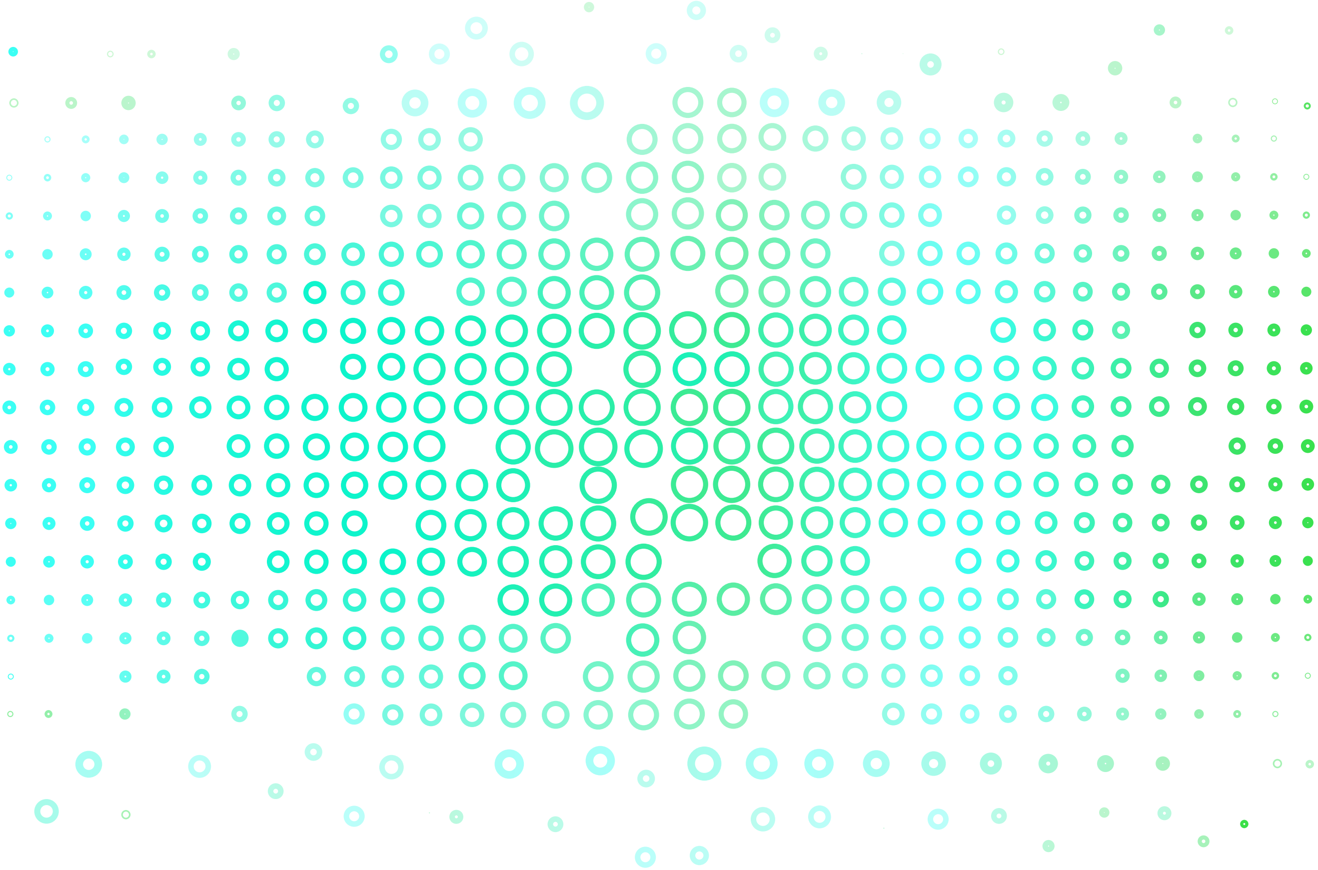
Book of Abstracts

III Workshop

On Branching Processes and their Applications



April, 7-10, 2015

Badajoz, Spain

Book of Abstracts

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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 held in Varna (Bulgaria) in 1993 to celebrate the first 150 years of branching processes. In last decade, it is worth to mentioning those took place in Goteborg (Sweden) in 2005, in Luminy (France) in 2007 and 2011, in Beijing (China) in 2011 or in Pomorie (Bulgaria) in 2012 and 2014.

In the 90's, a research group in branching processes was born at the University of Extremadura. We are now eight members investigating in several fields of the branching theory. With the aim of contributing to those interesting meetings, our group promoted the I and II Workshop in Branching Processes and their Applications held in Badajoz in 2009 and 2012. Now we are delighted to promote the third edition of these workshops to be held from 7th to 10th April, 2015.

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 12 sessions. The conference venue is the Faculty of Sciences of the University of Extremadura in Badajoz.

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 acceptation 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 Ministerio de Economía y Competitiviad, Gobierno de Extremadura, Ayuntamiento de Badajoz and University of Extremadura itself. Furthermore the Spanish Society of Statistics and Operations Research (SEIO) and the Instituto de Computación Científica Avanzada de Extremadura (ICCAEx) support 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.

Inés M. del Puerto
Chair of the WBPA

	Tuesday, 7	Wednesday, 8	Thursday, 9	Friday, 10
09:00-9:30	Opening ceremony			
9:30-10:00	K.B. Athreya			N.M. Yanev
10:00-10:30	G. Kersting	V. Vatutin	P. Jagers	O. Hyrien
10:30-11:00	R. Griffiths	V. Afanasyev	F. Klenaner	V. Topchii
11:00-11:30	Coffee Break	C. Braumann	F.T. Bruss	P. Trayanov
11:30-12:00	R. Abraham	Coffee Break	Coffee Break	Coffee Break
12:00-12:30	J.F. Delmas	F. Ball	G. Alsmeyer	M. Ispany
12:30-13:00	Y. Hu	R. Martínez	M. Bojkova	K. Mitov
13:00-13:30	Z. Li	Lunch	M. Mota	Lunch
13:30-16:00	Lunch		Lunch	
16:00-16:30	E. Yarovaya	Guided Visit: Cáceres and Mérida	U. Rösler	G. Pap
16:30-17:00	H. Wang		A. Lindo	K. Körmendi
17:00-17:30	Coffee Break		Coffee Break	Coffee Break
17:30-18:00	D. Atanasov		G. Yanev	A.N. Vidyashankar
18:00-18:30	C. Minuesa		D. Hull	C. Gutiérrez
18:30-				Closing Ceremony
19:00-	Reception			
20:30-			Concert	Social dinner

Tuesday, April 7	
	Session I: Coalescent branching processes Chairman: P. Jagers
9:30-10:00	**Krishna B. Athreya** Coalescence in branching processes
10:00-10:30	**Götz Kersting** Evolving beta-coalescents
10:30-11:00	**Robert Griffiths** A multi-type Λ-coalescent with mutation and selection
	Session II: Random trees Chairman: R. Griffiths
11:30-12:00	**Romain Abraham** Local limits of conditioned Galton-Watson trees
12:00-12:30	**Jean-François Delmas** On the genealogical tree of a stationary (quadratic) branching process
12:30-13:00	**Yueyun Hu** Randomly biased walks on trees
13:00-13:30	**Zenghu Li** Branching processes and stochastic equations
	Session III: Branching random walks Chairman: V. Vatutin
16:00-16:30	**Elena Yarovaya** Stochastic particle systems on non-homogeneous spatial lattice structures
16:30-17:00	**Hua-Ming Wang** Intrinsic branching structures within random walks on $\mathcal{Z}$ and their applications
	Session IV: Statistical inference I Chairwoman: I. del Puerto
17:30-18:00	**Dimitar Atanasov** Point estimation in multivariate power series offspring distributions
18:00-18:30	**Carmen Minuesa** Robust estimation on controlled branching processes: minimum disparity approach

