VLSCI 2015 ANNUAL REPORT

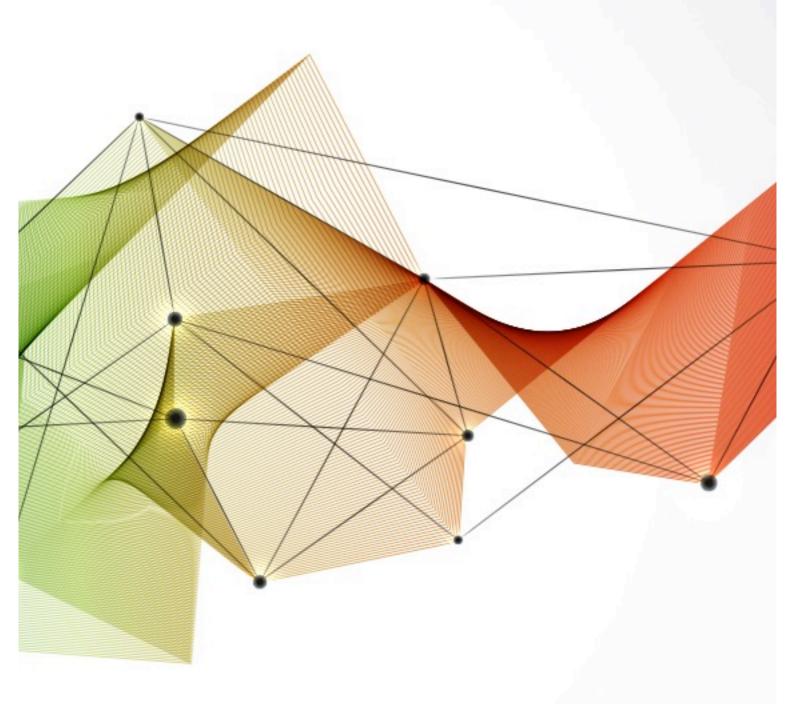






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Director's Report

As I finalise this report (March 30, 2016) the New York Times has just reported on successful international efforts to visualise the genome of the mosquito which is the vector for the frightening Zika virus to try to understand the virus is spread. As is the case today with such complex biological research, it has taken an international team of experts to get to this point. One crucial tool they used for this visualisation, Bandage, was created here at the University of Melbourne by a team which included Ryan Wick, a student in our Masters of Science in Bioinformatics. In 2015 Ryan was awarded the prestigious student prize in the post-graduate tertiary division at the iAwards in Canberra for Bandage.

Key to Ryan's success were his supervisors, VLSCI power user, Dr Kat Holt and her colleague Dr Mark Schultz, and to support his efforts he was provided the bursary from VLSCI that is available to exceptional bioinformatics Masters students each year.

Ryan's success shows what can be achieved when training, mentoring, intellectual environment and sophisticated tools and infrastructure come together, facilitating great research outcomes. This combination and concentration of efforts, a major feature of VLSCI, has delivered another successful year.

Our bioinformatics expertise and resources are delivering innovative products and services to the Melbourne Biomedical Precinct and contributing to Victoria's ICT industry that now generates more than \$34 billion revenue each year and employs 91,300 people.

Since 2010 the collaborative research between VLSCI's computational specialists and Victorian researchers has built an exceptionally skilled staff that have the capacity to transform life science research projects. Access to sophisticated computational infrastructure and expertise has resulted in the rapid increase in demand for the LSCC services. The natural evolution from a supercomputer resource to a centre of computational life science expertise blends talent, training, high-end and cloud-based computing, international networks and collaborations, software development and project management and expertise into several major national research infrastructure initiatives to serve the Australian research community.

Adding to that pool of talent, in 2015 we were thrilled to appoint leading experts Assoc Prof Torsten Seemann and Dr Daniel Park into the role of Lead, Microbial Genomics and Lead, Melbourne Bioinformatics Platform respectively. Along with the rest of the team, they have pivotal roles in major projects which are detailed in pages 12-13 of this Report.

Having partnered with the University of Queensland in the development of the Australian-made Genomics Virtual Laboratory (GVL) since 2012, it was pleasing to attend conferences in both Europe and the US where researchers were already using the GVL or wanting to adopt it for both research and training. Designed to take the 'IT' out of bioinformatics by simplifying access to the world's leading genomics tools and resources, the GVL is now being developed for major research collaborations in Australia and our staff are involved at all levels. Lead author of the October PLOS ONE paper which announced the GVL, Dr Enis Afgan, has now moved from VLSCI to Johns Hopkins University where he is involved in a project to pilot the GVL on the US research cloud in collaborations involving two of the top ranking universities in the world – Johns Hopkins and MIT (through the Broad Institute). The GVL is the best exemplar of this kind of platform in the world and it places Australia, and the participating Australian institutions, in an enviable leadership position on the world stage.

Throughout the year the management team worked to fulfil the terms of our 2015/16 Victorian Government Grant (the Grant). No longer restricted to supporting only life sciences research under that Grant, it was nevertheless important to strike a balance between the fact that our team of computational life sciences experts and significant software environment of some 240 life science-focused software packages does offer a valuable point of differentiation.

In successfully bringing RMIT, La Trobe and Deakin Universities in as financial members, we were pleased that their users are mostly working in life sciences or related fields such as biophysics (RMIT), molecular modelling (La Trobe) and bio-nanofabrication (Deakin). Considerable planning was also undertaken to investigate new hardware requirements in light of the future needs of members and to ensure their ongoing investment.

The Grant included budget for system upgrades and in September we concluded a lengthy tender process and subsequently installed a new Lenovo system "Snowy", purchased to replace aging x86 hardware. Its arrival was met with significant media coverage.

A major development for 2015 was the awarding of Australian Government research infrastructure funding, through Bioplatforms Australia (BPA), to host the EMBL Australia Bioinformatics Resource (EMBL-ABR). The Resource is a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia, set up in collaboration with the European Bioinformatics Institute (EMBL-EBI) to maximise Australia's bioinformatics capability. National funding was obtained to support the EMBL-ABR Director's position, seed some national activities and create a new position of Deputy Director, EMBL-ABR. BPA's review of Australian bioinformatics, undertaken in 2014 identified a growing need for more and better training for life scientists in Australia. So it was with great pleasure that at the end of the year we announced the appointment of high-profile bioinformatician Assoc Prof Vicky Schneider to that role. Coming from the Genome Analysis Centre, UK, where she worked as Head of Scientific Training, Education and Learning and prior to that having responsibility for the strategic coordination and implementation of the EMBL European Bioinformatics Institute's User-Training program, Assoc Prof Schneider's extensive training networks and activities are vital to help us grow Australian talent but also to contributing to the global data exchanges which have become the norm in biological research today.

As a further strategy to position Australia to benefit and contribute to international data conventions and initiatives, in late November/early December we were delighted to host Dr Niklas Blomberg, Director, ELIXIR, to discuss Australia's participation in this important European data sharing initiative. This was an extremely successful visit and we continue to develop this relationship. (More details about this visit are on page 13).

VLSCI ended the year having taken significant steps towards securing its future sustainability through a simpler governance structure, exploration of enhanced and new collaborations at a national and international level, and ongoing commitment to deliver valuable expertise, services and infrastructure. With the endorsement by Council for that strategic direction, we are now confident that 2016 will see this work grow and solidify into a firm footing for future provision of a range of resources for the Australian research community and its industry collaborators and partners.

The team at VLSCI is a professional, committed, dedicated and resourceful one and I am pleased to be able to continue to work with them to build the necessary tools, platforms, infrastructure, collaborations and training resources which are contributing to Australian research excellence.

On behalf of all concerned with the governance, sustainability and the ongoing success of the VLSCI

throughout 2015, I commend the 2015 VLSCI Annual Report to all.

Director Assoc Prof Andrew Lonie



Governance

In April 2015 VLSCI submitted its 2014 Annual Report to the Victorian Department of Economic Development, Jobs, Transport and Resources (DEDJTR) and in doing so, formally recorded its first five years of successful operation. This date also marked the retirement of its governing body, the VLSCI Steering Committee and its Chair, Prof John Zillman, who served in this capacity from 2010-2105. After five years as Director, Prof Peter R. Taylor returned to Europe in March and was replaced by Prof Justin Zobel who oversaw the appointment process for the role of Director and the establishment of a new Advisory Council for VLSCI. Prof Zobel's other tasks were to secure institutional agreements attached to financial memberships from other Victorian institutions, and continue to investigate federal and other funding options.

Throughout the year the University of Melbourne's Life Sciences Computing Steering Group (LSCSG) provided governance and strategic oversight of the VLSCI. Its role in relation to VLSCI is to oversee contractual obligations between the University, as host and institutional partner of the VLSCI, and the Victorian State Government as its major funder through the current Grant.

The LSCSG was delighted that Assoc Prof Jan Tennent, CEO, Biomedical Research Victoria accepted Prof Zobel's invitation to act as Independent Chair of the Advisory Council.

VLSCI's Five Year Evaluation Report, the final report of the VLSCI initiative to the end of 2014 (pursuant to the requirements of the original grant from the State of Victoria) was completed by ACIL Allen Consulting Pty Ltd and submitted as required to the Victorian Government on 7 September 2015. The Report was extremely positive about the returns to the Victorian research community from its investment in VLSCI. Its recommendations about the complex governance arrangements have been heard and are reflected in the new arrangements implemented in 2015. The full report is available on the VLSCI website.

Prof Zobel oversaw the selection process which led to the appointment of Assoc Prof Andrew Lonie, Head, VLSCI Life Sciences Computation Centre, as the new VLSCI Director commencing in mid-October.

University of Melbourne Life Sciences Computing Steering Group

The LSCSG met in May, June and August and its membership comprised Prof Jim McCluskey, Deputy Vice-Chancellor (Research) (Chair), Prof Liz Sonenberg, Pro Vice-Chancellor (Research Collaboration and Infrastructure) (and DVCR alternate), nominees from the Deans, Faculty of Medicine, Dentistry and Health Sciences, Science and Engineering, Prof Justin Zobel, Head, Department of Computing and Information Systems, Melbourne School of Engineering, VLSCI Director and Dr Steven Manos, Associate Director Research Platforms, University Services and Assoc Prof Lonie, Head, Life Sciences Computation Centre and later Director, VLSCI.

VLSCI Advisory Council

With the new Grant in place, VLSCI's governance was restructured to help steer the organisation's transition to a role as a national life sciences computing resource. The Advisory Council was established with an independent Chair appointed by the University of Melbourne and with representatives from designated tertiary and research-based member institutions contributing to core operations over 2015-2016.

The role of the Council is to monitor VLSCI activity to ensure that it continues to serve its community, and to provide advice on both strategic and operational matters to the Director, VLSCI and to the University of Melbourne, via the Deputy Vice-Chancellor (Research).

The Advisory Council met for the first time in September in the new home of the VLSCI at Lab-14 Carlton Connect Initiative, 700 Swanston Street, Carlton and again in November.

Members

Assoc Prof Jan Tennent (Chair), CEO, Biomedical Research Victoria

Prof Ricky Johnstone (LSCC Community Representative), Assistant Director, Cancer Research; Cohead, Cancer Therapeutics Program; Group Leader, Gene Regulation Laboratory, Peter MacCallum Cancer Centre

Prof Heinrich Schmidt (Institutional Subscriber), eResearch Director, Research & Innovation, RMIT University; Australia-India Research Centre for Automation Software Engineering, RMIT University; Adjunct Professor, Mälardalen University, Västerås, Sweden

Prof Brian Smith (Institutional Subscriber), Department Head, Chemistry & Physics, La Trobe University

Assoc Prof Michael Kearney (University of Melbourne Representative), Conservation and Wildlife Biology, School of BioSciences, University of Melbourne

Prof Melissa Southey (University of Melbourne Representative), Professorial Fellow/Deputy Head of Department, Pathology, University of Melbourne

Prof Tiffany Walsh (Institutional Subscriber), Veski Innovation Fellow; Professor, BioNanotechnology, Institute for Frontier Materials, Deakin University

Observers

Assoc Prof Andrew Lonie, Director, VLSCI

Dr Michael Lynch, Senior Program/Policy Officer, Innovation & Technology Research, Department of Economic Development, Jobs, Transport and Resources

VLSCI Management Team Representative (a member of the VLSCI Management Team whose attendance is to be rotated as business requires, with the approval of the Chair and VLSCI Director).

