Women in Networks (WiN) Workshop

School of Mathematics, Leeds University

27th February - 1st March 2019

Sponsors

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EUROPEAN COOPERATION IN SCIENCE AND TECHNOLOGY

COST Action CA15109.
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EU Framework Programme
Horizon 2020.

The electronic version of this booklet can be found at:
https://win.leeds.ac.uk
The codes used to generate this booklet, including the reference to the LaTeX template,
are available at `https://github.com/luisacutillo78/WiN-Workshop`

Contents

About

WiN: Woman in Networks Workshop

The COSTNET Woman in Networks Workshop will bring together senior and junior (mainly) women international scientists working in the field of Networks modelling and Networks applications. Activities will be spread over three days.

During the first two days, there will be afternoon interactive breakout discussion sessions in which participants will form small groups to independently discuss important topics in the field.

In particular, the first session will be devoted to highlight the main challenges and open questions in the modelling and validation of Networks.

The second interactive session will address the identification of potential solutions to the problems discussed.

The objectives of the interactive afternoon sessions will be:

- identifying main challenges;
- propose possible problems solutions;
- deciding priorities, strategy, and vision;
- improving/establishing scientific collaborations and networking;
- gathering ideas for research grant proposals;
- ascertaining user requirements for bioinformatics tools;
- generating ideas for designing web/software interfaces.

The 3rd, and last day, afternoon session will be dedicated to the discussion of poster presentations. Participants' posters will be displayed over the workshop around the lunch break area.

COSTNET: the European Cooperation for Statistics of Network Data Science.

COSTNET is COST Action CA15109 (`https://costnet.webhosting.rug.nl/`) which aims to foster an international European collaboration on the emerging field of statistics of network data science. COSTNET facilitates interaction and collaboration between diverse groups of statistical network modellers, establishing a large and vibrant interconnected and inclusive community of network scientists.

Organizing committee

Luisa Cutillo	School of Mathematics,University of Leeds
Jeanine Houwing-Duistermaat	School of Mathematics, University of Leeds

Logistic

Special thanks for the conference arrangements to:

Helen Copeland	Secretarial Assistant, School of Mathematics, University of Leeds
Iris Burger	Secretarial Office, Department of Statistics, University of Munich

Timetable

CT: Contributed Talk, KL: Keynote Lecture.

Wed 27 Feb, MALL 2, Level 8, School of Mathematics

9:00-9:45	**Welcome by Jeanine Houwing-Duistermaat and Luisa Cutillo**		
9:45-10:00	**Arrival and Registration, Level 9, School of Mathematics**		
10:00–11:00	KL	**Veronica Vinciotti** Brunel University, London	Network inference in genomics under censoring
11:00–11:30	**Coffee**		
11:30–12:00	CT	**Pariya Behrouzi,** Wageningen University, NL	Construction of High-resolution Linkage Maps Using Discrete Graphical Models
12:00–12:30	CT	**Rafiazka M. Hilman** Central European University (CEU),Budapest, Hungary	The Dynamics of Mass and Elite in Dutch Dividend Tax Discourse
12:30–14:00	**Lunch**		
14:00–15:00	KL	**Gesine Reinert** University of Oxford	Anomaly detection in networks
15:00–16:30	**Breakout 1: Challenges in Biological Networks**		
15:30–16:00	**Coffee**		
16:30–17:00	**Report back and plenary**		
19:00	**Social Dinner**		

Thur 28 Feb - Morning session: Worsley Building, 8.34a. Afternoon session: LT E, Chemistry West Block

9:30-9:45	**Registration, Level 9, School of Mathematics**		
9:45-10:00	**Sustainable garden tour and walk to Worsley Seminar Room 8.34a**		
10:00–11:00	KL	**Claudia Angelini** School of Mathematics, University of Leeds, UK	An overview on penalized network regression approaches
11:00–11:30	**Coffee**		
11:30-12:00	CT	**Marija Mihovar** Ss. Cyril and Methodius University, FINKI, Skopje	Efficient Algorithm for Finding all Minimal Path Vectors in Two-terminal Flow Network
12:00-12:30	CT	**Martin Lopez Garcia** School of Mathematics, University of Leeds, UK	On the exact analysis of stochastic epidemic processes on networks
12:30–14:00	**Lunch - Afternoon session at LT E, Chemistry West Block**		
14:00–15:00	KL	**Luisa Cutillo** School of Mathematics, University of Leeds, UK	Main challenges in Networks community structure validation
15:00-15:30	CT	**Valeria Policastro** IAC-CNR Naples, Italy	ROBIN: an R package for validation of community robustness
15:30–17:00	**Breakout 2: Identifying potential solutions**		
15:30–16:00	**Coffee**		
17:00–17:30	**Report back and plenary**		

