Mathematics of Large Networks Workshop
Abstracts

2022 May 9-13

Contents

Chapter 1

Invited talks

1.1 Albert-László Barabási

Title: **TBA**

Abstract: TBA

1.2 David Gamarnik

Title: **Overlap gap property: A topological barrier to optimizing over random structures**

Abstract: Many decision and optimization problems over random structures exhibit a gap between the existential and algorithmically achievable values, dubbed as statistics-to-computation gap. Examples include the problem of finding a largest independent set in a random graph, the problem of finding a near ground state in a spin glass model, the problem of finding a satisfying assignment in a random constraint satisfaction problem, and many many more. At the same time, no formal computational hardness of these problems exists which would explain this persistent algorithmic gap.

In the talk we will describe a new approach for establishing an algorithmic intractability for these problems called the overlap gap property. Originating in statistical physics, and specifically in the theory of spin glasses, this is a simple to describe property which a) emerges in most models known to exhibit an apparent algorithmic hardness; b) is consistent with the hardness/tractability phase transition for many models analyzed to the day; and, importantly, c) allows to mathematically rigorously rule out a large class of algorithms as potential contenders, specifically the algorithms which exhibit noise insensitivity.

We will specifically show how to use this property to obtain stronger than the state of the art lower bounds on the depth of Boolean circuits for solving two of the aforementioned problems: the problem of finding a large independent set in a sparse random graph, and the problem of finding a near ground state of a p-spin model.

Joint work with Aukosh Jagannath and Alex Wein

1.3 James Gleeson

Title: **Data-driven modelling of cascades on networks**

Abstract: Network models may be applied to describe many complex systems, and in the era of online social networks the study of dynamics on networks is an important branch of computational social science. Cascade dynamics can occur when the state of a node is affected by the states of its neighbours in the network, for example when a Twitter user is inspired to retweet a message that she received from a user she follows, with one event (the retweet) potentially causing further events (retweets by followers of followers) in a chain reaction. In this talk I will review some mathematical models that can help us understand how social contagion (the spread of cultural fads and the viral diffusion of information) depends upon the structure of the social network and on the dynamics of human behaviour. Although the models are simple enough to allow for mathematical analysis, I

will show examples where they can also provide good matches to empirical observations of cascades on social networks.

1.4 Peter Mörters

Title: **The contact process on dynamical scale-free networks**

Abstract: We investigate the contact process on four different types of scale-free inhomogeneous random graphs evolving according to a stationary dynamics, where each potential edge is updated with a rate depending on the strength of the adjacent vertices. Depending on the type of graph, the tail exponent of the degree distribution and the updating rate, we find parameter regimes of fast and slow extinction and in the latter case identify metastable exponents that undergo first order phase transitions. Joint work with Emmanuel Jacob (ENS Lyon) and Amitai Linker (Universidad Andrés Bello).

1.5 Sofia Olhede

Title: **Local linear graphon estimation**

Abstract: We consider local linear estimation of the graphon function, which determines probabilities of pairwise edges between nodes in an unlabelled network. Real-world networks are typically characterized by node heterogeneity, with different nodes exhibiting different degrees of interaction. Existing approaches to graphon estimation are limited to local constant approximations, and are not designed to estimate heterogeneity across the full network. In this paper, we show how continuous node covariates can be employed to estimate heterogeneity in the network via a local linear graphon estimator. We derive the bias and variance of an oracle-based local linear graphon estimator, and thus obtain the mean integrated squared error optimal bandwidth rule. We also provide a plug-in bandwidth selection procedure that makes local linear estimation for unlabelled networks practically feasible.