Wednesday, April 8	
	Session V: Population growth models in random environments Chairman: N.M. Yanev
10:00-10:30	**Vladimir Vatutin** Some limit theorems for subcritical branching processes in random environment
10:30-11:00	**Valeriy Afanasyev** On subcritical branching processes in random environment
11:00-11:30	**Carlos Braumann** Consequences of an incorrect model specification for population growth in random environments
	Session VI: Applications in epidemiology Chairman: M. Molina
12:00-12:30	**Frank Ball** Inference for emerging epidemics among a community of households
12:30-13:00	**Rodrigo Martínez** Vaccination in epidemic modelling: branching processes *versus* stochastic epidemic models

Thursday, April 9	
	Session VII: Size/Density/Resource-dependent branching models Chairman: K.B. Athreya
10:00-10:30	**Peter Jagers** Structure dependent branching processes
10:30-11:00	**Fima Klebaner** Escape from the boundary in Markov population processes
11:00-11:30	**F. Thomas Bruss** Envelopment in resource dependent branching processes and directives of control
	Session VIII: Applications in biology Chairman: F. Klebaner
12:00-12:30	**Gerold Alsmeyer** Branching within branching: a general model for host parasite evolution
12:30-13:00	**Maroussia N. Slavtchova-Bojkova** On multi-type decomposable branching processes in continuous time and time to escape extinction
13:00-13:30	**Manuel Mota** Branching processes as models for biological populations with sexual reproduction
	Session IX: Special branching models Chairman: G. Alsmeyer
16:00-16:30	**Uwe Rösler** The weighted branching process
16:30-17:00	**Alexey Lindo** A special family of Galton-Watson processes with explosion
17:30-18:00	**George P. Yanev** Revisiting limit results for controlled branching processes
18:00-18:30	**David Hull** The standard Galton-Watson branching process with a reflecting barrier

Friday, April 10	
	Session X: Age-dependent branching models Chairwoman: M.N. Slavtchova-Bojkova
9:30-10:00	**Nikolay M. Yanev** Sevastyanov age-dependent branching processes with non-homogeneous Poisson immigration
10:00-10:30	**Ollivier Hyrien** Classes of equivalence and identifiability of age-dependent branching processes
10:30-11:00	**Valentin Topchii** Two types critical Bellman-Harris processes with long-lived and short-lived particles. Renewal theorems and moments increments
11:00-11:30	**Plamen Trayanov** Crump-Mode-Jagers branching process: A numerical approach
	Session XI: Branching processes in varying environments Chairman: N.M: Yanev
12:00-12:30	**Márton Ispány** On critical branching processes with immigration in varying environment
12:30-13:00	**Kosto V. Mitov** A branching process with immigration in varying environments
	Session XII: Statistical Inference II Chairman: M. González
16:00-16:30	**Gyula Pap** Statistical inference for 2-type doubly symmetric critical irreducible CBI processes
16:30-17:00	**Kristóf Körmendi** Statistical inference for critical 2-type Galton-Watson processes with immigration
17:30-18:00	**Anand N. Vidyashankar** Unified robust empirical likelihood confidence regions for parameters of branching processes with immigration
18:00-18:30	**Cristina Gutiérrez** ABC methodology for two-sex branching models with mutations

Session I

Coalescent branching processes

Coalescence in branching processes

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Keywords:

AMS:

Abstract

In a tree generated by a Galton Watson branching processes go to the nth generation . If it has at least two individuals pick two of them at random by srswor and trace their lines back till they meet. Call that generation X_n. In this talk we discuss the limit behavior of X_n as n gets large for a variety of cases:single type subcritical, critical, supercritical, explosive and multitype extensions. We give applications to branching random walks as well.

Evolving beta-coalescents

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Keywords: Branching processes

AMS: 60J80

Abstract

Beta-coalescents are favored models for ancestral relationships, from a theoretical as well as practical point of view. They can be understood as limits of ancestral trees within supercritical Galton-Watson trees. More precisely Schweinsberg (2003) proved: Take a supercritical GW-process $Z = (Z_m)_{m \geq 0}$ with an offspring distribution satisfying $P(\xi > k) \sim ck^{-a}$, where $a > 1$, $c > 0$. Let $n \geq 1$ be some natural number and choose n individuals in generation m of the GW-process. Then, as $m \to \infty$, the ancestral tree of these individuals converges after a suitable scaling to a n-Beta-coalescent (with parameters $2 - \min(2, a), \min(2, a)$).

The evolving n-Beta-coalescent is a tree-valued process. Roughly speaking one consideres the ancestral trees of samples of n individuals at different times. Mathematically it is constructed from a shift-invariant Poisson point process. We shall discuss different functional limit theorems in the limit $n \to \infty$. Here we focus on functionals of the n-coalescents which are of some biological interest, like the total lengths and the total external lengths of the n-coalescents ([**?**, **?**, **?**]).

Acknowledgements: The research was partially supported by the DFG priority program SPP 1590 “Probabilistic Structures in Evolution”.

References

[1] Dahmer, I., Kersting G.: The total external length of the evolving Kingman coalescent. arXiv: 1412.6635 (2014)

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A multi-type Λ-coalescent with mutation and selection

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Keywords: Ancestral Selection Graph, Coalescent process, Dual process, Multi-type Λ-coalescent

AMS: 60J85

Abstract

The Λ-coalescent is a random tree where multiple lines can coalesce back in time. It was introduced by [?] and [?]. A multi-type coalescent occurs naturally when mutation determines types of individuals. An underlying population model forward in time which gives rise, as a limit, to the Λ-coalescent as a genealogy back in time is a Moran model of fixed population size, where an individual can give birth to multiple offspring. If mutation and selection occur in families then a multi-type Λ-coalescent arises. Selection has the effect of a differential birth rate for different types of individuals. The genealogy back in time is then a modified typed Λ-coalescent which becomes a branching coalescing random graph. Let $\boldsymbol{X}(t)$ be the relative frequencies of types at time t in a large population limit model from a Moran model. The generator for the population frequencies is specified by

$$\mathcal{L}g(\boldsymbol{x}) = \int_{|\boldsymbol{y}|\leq 1} \sum_{i=1}^{d} x_i \big(g(\boldsymbol{x}(1-|\boldsymbol{y}|)+\boldsymbol{y}) - g(\boldsymbol{x}) \big) \frac{G_i(\boldsymbol{dy})}{|\boldsymbol{y}|^2}, \tag{1}$$

with notation $|\boldsymbol{y}| = y_1 + \cdots + y_d$. The process is a jump process where, given frequencies $\boldsymbol{x}$, a type i individual gives birth with probability x_i, and adds multi-type frequencies $\boldsymbol{y}$ into the population and rescales as $\boldsymbol{x}(1-|\boldsymbol{y}|)+\boldsymbol{y}$, with a non-negative measure $G_i(\boldsymbol{dy})/|\boldsymbol{y}|^2$ for $\boldsymbol{y}$. The Λ-branching-coalescing graph is a dual process to this population model. This research is joint with Matthias Birkner from Johannes-Gutenberg-University at Mainz, and Alison Etheridge, Luke Miller from Oxford.

