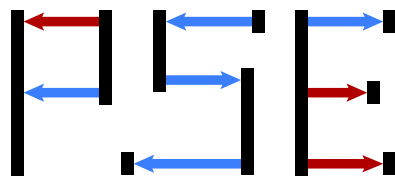# Geographic spaces for evolution: From lattices to graphs to continuum

A workshop within the DFG Priority Program 1590

December 12–13, 2019

Program

December 12th, 2019 (Thursday)	
08:30–09:20	Registration
09:20–09:30	Opening
09:30–10:30	NIC FREEMAN Extensive condensation in preferential attachment with choice
10:30–11:30	MATTHIAS BIRKNER Limit theorems for ancestral lineages in logistic branching random walks
11:30–12:00	Coffee Break
12:00–13:00	MAITE WILKE BERENGUER Spontaneous and simultaneous switching in the geometric seed bank model
13:00–14:00	Lunch Break
14:00–15:00	ANTON KLIMOVSKY Evolving networks and interacting particle systems on them
15:00–16:00	FRANK DEN HOLLANDER Graphon dynamics
16:00–16:30	Coffee Break
16:30–17:30	MATTHIAS HAMMER The stochastic F-KPP equation with dormancy and on/off-branching-coalescing Brownian motion
17:30–18:30	MARGRIET OOMEN Hierarchical seed-banks
19:30–22:00	Conference Dinner

	December 13th, 2019 (Friday)
9:00–10:00	RONGFENG SUN The 2-dimensional KPZ equation in the entire subcritical regime
10:00–11:00	JAN SWART Frozen percolation on the 3-regular tree
11:00–11:30	Coffee Break
11:30–12:30	RAPHAEL FORIEN The stepping stone model in a random environment - the effect of spatial heterogeneities on isolation by distance patterns.
12:30–13:30	Lunch Break
13:30–14:30	DANIEL VALESIN On the threshold of spread-out contact process percolation
14:30	End of the Workshop

Maite Wilke Berenguer (Bochum)
Spontaneous and simultaneous switching in the geometric seed bank model

The geometric seed bank model was introduced to describe the evolution of a population with active and dormant forms ('seeds') on a structure Markovian in both directions of time, whose limiting objects posses the advantageous property of being moment duals of each other: The (biallelic) Fisher-Wright diffusion with seed bank component describing the frequency of a given type of alleles forward in time and a new coalescent structure named the seed bank coalescent describing the genealogy backwards in time.

In this talk more recent results on extensions of this model will be discussed, focusing on the seed bank model with simultaneous migration: in addition to the spontaneous migration modeled before, where individuals decided to migrate independently of each other, correlated migration where several individuals become dormant (or awake) simultaneously is included.

In particular, we will discuss the effect of the correlation on the property of coming down from infinity.

This is joint work with J. Blath (TU Berlin), A. González Casanova (UNAM), and N. Kurt (TU Berlin).

Matthias Birkner (Mainz)
Limit theorems for ancestral lineages in logistic branching random walks

We study joint fluctuations of two ancestral lineages drawn from a non-trivial equilibrium of a system of d-dimensional logistic branching random walks. Furthermore, we apply this to derive a "quenched" central limit theorem for the spatial position of the ancestor of a typical individual.

Based on joint work in progress with Andrej Depperschmidt and Timo Schlüter

Frank den Hollander (Leiden)
Graphon dynamics

This lecture presents joint work with Siva Athreya (Bangalore) and Adrian Roellin (Singapore).

The aim is to develop a theory of graphon-valued stochastic processes, and to construct and analyze a natural class of such processes arising from population genetics. We consider finite populations where individuals change type according to Wright-Fisher resampling. At any time, each pair of individuals is linked by an edge with a probability that is given by a type-connection matrix, whose entries depend on the current empirical type distribution of the entire population via a fitness function. We show that, in the large-population-size limit and with an appropriate scaling of time, the evolution of the associated adjacency matrix converges to a random process in the space of graphons, driven by the type-connection matrix and the underlying Wright-Fisher diffusion on the multi-type simplex. In the limit as the number of types tends to infinity, the limiting process is driven by the type-connection kernel and the underlying Fleming-Viot diffusion.

Raphael Forien (Avignon)
The stepping stone model in a random environment - the effect of spatial heterogeneities on isolation by distance patterns

I will present a mathematical model for the genetic evolution of a population which is divided in discrete colonies along a linear habitat, and for which the population size of each colony is random but constant in time. I will show that, under reasonable assumptions on the distribution of the population sizes, over large spatial and temporal scales, this population can be described by the solution to a stochastic partial differential equation with constant coefficients. These coefficients describe the effective diffusion rate of genes within the population and its effective population density, which are both different from the mean population density and the mean diffusion rate of genes at the microscopic scale. To show this, I will present a duality technique and a new convergence result for coalescing random walks in a random environment.

Nic Freeman (Sheffield)
Extensive condensation in preferential attachment with choice

I will introduce a new preferential attachment model in which each vertex has an associated fitness value. I will discuss the behaviour of the model as the number of nodes tends to infinity, including the existence of a "condensation" phase in which a small number of especially fit vertices are able to gain disproportionately large degrees. The work relies on a new connection between preferential attachment with fitnesses, and branching-coalescing particle systems; it leads to a clear and intuitive explanation for why the condensation phenomenon occurs. Moreover, we will see that in this model the condensation is "extensive", meaning that some such vertices become, each only for a limited time, connected to a positive fraction of the current graph.

Joint work with Jonathan Jordan.

