White paper

Review of Bioinformatics in the University of Auckland: Looking forward from 2010 to 2013

15th November 2010: Cristin Print, Howard Ross and James Curran

Executive summary

During 2010 the Bioinformatics Institute at the University of Auckland gathered information about bioinformatics in New Zealand, in order to plan its goals and establish key performance indicators for 2011. In addition to informal disucssions with bioinformatcians from New Zealand and overseas, we have hosted a bioinformatics symposium attended by 108 people and conducted a web-based survey of 79 University of Auckland research groups. Key points and recommendations are summarised below:

(i) The use of research methods involving bioinformatics is likely to continue to grow at a moderate rate over the next three years.

(ii) Bioinformatics work is likely to become increasingly common within biological research laboratories that do not specialise in bioinformatics. Therefore, we recommend that the Bioinformatics Institute specially target support and training towards the members of Auckland research groups who are not formally trained in bioinformatics but who have an aptitude for data analysis.

(iii) High content biology and bioinformatics are rapidly penetrating many scientific disciplines, however the undergraduate training received by many Auckland students does not appear to adequately prepare them in these fields. contains. Therefore, we recommend that Auckland undergraduate biology and medical students to routinely receive additional basic education in computing and biostatistics, as appropriate for their courses.

(iv) Provision of scientist-focused software that allows mainstream laboratories to perform analysis of high content data from simple experiments will be important.

(v) We need to be prepared for journals, as a condition of publication, to require access to the precise bioinformatics analysis pipelines used, in addition to data.

(vi) Despite the increasing levels of bioinformatics skill in mainstream research laboratories, specialist bioinformaticians are likely to be required in increasing numbers. These bioinformaticians would be involved in difficult or cutting edge analysis, integrative biology, liaison roles and education.

(iv) Integrative biology is a growing part of the work of specialist bioinformaticians and can be important for research outputs. Therefore we recommend that the Bioinformatics Institute investigate purchasing a license for an integrative biology application for the use of Auckland researchers who contribute to the cost.

(vii) There appears to be a demand from outside the University for specialist bioinformatics consulting; providing external consulting services could benefit the Institute in several ways. Therefore we recommend that the Bioinformatics Institute discuss a framework for external consulting with Uniservices, after which the Institute's management group should establish a policy around this.

(viii) We recommend that the education of specialist bioinformaticians in Auckland needs to be flexible with several alternative entry paths to our postgraduate bioinformatics programs. Bridging/retrofitting courses may be required to provide the necessary prerequisite skills to students entering these programs. In addition, the Bioinformatics Institute should discuss with the Faculty of Science whether the current undergraduate program should be continued, or replaced with expanded postgraduate programs, mentoring schemes and internships.

(ix) Research groups in Auckland require ongoing bioinformatics assistance. For example, during the last 3 years, 52 of the 79 research groups that responded to the survey had obtained assistance from outside their groups for the analysis of biological data. 11 Auckland research groups have already secured research grant funding for external bioinformatics assistance during the next three years. In addition, 14 other groups have already applied for or intend to apply for funding for external bioinformatics assistance in the next three years. In many cases this assistance is most appropriately provided through collaborations with other research groups. However, for more complex tasks the Bioinformatics Institute may be best placed to provide help. We recommend that while the Bioinformatics Institute endeavour to provide researchers with small amounts of bioinformatics assistance free of charge, it should encourage research groups to include funding for any substantial blocks of bioinformatics assistance in research grant budgets. In addition to assuring assessment committees that the bioinformatics component of the work will be carried out to a high standard, the early involvement of bioinformaticans provides an opportunity to give expert input into research design, which is likely to reduce later problems.

(x) We recommend that the University of Auckland and the Bioinformatics Institute take a leadership role in developing collaborative activities and structures across the New Zealand bioinformatics community. While a national bioinformatics infrastructure is being developed, it may be prudent for Auckland to retain full bioinformatics capabilities and slowly merge these into national collaborative structures as they begin to function effectively.

(xi) We recommend that the Bioinformatics Institute set as one of its goals encouraging bioinformatics integration across the university, by arranging seminars and symposia, and by facilitating collaborative research projects.

(xii) We suggest that Auckland needs to recruit two additional bioinformaticians, one at least research fellow or lecturer level, and one at research assistant level. These staff should have a special focus on developing capabilities in next generation sequencing (NGS) data analysis and in integrative biology.

