Probability and Biological Evolution
June 15 - 19, 2015

Tibor Antal: Multitype branching processes: from bacteria to cancer.

We'll review recent developments in the theory of two type birth-death branching processes. These studies were pioneered by Salvador Luria and Max Delbruck in 1943 to model genetic mutations arising in bacterial populations. More recent applications include the development of resistance to chemotherapy for cancer.

Ellen Baake: Ancestral selection graph meets lookdown construction.

In a (two-type) Wright-Fisher diffusion with directional selection and two-way mutation, let x denote today?s frequency of the beneficial type, and given x, let h(x) be the probability that, among all individuals of today?s population, the individual whose progeny will eventually take over in the population is of the beneficial type. Fearnhead (2002) and Taylor (2007) obtained a series representation for h(x). We develop a construction that contains elements of both the ancestral selection graph and the lookdown construction and includes pruning of certain lines upon mutation. Besides being interesting in its own right, this construction allows a transparent derivation of the series coefficients of h(x) and gives them a probabilistic meaning. This is joint work with Ute Lenz, Sandra Kluth, and Anton Wakolbinger.

Vincent Bansaye: Coming down from infinity for some population models.

In the first part, we are describing the way birth and death processes come down from infinity. We will focus on the hitting time of large integers and make appear two regimes (weak and strong). We then derive under general conditions a deterministic speed for the speed of coming down from infinity, given by a dynamical system . It is based on a joint work with Sylvie Méléard and Mathieu Richard. In a second part, we give some general results on the coming down from infinity of population models described by (multi-dimensional) SDE using properties of flow of dynamical systems and martingales technics inspired from the work of Bertesycki, Berestycki and Limic for Lambda coalescent. This work is in progress.

Nick Barton and Alison Etheridge: Extending the infinitesimal model.

The infinitesimal model is a simple model for the evolution of quantitative traits. In its most basic form, the model is that offspring have trait values that are normally distributed around the average of their parents, and that the variance amongst offspring is independent of the parental trait values. It can be justified in the limit where traits are influenced by very many unlinked Mendelian genes. We show how the infinitesimal model extends to allow for random drift, mutation, and non-additive inheritance, and investigate the limits of its applicability.

Franz Baumdicker: The site frequency spectrum of dispensable gene sequences.

The number of completely sequenced genomes is growing to an enormous number. Especially in procaryotes, this brought to light an unexpected amount of genes present only in a subset of the population. These genes are distributed over the population and constitute the pan-genome of the population. Interestingly, for some bacterial populations the total number of genes in the population seems to be an arbitrary large number, while the genome size of any single individual is finite. I will give a short introduction to the neutral evolution of dispensable genes, particularly the infinitely many genes model, where genes are gained and lost along Kingman's coalescent. The frequency of one dispensable gene can be described by a diffusion, which gives rise to the gene frequency spectrum, i.e. the number of genes present in a certain fraction of the sample. In addition mutations can hit the dispensable DNA-sequences such that they differ within a population. Within the classical infinitely many sites model, it is possible to estimate the mutation rate based on the site frequency spectrum. Classical results can be used to compare the observed site frequency spectrum with its neutral expectation. For dispensable gene sequences we have to relax the classical assumption that all individuals only carry homologous genetic material. We link the presence and absence of genetic material with the number of site mutations seen within each gene. We use an urn model to derive the expectation of the joint gene and site frequency spectrum, i.e. the number of mutated sites occurring in exactly s gene sequences while the corresponding gene is present in exactly k individuals. We show that the site frequency spectrum of dispensable genes differs from the classical result and that standard estimators of the mutation rate are biased for dispensable genes.

Julien Berestycki: Branching processes with competition by pruning of Levy trees.

There are several ways to describe the evolution of a population with no interactions between individuals. One approach is to use the local time process of a forest of Lévy trees, or, following the work of Dawson and Li, one can construct the whole population flow as the solution to a certain system of Lévy driven stochastic differential equation. The equivalence between these two constructions is a generalization of the well-known Ray-Knight Theorem.

When one wants to introduce a form of competition in the population, the situation becomes more involved. The stochastic differential approach still works (with an added negative drift term) and the purpose of this talk is to present a novel construction based on the interactive pruning of the Lévy forrest.

The case of a positive drift, which corresponds to an interactive immigration, is also of interest as it is related to the question of existence of exceptional times for Generalized Fleming-Viot processes with mutations at which the number of genetic types in the population is finite.

