



Melbourne Bioinformatics
BIOINFORMATICS + DATA SERVICES + INFRASTRUCTURE, FOR LIFE SCIENCES TODAY

20 February 2017

VLSCI becomes Melbourne Bioinformatics: a letter from the Director

It seems fitting that on the day we re-launch as [Melbourne Bioinformatics](#), it has been seven years since VLSCI started. Doesn't it take seven years to grow a child? This evolution definitely marks a maturing of our project. We are now firmly embedded in the life of the Melbourne biomedical and biosciences precinct and every day we are empowering world-class research.

While we write our final report to the Victorian Government, we are also preparing a new report on the exciting progress made over the past 12 months. Late in 2015, we were granted support from the NCRIS-funded Bioplatforms Australia and the University of Melbourne to host the Hub of the EMBL Australia Bioinformatics Resource (EMBL-ABR). We then became an EMBL-ABR Node and have since been working with colleagues around the country to build the Resource into an exciting national network.

Several recent reviews by us and our stakeholders, nationally and internationally, have all pointed out that the exponential growth in life sciences data is not slowing down and as we get smarter with handling that data, we are finding new ways to analyse, manipulate, disseminate and store it. Many of us now rely on a range of resources to do our work, including desk-top systems, local high-end systems, cloud-based services and national infrastructure, along with the resources of our collaborators. Anticipating the retirement of Avoca at the end of 2016, we had applied for and won a LIEF grant to get a new GPU-based high-performance system (coming mid-2017) to add to our two other systems. With our ongoing participation in University of Melbourne computing requirements planning and national infrastructure projects such as the Australian Research Cloud, we are well-positioned to ensure researchers engaging with us get the right system for the work they want to do.

Demand for training continues to grow as life science transitions into a data science. Our linking with EMBL-ABR gives us an opportunity to bring resources available through that network to Melbourne and Australia to deliver world-class skills and training to our community. [EMBL-ABR's February newsletter](#) has more details about these activities. Through Bioplatforms Australia, three of our bioinformaticians are now trainers in the Genome Analysis Toolkit (GATK) which is a widely-used software package developed by the Data Science and Data Engineering group at the Broad Institute, to perform variant discovery analysis on high-throughput sequencing data. There is currently an expression of

interest out to determine where to run workshops in GATK in 2017 - you will see it in the events section on our homepage.

On the new site, you will also read about developments in our Human Genomics Group, led by Assoc Prof Daniel Park and Dr Bernard Pope. Daniel Park also led the project to build the Melbourne Bioinformatics Platform for the Parkville Precinct and the project now has a new face to the community through Melbourne Bioinformatics.

There have been some promising developments also in the Pan-Prostate Genomics Consortium project led by Prof Chris Hovens (University of Melbourne and Royal Melbourne Hospital). Vital to this project is the establishment of a robust analysis pipeline to process data coming in from samples around the world. This is the largest whole genome sequencing ever carried out in cancer research, with thousands of samples to be analysed, several hundred of which come from Prof Hovens' team. We look forward to further updates on this project from our bioinformaticians Dr Bernard Pope and Mr Peter Georgeson as they delve into all that data.

In the news section today, University of Melbourne's Assoc Prof Vicky Schneider, Deputy Director, EMBL-ABR, is featured for a recent paper published in *Integrative Biology*, co-authored with Dr Tamas Korcsmaros (Earlham Institute) and Professor Giulio Superti-Furga (CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences). The paper, *Next Generation of Network Medicine: Interdisciplinary Signalling Approaches*, reports on the outcomes of a cross-disciplinary workshop they ran to map out how to deliver on the outcomes as promised by 'network medicine'.

So, after seven years we have become fully immersed in the local and international bioinformatics landscape, acting locally and interacting globally.

To keep up to date with all our developments, please follow us on Twitter @MelBioInf and @EMBL_ABR and visit www.embl-abr.org.au to sign up to receive the EMBL-ABR news also.

Finally, for those of you with whom we have partnerships needing to be acknowledged with the new name, we will be contacting you separately with logo/branding details.

Thank you all for your support and involvement to date. We look forward to working with many of you in 2017 and beyond.

Sincerely,

Andrew Lonie
Director
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