Description of the symposium

On the 3rd May 2010 the Bioinformatics Institute hosted a one-day symposium in the Owen G Glenn Building at the University of Auckland. 108 participants from around New Zealand attended the symposium including: University academics, Crown Research Institute (CRI) scientists, commercial scientists, and science administrators. The goal of this symposium was to identify the direction of bioinformatics worldwide and in New Zealand, and then based on this exercise, to identify the capability gaps we need to address in New Zealand. A secondary goal of this symposium was to reinforce collaboration among New Zealand’s bioinformatic leaders so they develop their field across New Zealand in a more coordinated way.

Cris Print (FMHS) opened the symposium. This was followed by a session discussing the challenges facing bioinformaticians and the end users of bioinformatics worldwide, and the role of tertiary bioinformatics education in meeting these challenges. Mark Ragan (Queensland) and John Fraser (FMHS) summarised the world bioinformatics scene and the history of bioinformatics in New Zealand. Mark Ragan described a tsunami of bioinformatics approaching New Zealand science. John Mattick (Queensland) gave examples of best-practice biomedical bioinformatics from his laboratory. Howard Ross (FoS) summarised current tertiary bioinformatics education and the role played by education in increasing bioinformatics capability.

Following this was a session discussing the impact of new genetic and computing technologies and new infrastructure developments. Liam Williams (FoS), Marcus Davy (Plant and Food), and Les McNoe (Otago) jointly chaired a panel discussion about the rapid and continuous advances in ‘omics technologies and their likely impact on NZ science. Tony Reeve (Otago) and Stan Rodger (New Zealand Genomics Limited; NZGL), then described the scientific and organisational aspects of NZGL which is set to inject significant funds into genomic and genetic analysis in New Zealand from 2011. Anette Becher (AgResearch) discussed capability gaps in New Zealand Bioinformatics and how, as a community, we could take collaborative approaches to fill them. Mark Gahegan (FoS) discussed the emerging role of eResearch and High Performance Computing in NZ, and Nick Jones (FoS) discussed the impact that BeSTGRID will have on New Zealand bioinformatics.

After a lunch break the symposium continued with a session discussing the way in which advances in computer hardware and bioinformatic methods are changing the way in which bioinformaticians address biological problems. Satoru Miyano (Tokyo) described new insights into breast cancer biology that were made possible using massively parallel supercomputers. Robert Gentleman (Seattle) discussed the features of bioinformatic tool development that lead to a tool’s successful future use and showed examples of bioinformatic research from the field of transposons. Murray Cox (Massey) discussed the need to engage with biologists and up-skill them to fill capability gaps, and Roy Storey (Plant and Food) discussed the nuts and bolts of what is required to analyse NGS data on a large scale.

The symposium ended with a session focusing on what is required to enable end users of bioinformatics to achieve academic and commercial research outputs. Rod Dunbar (FoS) gave the perspective of a biological scientist and described the need for easily useable bioinformatic tools and for communication at the level of ‘end users’ rather than ‘power users’. Jack Flanagan (FMHS) described his molecular modelling work as an example of applied bioinformatics that requires intense computation and good communication between computer scientists and biologists. Tony Merriman (Otago) described the MapNet and Virtual Institute of Statistical Genetics (VISG) initiatives that apply bioinformatics to gene mapping. Mik Black (Otago) described the GenePattern project from the Broad Institute, which is being used in New Zealand within BeSTGRID to make bioinformatic applications that previously used command line interfaces more accessible to end users who are not used to this type of interface. James Curran (FoS) then summarised the day.

We are grateful to the organising committee: Dr Jack Flanagan (Auckland), Dr Mik Black (Otago), Dr Anette Becher (AgResearch), Marcus Davy (Plant and Food), and to University of Auckland staff who assisted with the survey including: Dr Emma Marks, Pui Shan Wong, Vicky Fan, Peter Tsai and Alexandra Miliotis. We are also grateful to the following organisations who sponsored this symposium: The Faculty of Science, The School of Medical Sciences in the Faculty of Medical and Health Sciences, The Maurice Wilkins Centre for Research Excellence, Roche, Illumina, Millennium Science, Life technologies and Agilent.

Description of the survey

79 research groups responded to an anonymous web-based survey conducted in the University of Auckland during the period 7th July - 6th August 2010. The aims of this survey were to: (i) assess how much bioinformatics is currently performed as part of University of Auckland research, and (ii) to predict the future needs for bioinformatics in the University of Auckland and how they can best be met. The survey was advertised by email to staff in the Faculties of Science and Medical and Health Sciences. Participation was encouraged by an 'iPod Touch' prize randomly drawn from participant names. A pdf version of this survey is appended to this report. The survey collected information about the responding research groups, the type of bioinformatics work they have done/plan to do, and how it was/will be funded.

