Ellen Baake, Universität Bielefeld
A probabilistic view on the deterministic mutation-selection equation: dynamics, equilibria, and ancestry via individual lines of descent

We review recent progress on ancestral processes related to mutation-selection models in the deterministic limit. We mainly rely on two concepts, namely, the killed ancestral selection graph and the pruned lookdown ancestral selection graph. The killed ancestral selection graph gives a representation of the type of a random individual from a stationary population, based upon the individuals potential ancestry back until the mutations that define the individuals type. The pruned lookdown ancestral selection graph allows to trace the ancestry of individuals from a stationary distribution back into the distant past, thus leading to the stationary distribution of ancestral types. We illustrate the results by applying them to a prototype model for the error threshold phenomenon.

[1] E. Baake, F. Cordero, S. Hummel, A probabilistic view on the deterministic mutation-selection equation: dynamics, equilibria, and ancestry via individual lines of descent, J. Math. Biol., appeared online first

[2] E. Baake, A. Wakolbinger, Lines of descent under selection, J. Stat. Phys., appeared online first

Vincent Bansaye, École Polytechnique, Palaiseau
Some stochastic functional responses for interactions in ecology

Functional responses are largely used in many biological systems and models in ecology to describe the speed and impact of interactions as a function of the population sizes. In particular, a great variety of functions as been proposed to describe prey-predator interactions at macroscopic level and are used in dynamical systems for prediction and estimations. In some cases, they have been mathematically linked to a stochastic and mathematical individual based model and in particular Monod's function (or Holling's) appears in slow fast dynamics as for Michaelis Menten enzymatic kinetics and chemical reactions [see in particular recent works of Kang, Kurtz and Popovic]. The aim of this talk will be to present some results and issues on the stochastic framework : - A unified approach to derive functional responses from individual behavior and their first order fluctuations, based on a joint work with Sylvain Billiard and Jean René Chazottes - Approximations in large population for some prey predators systems with multiple scales, work in progress with Bertrand Cloez. - Issues and questions on genealogical structures with interacting species and estimations

Nick Barton, IST Austria / Alison Etheridge, University of Oxford
Establishment in a new habitat under the infinitesimal model

Maladapted individuals can only colonise a new habitat if they can evolve a positive growth rate fast enough to avoid extinction - evolutionary rescue. We use the infinitesimal model to follow the evolution of the growth rate, and find that the probability that a single migrant can establish depends on just two parameters: the mean and genetic variance of fitness. With continued migration, establishment is inevitable. However, above a threshold migration rate, the population may be trapped in a sink state, in which adaptation is held back by gene flow. By assuming a constant genetic variance, we develop a diffusion approximation for the joint distribution of population size and trait mean.

Matthias Birkner, Johannes-Gutenberg-Universität Mainz
A conditional coalescent limit in fixed pedigrees

Kingman's coalescent is a standard model for the genealogies of samples in mathematical population genetics; it is usually derived by averaging out the demographic stochasticity in a population model. Wakeley, King, Bobbi and Ramachandran (2012) argued that the way random models of reproduction are used in coalescent theory is not justified for diploid biparental organisms and that the population pedigree for diploid organisms should be treated as a fixed parameter, not as a random quantity. However, using simulations they observed that distributional properties of samples often resemble those under Kingman's coalescent even if the population pedigree is kept fixed and randomness comes only from the Mendelian mechanism of inheritance. Inspired by this observation, we prove that the conditional distribution of the gene genealogy of a finite sample given the pedigree converges to the law of Kingman's coalescent as the population size tends to infinity for a relatively general class of diploid biparental population models. This is based on joint work with Andrey Tyukin.

Jochen Blath, TU Berlin
Further new models for seed banks in population genetics

In population genetics, the presence of seed banks is expected to signfiicantly influence the interplay of classical evolutionary forces such as selection, mutation and genetic drift. However, the development of a comprehensive population genetic theory incorporating seed banks is still in its early stages. Recently, some mathematical models have been introduced, including models for ‘weak and ‘strong seed banks. While the former lead to genealogies still governed by a (time change of) a Kingman coalescent, in the latter case, one obtains a ‘seed bank coalescent, in which lineages are turned on and off independently. In this talk, we will review these models and present some new results for the scaling limits of ‘strong’ seed bank models including their degenerate diffusion limits. Further, we introduce an entirely new class of models, leading to a family of on-off coalescents different form the now well-known seed bank coalescent. The point here is that we distinguish between the ‘spontaneous switching regime for the initiation and resuscitation from dormancy, and large-scale ‘trigger events that affect the active as well as dormant population. The talk is to a significant part on research in progress. If time permits, we wish to discuss the prediction for patterns of genetics variability under the different seed bank models and discuss model selection and calibration.