Based on joint works with : a) L. Doering, L. Mytnik and L. Zambotti and b) J. Fontbona and M.C. Fittipaldi

Matthias Birkner: Random walks in dynamic random environments and ancestry under local population regulation.

The spatial embeddings of ancestral lineages in population models with local regulation form (relatively complicated) random walks in a space-time dependent random environment

given by the time reversal of the local population size process. We develop abstract conditions that allow to implement a regeneration construction and then deduce a law of large numbers and a CLT in this context. We verify these conditions for two prototypical examples, the discrete time contact process and logistic branching random walks in a high density regime, and discuss implications for the spatial distribution of types.

Jochen Blath: Genetic variability under the seed bank coalescent.

We analyse patterns of genetic variability of populations in the presence of a large seed bank with the help of a new coalescent structure called seed bank coalescent. This ancestral process appears naturally as scaling limit of the genealogy of large populations that sustain seed banks, if the seed bank size and individual dormancy times are of the same order as the active population. Mutations appear as Poisson process on the active lineages, and potentially at reduced rate also on the dormant lineages. The presence of 'dormant' lineages leads to qualitatively altered times to the most recent common ancestor and non-classical patterns of genetic diversity. To illustrate this we provide a Wright-Fisher model with seed bank component and mutation, motivated from recent models of microbial dormancy, whose genealogy can be described by the seed bank coalescent. Based on our coalescent model, we derive recursions for the expectation and variance of the time to most recent common ancestor, number of segregating sites, pairwise differences, and singletons. Commonly employed distance statistics, in the presence and absence of a seed bank, are compared. The effect of a seed bank on the expected site-frequency spectrum is also investigated. Our results indicate that the presence of a large seed bank considerably alters the distribution of some distance statistics, as well as the site-frequency spectrum. Thus, one should be able to detect the presence of a large seed bank in genetic data. Joint work with Bjarki Eldon, Adrián González Casanova, Noemi Kurt, Maite Wilke-Berenguer

Anton Bovier: Limits in adaptive dynamics.

Intersting features in individual based models for adaptive dynamics arise in limits of large populations, small mutations, and small mutational steps, and under proper rescaling of time. Taking all limits in one step poses severe technical problems which need novel techniques that allow to control the system. I will present some recent results that have emerged over a very long term collaboration with Martina Baar and Nicolas Champagnat.

Eric Brunet: Existence of open evolutionary paths in a rugged landscape.

An evolving population under selection explores its fitness landscape by fixing favorable mutations. If one assumes that deleterious mutations cannot be fixed, it is however not obvious that the population can find an evolutionary path leading to the fittest possible state when the fitness landscape is rugged . I will present some rigourous results (and some conjecture, and some open questions) on the existence and the number of acceptable evolutionary paths in the "House of Cards" model.

Nicolas Champagnat: The limit of small mutations in a stochastic individual-based model and the canonical equation of adaptive dynamics.

The goal of this talk is to present a new approach to justify the canonical equation of adaptive dynamics, intermediate between the historical one of Metz, Geritz et al. (1996), based on a limit of rare mutations in a large population, followed by a limit of small mutation, and the PDE approach of Diekmann, Jabin, Mischler, Perthame (2005), based on a limit of small mutations in an infinite population. The canonical equation arises on a very long time scale in the first one, and the second one suffers from an irrealistic influence of very small population densities. Our approach assumes small mutations in a large but finite, stochastic population. The convergence to the canonical equation follows from a decomposition of the population dynamics on slow-fast scales, and from a careful study of the genealogy of the population.

Loren Coquille: A stochastic individual-based model for immunotherapy of cancer.

I will present an individual-based model of adaptive dynamics which is motivated by the modelling of immunotherapy for malignant tumors. On the one hand, we show that the interplay of genetic mutations and phenotypic switches on different timescales as well as the occurrence of metastability phenomena raise new mathematical challenges. On the other hand, we argue why understanding purely stochastic events (which cannot be obtained with deterministic systems) may help to understand the resistance of tumors to various therapeutic approaches and may have non-trivial consequences on tumor treatment protocols. We demonstrate this through numerical simulations. Joint work with Martina Baar, Hannah Mayer, Michael Hölzel, Meri Rogava, Thomas Tüting, and Anton Bovier. University of Bonn and University Hospital of Bonn.

