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Workshop on Branching Processes and Applications

Conference Proceedings and Abstracts

Edited by E. Stoimenova and M. Slavtchova-Bojkova

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KEYNOTE INVITED SPEAKERS
Extinction probability of some recessive alleles of X-linked genes in the context of two-sex branching processes

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Some defective alleles of certain genes can cause severe diseases or serious disorders in the organisms that carry them. Some of these genes, as could be the responsible for hemophilia, are linked to X chromosome. If the alleles causing the disorder are dominant, all the carriers are affected and most of them do not reach breeding age so they are rarely detected in a population. However, recessive pernicious alleles can survive since they only affect to carrier males and homozygous carrier females (the last ones must be daughters of a carrier male, so they rarely exist). Hence, heterozygous carrier females are not affected but can pass the allele onto offspring. In this work, we study a multitype two-sex branching process for describing the evolution of the number of individuals carrying the alleles, $R$ and $r$, of a gene linked to X chromosome. The $R$ allele is considered dominant and the $r$ allele is supposed to be recessive and defective, responsible of a disorder. In this model we study the fate of the recessive allele in the population, i.e. under which conditions it eventually disappears. We also investigate conditions for the fixation of the dominant allele and the extinction of the population. Finally, conditions for the coexistence of both alleles are conjectured.

Keywords: two-sex branching processes, extinction probability, X-linked genes.

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Statistical model of Microenvironment-Dependent Carcinogenesis: estimation and applications

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One important aspect of carcinogenesis is the time to emergence of the first cancerous tumor after exposure to a carcinogen, also known as tumor latency time. The extreme-value theory (EVT) approach is particularly suitable for modeling of tumor latency time, and was first proposed by M.C. Pike in 1966. We have formulated in the past a statistical parametric model that extends the EVT approach, and have derived its survivor function. Our model was the first attempt to account for the interdependence of initiated cells while they are becoming cancerous within the microenvironment of the emerging tumor. Here we fit our model to experimental, observational, and simulated data of small and larger size, and compare several estimation procedures, including ones based on the maximum-likelihood (ML), the method of moments (MOM), and simulated annealing. Also, our model is compared with other EVT-based models.
Perpetual Integral Functionals of Brownian Motion and Blowup of Semilinear Systems

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We investigate existence of nonglobal positive solutions of a system of nonlinear heat equations perturbed by a multiplicative Gaussian noise, where the noise factor is a Wiener process $W(t)$. We obtain a lower bound for the probability of explosion in finite time of such solutions, which is given in terms of a perpetual integral functional of $W(t)$.

Bayesian estimation on controlled branching processes via disparities: robust estimators for the offspring parameters

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Branching processes are one of the most remarkable models for the description of the dynamic of populations. Within the class of these processes, our work is focused on the controlled branching process. This stochastic model is a generalization of the classical process that presents the novelty of incorporating a random control function which determines the number of progenitors in each generation.
The strong relation between the value of the parameters of this process and its behaviour has led the recent research in this field to focus on the inferential theory. The aim of this work is to develop a methodology which provides robust estimators against outliers for the offspring parameters in a Bayesian outlook. This work presents pioneer results due to the fact that robust procedures against outliers have been barely studied in this field and no result has been obtained in a Bayesian context. Assuming that the offspring distribution belongs to a parametric family, we consider the sample given by the whole family tree and we make use of disparity measures. The proposed procedure consists of replacing the log likelihood with an appropriately scaled disparity in the expression of the posterior density function. The resulting function is called D-posterior density function and Bayesian point estimators for the offspring parameters are obtained from it. The asymptotic properties and robustness measures of these estimators are analysed. Finally, the accuracy of the method is illustrated by the way of simulated examples developed with the statistical software R.

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New research lines in controlled branching processes

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Controlled branching processes (CBPs) are a class of discrete-time stochastic growth population models characterized by the existence of a
random control mechanism for determining in each generation (nonoverlapping generations) how many progenitors participate in the subsequent reproduction process. Once the number of progenitors is known, each one reproduces independently of the others according to the same probability law. The novelty of adding to the branching notion a mechanism that fixes the number of progenitors in each generation allows to model a great variety of random migratory movements. It is the aim of this work to extend this kind of model to new practical situations. CBPs can be also used to model the evolution of the number of individuals of a population in which the rate of growth not only depends on the current population size but also on the distance between this size and the carrying capacity of the environment, that is the maximum population size that the environment can admit in view of its resources. Another possible extension we consider is to introduce the continuous time, that is, to define branching processes allowing random migration according to some point process and by considering the lifetime of each individual is random. A first approach to deal with these new situations will be presented.

