

## Titles and Abstracts

**Eugenio Buzzoni (TU Berlin)** *Boundary behavior in the seed bank diffusion*

Abstract: For the one-dimensional Wright-Fisher diffusion with mutation, the question whether the boundary points can be touched with positive probability has a well-known answer. The standard proof is based on a rescaling via scale function and speed measure. However, for the seed bank model, a similar two-dimensional diffusion process reflecting a population subdivided between active and dormant individuals, this method can't be applied. We will see how the usage of polynomial diffusions (Filipovic, Larsson, 2016; Larsson, Pulido, 2017), combined either with a martingale argument (McKean, 1969) or with an argument based on Foster-Lyapunov inequalities for the infinitesimal generator (Meyn, Tweedie, 1992 and 1993) can give us a solution in those cases, too.

**Adrián González Casanova (UNAM)** *The seedbank random graph*

Abstract: In this talk we construct a random graph version of the Kaj, Krone and Lascoux (2001) seed bank model and use it to draw in the same picture forward and backward results on the effect of dormancy at different temporal scales. We will then discuss in more details one of its limiting objects: the seedbank coalescent.

**Felix Hermann (TU Berlin)** *Evolutionary advantages of seed-banks in randomly fluctuating environments*

Abstract: We investigate three distinct Bienayme-Galton-Watson (BGW) processes in a random environment that oscillates between a healthy and a harsh state, in which the processes will be supercritical and subcritical respectively.  $(X_n)$  will be a standard 1-dimensional BGW process. By  $(Y_n)$  and  $(Z_n)$  we denote 2-type BGW processes, which both model an active and a dormant part of the population but differ in their switching behavior between states.  $(Y_n)$  will be aware of the environment and adjust to it in a reasonable way ('responsive switching'), while  $(Z_n)$  follows a strategy independent of the environment ('spontaneous switching'). We derive and discuss fitness values of these processes as functions of the environment parameters. As it turns out, there are scenarios for both switching strategies where the seed-bank process survives with positive probability while  $(X_n)$  goes extinct almost surely.

**Frank den Hollander and Margriet Oomen (Leiden)** *Hierarchical Seed-banks*

Abstract: We consider a system of interacting Wright-Fisher diffusions with seed-bank. Individuals live in colonies 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. As geographic space we consider the hierarchical group  $\Omega = \Omega_N, N \in \mathbb{N}$ . Our goal is to identify the change in behaviour induced by the seed-bank.

We carry out a multi-scale renormalisation analysis when, in addition to hierarchical migration, the system also has a hierarchical seed-bank, i.e., active individuals can become dormant into a hierarchy of dormant states, each with its own rate. In the hierarchical mean-field limit  $N \rightarrow \infty$ , we show that block averages on hierarchical space-time scale  $k \in \mathbb{N}$  perform a diffusion with a renormalised diffusion function that depends on  $k$ . Finally we show a criterion under which the renormalised diffusion function converges to the Wright Fisher

diffusion and we show how the seed-bank influence this criterion depending on its structure. Joint work with Andreas Greven.

**Jere Koskela (Warwick)** *Model selection between seed banks and related coalescents*

Abstract: There are (at least) two modelling regimes for seed banks in coalescent processes: the so-called weak seed bank, which arises from short periods of dormancy (measured in numbers of generations), and the strong seed bank, which arises from periods of dormancy on the order of the effective population size. The weak seed bank is equivalent to the Kingman coalescent with an altered effective population size, while the strong seed bank resembles the structured coalescent, albeit with an infinite effective population size in the seed bank subpopulation. I will review all four models, and show that a modest amount of DNA sequence data distinguishes between them with high confidence, at least in the idealised setting of simulated data.

**Jay Lennon (Indiana)** *Microbial seed banks: ecological and evolutionary significance of dormancy*

**Shubhamoy Nandan (Leiden)** *Homogeneous evolution with inhomogeneous seed-banks*

Abstract: We consider a system of interacting Moran models with seed-banks. Individuals live in colonies 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 via exchange, suspending their resampling and migration until they become active again. The colonies are labeled by  $\mathbb{Z}^d$ ,  $d \geq 1$ , playing the role of geographic space. The sizes of the active and the dormant population are finite and fixed throughout the evolution and depend on the location of the colony. Migration is driven by a random walk transition kernel. Our goal is to describe the equilibrium behavior of the system as a function of the underlying model parameters with the help of duality, coupling techniques, etc.

