

Book of Abstracts

WORKSHOP **On Branching Processes** **and their Applications**

April 20-23, 2009
BADAJOS, SPAIN

Organizing and Scientific Committee

Research Group at the University of Extremadura (Spain):
Procesos de Ramificación y sus Aplicaciones
Spanish Branching Processes Group

Miguel González, *Chairman*
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Presentation

The theory of branching processes was essentially motivated by the observation of the strange phenomenon of the extinction of certain family lines of the European aristocracy in a context of rapid exponential growth of the whole population. Since then, this theory has developed from the simplest to the most realistic models. Added to the theoretical interest in these processes, there was a major practical dimension due to their potential applications in such diverse fields as biology, epidemiology, genetics, medicine, nuclear physics, demography, actuarial mathematics, algorithm and data structures, etc. Nowadays, this theory goes on being an area of active and interesting research. Several meetings to facilitate the exchange of research ideas in the field of branching processes and their applications and related processes have been celebrated. The First World Congress on Branching Processes was held in Varna (Bulgaria) in 1993, to celebrate the first 150 years of branching processes. Recently, it is worth to mentioning those took place in Goteborg (Sweden) in 2005 or in Luminy (France) in 2007.

In the 90's, a research group in branching processes was born at the University of Extremadura. We are now seven members investigating in several fields of the branching theory. With the aim of giving continuity to those interesting meetings, our group has promoted this Workshop on Branching Processes and their Applications, which will be held in the Faculty of Sciences of our University.

The meeting will consist of a series of invited talks, keeping a healthy balance between the theoretical and practical aspects of branching processes theory. The talks are organized accordingly in 8 sessions. Besides the talks there will be plenty of time for informal discussions so that we can meet at leisure and as such a basis for future scientific collaboration will be formed. On the other hand, the programme also offers cultural events that will allow to discover the cities, gastronomy and sights of the dynamic and historical Spanish Region of Extremadura as well as the charm and hospitality of its people. We hope that these intensive program of activities will be found interesting and attractive.

It is a great honour for us to welcome you to the University of Extremadura, a young yet firmly consolidated, dynamic and diverse institution, and to the city of Badajoz, a town in which you feel at home. Moreover, we would like to thank you the acceptance of our invitation to take part in this event.

We also would like to thank all people that have actively participated in organizing the workshop and those entities that have provided financial and scientific support. Main funding come from the Spanish Ministry of Science and Innovation (Ministerio de Ciencia e Innovación), the University of Extremadura itself and local Administration. Furthermore the Spanish Society of Statistics and Operations Research (SEIO) supports the meeting scientifically.

Finally, we wish you an enjoyable and successful meeting in Badajoz, hoping that you will find the conference and the city a suitable setting to share your ideas and time.

Miguel González
Chair of the WBPA

Schedule

	Monday, 20	Tuesday, 21	Wednesday, 22	Thursday, 23
09:30-10:00	Opening ceremony			
10:00-10:30	P. Jagers	F. Ball	V. Vatutin	
10:30-11:00	M.C. Serra	C. Jacob	C. Braumann	U. Roesler
11:00-11:30	Coffee Break	S. Penisson	Coffee Break	F. Klebaner
11:30-12:00	G. Alsmeyer	Coffee Break	P. Mayster	Coffee Break
12:00-12:30	J. Biggins	M. Bojkova	M. Mota	K. Mitov
12:30-13:00	G. Yanev	D. Heinzmann	Lunch	V. Topchii
13:00-16:00	Lunch	Lunch	Excursion to Cáceres	Lunch
16:00-16:30	N. Yanev	I. Rahimov		D. Hull
16:30-17:00	M. Kimmel	M. Ispany		M. Molina
17:00-17:30	Coffee Break	Coffee Break		Closing Ceremony
17:30-18:00	R. Martinez	G. Pap		
18:00-18:30	M. Bichsel	I. del Puerto		
19:00-	Reception			
20:00-				Social dinner

Monday, April 20	
	Session 1: Extinction vs Survival Chairman: Miguel González
10:00-10:30	Peter Jagers The last minutes before extinction
10:30-11:00	Maria Conceição Serra Multitype Bienaymé-Galton-Watson processes escaping extinction
	Session 2: Branching Random Walks and Branching Trees Chairman: Peter Jagers
11:30-12:00	Gerold Alsmeyer On the transience of critical branching random walks on the line
12:00-12:30	John D. Biggins Random self-similar measures: "Multifractal spectra"
12:30-13:00	George Yanev Complete N-ary subtrees on branching family tree
	Session 3: Applications in Cell Kinetics and Genetics Chairwoman: Christine Jacob
16:00-16:30	Nikolay Yanev Branching processes in cell proliferation kinetics
16:30-17:00	Marek Kimmel Modeling the evolution of Alu repeats in human genome
17:30-18:00	Rodrigo Martínez On Y-linked branching models
18:00-18:30	Manuel Bichsel Branching process model of the early phase of a bacterial insertion sequence invasion

Tuesday, April 21	
	Session 4: Applications in Epidemiology Chairman: Nikolay M. Yanev
10:00-10:30	Frank Ball Applications of branching processes to a network epidemic model with casual contacts
10:30-11:00	Christine Jacob A branching process approach for the propagation of the Bovine Spongiform Encephalopathy in Great-Britain
11:00-11:30	Sophie Pénişon Limit theorems for conditioned multitype branching processes and Feller diffusions. Application to the BSE epidemic
12:00-12:30	Maroussia Slavtchova-Bojkova Stochastic modelling of vaccine preventable diseases by age-dependent branching processes
12:30-13:00	Dominik Heinzmann Approximating extinction times in multitype Markov branching processes
	Session 5: Limit Theorems and Statistics Chairman: Manuel Molina
16:00-16:30	Ibrahim Rahimov Approximation of a sum of martingale-differences generated by a bootstrap branching process
16:30-17:00	Márton Ispány Limit theorem for critical inhomogeneous branching processes with immigration
17:30-18:00	Gyula Pap Statistical inference of critical multitype branching processes with immigration
18:00-18:30	Inés M. del Puerto Weighted conditional least squares estimation in controlled branching processes