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Bernstein-Gamma functions and their applications in probability theory

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Motivated by questions in spectral theory we introduce a general class of functions (Bernstein-Gamma functions) that naturally extend the Gamma function via its recurrent equation wherein the multiplier is taken
to be any Bernstein function. We analyze in detail the analytic properties of these functions and derive all the essential quantities that characterize them as meromorphic functions. Most notably we develop a general asymptotic representation for the Bernstein-Gamma functions which is reminiscent of the celebrated Stirling asymptotic for the Gamma function. Using this information we solve more general recurrent equations which are also satisfied by the moment transform of the exponential functionals of Levy processes. Then we proceed to obtain various new and general results for the law of these random variables. For example, as a by-product, we recover a number of results on the density of the supremum of a stable Levy process.

**Family trees for decomposable branching processes**

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A critical Galton-Watson branching process \((Z(1; n), ..., Z(N; n))\) with \(N\) types of particles labelled \(1, 2, \ldots, N\) is considered in which a type \(i\) parent may produce individuals of types \(i, i+1, \ldots, N\) only. This model may be viewed as a stochastic model for the sizes of a geographically structured population occupying \(N\) islands, the location of a particle being considered as its type. The newborn particles of island \(i < N\) either stay at the same island or migrate, just after their birth to the islands \(i+1, i+2, \ldots, N\). Particles of island \(N\) do not migrate. Let \(Z(i; m, n)\) be the number of type \(i\) particles existing in the process at moment \(m < n\) and having nonempty number of descendants at moment \(n\). Assuming that the initial process is critical we study the structure of the process \((Z(i; m, n), i = 1, 2, \ldots N)\) given that \(Z(1; n) + \ldots + Z(N; n) > 0\).
Monotone empirical Bayes estimators for the reproduction parameter of Borel-Tanner distributions

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The Borel-Tanner (BT) distribution arises in stochastic models including branching processes and queuing theory. Originally it was derived as the distribution of the number of customers served in a busy period of a single server queuing process, assuming Poisson arrivals and constant service time. Later it appeared in the theory of branching processes. If the number of offspring of an individual is Poisson distributed with offspring mean $0 < m < 1$, then the total progeny of a Galton-Watson branching process is a BT random variable. More recently, the distribution has been used to model a variety of real-world phenomena including coalescence models, highway traffic flows, propagation of internet viruses, cascading failures of energy systems, and herd size in finance modeling.

Our interest in estimating the parameter $m$ stems from its role as the reproduction number of an epidemic infection modeled by a branching process. We construct a monotone version of an empirical Bayes estimator for the parameter $m$ of the BT distribution. Properties of the estimator's regret risk are illustrated through simulations. Some open questions will be discussed.
SHORT COMMUNICATIONS
A punctuated stochastic model of adaptation

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KB was supported by the Knut and Alice Wallenberg Foundation.

Abstract
Contemporary stochastic evolution models commonly assume gradual change for a phenotype. However the fossil record and biological theory suggests that development should be rather treated as undergoing punctuated change. In this work we present weak convergence results on for such an evolutionary model with jumps and illustrate it with simulations.

1 Introduction

Continuous trait evolution is currently modelled by stochastic differential equations (SDE) mainly in the framework of the Ornstein–Uhlenbeck (OU) process

\[ dX(t) = -\alpha(X(t) - \theta(t))dt + \sigma dB_t, \]

where \( \theta(t) \) can be piecewise linear. These models take into account the phylogenetic structure between the contemporary species. The trait follows the SDE along each branch of the tree (with possibly branch specific parameters). At speciation times this process divides into two independently evolving processes. However the fossil record indicates that change is not as gradual as Eq. (1) suggests. Rather that jumps occur and that the framework of Lévy processes is more appropriate.

The phylogeny is modelled by a pure birth process with speciation rate \( \lambda \) and conditioned on \( n \) contemporary tips. The key property of this branching process is that the time between speciation events \( k \) and \( k+1 \) is exponential with parameter \( k \). This is immediate from the memoryless property of the process and the distribution of the minimum of exponential random variables.

