Ancestral lines under selection and recombination

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ABSTRACT

Following up on the talk by Sebastian Hummel, we consider the deterministic limit of the Moran model, this time under selection and recombination taking place on the same time scale. For a single selected site and an arbitrary number of linked neutral sites, we formulate the ancestral selection recombination graph (in the deterministic limit) and use it to establish the type distribution of individuals along with their genealogy, thus providing a closed solution of the deterministic selection-recombination equation, along with a genealogical interpretation.

This is joint work with Carolin Herrmann.

Stochastic domination in space-time for the supercritical contact process

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ABSTRACT

The contact process is a classical model for the spread of infections in a population. In this talk, we focus on the contact process in the supercritical regime for which infections may spread forever with positive probability. Our goal is to understand how this process behaves compared with a process having no spatial correlations. In particular, does the contact process stochastically dominate a non-trivial independent (in space) spin-flip process? Such questions were studied by Liggett and Steif (2006) who proved that, for the process on $\mathbb{Z}^d$, the upper invariant measure stochastically dominates a Bernoulli product measure. We present some space-time versions of their results for the contact process on general graphs. From our methods, we furthermore deduce strong (uniform) mixing properties for certain space-time projections of the contact process. Based on joint work with Rob van den Berg (CWI Amsterdam and VU Amsterdam).

Infinite bridges for Rémy's algorithm

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ABSTRACT

An infinite bridge for a transient Markov chain is a Markov chain that has the same backwards-in-time transition probabilities. Delineating all the infinite bridges for a given Markov chain is equivalent to describing all the ways it is possible to condition that Markov chain to "do something at large times" or, analytically, to describing the Doob-Martin boundary of the state space. Rémy (1985) introduced a simple tree-valued Markov chain that at step n produces a random tree which is uniformly distributed over the rooted, planar, binary trees with $n + 1$ leaves. We obtain a concrete description of the infinite bridges for this Markov chain in terms of a certain class of real-trees (that is, tree-like metric spaces) equipped with additional structure.

Branching Brownian Motion, mean curvature flow and the motion of hybrid zones

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ABSTRACT

I will discuss a new connection between Branching Brownian Motion, the Allen-Cahn equation, and mean curvature flow. This connection can be used to show that so-called ”hybrid” zones form in (scaling limits of) the Spatial Lambda-Fleming-Viot process, with a suitably chosen selection mechanism. The arguments are probabilistic, and are based on understanding the spatial structure of genealogies formed by systems of branching-coalescing random walkers.

(The talk is built around https://arxiv.org/abs/1607.07563 and its continuations.)

Scaling limit of inclusion particles

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ABSTRACT

The inclusion process is a relative of the well-know exclusion process in which the exclusion rule is replaced by an attractive interaction among particles. As discussed in the Learning Session, due to its algebraic structure, the inclusion process enjoys duality properties that allow several exact computations.

In this talk we shall discuss its scaling limits: (1) infinite population limit; (2) diffusive limit. In part (1), if the inclusion parameter (tuning the spreading of the particles) stays fixed, then the scaling limit yields a diffusion on the simplex. If instead the inclusion parameter is scaled to zero, then a condensation effect occurs, with all particles on a single site. I shall present the results of the work [A. Bianchi, S. Dommers, C. Giardinà, "Metastability in the reversible inclusion process", arXiv:1605.05140] where it is shown that, in the presence of condensation, the dynamics has up to three relevant time scales.

In part (2) we consider the diffusive scaling limit of two inclusion particles. Particularly interesting is the condensation regime, yielding sticky Brownian motion for the distance between the two particles. This second part is work in progress with G. Carinci and F. Redig.

On large deviation probabilities for empirical distribution of branching random walks: Schröder case and Böttcher case

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ABSTRACT

Given a super-critical branching random walk on $\mathbb{R}$ started from the origin, let $Z_n(\cdot)$ be the counting measure which counts the number of individuals at the n-th generation located in a given set. Under some mild conditions, it is known that for any interval $A \subset \mathbb{R}$, $\frac{Z_n(\sqrt{n}A)}{Z_n(\mathbb{R})}$ converges a.s. to $\nu(A)$, where ν is the standard Gaussian measure. In this work, we investigate the convergence rates of

$$\mathbb{P}\left(\frac{Z_n(\sqrt{n}A)}{Z_n(\mathbb{R})} - \nu(A) > \Delta\right),$$

for $\Delta \in (0, 1 - \nu(A))$, in both Schröder case and Böttcher case. This is a joint work with Xinxin Chen.

Mutation, selection, and ancestry in the deterministic limit of the Moran model

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ABSTRACT

We consider a haploid Moran model with selection, mutation, and two allelic types. The large population limit, in which neither parameters nor time are rescaled, is called the deterministic limit of the Moran model. In this limit, the proportion of types over time is the solution of an ordinary differential equation. Despite the deterministic nature of this process, the ancestry of single individuals in the population is still stochastic. We describe it via a killed ancestral selection graph and connect it with the deterministic process via duality; this leads to a stochastic representation of the deterministic solution. In particular, the stationary state obtains a nice probabilistic interpretation. We generalise the construction to the multi-locus case with additive selection and provide probabilistic proofs for results previously obtained via multilinear algebra.

This is joint work with Ellen Baake and Fernando Cordero.

Modeling evolving phylogenies by means of marked metric measure spaces

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ABSTRACT

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.

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.