Wednesday, April 22	
	Session 6: Population Growth Models in Random and Varying Environments Chairman: John D. Biggins
10:00-10:30	Vladimir Vatutin Sudden death versus slow extinction of branching processes in random environment
10:30-11:00	Carlos A. Braumann Stochastic differential equation models of population and individual growth in a random environment
11:30-12:00	Penka Mayster Criticality for alternating branching processes
12:00-12:30	Manuel Mota A note on controlled branching processes in varying environment

Thursday, April 23	
	Session 7: Special Branching Processes Chairman: Gerold Alsmeyer
10:30-11:00	Uwe Roesler Stochastic fixed point equations
11:00-11:30	Fima Klebaner Population-dependent branching processes
12:00-12:30	Kosto Mitov Limit theorems for randomly indexed branching processes
12:30-13:00	Valentin Topchii Fixation time estimates in bounded populations
	Session 8: Two-sex Branching Models Chairman: Vladimir Vatutin
16:00-16:30	David Hull Elementary proofs for certain extinction in bisexual Galton-Watson branching processes
16:30-17:00	Manuel Molina Two-sex branching process literature

Session 1

Extinction vs Survival

The last minutes before extinction

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AMS: 60J80

Abstract

A big subcritical (and even general multi-type) branching population first declines exponentially, by the law of large numbers, and then it will survive according to some extreme value distribution. Indeed, under broad conditions the time to extinction T is proportional to the logarithm of the starting number plus a translated Gumbel random variable, ([1]).

As a consequence, the population size at time uT , $0 < u < 1$, properly normed, converges in distribution, as the starting number tends to infinity. The approximation is bad, though, for u close to one. We study the population size at time $T-u$, and have explicit results for continuous time Markov branching.

References

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Multitype Bienaymé-Galton-Watson processes escaping extinction

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Keywords: Bienaymé-Galton-Watson process, decomposable, escape from extinction, multitype, wild type branching process

AMS: 60J80

Abstract

In the framework of multitype Bienaymé-Galton-Watson (BGW) process, the event that the daughter's type differs from the mother's type can be viewed as a mutation event. Assuming that mutations are rare, we study a situation where all types except one produce on average less than one offspring. We establish a neat asymptotic structure for the BGW process escaping extinction due to a sequence of mutations toward the supercritical type.

The asymptotic analysis is performed by letting mutation probabilities tend to 0. The limit process, conditional on escaping extinction, is another BGW process with an enriched set of types permitting to distinguish a stem lineage of particles that leads toward the escape event. The stem lineage can be described by a simple Markov chain on the set of particle types. The total time to escape becomes a sum of a random number of independent geometrically distributed times spent at intermediate types. (This is joint work with Serik Sagitov)

Session 2

Branching Random Walks and
Branching Trees

On the transience of critical branching random walks on the line

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Keywords: Branching random walk, critical regime, recurrence, transience, minimal and maximal position, random weighted location measure, renewal theory

AMS: 60J80

Abstract

Gantert and Müller [2] recently proved that a critical branching random walk (BRW) on the integer lattice is transient by analyzing this problem within the more general framework of branching Markov chains and making use of Lyapunov functions. The main purpose of this talk based on the recent publication [1] is to explain how the same result can be derived quite elegantly and even extended to the nonlattice case within the theory of weighted branching processes. This is done by an analysis of certain associated random weighted location measures which, upon taking expectations, provides a useful connection to the well established theory of ordinary random walks with i.i.d. increments.

Acknowledgements: This is joint work with Matthias Meiners (Münster).

References

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Random self-similar measures: “Multifractal spectra”

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Keywords: General branching processes, local dimension of a measure, Hausdorff dimension

AMS: 28A80, 60J80, 60G18

Abstract

Given a compact set $K (\subset \mathbb{R}^d)$, an associated scaling law produces a random number of randomly scaled copies of K inside K . The scaling law is then used to produce even smaller copies of K inside the first generation ones, and so on. The division and scaling used on each set are independent, so this is a branching process. The union of the n th generation sets converges as n goes to infinity to a random fractal set. As well as its physical scale (its diameter, say) already described, each copy of K has second scale factor, generated in the same way as its physical scale. In the limit these translate to a measure on the random fractal. The objective is to provide a description of the variation of what is called the local dimension of this measure. (The local dimension is α at a point when the log of the measure of a ball of radius r around that point divided by the log of r converges to α .) Good results of this kind are already available when the measure is defined on the boundary (the infinite lines of descent) of the Galton-Watson tree. The main contribution in this work is dealing with the extra geometry resulting from building realisations in \mathbb{R}^d , extending the results in Arbeiter and Patzschke (1996).

Acknowledgements: This will be a report of joint work with Ben Hambly (Oxford) and Owen Jones (Melbourne).

References

- [1] M. Arbeiter and N. Patzschke. (1996). *Random self-similar multifractals*. Math. Nachr., 181:5–42.

