Vincent Bansaye

Branching model for proliferating parasites in dividing cells.

We consider a branching model introduced by M. Kimmel for cell division with parasite infection. Cells contain proliferating parasites which are shared randomly between the two daughter cells when they divide. We determine the probability that the organism recovers, meaning that the asymptotic proportion of contaminated cells vanishes. We study the tree of contaminated cells, give the asymptotic number of contaminated cells and the asymptotic proportions of contaminated cells with a given number of parasites. This depends on domains inherited from the behavior of branching processes in random environment (BPRE) and given by the bivariate value of the means of parasite offspring. In one of these domains, the convergence of proportions holds in probability, the limit is deterministic and given by the Yaglom quasistationary distribution. We can add random immigration of parasites from outside the cell population and get other asymptotic results.

Daniela Bertacchi

Ecological equilibrium for restrained branching random walks

We study a generalized branching random walk where particles breed at a rate which depends on the number of neighbouring particles. Under general assumptions on the breeding rates we prove the existence of a phase where the population survives without exploding. We construct a non trivial invariant measure for this case.

Lamia Belhadji

Ergodicity and hydrodynamic limits for an epidemic model

We consider two approaches to study the spread of infectious diseases within a spatially structured population distributed in social clusters. According whether we consider only the population of infected individuals or both populations of infected individuals and healthy ones, two models are given to study an epidemic phenomenon. Our first approach is at a microscopic level, its goal is to determine if an epidemic may occur for those models. The second one is the derivation of hydrodynamics limits. By using the relative entropy method we prove that the empirical measures of infected and healthy individuals converge to a deterministic measure absolutely continuous with respect to the Lebesgue measure, whose density is the solution of a system of reaction-diffusion equations.

Carl Boettiger

Demographic Noise
Demographic noise is an important phenomenon of natural populations. A method motivated from physicist van Kampen physics reveals some interesting insights often overlooked by conventional approaches. These include identifying regimes in a given model where diffusion approximations and deterministic models do and do not provide accurate descriptions and a general fluctuation-dissipation theorem for birth death processes around an equilibrium.

Jean-Stephane Dherin

Asymptotic results on the length of a coalescent trees

We consider $\Lambda$-coalescents including the Beta coalescent with parameter $\alpha$ in (1,2). Denote by $\tau_n$ the number of coalescence times of the n-coalescent. Using martingale arguments, we prove that $n^{-1/\alpha}(n-\tau_n/\{\alpha-1 \})$ converges in distribution to an $\alpha$-stable r.v. We also consider $L^{(n)}_t$ the total length of the n-coalescent up to the nt-th coalescence. For $t<\alpha-1$, we get that $n^{-2+\alpha}L^{(n)}_t$ converges in probability to a limit, say $a(t)$. We prove that for $\alpha$ small enough the process $n^{-\alpha}L^{(n)}_n-a(t)n^{2-\alpha}$ properly rescaled has a non trivial limit in distribution. In the case of neutral mutations, we use this result to describe asymptotic behaviour of the number of mutations. This is a first step to get an estimator of the rate of mutation.

Janos Englander

A spatial population model with random obstacles

We discuss the population size and the spatial spread in a model with randomly located ‘blocking’ areas in which breeding is partially suppressed.

Richard Geji

Understanding the evolutionary responses of a butterfly population to climatic change using a stochastic, individual-based model

Populations may evolve in response to anthropogenic climate change by altering the frequency of alleles and, in some cases, enabling population persistence. To study the effects of mean increases in temperature on the evolutionary dynamics of populations, we built a discrete computational model and a stochastic mathematical model based on the butterfly Colias spp. These models simulate a population composed of three genotypes where each genotype confers a different heat sensitivity and probability of flight as a function of environmentally determined body temperature. Time permitting, both models will be presented as well as a comparison of their results.
Patric Karl Gloede

Genealogies of autocatalytic branching populations

I present stochastic processes which describe the evolution of the genealogies of autocatalytic branching populations both on the level of discrete particle systems and on the level of their diffusion limits. The state spaces for these models are certain metric measure spaces equipped with the Gromov-weak topology which was introduced by Greven, Pfeffelhuber and Winter in 2006. The dynamics are defined by the means of martingale problems on separating subalgebras of bounded continuous functions on metric measure spaces.

Vishwesha Guttal

Indicators of regime shifts in spatial ecological systems.

Ecological systems such as lakes and vegetation in semi-arid ecosystems can undergo rapid transition from one state to an alternative stable state. They are referred to as catastrophic regime shifts. Recently, several studies have suggested leading indicators which can serve as an early warning signal of an impending transition (Carpenter et al, 2006, Ecology letters, Vol. 9, 311-318; van Nes et al, Am Nat 2007. Vol. 169, pp. 738747; Guttal and Jayaprakash, 2008, Ecology Letters, in press). These studies do not include spatial fluctuations in ecological systems. Aim of this research work is to develop indicators of regime shifts in spatial ecological models and study their utility.

