19w5071 - Scaling Limits of Dynamical Processes on Random Graphs

Grzegorz Rempała (The Ohio State University, rempala.3@osu.edu)
Heinz Koeppl (Technische Universität Darmstadt, heinz.koeppl@bcs.tu-darmstadt.de)
Rick Durrett (Duke University, rtd@math.duke.edu)
Remco van der Hofstad (Eindhoven University of Technology, rhofstad@win.tue.nl)

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1 Overview of the Field

The field "dynamical processes on networks" is the marriage of two diverse disciplines that have long been studied independently. Given a random graph with n vertices, we endow each vertex a "state" that changes over time as the vertex interacts with its neighbors. This defines a stochastic process on the graph. The probability law of the stochastic process depends on the rules of interaction among the vertices. Such systems arise naturally in physics, epidemiology, computer science and engineering disciplines. An example from epidemiology would be the spread of an infectious disease over a human population, which, in the eyes of a computer scientist, also describes the spread of virus, or information dissemination over a computer network. In this workshop, we specifically focused on scaling limits of such systems as the size of the network grows arbitrarily large. For instance, we asked questions like "can we approximate the limiting process by a simpler mathematical description? If so, under what conditions? How accurate are the standard statistical physics mean-field scaling limits? When do the mean-field limits become exact, if at all? How does the structure of the network impact the limiting process? Is the degree distribution sufficient to describe the limiting process? If there are two or more competing processes such as infectious diseases, which one will eventually pervade the entire graph? Is steady co-existence of two or more competing processes possible? If so, for which class of random graphs" etc.

Dynamical processes on networks have accrued growing research interest over the years primarily because of its vast applicability. We come across a host of dynamical processes arising from epidemiology [17], biology [19, 18, 20, 21], statistical physics [22, 23, 24], and computer science [30, 31, 32, 33]. These dynamical processes are often similar and hence, lend themselves to application across disciplines [27, 28, 29]. An account of major developments in the field can be found in [10, 11, 12]. With the overwhelming proliferation of social networks, never has it been more important to understand and model the spread of rumour, the dissemination of propaganda, or the very behaviour of social networks in general, which is often quite complex and adaptive. As our dependence on computer networks grows, so does the need to better understand and prevent the spread of computer viruses. Similarly, incorporating network structure and studying its impact on various epidemic process is also the need of the hour. The proposed workshop would therefore be opportune.

Although dynamical processes on random graphs themselves have been studied by mathematicians, physicists, epidemiologists, computer scientists and engineers for some time now, a comprehensive and mathematically rigorous body of work on various scaling limits (such as laws of large numbers, central limit theorems, large and moderate deviations) under general settings remains elusive. Such scaling limits have been derived rigorously only for a handful of special cases till date. Notable breakthroughs in the context of epidemiological processes include [43, 45, 42, 2, 1], appearing primarily in probability literature. Classical models arising from statistical physics have also been transferred to a random graph setting from the traditional lattice assumption. First passage percolation, for instance, has been studied rigorously on random graphs and several scaling limits have been derived, see [4, 6] and the references therein. Another example is scaling limits of (critical) percolation clusters, see [5, 7, 8, 9] and the (many) references therein. For an extended discussion, we refer to [10], where also thermodynamic limits of the Ising model are discussed and a rather complete overview of the literature is given.

The above models are especially interesting from a non-equilibrium perspective. Competition on random graphs has also attracted some attention of late [15, 14, 16]. There has already been a considerable amount of research work in the network science discipline, covering various statistical features of static networks. These aspects will not be covered in this workshop. We specifically focus on scaling limits as we believe a rich body of rigorously derived mathematical results on scaling limits still needs to be consolidated. We also consider models where the random graph itself may change as a result of the interactions among the vertices, as we would expect in many real life applications.

