Ancestral lines in population models with interaction

BOKU University, 24-26 September 2025
Seminar room 29 - Ilse Wallentin Haus
Peter Jordan Straße 82, 1190 Vienna

Wednesday, 24.09.2025

09:00 – 09:25 : Registration

09:25 – 09:30 : Opening

09:30 – 10:30 : Paul Jenkins (Warwick)

Sampling probabilities, diffusions, ancestral graphs, and duality under strong selection

10:30 – 11:00 : Coffee break

11:00 – 12:00 : Sebastian Hummel (Zurich)

Fixation and stationary times for the Λ*-Wright–Fisher process*

12:00 – 14:00 : Lunch + short walk at Türkenschanzpark

14:00 – 15:00 : Matthias Birkner (Mainz)

Conditional coalescent limits given the pedigree for diploid exchangeable population models

15:00 – 15:30 : Coffee break

15:30 – 16:30 : Cornelia Pokalyuk (Lübeck)

Neutral diversity patterns in a host-virus model with persistence and reinfection

16:30 – 17:30 : Florin Boenkost (Vienna)

Nested coalescent and their connection to the Brownian snake

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Thursday, 25.09.2025

09:30 – 10:30 : Martin Möhle (Tübingen)
On the genealogy of multi-type Cannings models
10:30 – 11:00 : Coffee break + Group picture
11:00 – 11:45 : Hannah Dopmeyer (Bielefeld)
The two-size Wright–Fisher model: (uniform) renewal theory, duality, and ancestral structures
11:45 – 12:30 : Mathilde André (Paris, Vienna)
Genealogies in structured frequency-dependent branching processes
12:30 – 14:00 : Lunch
14:00 – 15:00 : Emma Horton (Warwick)
Conditioned exit measures of non-local branching processes
15:00 – 15:30 : Coffee break
15:30 – 16:30 : Vitali Wachtel (Bielefeld)
Critical multitype branching: a functional limit theorem and ancestral processes
16:30 – 17:30 : Andreas Kyprianou (Warwick)
The Brownian marble
18:30 – : Conference Dinner at the Heurigen *Weinbau Zawodsky* (with outdoor seating, weather permitting)

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Friday, 26.09.2025

09:30 – 10:30 : Vincent Bansaye (Palaiseau)
A spine construction for density dependent population models

10:30 – 11:00 : Coffee break

11:00 – 12:00 : Michael Baake (Bielefeld)
The embedding problem with applications to reversible Markov matrices and recombination

12:00 – 14:00 : Lunch

14:00 – 15:00 : Charline Smadi (Grenoble)
Muller's ratchet with tournament selection

15:00 – 15:30 : Coffee break

15:30 – 16:30 : Anton Wakolbinger (Frankfurt)
From competing random populations to Poissonian interacting trajectories