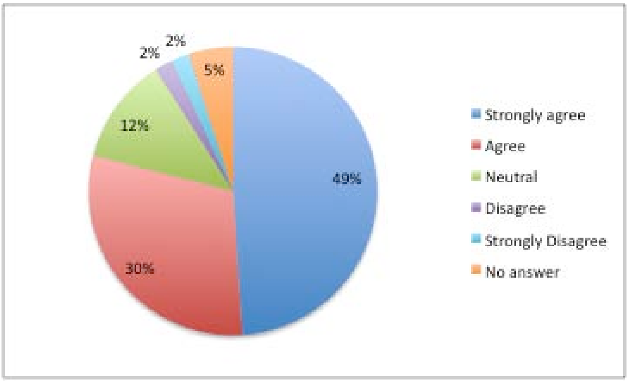
Participation was limited to principal investigators directing research projects related to biology or biological information, who answered on behalf of their research groups. The 79 research groups who responded ranged in size from one to greater than ten members, with 44% having 5 members or less. Most of the responding groups were academically funded - only 17% of the groups received more than 25% of their funding from commercial sources, and only 6% received more than 75% of their funding from commercial sources. We do not know what proportion of the population of University of Auckland research groups who use bioinformatics we managed to sample in our survey. Nevertheless, the survey is able to inform our planning by identifying the minimum numbers of groups involved in various types of bioinformatics in our university. We are grateful to Dr Deborah Wright (Department of Molecular Medicine and Pathology, University of Auckland) and Dr Rob McNeil (Survey Research Unit, University of Auckland) who collaborated in this survey.

Below we discuss the key issues that emerged from the symposium and survey:

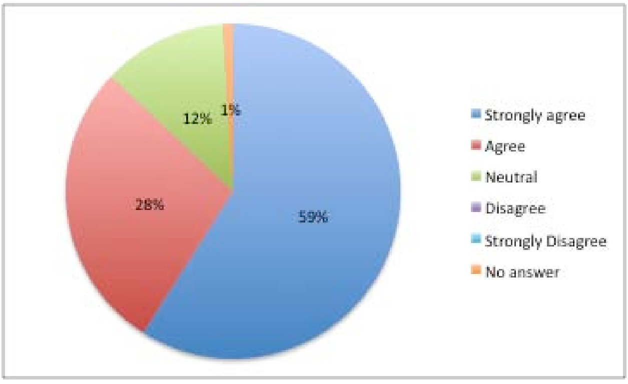
The field of bioinformatics has relatively strong support from Auckland biological science researchers

Based on the symposium and survey, it seems probable that the use of research methods involving bioinformatics may continue to grow at a moderate rate. Mark Ragan and John Mattick pointed out at the symposium that a tsunami of data is approaching bioinformaticians, and that research groups with deep bioinformatics skills in addition to traditional reductionalist experimental skills are likely to dominate their fields. To publish papers in the high impact scientific journals, investigators will increasingly need to use high content technologies in their laboratories. However, the rate and extent that this growth in bioinformatic activity occurs in New Zealand will depend on research funding.

When survey respondents were asked how strongly they agreed with the statement that; “large-scale measurement technologies (e.g. microarrays or NGS) are relevant to their research area”, 79% either agreed or strongly agreed, see below:



When asked how strongly they agreed with the statement that; “their research group will be more effective and more competitive in the future if they can use bioinformatics alongside the traditional methods used in their field”, 87% either agreed or strongly agreed, see below:



Bioinformatics work will become increasingly common within research laboratories that do not specialise in bioinformatics

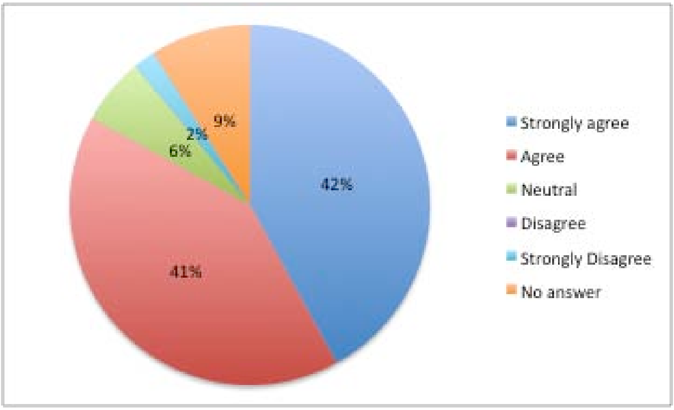
Many bioinformatics tasks that were once in the domain of expert bioinformaticians are now tasks that competent postdoctoral fellows could reasonably be expected to undertake. It is likely that the ability to perform basic bioinformatics will increasingly be part of postdoctoral fellow job descriptions in the biological sciences. This already seems to be occurring in Auckland. Of the 79 research groups that responded to our survey, 11 groups have contained, at some point in the last 3 years, a staff member with a bioinformatics degree or diploma qualification, with a further 17 groups containing a staff member with a statistics or computer science degree or diploma. 11 groups contained an individual who is confident using the “R” computing environment. A further 27 groups contained during the last 3 years a staff member who, while not formally trained in bioinformatics, has an aptitude for using computing and statistics to help solve biological problems.

