

List of abstracts for workshop on
**Population Models with Interaction:
New Trends and Developments**

16./17. September 2021 in Bielefeld and online

Dedicated to the 60th birthday of Ellen Baake

16.09.2021, 10:15–11:05

Frank den Hollander

Leiden University, The Netherlands

Spatial populations with seed-bank

In this lecture we consider a system of interacting Fisher-Wright diffusions with seed-bank. Individuals carry one of two types, live in colonies labelled by countable Abelian group playing the role of geographic space, 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. Our goal is to understand in what way the seed-bank *enhances genetic diversity*.

When individuals become dormant they adopt a *random colour* that determines their wake-up time. The system of continuum stochastic differential equations describing the population in the large-colony-size limit has a unique strong solution that converges to an equilibrium parametrised by the initial type densities. This equilibrium exhibits a dichotomy between two phases: *coexistence* (= locally multi-type equilibrium) versus *clustering* (= locally mono-type equilibrium). We identify the parameter regimes for which these two phases occur. We also establish the *finite-systems scheme*, i.e., identify how a finite truncation of the system (both in the geographic space and in the seed-bank) behaves as both the time and the truncation level tend to infinity, properly tuned together.

Joint work with Andreas Greven (Erlangen) and Margriet Oomen (Leiden)

16.09.2021, 11:10–12:00

Anita Winter

Duisburg-Essen, Germany

Self regulating branching populations under cell division

Abstract: TBA

16.09.2021, 14:00–14:50

Paul Jenkins

University of Warwick, United Kingdom

Lessons from population genetics for computational
statistics: genealogies of interacting particle systems used in
Sequential Monte Carlo

Interacting particle systems are a broad class of stochastic models for phenomena arising across physics, engineering, biology, and finance. A prominent class of such models can be expressed as a 'sequential Monte Carlo' algorithm in which the aim is to construct an empirical approximation to a sequence of measures. The approximation is constructed by evolving a discrete-time, weighted population of particles, alternating between a Markov update and a resampling step. This setup is familiar in population genetics, being mathematically equivalent to a Cannings model in a moving environment. Conditions under which the genealogy of a sequence of Cannings models in a fixed environment converges to a given scaling limit are well-studied. In this talk I discuss how such results can be extended to cover a much broader class of interacting particle systems commonly used in computational statistics. More precisely, under given conditions we can show that a certain time rescaling ensures that the genealogy converges (as the number of particles grows) to Kingman's coalescent.

This is joint work with Suzie Brown, Adam Johansen, Jere Koskela, and Dario Spanò.

16.09.2021, 14:55–15:45

Martin Möhle

Universität Tübingen, Germany

A restaurant process with a cocktail bar

The Chinese restaurant process (CRP) has applications in several disciplines, for example in Bayesian statistics and in mathematical population genetics. In addition to the features of the two-parameter CRP, the restaurant under consideration has a cocktail bar and hence allows for a wider range of (bar and table) occupancy mechanisms. The model depends on three real parameters α , θ_1 and θ_2 fulfilling certain conditions. Results known for the two-parameter CRP are carried over to this model. We study the number of customers at the cocktail bar, the number of customers at each table and the number of occupied tables after n customers have entered the restaurant. For $\alpha > 0$ the number of occupied tables, properly scaled, is asymptotically three-parameter Mittag-Leffler distributed as n tends to infinity. We provide representations for the two- and three-parameter Mittag-Leffler distribution leading to efficient random number generators for these distributions. The proofs draw heavily from methods known for exchangeable random partitions, martingale methods known for generalized Pólya urns and results known for the two-parameter CRP.

16.09.2021, 16:40–17:30

John Wakeley

Harvard University, U.S.A.

Effects of introgression on two-locus gene trees within species trees.

Abstract: TBA

16.09.2021, 17:30–18:00

Warren Ewens

University of Pennsylvania, U.S.A.

Some thoughts about population genetics theory and its
association with prime numbers and permutations, interesting
numbers, and physic

This talk considers three topics, the first two of which are perhaps whimsical. Topic 1 considers aspects of the well-known relation between the prime factorization of a random "large" integer and properties of random permutations. Topic 2 takes up constants involving the three central numbers e , γ and π . Topic 3 is an attempt to reconcile the fact that fitness is a while genome property with the study of evolution using gene frequencies.

17.09.2021, 09:00–09:50

Matthias Birkner

Johannes Gutenberg-Universität Mainz, Germany

An analogue of Haldane's formula when the variance
asymptotically is infinite

Haldane's classical formula approximates the fixation probability of a single beneficial allele with (small) selective advantage s in a large haploid population as $2s/\sigma^2$, where σ^2 is the individual offspring variance. By contrast, we consider a family of models for populations of size N where individual offspring numbers have tail exponent $-\alpha$ with $1 < \alpha < 2$, in particular, they have (asymptotically as N diverges) infinite variance. It turns out that then there is a regime where the fixation probability is proportional to $s^{1/(\alpha-1)}$. We also investigate the time scale on which fixation occurs.

Based on work in progress with Iulia Dahmer and Bjarki Eldon.

17.09.2021, 10:20–11:10

Meike Wittmann

Universität Bielefeld, Germany

Extinction vortices and minimum viable populations:
Interactions between ecology and evolution and between
different selection mechanisms

Joint work with Peter Nabutanyi

Small populations can suffer from genetic problems like inbreeding depression, mutation accumulation, and loss of genetic variation. In this talk, I will present stochastic models for the joint dynamics of population sizes and allele frequencies in such populations. We explore under what conditions populations enter an eco-evolutionary extinction vortex where a decrease in genetic variation leads to population decline, which leads to even faster loss of genetic variation, and so on, until the population goes extinct. We will also quantify minimum viable population sizes for the long-term persistence of populations experiencing a combination of genetic problems of small population size.

17.09.2021, 11:15–12:05

Anton Bovier

Universität Bonn, Germany

Branching Brownian motion with social distancing

We consider a model of branching Brownian motion with self repulsion. Self-repulsion is introduced via change of measure that penalises particles spending time in an ε -neighbourhood of each other. We derive a simplified version of the model where only branching events are penalised. This model is almost exactly solvable and we derive a precise description of the particle numbers and branching times. In the limit of weak penalty, an interesting universal time-inhomogeneous branching process emerges. The position of the maximum is governed by a F-KPP type reaction-diffusion equation with a time dependent reaction term.

This is joined work with Lisa Hartung.

17.09.2021, 13:40–14:30

Reinhard Bürger
Universität Wien, Österreich

The effects of epistasis and linkage on the invasion of locally
beneficial mutations.

Abstract: TBA

17.09.2021, 14:30–15:20

Anton Wakolbinger
Universität Frankfurt, Germany

Genealogies in evolution: looking backward and forward

Abstract: TBA