Secretariat

Ms Fiona Kerr, Executive Officer, VLSCI



The VLSCI Advisory Council L-R: back row H. Schmidt, A. Lonie; middle row J. Tennent, M. Lynch; front step M. Southey, B. Smith; floor M. Kearney, T. Walsh (Note: R. Johnstone absent).

Our People

VLSCI Staff

Directorate

Assoc Prof Andrew Lonie Director
Ms Karin Diamond Business Manager
Ms Fiona Kerr Executive Officer
Ms Claudia Curcio Reception/Administration Assistant
Ms Laura Williams P/T Reception/Administration Assistant

Communications, Skills and Development

Ms Helen Gardiner Communications Manager Dr Christina Hall Communications Officer

The Facility

Dr Vera Hansper Facility Manager
Dr Andrew Isaac Specialist Programmer
Dr Jeff Tan HPC Specialist IBM
Dr Michael Kuiper Computational Molecular Scientist
Mr Matthew Wallis HPC Specialist IBM (to March 2015)
Mr Ben Moran Systems Administrator
Mr Chris Samuel Senior Systems Administrator
Mr Carl Thomas Storage and Infrastructure Administrator
Ms Jin Zhang Systems Administrator

Life Sciences Computation Centre

Assoc Prof Torsten Seemann Lead, Microbial Genomics
Dr Bernard Pope Lead, Cancer & Clinical Genomics
Dr Daniel Park Lead, Melbourne Bioinformatics Platform
Dr Mathew Wakefield Senior Research Fellow
Dr Dieter Bulach Senior Research Scientist
Ms Charlotte Anderson Bioinformatician (to September 2015)
Ms Jessica Chung Bioinformatician/Research Assistant
Mr Peter Georgeson Bioinformatics Platforms Developer
Dr Anthony Marty Research Scientist
Dr Ira Cooke Research Scientist
Ms Harriet Dashnow Research Scientist (to March 2015)
Dr Nathan Hall Senior Research Scientist
Dr Nuwan Goonasekera Software Engineer
Mr Simon Gladman Research Scientist
Dr Chol-hee Jung Research Scientist

Dr Yousef Kowsar Scientific Software Developer Dr Khalid Mahmood Research Scientist Dr Juan Nunez-Iglesias Research Scientist

Dr Gayle Philip Research Scientist Dr Clare Sloggett Research Scientist

Mr Andrew Robinson Scientific Programmer

Our Machines

The peak computing facility at VLSCI is a world leader in the provision of high end computer processing infrastructure and computational expertise specialised for life sciences research. The petascale facility consists of three systems built on two architectures (BlueGene/Q and x86), with each system offering varying memory and data-handling capacities to suit the large memory computational resources required from genomics through to high capacity processing of computational imaging data.

VLSCI systems have now supported over 16 million jobs, involving 1.4 billion CPU hours of research compute since 2010.

In 2015, 64 projects existing and new users received grants to use VLSCI from the beginning of the year. During the year 15 new projects from member organisations were allocated access through a lightweight application process.

With 15% of the BlueGene/Q ('Avoca') system made available at the national level through the National Computation Merit Allocation Scheme (NCMAS), a total of 10 national projects were approved through this scheme.

A new x86 system to replace the aging 'Merri' iDataPlex was tendered in early February, and the winning bid was granted to LENOVO for a System-X cluster. The new cluster was named 'Snowy' after the Snowy River.

The Merri cluster was decommissioned and re-purposed in August 2015 with some terabyte nodes used to form a specialised cluster for the Melbourne Genomics Health Alliance, a \$25m Victorian clinical genomics initiative in which VLSCI is a funded participant and contributor.

Expertise

- HPC Systems Administration
- HPC programming
- Specialist HPC programming parallelising of algorithms
- Molecular Modelling and Dynamics

The VLSCI is local and has deep expertise in the life sciences.

The compute facilities available are also world class

Matthew Perugini, La Trobe University

Compute Systems

IBM Blue Gene/Q - Avoca

- Peak performance of 838.86 teraFLOPS
- 65,536 PowerPC based 1.6GHz cores
- A total of 64TB RAM
- Interconnect between compute nodes forms a five-dimensional torus providing excellent nearest neighbour and bisection bandwidth
- Suitable for large-scale parallel processing
- Compute nodes run a custom lightweight operating system called Compute
- Node Kernel (CNK) that is similar to Linux and mostly POSIX compliant
- The head node runs the RHEL 6 operating system, a variety of Linux

IBM iDataplex x86 system – Barcoo

- Peak performance compute nodes currently performing at 20 teraFLOPS with Xeon Phi cards running nominally at 1 teraFLOPS each
- 1120 Intel Sandybridge compute cores running at 2.7GHz
- 67 nodes with 256GB RAM and 16 cores per node
- 3 nodes with 512GB RAM and 16 cores per node
- 20 Xeon Phi 5110P cards installed across 10 nodes

LENOVO NeXtScale - Snowy (delivered August 2015, in production October 2015)

- Peak performance of 28 teraFLOPS
- 31 nodes, each with 32 cores of the latest Haswell processor, running at 2.3GHz
- 29 nodes have 128GB of memory
- 2 FAT nodes have 512GB of memory

IBM iDataplex x86 system – Merri (until August 2015)

- Peak performance of 7.3 teraFLOPS
- 688 Intel Nehalem compute cores running at 2.66GHz
- 36 nodes with 96GB RAM and 8 cores per node
- 44 nodes with 48GB RAM and 8 cores per node
- 3 nodes with 1024GB RAM and 16 cores per node

All x86 compute clusters run the RHEL 6 operating system, a variety of Linux and are connected to a high speed, low latency Mellanox FDR14 InfiniBand switch for inter-process communications.

Storage infrastructure

The storage infrastructure is connected via a high speed, low latency Mellanox FDR14 InfiniBand network for fast data-handling.

- 700TB GPFS Parallel Data Store (shared by Barcoo, Snowy, Merri and Avoca)
- 1PB HSM tape system, made available through GPFS (shared by Barcoo, Snowy, Merri and Avoca).

Hardware Hosting

VLSCI hosts hardware for Life Sciences research groups as requested. The specialised compute node, TURPIN continues to be hosted for Assoc Prof Andrew Turpin from the University of Melbourne.

Software

From 'ACG' to 'Zlib' over 220 licensed software applications specific to life sciences are installed on VLSCI's systems. A key activity to support the Life Science user community is the installation of their software. To date there has been over 2,000 software requests (over six years).



Facility Manager, Vera Hansper, and Acting Director, Justin Zobel, at the launch of 'Snowy' with Matt Codrington, Managing Director, Lenovo Australia and New Zealand.

Our Projects - Highlights

Genomics Virtual Laboratory

Since 2012, the VLSCI has partnered with UQ to develop a National eResearch Collaboration Tools and Resources project (Nectar) funded platform designed to make genomic data analysis more accessible to the Australia researcher community. The Genomics Virtual Lab (GVL: http://genome.edu.au) is a computational workbench providing a highly accessible cloud-based genomics analysis environment preconfigured with best practice genomics tools and supplemented with comprehensive tutorial materials and protocols, managed services and user support.

Large installations are at Monash, Queensland and Melbourne universities, with more to follow in Western Australia, New South Wales and Tasmania in 2016. Adopted both locally and overseas, the GVL has already been recognised as a quality platform to help address the shortage of bioinformatics expertise around the world and manage the complex, multiple-layered data analysis tasks confronting life scientists today. Recognition of the value of the Australian-made platform was boosted with the publication of 'Genomics Virtual Laboratory: A Practical Bioinformatics Workbench for the Cloud' 26 October in PLOS One.

Cancer Genomics Theme

The Cancer Genomics theme at VLSCI provides bioinformatics expertise and leadership in the critical area of cancer research, working closely with several key projects from The University of Melbourne and Cancer Council Victoria. Recent research has contributed significant results in fields such as breast, prostate and colorectal cancer, resulting in publications in leading research journals, and the development of publicly available software resources to support bioinformatics analysis, including the Methpat and Cpipe tools. The team has provided leadership on competitive cancer-related research grants, and presented their findings at leading national and international conferences.

Research highlights for my team during 2015 include an increase by an order of magnitude in the size of our research networks that has corresponded to a similar increase in demand for computation capacity and bioinformatic support. Without the collegial and flexible working relationships we enjoy with the VLSCI team we would not have been able to demonstrate the feasibility of our research vision that now enjoys National, US and European funding that is advancing the translation of new genetic information into breast cancer clinical genetics practice internationally.

Prof Melissa Southey Head Genetic Epidemiology Laboratory, Department of Pathology The University of Melbourne

Clinical Genomics Theme

The team of experts in bioinformatics, software engineering and data analytics is now involved in collaborations with a wider community of clinicians and medical researchers across ten major health providers in Victoria and beyond. New collaborations include one with the Leiden University Medical Centre in the Netherlands, developing databases to support the needs of clinical genomics. Additionally, the clinical genomics team, following on from its successful contributions to the Melbourne Genomics Health Alliance (MGHA) now provides leadership and expertise for the Australian Genomics Health Alliance, a \$25m federally funded project aiming to increase collaboration between leading clinical genomics providers across the country.

Melbourne Genomics Health Alliance

A Dutch study published in Genetics in Medicine on 4 February 2016 applies a cost analysis to the early use of whole-exome sequencing in diagnosing difficult-to-diagnose patients with intellectual disability. It reported that this new technology would save an average of US\$3,500 in patients who obtain a diagnosis and US\$1,700 in patients who do not, by avoiding doing unnecessary tests. Since a successful pilot in 2014 led to \$25m funding from the Victorian Government from 2015-2018, the team at the Melbourne Genomics Health Alliance (MGHA) in 2015 produced similarly impressive figures, yet to be published officially, supported in their work by our staff in the Clinical Genomics theme.

The clinical genomics team is a major contributor to the MGHA, leading the development of clinical grade bioinformatics analysis pipelines and variant curation databases. It is intended that the MGHA findings will contribute directly to future health practices and budgets, by determining where genomics has the most benefit to offer and how it might be applied across the Victorian hospital system and involvement in further national and international efforts will ensure Australia's health system benefits from those.

Microbial Genomics Theme

This theme is focussed on using bioinformatics and genomics to better understand and monitor the spread of pathogens and antimicrobial resistance at local, national and international levels. Through their role in these projects, the VLSCI microbial genomics team have become key contributors and leaders in the application of genomics and bioinformatics for the Australian microbiology community.

The Microbiological Diagnostics Unit and the Doherty Applied Microbial Genomics are together leading a national initiative to modernise public health and clinical microbiology by providing the infrastructure, tools and expertise to transition from traditional low resolution assays to the fine resolution that whole genome sequencing provides, allowing the earlier detection of better management of outbreaks. The inaugural July symposium 'Embracing the Genomic Revolution - Applied Microbial Genomics in Public Health and Clinical Microbiology' kick-started the process of establishing collaborative research aimed at translating microbial genomics into public health and clinical practice in Australia, while introducing the Doherty Centre of Applied Microbial Genomics to researchers, clinicians and public health professionals. Sponsored by VLSCI, the symposium featured a presentation by the VLSCI Microbial Genomics theme leader, Torsten Seemann.

The Bioplatforms Australia SEPSIS project is generating an exemplar multi-omics dataset on ten key Australian pathogens, and the VLSCI team is developing the tools, training materials, and web portal to enable the research community to access, explore and reproduce the analyses performed using this unique data set which may provide insight into new potential drug targets for some of our worst superbugs. The tools and training will be based on the Microbial Genomics Virtual Lab developed at VLSCI, a richly featured analysis platform running on the national Nectar research cloud, which relieves scientists of the burden of purchasing and maintaining their own computer system, and provides a turnkey solution to using the key software tools and databases they require.

