

Cambridge Networks Day – 7th of May 2013:

9:00 Registration/Coffee

9:30 Welcome

09:45 Albert-László Barabási: “Network Science: From structure to control”

10:45 Marc Barthélémy: “Evolution of road networks”

11:30 coffee for 30 min

12:00 Ed Bullmore: “The economy of brain network organization”

12:45 Ginestra Bianconi: “Statistical mechanics of multiplex networks”

13:15 lunch + posters

14:45 Jörg Menche: “Human diseases within the Interactome”

15:30 Cecilia Mascolo: “Evolving geo-temporal social networks and their applications”

16:15 coffee for 30 min

16:45 Felix Reed-Tsochas: title TBC

17:30 Poster orals

17:45 Poster prize + closing remarks

Albert-László Barabási

*Center for Complex Network Research, Northeastern University (USA) and
Department of Medicine, Harvard Medical School (USA)*

Network Science: From structure to control

Systems as diverse as the world wide web, Internet or the cell are described by highly interconnected networks with amazingly complex topology. Recent studies indicate that these networks are the result of self-organizing processes governed by simple but generic laws, resulting in architectural features that makes them much more similar to each other than one would have expected by chance. I will discuss the order characterizing our interconnected world and its implications to network robustness, and control. Indeed, while control theory offers mathematical tools to steer engineered and natural systems towards a desired state, we lack a framework to control complex self-organized systems. I will discuss a recently developed analytical framework to study the controllability of an arbitrary complex directed network, identifying the set of driver nodes whose time-dependent control can guide the system's dynamics.

Marc Barthélémy

CEA Institut de Physique Theorique, Saclay (France)

Evolution of road networks

The road network is a crucial component of urban systems: its growth and evolution reflect how a city changes in time. This network is both embedded in space and evolves in time, and we thus have to face the difficulty of measuring and characterizing its evolution, and to extract useful information. I will illustrate in this talk these various problems and present some recent results on empirical case studies. If time allows, I will also mention various directions for modeling these systems.

Ed Bullmore

The Brain Mapping Unit, University of Cambridge (UK)

The economy of brain network organization

Brains are expensive, incurring high material and metabolic costs relative to their size, despite many aspects of brain network organization being largely explained by a parsimonious drive to minimize fixed and running costs.

However, brain networks also have high topological efficiency, robustness, and other advantageous properties that may entail a wiring cost premium. We propose that brain organization is shaped by an economic trade-off between pushing down costs versus allowing the emergence of adaptively valuable topological properties. This economical trade-off between wiring cost and adaptive value is re-negotiated over long (decades) and short (millisecond) time scales as brain networks evolve, grow, and adapt to changing cognitive demands. An economical analysis of brain network disorders highlights the vulnerability of the most costly elements of brain networks to pathological attack or abnormal development.

Ginestra Bianconi

Queen Mary University of London (UK)

Statistical mechanics of multiplex networks

Many networks do not live in isolation but are strongly interacting, with profound consequences on their dynamics. Examples of interacting networks are everywhere, from multimodal transportation networks, to climatic systems, economic markets, energy supply networks, social networks and the human brain. In this talk I present new results aimed at modelling evolving and static multiplex networks with given structural properties such as interdependence and overlap. Moreover I will present works on critical phenomena unfolding on such networks, mainly I will focus on a new type of percolation transition in presence of antagonistic interactions between the nodes in different layers of the multiplex. The solution of this model show that in presence of antagonistic interactions the percolation steady state is degenerate and is bistable, moreover the percolation transition can be both first or second order. Finally I will comment on the implications that the multiplexity has on the network structure and dynamics.

Cecilia Mascolo

The Computer Laboratory, University of Cambridge (UK)

Evolving geo-temporal social networks and their applications

While in the last years massive online social networks have become extremely popular, gathering and engaging millions of users, only recently these social services are becoming location-aware. This provides broad and fine-grained data to investigate how spatial and social structure blend together, opening exciting research directions with promising scientific and practical applications.

In this talk we describe a number of modelling efforts we have pursued on geo-social networks including urban mobility modelling through place ranking, a network evolution that keeps into account the geographical and social aspects of the network and geographical community dynamics modelling that factors in users place visits as well as social ties.

There a number of possible applications of geo-social models for social networks that we will briefly illustrate including geographical and social recommendation, mobility prediction and epidemic spreading.

Jörg Menche

Center for Complex Network Research, Northeastern University (USA) and Central European University (Hungary)

Human diseases within the Interactome

During the past decade significant efforts have been made to uncover the genetic origin of various human diseases. It has become apparent that diseases are rarely a consequence of an abnormality in a single effector gene product. Instead they result from an interplay of multiple molecular processes that interact with

each other through complex molecular networks integrated in the human interactome. In my talk I will introduce some of our recent results on the relationship between disease-associated genes and the human interactome. We find that diseases are localized in well defined interactome neighborhoods.

The resulting disease maps offer a first glimpse of the localization of various diseases, as well as their relative position to each other.

Our measurements show that the relative position of diseases in the interactome strongly correlates with their biological similarity: the closer two diseases are in the interactome, the more symptoms they share, the higher is their comorbidity pattern, and the more similarity is seen between their disease genes as well as the pathways in which they are involved.

Felix Reed-Tsochas

Saïd Business School, Oxford (UK)

Title and abstract TBC