

NZ BioGrid

Travel Grant from REANNZ Capability Building Fund

10 October 2008

Background

The NZ BioGrid project was initiated to investigate the opportunities of developing a grid based system that took advantage of the KAREN network in the field of Bioinformatics.

Bioinformaticians use a variety of tools to analyse DNA and protein sequence data, data arising from gene expression studies as well as specialised systems involving evolutionary analysis and biological systems analysis. These tools range from those that can operate satisfactorily on a desk-top computer to those that require high computer power and which operate best using highly-parallelised systems.

The KAREN network and the BestGrid project were seen as opportunities to extend the availability of the high-end technologies to the New Zealand bioinformatics community. We were keen to learn from Australian colleagues who were about a year ahead of us in undertaking a similar process.

Learnings from across the ditch

Several meetings have been held in New Zealand and Australia. The first of these meetings was held in Auckland on 23 May 2007. Professor Shoba Ranganathan (Macquarie University) and Dr Lindsay Hood (Australian Partnership for Advanced Computing, APAC) were invited from Australia to attend and lead our discussions. Members of the New Zealand bioinformatics community representing all the major universities attended either in person or electronically.

This meeting was useful in several ways. It was noted that Australian bioinformaticians had not taken full advantage of the facilities of APAC (now morphed to National Collaborative Research Infrastructure Strategy or NCRIS). There were clear State/Federal conflicts. Portals that had been developed for various bioinformatic applications were non-intuitive for users without extensive IT experience.

The second meeting focussed on proteomics and was held in Auckland in July (timed to match KAREN meeting). Dr Bob Moritz (Ludwig Institute, Melbourne) who was responsible for the establishment of the Australian Proteomics Computer Facility (APCF) as a large-scale computational solution for mass spectrometry-based proteomic analyses for researchers in Australia. Researchers from several New Zealand universities attended. Dr Moritz described the facility in Melbourne and how New Zealand researchers could take advantage of it.

In November 2007, Dr Annette McGrath (Australian Genome Research Facility and Genomics Australia, Melbourne) met with researchers in Auckland to discuss assembly problems with sequences from the new high-throughput sequencers that are now available. It was clear from this meeting and at the Bioinformatics Australia meeting (see below) that there are major problems in achieving reliable sequences from the small reads produced by these technologies.

In November Dr Murray Grigor (University of Auckland) attended the Bioinformatics Australia annual meeting in Brisbane. This meeting was held in conjunction with the AusBiotech meeting.

Observations from this meeting include that the bioinformatics community in Australia is still largely fragmented and there has been only limited success in bringing it together.

A presentation on the Australian Bioinformatics Facility a new initiative under NCRIS was received with some reservations. This is a Federal Government-led project with emphasis on Genomics, Proteomics and Metabolomics. Bioinformaticians in Australia were also struggling with the same issues as their New Zealand counterparts in whether bioinformatics has matured to become a discipline in its own right and how funding might be captured for it.

Outcomes

In combination these meetings have provided a clear message that the tools of bioinformatics and the access to systems like KAREN must be set up to enhance the wider field of biology. The users, for the most part, molecular biologists have only limited skills in computer science, mathematics and statistics, disciplines that underpin bioinformatics.

Several observations arise:

- The interfaces have to be simple and intuitive to use.
- Information needs to be provided as to the nature of the tools and how best they can be used and, more importantly, when they should not be used.
- The bioinformatic portals in use in Australia tend to be non-intuitive and are generally user-unfriendly.

We have used these concepts to develop NZBioGrid further supported by another grant from REANNZ.

This project is nearing completion and will be reported on in due course. In addition, it is important to provide ongoing funding for bioinformatic projects. In both New Zealand and Australia we have pools of talented people who can develop new tools but this can rarely be achieved in the one to two year period covered by grants from agencies such as REANNZ.

Travel grant appropriations

In summary, this grant has been used to cover the costs of travel as follows:

Professor Shoba Ranganathan (Macquarie University)

Dr Lindsay Hood (APAC)

To lead workshop on grid computing and bioinformatics, University of Auckland, 23 May 2007

Dr Rob Moritz (Ludwig Institute, Melbourne)

To lead workshop on computing and proteomics and introduce the Australian Proteomics Computational Facility (APCF)

Dr Annette McGrath (Australian Genome Research Facility (AGRF), Melbourne)
For discussions in Auckland on developments in computing and sequence
analysis, 26 November 2007

Dr Murray Grigor (University of Auckland)
To attend Bioinformatics Australia annual meeting in Brisbane, November
2007

The total cost of travel and accommodation associated with these visits/meetings is
\$6,878.

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