We show from studies of spatially explicit ecological models of stochastic integro-differential equations that spatial variance and spatial skewness determined from snapshots of spatial data of an ecological system can be robust indicators of proximity to a transition. Moreover, spatial data can be used reliably even with much shorter length of time series thus substantially enhancing the predictive capabilities. These results are shown to hold for various kernels of spatial interactions such as local (Gaussian), fat tailed and heavily fat tailed (Cauchy) kernels and hence they are potentially applicable across wide variety of ecological systems.

Amaury Lambert

How many types in a branching population undergoing mutations ?

We consider a branching population whose individuals have i.i.d. lifespans with general distribution, during which they give birth at constant rate, independently, to copies of themselves. We show that for any fixed time t, alive individuals can be ranked in such a way that the coalescence times between consecutive individuals are i.i.d. with specified
distribution. The ranked sequence of these coalescence times, or branch lengths, is called a coalescent point process, and encodes all the information about the genealogical structure of the population at time $t$.

When individuals are given DNA sequences, there are two quantities of interest for a sample of $n$ DNA sequences, each belonging to a distinct individual of the population: the number $S_n$ of polymorphic sites (sites at which at least two sequences differ), and the number $A_n$ of distinct haplotypes (sequences differing at one site at least). It is standard to assume that mutations arrive at constant rate $\mu$ (on germ lines), and never hit the same site on the DNA sequence. Then for the Wright-Fisher model with large population size, it is well-known that both $S_n$ and $A_n$ grow as $\mu \log n$ as the sample size $n$ grows.

We show that for coalescent point processes with integrable branch lengths, $S_n$ and $A_n$ grow linearly with $n$, with explicit rate. For critical branching populations, $S_n$ grows as $\mu n \log n$. In addition, we study the frequency spectrum of the sample, that is, the numbers of polymorphic sites/haplotypes carried by $k$ individuals in the sample. In particular, the site frequency spectrum for critical branching populations is $n\mu/k$, similarly as for the Wright-Fisher model.

Belhadji Lamia

Ergodicity and hydrodynamic limits for an epidemic model

We consider two approaches to study the spread of infectious diseases within a spatially structured population distributed in social clusters. According whether we consider only the population of infected individuals or both populations of infected individuals and healthy ones, two models are given to study an epidemic phenomenon. Our first approach is at a microscopic level, its goal is to determine if an epidemic may occur for those models. The second one is the derivation of hydrodynamics limits. By using the relative entropy method we prove that the empirical measures of infected and healthy individuals converge to a deterministic measure absolutely continuous with respect to the Lebesgue measure, whose density is the solution of a system of reaction-diffusion equations.

Sivan Leviyang

A Coalescent Analysis of the Population Structure Statistic $F_{st}$

Populations are often divided into subpopulations. Determining whether a population evolves as a single population or as several interacting subpopulations is a crucial step in answering many genetic and ecological questions. Biologists use a statistic called $F_{st}$ to perform hypothesis tests for the existence of population subdivision and to estimate migration rates between subpopulations. While $F_{st}$ is broadly used for statistical analysis of populations, little is known about its distribution under different evolutionary models.
In this talk we consider Fst under a stochastic model of evolution for a subdivided population known as the finite island model. We use coalescent theory to prove rigorous results describing the distribution of Fst under this model. We show that under different scaling limits on the parameters of the model, Fst converges to different distributions in the large population limit. We derive explicit formulas for the distribution of Fst under these different scaling limits.

Finally, we discuss the implication of our results for biological applications. We emphasize the current need to provide ecologists with statistical tools that help in the study of structured populations. We comment on the implication of our results for Fst under different models of structure such as the stepping stone model.

Piotr Milos

Occupation time fluctuations of branching particle systems with immigration.

Consider a system consisting of particles evolving according to alpha-stable symmetric Levy motion in $\mathbb{R}^d$ and branching after exponential time due to binary critical or subcritical law. New particles immigrate to the system according to homogeneous in time and space Poisson random field. For such a system I will define rescaled occupation fluctuations process and show its weak convergence when time scale goes to infinity. The results differ substantially in critical and subcritical branching case.

Eduardo Jordao Neves

Modelling biological signaling networks with type-dependent interacting particle systems.

Type-dependent interacting particle systems are stochastic processes where particles change states with rates that depend not only on their environment but also on their types. This sort of stochastic dynamics, which somehow tries to mimic the typically quite asymmetric molecular interactions in a biochemical network, is not reversible and therefore harder to analyse. We present a simple mean-field model of this sort for which we show that empirical densities have, in the thermodynamic limit, complex deterministic behaviour.

Todd Parsons

Some Results Regarding a Model of Haploid Populations Exhibiting Density Dependence

Stochastic models have been used extensively in population genetics for almost a century, with great success. Standard models, such as the Wright-Fisher model and the
Moran model, tend to assume fixed or deterministically varying population sizes, in the interests of analytical tractability. I will present asymptotic results for a model of haploid organisms that allows the population size to vary stochastically according to the same birth and death events that result in a change in allele number. For this model, some novel phenomena appear that may have implications for inference in population genetics.

