

Abstracts: Probabilistic models in evolutionary biology

Workshop at the Georg-August-Universität Göttingen, November 24th-25th, 2016

Invited talks:

Thursday, 10.30 am

Chi Viet Tran: *Phylogenies in a population with competition*

Abstract: We consider a population structured by a neutral marker and an adaptive trait, that are supposed to be completely linked (hence neglecting recombination). The population evolves through births and deaths, and individuals compete together, in a logistic way and depending on their adaptive traits. The marker is neutral with respect to competition and selection.

In a large population with rare mutations, we show that the stochastic individual-based model can be approximated by the following process. Restricting to the trait distribution, we recover the Trait Substitution Sequence process (Metz et al. 96, Champagnat 06) or the Polymorphic Evolution Sequence (Champagnat Méléard 11), depending on whether the invasion of an advantageous mutant implies or not its fixation. During the invasion, the neutral marker associated with the original mutant hitchhikes, thus creating a bottleneck. Then, genetic diversity is rebuilt following a Fleming-Viot or Wright-Fisher (in bi-allelic cases) process.

From these results, we can show that the phylogenies in this limit are Kingman coalescent processes whose characteristics depend on all the traits present in the population, and with bottlenecks. The effective population sizes appear to be the stationary solutions of the dynamical system associated with the traits present in the population.

The first part is a work with S. Billiard, R. Ferrière and S. Méléard. The second part is a work in progress with F. Austerlitz, S. Méléard and M. Porte.

Friday, 10 am

Amaury Lambert: *From individual-based population models to lineage-based models of phylogenies*

Abstract: We seek to infer from a species tree the process of diversification (speciations and extinctions) that has produced this tree. For this we need a stochastic model specifying how species give birth to new species and become extinct. We show various examples of such models, ranging from the most fine-grained (individual-based) to the most coarse-grained (where the number of species follows a birth-death process). For each of these models, we show how to derive the likelihood of a given reconstructed species tree, and what kind of inferences we obtain based on various clades (Mammals, Cetaceans, Birds).

Friday, 3 pm

Charline Smadi Lasserre: *The effect of recurrent mutations on genetic diversity in a large population of varying size*

Abstract: Recurrent mutations are a common phenomenon in population genetics. They may be at the origin of the fixation of a new genotype if they give a phenotypic advantage to the carriers of the new mutation. In this talk, we are interested in the genetic signature left by a selective sweep induced by recurrent mutations at a given locus from an allele A to an allele a, depending on the mutation frequency. We distinguish three possible scales for the mutation probability per reproductive event, which entail distinct genetic signatures. Besides, we study the hydrodynamic limit of the A- and a-population size dynamics when mutations are frequent, and find non trivial equilibria leading to several possible patterns of polymorphism.

Contributed talks:

Thursday, 11.30 am

Sandra Kliem: *Nonlinear historical superprocess approximations for population models with trait-dependence*

Abstract: We consider an approximating sequence of interacting population models with branching, mutation and competition. Each individual is characterized by its trait and the traits of its ancestors. Birth- and death-events happen at exponential times. Traits are hereditarily transmitted unless mutation occurs. The model I shall take about is an extension of the model used in [S. Méléard and V.C. Tran, EJP, 2012], where for large populations with small individual biomasses and under additional assumptions, the diffusive limit is shown to converge to a nonlinear historical superprocess.

One of the major strengths of historical processes is that they allow for a control of the traits of historical particles, present in the population at time t , uniformly in $t \in [0, T]$. That is, we obtain a control on the history of the trait of the particle through its ancestry as well. For instance, suppose that in the n th-approximating population we increase genetic distance between two particles by $1/n$ at each birth with mutation. By interpreting genetic age of a particle as a trait, we obtain some control on genetic distance backwards in time. One of the major mathematical difficulties of this model is the non-equidistant setup due to the use of exponential times. The number of trait-changes (that is, birth with mutation) until time T now plays a major role in establishing tightness of the approximating sequence.