Matthias Hammer (Berlin)
The stochastic F-KPP equation with dormancy and on/off-branching-coalescing Brownian motion

We introduce a class of stochastic partial differential equations with dormancy modeling the spread of two competing alleles in a spatial population where individuals may switch between active and dormant states. We discuss (weak) existence and uniqueness of solutions to the SPDEs and provide an equivalent delay representation of the system. It turns out that these SPDEs give rise to an interesting class of "on/off"-branching-coalescing moment duals. For example, in the special case of the F-KPP equation with dormancy (but no noise), the moment dual is given by a system of "on/off"-branching Brownian motions. This system differs from a classical branching Brownian motion in the way that independently for all individuals, motion and branching may be "switched off" for an exponential amount of time, until they get "switched on" again. As an application of the duality, we show that the spread of the beneficial allele is slowed down in the Fisher-KPP model with dormancy compared to the classical Fisher-KPP model. This shows that dormancy has the potential to slow down fitness waves, in line with intuitive reasoning from ecology.

Anton Klimovsky (Essen)
Evolving networks and interacting particle systems on them

Most of the complex networks evolve over time and this can have substantial impact on the processes unfolding on them. We will give a brief overview of the very recent steps towards the asymptotic theory of large interacting particle systems on evolving networks focusing on the case of dense networks. In particular, we will discuss the ideas based on extending the graph limit theory.

Partially based on joint work with Jiri Cerny.

Margriet Oomen (Leiden)
Hierarchical seed-banks

We consider a system of interacting Wright-Fisher diffusions with seed-bank. Individuals live in colonies and are subject to resampling and migration as long as they are active. Each colony has a seed-bank into which individuals can retreat to become dormant, suspending their resampling and migration until they become active again. As geographic space we consider the hierarchical group $\Omega = \Omega_N, N \in \mathbb{N}$. Our goal is to identify the change in behaviour induced by the seed-bank.

We carry out a multi-scale renormalization analysis when, in addition to hierarchical migration, the system also has a hierarchical seed-bank, i.e., active individuals can become dormant into a hierarchy of dormant states, each with its own rate. In the hierarchical mean-field limit $N \to \infty$, we show that block averages on hierarchical space-time scale $k \in \mathbb{N}$ perform a diffusion with a renormalized diffusion function that depends on k. Finally we show a criterion under which the renormalized diffusion function converges to the Wright Fisher diffusion and we show how the seed-bank influence this criterion depending on its structure.

Joint work with Andreas Greven and Frank den Hollander.

Rongfeng Sun (Singapore)
The 2-dimensional KPZ equation in the entire subcritical regime

We consider the KPZ equation in space dimension 2 driven by space-time white noise. Previously, we showed that if the noise is mollified in space on scale epsilon and the noise strength scaled appropriately, then a phase transition occurs. Chatterjee and Dunlap then showed that the solution admits non-trivial sub-sequential scaling limits deep within the subcritical regime. In recent joint work with F. Caravenna and N. Zygouras, we showed that the limit exists in the entire subcritical regime, and we identify it as the solution of an additive Stochastic Heat Equation, establishing so-called Edwards-Wilkinson fluctuations. Deep within the subcritical regime, the same result was obtained independently by Y. Gu.

Jan Swart (Prag)
Frozen percolation on the 3-regular tree

In frozen percolation, i.i.d. uniformly distributed activation times are assigned to the edges of a graph. At its assigned time, an edge opens provided neither of its endvertices is part of an infinite open cluster; in the opposite case, it freezes. David Aldous (2000) showed that such a process can be constructed on the infinite 3-regular tree and asked whether the event that a given edge freezes is a measurable function of the activation times assigned to all edges.

In joint work with Antar Bandyopadhyay (2005), Aldous showed that the question can be reformulated in terms of a "Recursive Tree Process" (RTP), which is a sort of Markov chain in which time has a tree-like structure and the state of each vertex is a function of its descendants and some i.i.d. randomness. They called such an RTP endgenous if the state at the root is is a measurable function of the i.i.d. randomness attached to the vertices and showed that endogeny is equivalent to the statement that a certain bivariate recursive distributional equation has a unique solution.

In joint work with Balázs Ráth and Tamás Terpai, we were able to settle Aldous' original question by showing that for frozen percolation on the binary tree, bivariate uniqueness does not hold. An essential role in our proofs is played by a frozen percolation process on a continuous-time binary Galton Watson tree that has nice scale invariant properties.

DANIEL RODRIGUES VALESIN (Groningen)

On the threshold of spread-out contact process percolation

We study the stationary distribution of the (spread-out) d-dimensional contact process from the point of view of site percolation. In this process, vertices of $\mathbb{Z}^d$ can be healthy (state 0) or infected (state 1). With rate one infected individuals recover, and with rate λ they transmit the infection to some other vertex chosen uniformly within a ball of radius R. The classical phase transition result for this process states that there is a critical value $\lambda_c(R)$ such that the process has a non-trivial stationary distribution if and only if $\lambda > \lambda_c(R)$. In configurations sampled from this stationary distribution, we study nearest-neighbor site percolation of the set of infected sites; the associated percolation threshold is denoted $\lambda_p(R)$. We prove that $\lambda_p(R)$ converges to $1/(1-p_c)$ as R tends to infinity, where p_c is the threshold for Bernoulli site percolation on $\mathbb{Z}^d$. As a consequence, we prove that $\lambda_p(R) > \lambda_c(R)$ for large enough R, answering an open question of [Liggett, Steif, AIHP, 2006] in the spread-out case.

Joint work with Balázs Ráth.