The two main mathematical objects are: i) a random graph $G = (V, E)$, where $V = \{1, 2, \ldots, n\}$, for some natural number n, is the set of vertices and $E \subseteq V \times V$ is the set of edges; and ii) a (multivariate) stochastic process X capturing the dynamical process on G. Depending on the dynamical process, X will often be a vector of counts or proportions (corresponding to a partition of the population), for example, counts of susceptible, infected and recovered (or removed) individuals in a stochastic compartmental SIR model [13]. The law of X depends on n and the properties of the random graph G. Given a class of random graphs, we seek to find a scaling sequence $a_n > 0$ (a non-decreasing sequence of positive real numbers) such that: i) $\sup_t ||a_n^{-1}X(t) - x(t)|| \to 0$ in probability as $n \to \infty$ where x satisfies some suitable ordinary differential equation (ODE); or ii) $a_n^{-1}X \Rightarrow \tilde{X}$ weakly in some appropriate topology, where $\tilde{X}$ is some limiting process such as a gaussian (vector) martingale. We ask questions like "what restrictions do we need to impose on the class of random graphs to ensure existence of such a scaling sequence a_n? Under what (additional) condition(s) can the results be strengthened to almost sure convergence or L^r-convergence for some $r > 0$"? Establishing corresponding large and moderate deviations principles will also be crucial. It will be interesting to compare these limiting results with those obtained by tools from statistical physics such as the mean field techniques.

2 Recent Developments and Open Problems

One line of research has been inspired by the mean-field approach from statistical physics. Direct applications can be found in [27, 28] where the authors study epidemic dynamics on scale-free networks of [35]. A majority of work in this direction aims at obtaining limiting ODEs for the proportions of different compartments of the population. Notwithstanding the simplicity of these methods, the scaling limits presented are by design approximate and lack mathematical rigour. See [11, Chapter 1] for a critique.

The standard mean-field method was further improved by use of pair-approximation in [36, 37, 38]. Several other improvements yielding less approximate results have been proposed afterwards. A detailed account is presented in [12]. Some of these approximate results have been followed up by probabilists and improved upon [11, 40, 39]. Several of the classical models from statistical physics that were traditionally studied on lattices, have been transferred to a random graph setting. For instance, several scaling limits have been rigorously derived for first passage percolation on random graphs [10]. Competing first passage percolation on random graphs is also an emerging research topic [16].

Some promising developments have been made in the mathematical epidemiology literature. Anderson [45] provided limits theorems for a discrete-time random graph epidemic model. However, he made stringent assumptions on the degree sequence of the underlying random graph, for example, finiteness of $(4+\delta)$-th moment, for some $\delta > 0$. The work of Erik Volz in [41] aroused much interest among probabilists. He presented ODE limits for an SIR model on random graphs. Decreusefond et al. [43] later on provided rigorous proof of Volz's results. They considered configuration model random graphs and summarised the epidemic process into three measure-valued equations. Several works with the aim to provide laws of large numbers-type scaling limit came out in quick succession and under varying sets of technical assumptions. For example, [46, 47] assume uniformly bounded degrees, [44] assumes degree of a randomly chosen susceptible vertex is uniformly integrable and the maximum degree of the initially infected vertices is not too large. Recently [42] derived similar laws of large numbers for stochastic SIR on a multilayer configuration model assuming finiteness of the second moment of the underlying degree distribution. Two recent works developed diffusion approximations of such epidemic processes on random graphs. A functional central limit theorem for a susceptible-infected (SI) process on configuration model random graphs was developed in [2]. On the other hand, [1] developed a diffusion approximation for a partner model (susceptible-infected-susceptible) with random formation and dissolution of partnerships.

Recent developments in the context of biochemical reactions and social networks merit a mention. While there is no explicit graph structure (due to the classical well mixing assumption) in the biochemical reaction setting, the literature is rich with plentiful mathematical results (including scaling limits) for the underlying Markovian population model, making use of probabilistic tools. See, for example, [49, 48]. On the social networks side, emerging complex adaptive behaviour has received much attention. These works do not directly address the research questions of this workshop, but do reveal connections to game theory, agent-based models [52].