Our partnership with the microbial genomics team at VLSCI is a key driver behind our program to bring the full power of genomics to Australian public and clinical microbiology laboratories. Genomics is revolutionising our ability to track disease outbreaks and stop the spread of antibiotic resistant bacteria. The VLSCI team is critical to our efforts by providing accessible software tools and analysis platforms to interrogate the genome data in a framework that can then be deployed across Australia, and potentially across the globe for the benefit of all.

Tim Stinear, Professor, Department of Microbiology and Immunology Scientific Director, Doherty Applied Microbial Genomics The Doherty Institute for Infection & Immunity, The University of Melbourne

Melbourne Bioinformatics Platform

The University of Melbourne funded Melbourne Bioinformatics Platform (MBP) engaged in productive and exciting collaboration with Parkville Precinct researchers in 2015 with 467 University of Melbourne-affiliated researchers working on 50 distinct projects distributed across the Faculties of Medicine, Dentistry and Health Sciences, Science, Veterinary and Agricultural Sciences and the Melbourne School of Engineering. The projects continue to be many and varied and include those focused on better understanding and preventing bacterial sepsis, cancer and malaria. In 2015 MBP bioinformaticians authored at least 39 peer-reviewed original research articles, including those in Nature, Nature Biotechnology and Nature Communications, as well as supporting many more publications. Our bioinformaticians are Chief Investigators of four NHMRC grants awarded in 2015 and Associate Investigators on an additional NHMRC grant for a total value of \$12.5 million, in addition to other funded projects that were supported. MBP trained 369 researchers across 28 workshops and the Masters of Bioinformatics course.

EMBL Australia Bioinformatics Resource

VLSCI was announced as the host of the state-of-the-art bioinformatics resource hub in May following a joint agreement between the University of Melbourne and EMBL Australia and supported through funding from Bioplatforms Australia.

The EMBL Australia Bioinformatics Resource (EMBL-ABR) represents a significant opportunity to advance bioinformatics expertise and to support broader biological sciences research across an Australian network of Universities and Research Institutes. The agreement to base the facility in Victoria is an acknowledgement of the mature expertise and infrastructure dedicated to life sciences computing thriving in the State.

Assoc Prof Andrew Lonie, was appointed as EMBL-ABR's Director in December and announced that computational biologist Dr Vicky Schneider would join the University of Melbourne, as Assoc Prof and Deputy Director, EMBL-ABR in early 2016. Assoc Prof Schneider has been pivotal to bioinformatics capacity building and training in Europe for some years, through appointments at EMBL-EBI, The Genome Analysis Centre, and ELIXIR, and has exactly the experience and expertise needed in Australia. The appointment promises to deliver a significant advantage to the Australian bioinformatics community by building on both our national presence and international engagement.



Photo: Assoc Prof Vicky Schneider takes on the role of Deputy Director, EMBL-ABR from 2016.

Visit by EU's ELIXIR Director

Dr Niklas Blomberg, Director, ELIXIR – the EU's response to the growing need to build a distributed infrastructure for life science tools and data – visited Australia in Nov/Dec 2015, to interact with policy-makers, representatives of funding bodies and senior researchers from many key life sciences institutions. ELIXIR, a research infrastructure founded by 15 European countries and EMBL-European Bioinformatics Institute (EBI) formed to orchestrate the collection, quality control and archiving of large amounts of biological data produced by life science experiments.

Over four packed days Dr Blomberg met with policy-makers, senior researchers, representatives of funding bodies and many in the life sciences computation community from six States, providing insight into the development and management of life science infrastructure.

In Melbourne, as well as meeting local senior bioinformaticians, Dr Blomberg took part in a high level roundtable hosted by the University of Melbourne. The discussions included representatives from the Victorian Government Departments of Innovation and Health, Melbourne Genomics Health Alliance, Australian Genome Research Facility, EMBL Australia, eResearch and major research institutes, and included two representatives supported to attend from the South Australian node of the EMBL Australia Bioinformatics Resource based at the South Australian Health & Medical Research Institute. An evening public talk hosted by the Convergence Science Network was followed by a lively supper with network members.

At the University of Queensland, Dr Blomberg met with a group of Infrastructure managers followed by discussions on the supply of HPC and Cloud services and the Genomics Virtual Laboratory. The Institute of Molecular Biology in the Queensland Biosciences Precinct, hosted a public seminar in the afternoon. Several hours of meetings followed with invited groups of academics representing infrastructure power users and life science imaging researchers.

For the Canberra roundtable, Dr Vivien Bonazzi, Senior Advisor, Data Science Technologies & Innovation, Office of the Associate Director for Data Science at the US National Institute of Health, joined a group that heard Dr Blomberg's and global reflections on the virtues of standards and training in data curation and sharing for life sciences researchers. The event was attended by representatives from host institution, the Australian National University, and the National Computational Infrastructure, the ARC, the NHMRC, Queensland Cyber Infrastructure Foundation, Bioplatforms Australia, Population Health Research Network (Perth), University of Canberra, Research Data Services, EMBL Australia, ANDS, CSIRO and Australian Government Departments of Health and Education. The evening provided an opportunity to have more casual discussions with members of the local bioinformatics community.

A final visit was arranged at the Kinghorn Centre for Clinical Genomics, Garvan Institute of Medical Research. Dr Blomberg met with Garvan Director, Prof John Mattick, before giving a seminar to an audience invited from various NSW institutes including the Garvan, Victor Chang, St Vincents, AMR, Intersect, CSIRO, and Bioplatforms Australia. Garvan's Chief of Informatics, Dr Warren Kaplan hosted a lunch before Dr Blomberg's departure.

By bringing Dr Blomberg to Australia, VLSCI & the EMBL Australia Bioinformatics Resource (with funding from Bioplatforms Australia) aimed to strengthened existing connections and collaborations to drive quality Australian life sciences research, building on major investments in research infrastructure to date.

Software Development

The following list is a selection of important software published by LSCC bioinformaticians:

Methpat, published in Gigascience: Exemplary multiplex bisulfite amplicon data used to demonstrate the utility of Methpat (http://gigascience.biomedcentral.com/articles/10.1186/s13742-015-0098-x)

HiTIME, published in Analytical Chemistry: High-Resolution Twin-Ion Metabolite Extraction (HiTIME) Mass Spectrometry: Nontargeted Detection of Unknown Drug Metabolites by Isotope Labeling, Liquid Chromatography Mass Spectrometry, and Automated High-Performance Computing (http://pubs.acs.org/doi/abs/10.1021/ac504767d)

Cpipe, a shared variant detection pipeline designed for diagnostic settings published in Genome Medicine: https://genomemedicine.biomedcentral.com/articles/10.1186/s13073-015-0191-x

Genomics Virtual Laboratory: A Practical Bioinformatics Workbench for the Cloud published in PLOS ONE: http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0140829

Hi-Plex update: The paper documenting improvements to the Hi-Plex tool and workflow, 'Abridged adapter primers increase the target scope of Hi-Plex' was listed in the Top Ten Biotechniques Peer reviewed papers for 2015 (http://www.biotechniques-Of-2015/biotechniques-Of-201

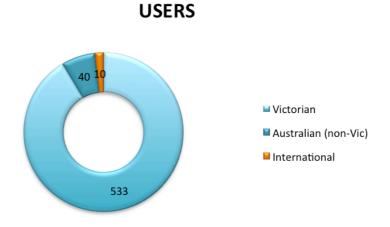
Nullarbor: https://github.com/tseemann/nullarbor
Snippy: https://github.com/tseemann/snippy
MLST: https://github.com/tseemann/mlst
ABRicate: https://github.com/tseemann/abricate

Over 50 'recipes' for Homebrew Science make it easy for people to install bioinformatics software: http://brew.sh/homebrew-science/.

Prokka update: The high-profile Prokka software has reached 374 citations in less than two years https://scholar.google.com/scholar_lookup?title=Prokka%3A+rapid+prokaryotic+genome+annotationauthor=Seemann&publication_year=2014.

Our Users

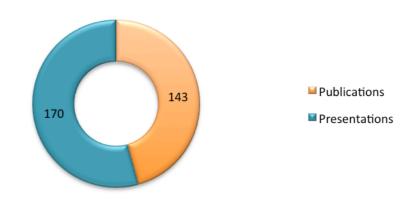
There were 583 researchers from 46 different research institutions or organisations using VLSCI systems in 2015. Of these, 91% were from Victoria, with 40 individual users from other states, and 10 logging on from international institutions.



All projects using VLSCI systems in 2015 were asked to complete a report with a range of questions and reporting criteria. The figures presented here represent data from the 80 responses received from the 92 Chief Investigators (CIs) contacted.

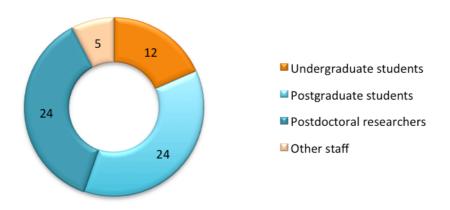
There were a reported 143 papers published involving research on VLSCI systems, and 170 presentations made. In 2015, 70% of journals in which publications from VLSCI projects appear being in the first quartile of their discipline category, as ranked by Thomson Reuters.

COMMUNICATING OUTCOMES



30 CIs allocated resources on VLSCI systems reported increased capacity to employ additional staff or students.

EMPLOYMENT



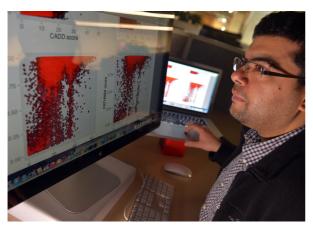
The VLSCI resources were vital to a number of our projects. The computations that that we have been doing required more CPU time and memory than was otherwise available to us. Without access to the VLSCI, the publications that are currently under review and in preparation would not have happened.

Anthony Burkitt, Bionic Vision Australia.

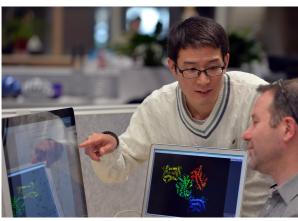
Project CIs were asked what grant income supported for their work on VLSCI machines in 2015. A total of \$50,428,561 in grants was received by the projects that responded.

GRANT INCOME













Our Collaborations

Researchers with projects utilising VLSCI machines were actively involved in a variety of collaborations.

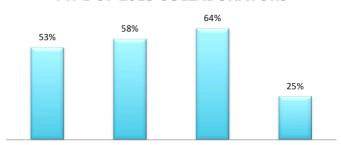
Collaborators were involved in 74% of projects, and 38% reported that the 2015 project resulted in the formation of new collaborations.

PROJECT COLLABORATIONS 74% 38% Active collaborations in 2015 project New collaborations resulting from

Many projects had a variety of types of collaborations, with 53% reporting having Victorian collaborators, 58% having other Australian collaborators, 64% International, and 25% nominating Industry collaborators. Of the 58 projects who had external collaborators (74% of total), 25% of CIs reported their projects had industry collaborators (representing 18% of all projects).

project

Industry



TYPE OF 2015 COLLABORATORS

The majority of new collaborations that resulted from 2015 projects were with International collaborators.

