



Mini-Workshop

Multiple merger coalescents in population genetics

Schedule

Thu., 28 November 2013

Morning: Room 05-432 (Hilbertraum), afternoon: Room 05-522

9:00–9:30	Registration	
9:30	Welcome	
9:30–10:20	Vlada Limic	A zoom into exchangeable coalescents viewed on fine scales at small times
10:20–11:00	Coffee/Tea	
11:00–11:30	Bjarki Eldon	Statistical properties of the site-frequency spectrum associated with Lambda-coalescents
11:30–12:00	Fabian Freund	The minimal clade size of a randomly chosen gene in the Bolthausen-Sznitman n -coalescent
12:00–14:30	Lunch break	
14:30–15:00	Iulia Dahmer	Beta-coalescents and their lengths
15:00–15:30	Götz Kersting	External and internal branch lengths in the Kingman coalescent
15:30–16:10	Coffee/Tea	
16:10–17:00	Aurélien Tellier	A biologist's guide to the Multiple Merger Coalescent: suggestions for possible applications
18:00	Conference Dinner	(Room 05-514)

Fr., 29 November 2013

Room 05-432 (Hilbertraum)

9:00–9:30	Patric Glöde	Dynamics of genealogical trees of autocatalytic branching processes
9:30–10:20	Robert Griffiths	Mutations within families in a multiple-offspring Moran model and a Ξ -coalescent limit
10:20–10:50	Coffee/Tea	
10:50–11:20	Richard Neher	Multiple merger coalescents in rapidly adapting populations
11:20–11:50	Benjamin Heuer	The spatial Cannings model and robustness of its coalescent
11:50–12:10	Quick Coffee/Tea	
12:10–13:00	Alison Etheridge	Some models for selection in spatially structured populations
13:00	Closing	
13:05–	Lunch, open discussions	

Sat., 30 November 2013 A seminar room for discussions will be available

List of abstracts

Iulia Dahmer, Beta-coalescents and their lengths

We consider $\text{Beta}(2 - \alpha, \alpha) - n$ -coalescents with parameter range $1 < \alpha < 2$. The (total, external and internal) lengths of the coalescent tree - the sums of the lengths of its branches - play a central role in the statistical analysis of the number of mutations that affect the individuals in the population for which the genealogy is described by the coalescent. We review recent results on the fluctuations of the a) total branch length and b) total external branch length in a $\text{Beta}(2 - \alpha, \alpha)$ -coalescent as the population size n tends to infinity.

This is based on joint work with Götz Kersting and Anton Wakolbinger.

Bjarki Eldon, Statistical properties of the site-frequency spectrum associated with Lambda-coalescents

Recursions for the expected values and covariances of the site-frequency spectrum associated with Lambda-coalescents are given. The recursions are used to obtain estimates of coalescent parameters associated with certain Lambda-coalescents. Our methods are applied to data on the high-fecundity Atlantic cod. Ways to distinguish Lambda-coalescents from population growth will also be discussed.

Joint work with Matthias Birkner and Jochen Blath.

Alison Etheridge, Some models for selection in spatially structured populations

Since the pioneering work of Fisher, Haldane and Wright at the beginning of the 20th Century, mathematics has played a central role in theoretical population genetics. One of the outstanding successes is Kingman's coalescent. This process provides a simple and elegant description of the way in which individuals in a population are related to one another. However, it only really applies to very idealised 'unstructured' populations in which every individual experiences identical conditions. Spurred on by the need to interpret the recent flood of DNA sequence data, an enormous industry has developed that seeks to extend Kingman's coalescent to incorporate things like variable population size, natural selection and spatial and genetic structure. But, until recently, a satisfactory approach to populations evolving in a spatial continuum has proved surprisingly elusive. In this talk we describe a framework for modelling spatially distributed populations that was introduced in joint work with Nick Barton (IST Austria) and some of the ways in which it can be extended to incorporate different forms of selection. As time permits we'll not only describe the application to genetics, but also some of the intriguing mathematical properties of some of the resulting models.

Fabian Freund, The minimal clade size of a randomly chosen gene in the Bolthausen-Sznitman n -coalescent

Consider the Bolthausen-Sznitman n -coalescent as a model for the genealogical tree of a sample of n genes, e.g. from a population evolving under rapid selection. We analyse the minimal clade size of a randomly chosen gene in the Bolthausen-Sznitman n -coalescent. The minimal clade is the equivalence class of the chosen gene at the time of the first merger this gene participates in. The minimal clade can be interpreted as the smallest family of the chosen gene within the sample.

Using the connection of the Bolthausen-Sznitman n -coalescent with random recursive trees, we analyse the distribution of the minimal clade size for fixed n as well as the asymptotics for $n \rightarrow \infty$. Asymptotically, we show that the minimal clade size behaves as n^U for U a uniform r.v. on $[0, 1]$. We compare this result to the behaviour of the minimal clade size in Kingman's n -coalescent as the standard genealogical tree model for a sample of n genes from populations under neutral evolution.

