

Booklet of abstracts

Ancestral lines for (multitype) genetic models

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Labelled partitions in action: recombination, selection, mutation and more

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The investigation of mathematical models that describe the interplay of genetic recombination with other forces of evolution such as selection and/or mutation is among the major challenges of mathematical population genetics. In particular, the *deterministic selection-recombination equation*, a high-dimensional system of nonlinear differential equations, has long defied all attempts at its solution. Recently, we solved this equation in the special case of a single selected locus linked to an arbitrary number of neutral loci, and single-crossover recombination [1]. The key to our solution is a connection (via a duality of Markov processes) between the solution of the selection-recombination equation, forward in time, and a stochastic process that describes the random evolution of the genealogy of a sample, backward in time. This process is derived from the *ancestral selection-recombination graph*, which in turn combines the *ancestral selection graph* introduced by Krone and Neuhauser with the *ancestral recombination graph*. Ultimately, this led to an explicit representation of the solution in terms of iterated integrals. This contribution complements our aforementioned work [1] by exploring the interaction between recombination and additional evolutionary forces in a more general setting. We will see that, under certain natural assumptions, the genealogy of a sample can be described as a partitioning process whose blocks carry independent Markovian labels. Intuitively speaking, the partitioning process describes the fragmentation of the genetic material of an individual across its ancestors, while the Markovian labels encode the evolution under the additional evolutionary forces. On the one hand, this deepens our insight into the mathematical structure underlying our results in [1] and on the other, it allows us to construct explicit solutions for a wider class of models. We will illustrate these ideas at the example of the selection-mutation-recombination equation.

[1] F. Alberti and E. Baake, Solving the selection-recombination equation: Ancestral lines and dual processes, Documenta Mathematica 26 (2021), 743–793.

The genealogy of nearly critical branching processes in a varying environment

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Branching processes in varying environment (BPVE) are a natural generalisation of classical Galton-Watson processes allowing for a time inhomogeneous offspring distribution. In this talk we introduce a notion of *near-criticality* for BPVEs and discuss Kolmogorov’s asymptotics, Yaglom’s law and the genealogical structure of nearly-critical BPVEs. Building on the spinal decomposition in [Foutel-Rodier, Schertzer, 22] we prove that the genealogy seen as a random metric space converges in the Gromov-Hausdorff-Prohorov topology to a time-changed Brownian coalescent point process. Through this convergence result we are able to deduce Yaglom’s law, the time to the most recent common ancestor and convergence of the reduced process. This talk is based on joint work with Félix Foutel-Rodier and Emmanuel Schertzer.

Extinction times of multitype continuous-state branching processes

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The distribution of a multitype (d -type) continuous-state branching process (MCSBP) is characterised by its branching mechanism, that is the data of d Laplace exponents of \mathbb{R}^d -valued spectrally positive Lévy processes, each one having $d - 1$ increasing components. We give an expression of the probability for a MCSBP to tend to 0 at infinity in terms of its branching mechanism. Then we prove that this extinction holds at a finite time if and only if some condition bearing on the branching mechanism holds. This condition extends Grey's condition that is well known for $d = 1$. Our arguments bear on recent results of fluctuation theory for spectrally positive additive Lévy fields and an extension of the Lamperti representation in higher dimension.

(This is a joint work with Marine Marolleau.

