



BIOPLATFORMS AUSTRALIA

2012 ANNUAL REPORT



An Australian Government Initiative
National Collaborative Research
Infrastructure Strategy



THE AUSTRALIAN NATIONAL UNIVERSITY

THE JOHN CURTIN SCHOOL
OF MEDICAL RESEARCH



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WAIMR
Western Australian Institute
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FOR HEALTHIER LIVES



THE UNIVERSITY
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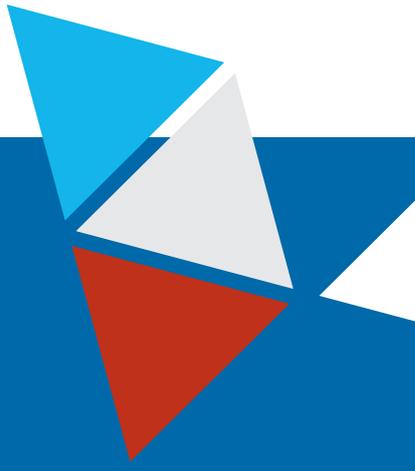
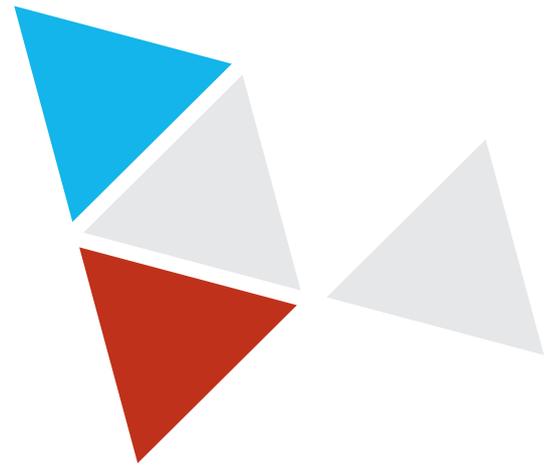


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FROM THE CHAIRMAN



“We have leveraged new scientific infrastructure with initiatives that foster collaboration and cross-discipline integration”

Over the last five years, Bioplatforms Australia has made targeted investments in ‘omics technology and bioinformatics expertise that have enhanced Australia’s research capacity. At the same time we have leveraged new scientific infrastructure with initiatives that foster collaboration and cross-discipline integration since these factors are fundamental to a systems biology approach.

Collaboration is integral to modern science. As life scientists seek answers to more complex questions, the range and depth of engagement with other disciplines is reaching new boundaries. Novel insights are more frequently relying on the application and integration of knowledge and technologies drawn from many different disciplines. Systems biology demands a multi-discipline approach, and as scientists strive to integrate experimental biology with computational biology and reductionist knowledge with a systems perspective; new technology and collaborative approaches are emerging.

The interdisciplinary nature of systems biology necessitates that investigators work in teams from the outset. However, this challenges traditional approaches to research where scientists and funding are organised along disciplinary lines effectively separating biology, engineering and computer science. Historically, democratic access to major scientific infrastructure has been minimal which has also hampered ready access to the multiple technologies needed for systems-wide analysis. A lack of data harmonisation

and standard annotation can also be added to the mix of impediments faced in systems-based approaches.

Within this context, Bioplatforms Australia’s mission to advance systems biology in Australia clearly reaches beyond increasing access to scientific infrastructure. In our view, a culture of shared infrastructure and cross collaboration is as essential as the technology and tools needed to conduct the research. This philosophy remains at the core of our endeavours and we are pleased to report that many of our strategic initiatives are facilitating broader collaborations, tackling integration issues and building valuable ‘data-based’ infrastructure in the process.

Framework datasets promote collaboration and integration

Bioplatforms Australia’s framework dataset program is an important element of our strategic efforts to facilitate research collaboration and systems biology. Simply providing new tools and equipment will not achieve these objectives. Having built up and connected ‘omics capabilities in Australia, we are now in a position to exploit our coupling of expertise and state-of-the-art infrastructure for more strategic purposes. Our dataset program is stimulating unprecedented levels of national collaboration and pivotal in enabling integration across many dimensions including technology; scientists from different disciplines; and integration of academia with industry. By building tangible data resources for the research community, we are convinced

FROM THE CHAIRMAN - MR JOHN GRANT AM

that both the process and the final outcome will translate the enormous potential of systems biology to continued innovation in Australian science.

Our dataset program was launched over a year ago with wheat as the first core theme for generating and collating large-scale datasets. Since then, additional themes offering broad national benefits such as soil biodiversity, melanoma and protection of the Great Barrier Reef have been included in the dataset program. Given the support we have received from the scientific community and our successes to date, we anticipate that Bioplatforms Australia will continue to develop new dataset projects to further collaboration opportunities and provide soft infrastructure resources for Australian researchers.

Bioinformatics remains a high priority

Bioplatforms Australia's focus on facilitating collaboration encompasses both a technical and cultural perspective. On the technical side, bioinformatics initiatives remain a high priority and we are continuing our efforts to alleviate noted skill shortages and boost bioinformatics capabilities. Our intention to form the Australian

Bioinformatics Network with the help of EMBL Australia and the CSIRO was cemented over the last year and this organisation is already delivering bioinformatics training and new collaborative opportunities to Australian scientists.

The framework dataset projects continue to provide a test bed for the bioinformatics analytical environment that will eventually provide scientists with on-line data resources and access to critical software tools and bioinformatics know how. Of course, on-going investments in infrastructure and expertise within the Bioplatforms Australia network continue to service the computational demands of high throughput technologies.

It is worth mentioning our wine yeast project as another tactic to illuminate and tackle the practical challenges of technology integration both in terms of data challenges and managing cross-discipline teams. This project has made excellent progress towards its research goals and consequently attracted international collaboration to sequence and analyse chardonnay genomes.

As a systems biology 'demonstration' project, it has been significant in defining challenges, generating

solutions and building valuable experience which is being shared through public workshops and publications.

Client growth continues

Bioplatforms Australia continues to achieve annual increases in the number of fee-for-service clients accessing the network. Genomics services are in high demand and show particular acceleration over the last year. Next generation sequencing technologies have been an important component of our investment strategy and new levels of capacity and affordability have prompted broad applications of genomic sequencing.

Acknowledgements

Bioplatforms Australia has been evolving its role in the research landscape and is making good progress towards its objectives. It now offers far more than a fee-for-service research capability and is generating much greater value by leveraging its integrated infrastructure network to promote broad collaboration on national-scale projects and giving genuine support to systems biology.

In these endeavours, I would like to thank my fellow Directors, Dr Les Trudzik and Professor John de

Jersey for their on-going commitment and respected leadership. I also take this opportunity to officially welcome Dr Sue Meek to the Board. Her in-depth experience and exposure to Australian science and insightful understanding of the interface between government, industry and academia will bring significant strategic value to our future plans and efforts.

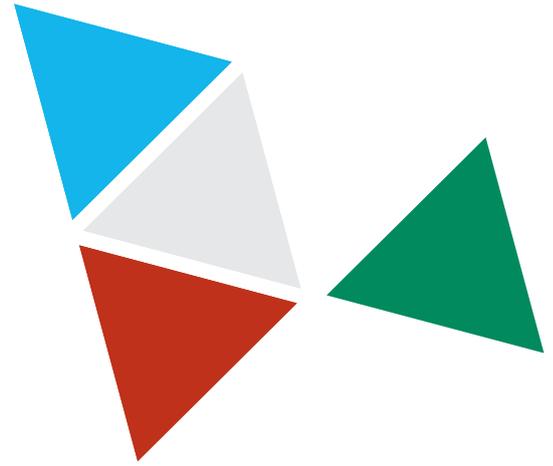
The effort and commitment of our facility leaders and platform convenors has not wavered over the last year and I thank them for their ongoing work to provide first class research services and support for our strategic programs.

Finally, I also wish to thank Andrew Gilbert, Anna Fitzgerald and Catherine Shang, for their continuing enthusiasm, energetic commitment and hard work behind our many achievements.

Yours sincerely,



Mr John Grant AM
Chairman



WHAT WE DO



“We endeavour to accelerate systems biology in Australia through initiatives that facilitate multi-discipline integration and build bioinformatics capabilities.”

Bioplatforms Australia builds Australian research capability and capacity in the fields of genomics, proteomics, metabolomics and bioinformatics.

Our national network of leading universities, research institutes and bioscience companies provides access to world class 'omics expertise and state-of-the-art infrastructure through contract services and research collaborations.

Bioplatforms Australia receives government funding to develop and implement investment strategies that boost Australian bioscience capabilities. We endeavour to accelerate systems biology in Australia through initiatives that facilitate multi-discipline integration and build bioinformatics capabilities. We also strive to foster greater scientific collaboration among researchers and between researchers and industry.

Our Vision

Bioplatforms Australia seeks to catalyse world class bioscience through access to integrated biomolecular research capability.

Our Goals

- ensure broad access to state-of-the-art biomolecular research capability;
- facilitate greater multi-discipline integration in Life Science research;
- contribute collaboratively to addressing challenges of national economic and social significance;
- advance world class research and innovation in Australia.