Anton Bovier, Universität Bonn
Stochastic individual based models with application to modelling of cancer theraphies

Stochastic individual based models, that is, measure valued Markov processes describing the evolution of interacting biological populations, have proven over the last years to be effective models in deriving key features of the theory of adaptive dynamics, such as the canonical equation of adaptive dynamics, the trait substitution sequence and the polymorphic evolution sequence. In this talk I report on recent progress in applying such models to the modelling of cancer therapies, and in particular to immunotheraphy and combination therapies of melanoma based of melanoma in mice, based on experimental data by colleagues from the Bonn university hospital. This work is based on collaborations with Martina Baar, Loren Coquille, Nicole Glodde, Michael Hlzel, Anna Kraut, Hannah Mayer, Meri Rogova, and Thomas Tting.

Nicolas Champagnat, Université de Lorraine, Site de Nancy
A large deviations approach to Hamilton-Jacobi scaling limits of PDE models of adaptive evolution of quantitative traits

This is joint work with Benot Henry (IECL, Universit de Lorraine). We consider partial differential equations modeling adaptive evolution of a quantitative trait in a population in which mutations are due to a Laplace operator and selection is due to the competition for finitely many resources described by integrals of the population density. A small population and large time/strong selection scaling of this equations gives rise to a Hamilton-Jacobi limit equation with constraints, first described by Diekmann, Jabin, Mischler, Perthame (2005), allowing to describe the evolution of the population as moving Dirac masses. We use a probabilistic interpretation of the solution of the PDE as the expectation of a functional of Brownian paths, and large deviations estimates to provide a variational characterization of the limit Hamilton-Jacobi problem. This variational problem can be obtained under more general conditions than those known for the Hamilton-Jacobi limit to hold. In addition, the method can be applied to a large range of mutation operators. We detail the case of finite trait spaces with exponentially small rates of mutations, where uniqueness properties for the limit variational problem can be obtained in some particular cases.

Yu-Ting Chen, University of Tennessee, Knoxville
Mean-field diffusions in stochastic spatial death-birth models

The Moran process is a canonical probability model for death and birth of species. In the limit of a large population, the model is well-known for its rich probability structure by several perspectives including coalescence in the time-reversed genealogy. On the other hand, central studies in evolutionary game theory have significantly relied on the generalization of the Moran process for populations organized by graphs, known as the voter model, and a further generalization featuring complex asymmetry in reproductive rates. There are particular interests in the generality of spatial structure as a way to explain the ubiquitous game behavior in biological evolutions. In this talk, I will discuss the recent mathematical results for these generalized Moran processes. The discussion will be centered around connections with mixing Markov chains and a seminal discovery in evolutionary game theory. The discovery remarkably predicts by some advanced mean-field method to cut off growing dimen- sions in the dynamics and thereby leads to the quantification of fixation by appropriate one-dimensional WrightFisher diffusions.

Camille Coron, Université Paris-Sud
Demography and its impact on genetics

We consider a population of diploid individuals modeled by a multi-dimensional diffusion process giving the joint dynamics of population size and genetic composition. This model can be obtained as the limit of a rescaled birth-and-death process. We give conditions on population size dynamics during extinction under which alleles can get extinct simultaneously.

Steven N. Evans, University of California at Berkeley
Bayesian inference of natural selection from allele frequency time series

We develop a novel approach for inference of general diploid selection and allele age from allele frequency time series obtained from ancient DNA. The key innovation of our approach is that we impute the allele frequency trajectory between sampled points when they are sparsely-sampled. This approach to inferring parameters from a sparsely-sampled diffusion is known as high-frequency path augmentation, and has been successfully applied in a number of contexts. The Wright-Fisher diffusion, however, has several features that are atypical in the context of high-frequency path augmentation, including a time-dependent diffusion coefficient and a bounded path-space. We apply this new method to several datasets and find that we have power to estimate parameters of interest from real data. This is joint work with Joshua Schraiber and Montgomery Slatkin.