Regarding the phenotype I recently considered the Yule–Ornstein–Uhlenbeck with jumps (YOUj) model [3]. The trait follows an OU process but just after a branching point on the phylogeny, with a probability \( p_n \), independently on each daughter lineage, a jump can occur. The jump is assumed to be normally distributed with mean 0 and variance \( \sigma^2 c, n < \infty \). Just after a speciation event at time \( t \), independently for each daughter lineage, the trait value \( X(t) \) will be
\[ X^+(t) = (1 - Z)X(t^-) + Z(X(t^-) + Y). \] (2)

In the above Eq. (2) \( X(t^-/+) \) means the value of \( X(t) \) respectively just before and after time \( t \), \( Z \) is a binary random variable with probability \( p_n \) of being 1 (i.e. jump occurs) and \( Y \sim \mathcal{N}(0, \sigma^2_{c,n}) \).

## 2 Weak convergence results

Branching Ornstein–Uhlenbeck processes have been previously studied [e.g. 1, 4]. It was found that they have three asymptotic regimes depending on the relationship between the adaptation rate \( \alpha \) and the branching rate \( \lambda \). If \( \alpha \geq \lambda / 2 \) then with appropriate scaling the contemporary sample average converges weakly to a normal distribution and behaves essentially as the mean of an i.i.d. sample. However if \( 0 \leq \alpha < \lambda / 2 \) then the process has “long memory” [“local correlations dominate over the OU’s ergodic properties”, cf. 1]. Denote \( \kappa_n = 2p_n\sigma^2_{c,n}/(2p_n\sigma^2_{c,n} + \sigma^2_a) \), \( \gamma_n := (\sigma^2_a + 2p_n\sigma^2_{c,n})/2\alpha \), \( \delta^*_n := (X_0 - \theta)/\sqrt{\gamma_n} \) and without loss of generality we take \( \lambda = 1 \) in what follows.

**Theorem 2.1** Let \( \bar{Y}_n = (\bar{X}_n - \theta)/\sqrt{\gamma_n} \) be the normalized sample mean of the \( \text{YOU}_j \) process with \( \bar{Y}_0 = (X_0 - \theta)/\sqrt{\gamma_0} \). If \( \sigma^2_{c,n}\kappa_n \rightarrow 0 \) then, depending on \( \alpha \), the process \( \bar{Y}_n \) has one of the following asymptotic (with \( n \)) types of behaviour.

- **(I)** If \( 0.5 < \alpha \) then \( \sqrt{(n/\ln n)} \bar{Y}_n \) is asymptotically normally distributed with mean 0 and variance \( (2\alpha + 1)/(2\alpha - 1) \).

- **(II)** If \( 0.5 = \alpha \) then \( \sqrt{(n/\ln n)} \bar{Y}_n \) is asymptotically normally distributed with mean 0 and variance 2.

- **(III)** If \( 0 < \alpha < 0.5 \) then we can allow \( \kappa_n \) to take any value in \([0, 1]\) and \( n^\alpha \bar{Y}_n \) converges almost surely and in \( L^2 \) to a random variable \( Y_{\alpha, \gamma_\infty, \kappa_\infty} \) with first two moments

\[
\begin{align*}
E[Y_{\alpha, \gamma_\infty, \kappa_\infty}] &= \gamma_\infty \Gamma(1 + \alpha), \\
E[Y^2_{\alpha, \gamma_\infty, \kappa_\infty}] &= (\gamma^2_\infty + (1 - \kappa_\infty)\frac{4\sigma_a}{1 - 2\alpha}) \Gamma(1 + 2\alpha).
\end{align*}
\]

The proof of the Central Limit Theorem 2.1, is based on a series of asymptotics, Lemma 2.1. Let \( \mathcal{Y}^*_n \) denote the \( \sigma \)-algebra that contains information on the Yule tree and jump pattern.
Lemma 2.1

$$\text{Var} \left[ E \left[ e^{-2\alpha \tau^{(n)}} | \mathcal{Y}_n^* \right] \right] = \begin{cases} O(n^{-4\alpha}) & 0 < \alpha < 0.75, \\ O(n^{-4\alpha} \ln n) & \alpha = 0.75, \\ O(n^{-3}) & 0.75 < \alpha, \end{cases}$$ (3)

where $\tau^{(n)}$ is the time to coalescent of a randomly sampled pair of tip species [4].