This is joint work with Swati Chandna and Patrick Wolfe

1.6 Tiago Peixoto

Title: **Disentangling homophily, community structure and triadic closure in networks**

Abstract: One of the most typical properties of social networks is the presence of homophily, i.e. the increased tendency of an edge to exist between two nodes if they share the same underlying characteristic, such as race, gender, class and a variety of other social parameters. More broadly, when the underlying similarity parameter is not specified a priori, the same homophily pattern is known as community structure. Another pervasive pattern encountered in the same kinds of network is transitivity, i.e. the increased probability of observing an edge between two nodes if they have a neighbor in common. Although these patterns are indicative of two distinct mechanisms of network formation, namely choice or constraint homophily and triadic closure, respectively, they are generically conflated in non-longitudinal data. This is because both processes can result in the same kinds of observation: 1. the preferred connection between nodes of the same kind can induce the presence of triangles involving similar nodes, and 2. the tendency of triangles to be formed can induce the formation of groups of nodes with a higher density of connections between them, when compared to the rest of the network. This conflation means we cannot reliably interpret the underlying mechanisms of network formation merely from the abundance of triangles or observed community structure in network data.

In this talk I present a solution to this problem, consisting in a principled method to disentangle homophily and community structure from triadic closure in network data. This is achieved by formulating a generative model that includes community structure in a first instance, and an iterated process of triadic closure in a second. Based on this model, we develop a Bayesian inference algorithm that is capable of identifying which edges are more likely to be due to community structure or triadic closure, in addition to the underlying community structure itself. As we show, this reconstruction yields a detailed interpretation of the underlying mechanisms of network

formation, allowing us to identify macro-scale structures that emerge spontaneously from micro-scale higher-order interactions, and in this way we can separate them from inherently macro-scale structures. We show how the method can evade the detection of spurious communities caused solely by the formation of triangles in the network, and how it can improve the performance of link prediction when compared to the pure version of the SBM without triadic closure.

1.7 Gergely Röst

Title: **Non-Markovian pairwise epidemics and COVID-19 mitigation on the network of a large bank**

Abstract: TBA

1.8 Thomas Sauerwald

Title: **Choice and Bias in Random Walks**

Abstract: We consider two types of controlled random walks on graphs. In the choice random walk, the controller chooses between two given random neighbours at each step (similar to the power of two choices). In the biased random walk the controller instead has a small probability at each step of a free choice of neighbour. The goal of the controller can be, for example, to minimise hitting times (expected time to visit a vertex), to minimise cover times (expected time to visit all vertices), or to maximise the stationary distribution of a vertex.

Our results on graphs such as grids, bounded-degree trees and expander graphs show that the controller can significantly improve the performance of the random walk. We also discuss one useful tool to analyse controlled random walks, which is its general ability to boost the probability of any unlikely event.

This is based on joint works with Agelos Georgakopoulos, John Haslegrave, Sam Olesker-Taylor and John Sylvester.

1.9 Tamás Vicsek

Title: **Why we live in hierarchies?**

Abstract: Almost all of the systems made of many units are hierarchical, still many of the quantitative aspects of the corresponding hierarchical networks have remained unexplored. There are many questions to answer: Are there typical hierarchical networks and, if yes, what are their main features? Are these many networks hierarchical because such an arrangement makes the underlying structure more efficient? If more efficient, why? Because of better information spreading, or easier adaptation to changing conditions, etc.? This talk will present an overview of the topic mentioning open problems rather than providing solid solutions. Although much more is known about small hierarchical networks, I shall give examples for a few large ones as well.

Chapter 2

Contributed talks

2.1 Zsolt Bartha

Title: **Degree-penalized contact processes**

Abstract: We study degree-penalized contact processes on Galton-Watson trees and the configuration model. In the usual contact process each vertex of a graph is either infected or healthy with the following dynamics: infected vertices heal with rate 1, until which time they infect each of their neighbors with rate λ. We modify this model by replacing λ by a decreasing function of the degrees of the sending and receiving vertices, in order to slow down the spread to and from "superspreaders". We identify several phase transitions in the long-term behavior of the process as the parameters of the model vary.

2.2 Marianna Bolla

Title: **Spectra and Structure of Networks: Discrepancy Based Spectral Clustering and Mapping the Fiedler-carpet**

Abstract: Spectral graph theory started developing about 50 years ago (A.J. Hoffman, M. Fiedler, D.M. Cvetković, and F. Chung) to characterize certain structural properties of a graph by means of the eigenvalues of its adjacency or Laplacian matrix. The famous Fiedler-vector, the eigenvector, corresponding to the smallest positive Laplacian eigenvalue was used to classify the vertices into two parts. Here we use the ensemble of eigenvectors (what we call Fiedler-carpet) corresponding to the $k-1$ smallest positive normalized Laplacian eigenvalues $\lambda_1, \ldots, \lambda_{k-1}$ and prove that $S^2_{2^{k-1}} \leq (\lambda_1 + \ldots + \lambda_{k-1})/\lambda_k$, where $S^2_{2^{k-1}}$ is the minimum of the weighted k-means algorithm, applied to the vertex representatives obtained by the above $k-1$ eigenvectors and classified into 2^{k-1} clusters.