Our Capabilities

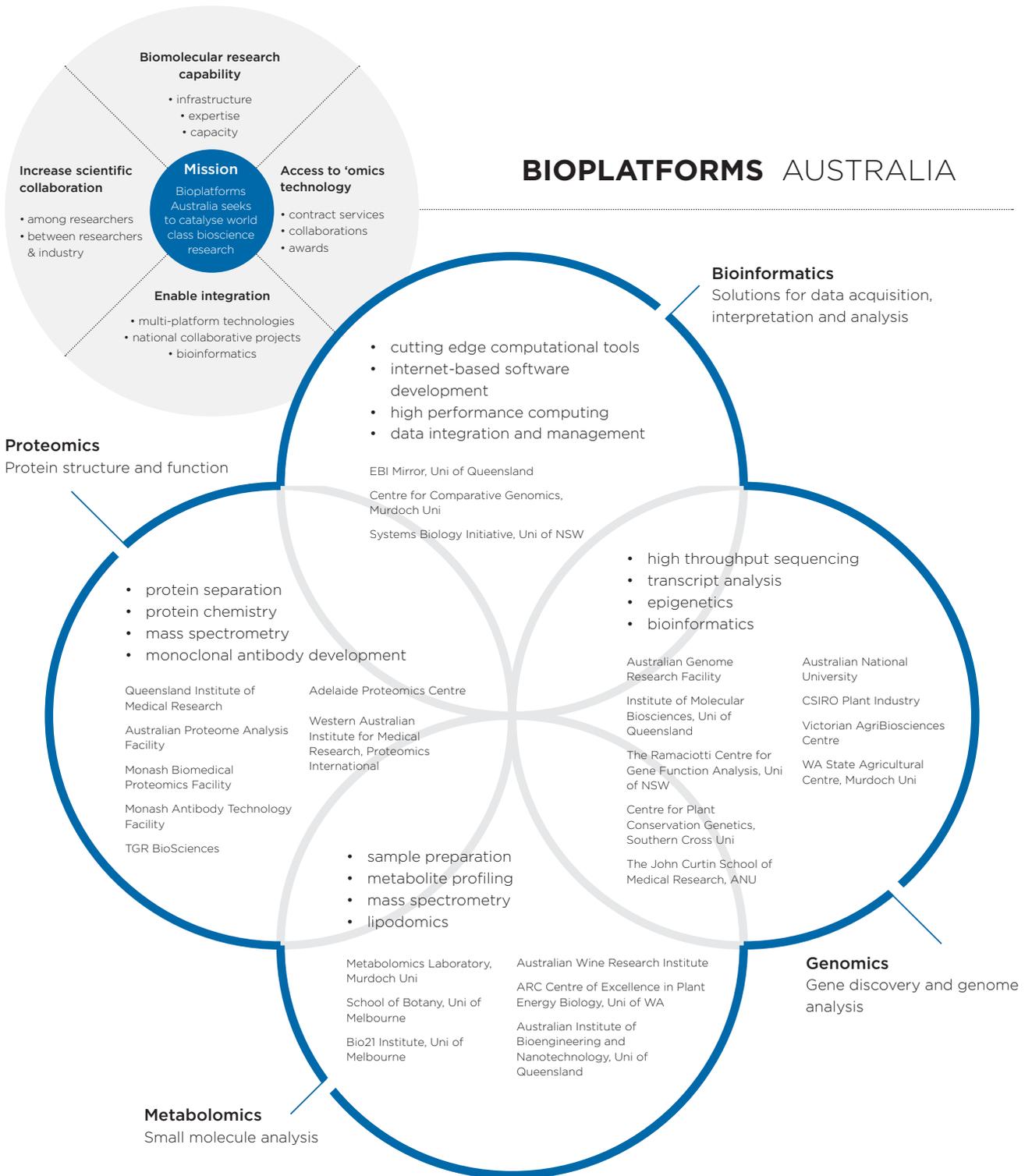
Bioplatforms Australia offers a broad range of complementary 'omics technologies relevant to the fields of food, agriculture, biomedicine and the environment. Users can access services from just one node or multiple network partners for more collaborative or complex projects.

Our Network

Our network is organised into four technology platforms - genomics, proteomics, metabolomics and bioinformatics. Services are offered through 17 separate nodes located around the nation with expert capabilities that can be accessed by the research community.

WHAT WE DO - BIOPLATFORMS AUSTRALIA

BIOPLATFORMS AUSTRALIA





11/12 YEAR IN REVIEW

During the last year, Bioplatforms Australia continued to leverage its 'omics network to promote broad collaboration in scientific projects offering significant strategic value for Australia.

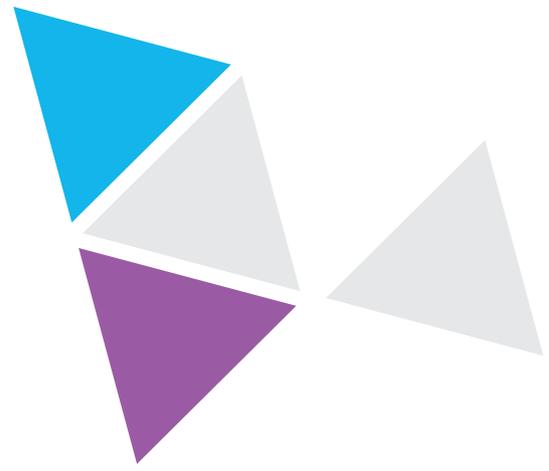
Our Framework Dataset Program has been a fundamental initiative in enabling systems biology for national research challenges. By generating large-scale 'omic datasets we are providing a pivotal resource while also facilitating the collaborative culture and cross-discipline approach essential to systems-based analysis.

Since launching the Wheat Dataset Program, additional projects on soil biomes, melanoma and the Great Barrier Reef have been instigated. Each project is being supported for its strategic value to national research efforts and significant potential to benefit from a systems biology approach. These projects have generated broad support and engagement and additional themes will be launched to extend Australia's data resources and foster new links with the scientific community.

We have also established collaborations that magnify our

efforts to build Australia's scientific capabilities and tackle research bottlenecks. The Australian Bioinformatics Network (ABN) is now formally established with dedicated leadership and represents the collective vision of Bioplatforms Australia, CSIRO and EMBL Australia. Over the last year, the ABN launched a world class training initiative to expand Australia's bioinformatics skills and will instigate further initiatives to support the bioinformatics sector and practitioners.

Other endeavours in 2011/12 revolve around our continuing commitment to increase access to 'omics infrastructure and enhance Australian bioscience capabilities. New initiatives and progress on existing work programs over the year are reported in the following pages.

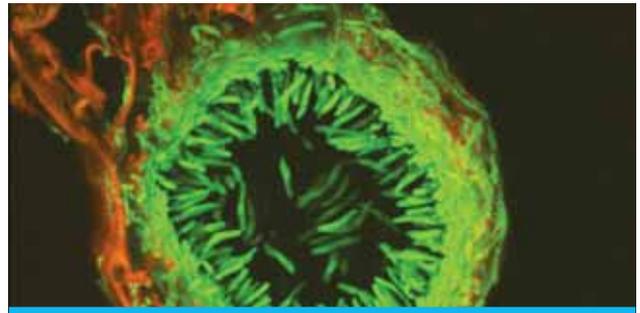


NATIONAL FRAMEWORK DATASETS

“By compiling large scale datasets around significant research themes within Australian science, existing resources and expertise can be leveraged to build ‘soft’ infrastructure that can be widely accessed for a range of downstream research.”

The Framework Dataset program was launched to address the lack of large scale, high quality, quantitative data needed for systems biology. By compiling large scale datasets around significant research themes within Australian science, existing resources and expertise can be leveraged to build ‘soft’ infrastructure that can be widely accessed for a range of downstream research.

So far the program has been successful in encouraging collective contributions and broad collaboration. A significant driver for such broad support is the shared recognition that the dataset program is able to transcend the discipline boundaries and financial limits associated with creating the massive cross-platform datasets that are vital to systems analysis. Indeed, our first dataset project on wheat has become something of a model for building the collaborative effort needed to tackle significant



research challenges. Over the year it has attracted the interest of a number of international organisations and been the theme of various discussions and workshops.

The core themes for each of our current dataset projects were all chosen for their relevance to national research challenges, collaborative opportunities and considerable potential to provide a lasting resource to Australian researchers. Our wheat and soil datasets projects are on-going from 2010 and the two new projects on melanoma and reef protection were instigated this year.

Bioplatforms Australia’s multi-platform network is making a core contribution to generating the bank

of data required for all four projects. We are also employing our bioinformatics workforce to solve integration and analysis issues and to ensure that the datasets can be broadly accessible.

On the bioinformatics front, the dataset program is proving to be an invaluable test bed. Numerous technical challenges related to data integration, harmonisation, management, accessibility and storage are generating new tools and techniques and this expertise will be broadly deployed to ensure on-going benefit to Australian researchers.

11/12 YEAR IN REVIEW - NATIONAL FRAMEWORK DATASETS

Wheat

Wheat was selected as Bioplatforms Australia's first dataset theme due to its significance to the Australian economy and its strategic value as a global food crop. Currently, Australian wheat research is particularly focused on food security, especially yield improvements; improved resistance to difficult climate conditions; and greater defence mechanisms against disease.

The wheat dataset program encompasses three elements: sequencing of wheat chromosome 7A; new datasets to define the genetic diversity of key Australian cultivars; and datasets on wheat interaction with pathogens and pests.

Chromosome 7A

While the genomes for rice and maize have already been sequenced, a reference genome for wheat is not yet available due to its much larger and more complex genome. In order to take advantage of biotech opportunities for crop improvement, the International Wheat Genome Sequencing Consortium (IWGSC) has taken on the mission to

sequence and assemble all wheat's 42 chromosomes and has engaged a number of countries to help with the process.

Australia's contribution to the IWGSC project is to sequence chromosome 7A. It is a strategic choice as it contains important genes that influence yield quality and disease resistance. Access to a wheat reference genome offers significant research prospects and will be invaluable to other components of our wheat dataset project. In particular, this data will be leveraged in a corresponding effort to map the genetic profile of key Australian varieties.

Funding from the Grains Research & Development Corporation (GRDC) for 7A sequencing has been leveraged with additional funds from Bioplatforms Australia. Sequencing work has progressed over the year and we expect to complete our component of this project in 2012/13. When completed, the full genome will be made publically and freely available.

Genetic variability in key Australian wheat varieties

New datasets of important Australian cultivars will enable meaningful

comparisons of genetic diversity and help researchers to identify the characteristics that impact on yield. A consortium of Australian wheat researchers and breeders from CSIRO, various Australian universities and relevant industry bodies have been collaborating with Bioplatforms Australia and some of our nodes to build datasets for 16 key varieties of particular importance to the Australian wheat industry.

