Limit models for a new general class of multitype branching processes with memory and population dependence
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Pruning Galton Watson trees and a tree-valued Markov process

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We present a new pruning procedure on discrete trees using a non-uniform percolation on the nodes of trees (the probability of deleting a node depends on its degree). This procedure allows us to construct and study a tree-valued Markov process \(\{G(u)\}\) by pruning Galton-Watson trees. This process is a “growing tree” process that starts from a degenerate tree with only one leaf and grows by adding trees on the leaves on the previous tree.

In particular, we study the law of the tree just before its ascension time (i.e. the time at which it becomes infinite) and give a representation of this tree in terms of a Galton-Watson tree conditioned to be infinite. Similar results were obtained by Aldous and Pitman\(^3\) in the special case of Poisson offspring distributions where they considered uniform percolation on the edges of Galton-Watson trees.

Our process can also be viewed as the discrete analogous of the continuum tree valued process introduced in \(^1\).

References


Acquaintance vaccination in epidemics on random networks

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Branching processes play a key role in the analysis of epidemic models. In particular, for stochastic SIR (susceptible \(\rightarrow\) infective \(\rightarrow\) removed) epidemics in large populations they provide a means for determining both the probability and expected relative size of a major outbreak. A main use of epidemic models is as a tool for evaluating control measures, such as vaccination strategies.

In this talk, we consider SIR epidemics on random networks, having arbitrary but specified degree distributions, and investigate acquaintance vaccination, a method for targeting vaccination at individuals with high degree; see \([2,3]\), which assume a perfect vaccine response. We extend the model in \([2,3]\) to allow for a more general vaccine response but this leads to difficulties since it introduces sibling dependence into the associated branching processes, which may then require infinite type spaces for their analysis. Thus we propose and analyse an alternative model for acquaintance vaccination, which avoids these difficulties. The analysis includes deriving a post-vaccination threshold parameter, which
determines whether or not an epidemic with few initial infectives can become established and lead to a major outbreak, and determining the probability and expected relative final size of a major outbreak. Properties of the two models for acquaintance vaccination are compared, assuming a perfect vaccine response.

The theory is extended to the network-households model (see [1]), in which the population is also partitioned into small households, and the performance of acquaintance vaccination is compared with that of households-based vaccination allocation schemes.

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References


Large deviations for branching processes in random environment

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Branching Processes in Random Environment (BPREs) are a generalization of Galton-Watson processes where in each generation the reproduction law is picked randomly in an i.i.d. manner. The associated random walk of the environment, whose increments are distributed like the logarithmic mean of the offspring distributions, plays a key role in the asymptotic behavior. We are interested in describing exceptional events in large times and consider the large deviations events. By contrast to the Galton-Watson case, here random environments and the branching process can conspire to achieve these events. We precise this phenomena and derive the rate functions.

Superspeed in the multitype branching random walk.

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Weinberger et al (2007) noticed that in certain multitype deterministic population models it is possible for types to ‘work cooperatively’ to produce a speed of spread that is faster than any single type could attain on its own even, when the type set is reducible. For the branching random walk it is possible to pin down this super-speed (which turns out to be an upper bound identified for the deterministic models). In the talk I will aim to set the scene, give an impression of how the branching random walk result arises and perhaps mention its connections with aspects of the deterministic theory (including certain coupled reaction-diffusion equations).

References

Limit theorems for multi-type subcritical age-dependent branching processes with two types of immigration

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This work continues the study of the classical subcritical age-dependent branching process (see [1]) and the effect of the following two-type immigration pattern in multi-dimensional case. At a sequence of renewal epochs a random number of immigrants of different types enters the population. Each subpopulation stemming from one of these immigrants is revived by new immigrants and their offspring whenever it dies out, possibly after an additional delay period. Individuals from the same type have the same lifetime distribution and produce offspring according to the same reproduction law. This is the $p$-dimensional Bellman-Harris process with immigration at zero and immigration of renewal type (BHPIOR). With this paper we complete the study of the one-dimensional case with its multi-type counterpart generalizing the strong law of large numbers and a central limit theorem for such processes. Similar conclusions are obtained for their discrete-time multi-type counterparts, namely Galton-Watson processes with immigration at zero and immigration of renewal type (GWPIOR).