Fri, 1st of March, MALL 2, Level 8, School of Mathematics

9:30–10:30	KL	**Jeanine Houwing-Duistermaat** School of Mathematics, University of Leeds, UK	Data integration using Network and Partial Least Square methods
10:30-11:00	CT	**Rebeka O. Szabo** Central European University (CEU),Budapest, Hungary	The micro-dynamic nature of team interactions
11:00–11:30	**Coffee**		
11:30–12:30	KL	**Marta Milo** University of Sheffield, UK	Bring Mathematics into Biology: Past, Present and Future Impact on Health
12:30-13:00	CT	**Denise De Gaetano** Malta College of Arts Science and Technology	Extracting the Value of Big Data
13:00-13:30	CT	**Arief Gusnato** School of Mathematics, University of Leeds, UK	Transcriptomic and Genomic Networks
13:30–15:30	**Lunch and Posters - Room 9.31, Level 9, School of Mathematics**		
15:30	**Coffee and Close**		

List of Abstracts – Talks

Wednesday 27th Feb

Network inference in genomics under censoring

Veronica Vinciotti, Brunel University, London, UK KL

Regularized inference of networks using graphical modelling approaches has seen many applications in biology, most notably in the recovery of regulatory networks from high-dimensional gene expression data. Under an assumption of Gaussianity, the popular graphical lasso approach provides an efficient inferential procedure under L1 sparsity constraints. In this talk, I will focus on a latest extension to censored graphical models in order to deal with censored data such as qPCR expression data. We propose a computationally efficient EM-like algorithm for the estimation of the conditional independence graph and thus the recovery of the underlying regulatory network. Similar techniques can be used also in the context of multivariate regression where censored outcomes are to be predicted from a set of predictors. Efficient inferential procedures are presented in the high-dimensional case and pave the way for the development of more complex models that integrate data from different sources and under different mechanisms of missingness.

Construction of High-resolution Linkage Maps Using Discrete Graphical Models

Pariya Behrouzi, Wageningen University, NL CT

Linkage maps are important for fundamental and applied genetic research. In this talk, we introduce an algorithm to construct high-quality and high-density linkage maps for diploid and polyploid species. We employ a sparse Gaussian copula graphical model and the nonparanormal skeptic approach to construct linkage maps. We compare our method with other available method when the data are clean and contain no missing observations and when data are noisy and incomplete. In addition, we implement the method on real genotype data of barley and potato. We have implemented the method in the R package "netgwas" which is freely available at CRAN.

The Dynamics of Mass and Elite in Dutch Dividend Tax Discourse

Rafiazka M. Hilman, Central European University (CEU), Budapest, Hungary **CT**

Political sphere in the Netherlands has been passing through torturous way due to the legislation process on Amendment to the Dividend Tax Act 1965 for the last 12 months. Among others, the government proposal on the abolishment of dividend tax (dividendbelasting) becomes the central point. Coalition parties who sponsor this bill, VVD, D66, CDA, and CU, deal with a lot of critiques from opposition in the parliament (Tweede Kamer). There are three enthralling observations to make in the introduction of this bill. First, it creates ideological distance among central-right coalition parties in which coalition partners D66, CDA, and CU attempt to minimise the political sentiment caused by VVD?s main agenda on the abolishment of dividend tax. On this side, the improvement of investment climate serves as a shield. Secondly, it induces ideological proximity among opposition parties in the parliament where cross-spectrum stands on the same rejection platform by questioning policy cost at 2 billion euros. Last, this political ambiguity leads to diverged public perception related to the importance of public spending over private incentive. It is the central interest of this research to identify the alignment between public perception and elite discourse captured during the parliamentary debate session. Synthesis and analysis are made in response to two questions: How does social network reflect interactions between political elites, political parties, and mass in dividend tax discourse in the Netherlands? How does the political ambiguity evolve amidst the dynamics of dividend tax discourse? In order to portray public perception towards elite interaction represented by political key players, social network data are extracted from Twitter in. On top of that minute of meetings recorded during parliament debate session are filtered out to construct the context and sentiment fragmentation among elites. Data are collected using Twitter API service during 4 weeks-period in October 2018. This period is selected to enable the tail-end of dividend tax issue as the government decided to withdraw the plan in the beginning of October 2018. Meanwhile, parliament record is analysed from the initial discussion in November 2017 to October 2018. The research proceeds as follows: first, the methodology comprising data and model are presented. Next, ideological spectrum and coalition formation becomes a foundation of the following discussion on political dynamics surrounding dividend tax discourse. The final part of the article concludes and discusses the results in terms of network structure and network properties.