Australian (other

than Victorian)

Victorian





Victorian Institutions

Bio21 Institute Bionics Institute

Cancer Council Victoria

Deakin University
La Trobe University
Monash University
Peter Doherty Institute

Peter MacCallum Cancer Centre

RMIT University

Royal Botanic Gardens Victoria

Royal Women's Hospital St Vincent's Hospital

St Vincent's Research Institute Swinburne University of Technology The Florey Institute of Neuroscience and

Mental Health

Walter and Eliza Hall Institute

Australian Institutions

ANDS

Australia National University

Australian Plague Locust Commission
Australian Rickettsial Reference Laboratory

Bioplatforms Australia

Centre for Cancer Biology, SA Pathology

Centre for Eye Research Australia

Curtin University

EMPathy Breast Cancer Network

Griffith University

Menzies School of Health Research National Vision Research Institute

NeCTAR

University of Technology Sydney

University of Adelaide

University of New South Wales University of Queensland University of South Australia

University of Sydney

University of Western Australia

University of Wollongong

Victor Chang Cardiac Research Institute

International Institutions

Aarhus University, Denmark Aix-Marseille Universite, France

Barcelona Supercomputing Centre, Spain Biomedical Instrument Institute, Shanghai Jiao

Tong University, China

CNR-NANO National Research Center, Italy

CNRS, France

Columbia University, USA Florida Atlantic University, USA Freie Universitaet Berlin, Germany Helsinki University, Finland Imperial College London, UK Institute Pasteur, France Leuven University, Belgium Linkoeping University, Sweden

Mahidol University, Thailand

MD Anderson Cancer Centre, The University of

Texas, USA

National Center for Microscopy and Imaging

Research, USA

National Heart Research Institute, Singapore National Institute of Animal Health, Japan National Institute of Plant Genome Research,

India

NeuroVista Corporation, USA Northwestern University, USA Princeton University, USA

RIKEN, Japan

Scuola Normale Superiore di Pisa, Italy Seoul National University, South Korea

Shanghai University, China St Jude Medical, USA

Thoraxcenter, Erasmus MC, Netherlands

University at Buffalo, USA

University College Dublin, Ireland

University of Auckland, NZ University of Bonn, Germany

University of Calgary, Canada University of Copenhagen, Denmark

University of Essex, UK University of Exeter, UK University of Gdańsk, Poland University of Hamburg, Germany

University of Iowa, USA University of Lancaster, UK University of Lincoln, UK

University of Lugano, Switzerland

University of Eugano, Switzenal University of Miami, USA University of Michigan, USA University of Miyazaki, Japan University of Notre Dame, USA University of Oklahoma, USA University of Oxford, UK University of Pennsylvania

University of Pottsdam, Germany University of Southern California, USA University of Utrecht, The Netherlands

University of Washington, USA

University of Wisconsin

Victoria University, New Zealand Warsaw University, Poland

Welcome Trust Sanger Institute, UK

York University, Canada

Industry Collaborators

Capsugel, France Abbot Vascular, USA

Biosensors International, Singapore

Carl Zeiss AG

CSL Ltd

Department of Health and Human Services,

Victoria

Floragenex Inc., USA General Electric

Genetic Technologies, Australia

IBM Research Australia

Meat and Livestock Australia

Medtronic Inc.

Melbourne Genomics Health Alliance Microbiological Diagnostics Unit, UoM

Servier Ltd.

The Department of Economic Development,

Jobs, Transport and Resources, Victoria

V3 Alliance

Victorian Infectious Disease Research

Laboratory

WHO Collaborating Centre for Reference and

Research on Influenza, Australia

Industry Representations

VLSCI supports and engages with a wide range of organisations:

AusBiotech

Australian Mathematical Science Institute

Australian National Data Storage Biomedical Research Victoria

BioMelbourne Network

Bioplatforms Australia

COMBINE

Convergence Science Network

HPC500

Melbourne Genomics Health Alliance

National Computational Merit Allocation

Scheme

Nectar

Research Data Storage Infrastructure

Victorian Government's Technology Voucher

Victorian Platform Technologies Network

VLSCI has provided a vital resource (both facilities and personnel) for the establishment and continuation of this project.

VLSCI has also enabled us to strengthen our cross-institute collaborations nationally and internationally. These collaborations will continue to yield research outputs leading, ultimately, to better health and treatment outcomes. VLSCI has also helped us establish further links with the existing computational biology community, and these will also ultimately benefit our research outcomes.

Andrew Hung, RMIT

Contributing Organisations











Engaging with Industry

Genomics to protect drinking water

On 17 March a VLSCI case study featuring ongoing collaboration with Melbourne Water was selected for presentation at the combined VPTN/BioMelbourne Network BioBreakfast entitled: Accelerating Innovation: Access to research.

Dr Melita Stevens, Manager, Research and Technology, Melbourne Water and non-executive Board Member, Water Research Australia and Prof Robin Gasser, School of Veterinary Science, University of Melbourne, presented their research which is hosted on VLSCI computer systems. The team investigate new microbial genomics technologies which will allow Melbourne Water to act only when harmful bugs are present in drinking water, thereby satisfying their public health obligations and minimising costs.

Of the 80 attendees, 35 represented industry, 27 were from academic institutions, facilities, and agencies and 18 were from State and Federal government agencies.

Supporting a Victorian start-up

VLSCI moved into the Carlton Connect Initiative (CCI) - Australia's premier innovation precinct anchored by the University of Melbourne - in March 2015. Staff are perfectly positioned to be actively involved in a range of student, academic and industry events run at Lab-14.

Victorian start-up, 2MRD, was offered a VLSCI start up allocation and hot-desk from July-December. This two-person operation is developing complex algorithms aimed at better calculations of radiation dosages for treatment regimes. Principals Chris Poole and Iwan Cornelius are both PhDs in physics with years of experience in research in radiation oncology medical physics, radiation protection, and scientific computing. They founded 2MRD as a research and development company to solve challenging problems in radiation oncology and radiation protection. The particular project 2MRD worked on with VLSCI involved a clinical application at the Epworth Hospital, which aimed to develop more targeted radiation treatment in a particular and substantial subgroup of patients. In July 2MRD received a City of Melbourne small business development grant.

Publications resulting from VLSCI staff collaborations

The dedicated team of bioinformaticians, computational biologists and high performance computing specialists at VLSCI work with external collaborators in research, training and platform development capacities. As a result of these activities our staff members authored the many high quality publications in 2015.

Ablordey, A. S., Vandelannoote, K., Frimpong, I. A., Ahortor, E. K., Amissah, N. A., Eddyani, M., Durnez, L., Portaels, F., de Jong, B. C., Leirs, H., Porter, J. L., Mangas, K. M., Lam, M. M. C., Buultjens, A., Seemann, T., Tobias, N. J. & Stinear, T. P. Whole genome comparisons suggest random distribution of Mycobacterium ulcerans genotypes in a Buruli ulcer endemic region of Ghana. *PLoS Negl. Trop. Dis.* **9**, e0003681 (2015).

Afgan, E., Krampis, K., Goonasekera, N., Skala, K. & Taylor, J. Building and provisioning bioinformatics environments on public and private Clouds. in 2015 38th International Convention on Information and Communication Technology, Electronics and Microelectronics (MIPRO) 223–228 (IEEE).

Afgan, E., Sloggett, C., Goonasekera, N., Makunin, I., Benson, D., Crowe, M., Gladman, S., Kowsar, Y., Pheasant, M., Horst, R. & Lonie, A. Genomics Virtual Laboratory: A Practical Bioinformatics Workbench for the Cloud. *PLoS One* **10**, e0140829 (2015).

Alioto, T. S., Buchhalter, I., Derdak, S., Hutter, B., Eldridge, M. D., Hovig, E., Heisler, L. E., Beck, T. A., Simpson, J. T., Tonon, L., Sertier, A.-S., Patch, A.-M., Jäger, N., Ginsbach, P., Drews, R., Paramasivam, N., Kabbe, R., Chotewutmontri, S., Diessl, N., Previti, C., Schmidt, S., Brors, B., Feuerbach, L., Heinold, M., Gröbner, S., Korshunov, A., Tarpey, P. S., Butler, A. P., Hinton, J., Jones, D., Menzies, A., Raine, K., Shepherd, R., Stebbings, L., Teague, J. W., Ribeca, P., Giner, F. C., Beltran, S., Raineri, E., Dabad, M., Heath, S. C., Gut, M., Denroche, R. E., Harding, N. J., Yamaguchi, T. N., Fujimoto, A., Nakagawa, H.,

Quesada, V., Valdés-Mas, R., Nakken, S., Vodák, D., Bower, L., Lynch, A. G., Anderson, C. L., Waddell, N., Pearson, J. V., Grimmond, S. M., Peto, M., Spellman, P., He, M., Kandoth, C., Lee, S., Zhang, J., Létourneau, L., Ma, S., Seth, S., Torrents, D., Xi, L., Wheeler, D. A., López-Otín, C., Campo, E., Campbell, P. J., Boutros, P. C., Puente, X. S., Gerhard, D. S., Pfister, S. M., McPherson, J. D., Hudson, T. J., Schlesner, M., Lichter, P., Eils, R., Jones, D. T. W. & Gut, I. G. A comprehensive assessment of somatic mutation detection in cancer using wholegenome sequencing. *Nat. Commun.* **6**, 10001 (2015).

Baines, S. L., Holt, K. E., Schultz, M. B., Seemann, T., Howden, B. O., Jensen, S. O., van Hal, S. J., Coombs, G. W., Firth, N., Powell, D. R., Stinear, T. P. & Howden, B. P. Convergent adaptation in the dominant global hospital clone ST239 of methicillin-resistant Staphylococcus aureus. *MBio* **6**, e00080 (2015).

Boekel, J., Chilton, J. M., Cooke, I. R., Horvatovich, P. L., Jagtap, P. D., Käll, L., Lehtiö, J., Lukasse, P., Moerland, P. D. & Griffin, T. J. Multi-omic data analysis using Galaxy. *Nat. Biotechnol.* **33**, 137–139 (2015).

Cooke, I. R., Whitelaw, B., Norman, M., Caruana, N. & Strugnell, J. M. in *Evolution of Venomous Animals and Their Toxins* 1–15 (Springer Netherlands, 2015).

Damiano, J. A., Afawi, Z., Bahlo, M., Mauermann, M., Misk, A., Arsov, T., Oliver, K. L., Dahl, H.-H. M., Shearer, A. E., Smith, R. J. H., Hall, N. E., Mahmood, K., Leventer, R. J., Scheffer, I. E., Muona, M., Lehesjoki, A.-E., Korczyn, A. D., Herrmann, H., Berkovic, S. F. & Hildebrand, M. S. Mutation of the nuclear lamin gene LMNB2 in progressive myoclonus epilepsy with early ataxia. *Hum. Mol. Genet.* **24,** 4483–4490 (2015).

Dugué, P.-A., English, D. R., MacInnis, R. J., Joo, J. E., Jung, C.-H. & Milne, R. L. The repeatability of DNA methylation measures may also affect the power of epigenome-wide association studies. *Int. J. Epidemiol.* **44**, 1460–1461 (2015).

Eddyani, M., Vandelannoote, K., Meehan, C. J., Bhuju, S., Porter, J. L., Aguiar, J., Seemann, T., Jarek, M., Singh, M., Portaels,

F., Stinear, T. P. & de Jong, B. C. A Genomic Approach to Resolving Relapse versus Reinfection among Four Cases of Buruli Ulcer. *PLoS Negl. Trop. Dis.* **9**, e0004158 (2015).

Gao, W., Monk, I. R., Tobias, N. J., Gladman, S. L., Seemann, T., Stinear, T. P. & Howden, B. P. Large tandem chromosome expansions facilitate niche adaptation during persistent infection with drug-resistant Staphylococcus aureus. *Microbial Genomics* **1**, (2015).

Harrison, P. F., Powell, D. R., Clancy, J. L., Preiss, T., Boag, P. R., Traven, A., Seemann, T. & Beilharz, T. H. PAT-seq: a method to study the integration of 3'-UTR dynamics with gene expression in the eukaryotic transcriptome. *RNA* **21**, 1502–1510 (2015).

Hong, M. K. H., Macintyre, G., Wedge, D. C., Van Loo, P., Patel, K., Lunke, S., Alexandrov, L. B., Sloggett, C., Cmero, M., Marass, F., Tsui, D., Mangiola, S., Lonie, A., Naeem, H., Sapre, N., Phal, P. M., Kurganovs, N., Chin, X., Kerger, M., Warren, A. Y., Neal, D., Gnanapragasam, V., Rosenfeld, N., Pedersen, J. S., Ryan, A., Haviv, I., Costello, A. J., Corcoran, N. M. & Hovens, C. M. Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. *Nat. Commun.* **6**, 6605 (2015).

