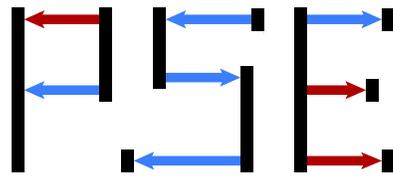


Genealogies, lines of descent and duality in population models

A workshop within the DFG Priority Program 1590



March 19–21, 2018

Program

March 19th, 2018 (Monday)	
13:30–14:00	Registration
14:00–14:15	Opening
14:15–15:15	MATTHIAS BIRKNER Ancestral lineages in spatial population models
15:15–15:45	Coffee Break
15:45–16:45	PAUL JENKINS Wright-Fisher diffusion bridges
17:00–18:00	ÉTIENNE PARDOUX Genealogy of a CSBP with jumps and interaction
18:45–21:00	Discussion and Snack Buffet

March 20th, 2018 (Tuesday)	
9:15–10:15	PETER PFAFFELHUBER Topological Aspects of genealogies and their evolution - MINICOURSE Part 1
10:30–11:30	ANITA WINTER Topological Aspects of genealogies and their evolution - MINICOURSE Part 2
11:30–12:00	Coffee Break
12:00–12:45	WOLFGANG LÖHR The Aldous chain on cladograms in a new state space of algebraic measure trees
12:45–14:15	Lunch Break
14:15–15:00	SANDRA KLIEM Evolving genealogies for finite branching populations under selection and competition
15:00–15:45	ANTON WAKOLBINGER Evolving genealogies for a two-type continuous state branch- ing population under selection and competition
15:45–16:15	Coffee Break
16:15–17:00	JOCHEN BLATH The seed bank diffusion, and its relation to the two island model
17:00–17:45	ANJA STURM On classifying genealogies for general diploid exchangeable population models
18:45–22:00	Conference Dinner Steinbach Bräu Erlangen

March 21st, 2018 (Wednesday)	
9:15–10:30	ELLEN BAAKE Ancestral lines under selection and recombination
10:30–11:15	ANTON KLIMOVSKY Stochastic population models on evolving networks
11:15–11:45	Coffee Break
11:45–12:30	STEIN ANDREAS BETHUELSEN Random walks on top of stochastic population models
12:30–13:30	Lunch Break
13:30–14:30	AMAURY LAMBERT Ultrametric trees, combs and neutral mutations

ANITA WINTER AND PETER PFAFFELHUBER
(Duisburg-Essen/Freiburg)

MINICOURSE
Topological Aspects of genealogies and their evolution

In this course we introduce metric measure spaces as state spaces of evolving genealogies. We discuss a notion of convergence which has two equivalent formulations which are of interest depending on the approach. From an application point of view we require that subtrees spanned by a typical sample from the population converge, while from a technical point of view we require the existence of an embedding in which the sampling measures converge.

The course has three parts. Part I is devoted to neutral populations without mutation. Part II extends the set-up to multi-type situations allowing for selection and mutation. Part III then introduces more recent developments such as topologies for multi-metric measure spaces (suitable for modeling recombination), for metric 2-level measure spaces (suitable for modeling host-parasite evolution or two-level selection), or bi-measure metric trees (allowing for including fossils into the modeling), and more.

ELLEN BAAKE (Bielefeld)

Ancestral lines under selection and recombination

We consider the deterministic limit of the Moran model under selection and recombination that take 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. This leads to a closed solution of the deterministic selection-recombination equation, together with a genealogical interpretation. As a matter of fact, the ancestral selection-recombination graph may be reduced further in this case. This results in a simple branching-partitioning process and a corresponding duality result.

This is joint work with Frederic Alberti and Carolin Herrmann.

STEIN ANDREAS BETHUELSEN (München)

Random walks on top of stochastic population models

Partly motivated by the applications to population models, the study of random walks on top of an interacting particle system (IPS) have gained increasing interest in recent years. So far general results have been obtained for such random walks whenever the IPS satisfies certain strong (and uniformly) mixing assumptions. On the other hand, for IPS in non-uniform mixing regimes only partial and very model specific results have so far been established.