Fabian Freund, Universtät Hohenheim
Multiple-merger coalescents - extended models, inference methods & evidence

Multiple-merger genealogies have been discussed as alternative genealogy models to the standard bifurcating genealogy models based on Kingmans n-coalescent. This talk presents recent extensions of these genealogy models (e.g. a rigorous derivation of adding exponential growth to different Λ-n-coalescents) and of inference methods to distinguish between them (e.g. enhancing inference by using information not coded in the site frequency spectrum). Using these extensions, we search for new evidence for multiple-merger genealogies in samples taken from a diverse set of organisms, both eukaryotic (plants, fungi, animals) and prokaryotic (bacteria and archea).
(Joint works with S. Matuszewski, J. Jensen (U. Arizona), M. Lapierre, A. Lambert(SMILE Paris), E. Kerdoncuff (SMILE Paris), G. Achaz (SMILE Paris), A. Siri-J?egousse (UNAM Mexico City) and F. Menardi (U. Basel))

Stephen Kissler, Queen's College Cambridge
Inferring the antigenic geography of influenza in the United States using molecular and epidemiological data

Evolution depends in part on spatial proximity: only organisms that are somehow 'close' to one another are able to compete, driving selection. The evolution of influenza has recently received much attention, but there still lacks a full account of how dominant strains arise from year to year. To better understand how influenza evolves, it is therefore necessary to know the geographic circulation patterns of influenza, in order to characterise potential competition between strains. Currently, however, molecular data on influenza strains is not collected widely enough to reconstruct fine-scale geographic patterns in the antigenic or genetic diversity of influenza. The coarse geographic patterns revealed by the molecular data might be resolved, however, by incorporating fine-scale epidemiological data. To demonstrate this, we examine the 2007-08 seasonal influenza outbreak in the United States, in which three distinct influenza strains (A/H1N1, A/H3N2, and B/Yamagata) co-circulated. Using case counts of influenza-like illness from 834 US cities inferred from electronic medical records, we fit a mechanistic geographic transmission model that describes the outbreak's spread across the US. By reverse-engineering the model, it is possible to probabilistically trace each city's outbreak to a most likely introduction site, revealing geographic 'basins' in which strains with a common ancestor likely circulated. Using antigenic data from the Centers for Disease Control and Prevention, it is possible to infer which strains may have been responsible for which introductions, giving a more detailed map of the antigenic diversity of that season's influenza viruses than the molecular data alone can provide. The methods may be easily extended to incorporate genetic, rather than antigenic, data. This marks an important step in the reconstruction of the phylogeography of influenza.

Katia Koelle, Emory University

Using genetic data at multiple scales to understand constraints on viral adaptation

Due to their high mutation rates, RNA viruses are thought to have the ability to rapidly adapt to changing or new environments. However, these viruses may also be faced with evolutionary constraints, including severe reductions in population size during transmission events and genetic linkage across their genomes. Here, I will present recent work that aims to quantify the extent of these constraints in the context of human influenza virus. I will first present two complementary methods for inferring transmission bottleneck sizes from deep sequencing data and apply these methods to a number of distinct flu datasets, indicating that different studies yield an intriguingly large range of bottleneck size estimates. I will then present an approach to infer the degree of genetic linkage across the gene segments of influenza virus and show evidence for extremely limited viral reassortment within human subjects. The studies I will present include collaborations with Ashley Sobel Leonard, Jeremy Harris, Chris Illingworth, Daniel Weissman, Elodie Ghedin, and Ben Greenbaum.

Amaury Lambert, Université Paris 6

Ranked tree shapes, nonrandom extinctions and the loss of phylogenetic diversity

Phylogenetic diversity (PD) is a measure of the evolutionary legacy of a group of species, defined as the total length of the phylogenetic tree subtending these species. When the phylogeny is given by a Kingman coalescent, an important loss of species diversity leads to a much less important loss of PD (Nee & May Science 1997). However, PD loss is expected to strongly depend on the shape of the species tree, on the clade relative ages and on the order in which species are lost.

Here, we propose a unifying framework to study these three different effects. Inspired by Aldous' beta-splitting model as well as self-similar fragmentations, we propose a new sampling-consistent, three-parameter model generating random trees with covarying shape, clade relative ages and clade relative abundances, the latter serving as proxy for robustness in the face of extinctions. This approach allows us to better understand the conditions in which species extinctions lead to a higher loss of PD.

We propose a procedure to compute the ML estimates of the three parameters on empirical ranked phylogenies and apply it to phylogenies of bird families. The values of parameters inferred lie close to a 'danger zone' of parameter space where the loss of PD can go faster than the loss of species, i.e., where phylogenetically distinct species disappear first.