Ancestral lineages in branching processes and somatic evolution

David Cheek

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Our ancestors reproduced more than typical members of the population, which could be said for any biological population. But ancestral reproductive bias doesn't need to be explained by Darwinian 'survival of the fittest' in a population with heterogeneous reproduction law. Even more simply, the bias arises in populations with homogeneous reproduction law. For a single-type branching process, we sample an individual uniformly at random, and we characterise reproduction along their ancestral lineage as a mixture of Poisson processes, determining the extent of ancestral bias as a function of the reproduction law and sampling time. We find that despite reproduction rates being constant in the population, reproduction rates continuously change along the ancestral lineage - the population size guides the degree of ancestral bias. For an extreme example, in a branching process with a constant reproduction rate and heavy-tailed offspring distribution, a randomly sampled individual's ancestors have reproduction rates increasing to infinity with the sampling time. Explicit results are available for birth-death branching processes too, and for a biological example, we suggest that ancestral bias can help to explain recently observed mutation rate variation along lineages of the developing human embryo. Then we measure ancestral lineages of human cancers, for example finding that lineages of lung cancer samples can predict patient survival. However a single-type model is too simplistic for cancer, where genetic heterogeneity always augments ancestral bias - we finish with some open questions on the meaning of cancer lineages.

Ancestral structures for Moran Models with general frequency-dependent selection and mutation

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Dealing with the interplay of mutation and selection is one of the important challenges in population genetics. One of the methods of study for the matter is looking at ancestral structures and exploiting duality relations. For this talk, we consider two variants of the two-type Moran model in the diffusion limit with mutations and frequency-dependent selection, that is, the case in which the selective advantage of fit individuals may depend on the rest of the population. The first one is the fittest-type-wins model (FTW), introduced by Baake et al [1], which encodes a particular type of frequency-dependent selection (nonlinear dominance). We briefly illustrate how and why the ancestral selection graph (ASG) and moment duality carry over from the classical genic case to this model, while arguing that these relations don't survive further generalizations. To do so, we will illustrate the second model, introduced by Cordero et al. [2], which includes general frequency-dependent selection via colouring rules acting during selective events. Rather than working with the relative ASG, they keep track of the conditional probability of the type of a sample, given the evolution of its ancestry backward in time, and encode it in what they denote as the Bernstein (coefficient) process, which we will present. Combining this idea with the intuition derived by working with the ASG, we propose an alternative process, the (monomial) coefficient process, together with a relative duality relation, in the case of deterministic colouring rules. We provide a graphical interpretation of the process, while highlighting advantages and disadvantages with the previous approach. We conclude by providing some criteria for the stochastic regularity of this process, and a first application in a parameter regime leading to its absorption.

[1] Baake, E., Esercito, L. and Hummel, S., Lines of descent in a Moran model with frequency-dependent selection and mutation. *Stoch. Proc. App.*, 160 (2023), pp. 409-457.

[2] Cordero, F., Hummel, S. and Schertzer, E. "General selection models: Bernstein duality and minimal ancestral structures." *Ann. Appl. Probab.* 32 (2022), pp. 1499-1556.

Ξ -coalescents arising from structured populations undergoing bottlenecks

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Ancestry models can be used for predicting genetic diversity of a population, and comparing it to observed data. In population genetics most theory and statistical tests have been developed using the classical Wright-Fisher model and the Kingman coalescent. Nevertheless, organisms having a genealogy not well described by the Kingman coalescent are not rare. One example is the Atlantic cod which presents shallow genealogies and high-variance offspring number that might be rather described by a multiple merger coalescent. The aim of our work is to find a realistic individual-based model fitting these data. We present a spatially structured model undergoing localized, recurrent bottlenecks, and describe its ancestral lines. Depending on the severity of the bottleneck, we derive as scaling limits different structured Ξ -coalescents featuring simultaneous multiple mergers and migrations. This talk is based on ongoing joint work with A. Etheridge, J. Koskela, M. Wilke-Berenguer.

On the boundary 1 of the Λ -Wright–Fisher process with “strong” selection and its dual process

