

# Network Science

## *Introduction*

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# Why this module?

Why you need Networks



# Generalities

# Who am I?

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# Emergence of metastability in frustrated oscillatory networks: the key role of hierarchical modularity

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Oscillatory complex networks in the metastable regime have been used to study the emergence of integrated and segregated activity in the brain, which are hypothesized to be fundamental for cognition. The parameters and the underlying mechanisms that determine the emergence of metastability are hard to identify, often relying on maximizing the correlation with empirical functional connectivity dynamics. Here, we propose and show that the brain's hierarchically modular mesoscale structure alone can give rise to robust metastable dynamics and (metastable) chimera states in the presence of phase frustration. We construct unweighted 3-layer hierarchical networks of identical Kuramoto-Sakaguchi oscillators, parameterized by the average degree of the network and the number of nodes per layer. The layers are fully connected and within blocks in the upper two layers. Together, these parameters affect the characteristic timescales of the system. Away from the critical synchronization point, we detect the emergence of metastable states in the lowest hierarchical layer coexisting with chimera and metastable states in the upper layers. Using the Laplacian renormalization group flow approach, we uncover two distinct pathways towards achieving the metastable regimes defined in these distinct layers. In the lower layer, the chimera states are characterized by strong stability on the local eigenmodes of the system. In the lowest layer instead, metastable dynamics can be achieved as the separation of timescales between layers reaches a critical threshold. Our results show an explicit relationship between metastability, chimera states, and the eigenmodes of the system, bridging the gap between harmonic based studies of empirical data and oscillatory models.

PLOS ONE

RESEARCH ARTICLE

# Temporal ordering of input modulates connectivity formation in a developmental neuronal network model of the cortex

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## Abstract

Preterm infant brain activity is discontinuous; bursts of activity recorded using EEG (electroencephalography), thought to be driven by subcortical regions, display scale free properties and exhibit a complex temporal ordering known as long-range temporal correlations (LRTCs). During brain development, activity-dependent mechanisms are essential for synaptic connectivity formation, and abolishing burst activity in animal models leads to weak disorganized synaptic connectivity. Moreover, synaptic pruning shares similar mechanisms to spike-timing dependent plasticity (STDP), suggesting that the timing of activity may play a critical role in connectivity formation. We investigated, in a computational model of leaky integrate-and-fire neurons, whether the temporal ordering of burst activity within an external neural driving input could modulate connectivity formation in the network. Connectivity evolved across the course of simulations using an approach analogous to STDP, from networks with initial random connectivity. Small-world connectivity and hub neurons emerged in the network structure—characteristic properties of mature brain networks. Notably, driving the network with an external input which encodes LRTCs in the temporal ordering of burst activity facilitated the emergence of these network properties, increasing the speed with which they emerged compared with when the network was driven by the same input with the bursts randomly ordered in time. Moreover, the emergence of small-world properties was dependent on the strength of the LRTCs. These results suggest that the temporal ordering of burst activity could play an important role in synaptic connectivity formation and the emergence of small-world topology in the developing brain.

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Mathematical  
Biology

ORIGINAL ARTICLE

## The Impact of Contact Structure and Mixing on Control Measures and Disease-Induced Herd Immunity in Epidemic Models: A Mean-Field Model Perspective

Francesco Di Lauro<sup>1</sup> · Luc Berthouze<sup>2</sup> · Matthew D. Dorey<sup>4</sup> · Joel C. Miller<sup>3</sup> ·  
István Z. Kiss<sup>1</sup>

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### Abstract

The contact structure of a population plays an important role in transmission of infection. Many ‘structured models’ capture aspects of the contact pattern through an underlying network or a mixing matrix. An important observation in unstructured models of a disease that confers immunity is that once a fraction  $1 - \bar{R}_0$  has been infected, the residual susceptible population can no longer sustain an epidemic. A recent observation of some structured models is that this threshold can be crossed with a smaller fraction of infected individuals, because the disease acts like a targeted vaccine, preferentially immunising higher-risk individuals who play a greater role in transmission. Therefore, a limited ‘first wave’ may leave behind a residual population that cannot support a second wave once interventions are lifted. In this paper, we set out to investigate this more systematically. While networks offer a flexible framework to model contact patterns explicitly, they suffer from several shortcomings: (i) high-fidelity network models require a large amount of data which can be difficult to harvest, and (ii) very few, if any, theoretical contact network models offer the flexibility to tune different contact network properties within the same framework. Therefore, we opt to systematically analyse a number of well-known mean-field models. These are computationally efficient and provide good flexibility in varying contact network properties such as heterogeneity in the number contacts, clustering and household structure or dif-

