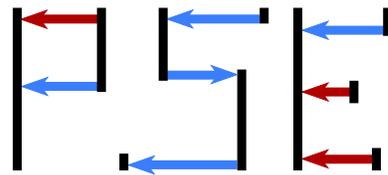# From Interacting Particle Systems to Population Genetics

in honor of the 60th birthday of Andreas Greven,

a workshop within the DFG Priority Program 1590

February 27–28, 2014

Program

	February 27th, 2014 (Thursday)
13:30–14:00	Registration
14:00–14:30	Opening
14:30–15:30	DON DAWSON From random walks to interacting diffusions on Ω_N and their hierarchical mean-field limits
15:30–16:00	GERHARD KELLER Exploring randomness in deterministic systems via transfer operators
16:00–16:30	Coffee
16:30–17:00	MICHAEL SCHEUTZOW Moments of recurrence times for Markov chains
17:00–17:30	JAN SWART Subcritical contact processes seen from a typical infected site
17:30–18:00	ANDREAS DEUTSCH Cellular automaton models for collective cell behaviour
18:30–	Reception

	February 28th, 2014 (Friday)
9:30–10:30	TED COX Convergence of finite voter model densities
10:30–11:00	ANJA STURM On a particle model with cooperative branching and coalescence
11:00–11:30	RONGFENG SUN Continuum space limit of the genealogies of interacting Fleming–Viot processes on $\mathbb{Z}$
11:30–12:00	Coffee
12:00–12:30	SANDRA KLIEM Modeling evolving phylogenies by means of marked metric measure spaces
12:30–13:00	ANDREJ DEPPERSCHMIDT Tree-valued Fleming–Viot dynamics
13:00–14:30	Lunch break
14:30–15:30	MATTHIAS BIRKNER Directed random walk on an oriented percolation cluster
15:30–16:30	FRANK DEN HOLLANDER Random walk in dynamic random environment

From random walks to interacting diffusions on Ω_N and their hierarchical mean-field limits

DONALD DAWSON (Ottawa)

This talk will begin with a review of some properties of random walk and the Evans Lévy process on the hierarchical group Ω_N and then consider certain classes of interacting diffusions on this space. In particular we consider the question of continuum limits including the super-Lévy process and mutual catalytic branching. The corresponding hierarchical mean-field continuum limits and their hot-spot behaviours will be analyzed.

This is based on a joint project with Iljana Zähle and Andreas Greven.

Exploring randomness in deterministic systems via transfer operators

GERHARD KELLER (Erlangen)

I will briefly review this broad field indicating

- the classes of chaotic deterministic systems that can be treated by operator methods,
- the variety of stochastic limit theorems that can be proved, and
- the spectral (perturbation) properties of the associated transfer operators that link the dynamical properties of the systems to their stochastic behavior.

Moments of recurrence times for Markov chain

MICHAEL SCHEUTZOW (Berlin)

It is well-known that if for an irreducible discrete time Markov chain with countable state space, the recurrence time for some state has a finite first moment, then the same is true for every state. Kai Lai Chung showed in the 1950-es that the same is true for all polynomial moments. In his famous monograph on Markov chains (1967), Chung asked for which other moments this property holds true. We provide an explicit description of all positive non-decreasing functions for which the property holds.

This is joint work with Frank Aurzada, Hanna Döring, and Marcel Ortgiese.

Subcritical contact processes seen from a typical infected site

JAN SWART (Prag)

In this talk, we will look at contact processes whose lattice can be any countable group. Starting with a single infected site, we size-bias on the number of infected sites at some later time and choose a 'typical' infected site with equal probabilities from all infected sites. Shifting this site to the origin, we obtain the contact process *as seen from* the typical site. I will sketch a proof that for subcritical processes, this law of the process as seen from a typical infected site converges to a limit as time tends to infinity. Whether such a limit law exists in general is an open problem. The limit law as seen from the typical site turns out to be closely related to the exponential decay rate of the expected number of infected sites. We will show that this exponential decay rate is continuously differentiable as a function of the recovery rate of the process, and give a formula for the derivative in terms of the limit laws as seen from the typical site for the process and its dual. An important role in the proofs is played by so-called eigenmeasures, which are a sort of equivalent of quasi-invariant laws.