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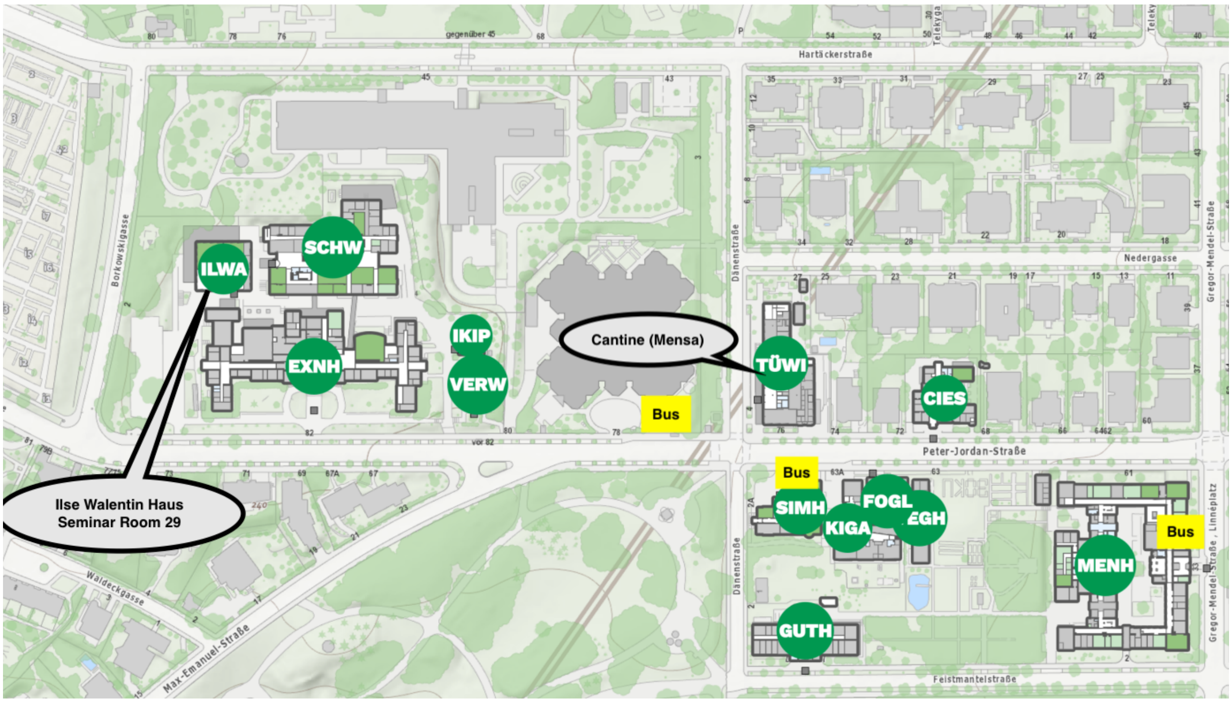

Abstracts

Paul Jenkins (Warwick)

Sampling probabilities, diffusions, ancestral graphs, and duality under strong selection

Wright-Fisher diffusions and their dual ancestral graphs occupy a central role in the study of allele frequency change and genealogical structure, and they provide expressions, explicit in some special cases but generally implicit, for the sampling probability distribution – the joint distribution of the allelic configuration of a sample taken from the population.

We study the asymptotic regime where the selective advantage of one allele is very large. In this regime, we identify two different scaling limits showing that the Wright-Fisher diffusion can be approximated either by a Gaussian process or by a collection of independent continuous-state branching processes with immigration. The latter provides a simple, analytic approximation for the leading term of the sampling probability even under non-reversible models of mutation. We also study the asymptotic behaviour of the corresponding ancestral selection graph and establish an asymptotic duality relationship between this and the diffusion. Joint work with Martina Favero (Stockholm University).

Sebastian Hummel (Zurich)

Fixation and stationary times for the Λ-Wright–Fisher process

We study the fixation and stationary behavior of the Λ-Wright–Fisher process with parent-independent mutation and finitely many types, a jump-diffusion model for allele frequency dynamics in large populations with potentially large offspring variance. Using a lookdown construction, we characterize the distribution of absorption times and the order of allele extinctions when mutations are absent, and identify a strong stationary time in the presence of mutations. Our results include explicit expressions for the mean fixation and stationary times for the Wright–Fisher diffusion, and mean fixation times in the Beta-coalescent case. A key component of our approach is the analysis of the fixation line: We extend this process to incorporate mutation, providing a unified framework for studying both fixation and equilibrium behavior.

This is joint work with Airam Blancas, Adrian González Casanova, and Sandra Palau.

Matthias Birkner (Mainz)

Conditional coalescent limits given the pedigree for diploid exchangeable population models

We study coalescent processes conditional on the population pedigree under a broad class of exchangeable diploid bi-parental population models. In the finite variance case, the large population limit agrees with its pedigree-averaged version, namely Kingman's coalescent. In the case of highly skewed offspring distributions, we characterise the limit as an inhomogeneous coalescent, which reflects certain fixed exceptional reproduction events in the past and differs from the usual (simultaneous) multiple merger coalescents. In particular, the fixed pedigree structure then impacts the distribution of the site frequency spectrum.