The 16 selected wheat varieties were drawn from a list of nearly 60 potential candidates. The consortium's final selection was based on the notable attributes and demonstrated productivity in different environments of each cultivar together with their associated economic impact. Over the year, the sequence data for all 16 wheat varieties was generated and is now being analysed. This data is now available for interested parties.

Wheat pathogen datasets

Disease represents a major constraint to wheat production and can have significant economic impact. Development of broad spectrum and more durable control mechanisms

in new wheat cultivars requires greater molecular understanding of how wheat pathogens infect their host and how wheat defends itself.

To help build this understanding, Bioplatforms Australia established a second wheat working group, the Australian Wheat Pathogenomics Consortium to generate large-scale genomic, transcriptomic, proteomic and metabolomic datasets of a diverse range of wheat pathogens. This integrated approach across biomolecular platforms is helping to define the pathogen interaction with the wheat host and highlight new opportunities



11/12 YEAR IN REVIEW - NATIONAL FRAMEWORK DATASETS



for crop protection.

The pathogenomics consortium comprises specialists from plant pathology research groups at CSIRO, a number of Australian universities and several Bioplatforms Australia nodes. The work program covers a range of pathogen species including those that cause stripe rust, stem rust, tan spot, glume blotch, septoria leaf blotch and crown rot/head blight.

A large proportion of the datasets for the wheat pathogenomics component were generated over 2011/12 with the remainder to be compiled by the end of 2012/13. When combined

with the wheat datasets, the pathogen data will offer new insights to fight significant wheat disease.

To ensure cohesion, data exchange and integration between the various project elements, the two wheat working groups meet at project forums and workshops.

Biome of Australian Soil Environments

The dataset project on soil biodiversity will provide a unique opportunity to map the diversity and ecological function of Australian soil biomes across a range of different sites. Although soil hosts diverse microbial

communities that play a critical role in many ecological processes, soil communities are not well quantified either in Australia or the rest of the world. Soil is rarely viewed as a natural resource but an understanding of the abundance, diversity and structure of soil communities will provide an invaluable insight into the response of soil microbes to land use practices as well as their potential for ecological stability and resilience.

Over the year, Bioplatforms Australia collaborated with scientists from CSIRO, National Parks, government agencies, universities and research and development corporations to define project goals and parameters including site selection criteria and sampling protocols. All collaborators are contributing resources and/or expertise to build molecular datasets that will relate each soil community to their site environment, vegetation and land use.

After defining project parameters, a pilot study was launched to collect samples from specific sites together with specified contextual data such as soil chemistry measurements, GPS information and environmental observations.

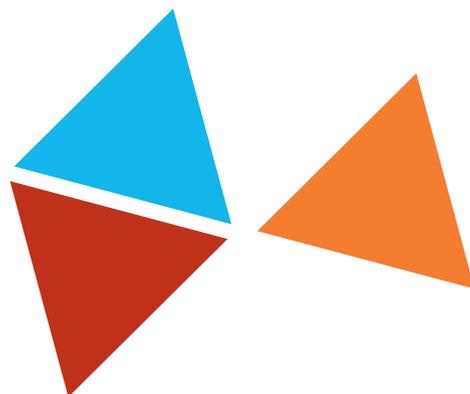
The AGRF will perform the DNA recovery and complete most of the sequencing work during 2012/13. An estimated 600 sites will be analysed in the first stage. The results will then inform future site selection and help to refine the methodologies being applied.

Melanoma Genome

During 2011/12 Bioplatforms Australia launched a new dataset project to support important research on melanoma cancer led by Melanoma Institute Australia. This collaborative venture aims to identify the genetic mutations that cause melanoma by analysing the DNA of over 500 melanoma tumours. The large-scale genomic datasets will allow researchers to compare mutant cells with 'normal' ones in order to identify new treatment targets based on the genetic characteristics of melanoma.

Melanoma is Australia's leading cancer killer, especially among the young and middle-aged. While it only represents around two per cent of skin cancers, it accounts for almost 76 per cent of all skin cancer deaths. Australia already has the highest incidence

11/12 YEAR IN REVIEW - NATIONAL FRAMEWORK DATASETS



of melanoma in the world but the number of cases has been increasing. Until recently there have been no effective therapies for treating melanoma cancer, but with greater knowledge of the genetic basis of the disease, researchers are confident that new treatments and better diagnosis will result.

The melanoma datasets will be critical to exploring the genetic and biochemical events that can transform cells into a melanoma and will hopefully reveal patterns of mutation and the consequent molecular changes that can occur. As different datasets will link various cellular processes, they are expected to become an invaluable resource for other cancer research and biological investigations.

Bioplatforms Australia nodes will help sequence 500 melanoma samples that have been drawn from the tissue bank collated by the Melanoma Institute over the last 20 years. The datasets will also include proteomic

and metabolomics analyses to profile the proteins and other small molecules expressed by the relevant genes. This data will provide further clues on the impact of melanoma gene mutations and help identify new drug targets.

The Melanoma Genome Project will take two years and represents a coalition of leading melanoma researchers from the Melanoma Institute of Australia, the University of Sydney, Royal Prince Alfred Hospital and NSW Health Pathology, Westmead Millennium Institute, Peter MacCallum Cancer Centre, Ludwig Institute for Cancer Research and the Queensland Institute of Medical Research.

In addition to the funding provided by Bioplatforms Australia, the project has also received financial support from the NSW Government, Cancer Council NSW and private donors who have pledged support to the Melanoma Institute of Australia.

Great Barrier Reef

Our newest dataset project will involve the Bioplatforms Australia network in generating genomic datasets for coral, their algal symbionts and associated microbes. This large scale data will serve a series of research projects to determine the response and resilience of corals to climate change which is expected to underpin new solutions for protecting and preserving coral reefs.

Climate change is considered to be the greatest risk facing the Great Barrier Reef with rising temperatures and pH changes placing on-going stress on corals and threatening long term repercussions for the sustainability of coral reefs and their complex ecosystem. In response to this threat, the Great Barrier Reef Foundation (GBRF) has established a consortium of national and international experts called ReFuGe 2020 (short for Reef Future Genomics). The Consortium's goal is to fast track genomics-based

research into coral climate adaptation in order to generate new approaches to reef protection.

Consortium members include Bioplatforms Australia, the Great Barrier Reef Foundation, James Cook University, the Australian Institute of Marine Science, the University of Queensland, the Great Barrier Reef Marine Park Authority, the King Abdullah University of Science and Technology, the Australian National University and corporate sponsor, Life Technologies. Rio Tinto is also a generous co-sponsor.

To date, the key research questions to be pursued have been established and all support fundamental objectives in reef management. Bioplatforms Australia's investment will deliver sequencing data for 10 priority corals and their associated symbionts. Sequencing work will commence in 2012/13 and, like all other datasets created by Bioplatforms Australia, will be openly available to Australian researchers.

BIOINFORMATICS



Currently, Australia's bioinformatics capacity and level of expertise is not yet keeping up with ever-increasing data outputs. Likewise, the practicalities of systems biology projects that revolve around data integration, data sharing and data management are putting a spotlight on harmonisation issues that need to be solved at a global level.

During 2011/12, Bioplatforms Australia continued to seek opportunities to tackle bioinformatics bottlenecks and, more importantly, foster Australia's emerging bioinformatics sector. A number of international collaborations have been established to forge links with global expertise and to keep track of international trends and advancements. These collaborations are already showing benefit especially in developing new training opportunities and establishing data commons. On the domestic front, the Australian Bioinformatics Network is now established and offers significant potential

to both leverage and grow Australian bioinformatics expertise.

The following highlights our bioinformatics activities for the year.

Australian Bioinformatics Network

Bioplatforms Australia, together with EMBL Australia and the CSIRO, founded the Australian Bioinformatics Network (ABN) as a mechanism to build a more coherent bioinformatics community in Australia and encourage greater links between researcher needs and bioinformatics capabilities. The ABN's mission is to connect people, resources and opportunities in order to increase the benefits Australian bioinformatics can deliver. During the year the ABN launched a new training program and recruited Dr David Lovell who will commence as Director in July 2012.

Dr Lovell is an electrical engineer by training and has been working in

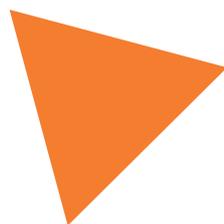
the field of quantitative biosciences since 2004. As ABN Director, Dr Lovell's ambition is for the organisation to encompass the full diversity of bioinformatics which extends beyond biology and informatics to many other quantitative disciplines. He intends to develop greater linkages between all the elements of bioinformatics needed for modern bioscience and will support and encourage the many bioinformatics communities and specialists that are already established around special topics of interest. Dr Lovell hopes to raise awareness of what's happening in the bioinformatics scene and facilitate opportunities for new and fruitful connections both in Australia and internationally.

The ABN's first priority will be to establish a useful online presence. The site will operate as an information hub for anyone interested in bioinformatics and offer a new forum for networking and collaboration opportunities. The website

will be launched early in 2012/13 together with other initiatives that support the ABN mission.



Dr David Lovell, *new*
Director of the Australian
Bioinformatics Network



11/12 YEAR IN REVIEW - BIOINFORMATICS

Bioinformatics Training Workshops

Bioplatforms Australia has developed new bioinformatics training workshops to support Australian life scientists undertaking systems biology research. This initiative was executed in collaboration with the European Bioinformatic Institute (EBI), a member of the European Molecular Biology Laboratory (EMBL) that is a renowned provider of diverse bioinformatics training including hands-on courses.

During 2011/12, a team of eight bioinformaticians from the Australian Bioinformatics Network were selected to deliver and develop Australia's first Next-Generation Sequencing workshop. All the trainers are highly experienced in bioinformatics and received further intensive training at the EMBL-EBI campus near Hinxton in the UK.