Julia Adela Palacios, Stanford University

State-space exploration of Tajima's Trees

Estimation of population genetic parameters from ancient and present-day samples of genomic data is a core goal of population biology. Modeling the sample's ancestry and the mutation processes of completely linked genomic segments allows such inference. Coalescent-based methods rely on the Kingman-coalescent genealogy to model the sample's ancestry. Unfortunately, the state space of genealogies grows superexponentially with the number of samples and hence, inference is computationally challenging for large number of samples. Here, we present a new Bayesian model that relies on a lower resolution coalescent process called Tajima-coalescent. A Tajima's genealogy includes coalescent times and a ranked tree shape, and has a drastically smaller state space than that of a coalescent genealogy which includes coalescent times and a labeled topology. We provide a new algorithm for likelihood calculation under the infinite sites model for mutation and provide an efficient algorithm for exploring the reduced latent state space. We compare the performance of our algorithm and lower resolution latent model with state-of-the-art algorithms in population genetics.

Peter Pfaffelhuber, Albert-Ludwigs Universität Freiburg
A two-locus model with interacting mutation rates and fluctuating selection

Usually, the mutation rates for different loci come as independent parameters in a population genetic model. We deviate from this and assume that individuals have an A-locus determining the mutation rate at a second, B-locus. In addition, selection intensities (depending on alleles at the B-locus) are fluctuating. We compute (using some approximations) an optimal mutation rate in the sense that the fixation probability for states in the A-locus is maximized. This is joint work with Franz Baumdicker and Elisabeth Huss (both Freiburg).

Cornelia Pokalyuk, Goethe-Universität Frankfurt am Main
A host-parasite model for the human cytomegalovirus

Inspired by DNA data of the human cytomegalovirus we propose a model of a two-type parasite population distributed over its hosts. The parasite is capable to persist in its host till the host dies, and to reinfect other hosts. Within a host, type diversity is maintained due to balancing selection. For a suitable parameter regime we show that in the limit of large host and parasite populations the host state frequencies follow a dynamical system with a globally stable equilibrium, guaranteeing that both types are maintained in the parasite population for a long time on the host time scale. The talk is based on joint work with Anton Wakolbinger.

Emmanuel Schertzer, Université Paris 6
A coagulation-transport equation and the nested Kingman coalescent

Consider the transport-coagulation equation

$$\partial_t n(t,x) \;=\; \partial_x(x^\gamma n)(t,x) \;+\; \frac{1}{2}\int_0^x n(t,x-y)n(t,y)dy \;-\; n(t,x)\int_0^\infty n(t,y)dy,$$

$t > 0$, $x \geq 0$. If we think of $n(t,x)dx$ as the "number" of clusters carrying a mass in an interval of size dx around x at time t, then the previous equation can be interpreted as the following dynamics: clusters coalesce at rate 1, and the mass of each cluster is depleted at a rate proportional to mass$^\gamma$.

In this work, we provide two natural probabilistic solutions of the latter PDE. The first solution is expressed in terms of a marking procedure of the Brownian Coalescent Point Process, whereas the second one is formulated in terms of branching CSBP.

Our main motivation for studying the latter PDE is the nested coalescent model in which gene lineages are constrained by a phylogeny, i.e., ancestral lineages can only coalesce if they belong to the same species. In particular, when $\gamma = 2$, we show that the latter PDE can be recovered the nested Kingman coalescent (where gene and species lineages are both described by a standard Kingman coalescent) at small time scales. In particular, we show that the existence of a self-similar solution for the PDE relates to the speed of coming down from infinity in the nested Kingman coalescent. I will also address some open problems related to the previous results.

This is joint work with A. Lambert.

Sebastian Schreiber, University of California, Davis
Stochastic persistence versus extinction for interacting populations with internal and external feedbacks

Species experience both internal feedbacks with endogenous factors such as trait evolution and external feedbacks with exogenous factors such as weather. These feedbacks often vary stochastically in their strength and can play an important role in determining whether populations persist or communities of species coexist. To provide a framework for studying these effects, I will present a general theory for analyzing stochastic persistence and extinction in stochastic difference equations accounting for internal and external feedbacks as well as species interactions. The theory will be illustrated with models of evolutionary rescue, evolution mediated coexistence, checkerspot butterflies, and Kansas prairies. This work is in collaboration with Michel Benaim.

Jason Schweinsberg, University of California, San Diego
Rigorous results for a population model with selection

We consider a model of a population of fixed size N in which each individual acquires beneficial mutations at a constant rate. Each individual dies at rate one, and when a death occurs, an individual is chosen with probability proportional to the individual's fitness to give birth. We obtain rigorous results for the rate at which mutations accumulate in the population, the distribution of the fitnesses of individuals in the population at a given time, and the genealogy of the population. Our results confirm predictions of Desai and Fisher (2007), Desai, Walczak, and Fisher (2013), and Neher and Hallatschek (2013).