In this talk I will focus on one particular example of such a random walk in the latter category, namely that of a random walk on top of a supercritical contact process. I will present an overview of the results obtained so far for this model and point at some of the challenges still remaining.

This talk is partly based on joint work with Markus Heydenreich (LMU Munich) and Florian Völlering (Bath).

MATTHIAS BIRKNER (Mainz)

Ancestral lineages in spatial population models

Genealogies in stochastic models for spatially extended populations, i.e. the space-time embedding of ancestral lines, typically form systems of coalescing - and possibly branching - ‘random walks’. In the classical stepping stone model with discrete space and fixed local population sizes, ancestral lines are literally independent random walks until coalescence, which facilitates detailed mathematical analysis and, via duality, gives insights into the genetic composition of a spatial population. We will discuss this and more recent modeling approaches which allow to consider continuous space and/or fluctuating local population sizes, where ancestral lines become correlated and inhomogeneous.

JOCHEN BLATH (Berlin)

The seed bank diffusion, and its relation to the two island model

We investigate various aspects of the (biallelic) Wright-Fisher diffusion with seed bank, including moments, stationary distribution and reversibility, for which our main tool is duality. We also provide a complete boundary classification for this two-dimensional sde. Further, we show that the Wright-Fisher diffusion with seed bank can be reformulated as a one-dimensional stochastic delay differential equation, thus providing an elegant interpretation of the age structure in the seed bank. Finally, we investigate several scaling limits of the seed bank model and find a new coalescent-related ancestral process describing the genealogy in a ‘rare-resuscitation’ regime over long timescales. Along the lines, we comment on the relation between the seed bank diffusion and the structured Wright-Fisher diffusion with two islands, which, despite their seeming similarity, exhibit remarkable qualitative differences.

PAUL JENKINS (Warwick)

Wright-Fisher diffusion bridges

There is a well known duality relationship between the neutral Wright-Fisher diffusion running forwards in time and its genealogical counterpart running backwards in time, the coalescent. In this talk I will extend this relationship to find a dual for Wright-Fisher diffusion bridges - that is, allele frequency trajectories conditioned on both start- and endpoint. To study the frequency of an allele at time t in a bridge starting at time 0 and ending at time T $\geq t$, the emerging genealogical structure is a coalescent running backwards from time t to 0 and another coalescent running forwards from time t to T . We can also extend this idea to incorporate natural selection, in which the genealogical processes are now branching and coalescing in two directions from time t . Finally I will discuss how these results can be used to draw exact samples from the transition function of a Wright-Fisher diffusions and their bridges.

This is joint work with Bob Griffiths (Oxford) and Dario Spano (Warwick).

SANDRA KLIEM (Duisburg-Essen)

Evolving genealogies for finite branching populations under selection and competition

In this talk we present a lookdown and a branching particle system version of a finite population evolving with time. Individuals have one of two types and the population dynamics include selection and competition. The population size varies with time. In both models, we record genealogical distances between as well as the types of all individuals. As we will explain, the processes are different when considering marked metric spaces as a state-space, but the same for their equivalence classes.

The talk is "in tandem" with Anton Wakolbinger's presentation, where we will have a look at a candidate for the infinite population limit, and reports on joint work (in progress) with him, Airam Blancas, Stephan Gufler and Viet Chi Tran.

ANTON KLIMOVSKY (Duisburg-Essen)

Stochastic population models on evolving networks

Populations of particles rarely interact via regular interaction networks such as lattices. Moreover, many interaction networks evolve over time and this can have an effect on the population dynamics. We discuss a modeling framework for interacting particle systems on evolving networks based on such familiar ingredients as exchangeability and Markovianity. In some simple cases, we discuss the genealogies of such population models.

(Based on joint work in progress with Jiří Černý.)

AMAURY LAMBERT (Paris)

Ultrametric trees, combs and neutral mutations

Ultrametric trees are trees whose leaves all lie at the same distance from the root. They model the genealogy of a population of particles coexisting at the same time. We will show how the boundary of an ultrametric tree, like any Polish ultrametric space, can be represented in a simple way via the so-called comb metric. We will give various nice examples of random combs and explain how they can be used in applications. In particular, we will examine some results concerning the genetic structure of the population in the presence of neutral Poissonian mutations on the skeleton of the tree.