Complete N -ary subtrees on branching family tree

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Keywords: Branching processes, Family trees, Binary trees

AMS: 60J80, 05C05

Abstract

We review the existing and present new results on certain subtrees of a branching tree. Consider the rooted subtrees of a Galton-Watson family tree. For a fixed positive integer N , define a complete N -ary tree to be the tree of a deterministic N -splitting. Let the random variable $V(N)$ be the number of complete infinite and disjoint N -ary subtrees of a branching tree, rooted at the ancestor. In [3], Yanev and Mutafchiev study the distribution of $V(N)$. The event $\{V(1) > 0\}$ implies that there is at least one infinite unary subtree and thus the process would never die. The event $\{V(2) > 0\}$ can be interpreted as the set of process' trajectories when the family tree grows faster than binary splitting. Dekking [1] raised and answered the question how to compute the probability for a branching process to possess the "binary splitting property", i.e., $\Pr(V(2) > 0) > 0$. Pakes and Decking [2] study the general situation when $N \geq 2$. Mutafchiev [4] proves limit results for the survival probability of a N -ary subtree. It is surprising that the case $N \geq 2$ is studied so late, whereas the classical question for extinction of a branching process, i.e., non-existence of an infinite unary tree has been studied extensively over the past 120-150 years.

References

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Session 3

Applications in Cell Kinetics and Genetics

Dedicated to the memory of Andrei Yu. Yakovlev

Branching processes in cell proliferation kinetics

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AMS: 60J80

Abstract

Some basic models and characteristics of cell proliferation kinetics using branching processes are considered in [1-4]. An important problem is the distribution of the discrete marks (labels) obtained in [3] and [4] using a model with infinite many types of Bellman-Harris branching processes. Generalizations in the case of continuous labels are given in [6] and [8]. Note that processes with continuous labels are first considered by Kolmogorov. New models of renewing cell populations (*in vivo*) using age-dependent branching processes with non-homogeneous Poisson immigration are proposed in [7]. Leukemia cell kinetics with a stem cell immigration component is studied in [5]. Multitype age-dependent branching processes with randomly chosen paths of evolution are proposed in [10] as models of progenitor cell populations (*in vitro*) with estimating of the offspring distributions using real data as well as bootstrap methods. An interesting and important problem arising from cell proliferation kinetics is the definition and the limiting behaviour of age and residual lifetime distributions for branching processes considered in [9].

The relative frequencies of distinct types of cells in multitype branching processes with a large number of ancestors are investigated in [11] and [12]. The reported limiting results are of advantage in cell kinetics studies where the relative frequencies but not the absolute cell counts are accessible to measurement. In [11] some relevant statistical applications are discussed in the context of asymptotic maximum likelihood inference for multitype branching processes. In [12] the asymptotic behavior of multitype Markov branching processes with discrete or continuous time is investigated in the positive regular and nonsingular case when both the initial number of ancestors and the time tend to infinity. Some limiting distributions are obtained as well as multivariate asymptotic normality is proved. The results from [11] and [12] have a specific applications in cell proliferation kinetics.

Finally it is worth to point out that new problems in the theory of branching processes appeared as a result of cell proliferation modeling and the talk will be focused on some of these new ideas.

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- [11] A. Yu. Yakovlev, N. M. Yanev (2008) Relative frequencies in multitype branching processes. *Ann. Appl. Probab.*, to appear.
- [12] A. Yu. Yakovlev, N. M. Yanev (2008) Limiting distributions in multitype branching processes. *Ann. Appl. Probab.*, submitted.

Modeling the evolution of Alu repeats in human genome

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Keywords: Branching process, infinite alleles model, Alu repeats, evolution

AMS: 60J80

Abstract

Alu elements occupy about eleven percent of the human genome and are still increasing in copy numbers. Since Alu elements substantially impact the shape of our genome, there is a need for modeling the amplification, mutation and selection forces of these elements. Our proposed theoretical neutral model follows a continuous-time branching process described by Pakes [3], or its equivalent discrete counterpart as described by [1]. From the model, we derived a limiting frequency spectrum of the Alu element distribution, which serves as the theoretical, neutral frequency to which real Alu insertion data can be compared to through statistical goodness of fit tests. Departures from the neutral frequency spectrum may indicate different types of selection. A comparison of the Alu sequence data (obtained by courtesy of Dr. Jerzy Jurka) with our model shows that the distribution of Alu sequences in subfamilies AluYa5 and AluYb8 does not follow the expected distribution derived from the branching process; for a thorough biological discussion see Ref. [2]. This observation suggests that Alu sequences do not evolve neutrally and might be under selection.

Acknowledgements: Marek Kimmel's research was partly supported by the Rice University - Texas Children Hospital Collaboration. Dr. Jerzy Jurka of the Genetic Information Research Institute (GIRI) kindly provided Alu sequence data for our analysis and provided important guidelines concerning their analysis. Help of Prof. Anthony Pakes in derivations related to his models is gratefully acknowledged.

References

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On Y-linked branching models

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Keywords: Sex-linked inheritance, bidimensional bisexual branching processes

AMS: 60J80

Abstract

A pair of chromosomes, called X and Y, determine the sex of many animal species, including most of mammals and human beings among them. In this system, females have XX chromosome and males have two distinct chromosome XY. Recent investigations have shown the importance of some Y-linked genes in populations of humans (see e.g., www.nature.com/nature/focus/ychromosome/) or in other species (see the review [1]). Determining the evolution of Y-linked characters in a population plays an important role to solve some relevant questions from a practical viewpoint, such as, the problem of Y-chromosomal Adam, infertility problems in males, or the extinction/spreading of marks such as the surnames or melanistic pigmentation. Recently, two bidimensional bisexual branching models have been introduced to describe the evolution of alleles associated to Y-linked genes (see [2] and [3]). In this work we summarize the results obtained for these models, related to their extinction conditions and asymptotic behaviour, and we also present new results about their estimation theories, from frequentist and Bayesian viewpoints.