3 Presentation Highlights

Epidemics on networks

Grzegorz Rempala: ***Survival dynamical systems on random graphs.***

The idea of a survival dynamical system (SDS) is to apply aggregated dynamics of a macro model at the level of an individual agent. SDS may be also viewed a limit of agents' dynamics obtained when replacing individual's random hazard function with its large volume limit. Under this second interpretation it is relatively simple to obtain an extension of the classical mass-action SDS to a configuration model random graph and to provide some basic results allowing for estimating the underlying epidemic parameters from micro-level data. As it turns out, in a certain class of degree distributions the SDS model takes a particularly simple from and its statistical analysis is only moderately more complicated than the classical mass- action SDS as given by the standard SIR equations.

Eban Kanah and Wasiur KhudaBukhsh: ***Population-level survival analysis from individual-level transmission models (Parts 1-2).***

In recent paper [55] it was shown that solutions to Ordinary Differential Equations (ODEs) describing the large-population limits of Markovian stochastic compartmental dynamical systems could be interpreted as survival or hazard functions when analyzing data from the individuals sampled from the population. An earlier paper by Kenah [54] showed that likelihoods from individual-level mass-action transmission models simplify in the limit of a large population when the depletion of susceptibles is negligible. In their presentations the speakers described generalizations of these results by deriving population-level survival and hazard functions from explicit individual-level models. This approach allows, for instance, for population-level survival analysis methods to be applied to a more general class of epidemic models and allows the asymptotic pairwise likelihoods to be applied throughout the course of an epidemic. In practice, this will provide a logically consistent framework for the analysis of both high-resolution outbreak investigations or household studies and population-level surveillance or sentinel data.

Samuel Scarpino: ***Behaviour-induced phase transitions in contagion models on networks.***

Seemingly trivial modifications to the classical model of contagion spreading can dramatically alter its phenomenology. For example, discontinuous phase transitions can occur due to complex or interacting contagions, accelerating transmission and hysteresis loops can occur when individuals modify their behaviour after becoming infectious, and double phase transitions can emerge in the presence of asymmetric percolation. Scarpino presented recent theoretical work on the effect of behaviour on contagion spreading and discussed empirical support for such new models. His findings nicely demonstrate the inherent complexity of biological contagion and we believe that his methods will advance the emerging field of disease forecasting.

Piet Van Mieghem: ***Epidemic Spread on Networks***

Epidemic models are increasingly applied in real-world networks to understand various kinds of diffusion phenomena (such as the spread of diseases, emotions, innovations, failures in economic networks) or the transport of information (such as news, memes in social online networks and activity in functional human brain networks). Van Mieghem focused in his talk on Susceptible-Infected-Susceptible (SIS) epidemics on networks. SIS Markovian epidemics on a given, fixed graph is one of the simplest "local rule - global emergence" models and allow for a remarkable level of mathematical analysis. Van Mieghem provided a review of known results for the SIS model in continuous time and give new mean field approximation results extending classical pair approximations.

Joel Miller: ***Contagion spread in clustered and unclustered small world networks***

He first discussed a class of random spatial networks and show that they have "small world"-like properties, but the level of clustering is tunable and can be made it arbitrarily small. In some limits we are able to derive a system of integro-differential equations which allows us to accurately predict both the temporal and spatial dynamics of SIR disease. These equations can be used to determine when the network behaves like a small world network with significant long-range transmissions and when the dynamics are dominated by the short-range transmission. Interestingly, the "small-world" properties of disease spread can exist even in the limit of no clustering, and thus the concept of a small-world network is determined more by whether the network has a combination of short-range and long-range connections than whether the network has many clustered connections.