Michael Desai: Genetic diversity in the interference selection limit.

Pervasive natural selection can strongly influence observed patterns of genetic variation, but these effects remain poorly understood when multiple selected variants segregate in nearby regions of the genome. Classical population genetics fails to account for interference between linked mutations, which grows increasingly severe as the density of selected polymorphisms increases. I will describe a simple limit that emerges when interference is common, in which the fitness effects of individual mutations play a relatively minor role. Instead, similar to models of quantitative genetics, molecular evolution is determined by the variance in fitness within the population, defined over an effectively asexual segment of the genome (a "linkage block"). I will describe how we can exploit this insensitivity in a new "coarse-grained" coalescent framework, which approximates the effects of many weakly selected mutations with a smaller number of strongly selected mutations that create the same variance in fitness. This approximation generates accurate and efficient predictions for silent site variability when interference is common. However, these results suggest that there is reduced power to resolve individual selection pressures when interference is sufficiently widespread, since a broad range of parameters possess nearly identical patterns of silent site variability.

Steve Evans: Recovering a tree from randomly sampled phylogenetic diversities.

Suppose that we sample the leaves of edge-weighted tree with n leaves in a uniform random order and record the lengths of the subtrees spanned by the first k leaves (that is, in biological terms, the phylogenetic diversity of the first k taxa) for k between 2 and n. In joint work with Daniel Lanoue (UC Berkeley) we consider the question, "Can we reconstruct the tree (up to isomorphism) from the joint probability distribution of this random increasing sequence of lengths?" We show that the answer is affirmative if we know a priori that the tree belongs to one of a number of families (e.g. trees with edge lengths in general position, ultrametric trees, and regular trees and caterpillars with equal edge lengths), but the general question is still open.

Adrian Gonzales Casanova et Linglong Yuan: An individual-based model for Lenski's long-term evolution experiment.

The Lenski experiment investigates the long-term evolution of bacterial populations. Its design allows the direct comparison of the reproductive fitness of an evolved strain with its founder ancestor. It was observed by Wiser et al. (2013) that the relative fitness over time increases sublinearly, a behaviour which is commonly attributed to effects like clonal interference or epistasis. In this talk, we present an individual-based probabilistic model that captures essential features of the design of the Lenski experiment. We assume that each beneficial mutation increases the individual reproduction rate by a fixed amount, which corresponds to the absence of epistasis in the continuous- time (intraday) part of the model, but leads to an epistatic effect in the discrete-time (interday) part of the model. Using an approximation by near-critical Galton-Watson processes, we prove that under some assumptions on the model parameters which exclude clonal interference, the relative fitness process converges, after suitable rescaling, in the large population limit to a power law function. The talk is based on a paper of the two speakers joint with Noemi Kurt and Anton Wakolbinger

Paul Jenkins: New evolutionary models for the long range dependencies of loosely linked loci.

For analysing multi-locus DNA sequence data, standard stochastic evolutionary models incorporating genetic drift and recombination include the Wright-Fisher diffusion with recombination and its dual genealogical process, the ancestral recombination graph (ARG). However, statistical inference under these models is intractable unless the loci are unlinked, in which case they are independent, or completely linked, in which case we are effectively back to a single locus. When the recombination parameter is finite but large we should expect our multi-locus model to be easier to describe: as an unlinked model except for some small ?linkage-driven? perturbations. In this talk I will make this statement precise, using two different approaches. The first is an application to the Wright-Fisher diffusion of a central limit theorem for density-dependent population processes, which fully describes the (Gaussian) fluctuations of linkage disequilibrium in the large-recombination limit. The second approach uses a probabilistic coupling of the ARG to a set of independent coalescent trees. These results reveal some hidden structure in these models and also have practical implications for genomic inference, since the likelihoods under these new models are analytically tractable.

Steve Krone: Directed evolution of phage lysins: using mathematical models

to explore feasibility/design of new antibacterial drugs.