Short courses and continuing education programs suitable for this last group, who are not bioinformatics specialists, are likely to become increasingly important. It is encouraging that 91% of the Auckland research group leaders who responded to the survey would be happy to send their staff on courses to allow them to gain specific bioinformatics skills, with 31 groups willing to pay up to $1,000 for each course. Research groups intending to use NGS, proteomics/metabolomics and phylogenetics in the next 3 years were especially keen on bioinformatics training; with 70%, 62% and 65% of these groups, respectively, being willing to pay up to $1,000 for training.

Recommendation*: that the Bioinformatics Institute specially targets support and training towards members of Auckland research groups who are not formally trained in bioinformatics but who have an aptitude for data analysis.* This training could be assessed and achievement of sufficient standards recognised by certificates. It could be linked with continuing education through NZGL and similar initiatives.

Bioinformatics education is likely to become an increasingly important component of undergraduate science and medical degrees

Murray Cox from Massey University spoke especially strongly at the symposium in support of up-skilling biologists in bioinformatics. The acquisition of bioinformatics skills by undergraduates may provide biologists with new research capabilities by enabling them to manipulate data and perform analyses, which hitherto were beyond either their skills or imagination. This attitude was mirrored by the survey responses. When asked how strongly they agreed with the statement that; “given recent technological developments, we now need to increase the statistics, computing and basic bioinformatics content in our postgraduate science and medical degrees”, 83% either agreed or strongly agreed, see below.



Recommendation*: As an Auckland bioinformatics community we push for undergraduate biology and medical students to routinely receive additional basic bioinformatics education including fundamentals of computing and statistics, as appropriate to their courses.*

Changes to hardware and software

Scientist-focused software that allows mainstream laboratories to perform statistically robust analysis of high content data will be important to reduce the workload of specialist bioinformaticians. Scientific hardware that produces high content data will continue to become less expensive and more common in individual university Departments. Computer hardware will also continue to advance in capability and reduce in price, even if not quite matching the increasing rate at which high content data is being produced. Along with this hardware there is likely to be a strong commercial drive to quickly produce easy to use and scientist-focused software for the basic analysis of high content data. A good example is the rapid development of the modules of the Geneious application that deal with NGS data. In parallel, the rapid development of more specialised/more cutting edge open source packages for "R" and other open source programming environments is likely to continue. To allow the use of these packages by mainstream scientists prior to commercial products incorporating their capabilities, initiatives such as GenePattern may become increasingly important. To facilitate collaborative research and access to high performance computing, programs such as BestGRID and Galaxy are likely to become more frequently used. Research journals are likely to increase their focus on reproducibility of high content data analysis by requiring researchers to provide access to their precise analysis pipelines, in addition to their data.

Specialist bioinformaticians are likely to be required in increasing numbers

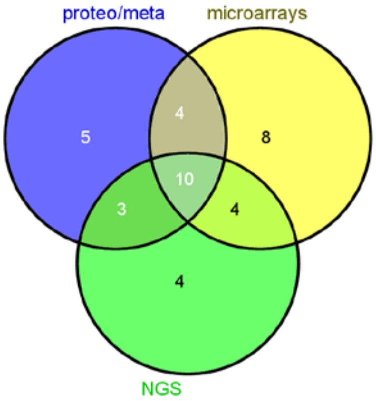
Despite the increasing level of bioinformatic capability in mainstream research laboratories, symposium participants suggested that specialist bioinformaticians are likely to be required in increasing numbers. While most of these specialists would be based in organisations like the Bioinformatics Institute or the AgResearch Bioinformatics group, several people suggested that small numbers of specialist bioinformaticians might also be embedded within individual research groups. John Mattick gave good examples of this. However, this seems unlikely to occur to a significant extent in Auckland, since over the next three years none of the 79 groups who responded to the survey intend to hire a new staff member with a bioinformatics degree or diploma, and only 3 plan to hire a staff member with a statistics or computer science degree or diploma.