Tom Britton: ***Epidemics in structured communities with social distancing***

Britton's talk was an example for recent works in the domain of changing networks. He again considered epidemics on large, structured networks. Infectious individuals spread the disease to each of their susceptible neighbors, independently, at rate λ, and each infectious individual recovers and becomes immune at rate γ. The social distancing is modeled by each susceptible who has an infectious neighbor rewires away this individual to a randomly chosen individual at rate ω. The main result of Britton is surprising and says: the rewiring is rational from an individual perspective in that it reduces the risk of being infected, but at the same time it may be harmful for the community at large since the outbreak may get bigger compared to no rewiring ($\omega = 0$).

David Sivakoff: ***The Contact Process with Avoidance***

Sivakoff's talk also considered time-varying networks. The classical contact process is a stochastic process on the vertices of a graph, which is a discrete, spatial model for the spread of a disease. The state of the contact process at time t is given by an infected subset of the vertices of the graph. At rate 1, each infected vertex becomes healthy, and therefore susceptible to reinfection. At rate $\lambda > 0$, each edge between an infected vertex and a healthy vertex transmits the infection, thus infecting the healthy vertex. The contact process has been thoroughly analyzed on the integer lattices and regular trees, where it is well-known to exhibit a phase transition: for large lambda, epidemics persist, while for smaller lambda, all vertices are eventually healthy. More recently, the community has made progress in analyzing the behavior of the contact process on (finite) complex networks, where epidemics may persist for all $\lambda > 0$ on graphs with 'heavy-tailed' degree distributions. Sivakoff presented recent progress on a version of the contact process in which the edges of the graph are also dynamic: at rate α, each edge from an infected vertex to a healthy vertex will deactivate; the edge will become active again when the infected vertex becomes healthy, and only active edges can transmit the infection. This emulates avoidance of infected individuals by healthy individuals. Sivakoff showed that the long-time qualitative behavior of this model may or may not differ from the classical contact process, depending on the underlying network topology.

Models and methods from physics

Souvik Dhara: ***Critical behavior for percolation on graphs with given degree***

He discussed the critical behavior of percolation on finite random networks. In a seminal paper, Aldous (1997) identified the scaling limit for the component sizes in the critical window of phase transition for the Erdos-Renyi random graph (ERRG). Subsequently, there has been a surge in the literature, revealing several interesting scaling limits of these critical components, namely, the component size, diameter, or the component itself when viewed as a metric space. Fascinatingly, when the third moment of the asymptotic degree distribution is finite, many random graph models have been shown to exhibit a universality phenomenon in the sense that their scaling exponents and limit laws are the same as the ERRG. In contrast, when the asymptotic degree distribution is heavy-tailed (having an infinite third moment), the limit law turns out to be fundamentally different from the ERRG case and in particular, becomes sensitive to the precise asymptotics of the highest degree vertices. In this talk, we will focus on random graphs with a prescribed degree sequence. We start by discussing recent scaling limit results, and explore the universality classes that arise from heavy-tailed networks. Of particular interest is a new universality class that arises when the asymptotic degree distribution has an infinite second moment. Not only it gives rise to a completely new universality class, it also exhibits several surprising features that have never been observed in any other universality class so far. This is based on joint works with Shankar Bhamidi, Remco van der Hofstad, Johan van Leeuwaarden and Sanchayan Sen.

Cristian Giardina: ***Quenched and annealed Ising models on random graphs***

Giardina considered the ferro-magnetic Ising model in a setting where the regular spatial structure is replaced by a random graph, which is often used to model complex networks. He discussed both the case where the graph is essentially frozen (quenched setting) and the case where instead it is rapidly changing (annealed setting). He showed that quenched and annealed case may have different critical temperatures, provided the graph has sufficient inhomogeneity. He also showed how universal results (law of large numbers, central limit theorems, critical exponents) are affected by the disorder in the spatial structure. The presented results emerged from collaboration with .H. Can, S. Dommers, C. Giberti, R.van der Hofstad and M.L.Prioriello.