Motivated by a mounting tide of drug resistant bacteria, the search for new antibacterial agents is embracing technologies that lie outside traditional bounds. One promising source of compounds is the lysins encoded by bacteriophages (viruses that infect and kill bacteria). These enzymes degrade the bacterial cell wall from the inside, leading to rupture the cell and subsequent dispersal of phage progeny. Lysins have evolved to not kill cells from the outside, thus preserving future hosts, but recent lab work has shown that they can be engineered to kill from without. Developing lysins that have desirable properties for therapeutic use is complicated by the fact that the molecular basis of improvement is not yet understood. A possible way forward is provided by directed evolution. Here we propose lab protocols that involve the co-culturing of two bacterial species–one producing a toxin/lysin that kills the other, leading to selective pressure for improved function of the toxin. We use mathematical models and simulations to explore the feasibility of this directed evolution and offer insights into various protocols.

Joachim Krug: Adaptive walks on correlated fitness landscapes.

Abstract: A random fitness landscape is a probabilistic mapping from the space of genetic sequences, commonly modeled as a binary hypercube of dimension L, to the real numbers. An adaptive walk is a discrete time Markov chain on this space that is constrained to move uphill in each step and terminates at a local fitness maximum. In the simplest case of uncorrelated and identically distributed fitness values, the number of steps to a local maximum is of order log(L) if the next fitter genotype is chosen at random (random adaptive walk) and of order unity if the most fit genotype is chosen deterministically (greedy adaptive walk). In this talk I will present a selection of recent results concerning adaptive walks on two types of correlated landscapes. Asymptotically exact results are available for random and greedy walks on the rough Mt. Fuji landscape, where uncorrelated random fitness components are superimposed on a linear fitness gradient, and a phase transition between short and long walks can occur in the random case [1]. For Kauffman's NK-model, a classic model of tunably rugged fitness landscapes, we focus on the comparison between different walk types with respect to the fitness value achieved at the endpoint (the 'height' of the walk) [2]. Remarkably, for certain parameter values 'reluctant' walks which follow the most shallow fitness ascent locally are most efficient in locating exceptionally high local maxima. The talk is based on joint work with Su-Chan Park, Stefan Nowak, Johannes Neidhart and Ivan Szendro.

[1] Phase transition in random adaptive walks on correlated fitness landscapes. Su-Chan Park, Ivan G. Szendro, Johannes Neidhart, and Joachim Krug, Phys. Rev. E 91 (2015) 042707.

[2] Analysis of adaptive walks on NK fitness landscapes with different interaction schemes. Stefan Nowak and Joachim Krug, arXiv:1503.07796.

Denise Kuehnert: Phylodynamic analysis of rapidly evolving pathogens.

The fast evolution of viral pathogens poses a big challenge to scientists, as well as an opportunity: Viral gene sequences, together with dates and locations of sampling, often contain useful information about the origin and transmission dynamics of virus epidemics.

Hence, when incidence data is rare or incomplete, virus sequences can give valuable insight into epidemic dynamics.

In phylogenetics we use branching processes to model the genetic ancestry of biological populations; simple birth-death processes can describe the spread of a pathogen - with a birth event relating to viral transmission, and death event corresponding to recovery.

The rapid evolution of viruses implies that in many cases the transmission tree can be approximated by the gene tree, such that we can estimate epidemiological parameters like the basic reproduction number R0 from sequence data.

Particularly, a birth-death model with migration allows phylogeographic analysis of viruses with a wide geographic range (such as seasonal influenza viruses), analysis of risk group dynamics of pathogens (e.g. HIV), or the incorporation of host population dynamics through compartmental models. The latter is particularly important for infectious diseases with long incubation periods such as ebola virus.

Tom Kurtz: Do it yourself lookdown constructions: It is safe to build them at home.

"Lookdown" constructions provide representations of population models in terms of countable systems of particles in which each particle has a ?type? which may record both spatial location and genetic type and a ?level? which incorporates the lookdown structure. At first glance, the constructions may appear very mysterious and difficult to apply. The goal of the talk will be to show how to break the population model of interest into pieces, to show how a lookdown process can be defined for each piece, and then to see that the pieces come together to give a lookdown construction for the full model. The talk is based on a forthcoming paper with Alison Etheridge.

Michael Laessig: Adaptive evolution of molecular quantitative traits.
Molecular phenotypes, such as gene expression levels or protein folding energies, link between genomic information with organismic functions, fitness, and evolution. Here we discuss the quantitative genetics and, in particular, the inference of adaptive evolution for complex molecular traits. We analyze trait evolution under mutations and genetic drift in a single-peak fitness seascape. The fitness peak performs a constrained random walk in the trait amplitude, which determines the time-dependent trait optimum in a given population. We derive analytical expressions for the distribution of the time-dependent trait divergence between populations and of the trait diversity within populations. Applying this model, we infer pervasive adaptation of gene expression in Drosophila: 63% of the observed expression divergence across seven Drosophila species are driven by directional selection.