Hosking, C. G., Driguez, P., McWilliam, H. E. G., Ilag, L. L., Gladman, S., Li, Y., Piedrafita, D., McManus, D. P., Meeusen, E. N. T. & de Veer, M. J. Using the local immune response from the natural buffalo host to generate an antibody fragment library that binds the early larval stages of Schistosoma japonicum. *Int. J. Parasitol.* **45**, 729–740 (2015).

Hovens, C., Hong, M., Macintyre, G., Wedge, D., Van Loo, P., Lunke, S., Alexandrov, L., Slogget, C., Cmero, M., Mangiola, S., Lonie, A., Naeem, H., Sapre, N., Phal, P., Kerger, M., Pedersen, J., Ryan, A., Haviv, I., Costello, A. & Corcoran, N. Tracking clonal diversity in metastatic prostate cancer progression. *J. Clin. Oncol.* **33**, 193 (2015).

Hsu, A. L., Kondrashova, O., Lunke, S., Love, C. J., Meldrum, C., Marquis-Nicholson, R., Corboy, G., Pham, K., Wakefield, M., Waring, P. M. & Taylor, G. R. AmpliVar: mutation detection in high-throughput sequence from amplicon-based libraries. *Hum. Mutat.* **36**, 411–418 (2015).

Jeffries, T. C., Ostrowski, M., Williams, R. B., Xie, C., Jensen, R. M., Grzymski, J. J., Senstius, S. J., Givskov, M., Hoeke, R., Philip, G. K., Neches, R. Y., Drautz-Moses, D. I., Chénard, C., Paulsen, I. T. & Lauro, F. M. Spatially extensive microbial biogeography of the Indian Ocean provides insights into the unique community structure of a pristine coral atoll. *Sci. Rep.* **5**, 15383 (2015).

Jung, C. H., O'Brien, M., Singh, M. B. & Bhalla, P. L. Epigenetic landscape of germline specific genes in the sporophyte cells of Arabidopsis thaliana. *Front. Plant Sci.* **6**, 328 (2015).

Kanwal, S., Lonie, A., Sinnott, R. O. & Anderson, C. Challenges of Large-Scale Biomedical Workflows on the Cloud -- A Case Study on the Need for Reproducibility of Results. in *Computer-Based Medical Systems (CBMS), 2015 IEEE 28th International Symposium on 220–225 (2015).*

Khong, J. J., Wang, L. Y., Smyth, G. K., McNab, A. A., Hardy, T. G., Selva, D., Llamas, B., Jung, C.-H., Sharma, S., Burdon, K. P., Ebeling, P. R. & Craig, J. E. Differential Gene Expression Profiling of Orbital Adipose Tissue in Thyroid Orbitopathy. *Invest. Ophthalmol. Vis. Sci.* **56**, 6438–6447 (2015).

Kuiper, M. J., Morton, C. J., Abraham, S. E. & Gray-Weale, A. The biological function of an insect antifreeze protein simulated by molecular dynamics. *Elife* **4**, (2015).

Leeming, M. G., Isaac, A. P., Pope, B. J., Cranswick, N., Wright, C. E., Ziogas, J., O'Hair, R. A. J. & Donald, W. A. Highresolution twin-ion metabolite extraction (HiTIME) mass spectrometry: nontargeted detection of unknown drug metabolites by isotope labeling, liquid chromatography mass spectrometry, and automated highperformance computing. *Anal. Chem.* 87, 4104–4109 (2015).

Li, S., Wong, E. M., Joo, J. E., Jung, C.-H., Chung, J., Apicella, C., Stone, J., Dite, G. S., Giles, G. G., Southey, M. C. & Hopper, J. L. Genetic and Environmental Causes of Variation in the Difference Between Biological Age Based on DNA Methylation and Chronological Age for Middle-Aged Women. *Twin Res. Hum. Genet.* **18**, 720–726 (2015).

Meumann, E. M., Globan, M., Fyfe, J. A. M., Leslie, D., Porter, J. L., Seemann, T., Denholm, J. & Stinear, T. P. Genome sequence comparisons of serial multi-drugresistant Mycobacterium tuberculosis isolates over 21 years of infection in a single patient. *Microbial Genomics* **1**, (2015).

Kwong, J. C., Mercoulia, K., Tomita, T., Easton, M., Li, H. Y., Bulach, D. M., Stinear, T. P., Seemann, T. & Howden, B. P. Prospective Whole-Genome Sequencing Enhances National Surveillance of Listeria monocytogenes. *J. Clin. Microbiol.* **54,** 333–342 (2016).

Moustafa, A. M., Seemann, T., Gladman, S., Adler, B., Harper, M., Boyce, J. D. & Bennett, M. D. Comparative Genomic Analysis of Asian Haemorrhagic Septicaemia-Associated Strains of Pasteurella multocida Identifies More than 90 Haemorrhagic Septicaemia-Specific Genes. *PLoS One* **10**, e0130296 (2015).

Murugesan, S., Tay, D. B. H., Cooke, I. & Faou, P. Application of dual tree complex wavelet transform in tandem mass spectrometry. *Comput. Biol. Med.* **63**, 36–41 (2015).

Nepal, S., Surya, N., Richard, S., Carsten, F., Catherine, W., Shiping, C., Sehrish, K., Jinhui, Y. & Andrew, L. TruXy: Trusted Storage Cloud for Scientific Workflows. *IEEE Transactions on Cloud Computing* 1–1 (2015).

Nguyen-Dumont, T., Hammet, F., Mahmoodi, M., Pope, B. J., Giles, G. G., Hopper, J. L., Southey, M. C. & Park, D. J. Abridged adapter primers increase the target scope of Hi-Plex. *Biotechniques* **58**, 33–36 (2015).

Nguyen-Dumont, T., Hammet, F., Mahmoodi, M., Tsimiklis, H., Teo, Z. L., Li, R., Pope, B. J., Terry, M. B., Buys, S. S., Daly, M., Hopper, J. L., Winship, I., Goldgar, D. E., Park, D. J. & Southey, M. C. Mutation screening of PALB2 in clinically ascertained families from the

Breast Cancer Family Registry. *Breast Cancer Res. Treat.* **149,** 547–554 (2015).

Patch, A.-M., Christie, E. L., Etemadmoghadam, D., Garsed, D. W., George, J., Fereday, S., Nones, K., Cowin, P., Alsop, K., Bailey, P. J., Kassahn, K. S., Newell, F., Quinn, M. C. J., Kazakoff, S., Quek, K., Wilhelm-Benartzi, C., Curry, E., Leong, H. S., The Australian Ovarian Cancer Study Group, Hamilton, A., Mileshkin, L., Au-Yeung, G., Kennedy, C., Hung, J., Chiew, Y.-E., Harnett, P., Friedlander, M., Quinn, M., Pyman, J., Cordner, S., O'Brien, P., Leditschke, J., Young, G., Strachan, K., Waring, P., Azar, W., Mitchell, C., Traficante, N., Hendley, J., Thorne, H., Shackleton, M., Miller, D. K., Arnau, G. M., Tothill, R. W., Holloway, T. P., Semple, T., Harliwong, I., Nourse, C., Nourbakhsh, E., Manning, S., Idrisoglu, S., Bruxner, T. J. C., Christ, A. N., Poudel, B., Holmes, O., Anderson, M., Leonard, C., Lonie, A., Hall, N., Wood, S., Taylor, D. F., Xu, Q., Lynn Fink, J., Waddell, N., Drapkin, R., Stronach, E., Gabra, H., Brown, R., Jewell, A., Nagaraj, S. H., Markham, E., Wilson, P. J., Ellul, J., McNally, O., Doyle, M. A., Vedururu, R., Stewart, C., Lengyel, E., Pearson, J. V., Waddell, N., deFazio, A., Grimmond, S. M. & Bowtell, D. D. L. Whole-genome characterization of chemoresistant ovarian cancer. Nature 521, 489-494 (2015).

Quek, C., Jung, C.-H., Bellingham, S. A., Lonie, A. & Hill, A. F. iSRAP - a one-touch research tool for rapid profiling of small RNA-seq data. *Journal of Extracellular Vesicles* **4**, (2015).

Sadedin, S. P., Dashnow, H., James, P. A., Bahlo, M., Bauer, D. C., Lonie, A., Lunke, S., Macciocca, I., Ross, J. P., Siemering, K. R., Stark, Z., White, S. M., Melbourne Genomics Health Alliance, Taylor, G., Gaff, C., Oshlack, A. & Thorne, N. P. Cpipe: a shared variant detection pipeline designed for diagnostic settings. *Genome Med.* 7, 68 (2015).

Shiller, J., Van de Wouw, A. P., Taranto, A. P., Bowen, J. K., Dubois, D., Robinson, A., Deng, C. H. & Plummer, K. M. A Large Family of AvrLm6-like Genes in the Apple and Pear Scab Pathogens, Venturia inaequalis and Venturia pirina. *Front. Plant Sci.* **6**, 980 (2015).

Takemura, S.-Y., Xu, C. S., Lu, Z., Rivlin, P. K., Parag, T., Olbris, D. J., Plaza, S., Zhao, T.,

Katz, W. T., Umayam, L., Weaver, C., Hess, H. F., Horne, J. A., Nunez-Iglesias, J., Aniceto, R., Chang, L.-A., Lauchie, S., Nasca, A., Ogundeyi, O., Sigmund, C., Takemura, S., Tran, J., Langille, C., Le Lacheur, K., McLin, S., Shinomiya, A., Chklovskii, D. B., Meinertzhagen, I. A. & Scheffer, L. K. Synaptic circuits and their variations within different columns in the visual system of Drosophila. *Proc. Natl. Acad. Sci. U. S. A.* 112, 13711–13716 (2015).

Wade, K. R., Hotze, E. M., Kuiper, M. J., Morton, C. J., Parker, M. W. & Tweten, R. K. An intermolecular electrostatic interaction controls the prepore-to-pore transition in a cholesterol-dependent cytolysin. *Proc. Natl. Acad. Sci. U. S. A.* **112**, 2204–2209 (2015).

Wong Doo, N., Makalic, E., Joo, J. E., Vajdic, C. M., Schmidt, D. F., Wong, E. M., Jung, C.-H., Severi, G., Park, D. J., Chung, J., Baglietto, L., Prince, H. M., Seymour, J. F., Tam, C., Hopper, J. L., English, D. R., Milne, R. L., Harrison, S. J., Southey, M. C. & Giles, G. G. Global measures of peripheral blood-derived DNA methylation as a risk factor in the development of mature B-cell neoplasms. *Epigenomics* **8**, 55–66 (2016).

Wong, N. C., Pope, B. J., Candiloro, I., Korbie, D., Trau, M., Wong, S. Q., Mikeska, T., van Denderen, B. J. W., Thompson, E. W., Eggers, S., Doyle, S. R. & Dobrovic, A. Exemplary multiplex bisulfite amplicon data used to demonstrate the utility of Methpat. *Gigascience* **4**, 55 (2015).

Yeoh, L. M., Goodman, C. D., Hall, N. E., van Dooren, G. G., McFadden, G. I. & Ralph, S. A. A serine–arginine-rich (SR) splicing factor modulates alternative splicing of over a thousand genes in *Toxoplasma gondii*. *Nucleic Acids Res.* **43**, 4661–4675 (2015).

Zhu, W., Ausin, I., Seleznev, A., Méndez-Vigo, B., Picó, F. X., Sureshkumar, S., Sundaramoorthi, V., Bulach, D., Powell, D., Seemann, T., Alonso-Blanco, C. & Balasubramanian, S. Natural Variation Identifies ICARUS1, a Universal Gene Required for Cell Proliferation and Growth at High Temperatures in *Arabidopsis thaliana*. *PLoS Genet.* **11**,e1005085 (2015).

Our Community

Skills development

Supporting skills development in students and sharing expertise amongst all levels of the research community is key to the sustainability of a healthy research ecosystem. Hundreds of researchers participated in a wide variety of VLSCI training activities in 2015. From aspiring scientists completing their high school work experience placements, to new graduates undertaking their first professional work placement or senior academics looking to pick up new bioinformatics skills at a hands-on workshop, VLSCI engaged with a diverse audience.