Thilo Gross: : ***A master-stability-function approach to diffusive instabilities in a meta-foodweb***

Gross presented work on diffusion-driven pattern formation in a class of multilayer systems, where different layers have the same topology, but different internal dynamics. Thereby agents are assumed to disperse within a layer by undergoing random walks, while they can be created or destroyed by reactions between or within a layer. Gross showed that the stability of homogeneous steady states can be analyzed with a master stability function approach that reveals a deep analogy between pattern formation in networks and pattern formation in continuous space. He considered a generalized model of ecological meta-food webs as an application. This fairly complex model describes the dispersal of many different species across a region consisting of a network of individual habitats while subject to realistic, nonlinear predator-prey interactions. In this example, the method reveals the intricate dependence of the dynamics on the spatial structure. The ability of the proposed approach to deal with this fairly complex system highlights it as a promising tool for ecology and other applications.

Silvio C. Ferreira: ***Eigenvector localization, dynamical correlations and epidemic thresholds on random networks with degree correlations***

Ferreira presented a comparison between large-scale stochastic simulations and mean-field theories for the epidemic thresholds and prevalence of the SIS model on networks with power-law degree distributions and degree correlations. The simulation confirm the vanishing of the threshold regardless of the correlation pattern and degree exponent. The thresholds are compared with heterogeneous mean-field (HMF), quenched mean-field (QMF) and pair quenched mean-field (PQMF) theories where the degree correlation patterns are explicitly considered. The PQMF, which additionally reckons dynamical correlations, outperforms the other two theories and its level of quantitative success depends on the type of degree correlation (assortative, disassortative or uncorrelated). Furthermore, Ferreira reported on the strong correlation between the success of PQMF theory and the properties of the prgincipal eigenvector such as the inverse participation ration (IPR) and the spectral gap. If the IPR is large and tends to a finite value at the limit of large networks the PQMF predictions deviate from numerical simulations. Otherwise, if the IPR is small, PQMF theory shows an excellent match with the simulations. Finally, Ferreira compared the epidemic prevalence near to the critical point for both the QMF theory and exact results.

Jan Nagler: ***Population growth, ergodicity breaking and optimal stategies in ecosystems and games*** Nagler introduced the notion of ergodicity breaking in various situations ranging from population growth in ecological foodwebs to climate prediction and discussed common pitfalls if one ignores ergodicity breaking. Mathematically, ergodicity breaking means that one cannot, in general, commute the evolution operator of a dynamical system with random parameters and the expectation operator. For instance, if a population model is embedded in a random environment, the mean growth dynamics cannot be obtained by running the growth dynamics with the mean environment. Nagler goes on to discuss the consequences of ergodicity breaking in evolutionary game theory and illustrates how new optimal strategies can be found if one accounts for ergodicity breaking.

Games on graphs

Rick Durrett: ***ODE limits for particle systems on graphs***

Durrett presented results voter model with perturbations in the sense of Cox, Durrett, and Perkins. He discussed results for two examples: evolutionary games with weak selection and the latent voter model in which individuals who adopt a new technology (e.g. buy an iPhone) have a latent period in which they will not change their state. These examples were analyzed in joint work with Ted Cox (EG) and Ran Huo (LVM).

Peter Caines: ***Graphon Mean Field Games and the GMFG Equations***

Caines presented methods for the analysis, design and control of very large networks linking dynamical agents. The emergence of the graphon theory of large networks and their infinite limits has recently enabled the formulation of a theory of the centralized control of dynamical systems distributed on asymptotically infinite networks. Furthermore, the study of the decentralized control of such systems has been initiated leasding to Graphon Mean Field Games (GMFG) and the GMFG equations are formulated for the analysis of non-cooperative dynamical games on unbounded networks. In Caines' talk the GMFG framework was presented followed by the basic existence and uniqueness results for the GMFG equations, together with an epsilon-Nash theorem. The latter relates the infinite population equilibria on infinite networks to that of finite population equilibria on finite networks.