The work that would be undertaken by specialist bioinformaticians may include:

Research projects outside the mainstream or at the cutting edge - although commercial biologist-focused bioinformatic tools are being developed rapidly to handle common analysis tasks, there is little commercial imperative to develop bespoke tools for unusual projects. This is likely to remain the purview of specialist bioinformaticians who can program effectively and use confidently use command line applications, scripting, local databases and open source tools. In addition, the analysis of especially large projects may only be doable by specialist bioinformaticians who have the facilities and skills to access grid or cloud computing.

Integrative biology – systems-level analysis in which various types of 'omic data are statistically combined; often with phenotype data (including high content imaging data), are likely to have an increasing impact on biological research. This is a technically difficult field, requiring expertise that is often beyond the capabilities of biological research groups. For example, specialist bioinformaticians/statisticians are sometimes required to estimate/control the false discovery rate of the *in silico* models that are produced by this analysis. Currently in New Zealand we know of at least five research groups taking genuine systems-level approaches to biological questions.

Interestingly, the survey revealed several groups that intend to use a combination of technologies in the next three years (see Venn diagram below), raising the prospect of more research in Auckland where the results from different technologies are combined at a 'systems' level.



A lot of integrative biology work involves the use of systems biology databases. Many research groups now use these databases to review the high content data they have produced on a regular basis, getting more value from their data each time. The expensive commercial systems biology databases appear to be gaining ascendency over their freely available competitors, and can give research groups a competitive advantage. Our survey suggested that 30 Auckland researcher groups would be willing to pay for access to this resource; 13 groups would pay up to $250/yr, 15 groups would pay up to $1,000/yr and 2 groups would be prepared to pay up to $2,500 a year for access.

***Recommendation**: that the Bioinformatics Institute investigates purchasing a license for an integrative biology application for the use of Auckland researchers who contribute to the cost.*

'Liaison' roles – some research groups have recruited a full- or part-time specialist bioinformatician who becomes embedded in the group. John Mattick provided good examples of this, and we know of at least three research groups in New Zealand who have taken this approach. This is likely to become increasingly common, as research groups require a bioinformatician to act as a 'translator' who can liaise with expert computer scientists and statisticians. In addition, these embedded bioinformaticians often support a research groups' experimental design, data analysis and databasing activities. Anecdotally, it seems that once a research group has access to an embedded bioinformatician a positive feedback cycle begins, where more experiments are proposed that require this person's expertise, leading to a stronger need for this person in the group.

Education – if we are correct in predicting an increased need for mainstream scientists to learn bioinformatics, as well as an increased need for specialist bioinformaticians, then specialist bioinformaticians will be needed to provide training and continuing professional development for both of these groups.

Bioinformaticians will be required to help groups in the Institute for Innovation in Biotechnology (IIB) within the Faculty of Science. Several New Zealand biotechnology companies employ bioinformaticians (e.g. Pacific Edge Biotechnology, ViaLactia, Livestock Improvement Corporation). There also appears to be a demand from outside the University for specialist bioinformatics consultants who can work on a project-by-project basis. Performing external consulting work for external companies would be in line with the Strategic Plans of the University and the Faculties. This may benefit the Bioinformatics Institute by growing its skills and knowhow and by providing an additional revenue stream. In addition, discussion with potential clients suggests that a significant proportion of external consulting work has the possibility of academic publications.

Recommendation*: that the Bioinformatics Institute should discuss a framework for external consulting work with Uniservices, after which its management group could establish a policy around this.*

How should we train specialist bioinformaticians in New Zealand?

Undergraduate education: The University of Auckland runs an undergraduate bioinformatics specialisation in which students train in biological sciences, maths, statistics and computer science (see http://www.bioinformatics.auckland.ac.nz/studying.php and also http://www.science.auckland.ac.nz/uoa/of-bioinformatics). This well rounded undergraduate bioinformatics specialisation is designed to train future academic leaders in bioinformatics (in addition to vocational bioinformaticians). The concept of such a solid grounding in the sciences that underlie bioinformatics is very attractive and is something that few other universities offer. However, current enrolments are low, and Howard Ross pointed out that Auckland's undergraduate specialisation in Bioinformatics requires an early and protracted commitment to a subject that few students understood early in their university studies. Some students also appear to 'drop out' during the course as their interests change, or as they find that they do not achieve equally well in all of the courses this specialisation prescribes. These points have resulted in difficulty in recruiting students and subsequently retaining them.