**Florian Nie (TU Berlin)** *Spread of the beneficial allele in a Fisher-KPP equation with dormancy*

Abstract: We introduce a class of stochastic partial differential equations with seed banks modeling the spread of two competing alleles in spatial populations where individuals may switch between active and dormant states. We discuss (weak) existence and uniqueness of the SPDEs and provide an equivalent delay representation of the systems. It turns out that the SPDEs give rise to an interesting class of “on/off” moment duals: For example, in the special case of the Fisher-KPP equation with seed bank, the moment dual will be given by a system of “on/off”-branching Brownian motions. This system differs from a classical branching Brownian motion in the sense that independently for all individuals, motion and branching may be “switched off” for an exponential amount of time, until they get “switched on” again. As an application of the duality, we show that the spread of the beneficial allele, which in the classical Fisher-KPP equation evolves as a pulled traveling wave with speed  $\sqrt{2}t$ , is slowed down in the seed bank Fisher-KPP model. In fact, by computing bounds on the position of the rightmost particle in the on/off branching Brownian motion, we obtain an upper bound for the speed of propagation of the beneficial allele given by

$\sqrt{\sqrt{5}-1}$ . This shows that seed banks have the potential to slow down fitness waves, in line with intuitive reasoning from ecology.

**Dario Spanò (Warwick)** *A wishlist of open problems for seedbank models*

Abstract: Our understanding of the mathematical properties of seedbank models has increased very rapidly in the past lustrum. This should make us optimistic on our ability to solve further open problems on which we would not like to remain dormant. This talk aims at initiating a discussion around some of the as-yet-unsolved questions on seedbank models which I find most enticing.

**Thibaut Sellinger (TU München)** *Inference of past demography and dormancy from whole genome polymorphism sequence data*

Abstract: Several methods based on the Sequential Markovian Coalescent (SMC) have been developed to use full genome sequence data to uncover population demographic history, which is of interest in its own right and a key requirement to generate a null model for selection tests. While these methods can be applied to all possible species, the underlying assumptions are sexual reproduction at each generation and no overlap of generations. However, in many plant, invertebrate, fungi and other species, those assumptions are often violated due to different ecological and life history traits, such as long term dormant structures (seed or egg-banking). We develop a novel SMC-based method to infer the rates of seed/egg-bank and the populations' past demographic history. Using simulated data sets, we demonstrate the accuracy of our method for a wide range of demographic scenarios and for sequence lengths from one to 30 Mb using four sampled genomes. Finally, we apply our method to the water flea *Daphnia pulex* and exhibit signature of a long lived egg-bank of three to 18 generations. In conclusion, we here present a novel method to infer accurate demographies and dormancy.

**Andr as T ob ias (TU Berlin)** *Emergence of dormancy under competitive pressure*

Abstract: Microbial dormancy is an evolutionary trait that has emerged independently at various positions in the tree of life. It describes the ability of a microorganism to switch to a metabolically inactive state to withstand unfavourable conditions. However, maintaining such a trait will use additional resources. In this talk, we aim at a basic understanding under which conditions an individual with a dormancy trait can invade a resident population lacking this trait, even if maintaining dormancy reduces the reproduction rate compared to the residents. Here, we follow a stochastic individual-based approach employing birth-and-death processes (leaving the usual population genetic framework), and dormancy is triggered by competitive pressure for resources. In the large-population limit, we identify a necessary and sufficient condition under which the invasion of mutants having a lower reproduction rate than the resident population has a positive probability. Further, we explicitly determine the limiting probability of invasion and the asymptotic time of fixation of mutants in the case of a successful invasion. In this case, we observe the three classical phases of invasion dynamics. The subject of this talk is joint work in progress with Jochen Blath and Noemi Kurt.