References

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Session II

Random trees

Local limits of conditioned Galton-Watson trees

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Keywords: Branching processes, conditioned Galton-Watson trees

AMS: 60J80

Abstract

This presentation is based on a joint work with Jean-François Delmas, [**?**, **?**]. We consider critical or sub-critical Galton-Watson trees conditioned on being large. We first give a general result for convergence in distribution of such trees toward Kesten's tree and apply this result to several special conditionings such as conditioning on the height on the tree, on the total progeny or the total number of leaves. In every previous cases, for critical Galton-Watson trees, the limiting tree is always the size-biased tree seen by Kesten as the critical tree conditioned on non-extinction. On the contrary, for sub-critical offspring distributions a condensation phenomenum may appear: the limiting tree has a single node with infinitely many offsprings.

References

[1] Abraham, R. and Delmas, J.-F. (2014). *Local limits of conditioned Galton-Watson trees: the infinite spine case.* Elec. J. of Probab., 19, Article 2, 1–19.

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On the genealogical tree of a stationary (quadratic) branching process

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Keywords: branching process, population model, genealogical tree

AMS: 60J80, 92D25

Abstract

We will first present the genealogy of a population with random size given by a quadratic stationary continuous-state branching processes. We will recall some properties such as the (mild) bottleneck effect at the time of the most recent common ancestor. Then, we will study the total length process for the genealogical tree and give an explicit formula for the one-dimensional marginal. This result is to be compared with the one obtained by Pfaffelhuber and Wakolbinger for constant size population associated to the Kingman coalescent. We also give a time reversal property of the number of ancestors process at all time, and give a description of the so-called lineage tree in this model.

Acknowledgements: This work is in collaboration with H. Bi.

Randomly biased walks on trees

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Keywords: Biased random walk on the GaltonŨWatson tree, branching random walk, slow movement, local time, convergence in law.

AMS: 60J80, 60G50, 60K37

Abstract

We are interested in the randomly biased random walk on the supercritical Galton–Watson tree. Our attention is focused on a slow regime when the biased random walk (X_n) is null recurrent, making a maximal displacement of order of magnitude $(\log n)^3$ in the first n steps. We study the localization problem of X_n and prove that the quenched law of X_n can be approximated by a certain invariant probability depending on n and the random environment. As a consequence, we establish that upon the survival of the system, $\frac{|X_n|}{(\log n)^2}$ converges in law to some non-degenerate limit on $(0, \infty)$ whose law is explicitly computed.

Acknowledgements: Joint work with Prof. Zhan Shi

Branching processes and stochastic equations

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Keywords: Branching process, stochastic equation, strong solution, stochastic flow, measure-valued process

AMS: 60J80, 60H10, 60H20

Abstract

We establish the strong existence of some stochastic flows of continuous-state branching processes. These unify and generalize the treatments of the flows of subordinators of Bertoin and Le Gall (2003, 2005, 2006). They also provide new perspectives into the tree-valued Markov processes of Aldous and Pitman (1998) and Abraham and Delmas (2012). The exploration is based on some general results on pathwise uniqueness and non-negative strong solutions of stochastic equations driven by time-space white noises and Poisson random measures.

Acknowledgements: The research was supported by by NSFC and MOSTC.

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[1] Abraham, R. and Delmas, J.-F. (2012). *A continuum tree-valued Markov process.* Ann. Probab. **40**, 1167-1211.

[2] Aldous, D. and Pitman, J. (1998). *Tree-valued Markov chains derived from Galton-Watson processes.* Ann. Inst. H. Poincaré Probab. Statist. **34**, 637-686.

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Session III

Branching random walks

Stochastic particle systems on non-homogeneous spatial lattice structures

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Keywords: Branching processes, random walks, symmetric operators, Green's functions, positive eigenvalues.

AMS: 60J80; 34K08; 34L05

Abstract

For simulation the evolution of complex stochastic systems whose elements can take several discrete states, systems with a finite number of sources in which elements may disappear or reproduce their copies are of particular interest. Taking this into account, in the framework of the continuous-time symmetric branching random walks (BRWs) on a multidimensional lattice, we give a formal statement of the problem of analysis of stochastic particle systems with a finite number of sources. The goal of the talk is to present a classification of the behavior of the process according to its intensities of reproduction and disappearance of the elements in the sources of equal intensities, as well as to study properties of the walk. To achieve this goal it was required to develop the methods of spectral theory for convolution-type operators with multipoint perturbations. Asymptotic analysis of the resolvent of bounded symmetric operators with multipoint perturbations generating a BRW on the lattice was studied in [**?**]. In previous studies the authors were limited by finding the leading positive eigenvalue for supercritical case. In the present work we study the order of appearance of positive eigenvalues in the discrete spectrum of the operator describing the evolution of the average number of particles, depending on the intensity of sources and their configuration on the lattice. This study allows us to understand the basic difference in the behavior of the process on continuous and discrete structures. A special attention is paid to the case when the spectrum of the evolution operator has a single eigenvalue. The results are applied to the study of population structure of elements (in BRWs they are usually called particles) inside a propagating front.

Acknowledgements: The research was supported by the Russian Science Foundation (RSF) 14-21-00162.

References

[1] Yarovaya, E.B. (2013). *Branching Random Walks with Several Sources.* Mathematical Population Studies: An International Journal of Mathematical Demography, 20:1, 14-26.

Intrinsic branching structures within random walks on $\mathbb{Z}$ and their applications

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Keywords: Branching structure; random walk; birth-and-death process; random environment.

AMS: 60J80; 60K37

Abstract

In this talk, we firstly introduce our results on intrinsic branching structure within random walk on $\mathbb{Z}$. The possible jumps of the random walk are assumed to be non nearest but bounded. The branching structure was founded very useful to prove the LLN of Random Walk in Random Environment (RWRE) with *bounded jumps* and give its explicit velocity. Secondly, we consider RWRE with *unbounded jumps.* The environment is stationary and ergodic, uniformly elliptic and decays *polynomially* with speed $Dj^{-(3+\varepsilon_0)}$ for some small $\varepsilon_0 > 0$ and proper $D > 0$. We prove an LLN with positive speed under the condition that the annealed mean of the hitting time of the positive half lattice is finite. Finally, taking the advantage of the branching structure and the LLN for RWRE with unbounded jumps, we prove an LLN with explicit velocity for Birth-and-Death Process with Bounded Jumps in Random Environment. This talk is based on our recent works [**?**, **?**, **?**] enumerated below.

Acknowledgements: Joint work with Prof. W.M. Hong.

References

[1] W. M. Hong and H. M. Wang, Intrinsic branching structure within (L-1) random walk in random environment and its applications, Infin. Dimens. Anal. Quantum Probab. Relat. Top., Vol. 16, 1350006 [14 pages], 2013.

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Session IV

Statistical inference I

Point estimation in multivariate power series offspring distiributions

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Keywords: Two-type branching processes, bivariate power series distributions, trimmed likelihood

AMS: Primary 60J80; Secondary 62F10, 62F15, 62F35

Abstract

We consider the two-type discrete-time branching process. We suppose that the individual distributions of both particle types belong to the bivariate power series distribution family. We consider the parametric estimation of the offspring distribution parameters - firstly we study the behaviour of the maximum likelihood estimates under the presence of outlier data and then find the trimmed likelihood estimators, introducing the lower bounds of their breakdown points. Here we address also the issue of the Bayesian estimation in the power series offspring distribution family in conjunction with the robust approach. The estimation is carried out under two sampling schemes - when the entire family tree is observed and when data on the generation sizes over one trajectory is collected. Simulational and computation examples are carried out.