Recommendation*: that the Bioinformatics Institute should discuss with the Faculty of Science whether the current undergraduate specialisation should be continued, or whether it is wise to now replace it with revised 300-level courses and an expanded postgraduate program. When doing this, it may be helpful to duplicate two of our current 700-level bioinformactics courses as 300-level courses.*

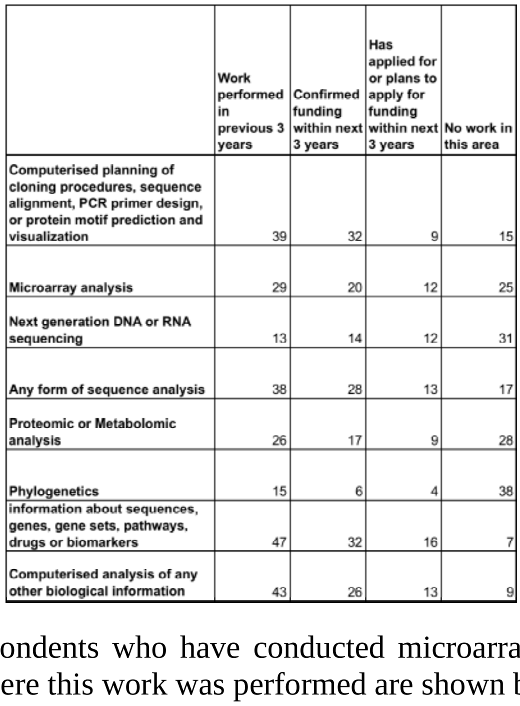
Postgraduate education: Currently, Auckland's BSc(Hons), PGDipSci and MSc in Bioinformatics primarily serve students from Auckland's BSc (Bioinfomatics) course (see above) or equivalent programmes, which restricts student numbers. The possibility was discussed of additional postgraduate bioinformatics teaching, where individuals with a prior degree in one of the constituent sciences were cross-trained in a graduate bioinformatics program. There was no consensus regarding from where such students should be recruited, whether from the life or computational sciences; successful examples from both sources were mentioned. It is possible that a broadened postgraduate course could either supplement or replace Auckland's undergraduate bioinformatics course to increase the numbers of vocational bioinformaticians we train. One aspect of this may be a duplication of two of our current 300-level bioinformactics courses as 700-level courses.

Recommendation*: Based on these points, we recommend discussion with the Faculty of Science about whether the postgraduate education of specialist bioinformaticians in Auckland is sufficiently flexible with sufficient alternative educational pathways.* Flexible pathways could provide opportunities for students from diverse backgrounds to enter bioinformatics provided they had sufficient prerequisite skills. Bridging/retrofitting programs may be required to provide these prerequisite skills.

It was recognised that New Zealand institutions are sufficiently small that each will lack teaching staff with expertise in many important domains, as for example in NGS. For bioinformatic courses to cover a reasonable amount of the field, the expertise held within the country would have to be pooled through collaboration among institutions. Anette Becher’s proposal to establish a virtual bioinformatics institute, through which teaching could be shared, is in line with these educational needs. The most promising vehicle for new educational opportunities discussed during the symposium was NZGL. However, given that the NZGL will be focused on genomics, it may contribute to the sharing of expertise and training opportunities, but is unlikely to be the sole agency. The possibility of industry-based internships as an important aspect of education was also identified.

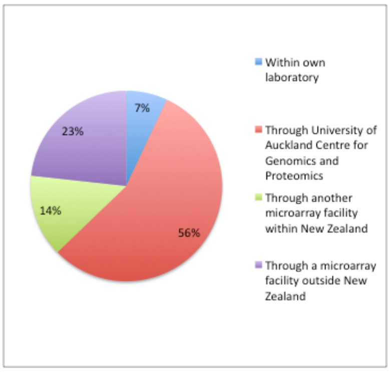
How much bioinformatics activity has there been in the last 3 years in the University of Auckland?

The survey identified how many groups have conducted/are planning to conduct the types of research for which bioinformatic assistance is required. Please see the table below, which shows research activities in rows and time/funding information in columns.



	Work performed in previous 3 years	Confirmed funding within next 3 years	Has applied for or plans to apply for funding within next 3 years	No work in this area
Computerised planning of cloning procedures, sequence alignment, PCR primer design, or protein motif prediction and visualization	39	32	9	15
Microarray analysis	29	20	12	25
Next generation DNA or RNA sequencing	13	14	12	31
Any form of sequence analysis	38	28	13	17
Proteomic or Metabolomic analysis	26	17	9	28
Phylogenetics	15	6	4	38
information about sequences, genes, gene sets, pathways, drugs or biomarkers	47	32	16	7
Computerised analysis of any other biological information	43	26	13	9

For the 43 survey respondents who have conducted microarray analysis in the last three years, the sites where this work was performed are shown below:



How do University of Auckland research groups view their bioinformatics expertise?