This is joint work with Anja Sturm (Göttingen).

Cellular automaton models for collective cell behaviour

ANDREAS DEUTSCH (Dresden)

Cellular automata are introduced as models for collective behaviour in interacting cell populations. We focus on mechanisms of collective cell migration, clustering and invasion and demonstrate how analysis of the models allows for prediction of emerging properties at the individual cell and the cell population level. Finally, we discuss applications of the invasion models to glioma tumours.

Ref.: A. Deutsch, S. Dormann: *Cellular Automaton Modeling of Biological Pattern Formation. Characterization, Applications, and Analysis*, Birkhäuser, Boston, 2005 (2nd ed. 2014)

Convergence of finite voter model densities

TED COX (Syracuse)

Let (S_n) be a sequence of finite sets such that $|S_n| \to \infty$. For each n let S_n be equipped with an irreducible Markov chain transition matrix q_n with stationary probability distribution π_n, and let ξ_t^n be the corresponding voter model. That

is, ξ_t^n is the Markov process taking values in $\{0,1\}^{S_n}$ such that $\xi_t^n(x)$ flips to $1 - \xi_t^n(x)$ at rate $\sum_{y \in S_n} q_n(x,y)1\{\xi_t^n(y) \neq \xi_t^n(x)\}$. Given a sequence of positive constants γ_n, the corresponding time-scaled voter model *density of 1's process* is $Y_t^n = \sum_{x \in S_n} \pi_n(x)\xi_{t\gamma_n}^n$.

It is well known that in the mean-field case $q_n(x,y) = 1/(|S_n| - 1)$ for $x \neq y$, if $\gamma_n = |S_n|/2$ then Y^n converges as $n \to \infty$ to the Wright–Fisher diffusion Y, the diffusion on $[0,1]$ which has generator $\frac{1}{2}u(1-u)\frac{d^2}{du^2}$. This convergence also takes place if S_n is the d-dimensional torus $[0,n)^d \cap Z^d$, $q_n(x,y) = 1/2d$ if $|x-y| = 1$, $\gamma_n = c_2|S_n|\log|S_n|$ for $d = 2$ and $\gamma_n = c_d|S_n|$ for $d \geq 3$. We give a general condition under which this convergence holds when γ_n is the expected first meeting time of two Markov chains with transition matrix $q^{(n)}$, with initial states chosen independently according to π_n. The condition is that the associated Markov chain mixing time t_{mix}^n be small relative to γ_n, i.e., $t_{\mathrm{mix}}^n/\gamma_n \to 0$ as $n \to \infty$.

By duality, this result is closely related to recent results of Oliveira on the coalescing times of Markov chains on finite sets.

On a particle model with cooperative branching and coalescence

ANJA STURM (Göttingen)

We consider a one-dimensional model of particles performing independent random walks on $\mathbb{Z}$ in which only pairs of particles can produce offspring (cooperative branching) and particles that land on an occupied site merge with the particle present on that site (coalescence). In a biological context, the resulting cooperative branching-coalescent describes a simple population dynamics with reproducing pairs of particles and death due to competition. In addition, the process also describes the interface dynamics of a multi-type voter model in which rare types have an advantage.

Mathematically, the cooperative branching-coalescent has interesting properties: We show that the system undergoes a phase transition as the branching rate is increased. For small branching rates the upper invariant law is trivial and the process started with finitely many particles a.s. ends up with a single particle. Both statements are not true for high branching rates. We also show that if the branching rate is small enough then the particle density of the process started in the fully occupied state decays as one over the square root of time, and that the same is true for the decay of the probability that the process still has more than one particle at a later time if started with two particles.

An essential method for establishing some of these results is the derivation of a process that is a subdual to the cooperative branching-coalescent.

This is joint work with Jan Swart (UTIA Prague).