The problem is generalized to directed edge-weighted graphs and rectangular arrays of nonnegative entries (e.g. microarrays); modularity matrices are also used to find clusters with small discrepancy between the pairs. In the rectangular case, we use the SVD of the normalized contingency table and the method of correspondence analysis. We are able to prove that

$$s_k \leq 9\mathrm{md}_k(C)(k + 2 - 9k \ln \mathrm{md}_k(C)),$$

provided $0 < \mathrm{md}_k(C) < 1$, where s_k is the k-th largest singular value of the normalized version of table C (except the trivial 1) and $\mathrm{md}_k(C)$ is the k-way discrepancy of C. However, in the discrepancy estimates, the number of clusters is one more than the number of non-trivial eigenvectors (singular vector pairs) entered into the classification. This is because here Davis-Kahan type subspace perturbation theorems are used that are also effective in case of generalized random or quasirandom graphs and for large networks. For example, in metabolic networks with bidirected edges between the vertices (enzymes), the weights representing the intensity of chemical reactions, so-called autocatalytic subnetworks could be found with our method, based on discrepancies.

2.3 Ivan Bonamassa

Title: **Critical stretching and extreme non-monotonic variations in geometric networks with a characteristic link length**

Abstract: A natural assumption that finds compelling evidence in many real-world networks is the presence of wiring cost functions characterizing the probability of nodes to be connected depending on their Euclidean distance. In particular, geometric networks featuring a finite characteristic link-length ζ, undergo a crossover at ζ from random graph structures to ordered lattices. We will show that this picture changes drastically close to the percolation threshold, where the crossover point *stretches non-linearly* in space and in time until the universal scales $\xi_* = \zeta^{6/(6-d)}$ and $\tau_* = \zeta^{2d/(6-d)}$, as we confirm also in SIR-epidemics. We will further show that the effective critical exponents measured when crossing over between universality classes exhibit extreme *non-monotonic variations*, sometimes with an excess of more than 50% of the total asymptotic change. We explain these effects as the result of the relative sign between the second- and third-order terms of the Wenger-series corrections to critical scaling. Since experimental measures of critical exponents in real-world systems can fall within the crossover region, the practical relevance of these results becomes evident: detailed knowledge of the variation of the effective exponents guarantees a correct interpretation of the data.

2.4 Shengfeng Deng

Title: **Critical synchronization dynamics on power grids**

Abstract: Power-grids are among the largest man-made complex systems, staying in the synchronization state of billions of nodes. Formerly power-law tailed cascade size distributions have been found by outage statistics and DC models. The spread of renewable resources poses unprecedented pressure on system stability. Here we show how this can be modeled by Kuramoto-like synchronization models, which describe the real power flow in AC systems. The combination of swing equations with line threshold failures allows us to describe the dynamical avalanche-like blackout failures in different HV power-grid networks. In particular, we compare the stability and blackout statistics for the US and the EU HV networks, taking into account the feedback effects. We show that nonuniversal power-law size and duration distributions emerge below the first-order transitions of the Kuramoto model, thus we see an example for hybrid transition known in other branches of physics.

joint work with Géza Ódor, Bálint Hartmann, and Jeffrey Kelling

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[2] I. Dobson, B. A. Carreras, V. E. Lynch and D. E. Newman, Complex systems analysis of series of blackouts: Cascading failure, critical points, and self-organization, Chaos Interdiscip. J. Nonlinear Sci. 17, 026103 (2007).
[3] B. Schäffer, D. Witthaut, M. Timme and V. Latora, Dynamically induced cascading failures in power grids, Nat. Commun 9, 1975 (2018).
[4] Géza Ódor and Bálint Hartmann, Heterogeneity effects in power grid network models, Phys. Rev. E 98, 022305 (2018).
[5] Géza Ódor and Bálint Hartmann, Power-Law Distributions of Dynamic Cascade Failures in Power-Grid Models, Entropy 22 666 (2020).