Acknowledgements: This is a joint work with Vessela Stoimenova. The research was partially supported by the National Fund for Scientific Research at the Ministry of Education and Science of Bulgaria, grant No DFNI-I02/17.

Robust estimation on controlled branching processes: minimum disparity approach.

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Keywords: Controlled branching processes, minimum disparity estimation, robustness.

AMS: 60J80, 62M05

Abstract

Controlled branching processes are appropriate probabilistic models for the description of population dynamics in which the number of individuals with reproductive capacity in each generation is controlled by a random control function. The probabilistic theory of these processes has been extensively developed, being an important issue to examine the inferential problems arising from them.

The aim of this work is to consider the minimum disparity estimators of the underlying offspring parameters. We assume that the offspring distribution belongs to a general parametric family. We obtain these estimators under three possible samples: given the entire family tree up to a certain generation, given the total number of individuals and progenitors in each generation, and given only the population sizes. We examine their asymptotic and robustness properties. For the supercritical case, we establish the strong consistency of the estimators proposed and the asymptotic normality of the minimum disparity estimator suitably normalized based on the observation of the entire family tree. Measures for robustness qualities against gross errors are also studied, such as the influence curve, α-influence curves, and the asymptotic breakdown point.

The provided results extend those given in [**?**] and are illustrated by simulated examples.

Acknowledgements: This work is coauthored by M. González and I. del Puerto. This research has been supported by the Ministerio de Economía y Competitividad (grant MTM2012-31235), the Gobierno de Extremadura (grant GR15105) and the FEDER.

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Session V

Population growth models in random environments

Some limit theorems for subcritical branching processes in random environment

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Keywords: Branching processes, survival probability, Yaglom limit theorem

AMS: 60J80

Abstract

Let Z_n be the number of individuals in a branching process evolving in the environment generated by i.i.d. probability distributions. Let X be the logarithm of the expected offspring size per individual given the environment. Assuming that $\mathbf{E}X < 0$ and, as $x \to \infty$ either

$$\mathbf{P}(X > x) \sim x^{-\beta} l(x)$$

or

$$p_X(x) \sim x^{-\beta-1} l(x) e^{-\rho x}$$

for some $\beta > 2$, a slowly varying function $l(x)$ and $\rho \in [0,1)$, we show that in both cases

$$\mathbf{P}(Z_n > 0) \sim C\mathbf{P}\left(\min_{1\le k\le n} S_k \ge 0\right)$$

where $S_0 = 0, S_n = X_1 + ... + X_n$ for $X_i, i = 1, ..., n$ being independent copies of X, prove Yaglom type conditional limit theorems for the process and describe the conditioned environments.

The proofs use, in particular, a fine study of a random walk (with negative drift and heavy tails) conditioned to stay positive until time n and to have (for the second case) a small positive value at time n, with $n \to \infty$.

Acknowledgements: The research was supported by the Program of the Russian Academy of Sciences "Mathematical problems of the contemporary control theory".

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On subcritical branching processes in random environment

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Keywords: Branching processes

AMS: 60J80

Abstract

We consider a subcritical branching process in random environment. The properties of these processes were intensively investigated for the last several years under survival condition and three different types of the asymptotical behavior of the trajectories of the processes were discovered. We investigate the properties of such processes from a different point of view. Namely, under the condition of attaining a high level x and the assumption that the moment generating function $\theta(t)$ of the increments of the associated random walk is equal to 1 for some $t = k > 0$.

We study the asymptotic behavior of the probability of attaining the level $x \to \infty$ and prove two laws of large numbers: 1) for the time of attaining the level x; 2) for the lifetime of the process under consideration. It turns out that the trend of trajectories of the process has, at the logarithmic scale an "up and down" form constituted by two segments of straight lines: the first segment starts at the point $(0,0)$ with the slope $\theta'(k) > 0$; the second segment starts at the point $\left((\theta'(k))^{-1} \ln x, \ln x\right)$ with the slope $\theta'(0) < 0$. We also prove a functional limit theorem which describes deviations of the trajectories of the process from the trend. The limit process is a standard Brownian motion.

Acknowledgements: The research was supported by the Program of RAS "Mathematical problems of modern control theory".

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Consequences of an incorrect model specification for population growth in random environments

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Keywords: stochastic differential equations, population growth, random environmenst, incorrect model specification, stationary distribution, extinction times

AMS: 60H10; 92D25

Abstract

We consider stochastic differential equations to model the growth of a population in a randomly varying environment. These growth models are usually based on classical deterministic models, such as the logistic or the Gompertz model, taken as approximate models of the "true" (usually unknown) growth rate. We study (see [**?**]) the effect of the gap between the approximate and the "true" model on model predictions, particularly on the asymptotic behaviour and on the mean and variance of the time to extinction of the population (expressions for the approximate models were obtained in [**?**],[**?**]).

Acknowledgements: Joint work with Clara Carlos. Escola Superior de Tecnologia do Barreiro, Instituto Politécnico de Setúbal, Rua Américo da Silva Marinho, 2890-001 Lavradio, Portugal (email: clara.carlos@estbarreiro.ips.pt).
Both researchers belong to the Centro de Investigação em Matemática e Aplicações, Universidade de Évora, a research centre supported by FCT (Fundação para a Ciência e a Tecnologia, Portugal).

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Session VI

Applications in epidemiology

Inference for emerging epidemics among a community of households

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Keywords: SIR epidemic, households, parameter estimation, branching process

AMS: 60J85, 62M05, 92D30

Abstract

This talk is concerned with estimation of the within-household infection rate λ_L for an SIR (susceptible → infective → recovered) epidemic among a population of households, from observation of the early, exponentially growing phase of an epidemic; cf. Ball et al. [**?**] and Fraser [**?**] . Specifically, it is assumed that an estimate of the exponential growth rate is available from general data on an emerging epidemic and more detailed, household-level data are available in a sample of households. Estimates of λ_L obtained using the final size distribution of single-household epidemics are usually biased owing to the emerging nature of the epidemic. A new method, which accounts correctly for the emerging nature of the epidemic, is developed by exploiting the asymptotic theory of a supercritical branching process that approximates the epidemic process and yields a strongly consistent estimator of λ_L as the population and sampled households both tend to infinity in an appropriate fashion. The methodology is illustrated by simulations which demonstrate that the new method is feasible for finite populations and numerical studies are used to explore how changes to the parameters governing the spread of an epidemic affect the bias of estimates based on single-household final size distributions.

Acknowledgements: The talk is based on joint work with Laurence Shaw (University of Nottingham), who was supported by an EPSRC Doctoral Training grant.

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Vaccination in epidemic modelling: branching processes *versus* stochastic epidemic models

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Keywords: Branching processes, SIR epidemic model, Sellke construction, vaccination policies

AMS: 60J80, 60J85, 60J05

Abstract

The derivation and analysis of optimal vaccination policies to control the spread of an infectious disease are matters of special relevance for health authorities. Recently, in [?], a Crump-Mode-Jagers branching process is used for describing the spread of an epidemic depending on the proportion of the population that is vaccinated. Stochastic monotonicity and continuity results for a wide class of functions (e.g., extinction time and total number of births over all time) defined on such a branching process are proved, leading to optimal vaccination schemes to control corresponding functions of epidemic outbreaks. This branching process provides an adequate model for the early stages of an epidemic in a closed homogeneously mixing population, provided that the number of susceptibles is sufficiently large (see [?]). However, when the population size is small, or the epidemic takes off, stochastic epidemic models which account for the depletion of susceptibles during an outbreak should be used. Thus, in this talk, we discuss similarities and differences between these two approaches for analyzing vaccination strategies in epidemic modelling.