Chemical and gene networks

Jae Kyoung Kim: ***Accurate reduction of multiscale biochemical reaction networks.***

Kim's talk was centered around biochemical reaction networks (BRNs) with disparate timescales. The stochastic simulations of such multiscale BRNs are prohibitively slow due to the high computational cost for the simulations of fast reactions. One way to resolve this problem is replacing the fast species with their quasi-steady state (QSS): their stationary conditional expectation values for given slow species. Kim described types of BRNs which can be reduced by deriving an exact QSS even in the presence of non-linear reactions. Furthermore, in the case when the exact QSS cannot be derived, Kim described how we could derive the approximate QSS and illustrated how the accurately reduced BRNs could be used to identify molecular mechanism underlying robust circadian rhythms and predict accurate drug clearance in the liver.

Konstantin Mischaikow: ***The DSGRN Database for Dynamics of Gene Regulatory Networks***

A common goal in the domain of systems and synthetic biology is to understand the relationship between design and function of gene regulatory networks. This is a significant challenge for several reasons. Typically understanding the behavior of a gene regulatory network means understanding the associated dynamics. Traditionally this requires having an acceptable nonlinear model, knowledge of parameter values, and knowledge of initial conditions, all of which are difficult to obtain in the setting of complex multi-scale problems. To circumvent these challenges the speaker has developed a novel approach to nonlinear dynamics based on order theory and algebraic topology. This method allows for efficient computations of rigorous combinatorial/algebraic topological descriptions of the global dynamics over large ranges of parameter space. As a consequence, given a regulatory network, we are able to construct a database describing all the associated dynamics. The talk discussed the theory behind this tool and demonstrated how it could be applied to some specific examples.

Daniel Linder: ***Inferring sparse regulatory networks in high dimensions***

Inferring gene regulatory networks from high-throughput omics data is a challenging statistical and computational problem. Classical inferential methods are known to break down due to the curse of dimensionality. Linder presented work his group has done in this area of statistical inference, and focused on recent work to learn the network structure in dynamical systems using Bayesian hierarchical modeling.

Miscellaneous mathematical analyses

Thomas G. Kurtz: ***Genealogies for stochastic population models.***

Stochastic models of populations have a long history beginning with branching processes and continuing with models in population genetics and models of the spatial distribution of populations. At the same time, models of population genealogies were developed in the population genetics literature. Work with Peter Donnelly [53] showed how to simultaneously construct models that include both the forward in time evolution of the population distribution and the backward in time genealogy starting at any time point in the forward in time evolution. These “lookdown” constructions were essentially restricted to neutral models, that is, models in which birth rates, offspring distributions, and death rates do not depend on the types or locations of the individuals in the population. Following some earlier preliminary results, work with Eliane Rodrigues [56] gave lookdown constructions for general Markov branching processes in which the birth rates, offspring distributions, and death rates can depend on the location/type of the individual. Extensions of these lookdown/genealogical constructions to very general Markov population models, to appear in a forthcoming paper with Alison Etheridge, were discussed.

Sayan Banerjee: ***Joining the shortest queue, non-elliptic reflected diffusions and stationarity***

In his talk Banerjee, considered a system of N parallel single-server queues with unit-exponential service time distribution and a single dispatcher where tasks arrive as a Poisson process of rate l(N). When a task arrives, the dispatcher assigns it to one of the servers according to the Join-the-Shortest Queue (JSQ) policy. Eschenfeldt and Gamarnik (2015) established that appropriately scaled functionals of the queueing network under the JSQ policy converge weakly to associated functionals for a certain non-elliptic reflected diffusion process as N grows. Banerjee talked about analyzing the detailed behavior of the steady state of this non-standard diffusion process using tools from renewal theory. The tails and bulk behavior of the steady state distribution and sample path fluctuations of the diffusion process were explored. He also showed that the steady state shows a stark difference in behavior between two regimes governed by a system parameter. The presented results are based on joint work with Debankur Mukherjee.

