

Bioinformatics Mini-Symposium at the University of Dundee

Thursday 8th September 2011, Dalhousie Lecture Theatre 1

This meeting should appeal to anyone who is analysing biological data, particularly from high-throughput methods such as DNA sequencing or developing methods to extract knowledge from large data collections. The meeting presents a rare opportunity to hear an international spectrum of speakers who have all made important contributions to the field of bioinformatics.

Come and hear **Dr Michele Clamp** who during her time at the **Wellcome Trust Sanger Institute** was the chief architect of the Ensembl genome analysis pipeline and has worked since at the **Broad Institute at MIT/Harvard** and is now at **Bioteam, Boston, USA**. Michele is an authority on large-scale genome analysis. **Dr Toby Gibson** from the **European Molecular Biology Laboratory (EMBL) Heidelberg**, is co-author of the clustalW multiple alignment program and one of the most highly cited scientists in any field. He is an expert on biological sequence and pathway analysis. **Dr Mike Gribskov** of **Purdue University, USA**, is famous for his development of early “profile” sequence database search methods. He is a former president of the International Society of Computational Biology (ISCB) and remains an authority on the application of computational methods in biology.

High Performance Computing and storage underpins modern biology, whether it is to store prodigious amounts of data or carry out calculations across it, so we are pleased that **Dr James Cuff** who is director of research computing at **Harvard University Faculty of Arts and Sciences USA** will also be speaking at the meeting. James is a world authority on high performance computing for scientific research. After creating the high performance computing infrastructure for the Ensembl project at the **Wellcome Trust Sanger Institute**, James moved to the **Broad Institute at MIT/Harvard** and then to his current position at Harvard where he is responsible for one of the largest research computing systems in the world.

As well as these international speakers, we will have talks from four speakers closer to home. **Dr Daniel Rigden** is senior lecturer in post-genomics bioinformatics at the **University of Liverpool**. His interests focus on protein sequence/structure analysis and the study of evolution. **Dr Jim Procter** from the **University of Dundee** is the main developer and co-ordinator of the popular Jalview multiple sequence alignment workbench and will be giving an update on the new developments to that tool while **Prof. Geoff Barton**, also from **Dundee** will describe some his group’s other work in bioinformatics technique development and applications to high-throughput sequencing. Last but not least, we are delighted that **Prof. Richard Baldock** of the **MRC-Human Genetics Unit** will be able to speak about his experiences in large scale image analysis on the mouse atlas.

There will be ample time over a buffet lunch and coffee/tea breaks to meet the speakers. The registration fee covers the cost of lunch and all refreshments.