WOLFGANG LÖHR (Duisburg-Essen)

The Aldous chain on cladograms in a new state space of algebraic measure trees

The Aldous chain on N -cladograms is a simple, mixing Markov chain on the set of binary trees with N labelled leaves. Its mathematical analysis was initiated by David Aldous, who also conjectured in a Fields Institute talk 1999 that there is an $N \rightarrow \infty$ limit diffusion “on some space of continuum trees”. Despite several attempts, however, constructing this limit diffusion in a space of metric (measure) trees has failed since then. Therefore, we propose to change the state space and instead of considering the graph distance, to focus on the tree-structure alone.

We present a new framework for a space of such (continuum) trees possessing no metric structure. We call them algebraic trees, because we formalize the tree-structure by a tertiary operation, namely the branch point map. We construct a natural topology on a space of (sufficiently nice) algebraic measure trees, which is closely related to convergence of triangulations of the circle. In this state space, we are able to prove convergence of the Aldous chain on N -cladograms to a limiting strong Markov process with continuous paths.

(joint work with Leonid Mytnik and Anita Winter)

ÉTIENNE PARDOUX (Marseille)

Genealogy of a CSBP with jumps and interaction

We extend previous work in collaboration with V. Le and A. Wakolbinger to the case of CSBP with jumps. We first describe the genealogy of a CSBP with jumps in case of the presence of a Brownian component. In such a case, we give a new representation of the height process of its genealogical tree, already discussed by Duquesne and Le Gall, in terms of a non Markovian SDE. We then extend this representation to a CSBP with interaction (which of course destroys the branching property). Finally we discuss the approximation by a sequence of renormalized Z^+ valued processes.

This is joint work with Ibrahima Dramé, Zenghu Li and Anton Wakolbinger.

ANJA STURM (Göttingen)

On classifying genealogies for general diploid exchangeable population models

The genetic variation in a sample of individuals/genes depends on their relatedness which is described by their genealogy. In this talk we consider classifying the genealogies of exchangeable diploid populations with fixed size N asymptotically as N tends to infinity.

In a diploid population (such as the human population) every individual carries two copies of each gene, one of which is inherited from one of the individual's two parents and the other copy from the other parent. Diploid populations have in the past most often been modeled in an approximate way by haploid population models (exchangeable Cannings population models) of size $2N$. In haploid populations each individual only carries one copy of a gene such that we may identify individuals and genes and each offspring (gene) has a unique parent (gene). Describing the relatedness of the $2N$ genes in a diploid population of N individuals by a haploid model thus ignores some of the special structure that is present.

In this talk we briefly review the limiting coalescents describing the genealogy for haploid Cannings models in the limit as N tends to infinity: Möhle and Sagitov (2001) classified all possible such limit processes and showed that depending on the tail behavior of the offspring numbers the limit process is Kingman's coalescent with coalescence of pairs or is given by coalescents with (simultaneous) multiple mergers in which (several) larger groups may find a common ancestor at the same time.

We then extend this result to diploid bi-parental analogues of the Cannings model. Here, the next generation is composed of offspring of parent pairs, which form an exchangeable (symmetric) array. Our result classifies the limiting coalescent processes describing the gene genealogies. Using this general result we determine the limiting coalescent in a number of examples of which some have been studied previously (in special cases) and some are new. The examples also show when a haploid approximation to a diploid population may be appropriate for describing its genealogy.

This talk is based on joint work with Matthias Birkner (Universität Mainz) and Huili Liu (Hebei Normal University).

ANTON WAKOLBINGER (Frankfurt)

Evolving genealogies for a two-type continuous state branching population
under selection and competition

The so-called lookdown space (Gufler 2017) allows for a pathwise construction of the evolving genealogy for a large class of neutral reproduction mechanisms. In this talk we focus on a classical continuous branching mechanism and explain how an evolving genealogy for a two-type population with selection and competition can be constructed on top of the (neutral) lookdown space, rendering a pathwise construction of the corresponding process of marked distance matrix distributions.

The talk is "in tandem" with Sandra Kliem's presentation, and reports on joint work (in progress) with her, Airam Blancas, Stephan Gufler and Viet Chi Tran.