References


Properties of states of super-$\alpha$-stable motion
with branching of index $1 + \beta$

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It has been well-known for a long time that the measure states of the process in the title are absolutely continuous at any fixed time provided that the dimension $d$ of space is smaller than $\frac{d}{\beta}$. Various properties of the corresponding densities functions are reviewed. If the branching is discontinuous, the densities have continuous versions or they are locally unbounded within that regime. Moreover, when they are continuous, the Hölder continuity is further illuminated. Also, some conjectures are formulated, in particular concerning the excluded boundary case of Neveu’s branching mechanism. This reports on joint work with Leonid Mytnik (Haifa) and Vitali Wachtel (Munich).

References


Hazard Rates of Introgression in Random Environments

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Introgression is the permanent incorporations of a gene from the genome of one population into another. It has become a large area of research with the increasingly rapid development of new genetically modified crops, with fears that genetically modified material might escape from cultivated plants into wild plants with unpredictable ecological consequences.

To quantify introgression risks would be a valuable tool for ecologists and policy makers. Since introgression involves the immigration of invaders, a successful invasion will almost certainly occur after a long time, so the probability of introgression always becomes one in the limit, and is thus a poor measure of risk. The extinction probability of a single invader fails to account for the effect of immigration in introgression. As a measure of risk in these scenarios, we propose the hazard rate. The hazard rate is the probability per time unit that an introgression event occurs given it has not occurred before.

This talk outlines the derivation of the hazard rate of introgression using multi-type Galton Watson branching process with immigration and random environments.

Parametric Bayesian inference for Y-linked bisexual branching models

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In the papers [1] and [2], two bidimensional bisexual branching models have been introduced to analyze the evolution of the number of carriers of some alleles of Y-linked genes from generation to generation in two-sex monogamous populations. In these models, genes which present two allelic forms are considered. The behavior of this sort of genes is strongly related to the reproduction law of each genotype. In practice, these offspring distributions are usually unknown and their estimation is necessary. In this work, we deal with this estimation problem in a parametric Bayesian framework when the available information does not allow us to distinguish the genotype of the males, i.e., we assume that only the total number of females and the total number of males up to some generation are observed. To approximate the posterior distribution of the main parameters of the reproduction law of each genotype, we provide an algorithm based on the Gibbs sampler. From these estimated posterior distributions, we also approximate the posterior predictive distributions of future population sizes. By way of simulated examples, developed with the statistical software R, we illustrate the accuracy of the proposed algorithm.

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References


Limit models for a new general class of multitype branching processes with memory and population dependence

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We present here a new general class of multitype branching processes in discrete time with memory and population dependent individual transitions. Except in simple particular cases (essentially BGW (Bienaymé-Galton-Watson) or asymptotically BGW processes), the asymptotic behaviour of this kind of processes, as time tends to infinity, is an open problem. So in order to be able to study this behaviour, we derive the limit models, as the initial size of the population tends to infinity, of either the process suitably normalized, when the types of interest are nonrare at the initial time, or of the process itself, when the types of interest are rare. In the first case, the normalized process has the same asymptotic behaviour as that of a deterministic dynamical system on densities or on probabilities. In the second case, the limit process, as the initial population size tends to $\infty$, is reduced to a multitype BGW process on the rare types with Poissonian transitions. We derive its asymptotic behaviour, and in the subcritical case, the distribution of its extinction time and of the size of its tree until extinction. We give some examples, and an error bound between the process and its limit.