The Next-Generation Sequencing Workshop developed for Australian researchers gives particular focus to those with minimal experience in next generation sequencing analysis or bioinformatics. The course allows participants to familiarise themselves with commonly

used software applications and workflows and offers hands-on exposure to computational elements. The course was delivered in a number of Australian cities and was very well received by participants. It will be offered again in the coming year along with other training initiatives.

Data Commoning

Bioplatforms Australia's framework dataset program has propelled the drive to establish data protocols that will enable greater data exchange and integration. To facilitate data sharing within our own projects and promote the reuse of growing data resources by others, we have been collaborating with a research team from the University of Oxford to adopt their open source software suite for managing omic' studies.

The Oxford team has developed a framework called ISA-Tab which provides a template to standardise the way data is captured, annotated and curated allowing greater data sharing with the growing international community that are using the ISA framework.

We have now adopted the ISA-tab format for our dataset projects and

also implemented another ISAtools component known as the BioInvestigation Index (BII) which facilitates storage of curated data and allows on-line accessibility.

Bioplatforms Australia is highly committed to improving data harmonisation in Australia and is supporting international efforts towards establishing data commons. During the year, we joined an international collaboration of 30 academic and commercial organisations which are all working to establish data standards based on the ISA-framework. To accelerate this initiative, Bioplatforms Australia and the CSIRO sponsored the Oxford ISAtools developers, Dr Philippe Rocca-Serra and Eamon Maguire to discuss data commoning with Australian research teams and run ISAtools training courses in Brisbane, Perth and Canberra.

Bioinformatics Analysis Environment

Bioplatforms Australia has been working with leading eResearch organisations from around Australia to scope and develop a bioinformatics analytical environment that can provide biologists with a web-based interface to open source and proprietary

bioinformatics tools and other capabilities. The aim is to empower scientists with a bigger range of bioinformatics tools for their workflows that can be readily accessed and used without advanced computer skills. The analytical environment is an important component of our Framework Dataset program as it will enable access to new data repositories as well as a range of analytical tools.

The NeCTAR's virtual laboratory program fits neatly with our objectives for data sharing and accessibility, so we are co-investing in the development of a Genomics Virtual Laboratory (GVL) that will allow genome researchers to connect with relevant datasets, sophisticated analytical tools and large-scale computation infrastructure. Besides the data repositories built by Bioplatforms Australia, the GVL will also allow researchers to access other national facilities such as the NeCTAR research cloud, Research Data Storage Infrastructure, National Computational Infrastructure Specialised Facility in Bioinformatics (NCI-SFB), Australian National Data Service and the Australian EMBL-EBI mirror. The GVL



“Bioplatforms Australia is highly committed to improving data harmonisation in Australia and is supporting international efforts towards establishing data commons.”

development is being co-lead by Dr Michael Pheasant of the University of Queensland’s Institute for Molecular Biosciences.

EMBL-EBI Mirror

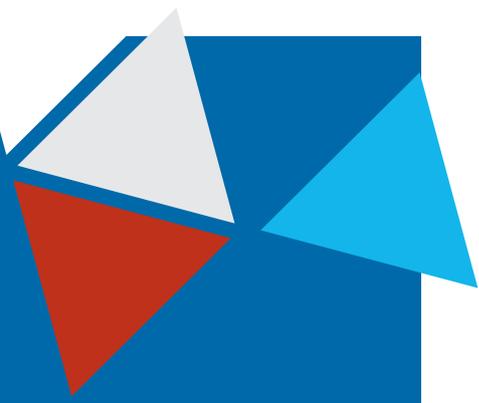
The Australian Mirror of EMBL-EBI facility at the University of Queensland was launched in June 2011 and provides a major bioinformatics resource for Australian scientists. The EBI mirror gives Australian scientists greater access to the data resources of the European Bioinformatics Institute (EBI) and other specialised datasets. It also provides access to the high-performance computing offered by the NCI-SFB

which is hosted on the same infrastructure.

Accessibility to analytical tools now available through the mirror facility has been greatly enhanced with the introduction of the YABI/Bioflow workflow engine developed by one of our bioinformatics nodes, the Centre for Comparative Genomics (CCG) at Murdoch University. Researchers are now able to use this intuitive web-based tool to create and manage new workflows to aggregate and integrate a wide range of bioinformatics tools with the available data. It also allows scientists to share their workflows and data with the scientific

community, facilitating dissemination and re-use.

The EBI mirror has recorded approximately 150 users per month in its first year of operation but visitor numbers are steadily increasing and this figure is expected to be higher over the next year and into the future.



COLLABORATIONS & PARTNERSHIPS

Bioplatforms Australia works hard to foster scientific collaboration as well as partnerships that enhance scientific capabilities for Australian researchers.

The Framework Dataset program represents a key tactic in this mission, but other partnerships such as that with EMBL Australia have been very valuable in delivering strategic opportunities to enhance skills and provide access to international scientific resources.

We are particularly keen to foster other international linkages for Australian scientists and have been developing new opportunities for greater collaboration and international engagement with the following initiatives.

International Internships

To more deeply engage with international science, Bioplatforms Australia's International Internship program offers our network partners an opportunity to build strategic, reciprocated and lasting collaborations with international organisations.

The program offers up to \$30,000 for travel, accommodation and scientific costs for a two to three month internship by an Australian or international scientist. The internship needs to demonstrate benefit to Australia's systems biology capabilities or projects and identify potential for an on-going relationship.

The first internship under this program facilitated a scientist exchange between the Ramaciotti Centre at the University of NSW and a leading Stem Cell lab in Denmark.

Chardonnay Genome Collaboration

The landmark project to map the chardonnay genome is well underway as a result of an international partnership between the Australian Wine Research Institute and Genome British Columbia.

COLLABORATIONS & PARTNERSHIPS



“Modern genomics technology represents an unprecedented opportunity to more deeply explore Australia’s genetic diversity.”

The project involves sequencing and analysis of 15 chardonnay clones from the vineyards of Australia’s Yalumba Wine Company. Sequencing work is being shared between the AGRF and University of British Columbia and is expected to be completed by the end of 2012. The complicated task of assembly will follow together with genomic comparisons to determine how genetic variations affect growth, fermentation, flavour and aroma. Wine will also be made from a subset of 10 clones at Hickenbotham Wine Science Laboratory in South Australia. This will allow researchers to align genetic variations in the cultivar with metabolomic and sensory profiles of the wine that is produced.

This project offers significant benefit to the winemaking industry in Australia as chardonnay is our most dominant white variety and second most widely grown wine cultivar. The collaboration will deliver important knowledge to help winemakers choose the best variety for their climate and

soil as well as enable them to produce better wine.

This unique project is also supported by the South Australian Research and Development Institute and funded by Bioplatforms Australia, the Grape and Wine Research and Development Corporation and Genome British Columbia.

Genetic Diversity Revealed from Unique Collections

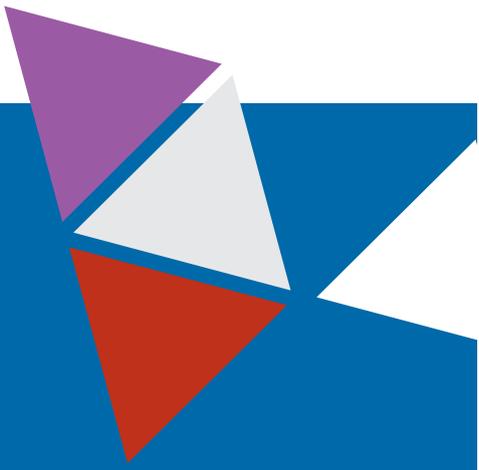
Australia’s rich and unique biodiversity is significantly captured in the expansive collections of our museums, zoos and gardens, however, the scientific benefit of such vast repositories is largely untapped. Modern genomics technology represents an unprecedented opportunity to more deeply explore Australia’s genetic diversity which has prompted a new program to engage curators of important flora and fauna collections.

Bioplatforms Australia is seeking new collaborations with Australian museums, zoos and gardens to unlock

further benefit from their biological collections and better leverage some of the rare and historic specimens that have been collated over the last two centuries. New genetic data from preserved specimens will be made publicly accessible to propel many diverse scientific endeavours including international projects such as the Barcode of Life.

Bioplatforms Australia will provide resources to extract and sequence DNA from significant biological specimens and has approached a number of curators to convey the analytical capabilities available across our ‘omics network. By making the data publicly accessible in the same manner as our framework datasets, we can add to the massive data resources being acquired for systems biology projects and ensure on-going value.

Bioplatforms Australia expects to announce new projects under this initiative in the coming year.



ACCESS

New Infrastructure & Technology

In 2011/12 further investments in next-generation sequencing have continued to enhance the capacity and technology breadth available across our genomics network.

Additional Illumina HiSeq capacity and the first foray into MiSeq and Ion Torrent technology were funded during the year. Existing Sanger sequencing capability has been maintained with various upgrades occurring at the Australian Genome Research Facility (AGRF).

Australian Proteome Analysis Facility (APAF) at Macquarie University acquired two additional Triple TOF 5600 mass spectrometers providing high capacity for advanced protein identification and quantification analyses.

The metabolomics node at the Australian Wine Research Institute acquired additional Gas Chromatography and Liquid Chromatography Mass Spectrometry capacity in response to growing customer demand. The metabolomics node at Murdoch University also acquired a Liquid

Chromatography Mass Spectrometer that will be shared with the Perth based proteomics node, Proteomics International.

The University of Western Australia facility acquired additional Agilent Gas Chromatography and Liquid Chromatography Mass Spectrometry instrumentation. They also signed a five year collaborative agreement with Agilent Technologies to adopt the company's platform technologies. Under this agreement, a high-resolution mass spectrometer was donated to provide accurate metabolomic analysis of molecules in complex samples.