Acknowledgements: This is a joint work with M. González, C. Gutiérrez and M. Mota. The research was supported by the Ministerio de Ciencia e Innovación and the FEDER through the Plan Nacional de Investigación Científica, Desarrollo e Innovación Tecnológica, grant MTM2006-08891.

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Branching process model of the early phase of a bacterial insertion sequence invasion

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Keywords: Multitype branching process, insertion sequence

AMS: 60J80

Abstract

Bacterial insertion sequences (ISs) are short DNA segments that can proliferate on their own inside a bacterial genome and can spread in a host cell population through horizontal gene transfer. With the help of a continuous-time, multitype Markov branching process model we examine the population dynamics of the early phase of an IS invasion into an uninfected cell population at carrying capacity. In particular, we are interested in the probability of a successful IS invasion depending on the rate of horizontal gene transfer, in the distribution of IS counts per cell over the host cell population and in the time needed to reach a certain threshold number of infected cells.

Acknowledgements: The author thanks Prof. Andreas Wagner and Prof. Andrew Barbour for their support in biological and mathematical matters, respectively. This work is supported by the Swiss National Science Foundation.

Session 4

Applications in Epidemiology

Applications of branching processes to a network epidemic model with casual contacts

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Keywords: SIR epidemics, random graphs, branching process approximations, threshold behaviour, final outcome

AMS: 92D30, 60J80

Abstract

Branching processes play a key role in the analysis of epidemic models. In this talk, I illustrate this by outlining some recent work with Peter Neal (University of Manchester) concerned with epidemics on random networks incorporating casual contacts (Ball and Neal [1]). I consider a stochastic SIR (susceptible \rightarrow infective \rightarrow removed) model for the spread of an epidemic on a finite network, having an arbitrary but specified degree distribution, in which individuals also make casual contacts, i.e. with people chosen uniformly from the population. The behaviour of the model as the network size n tends to infinity is investigated. In particular, its threshold behaviour is determined by exploiting an approximate branching process, with the approximation becoming exact in the limit as $n \rightarrow \infty$. The proportion of the population who are ultimately infected by an epidemic that becomes established is determined, using another approximating branching process, and a central limit theorem for the size of such an epidemic is obtained. Corresponding results for the epidemic without casual contacts, i.e. for the standard SIR network epidemic model, are discussed briefly. The theory is illustrated by numerical studies which demonstrate that the asymptotic approximations work well, even for only moderately sized networks, and that the degree distribution and the inclusion of casual contacts can each have a major impact on the outcome of an epidemic.

Acknowledgements: The research was supported by the Leverhulme Trust and by the UK Engineering and Physical Sciences Research Council, under research grant EP/E038670/1.

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A branching process approach for the propagation of the Bovine Spongiform Encephalopathy in Great-Britain

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Keywords: Branching processes; Extinction; Bayesian estimation; Epidemiology.

AMS: 60J80; 60J85; 92D30

Abstract

The goal of this work is the modelling of the propagation of BSE (Bovine Spongiform Encephalopathy) at the scale of a very large population (Great-Britain) in order to predict its extinction time and to evaluate the efficiency of the main feedback regulation. We first elaborate a multitype branching process in discrete time with age and population dependent individual transitions. The types are the health states at each age. Then, assuming that the disease is rare at the initial time, and assuming a Reed-Frost type assumption for the infection law, we derive from this model a limit process on the incidence of clinical cases, as the initial size of the population increases to ∞ . This limit process may be either considered as a singletype $(a_M - 1)$ -Markovian process with a Poissonian transition distribution, or a multitype Bienaymé-Galton-Watson process having $a_M - 1$ types corresponding to the memory of the process. We derive the bifurcation parameter, the extinction probability and the extinction time distribution from the limit process. Estimations are then done in the Bayesian setting.

Acknowledgements: This work is done in collaboration with L. Maillard, J.-B. Denis, C. Bidot, and was supported by the french government through the project GIS Prions and then by the european ReX Neuroprion

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Limit theorems for conditioned multitype branching processes and Feller diffusions. Application to the BSE epidemic

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Keywords: multitype branching process, limit theorems, epidemiology

AMS: 60J80, 60J85, 92D30

Abstract

We consider a multitype continuous-time branching process, and study in the critical and subcritical cases the conditioned distribution $\mathbb{P}(X_t \in \cdot | X_{t+\theta} > 0)$, for some $\theta \geq 0$. We investigate both limits as θ and t tend to ∞ , as well as the commutativity between them. The first limit stands for a conditioning on non-extinction in the remote future, while the second limit is a generalization of the Yaglom distribution (obtained for $\theta = 0$). We shall investigate the same limits for a multitype Feller diffusion process, as well as the connexion between the discrete and continuous-state cases.

In terms of risk analysis, the study of the conditioned distribution $\mathbb{P}(X_t \in \cdot | X_{t+\theta} > 0)$ for θ very large is of some interest. If the process represents the size of an infected population, this distribution corresponds indeed to the worst scenarios of the epidemic. We shall apply some of the above-mentioned results to the modelling of the propagation of BSE elaborated by C. Jacob. In [2], the authors model the incidence of clinical cases via a monotype Markovian process of order d , which can be considered as a multitype Bienaymé-Galton-Watson process having d types corresponding to the memory of the process. We would like to estimate parameters of this model in the previous setting, which would provide information about the worst scenarios of the epidemic.