In what follows $C$ is a constant not scaling to 0 if $p \to 0$. Let $J_i$ be a binary random variable indicating if a jump ($p$ probability of jump) took place on the $i$–th (counting from the origin of the tree) speciation event of a randomly sampled lineage. For a fixed jump probability $p$ we have

$$\text{Var} \left[ E \left[ \sum_{i=2}^{\Upsilon^{(n)}+1} J_i e^{-2\alpha (\tau_{i+1} + \ldots + \tau_k)} | \mathcal{Y}_n^* \right] \right] \sim pC \begin{cases} n^{-4\alpha} & 0 < \alpha < 0.25, \\ n^{-1} \ln n & \alpha = 0.25, \\ n^{-1} & 0.25 < \alpha, \end{cases}$$ (4)

where $\Upsilon^{(n)}$ is the number of speciation events on a random lineage, $t_{k+1}$ is the time between speciation events $k$ and $k + 1$ on a randomly chosen lineage,

$$\text{Var} \left[ E \left[ \sum_{i=2}^{\Upsilon^{(n)}+1} J_i e^{-2\alpha (\tau_{i+1} + \ldots + \tau_k)} | \mathcal{Y}_n^* \right] \right] \sim pC \begin{cases} n^{-4\alpha} & 0 < \alpha < 0.5, \\ n^{-2} \ln n & \alpha = 0.5, \\ n^{-2} & 0.5 < \alpha, \end{cases}$$ (5)

where $\Upsilon^{(n)}$ is the number of common speciation events for a random pair of tips bar the splitting them event [2].

References


Figure 1: Left: $\alpha = 0.25$ centre: $\alpha = 0.5$ and right: $\alpha = 1$. Top row: examples of simulated YOUj process trajectories, bottom row: histograms of sample averages scaled to theoretical unit variance. In all three cases $p = 0.5, \sigma_c^2 = 1, \sigma_d^2 = 1, X_0 = \theta = 0$. The phylogenetic trees are pure birth trees with $\lambda = 1$ conditioned on number of tips, $n = 30$ for the trajectory plots and $n = 200$ for the histograms. The histograms are based on 10000 simulated trees. The gray curve painted on the histograms is the standard normal distribution. The simulations are done using TreeSim [7] and mvSLOUCH [5] R packages.


Gamma distribution, random impulses in differential equations and p-moment exponential stability

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Abstract: Gamma distributed random moments of impulses in differential equation is studied. Some properties of the solutions being stochastic processes are studied and applied to be obtained sufficient conditions for p-moment exponential stability of the solutions.

Introduction

The modeling of real world phenomena in which the state of the investigated process changes instantaneously at uncertain moments lead to the application of an apparatus combining differential equations and probability theory. In the case the behavior of the studied variables are deterministically changed between two consecutive instantaneous changes at uncertain moments the adequate model is impulsive differential equations with random impulses. This type of equations is totally different than stochastic differential equation (see, for example, [3], [4]). Some considerations concerning deterministic differential equations with random impulses have been considered, for example, in [2], but there are some inaccuracies concerning properties of deterministic variables and random variables.

Random impulses in differential equations

Initially we will recall impulsive differential equations (IDE) with fixed points of impulses

\[ x'(t) = f(t, x(t)) \quad \text{for} \quad t \in (T_k, T_{k+1}], \quad k = 0, 1, 2, \ldots, \]
\[ x(T_k + 0) = I_k(x(T_k - 0)), \quad \text{for} \quad k = 1, 2, \ldots, \]
\[ x(T_0) = x_0, \]

(1)
where \( x, x_0 \in \mathbb{R}^n, f : [0, \infty) \times \mathbb{R}^n \to \mathbb{R}^n, I_k : \mathbb{R}_+ \times \mathbb{R}^n \to \mathbb{R}^n \) and the increasing sequence of nonnegative points \( \{T_k\}_{k=0}^{\infty} \) be given, \( \lim_{k \to \infty} \{T_k\} = \infty. \)

**H1.** \( f(t, 0) = 0 \) and \( I_k(t, 0) = 0 \) for \( t \geq 0, \ k = 1, 2, \ldots. \)

The solution \( x(t; T_0, x_0, \{T_k\}) \) of IDE (1) depends not only on the initial condition \((T_0, x_0)\) but on the moments of impulses \( T_k, \ k = 1, 2, \ldots. \)

The main goal of the paper is studying stability properties of the solutions of impulsive differential equation in the case the waiting time between two consecutive impulses is Gamma distributed.

