SORS: Network-based analyses of transcriptomics data: new approaches to define cell signatures from tissue data

Objectives

To access the presentation please click here

Abstract: Biological data continues to grow in size and complexity, and at the forefront of this growth has been data generated by transcriptomics analysis platforms. Microarrays and RNA-seq have now generated a vast amount of expression data but its analysis and interpretation remains a significant challenge.

For the past decade we have been exploring the use of networks to visualise, explore and interpret the transcriptional landscape of tissues and cells. Our approach has been to turn such data into gene correlation networks, where the enormous size and complexity of the graphs generated has necessitated the development of new tools to support these analyses. Recently, we have been building a new analysis platform called Graphia. This is faster, more scalable (1,000,000s of data points), includes dynamic rendering and a very much extended range of new functionality for network analysis of many data types.

We have been using these analysis platforms to analyse large collections of transcriptomics data, such as the GTEx resource, to define expression modules associated with pathways and cell types, and through such analyses better understand the altered transcriptional landscape associated with disease.

Short bio: Prof. Tom Freeman has a long history of working in the field of functional genomics and systems biology. As head of the Gene Expression Group, Sanger Institute he  developed, refined and used of a variety of contemporary expression analysis techniques for gene discovery and expression profiling, being one of the first in the UK to establish microarray technology in his lab. In 2000 he joined the HGMP-Resource Centre where he headed the newly formed UK National Microarray Programme funded by the MRC and BBSRC. As well as providing resources for the UK community, the group also had an active research programme particularly around technology development and data analysis.

Tom joined the University of Edinburgh in 2006 where his work has focused on exploring immune the

system in health and disease, particularly with respect to the macrophage. He currently holds the chair of Systems Immunology at The Roslin Institute where his group work on a number of projects analysing immune expression signatures, and developing novel network-based approaches and tools to support the analysis of complex data.

He was an instructor on the Welcome Trust Advanced course in Functional Genomics and Systems Biology for over 20 years, and now regularly instructs on other courses and workshops. He was a founder of Fios Genomics Ltd, a company offering data analysis services now in its 10th year of operation, and in 2015 founded Kajeka Ltd, a company developing advanced visual analytics software for big data analysis in the biosciences and beyond.



Speakers

Prof. Tom Freeman, The Roslin Institute, University of Edinburgh

Barcelona Supercomputing Center - Centro Nacional de Supercomputación

---

Source URL (retrieved on *29 Mar 2024 - 11:45*): https://www.bsc.es/es/research-and-development/research-seminars/sors-network-based-analyses-transcriptomics-data-new-approaches-define-cell-signatures-tissue-data