Acknowledgements: This research is done as part of a PhD thesis supervised by S. Roelly (Potsdam, Germany) and C. Jacob (INRA, France). It is supported by the Université Franco-Allemande and the International Research Training Group “Stochastic models of complex processes” .

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Stochastic modelling of vaccine preventable diseases by age-dependent branching processes

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Keywords: Age-dependent branching processes, extinction time, vaccine preventable diseases, Monte-Carlo method

AMS: 60J80

Abstract

The aim of this study is to provide tools to analyze the rate of vaccination coverage in case of fast newly emerging infectious disease, so that the spread cannot lead to large-scale epidemics. To this end, the epidemic spreading is modeled through an age-dependent branching process, appropriate for diseases with incubation period and allowing different transmission rates during the infection period. We investigate theoretically the properties of the time to elimination of an epidemic, depending on the rate of the immunized and/or extra-immunized individuals into the population. From these results, we are able to suggest a vaccination strategy to have the epidemic ceased before a given period of time. The results are simulation-based, without focusing on any specific disease. Finally, our model is widely applied in scope, in that it is in continuous time and allows heterogeneities in contact rates.

Acknowledgements: This is a joint research with M. González and R. Martínez from University of Extremadura, Spain. The research was partially supported by the Ministerio de Ciencia e Innovación and the FEDER through the Plan Nacional de Investigación Científica, Desarrollo e Innovación Tecnológica, grant MTM2006-08891 and by the NFSI, grant VU-MI-105/2005, Bulgaria.

Approximating extinction times in multitype Markov branching processes

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Keywords: Multitype branching process, extinction time, convergence rate

AMS: 60J80

Abstract

We derive a distributional approximation to the time to extinction in a sub-critical continuous-time multitype Markov branching process. The argument is to combine (i) the classical exponential approximation to the extinction probabilities and (ii) the branching property to finally derive a Gumbel approximation for the extinction time. We show that the upper bound on the error for the corresponding density approximation in total variation distance is inversely proportional to a positive power of a weighted sum of the number of individuals of the different types. The power depends on the means and higher moments of the offspring distribution.

The accuracy of the approximation is illustrated by a model of parasitic resistance of the parasite *Toxoplasma gondii*, a serious public health problem.

Acknowledgements: The author wishes to thank Andrew Barbour for many helpful suggestions. This work is supported by the Swiss National Science Foundation (SNSF), project no. 107726.

Session 5

Limit Theorems and Statistics

Approximation of a sum of martingale-differences generated by a bootstrap branching process

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Keywords: Branching processes, Bootstrap, Functional limit theorem.

AMS: 60J80

Abstract

Let $\{Z(k), k \geq 0\}$ be a branching stochastic process with non-stationary immigration given by offspring distribution $\{P_j(\theta), j \geq 0\}$ depending on unknown parameter $\theta \in \Theta$. We estimate θ by an estimator $\hat{\theta}_n$ based on sample $\mathcal{X}_n = \{Z(i), i = 1, \dots, n\}$. Given \mathcal{X}_n , we generate bootstrap branching process $\{Z^{(n)}(k), k \geq 0\}$ for each $n = 1, 2, \dots$ with offspring distribution $\{P_j(\hat{\theta}_n), j \geq 0\}$. The object of discussion is a weighted sum of martingale differences generated by this array of branching processes. We provide a general functional limit theorem for this sum, which includes critical or nearly critical processes with increasing or stationary immigration and with large or fixed number of initial ancestors. It also includes processes without immigration with increasing random number of initial individuals. Possible applications in estimation theory of branching processes will also be discussed.

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Limit theorem for critical inhomogeneous branching processes with immigration

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Keywords: Inhomogeneous branching process, limit theorem, square-root process

AMS: 60J80; 60J27, 60J85

Abstract

A zero start inhomogeneous branching process with immigration (IBPI) $(X_n)_{n \in \mathbb{Z}_+}$ is defined as

$$X_n = \sum_{j=1}^{X_{n-1}} \xi_{n,j} + \varepsilon_n, \quad n \in \mathbb{N}, \quad X_0 = 0,$$

where $\{\xi_{n,j}, \varepsilon_n : n, j \in \mathbb{N}\}$ are independent non-negative integer-valued random variables such that $\{\xi_{n,j} : j \in \mathbb{N}\}$ are identically distributed for each $n \in \mathbb{N}$. Assume that $m_n := \mathbb{E}\xi_{n,1}$, $\lambda_n := \mathbb{E}\varepsilon_n$, $\sigma_n^2 := \text{Var}\xi_{n,1}$, $b_n^2 := \text{Var}\varepsilon_n$ are finite for all $n \in \mathbb{N}$. The process $(X_n)_{n \in \mathbb{Z}_+}$ is called (nearly) critical if $m_n \rightarrow 1$ as $n \rightarrow \infty$. Introduce the random step functions

$$\mathcal{X}^{(n)}(t) := X_{\lfloor nt \rfloor} \quad \text{for } t \in \mathbb{R}_+, n \in \mathbb{N}.$$

We prove the following generalization of a result of Wei and Winnicki [1].

