptide analysis (Dr. Valerie Wasinger, Bioanalytical Mass Spectrometry Facility, UNSW, completed)
- Human leukocyte peptide analysis for transplant tissue typing (Dr. Wallace Bridge, Faculty of Science, UNSW, completed).
- Construction of microRNA metanetwork (protein-protein interactions, signal transduction, microRNAs) to identify microRNA regulated protein complexes. (Dr. Eileen McGowan, Centenary Research Institute, completed).
- Glycomics data analysis and viewer platform (Prof. Nicki Packer, Macquarie University, ongoing).
- Analysis of next generation sequencing data from human brain (Dr. Michal Janitz, Faculty of Science, UNSW, ongoing)
- Analysis of human colorectal cancer biomarkers data for tissue screening (A. Prof. Graham Robertson and Prof. Stephen Clarke, Cancer Pharmacology Unit, Concord Hospital, ongoing).
- Genomic assembly and annotation of *Campylobacter concisus* (Prof. Hazel Mitchell, Faculty of Science, UNSW, ongoing).
- Genomic assembly and annotation of *Campylobacter showae* (Prof. Hazel Mitchell, Faculty of Science, UNSW, ongoing).
- Annotation of gene lists from *Pseudomonas* (Dr. Jim Manos, Bacterial pathogens in Cystic Fibrosis group, University of Sydney)
- Analysis of microarray data from KLF knockout mice (Prof. Crossley, Dr. Richard Pearson, Laura Norton, Sydney University and UNSW)
- Plant genomics with next-gen sequencing (Dr. Mark Edwards, Susan Gillies, Peter Bundock of CPCG, Southern Cross University). Natalie Twine (from SBI) acted as the 'geek for a week', visiting and working with the CPCG at SCU.
- Analysis of the genome of the Australian Fruit Fly *Bactrocera tryoni* (Dr. Marianne Frommer, Dr. John Sved, ongoing)
- 454 analysis of antisense RNAs (Dr. Greg Arndt, Radhika Das, Childrens Cancer Institute of Australia, underway).
- 454 analysis of amphipod RNA (Sharon Hook, CSIRO, scheduled 2011).

Smaller Projects or project advice:

- Network analysis of sphingosine kinase SK1 in breast cancer (Dr. Eileen McGowan, Centenary Institute, ongoing).
- Experimental design for microarray, Dr. Miriam Calao, Children's Cancer Institute Australia for Medical Research (completed).

- SILAC data analysis (Dr. Alice Len, Children's Cancer Institute Australia for Medical Research).
- Australian Wine Research Institute / Bioplatforms Australia Wine Yeast Systems Biology Demonstration Project (Dr. Paul Chambers, AWRI, Adelaide South Australia, ongoing)
- ELAND analysis of next generation sequencing data (Dr. John Pimanda and Dr Jason Wong, School of Medicine, UNSW)
- REACTOME analysis of expression data (Nikki Curthoys and Dr. Thomas Fath, School of Medicine UNSW).
- Functional analysis and use of DAVID tools (Eliza Courtney, Dr. Michal Janitz, UNSW).
- Yeast protein interaction network analysis, processing and data extraction from UniProt (Prof. Ian Dawes, Eva Chen, Anita Ayer, Geoff Kornfeld, UNSW)
- General bioinformatics advice (A. Prof Peter White, John-Sebastian Eden, UNSW)
- GEOMI use (Dr. Roxane Legaie, Warwick Systems Biology Centre, UK).

6. International links

The SBI continued to expand its international links.

Links with EMBL (Europe) as part of next generation sequencing data analysis projects:
Dr. Clare Sloggett visited the EBI and the Sanger Centre in 2009.

Link with EMBNet, the European Bioinformatics Network;
The SBI became a new Specialist Node in EMBnet in 2009. Dr. Bruno Gaeta represents the SBI at the EMBnet meetings.

Link with the Swiss Institute of Bioinformatics:
Prof. Wilkins visited the SIB in Geneva in Sept 2009. Ongoing collaborations in glycoinformatics and proteomic informatics were discussed with Dr. Frederique Lisacek.

Link with the Institute for Systems Biology, Seattle
The SBI hosted 5 researchers from the Institute of Systems Biology to deliver a hands-on workshop in proteomic informatics in Sept 2010. This was co-ordinated with Dr. Rob Moritz.

Link with the European Bioinformatics Institute (EBI)
The SBI is building a relationship with the EBI, specifically with Dr. Henning Hermjakob. Specific projects are around the use of the Reactome database and associated visualization tools.