Acknowledgements: This is a joint work with Frank Ball, Miguel González and Maroussia Slavtchova-Bojkova. This research has been supported by the Ministerio de Economía y Competividad of Spain (grant MTM2012-31235), the Gobierno de Extremadura (grant GR15105), the National Fund for Scientific Research at the Ministry of Education and Science of Bulgaria (grant DFNI-I02/17) and the FEDER.

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Session VII

Size/density/resource-dependent branching models

Structure dependent branching processes

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Keywords:

AMS:

Abstract

Consider a general branching process where, at any moment, the individual birth and death intensities as well as the splitting probability distributions can be influenced by the size and composition of the whole population. The special case of population size dependence with a threshold such that reproduction turns subcritical when the population becomes larger than the threshold, yield a natural framework for populations in a habitat with a finite carrying capacity. But also two-sex reproduction, where the reproductivity of females is determined by the availability of males, can be formulated for general processes with the help of structure dependence.

Escape from the boundary in Markov population processes

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Keywords: Markov population processes, boundary behaviour, branching process

AMS: 92D30, 60J27, 60B12

Abstract

Density dependent Markov population processes in large populations of size N were shown by Kurtz (1970, 1971) to be well approximated over finite time intervals by the solution of the differential equations that describe their average drift, and to exhibit stochastic fluctuations about this deterministic solution on the scale $\sqrt{N}$ that can be approximated by a diffusion process. Here, motivated by an example from evolutionary biology, we are concerned with describing how such a process leaves an absorbing boundary. Initially, one or more of the populations is of size much smaller than N, and the length of time taken until all populations have sizes comparable to N then becomes infinite as $N \to \infty$. Under suitable assumptions, we show that the early stages of development, up to the time when all populations have sizes at least N^b , for $b < 2/3$, can be accurately approximated in total variation by a Markov branching process. Thereafter, the process is well approximated by the deterministic solution starting from the original initial point, but with a random time delay. Analogous behaviour is also established for a Markov process approaching an equilibrium on a boundary, where one or more of the populations become extinct.

Acknowledgements: This is joint work with Andrew Barbour (Zurich), Haya Kaspi (Technion) and Kais Hamza (Monash).

Session VIII

Applications in biology

Branching within branching: a general model for host parasite evolution

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Keywords:

AMS:

Abstract

We consider a general host-parasite model for a cell population and proliferating parasites colonizing these cells. It can be viewed as an extension of a model studied by Bansaye [?]. Cells multiply in accordance with an ordinary Galton-Watson process. Morover, the multiplication mechanisms of cells and parasites obey some dependence structure since cells and parasites influence each other's reproduction in real biological settings. More precisely, the number of daughter cells determines the reproduction law of a parasite living in the mother cell and the way it shares its offspring to these daughter cells. We establish equivalent integral conditions for almost sure extinction of parasites by making use of a strong relation of this event to the behavior of parasite multiplication along a randomly picked cell line through the cell tree, the latter forming a branching process in random environment. We also provide results on the asymptotic behavior of the branching within branching process in the case when parasites survive. In particular, we look at the processes of contaminated cells and of parasites by using martingale theory. For both processes, we prove Kesten-Stigum type results and present equivalent integrability conditions for the martingale limit to be positive with positive probability. The case when these conditions are violated is also considered, and we determine exponential growth rates of the two processes in these cases. For the process of contaminated cells, we show that a proper (Heyde-Seneta) normalization exist, such that the limit is nondegenerate.

Acknowledgements: This is joint work with Sören Gröttrup.

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On multi-type decomposable branching processes in continuous time and time to escape extinction

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Keywords: Multi–type branching processes, probability of extinction

AMS: 60J80

Abstract

The main goal of this paper is to consider multi–type branching processes with continuous time to model the dynamics of different types of individuals, which due to a small reproductive ratio of individuals are fated to become extinct. However, mutations occurring during the reproduction process, may lead to the appearance of new types of individuals that may escape extinction. This is a typical real world situation with the emergence of scatters after local eradication of a certain type of cancer during the chemotherapy. Mathematically, we are deriving the numbers of mutations to the escape type and their moments.

Individual of the "mutation" type, which leads to the beginning of a lineage, that will never extinct is called "successful mutant". Using the results about the probability generating function of the single–type branching processes, an answer about the distribution of the waiting time to produce a "successful mutant" is obtained.

In general, our results aimed to prove the limits of expanding the methods used by Serra and Haccou (2007) for different schemes leading to mutation.

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Branching processes as models for biological populations with sexual reproduction

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Keywords: Two-sex branching processes. Mathematical modeling.

AMS: 60J80, 62M05

Abstract

In this work we develop appropriate mathematical models to describe the demographic dynamics of animal populations with sexual reproduction. More specifically we consider two branching processes, introduced in [1] and [2] with the motivation of modeling the evolution of salmonid populations.

In the first of these models we focus our attention on the numbers of couples that participate in an effective way in the reproduction process when the environment is non-predictable. On the other hand, in the second model we pay special attention to population whose individuals carry out different strategies for mating and reproduction depending on the number of females and males in the population. For both models we investigate some probabilistic and inferential features concerning the extinction of the population and the estimation of the offspring distribution and its main moments, respectively.

Acknowledgements: This is a joint work with Manuel Molina and Alfonso Ramos.

This research has been supported by the Ministerio de Economía y Competividad of Spain (grant MTM2012-31235), the Gobierno de Extremadura (grant GR15105) and the FEDER.

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Session IX

Special branching models

The weighted branching process

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Keywords: Branching processes

AMS: 60J80

Abstract

Weighted Branching Processes are Galton-Watson Processes, where each individual carries a weight inherited from his parent via a random transformation. Typical questions are about the n-th generation, like the sum Z_n of all weights or the largest weight.

These questions are closely connected to stochastic fixed point equations

$$X \overset{\mathcal{D}}{=} \sum_i A_i X_i + B$$

For example, the sequence $\frac{Z_n}{m^n}$ converges (under weak conditions) to a limit satisfying the above stochastic fixed point equation.

We will also point out the connection to random divide-and-conquer algorithm. This leads to new interesting processes. As an example we present Quicksort online, mathematically the almost sure convergence of the Quicksort process.

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A special family of Galton-Watson processes with explosion

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Keywords: Branching processes

AMS: 60J80

Abstract

The linear-fractional Galton-Watson processes is a well known case when many characteristics of a branching process can be computed explicitly. In [**?**] we extend the two-parameter linear-fractional family to a much richer four-parameter family of reproduction laws. The corresponding Galton-Watson processes also allow for explicit calculations, now with possibility for infinite mean, or even infinite number of offspring. We study the properties of this special family of branching processes, and show, in particular, that in some explosive cases the time to explosion can be approximated by the Gumbel distribution.

Acknowledgements: The research was supported by the Swedish Research Council grant 621-2010-5623.

