

## **Bioinformatics Mini-Symposium at the University of Dundee**

*Thursday 30<sup>th</sup> May 2019,*

*School of Life Sciences Building*

*Old Hawkhill*

*Dundee*

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 international speakers who have all made important contributions to the field of bioinformatics.

Come and hear **Dr Toby Gibson** from the **European Molecular Biology Laboratory (EMBL) Heidelberg, Germany** who is co-author of the Clustal family of multiple alignment programs and one of the most highly cited scientists in any field. He is an expert on biological sequence, motif 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.

As well as these international speakers, we will have talks from speakers across the UK. **Prof. Daniel Rigden** is based in the **Institute of Integrative Biology** at the **University of Liverpool**, his interests focus on protein sequence/structure analysis and the study of evolution. **Prof Christine Orengo** is a world authority on protein structure classification, evolution and bioinformatics, she leads the **CATH/Gene3D** protein domain database at **University College London** while **Dr Alex Bateman** is head of Protein and Protein Family Services at **EMBL-EBI, Cambridge**. He oversees key resources such as **UniProt, Pfam and Interpro**.

From **Dundee**, we will hear talks from **Dr Gabriele Schweikert** who is a Principal Investigator in Computational Biology at the **School of Life Sciences, Dundee** with a joint appointment in machine learning at the **University of Tübingen**, Cyber Valley Institute, Germany. Her research applies **machine-learning techniques to understanding epigenetics**. **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 work that brings together human population genetics with protein evolution and structure

There will be ample time over a buffet lunch and coffee/tea breaks to meet the speakers. Although unable to speak this year, we will also be joined by **Dr Michele Clamp** who during her time at the **Wellcome Trust Sanger Institute** was the chief architect of the **Ensembl genome analysis pipeline**. More recently, she was **Director of Informatics at Harvard University** and is now co-founder of consultancy firm **Witnix**. Michele is an authority on informatics and large-scale genome analysis.

The registration fee covers the cost of lunch and all refreshments.