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## Stochastic Processes in Evolution, Ecology and Genetics
## Processus stochastiques en évolution, écologie et génétique

(Org: **Don Dawson** (Carleton) and/et **Sylvie Méléard** (Ecole Polytéchnique-Paris X))

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**JULIEN BERESTICKY**, Université Paris 6, 175 rue du Chevaleret, 75013 Paris
*Is the Ewens Sampling formula valid for Oysters?*

Kingman's coalescent is a process which describes how ancestral lineages merge when one goes backward in time into the past. Since its introduction in the 80's, it has become the standard genealogy model in population genetics. One of the main question in this field is to try to detect the trace of natural selection's action in today's genomes. One of the main tool for doing so is the celebrated Ewens sampling formula which describes the expected genetic diversity in a neutral, constant-size population (for which Kingman's coalescent accurately describes the genealogy). As such, it gives the nil hypothesis for statistical tests designed to detect selection.

However, it is now known that for many species (particularly in marine biology) in which there is a strong variance of the reproductive success, other coalescents are better suited to model neutral genealogies. The purpose of the work presented here is to obtain an asymptotic analogue of Ewens formula in this framework. This requires studying some of the deep connections which links coalescence and branching processes.

Based on joint works with Nathanaël Berestycki and Jason Schweinsberg.

**NICOLAS CHAMPAGNAT**, INRIA Sophia Antipolis–Méditerranée
*A study of evolutionary branching in a logistically regulated population*

We are trying to give a mathematical basis to the notion of evolutionary branching introduced by Metz et al. in 1996 in the framework of adaptive dynamics, which studies the long-term evolution of ecologically explicit populations. It is said that evolutionary branching occurs in a population when the evolutionary dynamics drives the population from an (essentially) monotype population to an (essentially) 2-type population. We consider a finite stochastic population with birth, mutation, death and selection due to a logistic-type competition (nonlinearity in the death rates), where individuals are characterized by a finite dimensional phenotypic trait (such as body size, rate of food intake,...). We first consider the combination of the limits of large population and rare mutation, which allows one to simplify the dynamics as a jump process over the trait space describing the successive invasions of mutants, and which is based on a time-scale separation. This process allows transitions from monomorphic populations (with only one trait) to dimorphic populations.

This process is therefore a natural one to study evolutionary branching. In particular, when the size of mutations in the trait space converges to 0, we are able to justify the branching criterion proposed by biologists, to precisely describe the transition from a monomorphic population to a dimorphic one, and to explicitly compute the time-scale of mutation.

This is joint work with Michel Bénaïm, Anton Bovier and Sylvie Méléard.

**SHUI FENG**, McMaster University, Hamilton, Ontario, Canada L8S 4K1
*Asymptotic Behaviour of Poisson–Dirichlet Distribution*

Poisson–Dirichlet distribution is a one-parameter ($\theta$) probability measure on the infinite dimensional ordered simplex. It arises in number theory, combinatorics, ecology, and population genetics. The parameter $\theta$ ranges between zero and infinity. Asymptotic behaviour such as law of large numbers, central limit theorem, moderate deviations, and large deviations will be discussed in this talk. The limiting procedures involve both $\theta$ goes to zero and to infinity. Generalizations to the two-parameter Poisson–Dirichlet distribution will also be presented.

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**OLIVIER FRANÇOIS**, Universités de Grenoble
*Probabilistic analysis of tree shape statistics*

The explosion of phylogenetic studies not only provides a clear snapshot of biodiversity, but also makes it possible to infer how the diversity has arisen. To this aim, variation in speciation and extinction rates have been investigated through their signatures in the shapes of phylogenetic trees. This issue is of great importance, as fitting stochastic models to tree data would help to understand underlying macroevolutionary processes. Although the prevailing view is that it does not represent phylogenies so well, the most popular model of phylogenetic trees is a branching process introduced by Yule, in which lineages split at random. For two decades, the Colless index has been the most frequently used statistic for assessing the balance of phylogenetic trees. In this talk, this statistic is studied under two models of phylogenetic trees: the Yule and uniform model. The main tool of analysis is a coupling argument with another well-known index called the Sackin statistic. Asymptotics for the mean, variance and covariance of these two statistics are obtained, as well as their limiting joint distribution for large phylogenies. Under the Yule model, the limiting distribution arises as a solution of a functional fixed point equation. Under the uniform model, the limiting distribution is the Airy distribution. The cornerstone of this study is the fact that the probabilistic models for phylogenetic trees are strongly related to the random permutation and the Catalan models for binary search trees. Application to a large computer database of phylogenetic trees will also be shown.

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**AMAURY LAMBERT**, Université Pierre et Marie Curie (Paris 6), Paris
*The mutation and allele frequency spectra for the coalescent point process*

A *splitting tree* is the genealogical tree with edge lengths associated with 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. For any fixed time $t$, we show that individuals alive at $t$ 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 branches is called a *coalescent point process*, and encodes all the information about the genealogical structure of the population alive at time $t$.