Clément Foucart

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Consider a two-allele model in which the frequency of the deleterious allele is given by a Λ -Wright–Fisher process with frequency-dependent selection (Λ -WF with selection). The latter is a $[0, 1]$ -valued Markov process with jumps and the boundary 1 is reached when the whole population carries the deleterious allele. When the frequency-dependent term is very strong (typically non Lipschitz at 1), the selection and the genetic drift (governed by Λ) may interplay and the boundary 1 can be an exit, an entrance or a regular boundary (terms will be explained). In each case, the process satisfies some duality relationships with the block counting process of a simple exchangeable fragmentation-coalescent process (EFC processes). One-to-one correspondences are established between the nature of the boundaries 1 and ∞ of the processes involved. They provide new information on these two classes of processes. When the coalescence measure Λ and the selection mechanism verify some regular variation properties, conditions are found in order that the extended Λ -WF process with selection makes excursions out from the boundary 1. In this case, 1 is a transient regular reflecting boundary. This corresponds to a new phenomenon for the deleterious allele, which can be carried by the whole population for a set of times of zero Lebesgue measure, before vanishing in finite time almost surely.

From population genetics to statistical physics, and backward

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Well-known models of mathematical population genetics (Moran model, Wright–Fisher diffusion) can be interpreted as transport models of non-equilibrium statistical mechanics. This is useful to transfer results between the two areas, e.g. dualities. In the reverse direction, I will discuss in this talk a new family of integrable Markov processes (so-called “harmonic processes”, related to Yang–Baxter equation) recently introduced in statistical physics, which may again have a nice interpretation as population genetics models. The added values of those new models based on integrability (compared to pre-existing ones) is that they are exactly solvable, at least in one dimension.

Multitype Lambda-coalescents

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Consider a multitype coalescent process in which each block has a colour in $\{1, \dots, d\}$. Individual blocks may change colour, and some number of blocks of various colours may merge to form a new block of some colour. We show that if the law of a multitype coalescent process is invariant under permutations of blocks of the same colour, has consistent Markovian projections, and has asynchronous mergers, then it is a multitype Λ -coalescent: a process in which single blocks may change colour, two blocks of like colour may merge to form a single block of that colour, or large mergers across various colours happen at rates governed by a d -tuple of measures on the unit cube $[0, 1]^d$. We go on to identify when such processes come down from infinity. Our framework generalises Pitman's celebrated classification theorem for single-type coalescent processes, and provides a unifying setting for numerous examples that have appeared in the literature including the seed-bank model, the island model and the coalescent structure of continuous-state branching processes. This is joint work with Andreas Kyprianou and Tim Rogers.

The ancestral selection graph for a Lambda-asymmetric Moran model

Noemi Kurt

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Motivated by the question of the impact of selective advantage in populations with skewed reproduction mechanisms, we study a Moran model with selection. We assume that there are two types of individuals, where the reproductive success of one type is larger than the other. The higher reproductive success may stem from either more frequent reproduction, or from larger numbers of offspring, and is encoded in a measure Λ for each of the two types. Our approach consists of constructing a Λ -asymmetric Moran model in which individuals of the two populations compete, rather than considering a Moran model for each population. Under certain conditions, that we call the "partial order of adaptation", we can couple these measures. This allows us to construct what we call the Λ -asymmetric ancestral selection graph, which leads to a pathwise duality of the forward in time Λ -asymmetric Moran model with its ancestral process. Interestingly, the construction also provides a connection to the theory of optimal transport. We apply the ancestral selection graph in order to obtain scaling limits of the forward and backward processes, and note that the frequency process converges to the solution of an SDE with discontinuous paths. Another application is a Griffiths representation for the generator of the SDE which may be used to find a semi-explicit formula for the probability of fixation of the less beneficial of the two types.

Coalescents with migration in the moderate regime

Sophia-Marie Mellis

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We consider a population of size K^γ , $\gamma \geq 1$, that is divided into $d \geq 2$ colonies. Between these colonies individuals may migrate at a rate proportional to K . In this setting, we study the ancestral lines of said population by using a coalescent model where pairs of ancestral lines within the same colony coalesce at rate 1. More specifically, we work with a vector of empirical measures, such that each component keeps track of both the number of ancestral lines present in colony i at time t and the initial locations of all the lines they merged with. Our main concern then lies with its behavior as K goes to infinity for small times t . We will see that, in the proper rescaling of time and space, it converges to the solution of a d -dim. coagulation equation that has a probabilistic interpretation connected to either multitype branching processes (case $\gamma = 1$) or multitype Feller diffusions (case $\gamma > 1$). Joint work with Fernando Cordero, Sebastian Hummel and Emmanuel Schertzer.