Mike Steel, University of Canterbury, New Zealand
Deciphering a species phylogeny from conflicting gene trees

A phylogenetic tree that has been reconstructed from a given gene can describe a different evolutionary history from its underlying species tree. The reasons for this include: error in inferring the gene tree, incomplete lineage sorting, lateral gene transfer, and the absence of the gene in certain species. In this talk, I discuss probabilistic models and mathematical results that help address basic questions concerning the consistency and efficiency of different methods for inferring a species phylogeny from gene trees.

Viet Chi Tran, Université des Sciences et Technologies de Lille
Stochastic dynamics of a population of microorganisms with competition and horizontal transfers

We present a model for the dynamics of a population of bacteria with trait structure, who compete for resources and exchange horizontally (transfer) an otherwise vertically inherited trait with possible mutations. Competition and horizontal transfers influence individual demographics, affecting population size, which feeds back on the dynamics of competitions and transfers. We consider a stochastic individual-based pure jump process taking values in the space of point measures. The jumps describe the individuals' reproductions (possibly mutant), transfers and deaths. In this model there is a trade-off between the transfert and advantageous mutation effects: individuals with costly traits and hence smaller growth rates can transfer their traits to fitter individuals. Depending on the parameters of the model, different behaviours can be observed on simulations, including evolutionary suicides and cyclic phenomena. If the trait describes the resistance charge to some antiobiotics carried by plamids in a bacterium, this cyclic effect can be associated to the appearance of resistant strains for instance. In the limit of large populations and rare mutations, we explore mathematically these phenomena using and developing an approach introduced in a different context by Durrett and Mayberry. The idea is to consider the population sizes in a log scale to keep track of the smaller subpopulations that have negligible sizes compared with the population with resident trait. The explanation of the population dynamics is then based on limit theorems in this log scale and on couplings with branching processes with immigration. This is a joint work with Nicolas Champagnat and Sylvie Mlard.

Amandine Veber, École Polytechnique, Palaiseau
How to make good resolutions

In this presentation, we shall discuss the reconstruction of demographic parameters based on the genetic variability observed within a sample of individual DNA. In the family of models that we consider, the statistics describing this genetic diversity (number of mutations, distribution of the mutations amongst individuals in the sample) depend on a more or less coarse ‘resolution of (i.e., level of information on) the hidden genealogical tree that relates the sampled individuals. Considering the optimal resolution thus allows to greatly improve the exploration of the space of possible genealogies when computing the likelihood of demographic parameters, compared to classical methods based on full labelled trees such as Kingmans coalescent. We shall focus on two examples, based on works with Raazesh Sainudiin (Uppsala Univ.) and with Julia Palacios (Stanford Univ.), Sohini Ramachandran (Brown Univ.) and John Wakeley (Harvard Univ.).

John Wakeley, Harvard University
The Evolution of Cooperation in an Iterated Survival Game
(joint with Martin Nowak)

A new type of a simple iterated game with natural biological motivation is introduced. Two individuals are chosen at random from a population. They must survive a certain number of steps. They start together, but if one of them dies the other one tries to survive on its own. The only payoff is to survive the game. We only allow two strategies: cooperators help the other individual, while defectors do not. There is no strategic complexity. There are no conditional strategies. Depending on the number of steps we recover various forms of stringent and relaxed cooperative dilemmas. We derive conditions for the evolution of cooperation.

Specifically, we describe an iterated game between two players, in which the payoff is to survive a number of steps. Expected payoffs are probabilities of survival. A key feature of the game is that individuals have to survive on their own if their partner dies. We consider individuals with simple, unconditional strategies. When both players are present, each step is a symmetric two-player game. As the number of iterations tends to infinity, all probabilities of survival decrease to zero. We obtain general, analytical results for n-step payoffs and use these to describe how the game changes as n increases. In order to predict changes in the frequency of a cooperative strategy over time, we embed the survival game in three different models of a large, well-mixed population. Two of these models are deterministic and one is stochastic. Offspring receive their parent's type without modification and fitnesses are determined by the game. Increasing the number of iterations changes the prospects for cooperation. All models become neutral in the limit ($n \to \infty$). Further, if pairs of cooperative individuals survive together with high probability, specifically higher than for any other pair and for either type when it is alone, then cooperation becomes favored if the number of iterations is large enough. This holds regardless of the structure of pairwise interactions in a single step. Even if the single-step interaction is a Prisoner's Dilemma, the cooperative type becomes favored. Enhanced survival is crucial in these iterated evolutionary games: if players in pairs start the game with a fitness deficit relative to lone individuals, the prospects for cooperation can become even worse than in the case of a single-step game.