

6th Bioinformatics Day on "Bioinformatics and Network Biology" October 6th 2005 in the Oxford Centre for Gene Function, Oxford.

There is a need for researchers interested in network biology and bioinformatics to meet, so Jotun Hein, Chris Holmes, and Andrea Rocco have organised the Bioinformatics day with focus on Networks. It is our intention to have such a half day before every term. The day will be dedicated to an interesting topic and will also be used to announce Genomics/Bioinformatics in the following term: seminars, study group and other meetings. If you intend to attend this event, please send an email to Cathy Went (went@stats.ox.ac.uk) before October 4th 2005 with your name and affiliation.

1.00pm Jotun Hein: Introduction and Biology of Networks

The first 5 presentations will try to summarize different aspects of the field very briefly with appropriate references that should be useful to people getting into the field. The first presentation will focus on the variety of graphs used in modelling cellular dynamics and when the corresponding knowledge appeared historically.

1.20pm Chris Holmes: Inference of Networks

I will review some of the challenges faced in inferring network structure from experimental data; both for probabilistic and non-probability models. I will then discuss some approaches for integrating information from multiple sources, which offers some protection against false discovery.

1.35pm Andrea Rocco: Modelling structure and function in complex networks

I will briefly review the recent advances in the topological analysis of large networks, highlighting the properties, which distinguish classical random graphs from scale-free networks. I will also introduce the concepts of hubs, modules, and motifs, as possibly fundamental tools to infer biological function. Finally I will focus on the relevance and challenges posed by a dynamical approach to the modelling of networks.

1.50pm Gesine Reinert: Statistics for small-world networks

We shall present rigorous results for the approximate distribution of the shortest path length and the clustering coefficient in small-world networks. In addition a distributional approximation for the joint count of circle motifs will be given. The emphasis is on describing not only the results but also sketch their derivation, as the methods used are transferable to other types of networks.

2.05pm Michael Stumpf: Comparative Biology of Networks

Present biological network data are incomplete and subject to high error rates. These shortcomings will affect evolutionary inferences and comparisons of networks between model organisms and I will discuss recent progress in the evolutionary and comparative analysis of biological networks.

2.25-2.45pm mini-BREAK

2.45pm Imre Vastrik: The Reactome

Life on the molecular level is an intricate network of biochemical reactions and pathways. Biologists have been elucidating fragments of this network for a century. Yet this information remains largely inaccessible to computational investigation. I will present Reactome - a knowledgebase of human biochemical reactions and pathways - which aims at making existing knowledge more accessible for computation.

3.15 pm Hector Keun: Metabonomics and modelling metabolic networks

Metabonomics is in essence the process of systemic metabolic profiling through time. As such it provides a rich source of experimental data for understanding metabolic regulation in complex living systems. A key feature of metabonomics is that minimal pre-selection of metabolites to be measured is employed, such that novel regulatory structures can be revealed. I will introduce the field, the technologies employed, and exemplify our current strategies for data analysis.

3.45-4.15pm maxi-BREAK

4.15 pm Philip Bang: Machine Learning for Systems Biology

Systems biologists use graph-based descriptions of bio-molecular interactions, which describe cellular activities such as gene regulation, metabolism and transcription. Biologists build and maintain these network models based on the results of experiments in wildlife and mutated organisms. This presentation will provide an overview of recent ILP research within in this area.

4.45pm Gail Preston: Evolutionary Modelling of Nitrogen Metabolism in *Falciparum*

This talk will describe a collaboration doing comparative analyses of the composition, function and regulation of nitrogen assimilation genes and nitrogen assimilation activities in plant pathogenic *P. syringae* and non-pathogenic *P. fluorescens* strains can be used to construct and test models of the evolution and ecology of these bacteria. The results of this study will provide important insights into the metabolic evolution of pathogenic bacteria, and into the interaction of *Pseudomonas* with plant hosts, particularly when placed in the context of metabolomic, proteomic and transcriptomic data on plant nitrogen metabolism.

5.05 – 5.20 pm Neil Johnson: Complex Agent-Based Dynamical Networks

This talk summarizes the biological network projects that we (Complex Systems Group, Physics Dept.) are developing with collaborators across the University. In particular: (i) dynamical evolution of nutrient networks in fungal and slime-mold systems (with Mark Fricker, Plant Sciences), (ii) AVMs and supply networks in the brain (with Paul Summers, Radcliffe Infirmary, and Yiannis Ventikos, Engineering Science), (iii) virus spreading on networks (with Zoology), (iv) angiogenesis in cancer tumour growth (with Tomas Alarcon). See also http://sbs-xnet.sbs.ox.ac.uk/complexity/complexity_splash_2003.asp