Anomaly detection in networks

Gesine Reinert, University of Oxford, UK

KL

Detecting financial fraud is a global challenge. This talk will mainly focus on financial transaction networks. In such networks, examples of anomalies are long paths of large transaction amounts, rings of large payments, and cliques of accounts. There are many methods available to detect specific anomalies. Our aim is to detect unknown anomalies. To that purpose we use a strategy with derives features from network comparison methods and spectral analysis, and then apply a random forest method to classify nodes as normal or anomalous. We test the method on synthetic data which we generated, and then on synthetic data without us having had access to the ground truth. This talk is based on joint work with Andrew Elliott, Mihai Cucuringu, Milton Martinez Luaces, Paul Reidy.

Thursday 28th Feb

An overview on penalized network regression approaches

Claudia Angelini, IAC Istituto per le Applicazioni del Calcolo "Mauro Picone", CNR Naples, Italy

KL

In this talk we will briefly review the main concepts and problems that arise when analyzing high dimensional data, then we describe recent approaches based on network penalized regression. As an illustrative example, we describe a novel method that combines variable screening and penalized network-based Cox-regression models for the identification of high- and low-risk groups in breast cancer and the selection of potential biomarkers. More in general, we illustrate most recent results and open challenges of network penalized approaches in the context of omic data analysis and integration.

Construction of High-resolution Linkage Maps Using Discrete Graphical Models

Marija Mihova, Ss. Cyril and Methodius University, FINKI, Skopje **CT**

Efficient Algorithm for Finding all Minimal Path Vectors in Two-terminal Flow Network Minimal path and minimal cut vectors are usually used for computing the reliability of a two- terminal flow network with discrete set of possible capacities of its arcs. This work unites the max-flow theory of two-terminal vectors and the theory of minimal path vectors in multi-state systems. Based on obtained theoretical results, we have designed an algorithm for computing all minimal path vectors for a given level d.

The Dynamics of Mass and Elite in Dutch Dividend Tax Discourse

Martin Lopez Garcia, University of Leeds, UK **CT**

On the exact analysis of stochastic epidemic processes on networks I will show in this talk how to analyse the SIR epidemic model in an exact way when the population under study is formed by a small highly heterogeneous group of N individuals, represented by means of a network. This approach, which amounts to the analysis of the exact 3^N-states continuous-time Markov chain (CTMC), makes special focus on algorithmic aspects, and requires a creative organization of the space of states S, I, R^N of the CTMC. The analysis of the epidemic dynamics is carried out in terms of a number of summary statistics for the disease: (i) the length and size of the outbreak; (ii) the maximum number of individuals simultaneously infected during the outbreak; (iii) the fate of a particular individual within the population; and (iv) the number of secondary cases caused by a certain individual until she/he recovers. I will illustrate this methodology by studying the spread of the nosocomial pathogen Methicillin-resistant Staphylococcus Aureus among the patients within an intensive care unit (ICU). The interest here is in analysing the effectiveness of different control strategies which intrinsically incorporate heterogeneities among the patients within the ICU. References: M. Lopez-Garcia (2016) Stochastic descriptors in an SIR epidemic model for heterogeneous individuals in small networks. Mathematical Biosciences 271: 42-61. A. Economou, A. Gomez-Corral, M. Lopez-Garcia (2015) A stochastic SIS epidemic model with heterogeneous contacts. Physica A: Statistical Mechanics and its Applications 421: 78-97.