Joint work with A. Siri-Jégousse (CIMAT, Guanajuato, Mexico)

Patric Glöde, Dynamics of genealogical trees of autocatalytic branching processes

I will talk about the dynamics of genealogical trees for autocatalytic branching processes. In such populations each individual has an infinitesimal death rate which depends on the total population size and, upon its death, it produces a random number of offspring. I will consider finite as well as infinite populations. Formally, processes take values in the space of ultrametric measure spaces. The dynamics are characterised

by means of martingale problems. Key issues are proving well-posedness for the martingale problems and finding invariance principles linking finite and infinite populations. In fact, infinite populations arise as scaling limits of finite populations in the sense of weak convergence on path space with respect to the polar Gromov-weak topology. I will also show that there is a close relationship between the genealogies of infinite autocatalytic branching processes and the Fleming-Viot process. Moreover, I will mention an abstract uniqueness result for martingale problems of skew product form which is of importance for the processes discussed before but also applies to more general settings.

Robert Griffiths, Mutations within families in a multiple-offspring Moran model and a Ξ -coalescent limit

Mutations occurring in a Λ -coalescent tree are usually assumed to occur at random on the edges of the tree. The tree process is dual to the Λ -Fleming-Viot population process. A different model is that mutations occur within families in a pre-limit Moran model with multiple offspring. Selection can be modelled in different ways to act on types of genes. Mutation and selection within families produces a multi-type offspring distribution. The Fleming-Viot population process for which the limit process is dual to is a Ξ -coalescent, where multi-type offspring in families causes simultaneous mergers. This talk will describe the Moran model with mutations in families, the Ξ -limit tree and Fleming-Viot process.

Benjamin Heuer, The spatial Cannings model and robustness of its coalescent

We look at the spatial Cannings model which is a model where a population is subject to critical reproduction and migration on a finite graph G . Sampling n individuals in the present yields a spatial coalescent process backwards in time. If the variance of the offspring distribution is relatively large and under some assumptions on the migration this process, with a proper time rescaling, will converge to a spatial Λ -coalescent. We will then look at the special case of G being a discrete torus of side length L . We show that a spatial Λ -coalescent on the discrete torus will converge for $L \rightarrow \infty$ to a nonspatial Kingman coalescent if we choose a proper time rescaling and sample the ancestral lines sufficiently far apart from each other. This is joint work with Anja Sturm (University of Göttingen).

Götz Kersting, External and internal branch lengths in the Kingman coalescent

The internal branch length L_k^n of order k in a Kingman n -coalescent is the sum of lengths of all branches, which carry k leaves. We present the result that in the limit $n \rightarrow \infty$ the random variables

$$\sqrt{\frac{n}{4 \log n}} \left(L_k^n - \frac{2}{k} \right)$$

are iid and $N(0,1)$ -distributed.

Joint work with Iulia Dahmer.

Vlada Limic, A zoom into exchangeable coalescents viewed on fine scales at small times

A few years ago Berestycki, Berestycki and Limic derived the first order asymptotic for the number of blocks at small times in any Λ -coalescent that comes down from infinity. Their result exhibits a function v such that N_t is asymptotic to $v(t)$ as t goes to 0. In a joint recent work with Anna Talarczyk, we study the second-order asymptotic for the number of blocks. Under conditions on the driving measure Λ near 0, we obtain convergence in Skorokhod J_1 topology for the appropriately rescaled process $(N_t/v_t - 1, t \geq 0)$.

Richard Neher, Multiple merger coalescents in models of rapidly adapting populations

The statistical properties of genealogies are well studied in neutral models of evolution. But those properties change dramatically when individuals differ in fitness. Building on work by Brunet, Derrida, Mueller and Munier, we investigate genealogies in models of adapting populations in which many small effect mutations are available to increase fitness. We provide evidence that some aspect of the genealogies converge against the Bolthausen-Sznitman coalescent in the limit of large populations. We then extend these ideas

to sexual populations and show how we can use these results to calculate levels of neutral diversity, site frequency spectra, and the scale of linkage disequilibrium from parameters of the model.

Aurélien Tellier, A biologist's guide to the Multiple Merger Coalescent: suggestions for possible applications

Population genetics theory has laid the foundations for genomics analyses including the recent burst in genome scans for selection and statistical inference of past demographic events in many prokaryote, animal and plant species. Identifying SNPs under natural selection and underpinning species adaptation relies on disentangling the respective contribution of random processes (mutation, drift, migration) from that of selection on nucleotide variability. Most theory and statistical tests have been developed using the Kingman's coalescent theory based on the Wright-Fisher population model. However, these theoretical models rely on biological and life-history assumptions which may be violated in many prokaryote, fungal, animal or plant species. Theoretical developments of the so called multiple merger coalescent (MMC) models have flourished recently, but their application to analysis of polymorphism data is still lagging behind. I will explicit how these new models may take into account various pervasive ecological and biological characteristics, life history traits or life cycles which were not accounted in previous theories such as 1) the skew in offspring production typical of marine species, 2) fast adapting microparasites (virus, bacteria and fungi) exhibiting large variation in population sizes during epidemics, and 3) the peculiar life cycles of fungi and bacteria alternating sexual and asexual cycles. Examples from coevolutionary models of plant-parasite interactions and preliminary analyses of polymorphism data will be used to highlight species and systems where MMC models may be applicable.