The journey of University of Melbourne undergraduate student, Edmund Lau, provides a great example of how VLSCI attracts young talent and can help to build a passion into a career. Edmund has always been interested in science - the way it describes the world objectively, its internal coherency and the universal applicability of its techniques. While studying for his BSc with a major in mathematical physics, Edmund sought practical research experience and was accepted into the 2015 Undergraduate Research Opportunities Program (UROP).

Edmund's exceptional mathematical, algorithmic and problem solving skills were immediately recognised, and he was offered a UROP position at VLSCI despite no previous experience in bioinformatics. His studies provided the foundation to understand complex research challenges, and he was excited to have the opportunity to solve an algorithmically complex problem in a biological context.

The 2015 UROP Conference Day was opened by the Hon. Frank McGuire MP, the Parliamentary Secretary for Medical Research, with a keynote talk by Deakin University's Dr Melanie Thomson.

The VLSCI prize for Best **Computational Research Presentation** was awarded to Yoshua Wakeham (Peter MacCallum Cancer Centre) for 'The impact of heterogeneity and genetic instability on tumour treatment response: an *in silico* investigation', and the runner up prize went to Julia McCoey (Monash University) for 'Modeling of Thyroid Peroxidase Reveals Insights into its Enzyme Function and Autoantigenicity'.

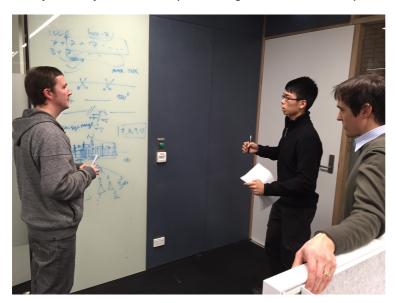
Other presentations at the Conference Day included VLSCI UROP students Roger Li (supervised by Bernard Pope and Daniel Park): UNDR ROVER - A fast and accurate variant caller for the Hi-Plex targeted DNA sequencing system, and Regina Zhang (supervised by Yousef Kowsar and Andrew Lonie): Testing Automation for GenomeSpace.



Photos: UROP's VLSCI prize winners Julia McCoey and Yoshua Wakeham; UROP student Regina working with VLSCI supervisor Yousef.

Supervised by Bernard Pope and Daniel Park, Edmund's project tackled a problem with multiplex-PCR primer design. He developed a software tool to automate the process of designing molecules which are central to the Hi-Plex targeted DNA sequencing technology. The program is designed to find the optimal solution in a vast space of possible solutions. It is able to explore large parts of that space in an efficient manner - analogous to finding the best set of DNA sequences from a huge volume of genomic information with reference to a particular biological context.

The abstraction of a biochemical problem to a model allows it to be tackled by mathematical methods and subsequently solved by the development of novel algorithms, ultimately making the real world search as fast and accurate as possible. Once optimised, the primer design tool can become widely used by researchers performing PCR and DNA sequencing.



As a first-time researcher, Edmund gained a whole new view of how previously disconnected knowledge can work together to generate new perspectives on problems:

I have learnt priceless lessons and gained valuable experience at VLSCI. Working with researchers here has taught me to always be attentive to alternative ideas and to be prepared to update my mental model of how things work. It has showed me that science truly is a lively community effort of smart and enthusiastic people.

Photo: Edmund works through a problem with VLSCI supervisors Bernie and Danny.

Edmund has now completed a summer internship at VLSCI where he developed a DNA folding tool to complement the main software. His exposure to the diversity of scientific challenges and interesting problems requiring new methods has inspired Edmund to stay on with VLSCI while he completes his 3rd year of studies in mathematical physics. Edmund will join a major new VLSCI project taking place in 2016 that will allow him to follow his enthusiasm for research and passion for scientific knowledge.



Photos: Work experience students Tushar (left, with supervisor Mike Kuiper) and Lewis (right).

Internships

Each year, VLSCI has employed a group of talented interns from December – February. The majority of our interns are postgraduate students, and the 2015 cohort of 11 interns worked on a diverse range of projects with VLSCI supervision across Murdoch Childrens Research Institute, La Trobe and Melbourne Universities, and at VLSCI.

Jumana Yousef: Assessment of normalisation methods for DNA methylation microarray data.

Susmita Saha: Feature selection for clustering of high throughput microscopy images.



Jordan Holland: Determining the relative stability of protein helices.

Tane Hunter: Diagnosis of childhood syndromes by analysis of clinical exome data.



Diego Montufar: Development of a web resource for analysing helices in proteins.

Luke Zappia: Analysis of Mass Spectrometry Data, metabolomics and high performance computing.

Simon Belluzzo: Easy deployment of tools with complex dependencies using Docker and Galaxy on the Cloud.

Andres Chaves: Improving efficiencies and generality of code used to compute animal and microclimate heat budgets.



Emanuel Birru: Molecular Dynamics Workflow.

Steffi Cheung: Development of techniques for the de novo assembly of genomes from metagenomic samples.

Hugh Ford: Spatiotemporal models of calcium dynamics within heart cells: a nuclear focus.

Direct Support for Students

STUDENT	HOST INSTITUTION	PRIMARY SUPERVISOR/S	PROJECT		
PHD TOP-UP STUDENTSHIPS (ceased 30 June 2015)					
Brendan Ansell	UoM, Veterinary Science	Aaron Jex Malcolm McConville	Investigating mechanisms of drug resistance in Giardia		
Daniel Brown	UoM, Pathology	Theo Mantamadiotis	Investigating signalling pathways in glioma stem cells		
Daniel Cameron	UoM, WEHI	Tony Papenfuss Terry Speed	Detecting somatic indels and other structural variants using high-throughput genomic sequencing		
Thomas Coudrat	Monash, MIPS	Patrick Sexton Denise Wootten	Development of methods for G- Protein Coupled Receptors (GPCRs) conformation modelling and investigation of the structural determinants for their activity		
Sarah Diepstraten	La Trobe, Genetics	Adam Hart	A new experimental model for analysis of human globin gene switching during embryonic stem cell differentiation		
Emma Hodges	Monash, Chemical Engineering	Ravi Jagadeeshan	Mesoscopic simulations and experimental observations of cell adhesion in hydrodynamic flow		
Danielle Ingle	UoM, Microbiolology & Immunology	Roy Robins-Browne Kathryn Holt Marija Tauschek Timothy Stinear	Virulence within atypical enteropathogenic <i>E. coli</i>		
Bernd Merkel	UoM, MDHS	Patricia Desmond Nicola Lautenschlager Matthias Guenther Christopher Steward	Investigation of white matter changes with MRI in older adults at risk of Alzheimer's Disease		
Ehtesham Mofiz	UoM, WEHI/MDHS	Tony Papenfuss	Scabies mite genome project		
Simon Sadedin	UoM, MCRI	Alicia Oshlack Terry Speed Andrew Sinclair	Improving detection of disease causing variants in targeted NGS data		
Luisa Teasdale	Museum Vic	Adnan Moussalli	Using 'next generation' sequencing to resolve deep phylogenetic relationships in the land molluscs (Panpulmonata)		
Jian D.L. Yen	Monash, Faculty of Science	Ralph MacNelly	Thermodynamic ecology: theoretical and empirical approaches.		
	MSC (BIOINF	ORMATICS) BURSARY	RECIPIENTS		
Cristian Pena (Peter Mac bursary)	Peter Mac	Tony Pappenfuss	De novo genome assembly of the scabies mite		

Luyi Tian (WEHI bursary)	WEHI	Matt Ritchie	Making sense of single-cell transcriptomes
Dong Hao Teng (VLSCI bursary)	UoM, VLSCI	Juan Nunez-Iglesias	Interactive clustering of high- content screen images with Microscopium
Alexis Lucattini	WEHI / AGRF	Lavinia Gordon Matt Ritchie	Comparison of long reads – MinION vs PacBio
Tony Pham (Pathology, UoM)	UoM, Pathology	Paul Waring Graham Taylor	Molecular Evolution of Meninigiomas
Daniel Esposito (VLSCI bursary)	UoM, Computational Biology	Melissa Davis	Analysis of functional modules in tissue- and cell-specific molecular interaction networks
	UROP ST	UDENTS WITH VLSCI	STIPEND
Jan Jarosz	UoM, Computational Biology	Vijay Rajagopal Edmund Crampin	Using 3D models of heart cells to understand how cell structure affects cell function
Max Plumley	MIPS	David Chalmers Colin Pouton Dallas Warren	Molecular Dynamics Modeling of drug formulations
Nick Rosa	CSIRO	Janet Newman	Thermal melt curves as predictors of crystallisation
BEST UROP I	PRESENTATION IN	I COMPUTATIONAL BIO	DLOGY VLSCI PRIZE WINNERS
Yoshua Wakeham (1 st prize)	Peter Mac	David Goode	The impact of heterogeneity and genetic instability on tumour treatment response: an <i>in silico</i> investigation
Julia McCoey (2 nd prize)	Monash	Ashley Buckle	Modeling of Thyroid Peroxidase Reveals Insights into its Enzyme Function and Autoantigenicity
	WOR	K EXPERIENCE STUDE	INTS
Tushar Nagar	WOR Melbourne High School	K EXPERIENCE STUDE Michael Kuiper	NTS
Tushar Nagar Lewis Barnes	Melbourne High		ENTS
	Melbourne High School Northcote High School Elizabeth Blackburn School of	Michael Kuiper	How does the New Delhi metallo- beta-lactamase 1 (NDM-1) protein influence bacterial resistance to
Lewis Barnes Sean Cartwright (year- long	Melbourne High School Northcote High School Elizabeth Blackburn School of Sciences	Michael Kuiper Michael Kuiper	How does the New Delhi metallo- beta-lactamase 1 (NDM-1) protein influence bacterial resistance to penicillin?
Lewis Barnes Sean Cartwright (year- long	Melbourne High School Northcote High School Elizabeth Blackburn School of Sciences	Michael Kuiper Michael Kuiper Michael Kuiper	How does the New Delhi metallo- beta-lactamase 1 (NDM-1) protein influence bacterial resistance to penicillin?
Lewis Barnes Sean Cartwright (year- long research project)	Melbourne High School Northcote High School Elizabeth Blackburn School of Sciences	Michael Kuiper Michael Kuiper Michael Kuiper ENTS WITH VLSCI SUF Ira Cooke Nick Hoogenraad Nathan Hall Kim Plummer	How does the New Delhi metallobeta-lactamase 1 (NDM-1) protein influence bacterial resistance to penicillin? PERVISION Differential expression of membrane proteins under heat
Lewis Barnes Sean Cartwright (year- long research project) Fiona Durand	Melbourne High School Northcote High School Elizabeth Blackburn School of Sciences RHD STUD	Michael Kuiper Michael Kuiper Michael Kuiper ENTS WITH VLSCI SUF Ira Cooke Nick Hoogenraad Nathan Hall	How does the New Delhi metallobeta-lactamase 1 (NDM-1) protein influence bacterial resistance to penicillin? PERVISION Differential expression of membrane proteins under heat shock Genomics and transcriptomic studies of Venturia host-pathogen
Lewis Barnes Sean Cartwright (year- long research project) Fiona Durand Shakira Johnson	Melbourne High School Northcote High School Elizabeth Blackburn School of Sciences RHD STUD PhD, La Trobe	Michael Kuiper Michael Kuiper Michael Kuiper ENTS WITH VLSCI SUF Ira Cooke Nick Hoogenraad Nathan Hall Kim Plummer Nathan Hall Ira Cooke	How does the New Delhi metallobeta-lactamase 1 (NDM-1) protein influence bacterial resistance to penicillin? PERVISION Differential expression of membrane proteins under heat shock Genomics and transcriptomic studies of Venturia host-pathogen responses Understanding of abalone heat