Based on joint work with Frederic Alberti, Louis Fan and John Wakeley.

Cornelia Pokalyuk (Lübeck)

Neutral diversity patterns in a host-virus model with persistence and reinfection

Some viruses including the widespread Human Cytomegalovirus (HCMV) show a high level of genetic diversity within hosts and across the whole virus population even in relatively conserved genomic regions. To investigate how this diversity is formed, we introduce and analyse a multi-locus population model with neutrally evolving viruses that persist in their host and are capable for reinfection. In a regime of rare mutation, occasional recombination and relatively frequent viral reproduction and reinfection we determine the asymptotic within host sequence type frequency distribution by investigating the ancestral lines of a sample of viruses.

Based on these results we fit our model to observed genotype frequencies from Austrian HCMV patients. We find that our neutral model describes the data surprisingly well.

This talk is based on joint work with Raphael Eichhorn, Irene Görzer, Büsra Külekci and Madlen Mollik.

Florin Boenkost (Vienna)

Nested coalescent and their connection to the Brownian snake

The nested Kingman coalescent $(\mathcal{K}_t^n, t \geq 0)$ is a model for the genealogy of lineages belonging to different species, which can be thought of as (gene-)trees within a (species-)tree. Here, we assume that the species tree is given as a Kingman coalescent and once species coalesce the gene lineages belonging to the merged species are allowed to coalesce. An important quantity is the empirical measure $g_t^n = \frac{1}{s_t^n}\sum_{i=1}^{s_t^n} \delta_{\Pi_t^n(i)}$ of species sizes in the nested coalescent, where $\Pi_t^n(i)$ denotes the number of gene lineages in species i. As the number of species s_0^n tends to infinity we show convergence towards a dust solution $u(t,x)$ of the Smoluchowski coagulation-transport equation

$$\partial u = \partial_x \left(\frac{x^2}{2} u \right) + \frac{1}{t}(u \star u - u).$$

In particular, if there are fewer lineages per species than species itself, g_t^n converges to a *dust solution* $u(t,x)$, meaning that $u(t,x) \to \delta_0(dx)$ as $t \to 0$. Dust solutions for the Smoluchowski coagulation-transport equation have appeared in [Lambert and Schertzer 2020]. We prove that dust solutions can be expressed in terms of the Brownian snake and through that connection we show existence and uniqueness (up to scaling) for solutions of this equation. This talk is based on joint work with Emmanuel Schertzer.

Martin Möhle (Tübingen)

On the genealogy of multi-type Cannings models

We study the multi-type Cannings population model. Each individual has a type belonging to a given at most countable type space E. The population is hence divided into $|E|$ subpopulations. The subpopulation sizes are assumed to be constant over the generations, whereas the number of offspring of type l of all individuals of type k is allowed to be random. Under a separate exchangeability assumption on the offspring numbers, the transition probabilities of the ancestral process of a sample of individuals satisfy a multi-type consistency property, paving a way to prove in the limit for large subpopulation sizes the existence of multi-type exchangeable coalescent processes via Kolmogorov's extension theorem. Integral representations for the infinitesimal rates of these multi-type exchangeable coalescents and some of their properties are studied. Examples are provided, among them multi-type Wright–Fisher models and multi-type pure mutation models. The results contribute to the foundations of multi-type coalescent theory and provide new insights into (the existence of) multi-type exchangeable coalescents.