On multi-allelic Cannings models and multi-type exchangeable coalescents

Martin Möhle

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A multi-type neutral Cannings population model with mutation and fixed subpopulation sizes is analyzed. Under appropriate conditions, as all subpopulation sizes tend to infinity, the ancestral process, properly time-scaled, converges to a multi-type coalescent with mutation sharing the exchangeability and consistency property. The proof gains from coalescent theory for single-type Cannings models and from decompositions into reproductive and mutational parts. The second part deals with a different but closely related multi-type Cannings model with mutation and fixed total population size but stochastically varying subpopulation sizes. The latter model is analyzed forward and backward in time with an emphasis on its behaviour as the total population size tends to infinity. Forward in time, multi-type limiting branching processes arise for large population size. Its backward structure and related open problems are briefly discussed.

Branching systems with noisy selection

Zsófia Talyigás and Emmanuel Schertzer

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There have been a lot of recent progress on branching particle systems with selection, in particular on the N -particle branching random walk (N -BRW). In the N -BRW, N particles have locations on the real line at all times. At each time step, every particle generates a number of children, and each child has a random displacement from its parent's location. Then among the children only the N rightmost are selected to survive and reproduce in the next generation. This is the truncation selection model.

In this talk we will investigate noisy versions of the N -BRW. That is, instead of truncation, we randomly sample N particles from the children to survive. For this class of models, the probability of selecting a given child depends on its location in such a way that particles more to the right are more likely to be selected. There are different versions of such models, which, according to our simulations, show some universal counter-intuitive behaviours and interesting phase transitions. In our talk we will discuss explanations of these phenomena by presenting rigorous results and conjectures on some of the noisy selection models.

A branching particle system as a model of pushed fronts

Julie Tourniaire

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We consider a system of particles performing a one-dimensional dyadic branching Brownian motion with space-dependent branching rate $r(x)$, negative drift $-\mu$, and killed upon reaching 0. More precisely, the particles branch at rate $\rho/2$ in $[0, 1]$, for some $\rho \geq 1$, and at rate $1/2$ in $(1, \infty)$. The drift $\mu = \mu(\rho)$ is chosen in such a way that the system is critical.

This system can be seen as an analytically tractable model for fluctuating fronts, describing the internal mechanisms driving the invasion of a habitat by a cooperating population. Recent studies by Birzu, Hallatschek and Korolev on the noisy FKPP equation with Allee effect suggest the existence of three classes of fluctuating fronts: pulled, semi-pushed and fully-pushed fronts.

In this talk, we will focus on the pushed regime. We will show that the particle system exhibits the same phase transitions as the noisy FKPP equation. We will then use this system to explain how the internal mechanisms driving the invasion shape the genealogy of expanding populations.

Scaling limit of an adaptive contact process

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We introduce and study an interacting particle system evolving on the d -dimensional torus \mathbb{Z}_N^d . Each vertex of the torus can be either empty or occupied by an individual of a given type; the space of all types is the positive real line. An individual of type λ dies with rate one and gives birth at each neighbouring empty position with rate λ . Moreover, when the birth takes place, the new individual is likely to have the same type as the parent, but has a small chance to be a mutant; the mutation rate and law of the type of the mutant both depend on λ . We consider the asymptotic behaviour of this process when the size of the torus is taken to infinity and the overall rate of mutation tends to zero fast enough that mutations are sufficiently separated in time, so that the amount of time spent on configurations with more than one type becomes negligible. We show that, after a suitable projection (which extracts just the dominant type from the configuration of individuals in the torus) and time scaling, the process converges to a Markov jump process on the positive real lines, whose rates we determine. Joint work with Adrián González Casanova and András Tobias.