Theorem. Suppose that $\sum_{n=1}^{\infty} |m_n - 1| < \infty$; $\sigma_n^2 \rightarrow \sigma^2 \geq 0$, $\lambda_n \rightarrow \lambda \geq 0$, $b_n^2 \rightarrow b^2 \geq 0$, and $n^{-2} \sum_{k,j=1}^n \mathbb{E}(|\xi_{k,j} - m_k|^2 \mathbb{1}_{\{|\xi_{k,j} - m_k| > \theta n\}}) \rightarrow 0$ for all $\theta > 0$ as $n \rightarrow \infty$. Then

$$n^{-1} \mathcal{X}^{(n)} \xrightarrow{\mathcal{D}} \mathcal{X} \quad \text{as } n \rightarrow \infty,$$

that is, weakly in the Skorokhod space $\mathbb{D}(\mathbb{R}_+, \mathbb{R})$, where $(\mathcal{X}(t))_{t \in \mathbb{R}_+}$ is the unique solution of a stochastic differential equation (SDE)

$$d\mathcal{X}(t) = \lambda dt + \sigma \sqrt{\mathcal{X}_+(t)} dW(t), \quad t \in \mathbb{R}_+,$$

with initial condition $\mathcal{X}(0) = 0$, where $x_+ := \max\{x, 0\}$ and $(W(t))_{t \in \mathbb{R}_+}$ is a standard Wiener process.

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Statistical inference of critical multitype branching processes with immigration

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Keywords: Multitype branching processes

AMS: 60J80

Abstract

We will investigate a d -type branching process $X_k = (X_k^1, \dots, X_k^d)^\top$, $k = 0, 1, \dots$, with immigration. By $\xi_{k,\ell}^{i,j}$ we denote the number of type j offspring produced by the ℓ^{th} individual who is of type i belonging to the $(k-1)^{\text{th}}$ generation. The number of type i immigrants in the k^{th} generation will be denoted by ε_k^i . Then

$$X_k = \sum_{i=1}^d \sum_{\ell=1}^{X_{k-1}^i} \xi_{k,\ell}^i + \varepsilon_k,$$

where $\varepsilon_k := (\varepsilon_k^1, \dots, \varepsilon_k^d)^\top$ and $\xi_{k,\ell}^i := (\xi_{k,\ell}^{i,1}, \dots, \xi_{k,\ell}^{i,d})^\top$. Assume that $m_\xi := (E(\xi_{1,1}^{i,j}))_{1 \leq i,j \leq d}$ and $m_\varepsilon := E(\varepsilon_1)$ are finite. Then $E(X_k | X_1, \dots, X_{k-1}) = m_\xi^\top X_{k-1} + m_\varepsilon$. If m_ε is known then the conditional least squares estimator \widehat{m}_ξ^n of m_ξ based on the observations X_1, \dots, X_n can be obtained by minimizing the sum of squares $\sum_{k=1}^n \|X_k - m_\xi^\top X_{k-1} - m_\varepsilon\|^2$ with respect to m_ξ , and we obtain

$$\widehat{m}_\xi^n = \left(\sum_{k=1}^n X_{k-1} X_{k-1}^\top \right)^{-1} \left(\sum_{k=1}^n X_{k-1} (X_k - m_\varepsilon)^\top \right).$$

We are interested in the asymptotic behaviour of the sequence \widehat{m}_ξ^n , $n = 1, 2, \dots$, in the critical case $\rho(m_\xi) = 1$, where $\rho(m_\xi)$ denotes the spectral radius of m_ξ .

Acknowledgements: The research was supported by Hungarian Foundation for Scientific Researchers under Grant No. OTKA-T048544/2004.

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Weighted conditional least squares estimation in controlled branching processes

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Keywords: Branching processes, weighted conditional least squares, asymptotic properties.

AMS: 60J80

Abstract

The controlled branching process with random control function provides a useful way to model generation sizes in population dynamics studies, where control on the growth of the population size is necessary at each generation. From a probabilistic viewpoint and in the framework of asymptotic linear growth of the expectation of the control variables, this model has been well studied. One of the main parameters describing the evolution of these models is known as the offspring mean. As in classical Galton-Watson process, this plays a crucial role as a threshold parameter, which drastically changes the behavior of the process in the three cases known as subcritical, critical and supercritical. However, few papers deal with the study of inference problems arising in this model. In this talk, we present the weighted conditional least squares (WCLS) estimator of the offspring mean proposed in Sriram et al. (2007) and derive the asymptotic limit distribution of the estimator in the tree cases. It turns out that the limit distribution depends on each case. In order to provide a unified solution, we present the bootstrap approximation to the sampling distribution of the WCLS estimator of the offspring mean.

Acknowledgements: This is joint work with T.N. Sriram and A. Bhattacharya, from University of Georgia (Athens, Georgia, USA), and M. González and R. Martínez, from University of Extremadura. This research was supported by the Ministerio de Educación y Ciencia and the FEDER through the Plan Nacional de Investigación Científica, Desarrollo e Innovación Tecnológica, grant MTM2006-08891.

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Session 6

Population Growth Models in
Random and Varying
Environments

Sudden death versus slow extinction of branching processes in random environment

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Keywords: Branching processes in random environment, stable law

AMS: 60J80, 60G52

Abstract

A branching process $Z(n), n = 0, 1, \dots$, is considered which evolves in a random environment generated by a sequence of iid generating functions $f_0(s), f_1(s), \dots$. Let $T = \min\{k : Z(k-1) > 0, Z(k) = 0\}$ be the extinction moment of the process, $S_0 = 0, S_k = \log f'_0(1) + \dots + \log f'_{k-1}(1), k \geq 1$, be the associated random walk and $\tau(m, n)$ be the left-most point of minimum of $\{S_k, k \geq 0\}$ on the interval $[m, n]$.