Main challenges in Networks community structure validation

Luisa Cutillo, University of Leeds, UK KL

High throughput technologies have led to an increased availability of data and to the need for novel statistical tools. Biological networks provide a mathematical representation of patterns of interaction between appropriate biological elements. We propose a novel approach to compare community structures in different networks. During this seminar we will try to address some open questions: How can we compare two (or more) networks and their community structures? Can we use Network Enrichment Analysis tools to do this? Is it an advantage to integrate metadata to infer communities?

ROBIN: an R package for validation of community robustness

Valeria Policastro , IAC Istituto per le Applicazioni del Calcolo "Mauro Picone", CNR Naples, Italy CT

In network analysis, many community detection algorithms have been developed. However, their applications leave unaddressed one important question: the statistical validation of the results. We present ROBIN (Robustness In Network), an R package that gives a statistical answer to the validation of the community structure by looking at the robustness of the network. The package implements a methodology presented in a previous paper that detects if the community structure found by a detection algorithm is statistically significant or is a result of chance, merely due to edge positions in the network. The software performs a perturbation strategy and runs a null model to build a set of procedures based on the Variation of Information as a clustering distance. In particular, it provides a procedure to examine the stability of the partition recovered against random perturbations of the original graph structure, a routine to compare different detection algorithms applied to the same network and a graphical interactive representation of networks. The package is useful not only to determine whether the obtained clustering departs significantly from the null model, but also to discover which algorithm better fits for the network of interest.

Friday 1st March

Data integration using Network and Partial Least Square methods

Jeanine Houwing-Duistermaat, School of Mathematics, University of Leeds, Uk **KL**

The availability of large omics datasets in epidemiological and clinical studies provides many opportunities for research in statistical bioinformatics. The hope is that the abundance of information will provide better understanding of underlying disease mechanisms and accurate prediction models enabling patient targeted screening and treatment. Statistical challenges are to deal with data wrangling, heterogeneity across omic datasets, high dimensionality, data integration and the presence of high correlation within and between datasets (Morris et al, 2017; Houwing-Duistermaat et al, 2017). In this talk I will present Partial Least Squares (PLS) and Network methods for data integration and dimension reduction when analysing several omics datasets simultaneously. The methods will be illustrated by analysis of glycomic datasets and of metabolomics and gene expression in relation with Body Mass Index.

The micro-dynamic nature of team interactions

Rebeka O. Szabo, Central European University (CEU), Budapest, Hungar **CT**

Teams have become a popular organization form since well-functioning task-focused groups are basic pillars of successful organizations. While there is much interest in contemporary social science in understanding team processes that lead to efficiency, most of these researches rely heavily on self-reported data yielding static and potentially biased information and tends to overlook actual interaction processes. We propose a novel approach that allows portraying a nuanced, complex picture of problem-solving group behaviour by measuring performance dynamics as it evolves in real-time, in a controlled environment. The research aims to explore how collaboration networks of small project teams evolve across time and team members, and how it relates to successful task performance. We investigate interaction patterns in escape rooms, where all teams are video recorded during the task-solving process in the same experimental environment. We expected and confirmed that homogeneous distribution of interaction ties across time and team members fosters successful problem-solving. Concerning the impact of the initial social roles on the dynamics of the interaction pattern, we hypothesized that flexible, less hierarchical team structures favour for problem-solving. In the case of the teams with random composition, the development of a new social structure during the dynamic performance of an unstructured task is expected to entail more tensions with the conversation rules than otherwise. This research aims to advance the new science of teams? by focusing on the network micro-mechanisms that allows us to treat teams as dynamic, adaptive, task- performing systems.

Bring Mathematics into Biology: Past, Present and Future Impact on Health

Marta Milo, University of Sheffield, UK KL

Last decade has seen a massive increase of data production in science. Particularly in the biomedical field, data has grown exponentially thanks to the development of technologies like next generation sequencing and high-throughput quantitative assays. The information that this data contains is only partially uncovered to this date, but the impact that it has on human progression and well-being is already very clear. Despite the ability to process large amount of data and to quantify fine details of biological processes, the costs, the time to perform such experiments and mainly the complexity of the systems remain in some cases still very prohibitive. For this reasons the use of mathematics to study complex systems in its entirety, looking at how they interacts, is having a great impact in current biology and healthcare. A variety of statistical, probabilistic and optimisation techniques methods, like machine learning techniques, taht allows to learn from the available data, to detect hidden patterns from large, noisy and complex datasets, is particularly suitable for application in medicine. In this talk I will present examples of using machine learning techniques for a variety datasets from medical and biological problems and what are the advantages and disadvantages of this approach. I will also give examples when tehse techniques enabled to discover infoirmative knowledge from a large complex system in the presence of small number of samples. Finally I will discuss how we use Machine Learning today for analysis of single-cell sequencing data and how we can use it for future more complex datasets generated integrating data from different sources.