ACCESS

Table 1: A summary of the main infrastructure purchases for 2011/12

Table 1: Infrastructure Purchases

Genomics Australia

Australian Genome Research Facility (AGRF)	<ul style="list-style-type: none"> - Next-generation sequencing instrumentation - Sanger based nucleotide sequencing instrumentation - Ion Torrent technology for nucleotide sequencing - MiSeq technology for nucleotide sequencing - Ancillary laboratory equipment
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Proteomics Australia

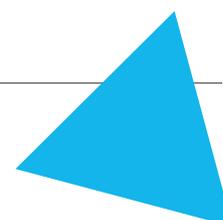
Monash University	<ul style="list-style-type: none"> - Robotic automation for monoclonal antibody production and mammalian protein production
Australian Proteome Analysis Facility (APAF)	<ul style="list-style-type: none"> - 2 AB Sciex 5600 high duty cycle Mass Spectrometer (one instrument purchased in partnership with Cancer Institute NSW)

Metabolomics

Australian Wine Research Institute	<ul style="list-style-type: none"> - LS Triple Quadrupole Mass Spectrometry - Gas Chromatography Mass Spectrometry - Auto sampling robotics and auxiliary laboratory equipment
University of Western Australia	<ul style="list-style-type: none"> - Gas Chromatography Mass Spectrometry - Liquid Chromatography Mass Spectrometry - Analytical software
Murdoch University	<ul style="list-style-type: none"> - AB Sciex 5600 Mass Spectrometer (this instrument will be jointly accessed by Proteomics International)

Bioinformatics

University of Melbourne Murdoch University University of Western Australia University of Queensland WA Institute of Medical Research Australian Wine Research Institute	<ul style="list-style-type: none"> - These nodes recruited bioinformaticians to provide embedded capacity for relevant services. - Funded bioinformatics capability at the Australian Wine Research Institute supports all platforms in Adelaide.
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ACCESS



Dr Chris Tonkin

2011/12 Access Voucher Awardee

Dr Chris Tonkin from Walter & Eliza Hall Institute of Medical Research was selected by the Australian Society for Biochemistry and Molecular Biology (ASBMB) to receive the 2012 Bioplatforms Australia Award. The award is presented to post-doctoral researchers for outstanding research in the field of genomics, transcriptomics, proteomics, metabolomics, or relevant bioinformatics and provides \$10,000 worth of services provided by any node of Bioplatforms Australia.

Dr Tonkin's research focuses on Apicomplexan parasites that cause a wide range of disease such as malaria, gastrointestinal disease and toxoplasmosis. Toxoplasmosis is mostly suffered by immune compromised individuals such as transplant recipients and AIDS patients but is also responsible for an eye infection that is a leading cause of blindness in some developing countries.

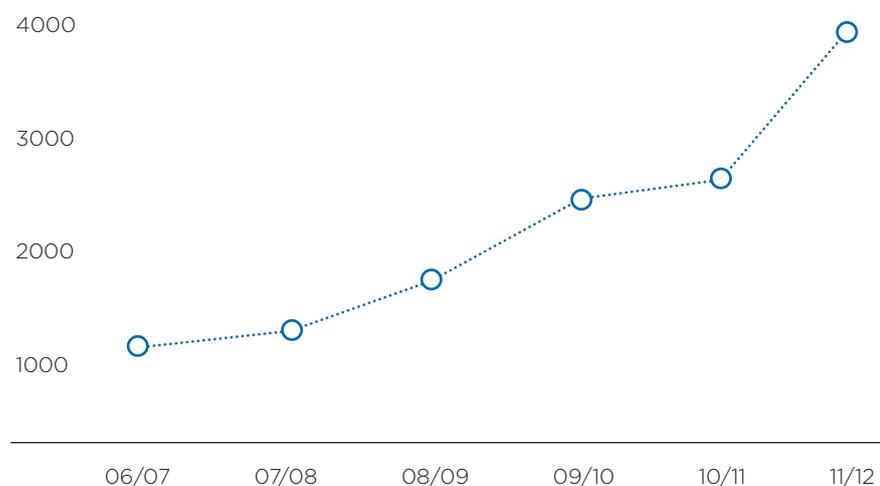
Dr Tonkin's research has been investigating how different apicomplexan parasites invade host cells in order to identify what aspects of invasion are common to all apicomplexan species. His latest research aims to reveal new genes that are involved in the process of activating invasion and he plans to utilise his Bioplatforms Australia access voucher for full genome sequencing of isolated *Toxoplasma gondii* lines.

Access Statistics

Bioplatforms Australia closely monitors access to its infrastructure network and collects data from the major nodes to determine access trends and the level of industry engagement. Our baseline data was collated in 2006 and represents the year prior to Bioplatforms Australia being established and implementation of the NCRIS funding strategy. Statistics for 2011/12 represent the fifth full year of nationally co-ordinated investments in scientific infrastructure and show continuing growth in both clients and revenue.

“the number of clients has increased every year with a notable acceleration in the last year.”

Figure 1: Access Trends between 2007 and 2011



ACCESS



“The significant jump in clients compared to previous years relates particularly to genomics where the introduction of next-generation sequencing technologies have been readily adopted by researchers and is in high demand.”

Figure 2: Client Numbers by Platform

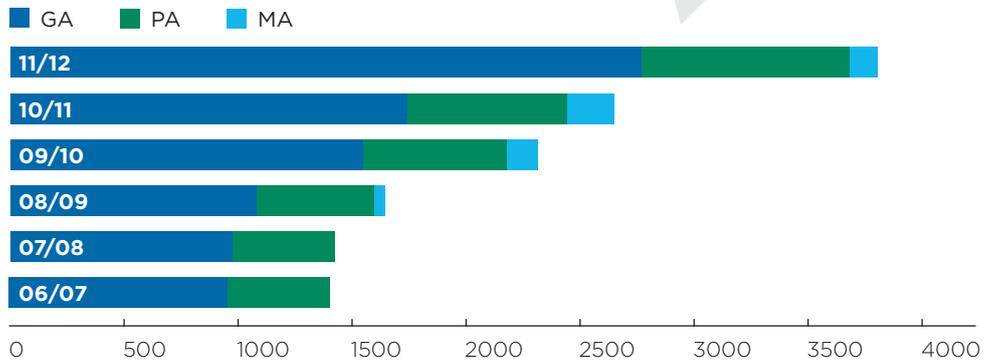
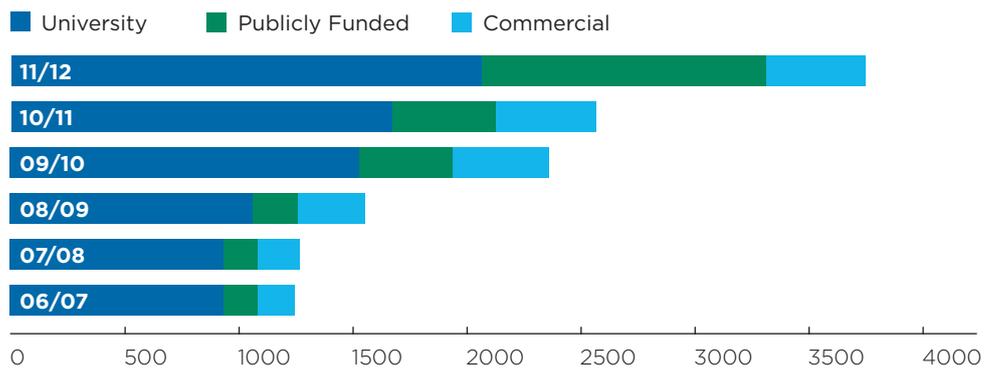


Figure 3: Client Numbers by Sector



Client Growth Continues

The number of fee-for-service clients increased by 44 per cent in the last 12 months with a total increase of 178 per cent over the five years since Bioplatforms Australia was established. A ‘client’ is defined as a researcher or group of researchers who access a service or services for a specific research project. As shown in Figure 1, the number of clients has increased every year with a notable acceleration in the last year.

Figure 2 indicates the numbers of clients serviced by each platform over the last five years. The significant jump in clients compared to previous years relates particularly to genomics where the introduction of next-generation sequencing technologies have been readily adopted by researchers and is in high demand. No clients were recorded for metabolomics until 2008/09 as it is a new scientific capability for Australia and went through a period of

instrument commissioning and methods development before it could offer services.

Clients and Revenue by Research Sector

As indicated by Figure 3, universities constitute 56 per cent of all 2011/12 clients while publicly funded researchers account for 34 per cent, an increase of 134 per cent since the previous year. Indeed, the number of publicly funded clients has more than trebled since 2008/09 making it the

ACCESS

“Despite the minor fall in the number of commercial clients, Figure 4 shows that this sector accounts for 25 per cent of 2011/12 service revenues which is a notable increase in the average client spend since last year.”