Assuming that the distribution of $\log f'_0(1)$ belongs to the domain of attraction of a stable law with parameter $\alpha \in (0, 2]$ and zero mean if $\alpha > 1$, we show that (under the quenched approach and given $T = n \rightarrow \infty$) the process approaches the extinction moment by passing through a number of bottlenecks, when the size of the population becomes very small, and periods of recovering, when the size of the population is of order $e^{S_m - S_{\tau(0, m)}}$ if $m < \tau(0, n)$ and of order $e^{S_m - S_{\tau(m, n)}}$ if $m \geq \tau(0, n)$. In particular, the size Z_{n-1} of the population is "not too big" and, therefore, the process dies out in a "natural" way. Similar phenomenon takes place under the annealed approach if $\text{Var} \log f'_0(1) < \infty$. If, however, $\text{Var} \log f'_0(1) = \infty$ then (under the annealed approach) $\log Z_{n-1}$ is very big, namely, of order $n^{1/\alpha}$. In this case the extinction of the process at moment n may be treated as it's sudden death under very unfavorable environment.

Acknowledgements: The research was supported in part by the DFG-RFBR grant 08-01-91954

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Stochastic differential equation models of population and individual growth in a random environment

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Keywords: Stochastic differential equations, population growth, individual growth, random environment, stationary distribution, extinction

AMS: 60H10, 92D25

Abstract

Consider a population growing in an randomly varying environment and let $N = N(t)$ be its size at time t . We assume that the *per capita* growth rate has mean behavior $g(N)$ (a general smooth function satisfying suitable assumptions dictated by biological considerations) and is affected by a (white) environmental noise with constant noise intensity σ . We thus obtain the general stochastic differential equation (SDE) model $\frac{1}{N} \frac{dN}{dt} = g(N) + \sigma \varepsilon(t)$ or, in traditional format, $dN = g(N)Ndt + \sigma NdW(t)$, where $\varepsilon(t)$ is a standard white noise and $W(t)$ is the standard Wiener process.

For the special case of Malthusian growth ($g(N)$ constant), comparing this model with the corresponding classical branching process model, that studies demographic noise (sampling variation in births and deaths), one notices that changes in population size have a standard deviation proportional to N in the SDE model (environmental noise) and proportional to \sqrt{N} in the branching process model (demographic noise).

We will examine the behavior of our general SDE model in what concerns the existence of a stationary density for the population size and in what concerns extinction. We then generalize the results to the case of density dependent noise intensities $\sigma(N)$.

Finally, we use similar models (work with Patrícia A. Filipe) to describe individual growth of animals from birth to maturity and illustrate with data on cattle weight.

Acknowledgements: Research done in the research center CIMA, also involving the research project PTDC/MAT/64297/2006, both supported by FCT (Fundação para a Ciência e a Tecnologia, Portugal).

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Criticality for alternating branching processes

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Keywords: Branching processes; controlled branching process; state-dependent emigration; random environment; extinction probability; critical case

AMS: 60J80

Abstract

This communication describes the correspondence between the models of Alternating branching processes, Controlled branching processes and Branching processes in random environment. The Control process consists of testing every particle from the n -th generation according to a dying branching process during an independent random time τ_n . The random environment is generated by the sequence of random variables (δ_n, τ_n) , representing the observation and treatment times, respectively, and by the probability generating functions of the Markov branching processes stopped at the random times δ_n or τ_n .

Acknowledgements: The research was completed during my visiting position at the University of Tunis-ISET de Rades.

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A note on controlled branching processes in varying environment

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Keywords: Branching processes, varying environment.

AMS: 60J80

Abstract

Branching processes are regarded as appropriate probability models for the description of the extinction/growth of populations (see [1]). In particular, controlled branching processes are useful to model some situations where some kind of control is required.

In order to model a control mechanism in the evolution of a population we assume a development in two phases: a reproductive phase where individuals give birth to their offspring according to a probability distribution, called reproduction law, and a control phase where some individuals are introduced or removed according to other probability distribution, called control law. In the literature on controlled branching processes the control phase is assumed to depend on the population size. On the other hand, in the vast majority of works, the reproduction law is assumed to be the same for every individual in any generation. However, it seems reasonable to think that the reproductive abilities of a population may vary from one generation to another and also that the control could change with the generation independently of the population size. These possibilities have not been considered until now, at least from a general viewpoint.

As a first approach to possible modifications for a controlled branching process, it is our purpose in this talk to introduce and research controlled branching processes that consider the reproduction law can vary. They will be called controlled branching processes in varying environment.

Acknowledgements: This is a joint work with I.del Puerto and A. Ramos (University of Extremadura). This research was supported by the Ministerio de Ciencia e Innovación and the FEDER through the Plan Nacional de Investigación Científica, Desarrollo e Innovación Tecnológica, grant MTM2006-08891.

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Session 7

Special Branching Processes

Stochastic fixed point equations

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Abstract

We will present an overview on solutions of Stochastic Fixed Point Equations,

$$X \stackrel{d}{=} \sum_n T_n X_n + C.$$

The random vector (C, T_1, T_2, \dots) is independent of the sequence $X_n, n \in \mathbb{N}$ of independent rvs with the same distribution as X .

The most well known solutions arise as limits in the context of Weighted Branching Processes, as the limit of the total weight in n -th generation correctly normalized. However there may be more. Prominent examples are the Quicksort, α -stable, and Weibull distributions.

Population-dependent branching processes

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Keywords: near-critical branching process, near-supercritical branching process

AMS: 60J80

Abstract

I shall give a survey of asymptotic behaviour of population-dependent branching processes concentrating on two cases: near-critical and near-supercritical processes. Precise description of these cases will be given in the models of Galton-Watson, Markov and Age-dependent branching processes. Single type as well as multitype processes will be considered.

