

Te Whare Wananga o Otago



Centre for Gene Research

NEWSLETTER

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Centre for Gene Research News

A note from the lame duck Director

As many of you will now know, I shall be leaving the University of Otago at the end of October to join Ag-Research in Hamilton. This has meant that I also needed to resign from the position of Director for the Centre for Gene Research and accordingly I submitted my resignation to take effect from the end of July. Whilst this has been accepted and a nomination for a new Director has been made, that person has not yet been appointed and indeed is not currently in the country. Those of you who receive the Medical School Newsletter will know that Jim Kalmakoff is the person nominated by the Dean of the School of Medical Sciences to the AVC and ultimately to the Council of the University. If Jim's experience is like mine was, he will learn of his appointment sometime round December! Whatever, I am delighted that Jim has agreed to take the position on. He is currently on leave but will be back in Dunedin round the middle of September, at which stage I will be pleased to pass filing cabinets, computer files etc on to him.

I have thoroughly enjoyed working with the Centre over the last three years and I think the success of the Centre lies in the loose structure we have, the willingness of those on our committee to be involved in the activities of the Centre and the quality of the staff we currently have in our DNA sequencer facility. I think the meetings or workshops that we now are holding annually are exciting and of a very high quality. The meeting on Ion Channels and Membrane Transporters we held in conjunction with the Otago Medical School Research Society last month was as good as one might expect to find anywhere in the world on this topic. The poster nights we have in November also demonstrate the quality of the work being done on this campus.

I need to thank two people particularly. Allan Crawford in his role as "technical advisor" for the DNA sequencer has worked hard to ensure that the quality of the service offered is excellent and that the equipment the kept up to date. Allan works well with Tracee and Janet who run the service on a day to day basis. Last year we sequenced close on 5000 templates and, while most of the customers come from within the Centre, others are as far away as Auckland. With the change in Director, it is expected that the sequencer facility will, however, remain based in the Department of Biochemistry and I am

sure the service provided will continue to be at its current high standard. Craig Marshall also has assisted greatly as Editor for this Newsletter over the last 4 or 5 issues. Anyone who gets involved with preparing Newsletters like this soon learns of the amount of work that is required to keep them going. Nevertheless, the positive comments that we have received about the Newsletter have made its preparation worthwhile. However, to be really effective, items from the membership are essential to keep the newsletter topical and interesting. These can be technical tips, meeting reports, reviews of interesting papers people have found etc. I hope that I can be added to the mailing list when I move to my new position.

Last year Gene Structure and Function was identified as a major research theme of the University. In the 8 months to August this year, there have been few developments that I am aware of with respect to this. I do not know just how the University plans to develop these themes but it appears to me essential that University must maintain its support for this area, which is a real strength at Otago. The only other matter of note for members of the Centre is that in conjunction with the Department of Biochemistry an application has been forwarded to the University for consideration for a Wellcome grant that, if funded, will enable a replacement sequencer to be purchased within the next year or so.

Happy gene researching,

Murray Grigor grigor@sanger.otago.ac.nz *********

Sequencer News

We have had considerable positive feed back recently regarding the quality of the sequencing data that our customers have been receiving. This is very gratifying but it is clearly still more important that we hear about problems so that the service can continually be upgraded.

Not only is quality important but we know that everyone wants their results yesterday. Over the last three months the average time taken from receiving the template to posting the results on the network is between 3 and 4 days. If you bring a template in on day 1 the sequencing reactions will be done on the second day and the samples run overnight. The results will therefore be available (after processing which

takes an hour or two) on day 3.

You should expect, on the majority of occasions, to get your sequence placed on the network 3 working days after bringing down the sample. The mail takes another day to get the printed chromatogram to you. Occasionally we have breakdowns, Tracee or Janet are sick, or a whole load of templates arrive at the same time, so it takes a day or two longer but this should be the exception rather than the rule.

The most crucial parameter determining the quality of the sequence obtained from the ABI373 is the template. Over the years a number of different methods have been suggested by us and others. To determine what the current "fashions" were and to see if there was some consensus developing as to the best method I asked a most of the local groups regularly using the sequencing service what their current method of template preparation was. The results are as follows

- Promega 373 Wizard Kit
 This is used by 4 groups (some in AgResearch, Virus Research, Clive Ronson and Warren Tate's group).
- ABI's recommended PEG method
 Used by 3 groups (some in AgResearch, Russell Poulter, 3rd floor Plant Group).
- Electroelution from Agarose Charles (Clive Trotman's group)
- Method of Stephen et al. Nucleic Acids Research 18: 7463
 George Petersen's Group (This group has got excellent sequence from templates stored for as long as 5 years in the freezer)
- Martin Kennedy is still getting excellent sequence of PCR products using the method described in a previous newsletter.

Recommendation: While there is clearly no consensus I would recommend starting out with either of the two most popular methods. The Wizard Kit is quicker but likely to be more expensive than the PEG method.

Allan Crawford

********** Women In Science Conference

"Science - Women and our Future", Plaza hotel, Wellington, May 29 - 31 1996.

Nearly 400 women from throughout the range of scientific disciplines in New Zealand came together for a celebration of the way in which women are being part of science. We were all made absolutely, positively welcome!

The keynote individual speakers, Dell Whihongi from the Pu Hao Rangi Trust, Kathleen Lennon from the Department of Philosophy, University of Hull and Dale Spender from Australia, challenged and inspired. As one keynote speaker was unwell, a panel of

women in science (including Diana Hill from Otago) spoke at a few hours notice of their visions and concerns for the future of science in New Zealand. This created lively and intense debate and was one of the highlights of the conference.