Hannah Dopmeyer (Bielefeld)

The two-size Wright–Fisher model: (uniform) renewal theory, duality, and ancestral structures

In the first part of the talk we consider a population with two types of individuals, distinguished by the resources required for reproduction: type-0 (small) individuals need a fractional resource unit of size $\vartheta \in (0,1)$, while type-1 (large) individuals require 1 unit. The total available resource per generation is R. To form a new generation, individuals are sampled one by one, and if enough resources remain, they reproduce, adding their offspring to the next generation. The probability of sampling an individual whose offspring is small is $\rho_R(x)$, where x is the proportion of small individuals in the current generation. We call this discrete-time stochastic model a two-size Wright–Fisher model, where the function ρ_R can represent mutation and/or frequency-dependent selection. We show that on the evolutionary time scale, i.e. accelerating time by a factor R, the frequency process of type-0 individuals converges to the solution of a Wright–Fisher-type SDE. The drift term of that SDE accounts for the bias introduced by the function ρ_R and the consumption strategy, the latter also inducing an additional multiplicative factor in the diffusion term. The proof relies on methods from renewal theory, in particular a uniform version of Blackwell's renewal theorem for binary, non-arithmetic random variables, established via ε-coupling.

In the second part, we explore a mysterious moment duality between that Wright–Fisher type SDE and a branching process with interactions. To do so, we construct a Moran model with frequency-dependent neutral reproduction, which on the evolutionary time scale converges to the same SDE as the two-size Wright–Fisher model. The natural ancestral graph of that Moran model exhibits a complicated hierarchical structure that is very different from the moment dual. By using the fact that moment duality is a property in expectation and constructing so-called Frankenstein processes (merging realizations of different ASGs), we bridge the gap between the natural ancestral graph and the analytical moment dual.

Mathilde André (Paris, Vienna)

Genealogies in structured frequency-dependent branching processes

We establish a broad class of regulated individual-based models going beyond exchangeable populations, yet whose genealogies are in the universality class of the celebrated Kingman coalescent (Kingman, 1982) which serves as baseline models for panmictic, neutral populations. We establish a broad class of regulated multitype individual-based models extending beyond exchangeable and fix-sized populations, yet for which the scaling limit of the genealogies sampled at a given time is still Kingman's coalescent.

The random marked metric measure space encoding genealogies is proved to converge in distribution for the Gromov-Weak topology (Greven et al, 2009) through using a martingale change of measure and building on the moment formalism developed in Foutel-Rodier and Schertzer (2023) for Galton–Watson processes. Besides extending the robustness of exchangeable coalescents, the underlying purpose is to formulate a versatile methodology to derive scaling limits of genealogies within structured and regulated particle systems. The latter streamlines computations on chronological forests to a stochastic analysis of the type frequencies in the population.

Kingman's coalescence rates are recovered from the contribution over large timescales of its deviations from equilibrium. T he underneath spatial structure only influences the effective population size, hence the genetic diversity of the population.

This is joint work with Félix Foutel-Rodier (MAP5) and Emmanuel Schertzer (University of Vienna).

Emma Horton (Warwick)

Conditioned exit measures of non-local branching processes

Motivated by the need to estimate rare events probabilities in fissile systems, we consider path decompositions for conditioned exit measures of non-local branching processes. In particular, we show that non-local branching processes conditioned to exit a domain via certain sets exhibit a many-to-few decomposition.

Vitali Wachtel (Bielefeld)

Critical multitype branching: a functional limit theorem and ancestral processes

We consider the long-term behaviour of critical multitype branching processes conditioned on non-extinction, both with respect to the forward and the ancestral processes. Forward in time, we prove a functional limit theorem in the space of trajectories of the linearly-scaled h-transformed process; the change of measure allows us to work on the same probability space for all times. Backward in time, we trace the lines of descent of individuals sampled from a (stationary) population and analyse the ancestral type distribution, that is, the type distribution of the ancestors in the distant past, as well as the type process along the ancestral line.