Limit theorems for randomly indexed branching processes

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Keywords: Branching processes, Random time change, Limit theorems

AMS: 60J80

Abstract

Let us have on the probability space $(\Omega, \mathcal{A}, \mathbf{P})$ two independent stochastic processes:
The Bienaymé-Galton-Watson process

$$Z_0 = 1, \text{ a.s. , } Z_{n+1} = \sum_{i=1}^{Z_n} X_i(n+1);$$

The renewal sequence

$$S_0 = 0, \quad S_n = \sum_{j=1}^n J_j, \quad n = 0, 1, \dots,$$

and the corresponding renewal counting process $N(t) = \max\{n \geq 0 : S_n \leq t\}$.

Then the continuous time process $\{Y(t), t \geq 0\}$ defined by

$$Y(0) = 1, \quad Y(t) = Z_{N(t)}, \quad t > 0$$

is called a randomly indexed BGW branching process.

In the talk we give some limit theorems for the process $Y(t)$.

Acknowledgements: The research was supported by NSF- Bulgaria (grant VU-MI-105/20-05).

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Fixation time estimates in bounded populations

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Keywords: Branching processes; Markov models

AMS: 60J80; 60J10

Abstract

Markov models are used widely in population dynamics and evolution. One of such sort models are fixed size haploid models without mutations. The discrete time model consisting of N particles each of which can belong to one of N types. If, at some moment, the number of particles of each type is defined by $\mathbf{k} = (k_1, \dots, k_N)$, where $k_j \in \{0, \dots, N\}$ and $|\mathbf{k}| = k_1 + \dots + k_N = N$, then, at the next moment, the number of particles of each type is described by the random vector (rv) $(\sum_{j \in K_1} \xi_j^{(N)}, \dots, \sum_{j \in K_N} \xi_j^{(N)})$, where $\xi_j^{(N)}$ is the number of offspring of the j -th particle, the sets K_1, \dots, K_N consist of the numbers of the particles with types $1, \dots, N$ (K_1, \dots, K_N have k_1, \dots, k_N elements and are pairwise disjoint) and $\xi_1^{(N)} + \dots + \xi_N^{(N)} = N$. The rv $(\xi_1^{(N)}, \dots, \xi_N^{(N)})$ have exchangeable distributions (i.e., the birth law does not depend on their type) are i.i.d. at each step. Let $\tau_{\mathbf{k}}$ be the fixation time of the population (i.e., supplanting all particles by particles of one type) with initial configuration \mathbf{k} . The main result is $\mathbf{E}\tau_{\mathbf{k}} \leq c \left((N-1)N \ln N - \sum_{j=1}^N (N-k_j) \ln(N-k_j) \right)$, for some constant c depends of N and moments of $\xi_1^{(N)}$ [1].

Let $Z_n(m)$ bounded by level N supercritical Galton-Watson process, defined as $Z_0 = m$, $Z_n(m) = \min \left(N, \sum_{j=1}^{Z_{n-1}(m)} \xi_{j,n} \right)$. The process $Z_n(m)$ is finite Markov chain with one absorbing state. But the extinction time for one very large and very long time we have $Z_n(m) \approx N$, as $m \approx N$ and $N \gg 1$ [1]. Empirical results show that $\mathbf{E}\tau_{\mathbf{k}}$ from previous model equivalent to analogy parameters for the branching process.

Acknowledgements: The research was supported by RFBR (Grant 09-01-00105), and the Foundation of the President of the Russian Federation (Grant 3695.2008.1).

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Session 8

Two-sex Branching Models

Elementary proofs for certain extinction in bisexual Galton-Watson branching processes

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Keywords: Bisexual branching processes, extinction

AMS: 60J80

Abstract

Interest in the standard Galton-Watson branching process can be motivated by a consideration of two questions. Given: a singular class of asexually reproducing individuals, what condition will guarantee certain extinction (i.e. an extinction probability of one)? (Answer: when the mean of the offspring probability distribution is less than or equal to one.) Also, if the extinction probability is known to be less than one, how can that probability be calculated? (Answer: solve the equation, the generating function of the offspring probability distribution (in terms of x) equal to x . The least positive solution will be the probability of extinction if there is one individual in the initial generation.) The mathematical arguments associated with the two answers are relatively simple and can be understood by novice probability students. These relevant questions should be asked in the context of the bisexual Galton-Watson branching process. However, the simplicity associated with asexual reproduction is lost when the model requires bisexual reproduction. A consideration of the first question with the assumption of a two-sex population will be considered in this paper. Proofs relating to this question has found in the literature are not simple and require a high level of mathematical sophistication. Perhaps, a greater interest in the bisexual model could be generated, if the proof associated with the first question, could be presented for a target audience with minimal mathematical backgrounds. That project will be attempted in this paper.

Two-sex branching process literature

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Abstract

With the purpose to describe the probabilistic evolution of populations where females and males coexist and form couples, Daley (1968) introduced the bisexual Galton-Watson branching process. Professor D. J. Daley, considering two interesting mating functions between females and males, provided necessary and sufficient conditions for the ultimate extinction of the bisexual process to occur with probability one. Since Daley's work, several papers on the extinction probability, the limiting behaviour, the statistical theory or the applications about the bisexual Galton-Watson branching process have been published, see Hull (2003). In the last years, in order to get an optimum modelling in more complex two-sex populations, new classes of discrete time two-sex (bisexual) branching processes, including models with immigration, in varying environments, in random environments, depending on the number of couples in the population, or controlled models, have been introduced and some theory and applications about them developed. Also, some general classes of continuous time two-sex branching processes have been studied, see e.g. Molina and Yanev (2003). This talk, will intended to be a survey of the literature associated with such classes of discrete or continuous time two-sex branching processes.

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