**Branching Processes with a Carrying Capacity**

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I describe simple and general branching processes which are supercritical below a so called carrying capacity and subcritical if population size is larger. What are their chances of taking off and reaching a vicinity of the carrying capacity? How long will they linger around it before finally dying out? What happens if there are mutations so that new and fitter morphs can arise? These and related matters will be discussed, and finally the intriguing phenomenon of evolutionary suicide, in a simple form.

**Heterogeneity of proliferating cell populations: Old models and new data**

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Recent years brought a deluge of technologies to observe biological processes at single-cell and sometimes at single-molecule levels. These include high-content microscopy as well as microfluidics and insertion of engineered fragments of genetic material into cells. Stochastic models introduced 20 or 30 years ago suffered from paucity or absence of such data. Some of these models can be now re-thought and re-applied in the new context. The talk, idiosyncratically, reviews two such models built by the author over past 20 years: (1) pseudo-stochastic model of unequal division of cells, and (2) branching process model of gene amplification, and confronts them with recent biological findings. Biological phenomena to explore include self-renewal and maturation of stem cells, variability of abundance of proteins in cells, and carcinogenesis.

**Markovian trees subject to catastrophes: would they survive forever?**

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We analyze criteria for almost sure extinction of multi-type Markovian branching processes subject to catastrophes which kill random numbers of living individuals at random epochs. Such criteria are related to the conditional growth rate of the population, given the history of the process of catastrophes, and are usually hard to numerically evaluate. We give a simple characterization in the case when all individuals have the same probability of surviving a catastrophe, and we determine upper and lower bounds in the case where survival depends on the type of the individual. The upper bound appears to be often better than the lower bound.
We unify, under a one-parameter family, the most commonly known estimators of the means and the covariance matrices of the offspring distributions for a supercritical multi-type branching process. Using martingale tools and contiguity techniques, we establish the Law of Large Numbers, the Law of Iterated Logarithm and the Central Limit Theorem for each estimator in this family. We also select, within this family, the “best” estimator for each one of the parameters means and covariance matrices. Using these optimum estimators, we perform a global estimation of the multi-parameter (means, covariance matrices), for which we specify the asymptotic multi-dimensional normality, and the asymptotic independence of the standardized errors.

References


Time to extinction of an infectious disease through Crump-Mode-Jagers branching processes

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When an infectious disease is strongly detrimental to the population in which it is spreading, control measures are needed to protect susceptible individuals. Vaccination programmes represent one of the most effective forms of control (see [3]). However, immunizing the whole population is not an option in most cases, so only a proportion of susceptible individuals can be vaccinated. How to determine the necessary proportion is an important public health problem in its own right, which depends on many factors. One of these factors, that is particularly significant for public health authorities to assess vaccination efficiency, is the time that elapses for the infectious disease to become extinct, known as the disease’s time to extinction.
The aim of the present work is to provide an approach to this problem by modeling epidemic spread using branching processes. Specifically, we use Crump-Mode-Jagers branching processes, which (see [1]) are appropriate for describing the early stages of a wide variety of epidemic models, notably SIR (susceptible→infective→removed) models. First, using coupling methods, we study the dependence of properties of a disease’s time to extinction on the proportion of immunized individuals in the population. We allow this proportion to vary over time. Thus, for example, it may be zero prior to vaccination, increase during the vaccination process and be constant after vaccination. In this way, the results obtained generalize those given in [2]. From these results, we suggest an optimal vaccination policy based on the quantiles of the disease’s time to extinction. Finally, we provide a simulation-based method to determine numerically the optimal vaccination level and show the accuracy of the method by way of an example.