Extracting the Value of Big Data

Denise De Gaetano, Malta College of Arts Science and Technology CT

Despite the large volumes of data, companies still struggle to access, manage and extract the information that their day-to-day processes generate. The growth of IT systems has provided these same companies, the ability to capture this potentially valuable data, within a number of applications, databases and organizations. Apart from a strong IT infrastructure, changes in the board and management, within a company also need to be carried out. This allows a number of departments to work in coordination and help ensure success of the utilization of the data at hand. Understanding what is required out of the data, is the first step to generate the best results from the company and customer data. The strategy is to understand how the information can enable an improvement in the business.

Transcriptomic and Genomic Networks

Arief Gusnanto, School of Mathematics, University of Leeds **CT**

Correlation network is an important tool in bioinformatics to find clusters of genes that are highly correlated in their expressions. The network can be used as a screening method to identify candidate biomarkers and therapeutic targets. This methodology has been successfully implemented in many biological contexts including cancer. While the interpretation may be natural in the context of gene expression data, network of copy number alterations (CNA) is not so straightforward because the data are in segments. CNA are structural variations in the human genome where some regions have more or less copy number than the normal two copies. Since the alterations happen in segments, the data exhibit stronger correlations than gene expression data and the correlations are in ?blocks?. The standard method is no longer adequate for an intuitive interpretation. This talk will describe the research problem, challenges, and our efforts so far in dealing with data from lung cancer patients. This is currently an ongoing joint work with (in alphabetical order) Mohammed Alshahrani, Luisa Cutillo, Charles Taylor, Peter Thwaites, and Henry Wood.

List of Posters

An unsupervised Machine Learning technique for dimensionality reduction of single cell data

Helena Andres-Terre, *University of Cambridge*

The introduction of single cell RNA-seq data was a major breakthrough in the field of biology, and particularly useful in research areas such as comparative transcriptomics or disease studies. It allows the characterization of gene expression levels for individual cells, and the potential to observe different stages of the Stem cell differentiation process. These datasets are known to be sparse and highly dimensional, with a large number of genes describing each cell. In order to interpret the experimental results, one of the main objectives is to identify the most relevant features of the underlying processes. After a first cut on the number of accounted genes based on their variability, current techniques use dimensionality reduction methods such as Principal Component Analysis (linear) or tSNE (non-linear). The new components are then used for plotting, performing further analysis on classification tasks or to describe differentiation processes. While these methods have been proved valid to address the aforementioned challenges, they also present some restrictions when trying to characterize the middle states of differentiation. We present an unsupervised Machine Learning technique for dimensionality reduction of single cell data. We used Variational Auto-Encoders to extract a number of significant components that characterize individual cells based on their gene expression, using a deep learning bottle-neck approach. The variational nature of this technique allows for certain levels of stochasticity in the original data, while learning an encoded representation that can be used to reconstruct and generate new samples. The methods that are based on linear dimensionality reduction techniques often require strong assumptions and constraints; for instance locally homogeneous distribution of samples in the high dimensional space, or not accounting for low variance dimensions. Variational Auto-Encoders (VAEs) provide an en- coding capable to identify and separate among relevant features in the dataset. VAEs can also be used to identify sets of relevant genes or drivers of the different processes captured by the latent encoding. Their generative potential also allows the exploration of the latent space, which can lead to defining a theoretical energy landscape that describes trajectories of differentiation.