Michael Raghib

A multi-scale approach to consensus in self-propelled swarms

It can be argued that a fundamental and unifying challenge in biology revolves around the integration of phenomena across a wide range of temporal, spatial and organizational scales. Typically, patterns observed at larger scales are driven by processes occurring over a broad range of scales involving time, space and system organization, with special roles being played by the smallest/fastest components. This picture is usually complicated by the existence of feedbacks from the environment or the larger scales into the smaller ones. An interesting example is related to the emergence of directed motion in swarms of self-propelled agents comprising naive and informed individuals. The central question here is to understand how information flows from the informed sub-population to the whole group. By treating the random walk of the swarm centroid as a continuous time random walk, it is possible to quantify the population-level drift, as well as the time scale at which it becomes apparent. We also discuss a multi-scale continuum approximation for the centroid walk in terms of the 2D Advection-Diffusion Equation with Memory (ADEM). This method allows the computation of long-time behaviors from a single, and short, simulation run of the swarm.

Daniel Remenik

Chaos in a spatial epidemic model

We study an epidemic model running on a random 3-regular graph. The dynamics occur in discrete time with two alternating processes: growth and epidemic. In the first step, thinking of annual plants, no occupied site survives and each one gives birth to a Poisson number of individuals, which are sent to a site chosen uniformly from the graph. In the second step, an infection lands at each site with some small probability. If the site is occupied, an infection starts and spreads to all neighboring sites, and all infected sites become vacant. We let the infection probability go to 0 as the number of sites grows so that in the limit only the giant component of the set of occupied sites is destroyed. We prove that the density of occupied sites converges weakly as a Markov chain to a deterministic dynamical system which can be computed explicitly and that, for a certain parameter range, this system is chaotic.

Next, we replace the random 3-regular graph by a 2-dimensional torus and introduce local interactions in the growth step: now each occupied site sends a Poisson number of individuals to locations chosen uniformly from the neighborhood of the site of a certain size. We show that if this interaction range goes to infinity at an appropriate rate
as the size of the system grows, then the sequence of occupation densities also converges to a deterministic system, which is also chaotic for a certain parameter range.

Matthias Steinrucken

Inference for Lambda-coalescents

The genealogy of neutral populations in the domain of attraction of generalized Fleming-Viot processes can be approximately described by their corresponding dual processes, the Lambda-coalescents. This includes the classical Fleming-Viot process and its dual the Kingman coalescent. The Lambda-coalescents allow for multiple merging of ancestral lines. Such multiple collisions appear when in the corresponding population model the offspring of one individual replaces a substantial fraction of the whole population. One biological scenario in which such extreme reproduction events do appear is described in Hedgecock '94 (Hedgecock's reproduction sweepstakes). I discuss methods used by Eldon & Wakely '06 and Birkner & Blath '08 to estimate likelihoods of evolutionary parameters in such models. These methods are then applied to simulated and various real data sets e.g., from Arnason, Genetics '04 (Atlantic Cod).

Joseph Stover

Attractive n-Particle Systems with Contact Interactions

The property of monotonicity is well understood for 2-particle systems such as the Contact Process and Voter Model, but the picture is much less complete for multi-particle systems such as the multi-type contact process and many multi-particle ecological models with contact process type interactions. Monotonicity is a desirable property since it allows the use of coupling from the past to look at the path leading up to stationarity and to take an exact sample from the stationary distribution of an ergodic process. In this talk, a framework for understanding monotonicity of multi-particle contact processes will be presented. This approach creates an "interaction map", which defines the allowable transitions for a model. Attractiveness has a natural extension to the interaction map framework. An attractive reformulation of the multi-type contact process, along with a modification to this process which splits the empty sites into two exclusive types will be presented.

Viet Chi Tran

Stochastic particle models for age-structured population and applications

A microscopic individual-centered population in continuous time is described. Each individual is characterized by an age and by hereditary variables called traits. Limit theorems are considered, with various applications concerning PDE approximations, behaviour before extinction, statistical estimation or evolution in adaptive dynamics.
Lee Worden

Evolutionary Graph Theory and Structural Power

The "evolutionary graph theory" analysis of selection in graph-structured populations, introduced by Nowak and co-workers, suggests that centralized or decentralized structures are more efficient at selection than distributed or source-sink-structured networks. By analogy, it is suggested that these structures are good ones for enhancing collective intelligence. Centralized or decentralized structures, however, are more vulnerable to disconnection by loss of nodes than distributed ones. I will argue that there is a second issue as well: that some nodes have significantly more influence over the outcome than others. I will quantify this influence using sensitivity analysis, both analytically and via simulations.

Fabio Zucca

Weak and strong survival for branching random walks

We consider BRWs on weighted graphs. We relate the strong critical value of the BRW to some (local) geometrical parameter of the underlying graph and we show that at this critical value the process dies out locally almost surely. We show that the weak critical value of the BRW is bounded from below by some (global) geometrical parameter of the graph. We give a sufficient condition for the equality and we prove that, under the same condition, at the weak critical value the process dies out globally almost surely. An example of weak survival at the critical value is given.