SYCS 1: Data Analysis in Complex Systems: From Data to Models

Time: Friday 10:15–13:30   Location: BAR SCHÖ

Invited Talk   SYCS 1.1   Fri 10:15   BAR SCHÖ
Eat, Drink, and Be Merry: The Spread of Health Phenomena in Complex, Longitudinally Resolved Social Networks — ●Nicholas Christakis — Harvard Medical School, Boston, MA, USA — Harvard Faculty of Arts and Sciences, Cambridge, MA, USA

Our work has involved the quantitative investigation of whether and how various health-related phenomena might spread from person to person in complex networks. We have developed various data sets to support these investigations, including a densely interconnected, longitudinally resolved network of 12,067 people assessed repeatedly from 1971 to the present. Each node in this network has an average of 11 ties of various kinds, including friends, siblings, spouses, offspring, coworkers, and neighbors. We observe discernible clusters of individuals with various traits, including obesity, smoking, eating, and happiness, and we document that these clusters are not solely due to selective formation of social ties between nodes. Rather, processes of social and emotional contagion are also apparent within the network. Various aspects of our findings suggest that the spread of social norms is a key mechanism underlying these inter-personal health effects. In other work, we have examined the genetic basis for social network formation and have developed a novel model for the social processes involved (the "attract and introduce" model). The recognition of the role of supra-individual, network effects on individual health lays a further foundation for public health by providing a rationale for the claim that health is not just an individual, but also a collective, phenomenon.

Invited Talk   SYCS 1.2   Fri 11:00   BAR SCHÖ
Transport efficiency and resilience in mycelial networks — ●Mark Fricker[1], Daniel Bebber[1], and Lynne Boddy[2] — [1]Dept. Plant Sciences, University of Oxford, Oxford, OX1 3RB, UK — [2]Cardiff School of Biosciences, Cardiff University, Museum Avenue, Cardiff, CF10 3AX, UK

Many fungi grow as a foraging mycelium, formed by branching and fusion of threadlike hyphae, that gives rise to a complex adaptive network without centralised control. These networks display both a high transport capacity and high resilience to damage with low relative cost. These properties are enhanced as the network grows, while the relative amount of construction material used decreases. Thus, mycelia achieve the seemingly competing goals of efficient transport and resilience, with decreasing relative investment, by selective reinforcement and recycling of transport pathways.

To test the transport predictions, we have imaged movement of radiolabelled nutrients. These show rapid flux with marked oscillations organised into discrete phase domains, preferential resource allocation and abrupt switching between different pre-existing transport routes. Furthermore, fusion between compatible individuals leads to rapid nutrient re-distribution and formation of a fully synchronised super-colony. This complex behaviour makes correlation between theoretical and experimental measures more challenging, and we are just beginning to develop a suitable modelling framework to understand these self-organised systems better.

Invited Talk   SYCS 1.3   Fri 11:30   BAR SCHÖ
From genetic variability between species to the inference of protein-protein interactions — ●Martin Weigt[1,2], Robert A. White[2], Hendrik Szurmant[3], James A. Hoch[3], and Terrence Hwa[2] — [1]Institute for Scientific Interchange, Turin — [2]Center for Theoretical Biological Physics, UC San Diego — [3]The Scripps Research Institute, La Jolla

The large majority of cellular functions are executed by interacting proteins. Their concerted specific interactions regulate the interplay of biochemical processes that are the essence of life. Many protein interactions are transient, allowing proteins to mate with several partners or travel in cellular space in order to perform their functions. Understanding these interactions is an outstanding challenges in systems biology.

Experimental approaches to identify surfaces of interaction between proteins are arduous and/or serendipitous. However, the availability of large protein databases generated from sequences of hundreds of bacterial genomes enables various statistical approaches to this problem. We propose a novel global inference approach based on the cavity method developed in the statistical physics of disordered systems. Applied to over 6900 representatives of the bacterial two-component signaling system, this method successfully and robustly identifies residue pairs that are proximal in space without resorting to ad hoc tuning parameters. This output is used to predict in-silico co-crystal structures. Further more, the method allows the accurate identification of new interacting protein partners.

Invited Talk   SYCS 1.4   Fri 12:00   BAR SCHÖ
Clustering and multiscale structure of graphs — ●Boaz Nadler — Weizmann Institute of Science, Rehovot, Israel

Clustering of data and graph partitioning are fundamental problems in many scientific fields. Both problems are related since many clustering algorithms can be formulated as solutions to graph partitioning problems.

In this talk we focus on two issues. The first is a probabilistic interpretation of eigenvalue/eigenvector based methods, such as spectral clustering and normalized cut. We show the connection of these methods to the properties of random walks on graphs, thus explaining both their successes, but also highlighting their fundamental limitations, specifically in the presence of structures at different scales.

The second issue is the study of the multiscale structure of data and graphs. Motivated by the properties of random walks on graphs, we present a multiscale algorithm and a diffusion based coherence score to reveal the structure of graphs and detect salient clusters at different scales.

Invited Talk   SYCS 1.5   Fri 12:30   BAR SCHÖ
Clustering, chance, and statistical mechanics — Marta Luksza[1], Michael Lässig[2], and ●Johannes Berg[3] — [1]Max Planck Institut für molekulare Genetik, Berlin — [2]Institut für Theoretische Physik, Universität zu Köln — [3]Physikalisches Institut, Albert-Ludwigs-Universität Freiburg

Clustering a set of points in a high-dimensional space is a core method of statistical data analysis. We consider the problem of clustering in random data: Given a set of randomly distributed vectors, how likely do some of them form a cluster with a given cluster score? This *cluster p-value* is crucial to assess the statistical significance of clusters found in real data. We use a mapping to a disordered spin-model to analytically solve the random clustering problem and discuss applications to the analysis of gene expression patterns.

Invited Talk   SYCS 1.6   Fri 13:00   BAR SCHÖ
Physics of recommendation mechanisms — ●Yi-Cheng Zhang — Department of Physics, University of Fribourg, Switzerland

Recommendation is a proactive way to bring the right information to the needy people, it complements to information searching. We shall outline the basic premises of recommendation and examine the possible applications on the WWW. We shall deal with the dilemma of ever-fine seggregation and the need of diversification. The models behind have closer analog with traditional physics than it is generally acknowledged.