Amaury Lambert: A non exchangeable coalescent arising in phylogenetics.

A popular line of research in evolutionary biology is to use time-calibrated phylogenies in order to infer the underlying diversification process. Most models of diversification assume that species are exchangeable and lead to phylogenetic trees whose shape is the same in distribution as that of a Yule pure-birth tree. Here, we propose a non-exchangeable,

individual-based, point mutation model of diversification where interspecific pairwise competition (rate d) is always weaker than intraspecific pairwise competition (rate c), and is only felt from the part of individuals belonging to younger species. The only important parameter in this model is d / c =: 1 ? a, which can be seen as a selection coefficient.

We show that as the initial metapopulation size grows to infinity, the properly rescaled dynamics of species lineages converge to a 'shift-down/look-up coalescent' where lineages are given levels: the species at level i is the i-th most recent extant species. At constant rate, all lineages simutaneously "shift down" their level by -1, while the lineage at level 1 "looks up" to a geometrically distributed (with parameter a) level and coalesces with the lineage present there.

By interlacement techniques, we propose a dimensionally-reduced version of this model allowing for fast simulation and likelihood computation of given trees. We use this algorithm and MCMC data augmentation methods to estimate a from real trees, and compare this estimate to classical measures of tree imbalance.

Sylvie Méléard: Competitive populations with vertical and horizontal transmissions.

Horizontal transfer of information is recognized as a major process in the evolution and adaptation of population, especially micro-organisms. There is a large literature but the previous models are either based on epidemiological models or population genetics stochastic models with constant population size. We propose a general stochastic eco-evolutionary model of population dynamics with horizontal and vertical transfers, inspired by the transfer of plasmids in bacteria. The transfer rates are either density-dependent (DD) or frequency-dependent (FD) or of Michaelis-Menten form (MM). Our model allows eco-evolutionary feedbacks. In the first part we present a two-traits (alleles or kinds of plasmids, etc.) model with horizontal transfer without mutation and study a large population limit. It's a ODEs system. We show that the phase diagrams are different in the (DD), (FD) and (MM) cases. We interpret the results for the impact of horizontal transfer on the maintenance of polymorphism and the invasion or elimination of pathogens strains. We also propose a diffusive approximation of adaptation with transfer. In a second part, we study the impact of the horizontal transfer on the evolution. We explain why it can drastically affect the evolutionary outcomes. Joint work with S. Billiard,P. Collet, R. Ferrière, C.V. Tran.

Richard Neher: Quantifying and predicting the evolution of RNA viruses.

In untreated HIV infected individuals, the virus population is constantly adapting to selection pressures imposed by the host immune system. We have sequenced the HIV populations in 11 patients at about 10 time points each spanning 3-10 years during which HIV diverges by about 1%. Using the time series data, we estimate the strength of purifying selection at loci conserved to different degrees on larger evolutionary time scales and quantify the extend of linkage disequilibrium and hitch-hiking. We find that the dynamics of alleles is well described by recent theories of rapid adaptation that assume that frequency changes are governed by selection on random genetic backgrounds of different fitness rather than neutral drift. I will further discuss how the shape of genealogical trees can be used to predict fitness of individuals corresponding to the tips of the tree. We use these fitness predictions

to anticipate the evolution of influenza viruses.

Todd Parsons: Escaping from the boundary in Density Dependent Population Processes.

In a series of papers in the 1970?s, Thomas G. Kurtz identified a class of models that he called Density Dependent Population Processes, which contained a variety of interesting examples from biology and chemistry. Kurtz and subsequent authors derived functional laws of large numbers and central limit theorems for this class, but outside of specific examples, the problem of the establishment of a new population from very small numbers - a question of fundamental interest in evolutionary biology - has remained largely unexamined. In my talk, I will present work in progress on the general case, and, time permitting discuss applications to specific models from epidemiology and from evolution under the Red Queen hypothesis.

Herman-Helmut Pitters: The hydrodynamic limit for beta coalescents that come down from infinity.