Andreas Kyprianou (Warwick)

The Brownian marble

Fundamentally motivated by the two opposing phenomena of fragmentation and coalescence, we introduce a new stochastic object which is both a process and a geometry. The Brownian marble is built from coalescing Brownian motions on the real line, with further coalescing Brownian motions introduced through time in the gaps between yet to coalesce Brownian paths. The instantaneous rate at which we introduce more Brownian paths is given by λ/g^2 where g is the gap between two adjacent existing Brownian paths. We show that the process "comes down from infinity" when $0 < \lambda < 6$ and the resulting space-time graph of the process is a strict subset of the Brownian Web on $\mathbb{R}x[0, \infty)$. When $\lambda \geq 6$, the resulting process "does not come down from infinity" and the resulting range of the process agrees with the Brownian Web.

Vincent Bansaye (Palaiseau)

A spine construction for density dependent population models

In this talk, we will be interested in uniform sampling within population models where births, deaths, or transitions may depend on population sizes. This will be achieved through a spine construction, in the spirit of the Kesten tree and works of Kurtz, Lyons, Peres, and Pemantle–namely, a Markov forward construction that describes a typical immortal individual and uses it to represent the ancestral lineage under uniform sampling.

This approach consists in defining a new process and a new genealogical tree, in which both the typical individual and the rest of the population follow modified dynamics. We will illustrate this construction with simple examples, including a transition phase in a neutral density-dependent growth-division model. We could also discuss premilinary results or perspectives for extensions, as well as more challenging questions, models and potential limitations.

Michael Baake (Bielefeld)

The embedding problem with applications to reversible Markov matrices and recombination

The question whether a given Markov matrix can occur in a continuous-time Markov chain is known as the Markov interpolation or embedding problem. It is fully solved only for matrices up to dimension 4, while only partial results exist beyond that. We review the problem and some of the known results, and discuss it for reversible Markov matrices and for the partioning processes of recombination.

Joint work with Ellen Baake and Jeremy Sumner.

Charline Smadi (Grenoble)

Muller's ratchet with tournament selection

Muller's ratchet, in its prototype version, models a haploid, asexual population whose size N is constant over the generations. Slightly deleterious mutations are acquired along the lineages at a constant rate, and individuals carrying less mutations have a selective advantage. In the classical variant, an individual's selective advantage is proportional to the difference between the population average and the individual's mutation load, whereas in the ratchet with tournament selection only the signs of the differences of the individual mutation loads matter. In a parameter regime which leads to slow clicking (i.e. to a loss of the currently fittest class at a rate $\ll 1/N$) we obtain the asymptotic click rates of the tournament ratchet as N goes to infinity, and derive and analyse the large population asymptotics of the empirical type frequency profile at moderately large times.

This is a joint work with Jan Lukas Igelbrink and Anton Wakolbinger.

Anton Wakolbinger (Frankfurt)

From competing random populations to Poissonian interacting trajectories

Motivated by mathematical models for experimental evolution, we consider a large population whose size is kept fixed over the generations and in which every once in a while some randomly chosen individual experiences a beneficial mutation, leading to a slightly increased reproduction rate of its offspring. In the so-called Gerrish-Lenski parameter regime, typically a finite number of such offspring populations (of mesoscopic size) is present together with one resident type (of macroscopic size). These subpopulations perform a contest for becoming resident, a phenomenon addressed as clonal interference. In this way some of the fitness increments caused by the beneficial mutations may get lost, leading to a reduction of the long time increase of fitness. In the Moran model with strong selection, it turns out that, in the limit of infinite population size, the rescaled logarithmic sizes of the contending subpopulations constitute a system of interacting piecewise linear trajectories, whose source of randomness is a Poisson point process.

We present a corresponding large population limit result, investigate the long time increase of fitness in the limiting system of "Poissonian interacting trajectories" and relate it to heuristic predictions. The talk is based on joint work with Felix Hermann, Adrián González Casanova, Renato Soares dos Santos, András Tóbiás, and Florin Boenkost.