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References

Random Time Changed Branching Processes and Lévy Processes
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We consider the jump structure of the subordinated Lévy process and subordinated Markov branching processes. Subordination provides a method of constructing a large subclass of Markov or Lévy processes

\[Y(t) = X(T(t)),\]

where \(X(t)\) is a Markov or Lévy process and \(T(t)\) is a continuous time subordinator-Lévy process with positive increments and \(T(0) = 0\). Let \(X(t)\) be a Lévy process, then subordination preserves the independence and stationarity of the increments, but it changes theirs amplitudes and the total mass of the Lévy measure. Let \(X(t)\) be a Markov branching process, then subordination (owing to the independence) preserves the Markov property, but it disturbs the branching property. The infinitesimal generator of the subordinated process \(Y(t)\) involves the total progeny of reproduction.

References

Birth-death branching models in random environments and their application to population dynamics
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We are interested in developing stochastic models to describe the demographic dynamics of animal populations. It is well known that many animal species live organized in socially structured groups, being the smallest units the lineages (families of kin-related individuals). Significant efforts have been made to develop mathematical models based on the assumption that all individuals behave identically with respect to reproduction (see Lefebvre et al. (2003) or Caron-Lormier et al. (2006)). They assume that environmental factors affecting reproduction do not change over time. Reality is more complex. As in any other biological process, reproduction has a major random component which depends on several environmental factors. Such phenomena can be described by using the theory of branching processes in random environments. In this work, we introduce a class of birth-death branching models in random environments which take such a reproductive behavior into account. The branching model comprises two sub-processes, a birth process and a death process. It is assumed that both, the offspring probability distribution which governs the birth process in each generation, and the sequence of death probabilities that governs the death process, change in a non-predictable manner. The motivation is to examine its practical implications in understanding the behaviour of animal populations. In this line, we determine the probability distributions of some random variables concerning the demographic structure of the population and discuss their biological significance. By way of illustration, we present some examples.

References


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Modeling prion dynamics in yeast
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Prions are infectious agents composed of misfolded proteins, responsible for illnesses such as mad cow disease in cattle and Creutzfeldt-Jakob disease in humans. We create a branching process model for yeast cells to describe how prions grow inside the cell and how they are transmitted from mother to daughter cell. We compare our model predictions to laboratory data and use it to estimate unknown parameters.

Several ways of conditioning branching processes
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We present several ways of conditioning branching processes: on non-extinction, on reaching a given state or level, and on the total progeny. Thanks to many existing results in the literature and to some additional results, we intend to compare these different ways of conditioning and to enlighten intuitive or counter-intuitive analogies and differences. When possible, we work in the context of multitype branching processes.

References

On some usual and some not-so-usual models of nucleotidic sequence evolution

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Some recent models of DNA sequences evolution take into account well documented, non-independent, features of their dynamics, such as those related to the biological role of CpG dinucleotides. We will describe the rather miraculous mathematical resolution of a class of these models with influence and the laborious extension of this miracle to models that are close enough to the previous ones for an underlying branching process summarizing the whole story to be subcritical. Every required notion of molecular biology will be recalled.

Work in collaboration with Jean Bérard (Lyon), Jean-Baptiste Gouéré (Orléans) and Laurent Guéguen (Lyon, biology).

References


Limit theorems for supercritical branching processes with neutral immigration

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We are interested in abundance distribution of species in a speciation model with immigration. The model that we consider is a generalization of Karlin and McGregor’s island-mainland model [2].

At rate $\theta$, individuals bearing types immigrate from mainland to island and begin a new population which evolves like an homogeneous, binary and supercritical Crump-Mode-Jagers process [1] that is, individuals have i.i.d. lifetime durations (and non necessarily exponential distribution which is a particular case treated in [3]) while they give births with constant rate $b$.

We make different assumptions about types: either each new migrant has a different type from previous ones or it is of type $i$ with probability $p_i$.

Then we are interested in asymptotic proportions of each type in the total population when time $t$ tends to $+\infty$. In the case ”new migrant=new type”, the limit has a GEM distribution with parameter $\theta/b$ and we remark that it does not depend on the law of individuals’lifespans.
References


Linear-fractional age-dependent branching processes

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We extend the framework of multitype branching processes with linear-fractional generating functions (cf [2], [4]) to the case of countably many types. Using this framework we introduce a convenient class of age-dependent branching processes constituting an important example of CMJ processes in discrete time (cf [1]). This class of branching processes is a discrete time counterpart of Lambert’s family of continuous time CMJ processes with the reproduction law governed by a Poisson point process (see [3]).