2.5 Tejas Iyer

Title: **A phase transition induced by competition in preferential attachment models with fitness**

Abstract: Motivated, in part, by the evolution of complex networks, we consider models of recursive random trees with inhomogenieties, so that the evolution of the degree of a node may depend on not only its degree, but on a (possibly random) weight associated to that node. These weights

lead to an interesting structure in the evolution of the network where newer nodes may compete for influence with older nodes. Under quite general conditions, we prove the existence of a phase transition in the limiting infinite tree where either every node has infinite degree, or there exists a unique infinite path in the model. In the latter case, every node has finite degree, but the maximal degree tends to infinity along the infinite path. We apply these results to some well-known models, including the Bianconi-Barabási model of preferential attachment with multiplicative fitness. We will also discuss applications of these results to models of evolving simplicial complexes, studied by Bianconi, Rahmede and other authors. Based on joint work with Bas Lodewijks.

2.6 Abbas Karimi Rizi

Title: **Herd Immunity and Epidemic Size in Networks with Vaccination Homophily**

Abstract: We study how the herd immunity threshold and the expected epidemic size depend on homophily with respect to vaccine adoption. We find that the presence of homophily considerably increases the critical vaccine coverage needed for herd immunity and that strong homophily can push the threshold entirely out of reach. The epidemic size monotonically increases as a function of homophily strength for a perfect vaccine, while it is maximized at a non-trivial level of homophily when the vaccine efficacy is limited. Our results highlight the importance of vaccination homophily in epidemic modeling.

`arXiv`: 2112.07538

2.7 Leah Keating

Title: **Multi-type branching process method for modelling complex contagion on clustered networks**

Abstract: Online social networks such as Twitter, Facebook, Instagram and TikTok serve as media for the spread of information between their users. We are interested in developing models for this information diffusion to gain a greater understanding of its drivers. Some models for the spread of online behaviour and information assume that the information behaves similarly to a virus, where infection is equally likely after each exposure, these dynamics are known as a simple contagion. In a simple contagion, the exposures are independent of each other. However, online adoption of some behaviour and content has been empirically observed to be more likely after multiple exposures from their network neighbours [1-2], the exposures are not independent of each other, we refer to this as a complex contagion. Analytically tractable descriptions of complex contagions have been developed for continuous-time dynamics. These extend mean-field and pair approximation methods to account for clustering in the network topologies [3]; however, no such analogous treatments for discrete-time cascade processes exist using branching processes. We describe a novel definition of complex contagion adoption dynamics and show how to construct multi-type branching processes which account for clustering on networks [4]. We achieve this by tracking the evolution of a cascade via different classes of clique motifs which contain different numbers of active, inactive and removed nodes. This description allows for accurate analytical calculation of cascade sizes, determination of critical behaviour and we also describe how the branching process description allows us, using probability generating functions, to derive full distributions of cascade sizes and other quantities of interest from the model.

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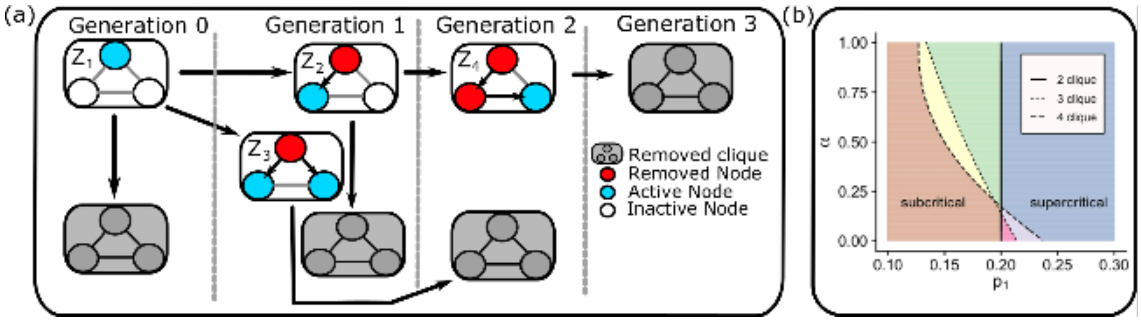

Figure 2.1: (a) The possible motifs in a network composed with 3-cliques. Active nodes are shown in red, inactive nodes are white and removed nodes are grey. The arrows represent the direction of the diffusion. (b) Critical behaviour for k-regular clique network we consider.