Tom Stent	PhD, Monash	Dieter Bulach, Julian Rood	Clostridial necrotic enteritis
Dan Brown	PhD, UoM	Andrew Lonie Theo Mantamadiotis	Genomic characterisation of Glioblastoma multiforme (GBM) subtypes
Andrew Buultjens	PhD, UoM	Torsten Seemann Tim Stinear	Tracking the source of myocbacterim ulcerans in Victoria
Kian Ho	PhD, UoM	Michael Kuiper Rao Kotagiri	Computational substrate querying and topology prediction of the beta-sheet
Sehrish Kanwal	PhD, UoM	Andrew Lonie Richard Sinnot	Informatics platforms for clinical genomics
Jason Kwong	PhD, UoM	Torsten Seemann Ben Howden	Genomics for public health microbiology
Ehtesham Mofiz	PhD, UoM	Torsten Seemann Tony Papenfuss	Scabies mite genome
Camelia Quek	PhD, UoM	Chol-Hee Jung Andrew Hill (Bio21)	Implication of small transcriptome in exosomes during Prion disease
Sabrina Rodriguez	PhD, UoM	Andrew Lonie Richard Huggins	Predicting Phenotypes through pathway analysis using conditional independence and central subspaces
Melissa Yeow	PhD, UoM	Dieter Bulach Melissa Southey	Using a high throughput sequencing strategy to detect microbial agents (viral or bacterial) associated with prostate cancer
Nikeisha Caruana	PhD, La Trobe	Ira Cooke Jan Strugnell	Proteomics and transcriptomics of squid toxins
Dong (Don) Hao Teng	MSc(Bioinf), UoM	Juan Nunez-Iglesias Kaylene Simpson	Features and metrics to compare high content screen images
Hongzi Luo	MSc(Bioinf), UoM	Gayle Philip	Analysis of Renal Disease Associated Gene Variants in Minature bull terriers
Brooke Whitelaw	BSc(Hons), La Trobe	Ira Cooke Jan Strugnell	Proteomics and transcriptomics of blue ringed octopus and octopus kaurna

MSc (Bioinformatics) Graduates

National iAwards winner, UoM student Ryan Wick, was recognised for developing Bandage - a bioinformatics application designed to help researchers in genetics and medicine. During his MSc (Bioinformatics) research project, Ryan was supported by a VLSCI bursary made available to exceptional students each year.

NAME	HOST INSTITUTION	PRIMARY SUPERVISOR/S	PROJECT
Ryan Wick	UoM	Kathryn Holt Justin Zobel	Analysing genes of interest in a set of microbial metagenomic sequencing reads
Helen Mitchell	UoM, Melbourne Dental School	Stuart Dashper	Prediction of Early Childhood Caries risk using bacterial biomarkers
Jumana Yousef	Peter Mac	Maria Doyle	Developing novel methods to distinguish somatic from constitutional germline DNA variants in tumour sequencing data in the absence of a control sample
Dharmesh Bhuva Dinesh	UoM, Engineering	Edmund Crampin Melissa Little	Cofactor Identification in cancer

Tiane Ryman	UoM, Biomedical Engineering	Melissa Davis	Identification and analysis of molecular interaction networks driving metastasis in diverse cancers
Luke Zappia	UoM	Fred Hollande Arthur Hsu	Human Circulating tumour cells: from biology to biomarkers
Janan Arslan	CERA/Dept of Opthamology	Paul Baird	Identification of genetic variants associated with poor treatment outcome in patients with age related macular degeneration (AMD) – a pharmacogenetic analysis
Madison Flannery	UoM, Biomedical Engineering	Melissa Davis	Identification and analysis of molecular interaction networks driving metastasis in diverse cancers
Lara Gonzalez Luis	Peter Mac	David Goode	Modelling the evolution of drug- resistant tumours
Stuart Lee	WEHI	Melanie Bahlo	Looking for selection signatures for malaria in high throughput sequencing data
Chang Liu	Peter Mac	David Goode	Biological pathway and gene-set enrichment analysis in cancer
Bahiyah Nor	UoM, Vet Science	Neil Young Robin Gasser	Parasite Genomics
David Stasiak	WEHI	Matt Ritchie	Evaluating the quality of ChIP-seq data in the context of a differential binding analysis
Agnes Tan	RWH	Sepehr Tabrizi Gayle Philip	Changes in microbial communities upon onset of Bacterial Vaginosis

Sponsorship of Travel and Conference Attendance

There was \$18,615 allocated in 2015 to funding the travel of Victorian research scientists. The majority of funds was allocated to postgraduate students to further their opportunities to attend conferences and collaborate with international peers. Where benefits to the broader research community could be demonstrated, grants were also used to support researchers' travel to strengthen international collaborations and networks.

RECIPIENT	POSITION	INSTITUTION	DESTINATION
Zak Hughes	Postdoctoral Researcher	Deakin	Spring Meeting of the American Chemical Society, Denver, Colorado (March).
Jane Hawkey	Postgraduate Student	UoM	Applied Bioinformatics & Public Health Microbiology conference, meet with collaborators at Sanger Inst, Cambridge (May)
Claire Gorrie	Postgraduate Student	UoM	Applied Bioinformatics & Public Health Microbiology conference, meet with collaborators at Sanger Inst, Cambridge (May).
Danielle Ingle	Postgraduate Student	UoM	Applied Bioinformatics & Public Health Microbiology conference, meet with collaborators at Sanger Inst, Cambridge (May).
Harriet Dashnow	Postgraduate Student	MCRI	Biology of Genomes conference, New York, lab meetings with collaborators,

			Cambridge (May)
Henry Whittler	Postgraduate Student	LTU	Traineeship at Gromacs software developers labs, Stockholm and Uppsala (June-August).
Caitlin Gionfriddo	Postgraduate Student	UoM, Earth Sciences	International Conference on Mercury as a Global Pollutant (June).
Jingyi Tang	Postgraduate Student	UoM - RMH	Winter School in Mathematical and Computational Biology, Software Carpentry Workshop, Brisbane (July).
Zoe Dyson	Postdoctoral Researcher	UoM)	Welcome Trust Infection Disease Genomics Conference, Lab visits to the Sanger Inst, University of Oxford, Public Health England (October).
Andrew Buultjens	Postgraduate Student	UoM	COMBINE Student Symposium, ABACBS Conference (October).

I am very grateful for the opportunity to attend the 2015 Winter School in Mathematical & Computational Biology and I am grateful to VLSCI for the financial support to attend this course.

I returned to Melbourne armed with solid bioinformatics knowledge. I strongly recommend my colleagues or anyone working in sciences attend this course next year to gain valuable experiences.

Travel grant recipient, Jingyi Tang, Royal Melbourne Hospital.

Sponsorship of Meetings and Conferences

Investing in the research community, VLSCI contributes funds and in kind support to a range of organisations and events. Major annual sponsorship of the bioinformatics/computational biology student group, COMBINE, and the Convergence Science Network strengthens existing training and networking activities. Providing financial support to a range events - from UoM's involvement in the IBM International Collegiate Programming Contest and the Codemasters Programming competition for high school students, to professional events such as the Metagenomics@Melbourne Symposium or the SOBR (Students of Brain Research) Professional Development Dinner and various other conference prizes - reach a diverse range of researchers.

Community capacity building was further supported by sponsoring tours by leading figures such as ELIXIR's Niklas Blomberg and CSIRO's Annette McGrath's trip to South Africa to successfully bid for Australia to host the 2016 Global Organisation for Bioinformatics Learning, Education and Training AGM.

DATE	ACTIVITY (LOCATION)	TYPE OF SPONSORSHIP
Annual sponsorship	COMBINE (student-run organisation for researchers in computational biology & bioinformatics)	Major sponsorship, plus in kind support for Sydney Symposium
Annual sponsorship	Convergence Science	Major sponsorship and provision of speakers
March	Graeme Clark Oration & activities (Melbourne Convention and Exhibition Centre)	Sponsored event, hosted a group of students at Oration and Oration Dinner.
April	Code Masters Challenge (Computing & Information Systems, UoM)	Sponsored event
June	Advanced Molecular Modelling Workshop	Primary sponsor and organiser (speakers: 3 international, 2 interstate, 1 local)
June	SOBR Professional Networking Dinner - Bridging the Translational Research Gap: A Successful Partnership Involving Neuroscientists and Industry. Keynote speakers: Professor Patrick McGorry, ORYGEN, Dr Krystal Evans BioMelbourne Network (Melbourne Convention and Exhibition Centre)	Sponsored event and provided speaker
July	Embracing the Genomic Revolution - Applied Microbial Genomics in Public Health and Clinical Microbiology Symposium (Doherty Institute for Infection and Immunity)	Sponsored event and provided speaker
July	UROP Conference Day (Melbourne Convention and Exhibition Centre)	Judging and prize for Best Computational Biology Presentation
September	South Pacific Regional Finals, IBM International Collegiate Programming Contest, New Zealand	Sponsored travel costs of UoM team (3 students) and their coach
October	Transcriptomics Workshop - satellite to ComBio2015 (La Trobe University)	Sponsored event
November	Metagenomics@Melbourne Symposium on microbiome research (Bio21 Institute)	Sponsored event
November	GOBLET AGM, South Africa	Funded travel of Dr Annette McGrath (Principal Research Sciencetist, DATA61, CSIRO) to represent BRAEMBL and successfully bid for 2016 GOBLET AGM
November- December	Financed and organised Australian visit of Niklas Blomberg, ELIXIR, who toured Melbourne, Canberra, Sydney and Brisbane.	Funded and organised tour
November	EMBL PhD Symposium, Bio21	Sponsored event
December	MM2015 (Molecular Modelling 2015), UNSW	Student travel bursaries

Hands-on Workshops

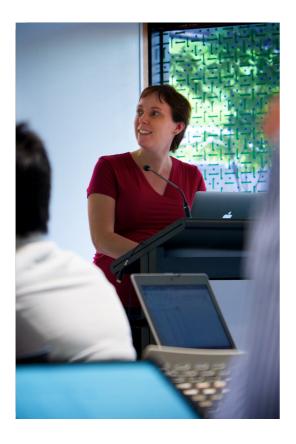


Photo: Clare Sloggett facilitates a hands-on workshop at Lab-14.

Staff from VLSCI were invited to institutions and conferences around the world to deliver workshops.

In July, Dr Simon Gladman presented a workshop on the use of the Genomics Virtual Laboratory (GVL) for microbial genomics for Applied Bioinformatics and the Public Health Microbiology conference at the Sanger Research Institute, UK. Simon also spent time discussing with UK officials on deployment of GVL onto their cloud infrastructure and presented at a UK Midlands Group Meeting and at a hackathon at the University of Birmingham.

In a demonstration of the breadth of workshops that VLSCI contributes to, the popular Australian public forum, Future Crunch, invited Dr Michael Kuiper to present his work to an enthusiastic audience for the 'Future of Biotechnology'.

There were 33 local workshops offered in 3 locations, reaching a total of 461 Victorian participants from a wide variety of research institutes or organisations.

33 WORKSHOPS



I have little programming knowledge and this workshop has given me tremendous confidence in using and learning more about R. Thank you very much!

Postdoctoral Researcher in Stem Cells, UoM

Wonderful course! I have learned heaps and am in a good position to keep learning shell scripts after this awesome intro.

Postdoctoral Researcher, Peter Mac







From Peter Mac researchers (left) to our youngest workshop participant yet (right – 10 year old 'CAKE'), VLSCI's 2015 workshops were well attended.