Among the most celebrated mathematical models in population genetics is Kingman's n-coalescent $Pi^n(t), t >= 0$. The stochastic process $Pi^n(t)$ takes its values in the partitions of 1, ..., n and models the genealogy of a sample of size n drawn from a large neutral population of haploid individuals. More precisley, individuals i and j have a common ancestor at time t in the past if i, j are in a common block of $Pi^n(t)$. In recent years natural generalizations of Kingman's coalescent, the so-called multiple merger coalescents, have been suggested as better null models for the genealogies in highly fecund populations or populations undergoing selection. We study an important subclass of multiple merger coalescents, namely the beta coalescents, parameterized by two positive real values a and b. We present a law of large numbers type of result for the beta coalescent Pi(t) that comes down from infinity, i.e. has a finite number of blocks at any time t>0. Approximating Pi(t) by its restriction $Pi^n(t)to1, ..., n$, the suitably rescaled block counting process $Pi^n(tn^a?1)/n$, (A denoting the cardinality of the set A) has a deterministic limit, c(t), as n tends to infinity. An explicit formula for c(t) is provided. The block size spectrum $(c_1Pi^n(t), ..., c_nPi^n(t))$, where $c_iPi^n(t)$ counts the number of blocks of size i in $Pi^n(t)$, captures more refined information about Pi^n. The block size spectrum also converges to a deterministic limit as n tends to infinity, with the same rescaling as before. This limit is characterized by a system of ordinary differential equations whose ith solution is the ith complete Bell polynomial, depending only on c(t) and a. We work out the parameters of this Bell polynomial explicitly. This is joint work with Luke Miller (University of Oxford).

Emmanuel Schertzer: Genealogy of a branching process with overlapping generations.

The genealogy of a (planar) critical Galton–Watson branching process is encoded by its contour path, which is obtained by recording the height of an exploration particle running along the edges of the tree from left to right. Crump-Mode-Jagers (CMJ) branching processes are a generalization of Galton-Watson processes, for which generations can overlap.

In general, this type of genealogy is difficult to characterize. However, we will show that under certain assumptions, the corresponding contour process is obtained by a simple transformation of the contour process of the underlying genealogical structure. This is joint work with Florian Simatos

Aurélien Tellier: Plant ecology influences population genetics: the role of seed banks in structuring genetic diversity.

Recent population genomics studies focus prevalently on the aspects of demography and adaptation, whereas age structure (for example, in plants via the maintenance of seed banks) has attracted less attention. Germ banking, that is, seed or egg dormancy, is a prevalent and important life-history trait in plants and invertebrates, which buffers against environmental variability and modulates species extinction in fragmented habitats. I will here summarize our recent findings investigating the intertwined effect of germ banking, time-varying population size and selection on genetic polymorphism in the wild tomato species. First, we examine the effect of seed banking on within species variability and local adaptation in the wild tomato Solanum chilense. Population genetic analyses and statistical inference of past demography was conducted on pooled-sequencing from 30 genes from an exhaustive sampling of 23 populations over Chile and Peru. We reveal a north-south colonization associated with relaxed purifying selection in the south as shown by a decrease of genetic variation and an increasing proportion of nonsynonymous polymorphism from north to south and population substructure with at least four genetic groups. We also uncover 1) a decreasing proportion of adaptive amino acid substitutions from north to south suggesting that adaptation is favoured in large populations, while 2) signatures of local adaptation predominantly occur in the smaller populations from the marginal ranges in the south. These results combined with additional germination data suggest that colonization of new habitats was accompanied by local adaptation for shorter seed banks in the marginal populations, shaping in return the available nucleotide diversity and effectiveness of purifying and positive selection. Second, we use ABC and polymorphism data to estimate population divergence times between two wild tomato species in presence of seed banks. We show that unknown seed banking also impedes our knowledge of the speciation process. Joint worjk with Katharina B. Böndel, Wolfgang Stephan.

Amandine Veber: Genealogies with recombination in spatial population genetics.

Discrete or continuous, the spatial structure of a population has an effect on the evolution of its genetic diversity. In recent studies, the random process of recombination has been used to reconstruct the past of a population over a few hundred generations. This reconstruction is based on the properties of the genealogical trees corresponding to such populations. We shall consider a couple of examples (in continuous space) in which the understanding of the correlations between the genealogies at neighbouring loci will offer new statistical methods to infer quantities such that the dispersal rate of a gene, or to test the presence of rare but recurrent catastrophes in the history of the population. Joint work with Alison Etheridge and Nick Barton.