For these processes we found explicit formulae for generating functions describing the joint distributions of different age-group sizes at arbitrary observation times. Our formulae imply basic asymptotic results for this class of CMJ processes without using the Perron-Frobenius theorem for infinite dimensional matrices. On the other hand, our asymptotic results illuminate the general Perron-Frobenius theory [5] providing interesting examples of R-transient and R-null cases.

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References


Trimmed Likelihood Estimation in a Class of Multitype Branching Processes

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We consider procedures for robust estimation of multitype discrete-time branching processes with a large (and increasing) number of ancestors. The studied trimmed likelihood estimators are based on the asymptotic properties of the relative frequencies of the processes. Computational algorithms are considered and simulational results are shown.
On the probability of random genetic mutations for various types of tumor growth

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In this work we consider the problem of estimating the probability for specific random genetic mutations to be present in a tumor of a given size. Previous mathematical models have been based on stochastic methods where, on average, the tumor was assumed to be growing exponentially. In contrast, due to the simplicity of the approach, analytical results are obtained also for cases where the exponential growth of cancer has been replaced by other, arguably more realistic types of tumor growth. The main result is that the probability that a given random mutation will be present by the time a tumor reaches a certain size, is independent of the type of curve assumed for the average growth of the tumor, at least for a general class of growth curves. The same is true for the related estimate of the expected number of mutants present in a tumor of a given size, if mutants are indeed present. An application of these results to chronic myeloid leukemia and cancer stem cell dynamics will be presented.

References


Limit Theorems for Multitype Branching Processes with Large Number of Ancestors

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First we consider multitype Markov branching processes with discrete or continuous time assuming a large number of ancestors. Usually the discrete and continuous time cases are developed separately while in the present paper they are considered simultaneously. The asymptotic behavior in the positive regular and nonsingular case is investigated when both the number of ancestors $N$ and the time $t$ tend to infinity. Some limiting distributions are obtained as well as multivariate asymptotic normality is proved. Note that the multitype branching processes are considered also from a new perspective: modeling of the relative frequencies of different types of individuals (instead of the usual counts of individuals) as functions of time. The need for such characteristics of cell kinetics arises in experimental situations where the relative frequencies but not the absolute cell counts are accessible to measurement. We obtain non-random limits for the frequencies and multivariate asymptotic normality when the initial number of ancestors is large and the time of observation increases to infinity. As a contrast of this results when the time is fixed the asymptotic normality is proved for any kind of branching processes (even non-Markov and reducible) assuming only the usual independence of individual evolutions. Finally it is shown that the obtained asymptotic results can be used to develop new statistical approach for estimation the basic parameters in branching processes with possible applications in the cell proliferation kinetics.

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References

Limit distributions for the number of particles in branching random walks with a few sources

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Recently continuous-time branching random walks (BRWs) on $\mathbb{Z}^d$ were applied to investigate evolutionary processes in spatially nonhomogeneous media [1]. Previous models of BRWs were studied for a medium with one source of branching (see, e.g., [2, 3, 4, 5]). In this sense, the medium was spatially nonhomogeneous. The offspring reproduction law was defined by the intensities of a Markov birth-and-death process at the source, and the underlying random walk was usually assumed to be symmetric. One of the main problems in models of BRWs is a study of limit distributions for the number of the particles. In the present work, the principal results of [4, 5] are extended to BRWs containing a few sources of branching situated at arbitrary lattice points under the assumptions that underlying random walks may be nonsymmetric. General methods are proposed to obtain conditions of an exponential growth for the number of particles in BRWs with several sources.

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References


Branching for ever!