Let the probability space \((\Omega, \mathcal{F}, P)\) be given. Let \( \{	au_k\}_{k=1}^{\infty} \) be a sequence of random variables defined on the sample space \( \Omega. \)

Assume \( \sum_{k=1}^{\infty} \tau_k = \infty \) with probability 1.

**H2.** The random variables \( \{\tau_k\}_{k=1}^{\infty} : \ \tau_k \in \Gamma(\alpha_k, \lambda) \) are independent where \( \lambda > 0 \) is the rate parameter and \( \alpha_k \) is the shape parameter.

Define the sequence of random variables \( \{\xi_k\}_{k=0}^{\infty} \) such that \( \xi_0 = T_0 \) and \( \xi_k = T_0 + \sum_{i=1}^{k} \tau_i, \ \ k = 1, 2, \ldots \) where \( T_0 \geq 0 \) is a fixed point. The random variables \( \tau_k \) define the time between two consecutive impulses and \( \xi_n \) give the arrival time of \( n \)-th impulses.

Consider the initial value problem for impulsive differential equations with random moments of impulses (RIDE)

\[
x'(t) = f(t, x(t)) \quad \text{for} \quad t \geq T_0, \ \xi_k < t < \xi_{k+1}, \ k = 0, 1, \ldots, \\
x(\xi_k + 0) = I_k(x(\xi_k - 0)), \quad \text{for} \quad k = 1, 2, \ldots, \\
x(T_0) = x_0.
\]

**Remark 1.** The random variables \( \Xi_n = \sum_{i=1}^{n} \tau_i \in \Gamma(\sum_{i=1}^{n} \alpha_i, \lambda). \)

**Proposition 1.** Let the condition (H1) be satisfied and the sequence of random variables \( \{\Xi_k\}_{k=1}^{\infty} \) be such that \( \Xi_n = \sum_{i=1}^{n} \tau_i = \xi_n - T_0, \ n = 1, 2, \ldots. \)

Then \( \Xi_n \in \Gamma(\sum_{i=1}^{n} \alpha_i, \lambda) \) are continuous dependent random variables with cdf \( F(t; \sum_{i=1}^{n} \alpha_i, \lambda) = P(\Xi_n < t) = \frac{\gamma(\sum_{i=1}^{n} \alpha_i, \lambda)}{\Gamma(\sum_{i=1}^{n} \alpha_i)} \) for \( t \geq 0, \) respectively, where \( \gamma(m, t) = \int_{0}^{t} x^{m-1} e^{-x} \, dx, \ m, t > 0 \) is the lower incomplete gamma function.

Let the point \( t_k \) be an arbitrary value of \( \tau_k, \ k = 1, 2, \ldots. \) Define the increasing sequence of points \( T_k = T_0 + \sum_{i=1}^{k} t_i, \ k = 1, 2, 3, \ldots \) that are values of the random variables \( \xi_k \) and consider (1).
Definition 1. The solution \( x(t; T_0, x_0, \{T_k\}) \) of the IVP for the IDE with fixed points of impulses (1) is called a sample path solution of the IVP for the RIDE (2).

Definition 2. A stochastic process \( x(t; T_0, x_0, \{\tau_k\}) \) with an uncountable state space \( \mathbb{R}^n \) is said to be a solution of the IVP for the system of RIDE (2) if for any values \( t_k \) of the random variable \( \tau_k \), \( k = 1, 2, 3, \ldots \) and \( T_k = T_0 + \sum_{i=1}^{k} t_i, k = 1, 2, \ldots \) the corresponding function \( x(t; T_0, x_0, \{T_k\}) \) is a sample path solution of the IVP for RIDE (2).

Gamma distributed moments of impulses

For any \( t \geq T_0 \) consider the events \( S_k(t) = \{ \omega \in \Omega : \xi_k(\omega) < t < \xi_{k+1}(\omega) \} \).