SusNet: a global retinal co-expression network

Annamaria Carissimo, *Istituto per le Applicazioni del Calcolo M.Picone, Naples, CNR*

Network analysis provides a useful framework to visualize and analyze complex biological problems. In biological networks, transcripts, genes or proteins are represented as nodes, and relationships between them as edges. These interactions can be reconstructed by inference methods starting from expression profiles. Co-expression networks use the transcriptional concordance of two gene expression profiles to build undirected graph representations of the biological system under observation. In our study, we generated a co-expression network of the adult porcine retina, SusNet, by calculating pairwise gene correlation among 47 Sus Scrofa Large White retina samples sequenced by RNA-Seq. We showed that SusNet captures the pan-retinal regulatory structure associated to retina-specific TFs. We further showed that mapping differentially expressed genes (DEGs) following somatic repression of the rod-specific gene Rhodopsin on SusNet enables the identification of a sub-GRN operating in a subcellular compartment.

COSMONET

Antonella Iuliano, *Telethon Institute of Genetics and Medicine (TIGEM), Pozzuoli, Italy*

We present an R package called COSMONET where screening-network methods are implemented for the prediction of survival outcome in cancer patients. The novelty is the combination of different types of screenings (biomedical-driven, data-driven, the union of both) and network-regularized Cox methods. This approach allows to improve the prediction capabilities, to discriminate patients in high-and low-risk groups using few potential biomarkers, and to help clinicians in the management of patients.

Graphical Markov Models with an Application on Traffic Accident Data

Gamze OZEL KADILAR , *Hacettepe University, Ankara, Turkey*

Undirected graphical models are widely used for modeling, visualization, inference, and exploratory analysis of multivariate data with wide-ranging applications. Graphical models are models based on graphs in which nodes represent random variables, and the edges represent conditional independence assumptions. Hence they provide a compact representation of joint probability distributions. Graphical Markov models started to be developed after 1970 as special subclasses of log-linear models for contingency tables and of joint Gaussian distributions, where conditional independence constraints are imposed such that conditioning is on all the other variables. The study of these models is an active research area, with many questions still open. In this study, graphical Markov models are described. Then, interpretations are illustrated with an application based on traffic accident data of Turkey. Furthermore, some of the more recent, important results for sequences of regressions are summarized. Keywords: graphical models; Markov property; categorical data analysis, traffic accident data.

Identification of cell subpopulations using ensMAP-DP approach

Monika Krzak, *Istituto per le Applicazioni del Calcolo M.Picone, Naples, CNR*

Single-cell RNA sequencing (scRNAseq) has emerged as an important technology that allows profiling gene expression at single-cell resolution. The great potential of this technique lies in the possibility to infer cellular diversity within the same organ, tissue or group of cells of interest. In the last years, several studies have been carried out for identifying novel or known cell populations. Despite the great collection of available methods, an accurate detection of cell subpopulations remains unresolved and several issues are still open. For example, most of the algorithms require to provide a fixed number of desired subpopulations. This might be a drawback when no prior knowledge about cell population is available or when the aim is to identify novel subtypes of cells. Motivated by these reasons, we developed a new method, ensMAP-DP, that uses probabilistic mixture modeling to reveal latent cell subpopulations. The method consists of several steps: first, it selects a number of most relevant features (i.e. so-called highly variable genes), then applies tSNE and performs MAP-DP clustering on a given number of components, finally the clustering solutions corresponding to different tSNE projections are combined into a consensus clustering using a meta-clustering algorithm. In this work, we demonstrate the superior performance of our approach to other widely used methods designed to infer the cellular heterogeneity in scRNAseq data.

TBD

Margherita Mutarelli, *Telethon Institute of Genetics and Medicine, Pozzuoli, italy*

The identification of the molecular cause of genetic diseases is one of the fundamental questions of medical research. Despite the availability of high-throughput techniques like Whole Exome and Whole Genome Sequencing that made now feasible to genotype patients at an unprecedented level of depth, still a high proportion of cases remain unsolved. We are building a gene and disease network based on the annotated phenotypes present in patients to improve candidate causative gene prioritization.

Inference on multilayer networks with latent layers

Alice Tapper, *University of Leeds*

Online social networks often represent one layer in a larger multilayer network of connections between people. Motivated by this, SIS dynamics occurring on two-layer systems with one visible layer and one latent layer are studied. A range of network structures and epidemic parameters are explored using mean field approximations and simulation, with an aim to identify cases where inference is inaccurate if solely the visible layer is analysed.