7. Grant applications and further funding

There are a series of successful grants that the SBI has led or been part of since its inception in 2008.

Importantly, the SBI has been able to raise funds to continue its activities until the end of 2013. It was awarded a total of \$1.5M from the EIF Super Science Scheme and \$500k from the University of New South Wales.

Awarded Grants:

- 1) **Wilkins**. The NSW Systems Biology Initiative: genomic data analysis and network biology. EIF Super Science Funding, Bioplatforms Australia and the University of New South Wales. \$2.0M
- 2) **Wilkins**, Molloy, Hart-Smith. The role and regulation of protein methylation: a study using the recently developed methylation network of yeast. ARC, DP11. \$300k.
- 3) **Wilkins**, Fung. Classification of colorectal cancer patients. Anzac Research Institute. \$20k.
- 4) **Wilkins**, Protein methylation, a fundamental regulator of the interactome. ARC, DP10. \$285k.
- 5) Botten, Ford, Poulton, Rahmani, Armfield, Kuyucak, Lewis, McPhean, Muller, Radom, Abbass, Ball, Bursill, England, Khanna, Leonardi, Pitman, **Wilkins**, Esselle, Ranganathan, Steel, Henskens, von Nagy-Felsobuki, Marchant. A high performance computing cluster and storage for the INTERSECT Consortium of NSW, ARC, LE09. \$500k.
- 6) **Wilkins**, Dawes, Henry, Shannon. Genomic Data Storage. Australian National Data Service (ANDS). \$125k.
- 7) Packer, **Wilkins**. ARDC-Linked International Glycomics Repository & Instrument Data Capture. Australian National Data Service (ANDS). \$125k.
- 8) Henry, **Wilkins**, Dawes, Shannon. Genomic Data Analysis. Intersect Innovation Project. \$180k.
- 9) Baker, Hancock, Molloy, Clark, **Wilkins**, He, Jiang, Sun, Xing, Proteomic Discovery in the Genesis, Spread and Treatment of Cancer, China – NSW Collaborative Research Program, OSMR, NSW. \$1.05M
- 10) Raftery, Guilhaus, Khachigian, Hogg, **Wilkins**, Marshall, Cheung, Haber, Daly, Corish, Butt, Christopherson, Orbitrap XL mass spectrometer with Electron Transfer Dissociation and multidimensional LC, NSW Cancer Institute. \$952k.

We are currently awaiting the outcome of LIEF 2011, in which a new supercomputer and mass spectrometer were requested.

8. Student training

The SBI is continuing to play an active role in training bioinformatics students in systems biology.

Amy Lo and Sally Tang undertook their bioinformatics honours projects with the SBI in 2009 / 2010. Both were awarded First Class Honours and Amy Lo was awarded the University Medal for her studies.

Students Apurv Goel and Lelin Zhang, who undertook their Honours projects in bioinformatics with the SBI, joined the SBI as PhD students in 2009 and 2010 respectively. Both were awarded an Australian Postgraduate Award.

PhD student Ignatius Pang submitted his PhD by publication. In 2010, this thesis was passed and was awarded the Best Thesis of the School of Biotechnology and Biomolecular Sciences 2010.

Students Apurv Goel, Lelin Zhang, Timothy Couttas and Jason Low were awarded conference bursaries for the HUPO 2010 Proteomics Congress.

Prof. Wilkins remains active in co-supervision of PhD students. Students co-supervised in 2009 and 2010 include Yose Widjaja (UNSW, Dr. Tim Lambert), Jerran Naidoo and Michael Medynskj (Macquarie, both with Assoc. Prof. Ben Herbert).

9. Outreach – conferences and workshops

2009:

SBI research was presented at the following national or international conferences:

- International Mass Spectrometry Conference IMSC2009, keynote speech 31st August, Bremen Germany. Wilkins.
- HUPO2009: plenary speech in The International Proteomics Forum, 26th September, Toronto, Canada. Wilkins.
- Australasian Proteomics Society, APS, Lorne Feb 2009. Couttas, Pang, Erce posters.
- Cardiac Society of Australia and New Zealand, 2009 Congress, Sydney August 16, 2009. Wilkins.
- AMATA 2009 conference (Australian Microarray and Affiliated Technologies), October 21, Katoomba, NSW. David Fung.
- “Systems Biology” in the Australasian Yeast Group meeting 2nd – 4th December 09, Adelaide. Simone Li, Wilkins.