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Revisiting limit results for controlled branching processes

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Keywords: branching process, extinction, limit theorem, immigration, emigration

AMS: 60J80

Abstract

The independence of individuals' reproduction is a fundamental assumption in classical branching processes. Since the 1960s, a number of authors have been studying models allowing different forms of population size dependence. Sevastyanov and Zubkov (1974) proposed a class of branching processes in which the number of reproductive individuals in one generation decreases or increases depending on the size of the previous generation through a set of control functions. The offspring distribution is not affected by the control and remains independent of population size. These processes are known as controlled or φ-branching processes (CBP). Yanev (1975) (no relation to the author) extended the class of CBP by introducing random control functions. This survey aims at presenting various limit results for some single-type controlled branching processes within a unified setting. Special attention is paid to migration processes with different regimes of immigration and emigration, controlled processes with continuous state space, and processes with reproduction dependent immigration. There is no doubt that CBPs have great potential as modeling tools. In my opinion, they deserve more attention from the branching process community.

Acknowledgements: The research was partially supported by the National Fund for Scientific Research at the Ministry of Education and Science of Bulgaria, grant No DFNI-102/17.

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The standard Galton-Watson branching process with a reflecting barrier

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Keywords: standard Galton-Watson branching process, time to extinction, reflecting barrier

AMS: 60J80

Abstract

The 20th century has been called the century of physics. It has been said that the 21st century will be the century of biology. It will be to our advantage to have biologists see branching processes as useful models. Unfortunately this is often not the case.

One of the main objections to the standard process is that survival requires that the population size may increase without bound. I propose an additional requirement to be added to the standard process. If the population size exceeds k individuals in a generation, only j members of this generation will have the capacity to produce the members of the next generation, where j is less than or equal to k.

We shall consider an effective method to calculate the "time to extinction" in this new process and then compare this value to "extinction time" in the standard process without this reflecting barrier.

Session X

Age-dependent branching models

Sevastyanov age-dependent branching processes with non-homogeneous Poisson immigration

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Keywords: Branching processes, Non-homogeneous immigration, Limit theorems

AMS: 60J80

Abstract

The first model of branching processes with immigration was introduced by Sevastyanov (TPA, 1957) in the continuous-time Markov case with a time-homogeneous Poisson immigration component. He obtained three limit theorems: a stationary distribution in the subcritical case, $\Gamma-$ distribution (using time-linear normalization) in the critical case and L_2 convergence to a positive r.v. (using a time-exponent normalization) in the supercritical case. These results were extended by many authors to the discrete time case and to the Bellman-Harris processes.

Sevastyanov (TPA, 1964) proposed a class of age-dependent branching processes in which the individual life span τ and the individual offspring ν were allowed to be dependent (see his monograph, 1971). In the age-dependent model of Bellman and Harris (1948) the random variables τ and ν are assumed to be independent.

In the present paper, we consider Sevastyanov age-dependent branching processes allowing an immigration component in the case when the moments of immigration form a non-homogeneous Poisson process with intensity $r(t)$. The resultant processes are non Markov and time-inhomogeneous. The asymptotic behavior of its moments and probability of non-extinction are investigated depending on the asymptotic behavior of $r(t)$. Corresponding limit theorems are also established using various normalizations adapted to the intensities $r(t)$. In particular, we obtained limiting distributions similar to the classical ones of Yaglom (1947) and Sevastyanov (1957), and we also discovered new phenomena due to the non-homogeneity. For example, we show that the processes satisfy LLN and CLT in all cases: subcritical, critical and supercritical. Some of the results in the critical case have been published in Mitov and Yanev (2013).

Acknowledgements: This is a joint work with Kosto V. Mitov from Faculty of Aviation, NMU, Pleven, Bulgaria and Ollivier Hyrien from Department of Biostatistics and Computational Biology, University of Rochester, New York, USA. The research was partially supported by the National Fund for Scientific Research at the Ministry of Education and Science of Bulgaria, grant No. DFNI-I02/17.

Classes of equivalence and identifiability of age-dependent branching processes

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Keywords: Branching processes, non-identifiability.

AMS: 60J80

Abstract

Age-dependent branching processes are increasingly used in analyses of biological data. Despite being central to most statistical procedures, the identifiability of these models has not been studied. We partition a family of age-dependent branching processes into equivalence classes in which the distribution of the population size remains identical and apply this result to study identifiability of the offspring and lifespan of families of branching processes. For example, we identify classes of Markov processes that are not identifiable. We show that age-dependent processes with (non-exponential) gamma-distributed lifespan are identifiable, and that Smith-Martin processes are not always identifiable.

Acknowledgements: This work was done in collaboration with Rui Chen and supported by grants from the National Institutes of Health.

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Two types critical Bellman-Harris processes with long-lived and short-lived particles. Renewal theorems and moments increments

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Keywords: moments and moments increments for two types critical Bellman-Harris branching process; local two-dimensional renewal theorems; regular varying functions

AMS: 60J80; 60E10; 60J85; 60K05

Abstract

Consider a critical Bellman-Harris branching process $\mathbf{Z}(t) = (Z_1(t), Z_2(t))$ with two types of particles. A particle of type $i \in \{1,2\}$ has the life–length distribution $G_i(t)$, and, at the end of its life, produces ξ_{i1} particles of the first type and ξ_{i2} particles of the second type. Denote $m_{ij} := \mathbf{E}\xi_{ij}$, $b^i_{jk} := \mathbf{E}\xi_{ij}\xi_{ik}$, $\mathbf{M}(t) := (m_{ij}G_i(t))_{i,j=1,2}$, $\mathbf{M} = \mathbf{M}(\infty)$ for $i,j,k = 1,2$, $\delta_{ij} = 1$, if $i = j$, and $\delta_{ij} = 0$ otherwise, $\mathbf{E}\{Z_j(t)|\mathbf{Z}(0) = (\delta_{i1}, \delta_{i2})\} = P_{ij}(t)$ for $i,j = 1,2$. Assume that $\mathbf{Z}(t)$ is an irreducible, nonperiodic, critical process and $b^i_{jk} < \infty$. This means, in particular, that there exists $n_0 \geq 1$ such that $\mathbf{M}^{n_0} > \mathbf{0}$, the Perron root of $\mathbf{M}$ is equal to 1. Define fundamental for research of $\mathbf{Z}(t)$ renewal matrix $\mathbf{U}(t) = \sum_{k=0}^{\infty} \mathbf{M}^{*k}(t)$.

Let $1 - G_1(t) = o(t^{-2})$, $1 - G_2(t) = \ell(t)t^{-\beta}$, were $t \to \infty$ and $\ell(t)$ is the slowly varying at infinity function, and for simplicity we suppose that $\beta \in (0,1)$ (case $\beta = 1$ is omitted). Under these conditions the renewal theorem $\mathbf{U}(t) \sim t^{\beta}\ell^{-1}(t)\mathbf{D}$, as $t \to \infty$, is true for some matrix $\mathbf{D}$. It leads to (see [**?**]) $P_{i1}(t) \sim D_{i1}t^{\beta-1}\ell^{-1}(t)$ and $P_{i2}(t) \sim D_{i2}$, as $t \to \infty$, for some constants D_{ij}, $i,j = 1,2$.

We offer the sufficient conditions under which the main part of the $\mathbf{U}(t)$, referred to as $\mathbf{U}_c(t)$, will be twice differentiable and $\mathbf{U}''_c(t) \sim \beta(\beta-1)t^{\beta-2}\ell^{-1}(t)\mathbf{D}$. It leads to $P'_{i1}(t) \sim D_{i1}(\beta-1)t^{\beta-2}\ell^{-1}(t)$ and $P'_{i2}(t) = o(t^{-1})$.

Acknowledgements: The research is supported by the project of Mathematical Department RAS "Modern methods approximability models, algorithms and theories".