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## 857

# Inferring Functional Connectivity From Time-Series of Events in Large-Scale Network Deployments

Antoine Messager, George Paricis<sup>②</sup>, Jetwan Z. Kise, Robert Harper, Phil Tee<sup>③</sup>, and Luc Berthouze<sup>④</sup>

**Abstract.** In response to rapidly and dynamically changing network and service outages, network operators must deal with a large number of events resulting from the interaction of various services operating on complex, heterogeneous and evolving networks. In this paper, we propose the concept of functional connectivity as an alternative approach to monitoring these events. Connectivity is defined in terms of the presence of statistical dependencies between nodes. We show that the concept of functional connectivity in brain networks, their straightforward application to commercial network deployment, a several challenges and opportunities. The first challenge is (a) the sparsity of the time-series of events, and (c) absence of an explicit model describing how events propagate through the network or system. The second challenge is that the events are not necessarily a novel inference approach whereby two nodes are defined as forming a functional edge if they emit statistically independent signals. The third challenge is that the events may be statistically independent. The output of the method is an undirected weighted graph, where the weight of an edge between two nodes is determined by the strength of the dependency between them. We develop a model of time-varying functional connectivity whose parameters are determined by maximising the model's likelihood function. We evaluate the performance of our model in terms of the accuracy, efficiency and scalability of our method on two real datasets of network events spanning multiple months. We compare our method against both a general-purpose time-varying network inference method and network management-specific event correlation methods. Our results indicate that in terms of sensitivity, accuracy and, importantly, scalability,

Network Science 981G5

www.nature.com/scientificreports/

# scientific reports

Check for updates

OPEN Network inference from population-level observation of epidemics

F. Di Lauro<sup>1</sup>, J.-C. Crois<sup>1</sup>, M. Dashti<sup>1</sup>, L. Berthouze<sup>2</sup> & I. Z. Kiss<sup>1,2,3</sup>

Using the continuous-time susceptible-infected-susceptible (SIS) model on networks, we investigate the problem of fitting the basic class of SIS models to observed data that is available at population level (i.e., the number of infected individuals at a fixed set of times during a single realization of the epidemic), the only information likely to be available in real world settings. To tackle this, epidemics on networks are approximated by a Birth-and-Death process which keeps track of the number of infected nodes at population level. The rates of this surrogate model encode both the structure of the network and the infection and recovery rates. We show that the proposed linear, Edge-based Bayesian model selection *for exact* fit to most likely underlying network class, based only on a single realization of the epidemic. We show that the proposed methodology yields good results on both synthetic and real-world networks.

# Module objectives

It is not a formal *graph theory* module!

- Learning outcomes:
  - Abstract real-world scenarios in terms of dynamics on networks (*and possibly dynamics of the networks*)
  - Systematically characterise network properties
  - Interpret and communicate network properties effectively
- Less formally:
  - Learn essential concepts and core ideas of network literacy
  - Acquire skills to load, manipulate, export, visualize networks
  - Recognize and describe a network's structural components and properties
  - Measure various centrality measures and their distributions, and apply them to detect important nodes and characterize their roles in the network
  - Model dynamic processes on networks, such as the spread of diseases and rumours
  - Appreciate and explore the broad relevance of network science to domains and applications such as biology, business, AI, search, recommendation, social media

# Schedule (Last updated: 27/01/2026)

- Week 1: Introduction (this lecture)
- Week 2: Generalities
- Week 3: Centralities
- Week 4: Network models
- Week 5: Modularity and network inference (Tutor: Enrico Caprioglio)
- Week 6: Dynamics on networks
- Week 7: Guest lecture: Dr Alex Penn, Title TBC
- Week 8: Guest lecture: Kieran Young/David Weir, Title TBC; Dataset Cards (extra)
- Week 9: Graph neural networks (Tutor: Ashfaq Salehin)
- Week 10: Guest lecture: Harry McCarney, Title TBC
- Week 11: Directed and weighted networks

# Assessment

- The module is assessed by **coursework** (i.e., worth 100% of the final mark)
- Format: report (3000 words) + code
- Submission deadline: **Monday 18 May 2026**, 4pm with submission on Canvas.