SBI research was also presented at a number of International institutes:

- Kurume University, Japan. 14th July 2009. Wilkins.
- Geneva University, Faculty of Medicine and the Swiss Institute of Bioinformatics, 2nd Sept 2009. Wilkins.

Presentations at Australian Institutes and at local workshops:

- Australian National Data Service (ANDS) – data lifecycle workshop (University of Sydney 11th Feb 2009). Wilkins, oral presentation.
- Australian Wine Research Institute systems biology two-day workshop – Simone Li Adelaide.
- Ramaciotti Centre – Launch of Next-Gen Sequencing - 11th June, University of New South Wales. Wilkins.
- University Western Sydney Faculty Seminar: Faculty of Medicine – 26th June. Wilkins.
- 2009 Teachers Professional Development Program: “Exploring Further Frontiers in Senior Biology” The University of New South Wales and the School of Medical Sciences. 3rd July. Wilkins.
- Next Generation Sequencing users’ group UNSW November 2009. Wilkins.
- Adelaide protein group meeting – December 2009. Wilkins.

Workshop attendance:

- 2009 NSW Bioinformatics Research Symposium, University of Sydney. Fung, Deshpande, Li.

2010:

SBI research was presented at the following national and international conferences:

- 4th Korea National Cancer Centre International Symposium. June 18. Wilkins.
- Australian Society for Microbiology, ASM 2010. July 8. Wilkins.
- International Human Proteome Organisation HUPO. 22nd Sept. Oral presentation: Wilkins. Poster presentations: Li, Goel, Couttas, Erce, Low.
- OzBio: Australian Society for Molecular Biology (ASBSB) and the International Society for Biochemistry and Molecular Biology (IUBMB). Oct 1. Melbourne, Australia. Wilkins.
- AMATA 2010, Hobart, Tasmania. 20th September. David Fung.
- 4th EuPA Meeting (European Proteomics Organisation) 25th October, Portugal. Wilkins.

Presentations at Australian Institutes and at local workshops:

- Lowry Symposium: Discovering Cancer Therapeutics 2010, University of New South Wales. 18th May. David Fung.
- ARC Australian Centre of Excellence for Bioinformatics: 2010 Winter School. 9th July. Wilkins.
- HUPO2010 SATELLITE SYMPOSIUM CHINA-NSW Cancer Proteomics Research Collaboration. 24th Sept, Macquarie University. David Fung.
- School of Medicine, Invited Seminar Series, University of New South Wales. Wilkins.
- SCRIPT Colon Cancer Proteomics Workshop. 12th October. Wilkins, Fung, Lo.
- Ramaciotti Centre Next Gen Sequencing Users Group meeting. Westmead Hospital. Twine.
- Bio21 Symposium: Systems Biology - moving towards the next generation biology. November 4, 2010. Wilkins.
- Centenary Institute Bioinformatics Symposium, Sydney. Nov 2010. Wilkins.
- Faculty of Engineering: Biological Systems Engineering Workshop, Nov 2010. Wilkins, Dawes.

Workshop attendance:

- 2010 Winter School in Mathematical & Computational Biology, University of Queensland. Deshpande, Fung attended.
- EBI bioinformatics workshop. 21-23 April. Deshpande, Twine, Li attended.
- Institute of Systems Biology (Seattle, USA) workshop in Proteomics Bioinformatics hosted by the SBI at UNSW. Li attended.
- Ramaciotti Centre Next Gen Sequencing Users Group meeting. Westmead Hospital. Deshpande attended.

Workshops and Conferences organized by the Systems Biology Initiative

2009

- Advanced data analysis for proteomics. 1 day workshop in association with BMSF. 13 attendees. Presenters included Wilkins, Li, Fung, Twine. Hands-on computer lab. 2nd July 2009.
- Next-generation DNA Sequencing Symposium. In affiliation with Sydney Bioinformatics. 120 attendees. 9th October 2009
- "Systems Biology" in the Australasian Yeast Group meeting 2nd – 4th December 09, Adelaide. Session Organiser and Chair

2010

- Advanced data analysis for proteomics. 1 day workshop in association with BMSF. 25 attendees. Presenters Wilkins, Li, Twine. Hands-on computer lab. 7th Sept 2010. 20 attendees.

- Workshop on Proteomic Bioinformatics. Collaboration with the Institute of Systems Biology (Seattle, USA) to host a 4 day hands-on workshop. Five experts from the Institute came to UNSW to deliver this workshop; this was the first time this workshop had been presented anywhere outside of the Institute in Seattle. 45 attendees. Organised by the SBI; Simone Li.
- The international congress of HUPO 2010 – 1,100 attendees. Wilkins was co-convenor, along with Profs. Baker, Smith and Nice. Wilkins was program co-ordinator.