Continuum space limit of the genealogies of interacting Fleming–Viot processes on $\mathbb{Z}$

Rongfeng Sun (Singapore)

We study the genealogies of a population of individuals modeled by an interacting Fleming–Viot process on $\mathbb{Z}$. We characterize the genealogical structure of the population in the Fleming–Viot process as a marked metric measure space, with each individual carrying its spatial location as a mark. We then show that its time evolution converges to that of the genealogy of a continuum-sites stepping stone model on $\mathbb{R}$, if space and time are scaled diffusively. We construct the genealogies of the continuum-sites stepping stone model as a functional of the Brownian web, and furthermore, we characterize its evolution as a solution of a martingale problem, where the generator has a singular feature: at each time, the resampling of genealogies only affect a set of individuals of measure 0.

Based on joint work with Andreas Greven and Anita Winter.

Modeling evolving phylogenies by means of marked metric measure spaces

Sandra Kliem (Duisburg)

In this talk, a model for evolving phylogenies, incorporating branching, mutation and competition is introduced. The state-space consists of marked tree-like metric measure (mmm)-spaces. The model arises as the limit of approximating finite population models with rates dependent on the individuals' traits and their genealogical distances.

The main focus of the talk will be on presenting the notion of mmm-spaces and to highlight their advantages in the given context. In particular, necessary and sufficient conditions for relative compactness of sets in mmm-spaces are explained. The route to verify these conditions to conclude the tightness of the approximating models from above is given.

A similar approximating model and its limit is treated in Méléard and Tran (2012) in the framework of nonlinear historical superprocess approximations. In the framework of mmm-spaces, work of (Depperschmidt, Greven, Pfaffelhuber and Winter, 2012–2013) introduces and studies tree-valued Fleming–Viot dynamics. During this talk, new ideas and challenges that arise from working with mmm-spaces in the context of evolving phylogenies are put into context of the above.

This is joint work with Anita Winter.

Tree-valued Fleming–Viot dynamics

Andrej Depperschmidt (Freiburg)

In population genetics Moran models are used to describe the evolution of types in a population of a fixed size N. The type of individuals may change due to mutation. Furthermore, due to selection the fitness (i.e. the ability to survive and produce offspring) of an individual depends on its current type. As the population evolves the configuration of types and the genealogy evolve as well. Both can be naturally read off from the graphical construction thus leading to a tree-valued version of the Moran model.

In the talk we review the construction and some properties of the tree-valued Fleming–Viot dynamics, the limiting object as $N \to \infty$. In the neutral case this construction was carried out in (Greven, Pfaffelhuber and Winter, 2013) and in the case with selection and mutation in (D., Greven and Pfaffelhuber, 2012)

Directed random walk on an oriented percolation cluster

Matthias Birkner (Mainz)

We consider a directed random walk on the backbone of the infinite cluster generated by supercritical oriented percolation, and exhibit suitable regeneration structures to obtain a law of large numbers and a quenched central limit theorem. The walk can be interpreted as the space-time embedding of the ancestral lineage of a sampled individual in the stationary discrete-time contact process. Extensions to more general population models, leading to random walks in correlated space-time environments, and also to several walkers are of interest in population genetic applications. I will discuss approaches to extend the results in this direction.

Based on joint work, in part in progress, with Jiří Černý, Andrej Depperschmidt and Nina Gantert.

Random walk in dynamic random environment

Frank den Hollander (Leiden)

Random motions in random media are of major interest in mathematics, physics and (bio)chemistry. They have been studied at the microscopic, mesoscopic and macroscopic level, through a range of different techniques: numerical, theoretical and rigorous. Within probability theory, over the past fifty years there has been much interest in studies of random walks in static random environments. More recently, the focus has shifted to dynamic random environments.

Most papers in the literature on random walk in dynamic random environment require fast space-time mixing conditions on the environment. In this talk we start by giving a brief overview of what has been achieved in the past ten years. After that we describe the challenges that come up in trying to weaken the mixing conditions. In particular, we describe examples where the dynamic random environment consists of an interacting particle system with particle conservation, for which mixing is typically slow.

We report on recent work where the dynamic random environment consists of a Poisson field of independent simple random walks. With the help of renormalisation techniques and the construction of so-called regeneration times, we can show that the displacement of the random walk satisfies a strong law of large numbers, a functional central limit theorem, as well as a large deviation bound.

Joint work with M. Hilario, V. Sidoravicius, R. Soares dos Santos and A. Teixeira.