Lemma 0.0.1. Let the condition (H2) be satisfied. Then the probability that there will be exactly \( k \) impulses until time \( t \), \( t \geq T_0 \) is given by

\[
P(S_k(t)) = \frac{\gamma(\sum_{i=1}^{k} \alpha_i, (t - T_0)\lambda)}{\Gamma(\sum_{i=1}^{k} \alpha_i)} - \frac{\gamma(\sum_{i=1}^{k+1} \alpha_i, (t - T_0)\lambda)}{\Gamma(\sum_{i=1}^{k+1} \alpha_i)}.
\]

Lemma 0.0.2. Let the condition (H1) be satisfied and \( m_i + \lambda \geq m_k \) for all natural \( i, k : i < k \). Then the solution of the IVP for the linear RIDE (2) is

\[
u(t; T_0, u_0, \{\tau_k\}) = \begin{cases} u_0 e^{-m_0(t-T_0)} & \text{for } T_0 < t < \tau_1 \\ u_0 \left( \prod_{i=1}^{k} b_i \right) e^{-\sum_{i=1}^{k} m_i - \sum_{i=1}^{k} \tau_i} e^{-m_k(t-\xi_k)} & \text{for } \xi_k < t < \xi_{k+1} \end{cases}
\]

and the expected value of the solution satisfies the inequality

\[
E(|\nu(t; T_0, u_0, \{\tau_k\})|) \leq |u_0| \left[ e^{-m_0(t-T_0)} \left( 1 - \frac{\gamma(\alpha_1, (t - T_0)\lambda)}{\Gamma(\alpha_1)} \right) \right] + \sum_{k=1}^{\infty} e^{-m_k(t-T_0)} \prod_{i=1}^{k} \left( |b_i| \left( \frac{\lambda}{m_{i-1} - m_k + \lambda} \right)^{\alpha_i} \right) \times \left( \frac{\gamma(\sum_{i=1}^{k} \alpha_i, (t - T_0)\lambda)}{\Gamma(\sum_{i=1}^{k} \alpha_i)} - \frac{\gamma(\sum_{i=1}^{k+1} \alpha_i, (t - T_0)\lambda)}{\Gamma(\sum_{i=1}^{k+1} \alpha_i)} \right). \tag{3}
\]
Remark 2. The estimate (3) is satisfied if \( \{m_i\}_{i=0}^{\infty} \) is a nonincreasing sequence bounded from below by \( M > 0 \) and there exists a number \( B \geq 1 \) such that \( \prod_{i=1}^{k} |b_i| \leq B, k = 1, 2, \ldots \). Then from (3) it follows \( E(|u(t; T_0, u_0, \{\tau_i\})|) \leq |u_0|Be^{-M(t-T_0)} \).

Remark 3. The estimate (3) is satisfied if \( m_i + \lambda \geq m_k \) for all natural \( i, k \) : \( i < k \), \( m_k \geq M > 0 \), \( k = 0, 1, 2, \ldots \) and \( \prod_{i=1}^{k} |b_i| \left( \frac{\lambda}{m_{i-1} - m_k + \lambda} \right)^{a_i} \leq B \) for \( k = 1, 2, \ldots \) where \( B \geq 1 \).

**p-exponential stability of RIDE**

**Theorem 0.0.1.** Let the following conditions be satisfied:

1. Conditions (H1), (H2) hold.
2. The function \( V \in A(\mathbb{R}_+, \mathbb{R}^n) \) and there exist positive constants \( a, b \) such that
   (i) \( a|x|^p \leq V(t, x) \leq b|x|^p \) for \( t \in \mathbb{R}_+, x \in \mathbb{R}^n \);
   (ii) there exists a constant \( m \geq 0 \) such that \( D_{(1)}^t V(t, x) \leq -mV(t, x), t \in \mathbb{R}_+, x \in \mathbb{R}^n \);
   (iii) for any \( k = 1, 2, \ldots \) there exist functions \( w_k \in C(\mathbb{R}_+, \mathbb{R}_+) \) and constants \( C_k > 0, w_k(t) \leq C_k \) for \( t \geq 0 \) such that \( \sum_{k=0}^{\infty} \prod_{i=1}^{k} C_i = C < \infty \) and \( V(t, I_k(x)) \leq w_k(t)V(t, x), t \in \mathbb{R}_+, x \in \mathbb{R}^n \).

Then the trivial solution of the RIDE (2) is \( p \)-moment exponentially stable.

Remark 4. If \( \alpha_k = 1 \) for all \( k \), i.e. \( \tau_k \in \text{Exp}(\lambda) \), the \( p \)-moment exponential stability is studied in [1].