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Crump-Mode-Jagers branching process: a numerical approach

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Keywords: General Branching Process, Leslie matrix projection, demographics, numerical method, renewal equation

AMS: 60J80

Abstract

The theory of Crump-Mode-Jagers branching processes presents the expected future population as a solution of a renewal equation (see Jagers [?]). As explained by the Renewal Theory, the theoretical solution of this equation is a convolution of two functions, one of which is called renewal function (see Mitov and Omey [?]). However in practice it is very time consuming to calculate the renewal function as a sum of convolutions with increasing order. This paper presents a General Branching Process model (GBP) relevant for the special case of human population and describes a numerical method for solving the corresponding renewal equation. The presented numerical method involves only simple matrix multiplications which results in a very fast calculation speed. Finally it is shown that the Leslie matrix projection, widely used in demographics, is actually a special case of the presented numerical solution and thus shows that this standard demographic method is actually related to the theory of Crump-Mode-Jagers branching process.

Acknowledgements: The research was supported by the National Fund for Scientific Research at the Ministry of Education and Science of Bulgaria, grant No DFNI I02/17.

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Session XI

Branching processes in varying environments

On critical branching processes with immigration in varying environment

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Keywords: Branching process with immigration, varying environment, criticality, functional limit theorem, inhomogeneous stochastic differential equation.

AMS: 60J80, 60F17

Abstract

Let $\{\xi_{k,j},\, \varepsilon_k \,:\, k,\, j \,\in\, \mathbb{N}\}$ be independent, non-negative, integer-valued random variables such that $\{\xi_{k,j} : j \in \mathbb{N}\}$ are identically distributed for each $k \in \mathbb{N}$. Define

$$X_k = \sum_{j=1}^{X_{k-1}} \xi_{k,j} + \varepsilon_k \quad \text{for} \quad k \in \mathbb{N}, \qquad X_0 = 0.$$

Assume that, for all $k \in \mathbb{N}$, $m_k := \mathsf{E}(\xi_{k,1}), \lambda_k := \mathsf{E}(\varepsilon_k), \sigma_k^2 := \mathsf{Var}(\xi_{k,1}), b_k^2 := \mathsf{Var}(\varepsilon_k)$ are finite. The sequence $(X_k)_{k\in\mathbb{Z}_+}$ is called a branching process with immigration in varying environment (BPIVE). Such processes have been investigated by several authors, mainly in the sub- or supercritical case, see, e.g, Cohn and Jagers (1994). A BPIVE is called nearly critical if $m_k = 1 + \alpha k^{-1} + \delta_k$ for some $\alpha \in \mathbb{R}$, where $\sum_{k=1}^{\infty} |\delta_k| < \infty$. The parameter α is called the index of criticality. Then, if $\lambda := \lim_{k\to\infty} \lambda_k$, the following asymptotic behavior holds for the expectation of the process: (i) $n^{-1}E(X_n) \to \lambda(1-\alpha)^{-1}$ if $\alpha < 1$; (ii) $(n \ln n)^{-1}E(X_n) \to \lambda$ if $\alpha = 1$; (iii) $n^{-\alpha}E(X_n) \to \mu$ if $\alpha > 1$, where $\mu \in \mathbb{R}_+$ is a constant, as $n \to \infty$.

In the talk, the fluctuation limit theorem $n^{-1/2}\left(\mathcal{X}^n - \mathsf{E}(\mathcal{X}^n)\right) \xrightarrow{\mathcal{L}} \widetilde{\mathcal{X}}$ as $n \to \infty$ is proved for the random step process $\mathcal{X}_t^n := X_{\lfloor nt \rfloor}$, $t \in \mathbb{R}_+, n \in \mathbb{N}$, under, among others, the assumptions $\alpha < 1/2$ and $k\sigma_k^2 \to \sigma^2$. Here, $(\widetilde{\mathcal{X}}_t)_{t\in\mathbb{R}_+}$ satisfies the inhomogeneous SDE

$$\mathrm{d}\widetilde{\mathcal{X}}_t = \alpha t^{-1} \widetilde{\mathcal{X}}_t \,\mathrm{d}t + \mathrm{d}\mathcal{M}_t, \qquad t > 0,$$

where $(\mathcal{M}_t)_{t\in\mathbb{R}_+}$ is a Wiener process with variance $\sigma_{\mathcal{M}}^2 := \sigma^2\lambda(1-\alpha)^{-1} + b^2$, with initial condition $\widetilde{\mathcal{X}}_0 = 0$. (Note that $b^2 := \lim_{k\to\infty} b_k^2$.) Similar result can be found in Ispány, Pap and van Zuijlen (2005). As a generalization of the functional limit theorem in Sriram (1994), under the assumptions $\alpha < 1$ and $\sigma_k^2 \to \sigma^2$ we have $n^{-1}\mathcal{X}^n \xrightarrow{\mathcal{L}} \mathcal{X}$ as $n \to \infty$, where $(\mathcal{X}_t)_{t\in\mathbb{R}_+}$ satisfies the inhomogeneous SDE

$$\mathrm{d}\mathcal{X}_t = (\lambda + \alpha t^{-1}\mathcal{X}_t)\,\mathrm{d}t + \sigma\sqrt{\mathcal{X}_t}\mathrm{d}\mathcal{W}_t, \qquad t > 0,$$

where $(\mathcal{W}_t)_{t\in\mathbb{R}_+}$ is a standard Wiener process, with initial condition $\mathcal{X}_0 = 0$.

A branching process with immigration in varying environments

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Keywords: Branching processes, Varying environments, Limit theorems

AMS: 60J80

Abstract

A branching process is said to be in varying environments if the offspring distribution of the particles changes with time. Most of the classical branching processes have been studied also in varying environments.

In the present paper we are interested in Bienaymé-Galton-Watson branching processes with varying offspring variance and an immigration component, concerning the critical case.

It is well known that the limiting behavior of critical branching processes essentially depends on the finiteness or infiniteness of the offspring variance. So, it is interesting what is the limiting behavior of the process when the offspring mean equals unit, but the variance increases to infinity. Second, the immigration component changes the behavior of any branching process, in dependence of the number of immigrants. By this reason we consider, two different regimes of immigration: finite and infinite mean number of immigrants in each generation. Let us mention also that both varying environment and the immigration make the BGW branching processes more flexible and enlarge the possible applications of these processes for modeling in biology, cell proliferation, finance. We derive asymptotic formulas for the moments and for the probability for non-extinction. Limit theorems are also proved.

Acknowledgements: This is a joint work with Edward Omey from Faculty of Economics and Business, KU Leuven, Brussels, Belgium. The research was partially supported by the National Fund for Scientific Research at the Ministry of Education and Science of Bulgaria, grant No. DFNI-I02/17.

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Session XII

Statistical inference II

Statistical inference for 2-type doubly symmetric critical irreducible CBI processes

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Keywords: continuous state and continuous time branching process with immigration (CBI process), conditional least squares estimator (CLS estimator)

AMS: 60J80, 62F12

Abstract

We study asymptotic behavior of conditional least squares estimators for certain critical irreducible continuous state and continuous time branching processes $(\mathbf{X}_t)_{t\in[0,\infty)}$ with immigration based on discrete time (low frequency) observations. We suppose that the process is doubly symmetric in the sense that the transformation rates of one type to the same type is $\gamma \in \mathbf{R}$ and one type to the other type is $\kappa \in [0,\infty)$. The model is called subcritical, critical or supercritical if $s < 0$, $s = 0$ or $s > 0$, respectively, where $s := \gamma + \kappa$ denotes the criticality parameter. For each $n \in \{1, 2, \ldots\}$, we derive the CLS estimators of the parameters s, γ and κ based on the observations $(\mathbf{X}_k)_{k\in\{1,\ldots,n\}}$. In the irreducible and critical case, i.e, when $\kappa > 0$ and $s = \gamma + \kappa = 0$, under some moment conditions, we describe the asymptotic behavior of these CLS estimators as $n \to \infty$.