2.8 Dániel Keliger

Title: **Switchover phenomenon of percolation models on graphs**

Abstract: We examine the pandemic size of SIR process with unit recovery time on networks. The problem is equivalent to finding the clusters of an initial seeding on a percolated graph. Conventional wisdom would tell that starting the infection from well-connected regions will inevitable lead to higher infection size as it is easier to reach other vertices from highly clustered regions. We would like to challenge this picture by showing the existence of a certain switchover phenomena: while for small infection rates starting the process from a central region does result in a higher pandemic size compared to a uniform seeding, the later takes the lead for larger infection rates. The phenomena is illustrated via numerical experiments on synthetical and real life networks attained from Hungarian mobility data, while rigorous results are provided for random power-law networks near criticality and for general networks under mild assumptions when the retention probabilities are close to 0 and 1.

Joint work with Gergely Ódor, Domonkos Czifra, Júlia Komlyáthy, László Lovász, Márton Karsai, Tamás Móri

2.9 Lukas Lüchtrath

Title: **The various phases of long-range inhomogeneous percolation**

Abstract: We consider a large class of inhomogeneous spatial random graphs where the vertex set is given by a Poisson process in Euclidean space and each vertex carries additionally an i.i.d. weight. Edges are drawn in such a way that short edges and edges to large weight vertices are preferred. This allows in particular the study of models that combine long-range interactions and heavy-tailed degree distributions. The occurrence of long edges together with the hierarchy of the vertices coming from the weights typically leads to very well connected graphs. We identify a sharp phase transition where the existence of a subcritical percolation phase becomes impossible. This transition depends on both the power law of the degree distribution and on the geometric model parameter, showing the significant effect of clustering on the graph's topology. We consider afterwards the specifics of dimension one in parameter regimes where a subcritical phase exists. Due to the geometric restrictions of the line, it is fairly hard to generate infinite clusters in this case and many established models admit no supercritical phase. We identify sharply how the combination of weights and long-range effects can lead to infinite clusters in situations where both effects alone are not strong enough for an infinite cluster to exist. Natural examples that are contained in our framework are for instance the random connection model, the Poisson Boolean model, scale-free percolation, the age-dependent random connection model and their soft versions.

Joint work with Peter Gracar, Christian Moench and Peter Moerters.

2.10 Xiangyi Meng

emphTitle: **Physical Network as a Manifold**

Abstract: A physical network, e.g., neurons, vascular system, tree, etc. is not only a combinatorial object – a graph of nodes and links – but also a geometric object that is tangible and smooth in the real world, hence mathematically best described as a differentiable d-manifold, i.e., a "morphologically shaped" d-dimensional space that is locally smooth everywhere.

Inspired by string theory, we find that a network can indeed be made such a manifold when $d > 1$, by minimally adding extra degrees of freedom (d.o.f.) that suffice to describe the shapes of individual nodes and links. For example, we find that each degree-k node needs $2(k-3)$ d.o.f. and each link needs 2 d.o.f. to minimally make a network a 2-manifold (surface), appearing as a bunch of tubes (as links) sewed together (through nodes).

This manifold-based description further motivates us to introduce a general manifold economy principle for physical networks, where the economy goal is not to optimize the total length of all links given fixed terminals to connect (i.e., a traditional wiring economy) but the total d-measure (surface area, volume, etc.) of the manifold. We focus on $d = 2$, introducing a special surface minimization scheme that keeps the circumference of each tube fixed, finding that the new economy principle predicts two novel structural transitions: a transition from bifurcation regime to trifurcation regime and a transition from a bifurcation regime with planar but crooked tubes to another bifurcation regime with straight tubes. Both transitions happen at some nontrivial length-over-circumference ratios of the tubes and are strictly forbidden by traditional wiring economy, but are often observed in real biological networks.