In this talk I will give an overview of the main probabilistic ideas and arguments of the above mentioned concepts.

Thursday, 2.15 pm

Gabriel Berzunza: *Convergence of multitype Galton-Watson forests to stable forests*

Abstract: Multitype Galton-Watson (GW) processes arise as a natural generalization of usual GW processes, in which individuals are differentiated by types that determine their offspring distribution. In this talk, we investigate the ancestor trees and forests associated with irreducible multitype GW processes, when the total number of types is finite. Under criticality hypotheses on the mean matrix, and such that the offspring distributions belong to the domain of attraction of a stable law, we show that these forests (after a proper rescaling) converge to the continuum random stable tree.

Thursday, 3 pm

Stephan Gufler: *Invariance principles for tree-valued Cannings chains*

Abstract: Möhle and Sagitov (Ann. Prob., 2001) showed that coalescents with simultaneous multiple mergers are robust limits for partition-valued processes that describe the genealogy in Cannings models at a fixed time. We give a robustness result on the level of evolving trees and show convergence to (neutral) tree-valued Fleming-Viot processes. A robustness of this kind was conjectured by Greven, Pfaffelhuber, and Winter (Probab. Theory Related Fields, 2013). Under the conditions of Möhle and Sagitov, the tree-valued processes that describe the genealogy in the Cannings models converge in the dust-free case. In the general case, they converge under these conditions when they are defined as processes with values in the space of distance matrix distributions. To show convergence to the tree-valued Fleming-Viot processes with values in the space of marked metric measure spaces in the case with dust, we make an additional assumption on the probability that a randomly sampled individual belongs to a non-singleton family. We give an example in which this assumption is violated

and exclude convergence as the empirical distributions of the external branch lengths in the Cannings models converge to the unit mass in zero, while the external branch lengths are positive in the limiting genealogy.

Thursday, 4.15 pm

Anton Klimovsky: *Is there more biodiversity in non-homogeneous environments than in homogeneous ones?*

Abstract: We consider a spatially structured multi-type population of individuals living in colonies embedded into a geographical space. Within the colonies, the individuals reproduce with heavy-tailed offspring distribution under a fixed amount of resources (Cannings model). The individuals move around from one colony to the other at given rates (= migration). Furthermore, the whole regions of the geographical space can suffer from occasional catastrophic events (droughts, floods, forest fires, meteorite impacts, etc.). How does the biodiversity in such a spatial Cannings process evolve? We will report on our findings in the case, where both the reproduction and the catastrophe mechanisms are spatially inhomogeneous. Spoiler: It turns out that the inhomogeneities increase biodiversity (comparing to the homogeneous environment).

This is joint work with Andreas Greven and Frank den Hollander.

Friday, 11.30 am

Airam Blancas Benítez: *On nested coalescent processes*

Abstract: In this talk we define a family of Markov processes with values in the space of nested bivariate partitions of the natural numbers N , called simple nested exchangeable coalescent, for short snec. Our motivation to introduce this class of processes arises from molecular biology where gene trees are nested in the species phylogeny, that is, gene lineages are allowed to coalesce while they are in the same branch of the species trees.

We present a Poissonian construction for a particular snec and we also establish a necessary and sufficient condition for this nested coalescent to come down from infinity, which means that almost surely the partitions associates with species and genes consists of only finitely many blocks for all $t > 0$.

Keywords: Random partitions; Coalescent processes; Genes and Species trees.

Friday, 2.15 pm

Adrian González Casanova: *Fixation in a Ξ coalescent with selection*

Abstract: In this talk we will introduce a generalisation of the Wright Fisher model, for a population with finite size and non-overlapping generations, allowing for several types of selection as well as simultaneous multiple mergers. The construction provides an almost sure dual relation between its frequency process and its ancestral process. The latter can be interpreted as a discrete analogue to the celebrated ancestral selection graph. We will also study a two type frequency process with general selection and general coalescent mechanism, and investigates in which cases the selective type goes to fixation with probability one.

This talk is based on a joint project with Dario Spano.