Amarjit Budhiraja: ***On Some Calculus of Variations Problems for Rare Event Asymptotics***

The theory of large deviations gives decay rates of probabilities of rare events in terms of certain optimal control problems. In general these control problems do not admit simple form solutions and one needs numerical methods in order to obtain useful information. In his talk, Budhiraja presented some large deviation problems where one can use methods of calculus of variations to give explicit solutions to the associated optimal control problems. These solutions then yield explicit asymptotic formulas for probability decay rates in several settings. The case of the Configuration Model was discussed in detail.

Laurent Decreusefond: ***Random walk on simplicial complexes***

In his talk Decreusefond considered random walks on simplicial complexes, also called hypergraphs, using some notions of topological algebra. It was shown that the transition matrix of this random walk was related to the higher order Laplacian, the generalization of graph Laplacian. He analyzed the limit behavior of this RW when the number of points in the simplicial complex tends to infinity.

4 Scientific Progress Made and Meeting Outcomes

The workshop brought together individuals from a diverse communities of international researchers. The main topic was epidemics on networks but models from physics such as percolation and the Ising model and the structure of various types of chemical and genetic networks were discussed as well. It is stimulating for researchers to see new perspectives on problems that they have previously studied. Several new collaborations were started and further progress in various areas is anticipated as a direct result of discussions during the workshop. Future meetings, like for instance the upcoming one in February, 2020, in CIRM (Marseille, France see https://www.cirm-math.fr) will provide opportunities for continued interactions. Some examples of scientific progress and specific outcomes are provided below.

- In the area of network models for infectious diseases there has been a realization during the conference that some of the recent results developed for non-Markovian epidemics in part of the reaction networks community have been in fact also recently reported in the communicable diseases literature although in a less mathematically formal way. In particular, extending the arguments presented in [57] allows to show that the non-Markovian results discussed in several talks at the workshop (Kenah, Miller, KhudaBukhsh) provide a nice connection and an extension of some earlier work reported e.g. in [58].

- A remarkable example of new contact came from the talks of Tom Britton and David Sivakoff, who talked in back-to-back presentations about the impact of link deactivation (susceptibles temporarily severing their contact with infecteds) on the spread of an infection. Britton focussed on the paradoxical result that link deactivation can cause the overall fraction of people who get infected to increase. Sivakoff concentrated on giving rigorous proofs of the existence of phase transitions. His collaborator Matt Wascher was a participant in the 2019 AMS Math Research Community held June 9-15 where this model was extensively discussed along with the version in which susceptibles connected to an infected can rewire their connection to another individual.

- Further progress was made in accumulating mathematical results developed by different communities and discovering new ones. Interesting theoretical results were presented that are likely to find new applications (eg in modeling vaccination and social distancing processes), which, in turn, should give rise to interesting new theoretical questions. This synergy is necessary to make sure the subject, as it grows into a mathematically rigorous discipline, remains equally appealing from both theoretical and applications points of view.

- The participants also explored new potential research domains. As discussed at the workshop, there has been extensive work on chemical reaction networks (CRNs) under mass-action assumption. The questions were posed about possible explicit graph structure comes into play in CRNs theory. Introduction of random graphs (possibly geometric) would help us refine all existing results and potentially improve our understanding of the chemical reaction systems. ii) Percolation on random graphs has emerged as an interesting research topic in the recent times [51, 50]. However, its possible connections with general dynamical processes on random graphs, especially from a non-equilibrium point of view, are not fully understood yet and hold great promise for future research.

Most rigorous works in the last few years [43, 46, 46, 44, 42] in epidemiological context seem to be followed by probabilists and mathematical epidemiologists, but their application to computer science in the context of spread of viruses, although reasonably achievable, does not seem to have gathered momentum. On the other hand, we are not aware of many rigorous efforts tailored to more complicated dynamical systems arising from, for example, peer-to-peer systems in computer science. During the workshop, several interesting specific open problems were identified that require new mathematical ideas. For instance, networks in which the structure of the network and the states of the vertices coevolve.

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