Figure 3: Service Revenue by Sector and Year

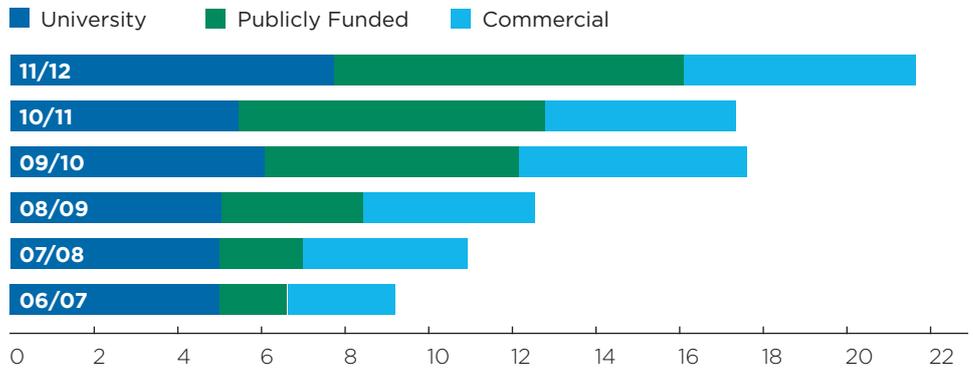
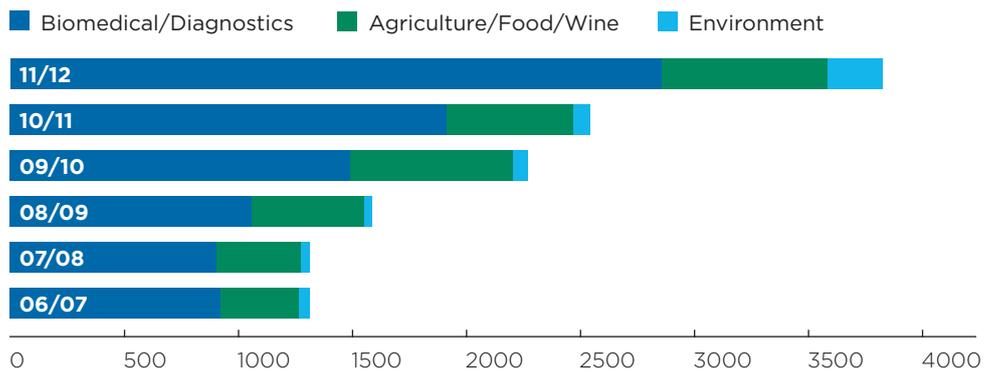


Figure 4: Client Numbers by Discipline and Year



fastest growing sector. The proportion of commercial clients has decreased slightly over the last 12 months to ten per cent.

Despite the minor fall in the number of commercial clients, Figure 4 shows that this sector accounts for 25 per cent of 2011/12 service revenues which is a notable increase in the average client spend since last year. Public research clients contributed 41 per cent of revenue representing minimal change since

last year due to a slight fall in the average spend for this sector. University clients delivered 34 per cent of recorded revenues and demonstrated only a marginal increase in their average spend.

While the number of clients from each research category increased in 2011/12, Figure 5 shows that research services are still predominantly provided to the biomedical/diagnostics sector which accounts for 74 per cent of

all clients and 76 per cent of revenues. Agriculture/food/wine clients constituted 19 per cent of clients and 16 per cent of revenues. The proportion of services delivered to the environment sector did not change significantly totaling six per cent with revenues reaching seven per cent of the total.

ACCESS



Summary

Bioplatforms Australia is pleased that access rates have accelerated this year and will continue to monitor capacity at each of our genomics nodes given the significant increases in client numbers. The growing importance of publicly funded and commercial clients is also welcome as Bioplatforms Australia is working hard to broaden access to its research network.

The continuing predominance of the biomedical sector is unsurprising given Australia's research strength in this area, the level of associated funding and the obvious relevance of 'omics applications to medical research. Agriculture and environmental researchers are increasingly applying 'omics technology and this trend is likely to continue.

Promotional Activities

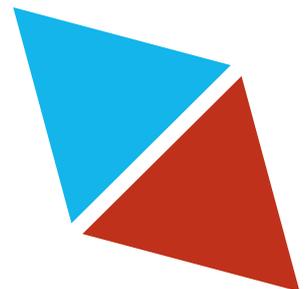
Promotional activities throughout 2011/12 sought to build awareness of 'omics capabilities and services and the role Bioplatforms Australia plays in sponsoring collaborative projects of national significance. Our network partners also undertake targeted marketing activities relevant to their technical expertise and service offering.

Bioplatforms Australia's main promotional activities include:

- Exhibits, presentations and/or attendance at a broad range of scientific forums and special interest meetings.
- Sponsoring targeted conferences, workshops and seminars.
- Publications in peer reviewed journals and science related websites.
- Promotional materials and corporate communications (including a regular newsletter).

Specific activities in 2011/12 included:

- Exhibit at Lorne Proteomics, Protein, Cancer and Genomics Conferences (in conjunction with AGRF and APAF).
- Sponsorship and organisation of the Metabolomics session at the Australasian Proteomics Society Conference at Lorne.
- Sponsorship of a pre-Lorne conference "Proteomics Mass Spectrometry Imaging Workshop" to highlight the new mass spectrometry imaging infrastructure now available at our proteomics node at University of Adelaide and metabolomics node at the University of Melbourne.
- Major upgrade and update of Bioplatforms Australia website.
- Workshops in Canberra and Perth for the wheat genomics and wheat pathogen consortiums collaborating on the wheat dataset project.





ADVOCACY & GOVERNANCE



Advocacy

Bioplatforms Australia's advocacy role aims to support 'omics research through on-going government liaison. We consult widely with the research community to build awareness of Australia's scientific capabilities and remain informed on emerging issues and technology trends. We also advocate for policy decisions and programs that support 'omics research and continued funding for the sector.

Discussions were held with all levels of government over the year as highlighted below. Dialogue sought to convey the impact of Bioplatforms Australia's strategic initiatives, promote the value of continued funding and seek new research partnerships.

State Government Liaison -

Bioplatforms Australia met with State Government departments from Queensland, Western Australia, South Australia, New South Wales and Victoria to report progress on our programs and projects and discuss possibilities for future partnership. The New

South Wales, South Australian and Queensland Governments provided co-investment funding to support various programs implemented under the EIF Super Science strategy.

Chief Scientist Liaison - Bioplatforms Australia representatives met with Chief Scientists from the Commonwealth, Western Australia, South Australia, Victoria and Queensland to advocate support for large scale genomics science and shared infrastructure strategies.

Department of Industry, Innovation, Science and Research - Bioplatforms Australia has been actively contributing to the 2012 National Research Investment Plan with written submissions and through a stakeholder meeting held in July 2012.

Government Agencies - Bioplatforms Australia provided verbal and written submissions to the ARC LIEF review and written submission to the ongoing NHMRC review.

ADVOCACY & GOVERNANCE



Governance

Bioplatforms Australia is managed by a Board of Directors with support from a Scientific Advisory Committee. During the year, Dr Sue Meek was welcomed to the Board and brings a wealth of experience in government liaison and a passion for formulating policies and programs to stimulate the application of research and development.

The Directors met on five occasions during 2011/12:

- 19 July 2011
- 22 September 2011
- 16 November 2011 (Annual General Meeting)
- 23 February 2012
- 18 May 2012

Board members also perform specific roles in addition to their fiduciary responsibilities:

John Grant - Financial oversight, Commonwealth Government liaison, NSW State Government liaison, NSW subcontractor liaison.

Les Trudzik - Performance and impact framework development, Victorian State Government liaison, Victorian subcontractor liaison, Western Australian State Government liaison, Western Australian subcontractor liaison.

John de Jersey - Chair of Scientific Advisory Committee, Queensland State Government liaison, Queensland subcontractor liaison, South Australian State Government liaison, South Australian subcontractor liaison.

Sue Meek - Communications, DIISR liaison, BPA representative to the Great Barrier Reef Foundation ReFuGe governance committee.

Scientific Advisory Committee

A Scientific Advisory Committee was established by the Board of Directors to oversee the scientific progress and needs of the platforms sectors.

Committee members are:

- Prof John de Jersey, Director, Bioplatforms Australia, Chair
- Dr Tim Littlejohn, IBM
- Prof John Mattick, University of Queensland
- Prof Peter Klinken, Western Australian Institute for Medical Research
- Prof Merlyn Crossley, University of Sydney.

The Scientific Advisory Committee met once during the year and advised the Board on:

- promoting and facilitating systems biology for researchers;
- strategic projects that demonstrate and build systems biology capabilities; and
- future infrastructure investments.

Executive Management Committee

The Executive Management Committee is responsible for executing the NCRIS Funding Agreement and implementing the strategic initiatives endorsed by the Board. Committee members are:

- Andrew Gilbert, Chair
- Dr Sue Forrest, Convenor Genomics
- Prof Jeff Gorman, Convenor Proteomics
- Prof Tony Bacic, Convenor Metabolomics
- Prof Matthew Bellgard, Convenor Bioinformatics



PLATFORM HIGHLIGHTS

Bioplatforms Australia offers comprehensive 'omics capabilities across four technology platforms - genomics, proteomics, metabolomics and bioinformatics.

Each node is responsible for managing NCRIS funded infrastructure and sharing their expertise with the broader scientific community through discrete scientific services or research partnerships and collaborations. The following projects highlight the capabilities of some of our nodes and diversity of research programs.

GENOMICS



“Next-generation DNA sequencing remains the cornerstone of most genomic projects undertaken by Bioplatforms Australia nodes over the last year.”

Next-generation DNA sequencing remains the cornerstone of most genomic projects undertaken by Bioplatforms Australia nodes over the last year. In addition to the substantial sequencing work required for the framework datasets of wheat, soil and melanoma, the following projects indicate the vast range of genomic research being conducted.

Safflower Genome

Safflower is a little used crop in Australian agriculture but is being developed as a technology platform for genetically-engineered oils with high contents of industrially-important derivatives of oleic acid. Dr Craig Wood and his colleagues at CSIRO have been working to determine the most important safflower genes for oilseed development and oil quality modification. High-quality sequencing data using the Illumina HiSeq2000 platform generated by AGRF was used to develop specific

gene silencing approaches (hairpin RNAi) to generate safflower seed containing the world’s highest concentration of oleic acid with more than 90 per cent purity. At such high purity, oleic acid is a highly valuable industrial oil and should help establish safflower as a profitable crop for Australian farmers.

Transcriptome Sequencing of Venom Toxins

Associate Professor Bryan Fry from the University of Queensland has noted that new insights into venom proteins have been limited by the very narrow taxonomical range studied. As entire groups of venomous animals are virtually unstudied, Fry partnered with the AGRF to complete transcriptome sequencing of more than 100 novel venom toxins including lineages such as the Antarctic Giant Octopus, the Komodo Dragon and vampire bat.