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

We study the mutation pattern associated to coalescent point processes. Here, $S_n$ and $A_n$ grow *linearly* as $n$ grows, with explicit speed. 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. These numbers are shown to grow also linearly with sample size, and we provide simple explicit formulae for mutation frequencies and haplotype frequencies.

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**NICOLAS LANCHIER**, Department of Mathematics, Arizona State University, Tempe, AZ 85287
*Survival and coexistence in spatially explicit metapopulations*

Interacting particle systems are usually defined as Markov processes on a state space that maps the regular lattice into a finite set of colors, and whose dynamics are described by local interactions. We extend this framework by replacing the usual lattice with a connected graph whose topology dictates how particles interact. This approach allows us to define a version of the multitype contact process including two levels of interactions, ideally suited to model metapopulations. Our main result indicates that, in the presence of two spatial scales, two species living on different time scales may coexist, whereas it was conjectured by Neuhauser that this does not hold on the regular lattice. This suggests that both spatial scales provide two resources, which allows coexistence of two species.

This is a joint work with Lamia Belhadji.

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**SABIN LESSARD**, Université de Montréal, C.P. 6128 Succursale Centre-ville, Montréal, Québec H3C 3J7
*Diffusion approximations for one-locus multi-allele kin selection, mutation and random drift in group-structured populations: a unifying approach to selection models in population genetics*

Diffusions approximations will be ascertained from a two-time-scale argument in the case of a group-structured diploid population with scaled viability parameters depending on the individual genotype and the group type at a single multi-allelic locus under recurrent mutation, and applied to the case of pairwise interactions within groups. The main step will consist in proving global and uniform convergence of the distribution of the group types in an infinite population in the absence of selection and mutation, using a coalescent approach. The results will show that kin selection can arise from interactions between relatives affecting reproductive success as a result of individual competition or group competition. Inclusive fitness formulations will be ascertained and a connection with the replicator equation in game dynamics will be established.

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**EDWIN PERKINS**, UBC, Department of Mathematics, Vancouver, BC
*Pathwise Uniqueness for Stochastic Heat Equations*

We prove pathwise uniqueness for solutions of parabolic stochastic pde's with multiplicative white noise if the coefficient is Hölder continuous of index $\gamma > 3/4$. The method of proof is an infinite-dimensional version of the Yamada–Watanabe argument for ordinary stochastic differential equations.

This is joint work with Leonid Mytnik, Technion.

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**LEA POPOVIC**, Concordia University, 1455 de Maisonneuve Blvd West, Montreal, QC, Canada H3G 1M8
*Genealogy of Catalytic Populations*

For neutral branching models of two types of populations there are three universality classes of behavior: independent branching, (one-sided) catalytic branching and mutually catalytic branching. Loss of independence in the two latter models generates many new features in the way that the populations evolve.

In this talk I will focus on describing the genealogy of a catalytic branching diffusion. This is the many individual fast branching limit of an interacting branching particle model involving two populations, in which one population, the "catalyst", evolves autonomously according to a Galton–Watson process while the other population, the "reactant", evolves according to a branching dynamics that is dependent on the number of catalyst particles.

We show that the sequence of suitably rescaled family forests for the catalyst and reactant populations converge in Gromov–Hausdorff topology to limiting real forests. We characterize their distribution via a reflecting diffusion and a collection of point-processes. We compare geometric properties and statistics of the catalytic branching forests with those of the "classical" (independent branching) forest.

This is joint work with Andreas Greven and Anita Winter.

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**DAVID STEINSALTZ**, University of Oxford
*Mutation and Selection in Age-structured Populations*

Many features of evolutionary theory depend upon considering the mutational load arising from the slow clearing of slightly deleterious mutations. Kimura, Kingman, Hamilton, and others have developed useful models for this process, and various versions of these models with increasingly sophisticated representations of the genome have been proposed. However, many of these models break down in the presence of epistasis.

This has been a particular challenge for the evolutionary theory of ageing. I will describe a new model, which combines a crude model of the genome with a perfectly general specification of fitness interactions, and describes the evolution in time of the distribution of mutant alleles in the population. The solutions may be derived formally from the Feynman–Kac formula. When we add a (sufficiently strong) recombination term, it turns into a dynamical system on the space of Poisson point processes.

One of the keystones of classic mutation-selection theory is Haldane's Principle, which states that the average mutational load depends only on the rate of mutation generation, and not on the size of the effect of each mutant allele. Our new model implies an age-structured version of this principle: In a stable population, the *aggregate population hazard* is invariant under changes in the strength of mutational effects.

This talk is based on joint work with Steve Evans and Ken Wachter.

**XIAOWEN ZHOU**, Concordia University, Montreal, Canada
*Reversibility of Interacting Fleming–Viot Processes*

The Fleming–Viot process is mathematics model in population genetics. It is a probability-measure-valued Markov process describing the evolution of the relative frequencies of different allelic types in a large population which undergoes possible mutation, selection, and recombination. The interacting Fleming–Viot process is a countable collection of Fleming–Viot processes that interact through migration.

The reversibility for Fleming–Viot processes is well understood. In this talk we are going to show that the interacting Fleming–Viot process can never be reversible when both migration and mutation are nontrivial.