10. Prizes, honours and publicity

Staff and students from the SBI have received a series of awards and honours in 2009 and 2010.

- Amy Lo was awarded the University Medal for her studies in bioinformatics. She undertook her honours research with the SBI.
- Lelin Zhang, who undertook her Honours project in bioinformatics with the SBI, was awarded an Australian Postgraduate Award to undertake PhD studies with the group.
- PhD student Ignatius Pang submitted his thesis in bioinformatics. This was awarded the Best Thesis of the School of Biotechnology and Biomolecular Sciences 2010.
- Students Apurv Goel, Lelin Zhang, Timothy Couttas, Jason Low and Melissa Erce were awarded conference bursaries for the HUPO 2010 Proteomics Congress.

Our work was featured in:

The Australian Life Scientist (2009) Volume 6, pages 10 to 16. “Another dimension in protein interaction” Research feature on the Interactorium.

Bio-IT World: story on the Interactorium.

http://www.bio-itworld.com/BioIT_Article.aspx?id=96473

Prof. Wilkins interviewed for *Expert Reviews in Proteomics* by Ryan De Vooght-Johnson. Published in Dec 2009.

The Australian Biochemist (2010) special issue on next-gen transcriptomic analysis.

11. Milestones

The milestones for year 2 / 3 were met or exceeded. This triggered the final year of funding for the SBI under the NSW State Government Science Leveraging Fund. UNSW funding from year 1 which was not fully expended in 2008 will be released in January 2011.

Milestones – year 3	Status
Annual report 2009	This document.

Stakeholder forum and agreement on proposed SBI projects	Consultation with stakeholder groups inside and outside UNSW.
Provision of services to 8 NCRIS –omics users	19 projects in 2009 / 2010.
Establishment and/or maintenance of 3 collaborative research programs	Major collaborations have been with Prof. Mitchell, Dr. Janitz, A. Prof. Robinson and Dr. Ruby Lin and Dr. McMullen.
Further Expansion of SBI membership / consortium to include 1 further member	Strong links have been forged with Southern Cross University as part of the GDA / GDS projects and Natalie Twine's visit to SCU in 2010. However the SCU centre lost its director in 2010. This relationship will be reviewed in early 2011.
Application for additional funds (ARC / NHMRC / charitable funding bodies)	Funds have been secured from Intersect, the Australian National Data Service and from the Australian Research Council.
Formulation of strategy for funding renewal (CRC / Centres of Excellence / NCRIS)	New funds have been raised from EIF Super Science for continuing operations of the SBI, until end of 2013.
Workshop on gene expression analysis in association with the Microarray Users Group	2009 and 2010 workshops have been held in next-gen sequencing, associated with the Ramaciotti Next-Gen users meeting.
Workshop on proteomic bioinformatics in association with APAF and the BMSF	Proteomic data analysis workshops delivered in 2009 and 2010.
Public presentations of collaborative research Public presentations of original Systems Biology research Publications of collaborative research	SBI was strongly represented at many conferences and was in demand for invited presentations.
Publication of original systems biology research	Done – see publications, below.
Recruitment of PhD students	Done - Apurv Goel, Lin Zhang. Others likely in

Participation of Honours and Masters research students	2011 (e.g. Xi Yao, Daniel Yagoub) Honours students Amy Lo, Sally Tang. Masters student Samantha Chia.
Production of Honours research theses	Theses from all students were completed and submitted to the University archives.

12. Management and committee meetings

The SBI is currently being managed by the Director, Prof. Marc Wilkins (UNSW). Prof. Ian Dawes (UNSW) is also actively involved in formulating the SBI strategy, and advising the Director on issues to do with the day to day running of the Initiative.

Our management committee is in a state of flux in 2010. Prof. Michael Guilhaus passed away in late 2009 and Prof. Mark Baker ceased to be the director of APAF. A. Prof. Jonathan Arthur ceased to be the director of Sydney Bioinformatics in 2009. Prof. Ian Dawes will retire from the University of New South Wales, but remain as Emeritus in 2011. The EIF funding will require a new management committee to be appointed.