2.11 András Molnár

Title: **Learning the parameters of a differential equation from its trajectory via the adjoint equation**

Abstract: The aim of the talk is to present a result strengthening the relation between machine learning and the theory of differential equations. In this context, the inverse problem of fitting the parameters, and the initial condition of a differential equation to some measurements constitutes a key issue. We present an abstraction that can be used to construct a family of loss functions with the aim of fitting the solution of an initial value problem to a set of discrete or continuous measurements. We show, that an extension of the adjoint equation can be used to derive the gradient of the loss function as a continuous analogue of backpropagation in machine learning. Lastly, we offer numerical evidence that under reasonably controlled circumstances the gradients obtained this way can be used in a gradient descent to fit the solution of an initial value problem to a set of continuous noisy measurements, and a set of discrete noisy measurements that are recorded at uncertain times.

2.12 Gergely Ódor

Title: **Source Identification via Contact Tracing in the Presence of Asymptomatic Patients**

Abstract: Inferring the source of a diffusion in a large network of agents is a difficult but feasible task, if a few agents act as sensors revealing the time at which they got hit by the diffusion. One of the main limitations of current source identification algorithms is that they assume full knowledge of the contact network, which is rarely the case, especially for epidemics, where the source is called patient zero.

In this talk, we propose a new framework inspired by recent implementations of contact tracing algorithms, which we call Source Identification via Contact Tracing Framework (SICTF). In the SICTF, the source identification task starts at the time of the first hospitalization, and initially we have no knowledge about the contact network other than the identity of the first hospitalized agent. We may then explore the network by contact queries, and obtain symptom onset times by test queries in an adaptive way, i.e., both contact and test queries can depend on the outcome of previous queries. We also assume that some of the agents may be asymptomatic, and therefore cannot reveal their symptom onset time. Our goal is to find patient zero with as few contact and test queries as possible. We propose two local search algorithms for the SICTF: the LS algorithm is more data-efficient, but can fail to find the true source if many asymptomatic agents are present, whereas the LS+ algorithm is more robust to asymptomatic agents. By simulations we show that

both LS and LS+ outperform state of the art adaptive and non-adaptive source identification algorithms adapted to the SICTF, even though these baseline algorithms have full access to the contact network. Extending the theory of random exponential trees, we analytically approximate the probability of success of the LS/ LS+ algorithms, and we show that our analytic results match the simulations. Finally, we benchmark our algorithms on a Data-driven COVID-19 Simulator, which is the first time source identification algorithms are tested on such a complex dataset.

joint work with Jana Vuckovic, Miguel-Angel Sanchez Ndoye, and Patrick Thiran

2.13 Géza Ódor

Title: **Critical dynamics on large connectome networks**

Abstract: Neural graphs, called connectomes, contain large number of nodes, $N \simeq 10^{11}$ for human $N \simeq 10^5$ for a fly brain, and average node degree of the order of $< k > \simeq 1000$. These connectomes exhibit hierarchical modular structure, with increasing complexity as we move from simple animals to humans. The weight distributions show power-law tails as the consequence of learning, but many of the incoming weights are suppressed or flipped to negative by inhibitors, providing a local homeostasis during brain operation. Optimal computing, storing and communicating capabilities are obtained by dynamics close to a critical point, edge of chaos, resulting in power-law activity avalanche size and duration, that has been confirmed in various electrode and other brain experiments. Here I show some simple models running on the connectomes of a fly and a human brain, reproducing such power-laws. In particular I compare the differences obtained on the almost Erdos-Renyi like fly and a large, whole human brain connectome.

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[4] Géza Ódor, Gustavo Deco and Jeffrey Kelling What makes us humans: Differences in the critical dynamics underlying the human and fruit-fly connectome, arXiv:2201.11084 to appear in Phys. Rev. Research.