List of Participants

Boshra Alarfaj	Leeds University, UK
Fatimah Almulhim	Leeds University, UK
Helena Andres-Terre	University of Cambridge, UK
Claudia Angelini	IAC National Research Council (CNR), Italy
Jason Anquandah	Leeds University, UK
Pariya Behrouzi	Wgeningen University, NL
Annamaria Carissimo	IAC National Research Council (CNR), Italy
Luisa Cutillo	Leeds University, UK
Tiziano Deangeli	Leeds University, UK
Denise Degaetano	Malta College of Arts Science and Technology
John Paul Gosling	Leeds University, UK
Arief Gusnato	Leeds University, UK
Rafiazka Hilman	Central European University (CEU), Hungary
Jeanine Houwing-Duistermaat	Leeds University, UK
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Kathryn Laing	Leeds University, UK
Sijia Li	Leeds University, UK
Haiyan Liu	Leeds University, UK
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Marija Mihove	Ss. Cyril and Methodius University, FINKI, Skopje
Marta Milo	Sheffield University, UK
Margherita Mutarelli	Telethon Institute of Genetics and Medicine, Italy
Alina Peluso	Imperial College, UK
Valeria Policastro	IAC National Research Council (CNR), Italy
Gesine Reiner	Oxford University, UK

Rebeca O. Szabo	Central European University (CEU), Hungary
Alice Tapper	Leeds University, UK
Veronica Vinciotti	Brunell University, London, UK
Jonathan Ward	Leeds University, UK

Useful Information

Talks will be held at the **School of Mathematics, room MALL 2** on Wednesday (morning and afternoon sessions) and Friday (morning session). MALL 2 is situated on the 8th floor of the School of Mathematics that has access through a lift located at the main entrance at level 9 of the School of Mathematics . On Thursday the morning session will be held at the **Worsley Building, room 8.34a**, while the afternoon session will be held at the lecture theather **LT E, Chemistry West Block**.
Coffee breaks will be offered in the the conference area.
Lunches will be held in the the refectory building in a dedicated area both on Wednesday and Thursday. Friday lunch will be delivered in the **Room 9.31 on the level 8** of the School of Mathematics.

The **poster session** will be held on Friday lunch and afternoon session night in the **Room 9.31 on the level 8** of the School of Mathematics.

WiFi: access to an eduroam network will be available on campus.

The **conference dinner** will be held at the "Brasserie Blanc Leeds", 4 The Embankment, Leeds' LS1 4BA, 0113 220 6060, leeds@brasserieblanc.com.

NOTE: the contribution required at the https://store.leeds.ac.uk/product-catalogue/faculty-of-maths-physical-science/women-in-networks will cover for your lunch(es), coffee break(s) and/or social dinner options you selected. If you did not book through the Leeds store system, you can always purchase a lunch on campus and join us in the dedicated lunch area. If you missed the social dinner booking and wish to join us on the day, please make your own arrangements with the "Brasserie Blanc Leeds".

Travel

You can travel to Leeds via the following airports:

- Leeds Bradford Airport, then travel by taxi or bus

- Manchester Airport, then travel by train or coach.

- London Airports, then travel by train or coach. (NB: London is around 320km away from Leeds. The fastest train takes about two hours to arrive to Leeds from London Kings Cross)

- Doncaster Sheffield Airport, then take a bus to the Doncaster Train Station and take a train to Leeds.

From Leeds-Bradford Airport , you can either take a taxi or catch the Flying Tiger bus 757 to City Square/Leeds Train station. From Manchester Airport, there are direct trains to Leeds approximately every half hour; the journey is about an hour and a quarter. See National Rail Enquiries for more details.