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**References**


Statistical inferences on binomial conditional autoregressive model of spatio-temporal data

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Abstract: Binomial conditional autoregressive model of spatio-temporal data is presented. Asymptotic properties of the maximum likelihood estimators of parameters for the binomial conditionally autoregressive model of spatio-temporal data are studied: asymptotic normality is proved and the asymptotic covariance matrix is found for the estimators. Results of computer experiments on simulated and real data are given.

Introduction

Studying the probabilistic models of spatio-temporal data is a new topical scientific direction. Statistical analysis and modeling of spatio-temporal data is a challenging task [1]-[5].

Models based on spatio-temporal data become widely used for solving practical problems in meteorology, ecology, economics, medicine and other fields. In [5] spatio-temporal model is used to analyse daily precipitation for 71 meteorological stations over 60 years in Austria. Bayesian spatio-temporal model is applied to predict cancer cases in [1].

Binomial conditional autoregressive model

Introduce the notation: $(\Omega, F, P)$ is the probability space; $\mathbb{N}$ is set of positive integers; $\mathbb{Z}$ is set of integers; $S = \{1, 2, \ldots, n\}$ is the set of indexed spatial regions or space locations (let us agree to call them sites), into which the analyzed spatial area is partitioned; $n$ is number of sites; $t \in \mathbb{Z}$ is discrete time; $T$ is the length of observation period; $x_{s,t} \in A = \{0, \ldots, N\}$ is a discrete random variable at time $t$ at site $s$;
$F_{<t} = \sigma\{x_{u,\tau} : u \in S, \tau \leq t-1\} \subset F$ is the $\sigma$-algebra generated by the indicated in braces random variables; $z_{j,t} \in R^l, (j = 1, \ldots, m)$ is an observed (known) level of the $j$-th exogenous factor at time $t$ which influences $x_{s,t}$; $L(\xi)$ means the probability distribution law of random variable $\xi$; $E\{\cdot\}$, $D\{\cdot\}$, $\text{cov}\{\cdot\}$ are symbols of expectation, variance, covariance of random variables; $Bi(\cdot; N, p)$ is the binomial probability distribution law of random variable $\xi$ with the parameters $N \in N, 0 \leq p \leq 1$:

$$P\{\xi = l\} = Bi(l; N, p) := \binom{N}{l}p^l(1-p)^{N-l}, l \in A; L\{\xi\} = Bi(\cdot; N; p), \quad (1)$$

We construct the binomial conditional autoregressive model for spatio-temporal data $\{x_{s,t}\}$, as in [3], [4]. Provided that prehistory $\{x_{s,\tau} : s \in S, \tau \leq t-1\}$ is fixed, random variables $x_{1,t}, \ldots, x_{n,t}$ are assumed to be conditionally independent and

$$L\{x_{s,t}|F_{<t}\} = Bi(\cdot; N; p_{s,t}), \quad (2)$$

$$\ln \frac{p_{s,t}}{1-p_{s,t}} = \sum_{i=1}^{n} a_{s,i} x_{i,t-1} + \sum_{j=1}^{m} b_{s,j} z_{j,t}, t \in Z, \quad s \in S, \quad (3)$$

where $a_s = (a_{s,1}, \ldots, a_{s,n})' \in R^n$, $b_s = (b_{s,1}, \ldots, b_{s,m})' \in R^m$, $s \in S$, $\theta_s = (\theta_1, \ldots, \theta_n)' \in R^{n+m}$ is the composed vector of the parameters of the model; $p_{s,t}$ can be calculated as follows:

$$p_{s,t} = p_s(X_{t-1}, Z_t) := \exp\left\{\theta_s' Y_t\right\} \left(1 + \exp\left\{\theta_s' Y_t\right\}\right)^{-1}, \quad s \in S, \quad t \in Z, \quad (4)$$

where $Z_t = (z_{1,t}, z_{2,t}, \ldots, z_{m,t})' \in R^m$ is the column vector specifying exogenous factors at time $t$; $X_t = (x_{1,t}, x_{2,t}, \ldots, x_{n,t})' \in A^n$ is the column vector specifying the time slice of the process under consideration at time $t \in Z; Y_t = (X_{t-1}' Z_t)' \in R^{n+m}, t \in Z$.

Let $L = \left\{l_j = (l_{1,j}, \ldots, l_{n,j})' \in A^n : j = 1, 2, \ldots, (N+1)^n\right\}$ be the ordered set of all admissible values of the vector $X_t$; $|L| = \nu = (N+1)^n$.