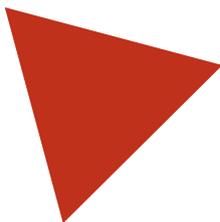
AGRF’s sequencing and bioinformatic analysis of

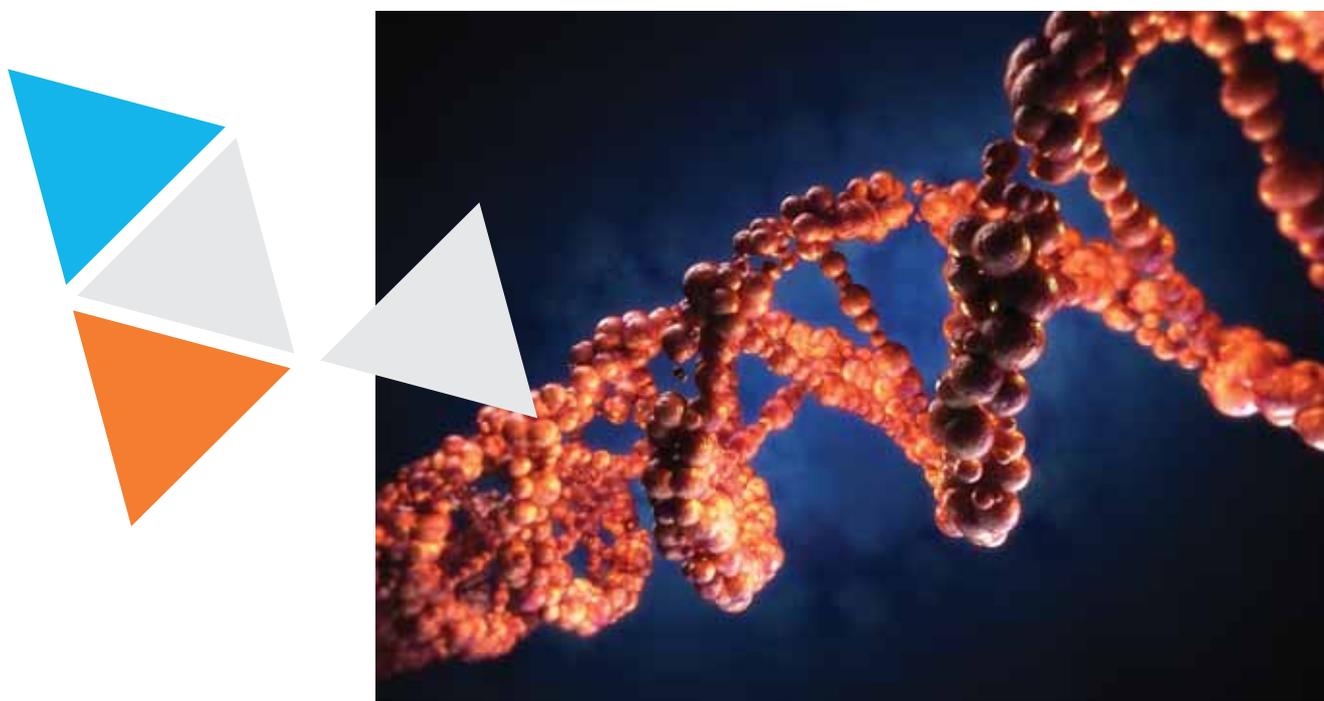
the toxins utilised a number of pipelines and databases. This work subsequently lead to a discovery in the unique way venom proteins are expressed and has so far facilitated nine papers including publications in elite journals.

Food Allergy Study

Professor Katie Allen, paediatric gastroenterologist and allergist at the Royal Children’s Hospital, Victoria is undertaking research in the field of food allergy and allergy epidemics. Professor Allen is working with the AGRF to combine a population-based food allergy study with a genome-wide association study (GWAS) to identify genetic variants linked to allergy. The aim of the project is to investigate the prevalence of food allergy and identify risk factors. It will also explore knowledge and attitudes toward food allergy in children and adolescents.

The project will include





“The results of the food allergy study are expected to provide important insights into the underlying mechanism of food allergy in children”

genomic analysis of 768 samples from a screened cohort with the aim of identifying genetic triggers which predispose an individual to allergic reactions. The results are expected to provide important insights into the underlying mechanism of food allergy in children.

The Role of Campylobacter concisus in Crohn’s Disease

Dr Nadeem Kaakoush and Professor Hazel Mitchell from the University of New South Wales sequenced the genome of an isolate of Campylobacter concisus, an enteric pathogen isolated from the gut of a child with Crohn’s disease. Sequencing

was done at the Ramaciotti Centre for Gene Function Analysis with assembly and annotation of the genome completed in association with the Systems Biology Initiative.

This research has revealed that the genome of this isolate showed dramatic differences to the non-pathogenic reference strain – especially in genes that might affect adhesion and invasion to cells that line the human gut. Dr Kaakoush and Professor Mitchell then showed that these genes, if transformed into non-pathogenic strains, increased their ability to attach to epithelial cells.

Another eight genomes of C. concisus were sequenced to expand this study and consistent genetic patterns are emerging which might explain the molecular basis of pathogenic strains.

PROTEOMICS



“Capabilities and capacity for protein identification and quantification analyses has significantly increased over the last two years.”

Capabilities and capacity for protein identification and quantification analyses has significantly increased over the last two years. This has been accompanied by improved bioinformatics support with the development of new workflows and an increase in embedded bioinformatics staff. In addition to proteomic studies on wheat pathogens, the following projects provide a snap shot of the research activities undertaken within Bioplatforms Australia’s proteomic network.

Glycoproteins in Sweat

APAF worked with an industrial cosmetics company to investigate a role for glycoproteins in the production of human sweat. Mass spectrometry was used to confirm such a role and research is now focused on establishing which glycans are associated with this finding. This work has led to a new research contract for Macquarie University to undertake further studies and, if successful, could

lead to new anti-perspirant products.

Biomarkers of Mesothelioma

APAF is working with Dr Glen Reid and his colleagues at the Asbestos Disease Research Institute to identify serum protein biomarkers that could be used to develop a novel diagnostic for malignant mesothelioma. Mass spectrometry experiments have identified several interesting leads and APAF is now designing targeted assays to quantitate these markers in a large cohort study. If successful, this research could improve prognosis for malignant mesothelioma, a disease with increasing prevalence in Australia, and pave the way for better treatment outcomes.

Protein Imaging Propels Cancer Research

Tissue banks in hospitals and research centres around the world have been collecting tumour samples for decades. Samples were

preserved with formalin and paraffin and archived for future research and pathological studies. With the advent of ‘omics technology, these archives now represent an invaluable resource for cancer research. In particular, proteomics techniques are revealing the molecular changes that occur with cancers and uncovering new insights for prognostic and diagnostic benefit.

Dr Peter Hoffmann, Director of the Adelaide Proteomics Centre and his team have been working on imaging proteins and peptides in formalin-fixed tumour samples using NCRIS funded MALDI imaging mass spectrometry (MALDI IMS). Exciting work is being undertaken in ovarian and other cancers but an important achievement has been new techniques for handling formalin-fixed paraffin embedded samples, an important first step before analysis.

The large number of tissue samples now available and technology advances

PLATFORM UPDATES - PROTEOMICS

like the MALDI IMS are expected to reveal more on the molecular progression of cancers and lead to new prognostic and diagnostic markers. Microarrays are being used to look at proteomic differences across hundreds of samples and investigate the changes that occur over tumour progression. The MALDI IMS has also been used to define drug activity in tissue samples and determine mechanisms of resistance with important implications for drug therapies.

Proteome Browser

Professor Ian Smith at Monash University is leading the development of an open-access web browser that can allow the integration and analysis of current proteome knowledge and make this huge volume of data more easily comprehensible, searchable and accessible to researchers worldwide.

The project has been undertaken in support of the Human Proteome Project aimed at cataloguing protein information associated with the 24 human chromosomes. The project represents an international effort where one chromosome is assigned to one or more countries. An Australian and New Zealand

consortium has taken on Chromosome 7 and will develop a gene by gene proteome where many of the proteins have yet to be experimentally confirmed. This work is largely led by Professor Mark Baker, Chair of Proteomics at Macquarie University.

The Proteome Browser being developed by Professor Smith's team will provide a traffic light system to indicate the quality of the information available on every protein where green indicates good quality data, amber indicates reasonable quality and red indicates poor quality data. Black signifies that there is no data available.

While its primary role is to underpin the Human Proteome Project, the Proteome Browser software is designed to be species and chromosome independent to allow comparisons of human and animal data. Phase 1 of the browser is expected to go live around December 2012 with a number of proteomic sources and will be completed in the following year with additional data sources, advanced filter capabilities, reporting and data-export functions.



Dr Peter Hoffman, Adelaide Proteomics Centre

Signaling Networks in Cancer Research

A collaboration of researchers from University of Sydney, Melanoma Institute Australia and Systems Biology Initiative, constructed four different protein-protein and signaling networks for the human cell. Transcriptomic and mutation data from four large scale clinical studies were analysed in the context of these networks, with a particular focus on the expression and interactions of hub proteins.

The results indicated a striking dysregulation of networks in bad outcome patients as compared to those of good clinical

outcome. Many cancer-related hub proteins were involved and suggest that these networks show promise as a new means of patient classification. The research results also suggest a way to identify novel dysregulated proteins for possible investigation as therapeutic targets.

METABOLOMICS



“All metabolomics nodes continue to build their research capabilities with significant effort in developing small molecule quantitation and analysis methodologies.”

All metabolomics nodes continue to build their research capabilities with significant effort in developing small molecule quantitation and analysis methodologies. Building bioinformatics capabilities remains a key focus and work to extend data management and storage systems is on-going together with the development of biostatistical tools for analysing metabolomics data.