Accommodation

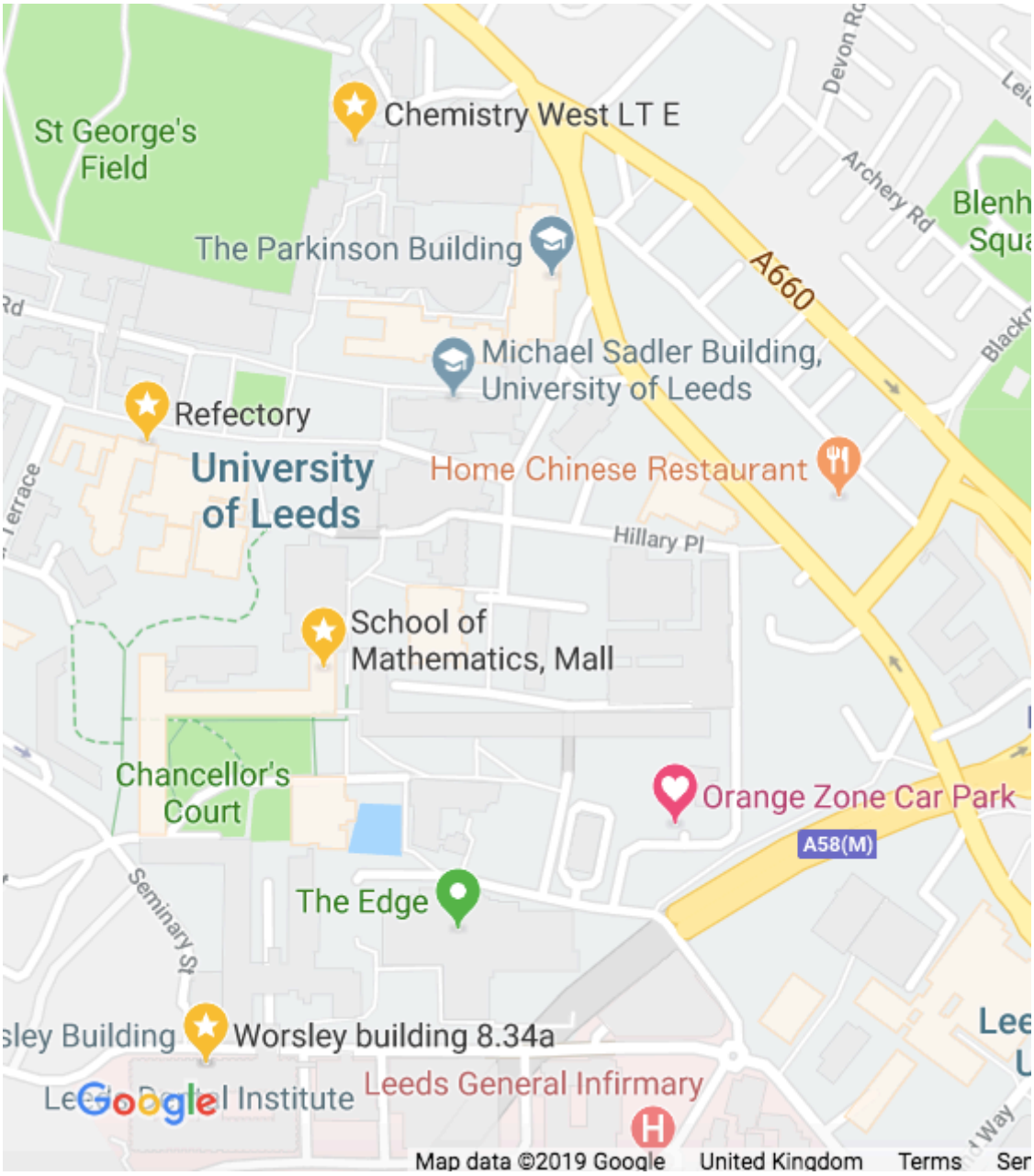
Most of the speakers (and some other participants) will stay at at the Ibis Leeds Centre Hotel. To arrive to the Hotel from Leeds Train Station there are several options:

- Taxi: This will take about 10 minutes and will cost approximately 5 pounds (NB: Uber also operates in Leeds)

- On foot: this should take about 12 minutes to the IBIS hotel.

- To get to the School of Maths from the IBIS hotel, you can walk for about 17 minutes.

A cheaper accommodation can be booked for example in Ibis budget Leeds Centre Hotel, about 30 minutes walk from The University (about 10 minutes by bus plus around 10 minutes walk).


St George's Field
Chemistry West LT E
The Parkinson Building
A660
Michael Sadler Building, University of Leeds
Refectory
University of Leeds
Home Chinese Restaurant
Hillary Pl
School of Mathematics, Mall
Chancellor's Court
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Partner Institutions and Sponsors

The WiN workshop, hosted at the University of Leeds, is one of the three European Cooperation for Statistics of Network Data Science (COSTNET) targeted events for 2019. In particular WiN workshop received the support for 16 fully funded women participants (travel, accommodation and subsistence according to the COST rules).

Sponsors