2.14 Márton Pósfai

Title: **Linear physical networks**

Abstract: Physical networks – networks with nodes and links that are physical objects embedded in space – are shaped by constraints such as volume exclusion, the cost of building and maintaining nodes and links, and local assembly. Examples of such networks include neural networks, vascular networks, polymer networks, and root systems. Although an increasing number of datasets are available that describe the full three dimensional structure of networks, it is difficult to disentangle the role of physical constraints and other processes. Therefore, we propose studying a minimal model of physical networks that is simple enough to remain tractable, yet captures mechanisms through which physicality manifests itself. Specifically, we introduce a random model of linear physical networks (LPN), where nodes are spheres and links are cylinders with fixed diameter. We generate an LPN by randomly placing N nodes in the unit cube and connect node pairs in random order if it does not violate physicality. We study the properties of the jammed state, i.e. networks with maximal number of physical links. We introduce the meta-graph, an auxiliary graph that captures the physical conflicts in the system, and we map the construction of physical networks to finding independent sets in the meta-graph. This mapping provides analytical tools to characterize the onset of physicality and the jammed state.

2.15 Sina Sajjadi

Title: **Structural inequalities exacerbate infection disparities: A computational approach**

Abstract: Official reports on the COVID-19 pandemic reveal disproportionate infection rates in lower socioeconomic groups whose economic insecurities outweigh concerns about the infection risk. Motivated by this issue, our research introduces a model for studying the effects of income inequality on infection rates during pandemics (or public health crises). We analyze the disparity of infection cases across different race and income groups within a context of residential segregation by constructing a novel agent based model which combines:
1. A network model for segregated communities using inter-group exposure indices
2. A decision making model governing agents' choices to go out to work vs. quarantining themselves.
3. An SIR model describing the infection spreading.

We develop both an individual-based model (ABM) and a mean-field model (ODE) and find that their results are in agreement. We find that infection rate is directly influenced by the existing level of income. More importantly, socioeconomic inequality increases the overall infection rate of the population. Our results convey a significant message for policy makers. Governments can slow down the spread of the infection by providing financial aids to low-income households; improving the latter's financial security will enable them to stay in. This study offers a modeling framework to understand socioeconomic factors affecting the dynamics of infection.

2.16 Ulysse Schaller

Title: **One-neighborhood biased first passage percolation on scale-free spatial random graphs**

Abstract: We study first-passage percolation in which the transmission time between two nodes increases by a penalty factor polynomial in the expected degree of the vertices, to model limited time and awareness of nodes with large degree. We consider two spatial scale-free random graph models: (finite and infinite) Geometric Inhomogeneous Random Graphs, and Scale-Free Percolation. In these spatial models, the connection probability between two vertices depends on their distance and on their expected degrees. We find that the transmission time between two far away vertices (the weighted distance with respect to first passage percolation) undergoes three phase transitions as the penalty exponent increases, and deviates more and more from classical first passage percolation. For small penalties, it was already known that the transmission time between two vertices at distance x converges in distribution as x grows, a phenomenon called explosion. We show that, as the penalty exponent gradually increases, the transmission time becomes longer and grows with x: first (at most) poly-logarithmically; then polynomially, but strictly sublinear; then linearly.

joint work with Júlia Komjáthy, John Lapinskas and Johannes Lengler

2.17 Eszter Sikolya

Title: **Stochastic reaction–diffusion equations on networks**

Abstract: We consider stochastic reaction–diffusion equations on a finite network, reperesented by a finite graph. On each edge of the graph, a multiplicative cylindrical Gaussian noise driven reaction–diffusion equation is given, supplemented by a dynamic Kirchhoff-type law perturbed by multiplicative scalar Gaussian noise in each vertex. The reaction term on each edge is assumed to be an odd degree polynomial, not necessarily of the same degree on each edge, with possibly stochastic coefficients and negative leading term. We utilized the semigroup approach for stochastic evolution equations in Banach spaces to obtain existence and uniqueness of solutions with sample paths in the space of continuous functions on the graph.

joint work with Mihály Kovács (PPKE ITK and BME)