Topics offered for workshops and parallel sessions ranged from "Making equity progress through strategic planning methods" to "Women in Africa: a visiting Kiwi Scientist's impressions", from "Assessing Science Learning" to "She who bleeds but does not die", from "Switching-on the Innovators of tomorrow" to "Gender and Science and Technology: and international Overview", from "Genetic research: the ethics of choosing metaphors" to "The 'Yes' trap" and many, many more. The choices were so diverse for small group listening, learning and participation, that one needed to be in several different places at once.

What a wonderful conference we had! Yet how difficult to capture its essence for people who were unable to go. The mere recital of all that went on does not convey the essence, joy or true value of this conference. The meeting and greeting of old friends and the making of new friends was part of it. The atmosphere of acceptance. Everyone who came had an opportunity to be heard, to express opinions, share knowledge and wisdom, ask questions, in confidence of justice and equality. This was a conference about doing science, about being in science and how we are achieving success for the commitment and vitality that we bring to science.

Lyn Dowsett

*********** The 1996 GCG Course

This year's GCG course proved to be a very successful follow on from last year's initial offer by the Centre for Gene Research. The course had not been advertised for one week before we were fully booked and the applications kept coming in. Not only did people associated with the University of Otago wish to attend, but even people from as far away as Massey University and Forest Research Institute, Rotorua signed up. In the end, 39 people applied for the 23 positions that we had available.

We started in on Monday morning covering configuration of a Macintosh computer to act as a terminal into one of our more powerful UNIX-based computers: sanger or biochem. Then, we began a rather intense session on the effective use of the UNIX operating system. The class rapidly mastered the easy commands, but many were grateful to move on from tildes, pipelines and 'grep' to the somewhat easier introduction of GCG programs and graphics. By the end of the day, everyone had mastered the basics and could manipulate graphical plots with skill.

Tuesday saw the class arriving early and starting in at the terminals with great vigour. We now began the more biological aspects of GCG: retrieving sequences and editing them to create new sequences. A very clear explanation by Peter Stockwell, taught most of us the theoretical basis of Blast and FASTA searches plus how to run the programs.

On Wednesday and Thursday, either the class understood more or the exercises had become easier. The atmosphere in the class was electric as we practised techniques for multiple sequence alignment and editing, fragment/contig assembly, translation of DNA sequence into peptide sequence, backtranslation, protein analysis and PCR primer design.

The last day, Friday, came as a bit of a "bad hair day". The projector blew a bulb, computer services didn't have the machines correctly configured for our exercises and someone managed to unplug one of the main computers, bringing half of our terminal sessions to an abrupt end. I was fuming at the problems as I raced along to finish up the lectures; next we had a fire alarm. Fifteen minutes later, with everyone back in class, trying to run the GCG point-and-click interface, WPI, we again managed to crash the computer when everyone pressed their "RUN" button at the same time. The demonstration of WPI ended up as an example how many things can go wrong when 20 people try what one has done before. Still, most people did learn how to run WPI which was the goal of the exercise; in addition, they learned a great deal about how a large computer behaves when it is overloaded.

My biased perspective on the course prevents me from reporting that everyone learned how to use the GCG collection of programs, however, the questions I received indicated a good understanding of the material covered. And there were a large number of smiling people at the end of the course - whether because the course was finally over, or because they had enjoyed themselves, I couldn't actually say.

Mark Dalphin

Participants Comments

The UNIX operating system and GCG (a suite of programmes for manipulating molecular data) are difficult for the uninitiated to use. With a good manual and logical structure to the 'Sequence analysis using GCG' course, Mark and Peter provided a substantial introducing these packages.

As with most computer programmes, greater understanding comes not from watching someone else but by having a go yourself. Ample time was set aside to work individually on exercises while Mark and Peter provided backup. This pair proved able tutors, no doubt spurred on by the thought that the acquisition of knowledge by participants during the course would reduce questions in the future.

I'm sure most participants would agree that the learning was intensive – we all looked forward to 11am (chocolate biscuits and coffee) and 1pm (the end of the session) – but I came away feeling that I could tackle data manipulation more efficiently than my

previous limited efforts. Of course the proof of this will come when I attempt my own data analysis without help immediately to hand.

Thanks Mark and Peter for a useful, well organised course.

Jamie Day

Computer Corner

This weeks computer corner looks at the World Wide Web again and suggests a few URL that might be interesting.

A number of new features have been added to the search engines at BCM. These are excellent places to look at your new sequences and contain links to other sequence databases, text databases including Medline and Entrez, related sequences, and sequences from related organisms. As well as homology searches, this site contains multiple sequence alignment tools, secondary structure prediction software (for what they are worth) and links to a number of databases including a YAC data search. The URL for this site is:

http://kiwi.imgen.bcm.tmc.edu:8088/search-launcher/launcher.html

Netscape 3 has now been released and more and more sites are now expecting visitors to a site to be using this browser. The new version of Netscape should be available from CWIS fairly soon, but beware, Netscape 3 takes even more memory and disk space than Netscape ever did before. Netscape 4, which is supposed to be smaller and faster, is likely to be released soon so you may prefer to wait. I have to admit that all the bells-and-whistles of Netscape 3 are fun when you download a page with images, sounds, movies and animation, but there is a price to pay in terms of computer resources.

The web site of the month is Science "Life on Mars" which can be found at:

http://www.eurekalert.org/E-lert/current/public_releases/mars/Prerelease.htm

The full text of the Science article can be found there, as well as a number of comments from several of perspectives. Look, learn and make up your own mind. Personally I think Ray Bradbury was right.

Craig Marshall