Spatial Cannings model with catastrophes in random environment

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ABSTRACT

We consider a system of (infinitely many) individuals structured in colonies. The individuals are subject to Cannings resampling, migration and occasional catastrophes affecting the whole patches of the geographical space at given rates. Specifically, the Cannings resampling substitutes a randomly chosen positive fraction of individuals in a colony by a copy of a randomly chosen individual. As a geographical space, we choose a countable hierarchical lattice called hierarchical group of order $N \geq 2$. The migration is modelled by independent random walks on the hierarchical group performed by all individuals. We assume that the catastrophes affect balls of any radius in the geographical space. This happens via panmictic Cannings resampling within a ball. Moreover, we allow for spatially inhomogeneous resampling and catastrophes rates. This is modelled via random environment. We show that in the long run with probability one the system displays dichotomic behaviour: either there is coexistence (= locally diverse equilibrium) or clustering (= equilibrium with monotype colonies). For finite N, a criterion for coexistence vs. clustering is provided. For $N \to \infty$, we identify the behaviour of the system upon space-time renormalization. It turns out that the renormalized system becomes a superposition of a Cannings dynamics and a Fleming-Viot diffusion with a deterministic volatility constant. In particular, we identify and study the scaling regimes for the volatility constants. These regimes lead either to coexistence or to cluster formation with different clustering speeds. In particular, it turns out that the spatial inhomogeneities reduce the clustering speed comparing to the spatially homogeneous case. This is joint work with A. Greven and F. den Hollander.

State spaces of (continuum) trees: R-trees versus Algebraic Trees

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ABSTRACT

In order to construct tree-valued stochastic processes, one needs a topological space of trees as state space. While this is not an issue for finite (or countable) graph-theoretic trees, we want to consider global limits as the number of vertices tends to infinity. We call the limiting objects also "tree" but have to make precise what we mean by this. The standard approach is to consider continuum trees to be metric (measure) spaces ($\mathbb{R}$-trees) and equip the space of them with Gromov-Hausdorff or Gromov-weak topology.

We argue that sometimes it is more natural to consider the *tree-structure* instead of the metric structure. First, because distances may behave very "wild" in certain cases and neglecting them makes proving some limit results more feasible. Second, because sometimes one might want to preserve structural properties such as being binary in the limit.

We present a framework for a space of such (continuum) trees possessing no metric- but only a tree-structure. We call them *algebraic trees*, because we formalise the tree-structure by a tertiary operation on the tree, namely the branch point map. We construct a natural topology on spaces of sufficiently nice algebraic trees. In the binary case, the resulting space is compact and intimately related to the set of triangulations of the circle as introduced by Aldous, equipped with the Hausdorff metric.

(joint work with Anita Winter)

A generating function approach to duality

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ABSTRACT

Besides the wide applicability of duality for Markov processes, effort has been employed also in unveiling all possible dualities between two processes via rather algebraic techniques (e.g. [1] in population genetics, [2, 3] in the context of particle systems).

In this talk, we present an alternative road map to duality suitable for interacting particle systems and diffusions with stationary product measures. Typical examples are independent random walkers, symmetric exclusion/inclusion processes and their continuum counterparts - all used as microscopic models of non-equilibrium phenomena such as heat conduction or mass transport.

Starting from a relation between the stationary product measures and the duality functions - the objects that ”link” the two dual processes - we obtain the full list of possible dualities in factorized form. Here, orthogonal polynomials w.r.t. the marginals of the stationary measure (also obtained in [4] via direct computation) appear.

At last, by passing to generating functions, we obtain equivalent formulations of duality: in one shot, we gain new dualities for the continuum processes and prove all dualities previously characterized.

Joint work with Frank Redig (TU Delft).

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Limit theorems for the partitioning process

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ABSTRACT

I will consider a haploid Wright–Fisher model with recombination, where each haplotype is a mosaic of its two parental chromosomes. Starting with uniformly colored and distinct chromosomes, each individual of the population at time t is a composite (or partition) of the colors originally present in the ancestral population. The partitioning process at time t is then defined as the color partition of a sampled chromosome. In particular, as time goes to infinity, it provides a description of the haplotype that will eventually fix in the population.

I will present some recent results on the partitioning process at stationarity. In particular, I will discuss the description of a typical color cluster, and a law of large numbers for the number of clusters inside a large portion of the chromosome.

Rigorous results for a population model with selection

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ABSTRACT

We consider a model of a population of fixed size N in which each individual acquires beneficial mutations at a constant rate. Each individual dies at rate one, and when a death occurs, an individual is chosen at random with probability proportional to the individual's fitness to give birth. We obtain rigorous results for the rate at which mutations accumulate in the population, the distribution of the fitness levels of individuals in the population at a given time, and the genealogy of the population. Our results confirm nonrigorous predictions of Desai and Fisher (2007), Desai, Walczak, and Fisher (2013), and Neher and Hallatschek (2013).

Phase Transition for the Contact Process in a Random Environment on $\mathbb{Z}^d \times \mathbb{Z}_+$

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ABSTRACT

Consider the basic contact process in a static random environment on the half space $\mathbb{Z}^d \times \mathbb{Z}_+$ where the recovery rates are constants and the infection rates are proportional to a series of independent and identically distributed random variables (need not be bounded). We show that, with probability one, the contact process at the critical value dies out. And the critical value exhibits the phase transition for the growth of the system. This is a generalization of the known results for the classical contact process in the half space case.

Convergence of branching-coalescing nonsimple random walks to the Brownian net

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ABSTRACT

The Brownian net is a collection of branching-coalescing Brownian motions starting from every point in the space-time plane $\mathbb{R}^2$, which has been shown to be the diffusive scaling limit of branching-coalescing simple random walks. The Brownian net is expected to be a universal scaling limit of one-dimensional interacting particle systems with branching-coalescence. However, up to now all the models known to converge to the Brownian net only have noncrossing paths. Showing the weak convergence of models with crossing paths remains a challenge. In this work, we considered the case of branching-coalescing nonsimple random walks, so that the paths can cross each other, and we partially obtained the convergence result.