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Statistical inference for critical 2-type Galton–Watson processes with immigration

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Keywords: multitype Galton–Watson process with immigration, conditional least squares estimation

AMS: 60J80, 62F12

Abstract

The well known Galton–Watson process can be generalized the following way; suppose the population consists of multiple types of individuals and allow the offsprings to have a different type than their parents. Denote the number of types by d. To describe this process we have to assign a d-dimensional offspring distribution to each of the types. The offspring mean matrix is a matrix whose columns consist of the expectation of these distributions.

In the single-type case we distinguish between subcritical, critical and supercritical processes based on the relation of the offspring mean to 1. For multi-type Galton–Watson processes we make the same distinction based on the spectral radius of the offspring mean matrix. Immigration can be introduced to the model exactly as in the single-type case, by adding i.i.d. random vectors representing the number of immigrants in each generation.

In this talk we examine the asymptotic properties of the conditional least squares estimate of the offspring mean matrix for critical 2-type Galton-Watson processes with immigration. We prove that under some conditions the estimation is weakly consistent, but the limiting distribution is tipically not normal. Then we discuss the prospect of generalizing the results for $d > 2$ types.

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Unified robust empirical likelihood confidence regions for parameters of branching processes with immigration

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Keywords: Empirical Likelihood, joint inference, Hellinger distance, Legendre-Fenchel transform, Ancestral Inference

AMS: 60J80

Abstract

Let $\{Z_n : n \geq 1\}$ denote a single-type branching process with immigration initiated by a single ancestor. The problem of developing a confidence region for (m, σ^2), the offspring mean and variance, with possibly unobserved immigration and without the prior knowledge of the range of values of m has been long open. In this presentation, we describe an empirical likelihood based approach for the construction of a joint confidence region and show that -2 times the logarithm of the joint empirical likelihood ratio converges in distribution to a chi-squared random variable with 2 degrees of freedom (χ^2_2) if $m \neq 1$ while it converges to a functional of Feller's diffusion if $m = 1$. We then describe an alternative approach, involving an observable stopping time T and show that the confidence regions indexed by T can be calibrated using the χ^2_2 distribution for all values of m provided the branching process with immigration is not a null-recurrent Markov chain. Additionally, we establish that, under the null-recurrent case the empirical likelihood ratio converges in probability to zero. Extensions to joint estimation of the parameters of the immigration distribution, robust non-parametric inference, and ancestoral inference will also be provided. (Parts of this presentation are based on a joint work with Pin Ren).

ABC methodology for two-sex branching models with mutations

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Keywords: Two-Sex Branching processes, mutations, ABC methodology

AMS: 60J80, 60J85

Abstract

The genetic causes of infertility in males or the history of paternal lineages are some relevant problems directly related to mutations in Y-linked genes. The interest of how these genes and their mutations evolve in a population led us to introduce a new two-sex branching process with blind-mating structure (see [**?**]). The present work focuses on the development of Bayesian inference for this model. The considered sample is given by the total number of females and males of each genotype (original allele and its mutations) up to some generation. Using the Approximate Bayesian Computation (ABC) methodology, we approximate the posterior distributions of the main parameters of this model. The accuracy of the procedure is illustrated by way of simulated examples covering the different interactions between the parameters.

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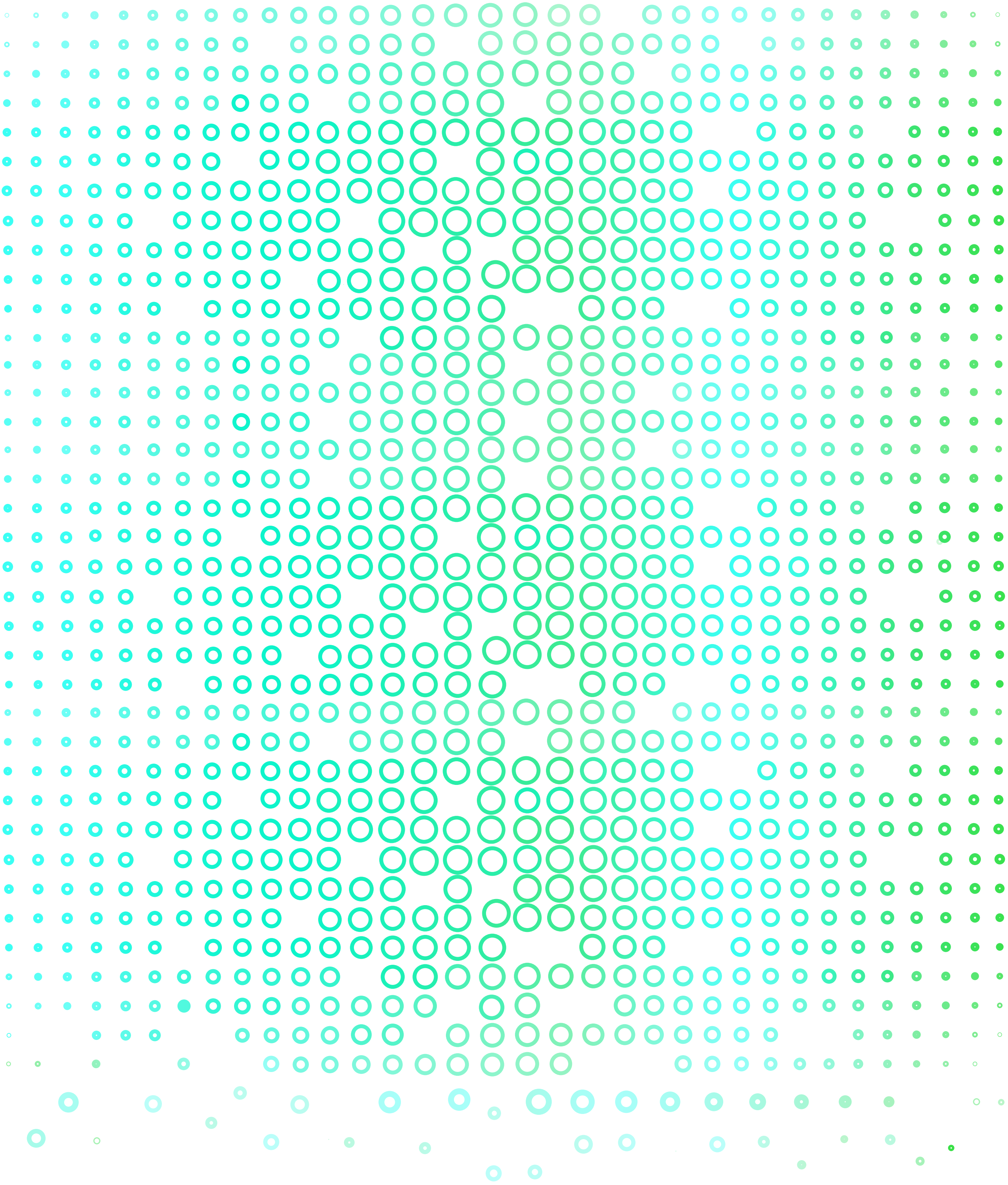

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