John M. Hancock, J Comput Sci Syst Biol 2013, 6:4
http://dx.doi.org/10.4172/0974-7230.S1.004

OMICS Group Conferences
Accelerating Scientific Discovery

International Conference on
Integrative Biology Summit
August 05-07, 2013 Embassy Suites Las Vegas, NV, USA

Integrating omics data with phenotype and disease using ontologies

John M. Hancock
University of Cambridge, UK

With the explosion in genome and exome sequencing and other High Throughput Sequencing applications attention is increasingly turning to the interpretation of large volumes of sequence data in a wide variety of contexts. Key data types that need to be integrated with sequence and other omics data to make this possible are phenotype and disease data. This is becoming increasingly important with the advent of the International Mouse Phenotyping Consortium and other high-throughput phenotyping projects using model organisms. Phenotype and disease data have historically suffered from a lack of appropriate forms of data representation for computational analysis but this is changing. I will review the current and developing formalisms for representing phenotype and disease and approaches for integrating them with omics data and their use in building heterogeneous data networks.

Biography

John Hancock obtained his B.Sc. in Cell and Molecular Biology at King's College, London in 1975 and a Ph.D. from the University of Edinburgh in 1980. After postdoctoral work at the Max-Planck-Institut für molekulare Genetik in Berlin, the Genetics Department, University of Cambridge and the Research School of Biological Sciences in Canberra he was a group head in the MRC Clinical Sciences Centre at Hammersmith Hospital from 1994-2000, Reader in Computational Biology at Royal Holloway University of London from 2000-2002 and was Head of Bioinformatics at the MRC Mammalian Genetics Unit, Harwell from 2002-2011.

jh818@cam.ac.uk