## Note

I am keen for you to explore your own ideas (e.g., feeding into your MSc project) so do get in touch early!

# Selected sample of past coursework (first cohort)

- A network analysis of women in British animation studios in the mid-twentieth century (own curated dataset)
- Where and how are products placed in a shop
- Helping lonely people: Impact of targeted within-community rewiring vs random edge addition on local clustering of social network nodes
- Analysing worm-virus dynamics with detection and prevention in peer-to-peer networks: the SIDR model
- Analysing influence and structure in the Higgs Twitter Retweet network
- Mapping innovation pathways in sustainable textiles: A network analysis of WIPO GREEN technologies (own curated dataset)
- Structure, complexity and network decomposition analysis of the Medullas synaptic network in *Drosophila melanogaster*

# Readings and Seminars

A list of textbooks is available [here](#) on Canvas. We will use *A first course in Network Science* as primary source for this module. Some of my slides are copied or modified from those provided by the authors.

There will be many papers mentioned during the lectures, for which links will be provided.

A lot of material is available from the [Network Science Society](#) including some special interest groups such as [Women in Network Science](#) or [the Society of Young Network Scientists](#) each with its own channels. Check them out!

Try to attend (remotely) the [NetSci Colloquium talks](#).

# Software

We will be using Python and the **Networkx** module.

There are two approaches possible:

- Jupyter notebooks on the cloud:
  - Google Colab ( [colab.research.google.com](https://colab.research.google.com) )
  - Kaggle Kernels ( [www.kaggle.com/kernels](https://www.kaggle.com/kernels) )
  - Azure Notebooks ( [notebooks.azure.com](https://notebooks.azure.com) )
  - Datalore ( [datalore.io](https://datalore.io) )
- Local installation: If you don't have Jupyter/IPython installed on your machine, we recommend installing the **Anaconda Python 3 distribution**. This option will require you to be comfortable with managing software packages (i.e., using `pip` or `conda`).

# Other software

See **NASCol - Network Analysis Software Collective** for a fairly comprehensive list.  
Below, I highlight a few.

- For analysis:
  - GraphTool (<https://graph-tool.skewed.de>) by the excellent **Tiago Peixoto**
- For temporal networks (see forthcoming lecture):
  - Raphtory (<https://www.raphtory.com>) for temporal graph analytics (in Rust with Python bindings)
- For multilayer networks:
  - MuxViz (<https://github.com/manlius/muxViz>), a R-package by complex scientist **Manlio de Domenico**. Consider reading his substack **Complexity Thoughts** which is always excellent.
- For visualisation:
  - Gephi ([gephi.org](http://gephi.org))
  - NetLogo ([ccl.northwestern.edu/netlogo](http://ccl.northwestern.edu/netlogo))
  - and see also this **review** of 16 tools

# Useful resources (Last updated: 7/01/2025)

- *D3 Graph Theory*, a nice interactive resource
- *how-to-draw-graphs-in-latex*, from StackExchange
- *MA30245: Graphs & Networks*, a more mathematical treatment from Bath University.

# Network repositories (Last updated: 27/01/2025)

- ICON – Colorado index of complex networks
- SNAP – Stanford Large Network Dataset Collection
- Network Repository. An Interactive Scientific Network Data Repository
- Konect – Koblenz Network Collection

## Specialised databases

- BCT – Brain-connectivity toolbox (biology)
- String – Protein-Protein Interaction Networks (biology)
- BioGRID – Biological General Repository for Interaction Datasets (biology)
- AMiner Citation and Co-Authorship Network (citation/authorship)
- CAIDA – Center for Applied Internet Data Analysis (web/internet)
- OSM – Open Street Maps (transportation/infrastructure)
- WIOD – World Input-Output Database (economic/financial)
- MovieLens Dataset (recommendations)

# Let's talk networks!

*"Networks are everywhere, and they are beautiful"* (**Jari Saramäki**)

# In-class activity