2.18 Péter L. Simon

Title: **On parameter identifiability in epidemic models**

Abstract: Fitting epidemic models to synthetic or real-world data is of great interest as it allows us to infer model parameters which in turn helps us to (i) learn more about the disease, (ii) implement and test control scenarios via simulations, and (iii) make short- or long-term predictions about the epidemic. A myriad of ODE-based epidemics are available with many providing explicit or implicit analytical expressions for quantities such as the basic reproduction number (or leading eigenvalue based on the linear stability analysis around the disease-free steady state), timing and/or peak prevalence, final epidemic size etc. Given a synthetic or real-epidemic and being able to measure several the aforementioned quantities, we investigate if it is possible to determine the parameters of the epidemic model that generated the data. We start with simple models such as the well-mixed susceptible-infected-recovered (SIR) compartmental model, followed by more complex models such as, the pairwise the edge-based compartmental model. We show that except for the simplest of models, there are clear parameter identifiability problems which we map out and explain analytically, where possible. In models with a larger number of parameters, it is often the case that many different combinations of the model parameters (with many individual parameters being far from their true values) result in output which is consistent with the true epidemic. From a parameter inference viewpoint this presents some important challenges which need to be mitigated carefully.

joint work with István Kiss

2.19 Ádam Tímár

Title: **Physical networks generated by loop-erased random walks**

Abstract: Physical networks are networks represented in the Euclidean space with edges thought of as physical objects with some constraint, e.g. they cannot intersect. We define a model through a dynamical process: a sequence of loop-erased random walks on the grid, run until they hit the previously constructed piece of the network. The trajectory of one such walk will then be a vertex of the corresponding abstract network, with adjacencies given by how the trajectories hit. We argue that in dimension at least 5 the network follows the same degree distribution $\P[\deg_i > t] = t^{-3+o(1)}$ as the Barabási-Albert preferential attachment trees. For dimension 2, the detailed knowledge coming from the conformally invariant scaling limit of the Uniform Spanning Forest suggests that 2.6 should be the tail exponent, separating it from the "mean field preferential attachment" exponent 3, and indicating an exciting phase transition. We also show various properties of the infinite-volume limit of this network and work towards a description of a scaling limit. This is a joint project with G. Pete, M. Pósfai and S. Ö. Stefánsson.

2.20 Rik Versendaal

Title: **Sampling simple random graphs under degree and edge-weight constraints**

Abstract: In [1], the problem was studied of sampling simple random graphs with degree constraints, which is typically a hard problem. Therefore, the authors proposed a sequential algorithm that samples such graphs asymptotically uniformly at random, when the number n of vertices tends to infinity.

In this talk, we will extend the algorithm in [1] to also include edge-weights. More specifically, we first assign random weights to all edges according to some probability distribution g_n and consider some target edge-weight distribution f_n. We then aim to sample random graphs satisfying some prescribed degree sequence, while additionally having empirical edge-weight distribution close to the target distribution f_n.

We make this statement precise by proving that with high probability the empirical edge-weight distribution of the random graph produced by our algorithm is close to f_n in Wasserstein distance. The key assumption for this is that the target edge-weight distribution f_n is not too large compared to the distribution g_n of the edge-weights, i.e., $f_n \leq C_n g_n$ for some constant $C_n > 0$. This constant is allowed to grow moderately with n, being $C_n = \mathcal{O}(n^\tau)$ for some $\tau < 1$. The proof of this result mainly relies on a variety of concentration inequalities.

Finally, we will discuss what happens in the boundary case where $C_n = \mathcal{O}(n)$. This for example occurs when studying graphs under geometric constraints in the box $[0,1]^d$, where the connection threshold is in the critical regime, i.e., of order $n^{\frac{1}{d}}$.

joint work with Ivan Kryven

[1] Mohsen Bayati, Jeong Han Kim, and Amin Saberi. "A sequential algorithm for generating random graphs". In: Algorithmica 58.4 (2010), pp. 860–910.

2.21 Anita Windisch

Title: **Dynamical effects of inhibitory neurons in neurobiological networks**

Abstract: Mathematical modelling of neuronal networks plays an important role in understanding how human brain and memory work. These models can be treated as dynamical systems enabling us to use bifurcation theory to investigate the changes in the states of neurons. Neuronal networks can be represented as directed graphs with weighted edges. Our main goal is to describe the dynamical behaviour for some special networks by applying analytical and numerical tools. We focus on the effect of weights to the number of steady states and to their stability.

joint work with Dr. Simon Péter