James Rennie Bequest Conference Report

O'Reilly Bioinformatics Technology Conference

January 28-31, 2002
Tucson, Arizona, USA

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Bioinformatics Overview

One of the main reasons for me attending this conference was to give me an overview of the bioinformatics. The conference was also useful as it gave speakers the chance to give their own insights into how the bioinformatics field will develop in the future and highlight new areas of bioinformatics, which will emerge in the near future. A broad range of topics were covered during the conference including:

- Computer Language choice / usage
- Prediction techniques
- Internet usage in bioinformatics
- Algorithm development
- Open source Vs Profiting from your software
- Database creation and maintenance
- Web site creation and maintenance
- Computer hardware considerations
- Medical applications of bioinformatics
- Document management

Meeting People

The conference gave me a chance to meet people from all the different fields incorporated in bioinformatics (i.e. computer scientists, biologists, chemists, pharmacologists, medical doctors & bioinformaticians) and from both academia and industry. Due to the different fields in bioinformatics there are great cultural divides between the fields. These differences include the literature, techniques and fundamental principals. For example biologists tend to hold back publishing work until they have got the work as near to perfect as possible. Where as computer scientists publish as often as possible regardless of whether the content is 100% viable as the reason for publishing is to put out ideas in to the computer science community. The conference was excellent in resolving communication barriers between the biologists and the computer scientists. One of the benefits of bringing people together from bioinformatics at conferences such as this is the development of a common language to allow biologists and computer scientists to communicate as easily as possible with minimal confusion.

Software

The conference provided the opportunity to find out benefits and pitfalls of marketing bioinformatics software to make a profit or making the software open source. This kind of discussion could help me decide what to do with my software at the end of my project. There are lots of opportunities for marketing software products for a profit, but this had limited benefit for the bioinformatics community. The current trend is for open source software, which has benefits outreaching the original scope of the software. People were also given the opportunity to talk about software that isn't mentioned in the scientific literature such as the BioPerl project and the new Apple Operating system OSX (developed with the bioinformatics community in mind). Software available was also discussed in terms of the next development steps, new features and the best ways to use the software to achieve the desired results.

Poster Session

Provided me with an opportunity to present and discuss my work at an international poster session attended by fellow PhD students and bioinformatics experts from both industry and academic backgrounds. During the conference I presented a poster entitled "Enzyme Function Prediction from Multiple Sequence Alignments", which covers my PhD work. I found the poster session invaluable in learning how to present my work to different target audiences. I had to be aware that my audience varied from molecular biologists to computer scientists.

Parsing in Perl for Bioinformatics Tutorial

This tutorial was given by Damian Conway, who is a lecturer in computer science and a significant contributor to the BioPerl project. The full day tutorial was aimed at Perl programmers wanting to improve their parsing techniques. This topic isn't extensively covered in textbooks so the tutorial provided and excellent opportunity to develop my Perl programming techniques. I found it especially useful to see how an expert would approach a parsing problem by going through some common bioinformatics parsing problems. The tutorial also gave me a chance to discuss the content with the other tutorial attendees.

Career Opportunities

I found out what the current trends are in bioinformatics and where the likely job vacancies will be emerge and be advertised. I also had the chance to meet potential employers in both academia (Post-doctoral work) and industry (permanent employment). I would like to continue my career in bioinformatics by taking a post-doctoral position possibly abroad (USA, Canada or Australia).