Many metabolomics based projects have a significant bio-medical focus, however, the wine yeast and chardonnay projects managed by the Australian Wine Research Institute demonstrate the growing potential of metabolomics for agricultural and environmental research. The following projects indicate the scope of metabolomics projects undertaken by platform nodes over the last year.

Stress Tolerance in Plants

The University of Melbourne is collaborating with the

Australian Centre for Plant Functional Genomics to understand abiotic stress tolerance in plants. Given Australia's propensity for drought conditions, seed companies and farmers are seeking more robust wheat varieties. The project involves a comprehensive metabolite characterisation of a large wheat mapping population grown under severe drought conditions in the field and aims to identify new genes involved in the metabolism of drought response and tolerance.

Another collaboration between the University of Melbourne and Australian Centre for Plant Functional Genomics involves a multidisciplinary approach to determining the effect of osmotic and ionic stress in barley roots. The work will combine physiological, growth, metabolite and transcript measurements of differing root zones with the aim of discovering new targets to improve salinity tolerance in cereal crops.

Metabolomic Stress Markers for Humans

The Defence Science and Technology Organisation (DSTO) have been working with the University of Melbourne to develop mechanisms to monitor the performance of personnel operating under physically and mentally stressful conditions. Metabolomic analyses of blood and urine samples are being used to identify specific metabolic biomarkers and fingerprints that can be used to monitor the physiological state of personnel experiencing high levels of physical activity and dehydration. Besides new research findings, this collaboration has facilitated new methods development for rapidly analysing and handling very large data sets.

Biomarkers for Metal Contamination

Dr Sara Long and Professor Ary Hoffman of the Victorian Centre for Aquatic Pollution Identification & Management have working with the University of



“The Australian Institute for Bioengineering and Nanotechnology (AIBN) is undertaking research to genetically modify sugarcane plants to manufacture biodegradable plastic.”

Melbourne to identify biomarkers of metal contaminated chironomids. The project examined the effects of metal contamination on chironomid metabolism in water ways. The results show different metabolic profiles for different types of metals and have laid the foundation for future collaborative work.

Sugarcane Manufacture of Bioplastics

The Australian Institute for Bioengineering and Nanotechnology (AIBN) is undertaking research to genetically modify sugarcane plants to manufacture the

biodegradable plastic polyhydroxybutyrate (PHB) at commercially relevant levels in the leaves of the plant. The project combines the node’s expertise in genome-scale metabolic modelling and genetic engineering to produce plants with improved PHB yields. It is also applying metabolomics (and other ‘omics technologies) to interrogate the biochemical effects of the manipulation and to direct further engineering strategies.

BIOINFORMATICS



The Australian Bioinformatics Facility (ABF) is responsible for delivering critical bioinformatics infrastructure and services to all nodes within Bioplatforms Australia's 'omics network. ABF's bioinformatics solutions are developed and delivered from its home base at Murdoch University as well as through embedded staff who work on site at various nodes in direct collaboration with 'omics scientists.

Over the last year the ABF has continued to improve handling and curation methods for datasets; developed new analytical tools; and established bioinformatics frameworks for uniform data pre-computing and integration. Project highlights are outlined below.

Wheat Dataset Program

The ABF had delivered significant support for the wheat dataset initiative with the implementation of a bioinformatics framework for standardised data

processing, pre-computing and analysis workflows that can be shared with the broader science community. Initial work focused on delivering a bioinformatics framework for the analysis of seven *Fusarium sp.* fungal pathogens. Several computational workflows have been implemented and validated and will be utilised to facilitate genome assembly and comparative analysis. All datasets and analysis are provided in standard formats and are compatible with open sourced software tools to facilitate integration with other 'omics data being generated for the wheat pathogen datasets.

Genomics

The ABF has been working closely with the AGRF in sequencing wheat chromosome 7A.

Chromosome 7A is complex and highly repetitive and represents a significant assembly challenge. To simplify and, most importantly, increase the accuracy of de novo

genome assembly when using next-generation DNA sequencing technologies, the ABF collaborated with the AGRF to develop a novel experimental approach which involved constructing BAC (fragment) libraries and utilising DNA fingerprinting to enable assembly.

Proteomics

ABF's web-based workflow application YABI provides a core technology for bioinformatics analysis and data integration that is continuously being extended with new tools and capabilities.

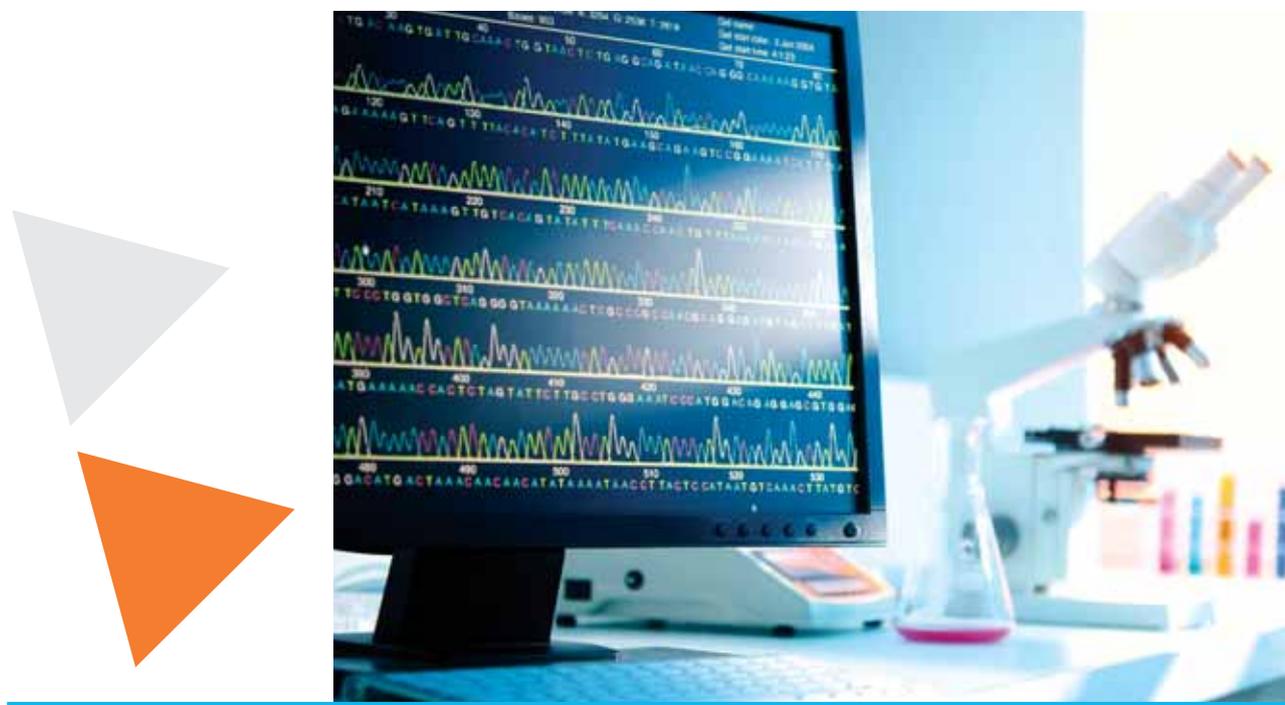
The Trans-Proteomics Pipeline (TPP) has been installed and tested extensively using reference datasets. The TPP tools, Peptide prophet, Protein prophet, and the iCAT labelling quantitation tool, ASAPRatio have been incorporated into YABI. Further work to include iTRAQ for labelling quantitation and Libra tools to fix incompatibilities will also be incorporated.

Proteogenomic pipelines for a number of proteomics nodes have been developed. Proteogenomics is the use of MS/MS proteomic data to assist with the annotation of genomes.

A tool developed by the University of California – San Diego (UCSD) called Inspect is well suited to proteogenomics analysis and has also been successfully installed into the YABI workflow environment along with other MS/MS database search tools.

As part of the wheat dataset program, a comprehensive wheat protein database is being assembled to assist with future wheat proteomics and proteogenomics projects. The database will be made available through ABF's locally installed Mascot server and other MS/MS database search tools. A collaboration between the ABF, Macquarie University, the UCSD and the US based Grape Research Coordination Network has been established to

PLATFORM UPDATES - BIOINFORMATICS



“Over the last year the ABF has continued to improve handling and curation methods for datasets; developed new analytical tools; and established bioinformatics frameworks for uniform data pre-computing and integration.”

leverage a proteogenomics pipeline developed at UCSD to assist with the annotation of the chardonnay genome.

Metabolomics

Over the last year, ABF has continued developing the metabolomics web-based analytical tools, Mastr-MS and Mambo-MS. These systems were installed at the Bio21 Institute in Melbourne during 2011 and have begun to see user activity. This user uptake marks an exciting phase in the development life-cycle of these applications and new solutions and features are now being designed and developed in response to user driven requirements.

The development of the Mastr-MS application has demonstrated particular progress. Application components are spread across three categories: Experimental Design; Experiment Configuration; and Data Capture to provide comprehensive data management, sample tracking and experimental design. The application allows a high degree of customisation and allows specified configurations to be deployed as “standards” throughout a laboratory or entire organisation if desired. User feedback has been invaluable in focusing future development efforts to make usability and interface improvements.



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Bioplatforms Australia is responsible for building scientific infrastructure in the specialist fields of genomics, proteomics, metabolomics and bioinformatics. It supports Australian life science research with crucial investments in state-of-the-art technologies and cutting edge expertise. Investment funding has

been provided by the Commonwealth Government's National Collaborative Research Infrastructure Strategy (NCRIS) and the 2009 Super Science initiative. Co-investments have also been made by State Governments, research institutes and commercial entities. Bioplatforms Australia aims to promote broad access to

Australia's world class 'omics capabilities to maximise the scientific endeavours of the Australian research community.

For more information please contact Andrew Gilbert of Bioplatforms Australia at agilbert@bioplatforms.com or call 0410 538648. www.bioplatforms.com