WORKSHOP	LOCATION	DATE
Introduction to Unix at VLSCI: hands-on workshop	Lab-14	12/02/15 6/10/15
Introduction to High Performance Computing at VLSCI	Lab-14	17/02/15 12/10/15
Introduction to Molecular Modelling & Visualisation	Lab-14	19/02/15 13/10/15
Introduction to Proteomics with Galaxy	La Trobe	24/02/15
Introduction to Galaxy	Lab-14	25/02/15 8/10/15
Intermediate Molecular Modelling & Visualisation for Life Sciences	Lab-14	26/02/15 19/10/15
Variant calling with Galaxy (beginners)	Lab-14	3/03/15 20/10/15
Open source science with Git and GitHub	Lab-14	5/03/15 4/11/15
RNA-Seq Differential Gene Expression Analysis using Galaxy	Lab-14	10/03/15 5/11/15
Introduction to Proteomics with Galaxy	Lab-14	11/03/15 29/10/15
Advanced Variant Calling with Galaxy	Lab-14	17/03/15 5/11/15
Advanced RNA-Seq DGE with Galaxy	Lab-14	19/03/15 25/11/15
Advanced proteomics analysis with Galaxy	La Trobe	14/04/15
Introduction to Unix at La Trobe: hands-on workshop	La Trobe	14/05/15
Advanced Molecular Modelling Workshop	La Trobe	3/06/15
Unix Revision at La Trobe	La Trobe	15/06/15
High Performance Computing at La Trobe	La Trobe	18/06/15
Python Programming for Physics	UoM	15/10/15 19/11/15 3/12/15
Introduction to EBI bioinformatics resources	Lab-14	9/11/15
Data Carpentry for Life Scientists	Lab-14	23/11/15
·		



Financials

Preamble

Grant Agreement

2015 is VLSCl's first year of operation under the new Grant Agreement 2014 (as signed on 29 September 2014) between the State of Victoria, represented by The Department of Economic Development, Jobs, Transport & Resources (DEDJTR) and The University of Melbourne. The period of the Funding Grant is for the 2015 and 2016 calendar years. The sum of the grant is \$6.65 million.

The purpose of the Grant is "to continue the operations of the Victorian Life Sciences Computation Initiative (VLSCI) to allow the University to fulfil its sustainability plan activities to transition the VLSCI into a national research infrastructure facility and position the VLSCI for Commonwealth research infrastructure grant funding..."¹

A significant direct cash investment made by The University of Melbourne of \$4.8 million in 2015 continues to support the Initiative. The University of Melbourne welcomed various funding contributions from member organisations (LaTrobe, Deakin, RMIT Universities) during the 2015 year.

The University of Melbourne

The University administers the Initiative's funds in accordance with the terms and conditions of the Grant and in accordance with approved University of Melbourne Finance Policies and Procedures and conventional accounting practices. Grant funds and University funds are audited internally and externally. Interest received on the Grant funds has been generated through investment of those funds and is returned to the Initiative for use in continued operations of VLSCI.

Account Structure

Grant Funds from DEDJTR reside in a separate interest-earning project account which generates interest at The Reserve Bank Rate less 40 basis points. Drawdown to the VLSCI Operations Project of Grant funds is authorised by DEDJTR upon VLSCI meeting specified project deliverables and milestones in accordance with the Grant Agreement. Funds are scheduled for draw-down in three instalments over the 2015 & 2016 years.

University of Melbourne funds including contributions from member organisations and subscription and fee-for-service income are held in a separate VLSCI Operations Project.

2015 Audit

The 2015 Accounts have been reviewed by The University's Internal Audit Department and an external audit was conducted by Oakton Accounting Services. Oakton's Audit Statement confirmed the Financial Statement of Income and Expenditure fairly presented the expenditure of Grant funds and University of Melbourne funds for the 2015 year.

Income

Income to the VLSCI in the 2015 year consisted of subscription and fee-for-service income, interest earned on Grant funds, University of Melbourne direct cash contributions, contributions from member organisations and DEDJTR Grant funds. These earnings and contributions largely met revenue expectations.

¹ Grant Agreement, Background, C., 29 September, 2014, (The VLSCI Project").

Initiative Expenditure

Expenditure met budget for 2015. Savings were sought throughout the year. Notable expenses included a Maintenance and Support contract for the IBM Blue Gene/Q hardware (\$1.3m) and the capital acquisition of X86 hardware (\$500,000).

Summary

2015 was the first year of a two year Grant from DEDJTR. Significant funds were expended in maintaining current hardware and capital acquisition of new hardware to upgrade and expand VLSCI's systems. Subscription income was somewhat less than in 2014, but overall was still strong with conservative forecasts for increased growth in 2016. Expenditure was in line with expectations. The finances of the VLSCI were managed in accordance with the relevant agreements, policies and procedures.

Consulting Technology





Department of State Development, Business and Innovation

ANNEXURE B - Audit Opinion - Project Expenditure

Department of State Development, Business and Innovation 121 Exhibition Street MELBOURNE VIC 3000

UNIVERSITY OF MELBOURNE

This Audit Opinion is prepared for the purposes of the Grant Agreement dated 29th September 2014 (the Agreement) between the State of Victoria and the University of Melbourne (the Recipient) for transitional operations funding for the Victorian Life Sciences Computation Initiative (VLSCI) as further described in the Grant Details of the Agreement (the Project).

Scope

We have conducted an independent audit in accordance with Australian Auditing Standards of the attached Statement of Income and Expenditure for the period 1 January 2015 to 31 December 2015 provided by the Recipient.

Our audit involved an examination, on a test basis, of evidence supporting the amount of Project Expenditure incurred and the value of equipment installed and used at the Project Site. This included an examination of the Recipient's financial records and receipts, and an evaluation of the policies and procedures used to calculate the Project Expenditure. These procedures have been undertaken to form an opinion as to whether the methodology used to calculate the Project Expenditure, is in accordance with the Agreement, and that the figure stated is true and fair.

This Audit Opinion expressed in this report has been formed on the above basis.

Audit Opinion

We confirm that in our opinion, the Financial Statement of Income and Expenditure presents fairly the expenditure of grant funds for the Victorian Life Sciences Computation Initiative for the period 1 January 2015 to 31 December 2015. As at 31 December 2015 the Recipient has incurred:

- \$3,650,000 in Project Expenditure in accordance with the terms of the Agreement;
- \$3,388,748.87 in expenditure from the University.

David Fraser

Date: 18 March 2016

Delivery Manager, Accounting and Assurance

Oakton Services Pty Ltd ABN 31 100 103 268 Melbourne Head office Level 8 271 Collins Street Melbourne VIC 3000 Australia \underline{t} +61 3 9617 0200 \underline{f} +61 3 9621 1951 Sydney Level 3 65 Berry Street North Sydney NSW 2060 Australia \underline{t} +61 2 9923 9800 \underline{f} +61 2 9929 6731 Canberra Unit 2 45 Wentworth Avenue Kingston ACT 2604 Australia \underline{t} +61 2 6230 1997 \underline{f} +61 2 6230 1919 Brisbane Level 5 200 Mary Street Brisbane QLD 4000 Australia \underline{t} +61 7 3136 2990 \underline{f} +61 7 3136 2999 Perth Level 14 Governor Stirling Tower 197 St Georges Terrace Perth WA 6000 Australia \underline{t} +61 8 6188 7607 Hyderabad Krishe-8 8-2-293 Plot 499 Road 36 Jubilee Hills 500033 Hyderabad India \underline{t} +91 40 23552694 \underline{volp} : +61 3 9617 0294

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Financal Statement (Annual Report) 31 December, 2015	ment (Annual Report) 31 December, 2015 Ytd Actual to 31/12/15		BREAKDOWN	
		Grant	University	
Carry Forward (University of Melbourne)	3,168,312.25		3,168,312.25	
Carry Forward (CODEV)	6,650,000.00	6,650,000.00	3,108,312.23	
TOTAL CARRY FORWARDS			2 160 212 25	
TOTAL CARRY FORWARDS	9,818,312.25	6,650,000.00	3,168,312.25	
INCOME				
Other Grant Income	966,976.64		966,976.64	
Fee for Service Income	33,629.36		33,629.36	
Investment Income	113,327.08		113,327.08	
Consulting and Contracted Services	495,000.00		495,000.00	
Internal Allocation	1,697,000.00		1,697,000.00	
University Contributions & Levy Income	200,000.00		200,000.00	
Grant Income ECODEV (Milestone 1 Drawdown)	3,650,000.00	3,650,000.00		
TOTAL INCOME + GRANT Draw Down	7,155,933.08	3,650,000.00	3,505,933.08	
EXPENDITURE				
Academic Salaries	2,243,554.98	1,616,779.09	626,775.89	
Professional Salaries	1,508,433.28	1,079,022.81	429,410.47	
TOTAL SALARY EXPENDITURE	3,751,988.26	2,695,801.90	1,056,186.36	
Non Salary Expenditure				
Non Salary Experiorcine				
Grant Expense	79,839.42		79,839.42	
Finance Related Costs	2,577.90		2,577.90	
Student Support	57,267.13		57,267.13	
Consumable Goods and Services	61,745.25		61,745.25	
Expert Services	458,833.85		458,833.85	
Travel, Conf & Entertainment	203,414.67		203,414.67	
Hardware Maintenance (IBM Blue Gene)	1,289,706.95	493,853.10	795,853.85	
Asset Expense > \$10,000 (X86 2015 Hardware Purchase)	460,345.00	460,345.00		
Asset Expense < \$10,000	19,180.37		19,180.37	
Infrastructure Related Assets	653,850.07		653,850.07	
TOTAL NON SALARY EXPENDITURE	3,286,760.61	954,198.10	2,332,562.51	
TOTAL EXPENDITURE	7.020.740.07	3 650 000 00	2 200 740 07	
TOTAL EXPENDITURE	7,038,748.87	3,650,000.00	3,388,748.87	
Total Carry Forward into 2016	\$ 6,285,496.46	\$ 3,000,000.00 \$	3,285,496.46	

Glossary

AGRF Australian Genome Research Facility Ltd
ANDS Australian National Data Service
ARC Australian Research Council
Baker IDI Baker IDI Heart and Diabetes Institute

Bio21 Bio21 Institute
Burnet Burnet Institute

CCS Monash University's Central Clinical School

CCV Cancer Council Victoria

CEC Cancer Council Victoria's Cancer Epidemiology Centre

CERA Centre for Eye Research Australia

Curtin University
Deakin Deakin University

DEPI Department of Environment & Primary Industries Victoria

EMBL European Molecular Biology Laboratory

Eng UoM Melbourne School of Engineering, University of Melbourne

FedUni Federation University

Florey Institute of Neuroscience and Mental Health
IBM IBM Research Collaboratory for Life Sciences - Melbourne
KAUST King Abdullah University of Science and Technology, Saudi Arabia

La Trobe University

LSCC Life Sciences Computation Centre – VLSCI
Ludwig Ludwig Institute for Cancer Research
Max Planck Max Planck Institute of Biochemistry

MBC Melbourne Brain Centre

MCRI Murdoch Children's Research Institute

MDS Melbourne Dental School, University of Melbourne

MHTP Monash Health Translation Precinct Medical Genomics Facility

MIMR Monash Institute of Medical Research
MIPS Monash Institute of Pharmaceutical Sciences

Monash. Monash University
Museum Vic Museum Victoria

NCI National Computational Infrastructure

NCMAS National Computational Merit Allocation Scheme
NeCTAR National eResearch Collaboration Tools and Resources
NHMRC National Health and Medical Research Council

NICTA National Information and Communications Technology Research Centre of Excellence

Oxford Oxford University, Britain
PCF Peak Computing Facility - VLSCI

PDI Peter Doherty Institute for Infection and Immunity

Peter Mac
RAS
Resource Allocation Scheme
RBG
ROYAL Botanic Gardens
RCH
ROYAL Children's Hospital
ROYAL Melbourne Hospital

RMIT RMIT University
RWH Royal Women's Hospital
Sanger Sanger Institute
SVH St Vincent's Hospital
SVI St Vincent's Institute

Swinburne University of Technology

SydneyUni
UC
University of Canterbury
UNSW
UoA
University of New South Wales
The University of Adelaide
UoM
UoN
UoN
University of Melbourne
UoN
University of Newcastle
UoSC
University of the Sunshine Coast

UoW University of Wollongong

UROP Undergraduate Research Opportunities Program (Biomedical Research Victoria)

UQ The University of Queensland
UWA The University of Western Australia
VABC Victorian AgriBiosciences Centre
VBC Victorian Bioinformatics Consortium

VCB Victorian Cancer Biobank

VIDRL Victorian Infectious Diseases Reference Laboratory VLSCI Victorian Life Sciences Computation Initiative WEHI Walter & Eliza Hall Institute of Medical Research