For microarray analysis specifically, only 2 research groups believed they have sufficient skill within their group to get full value from their microarray data without external assistance. 14 groups could perform basic analysis of microarray data but required assistance to get full value from this data, and a further 15 groups required help from outside their group for most aspects of microarray data analysis.

For NGS, 21 research groups knew enough about NGS to identify the advantages and disadvantages of the different sequencing technologies, and 6 research groups already have experience analysing NGS data. However, only one group felt they had sufficient skill to get full value from their sequencing data without external assistance. 15 groups could perform basic analysis of sequencing data but required assistance to get full value from the data, and 7 groups need help from outside their group for most aspects of NGS data analysis.

In the last three years, how often have Auckland research groups required bioinformatics help from *outside* their group, and what type of help was required?

During the last 3 years, 52 of the 79 research groups that responded to the survey had obtained assistance from outside their groups for the analysis of biological data. 32% of these groups had sought assistance for analysis of relatively simple data sets (with less than 20 variables and less than 100 measurements of each variable), 27% for analysis of larger or more complex data sets, and 34% for complex bioinformatics tasks such as the use of specialist computerised analysis tools or specialised computer hardware or the generation and use of databases.

Where did Auckland research groups obtain their bioinformatics assistance from?

42% of the research groups who responded to the survey had sought informal help from a colleague based in another Auckland group, 41% had sought formal assistance from a recognised statistician or bioinformatician within Auckland University, and 25% had obtained help from a recognised statistician or bioinformatician outside Auckland. Of those who sought assistance outside the University of Auckland, 43% went to other New Zealand universities, 21% found assistance in NZ but not in universities (anecdotally these people used the services provided by CRIs and by NZ’s small number of private bioinformatic contractors), and 36% found assistance overseas.

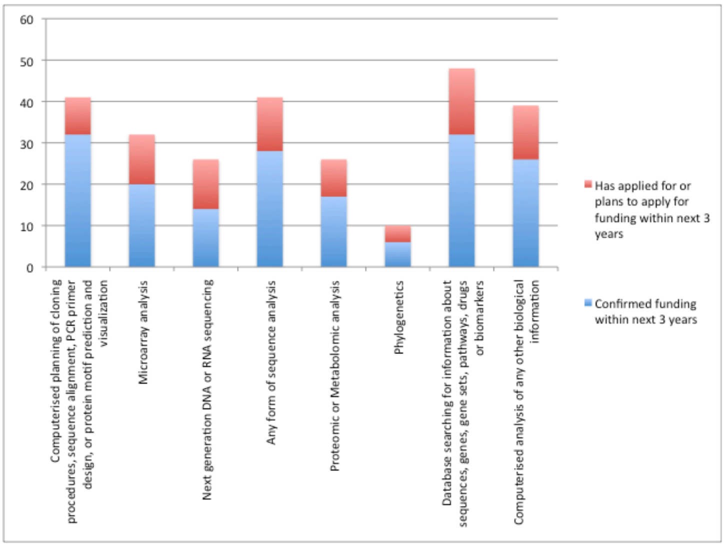
Was this bioinformatics assistance paid for, and if so from what source?

Of the 52 research groups who received bioinformatics assistance from outside their group in the last 3 years, only 43% fully or partially funded the assistance they received. Within this 43%, only 68% (15 groups) had obtained this funding by explicitly including these costs in a research grant application.

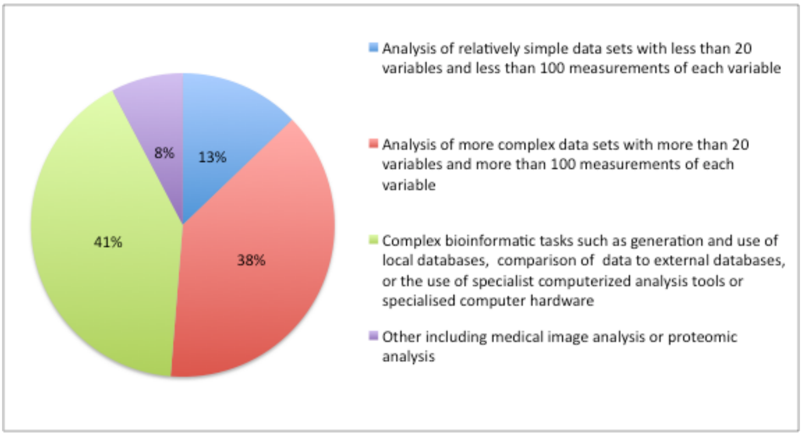
***Recommendation**: While the Bioinformatics Institute will endeavour to provide researchers with small amounts of bioinformatics assistance free of charge, it should encourage research groups to include funding for any substantial blocks of bioinformatics assistance in research grant budgets.* In addition to reassuring assessment committees that the bioinformatics component of the work will be carried out well, this provides an opportunity for expert input at the time of research design.