13. Recent publications (2008-2010)

Published and in press:

1. Erce M, Low J, Wilkins MR (2010) Analysis of the RNA degradosome complex in *Vibrio angustum* S14. FEBS Journal, in press.
2. Joshi HJ, Packer NH, von der Leith W, Wilkins MR (2010) A web based platform for glycomic analysis and comparison. Nucleic Acids Res. 2010 38: W667-70.
3. Fung DC, Wilkins MR, Hart D, Hong SK (2010) Using the clustered circular layout as an informative method for visualizing protein-protein interaction networks. Proteomics 10: 2723-7.
4. Pang CNI, Gasteiger E, Wilkins MR (2010) The *Saccharomyces cerevisiae* arginine- and lysine-methylproteome. BMC Genomics 11: 92.
5. Kaakoush N, Man SM, Lamb S, Raftery M, Wilkins MR, Kovach Z, Mitchell H. (2010) The secretome of *Campylobacter concisus*. FEBS Journal, 277: 1606-17.
6. Okoli AS, Wilkins MR, Raftery MJ, Mendz GL (2010) The response of *Helicobacter hepaticus* to bovine bile. Journal of Proteome Research, 9: 1374-84.
7. Ma L, Pang CNI, Li SS, Wilkins MR (2010) Proteins deleterious on overexpression are associated with unusual interaction domains, low abundance and biased physicochemical characteristics. Journal of Proteome Research, 9(3):1218-25.

8. Widjaja YY, Pang CNI, Li SS, Wilkins MR, Lambert TD (2009) The Interactorium: visualising proteins, complexes and interaction networks in a virtual 3D cell. *Proteomics*, 9, 5309–5315.
9. Wilkins MR (2009) Hares and tortoises: the high versus low throughput proteomic race. *Electrophoresis*, 30, 1-6.
10. Erce MA, Low JKK, March PE, Wilkins MR, Takayama KM. (2009) Identification and functional analysis of RNase E of *Vibrio angustum* S14 and two-hybrid analysis of its interaction partners. *Biochimica et Biophysica Acta - Proteins and Proteomics*, 1794 1107–1114.
11. Huang K-Y, Filarsky M, Padula MP, Raftery MJ, Herbert BR, Wilkins MR (2009) Micropreparative Fractionation of the Complexome by Blue Native Continuous Elution Electrophoresis. *Proteomics*, 9, 2494-2502.
12. Little PFR, Williams RB, Wilkins MR (2009) Inter-individual variation in expression: a missing link in biomarker biology? *Trends in Biotechnology* 27(1): 5-10.
13. Bek, E., Wilkins MR (2009) Using Yeast to Study Protein-Protein Interactions Relevant to Disease. In: *Yeast as a Model for Human Disease*. Ed. S. Witt. Signpost Research Press. pp 145-176.
14. Krycer JR, Pang, CNI, Wilkins MR (2008) High throughput protein-protein interaction data: clues for the architecture of protein complexes. *Proteome Science*, 6:32.
15. Couttas TA, Raftery MJ, Wilkins MR (2008) Immonium ion scanning for the discovery of post-translational modifications and its application to histones. *Journal of Proteome Research*, 7, 2632–2641.
16. Wilkins MR, Kummerfeld SK (2008) Sticking together? Falling Apart? Exploring the dynamics of the interactome. *Trends in Biochemical Sciences*, 33: 195-200.
17. Deshpande N, Wilkins MR, Packer NH, Nevalainen H (2008) Protein glycosylation pathways in filamentous fungi. *Glycobiology*, 18:626-37. [IF=3.7].
18. Pang CNI, Chen A, Hayen A, Wilkins MR (2008) Are protein complexes composed of core, module and attachment proteins? *Proteomics*, 8: 425-434.
19. Wilkins MR, Arthur JW, Junius FK, Harrison MJ, Traini MD, Bizannes P, Doggett PE, McDonald W. (2008) Information management for proteomics: a perspective. *Expert Reviews Proteomics*, 5: 663-678.

20. Ho E, Webber R, Wilkins MR (2008) Interactive three-dimensional visualization and contextual analysis of protein interaction networks. *Journal of Proteome Research*, 7: 104-12.

Other publications:

21. Wilkins MR (Ed.) (2009) A celebration of protein-protein interactions. *Proteomics*, volume 9, issue 23, 5207 - 5315. Includes editorial (p 5207-5208).
22. Janitz K, Twine N, Wilkins MR, Janitz M (2010) Comprehensive analysis of transcriptome by means of RNA-Seq next-generation sequencing. *Australian Biochemist*. 41, 18-21.
23. Wilkins MR (2009) Proteomic data mining. *Expert Reviews in Proteomics*, 6, 599-603.

Under revision or submitted:

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