How much bioinformatics activity is there likely to be in the next three years in the University of Auckland, and what type? Information from the survey:

The survey respondents have planned various types of future research that is likely to require bioinformatic analysis, see the graph below. The y-axis represents the number of groups with projects in each category (note that some groups plan to undertake research in several categories).



11 research groups who responding to the survey have already secured funding that specifically included bioinformatic analysis *to be conducted outside their group* during the next three years. In addition, 14 other groups have applied for, or intend to apply for, funding to support bioinformatic analysis to be conducted outside their group in the next 3 years. The type of external assistance these 25 groups will require is broken down below.



Should Auckland recruit additional bioinformaticians?

Based on the symposium discussions and the survey responses, we believe the answer to this question clearly "yes". As detailed above, Auckland research groups appear to be planning significant work in the next three years, which will require bioinformatics to achieve the expected research outputs. In addition, we need specialist bioinformaticians to be involved in training of non-specialist researchers and undergraduates. Currently we have limited bioinformatics capabilities, especially in the NGS and integrative biology fields. For example, the survey indicated that of the 26 groups that plan microarray analysis in the next three years, 19 have performed microarray analysis in the previous three years. However, this is not the case for NGS; of the 21 groups planning NGS research in the next three years, only 8 have performed this type of work in the previous three years. There is potentially funding available for new Auckland positions from NZGL and other sources. Due to NZGL and other infrastructure projects planned within New Zealand in 2010-2011, several institutions may simultaneously be recruiting specialist bioinformaticians. The organisations that advertise first may have a significant recruitment advantage.

Recommendation*: that the University of Auckland seeks funding to advertise at least two new bioinformatics positions, one at research fellow or lecturer level and one at research assistant level, before the end of 2010*. This would allow us to try to recruit good bioinformaticians who will be obvious targets for other organisations in 2011.

Recommendation*: That when recruiting new academic staff we target researchers with a focus on the use of NGS data.*

A coordinated approach to bioinformatics

Several symposium participants hoped that a coordinated national approach to bioinformatics would be possible. Mik Black pointed out the financial incentives for achieving this. BestGRID and VISG provide examples of national initiatives involving bioinformatics, and individual research consortia such as Nutrogenomics and AgResearch have conducted successful national bioinformatic programs. Anette Becher suggested an attractive plan of a national virtual bioinformatics institute over and above the NZGL bioinformatics program.

***Recommendation**: That the University of Auckland and the Bioinformatics Institute takes a leadership role in developing collaborative activities and structures across the New Zealand bioinformatics community.*

However, John Mattick and others with experience of national bioinformatics initiatives in Australia warned that national virtual institutes can degrade into local groups. In addition, for a truly national initiative many issues such as how confidentiality and intellectual property are handled and how lines of management are developed remain to be worked through. In addition, it appears especially important to have bioinformaticians sited near the biologists they collaborate with.

***Recommendation**: While a national bioinformatics infrastructure is being developed, it may be prudent for individual centres such as Auckland to retain full bioinformatics capabilities and slowly merge these into national collaborative structures as they begin to function effectively*.

In additional, a regional weakness in Auckland bioinformatics appears to be a relative lack of integration and coordination. Numerous initiatives are currently being developed in Auckland that involve bioinformatics with relatively little connection between them. As an example of this, in 2010 three separate initiatives have been started involving systems biology, all unconnected with one another. Another area where additional coordination could be useful is in the activities of the Faculty of Science’s statistics consulting services, the Bioinformatics institute and the Faculty of Medical and Health Sciences biostatistics group.

***Recommendation**: That the Bioinformatics Institute has as one of its goals successfully arranging seminars or symposia and initiating research projects that encourage integration across the university.*

Conclusion

Bioinformatics is likely to become increasingly crucial for the biological sciences. The University of Auckland may be putting research outputs at risk if it relies purely on the unstructured activities of individual research groups and external infrastructure-building schemes to provide bioinformatics capability for Auckland. Instead, based on the needs analysed above, we need to carefully plan Auckland’s bioinformatics capability in collaboration with other organisations. Alongside these plans, we need to ensure that Auckland remains strong in academic bioinformatics and expands its cohort of PBRF-eligible bioinformatics researchers and teachers.