**Theorem 1.** For the model (1)-(3) the observed vector process $X_t$ is the $n$-dimensional nonhomogeneous Markov chain with the finite state space $L$ and the one-step transition probability matrix $Q(t) = (q_{l,j}(\theta, t))$, $I = (I_s), J = (J_s) \in L$:

$$q_{l,j}(\theta, t) = \prod_{s=1}^{n} \frac{C_N^{J_s} \left(\exp\left\{a_s' I + b_s' Z_{t-1}\right\}\right)^{J_s}}{(1 + \exp\left\{a_s' I + b_s' Z_{t-1}\right\})^N}. \quad (5)$$
Corollary. Under conditions of Theorem 1, if vector of exogenous factors \( Z_t = Z = (z_1, \ldots, z_m) \in \mathbb{R}^m \) does not depend on \( t \), then the one-step transition probability matrix does not depend on \( t \), and Markov \( X_t \) chain is homogeneous:

\[
Q = (q_{I,J}(\theta)) \in [0,1]^{\nu \times \nu}, \quad I, J \in L,
\]

\[
q_{I,J}(\theta) = \prod_{s=1}^{n} C_{N}^{J} \left( \exp \left\{ a_{s}'I + b_{s}'Z \right\} \right)^{J_s} \left( 1 + \exp \left\{ a_{s}'I + b_{s}'Z \right\} \right)^{-N} ,
\]

the \( n \)-dimensional Markov chain is ergodic and single stationary distribution \( \pi = (\pi_{I}) \in [0,1]^{\nu} \) exists:

\[
Q'\pi = \pi, \quad \sum_{I \in A^n} \pi_{I} = 1.
\]

Lemma 1. For the model (1)-(3) the observed vector process \( X_t \) is nondegenerate process for any finite coefficients values \( \{\theta_s\} \) and finite \( \{z_{i,t}\} \), that means in (4):

\[
0 < p_{s,t} < 1, \quad s \in S, t \in \mathbb{Z}.
\]

Lemma 2. For the model (1)-(3) in case of any finite coefficients values \( \{\theta_s\} \) and finite \( \{z_{i,t}\} \) the covariance matrix \( \text{cov}\{X_t, X_t\} \) is positively defined and takes the form:

\[
\text{cov}\{X_t, X_t\} = N \text{diag} \{p_i(X_{t-1}, Z_t)(1 - p_i(X_{t-1}, Z_t))\} + D \in \mathbb{R}^{n \times n},
\]

\[
D = (d_{ij}) \in \mathbb{R}^{n \times n}, \quad d_{ij} = N^2 \text{cov} \left\{ (1 + \exp(-\theta_i Y_t))^{-1}, (1 + \exp(-\theta_j Y_t))^{-1} \right\}.
\]

Statistical estimation of parameters

Theorem 2. The log-likelihood function for the model (1)-(3) under the observed spatio-temporal data \( \{X_t : t = 1, 2, \ldots, T\} \) takes the additive form:

\[
l(\theta) = \sum_{s=1}^{n} l_s(\theta_s), \quad l_s(\theta_s) = \sum_{t=1}^{T} \left( x_{s,t} \theta_s Y_t - N \ln \left( 1 + \exp \left\{ \theta_s Y_t \right\} \right) + \ln C_{N,t}^{x_s,t} \right).
\]
To find the maximum likelihood estimators (MLE) \( \{ \hat{\theta}_s \} \) of the parameters of the model we need to maximize the log-likelihood function (8):

\[
l(\theta) \to \max_{\theta \in \mathbb{R}^{(n+m)}}.
\]

**Theorem 3.** In case of the model (1)-(3), if \( m = 1 \), \( z_{1t} = z \neq 0 \) does not depend on \( t \) and Markov chain \( X_t \in L \) is stationary, then for any finite coefficients values \( \{ \theta_s \} \) and finite \( z \in \mathbb{R}^1 \) the Fisher information matrix is nonsingular block-diagonal matrix \( (Y_t = (X_{t-1}', z)') \):

\[
G = Ndiag \left\{ E \left\{ Y_t Y_t' p_i(X_{t-1}, z)(1 - p_i(X_{t-1}, z)) \right\} \right\}, i = 1, ..., n.
\]

**Theorem 4.** Under Theorem 3 conditions, if \( T \to +\infty \) the constructed by (9) maximum likelihood estimators \( \{ \hat{\theta}_s \} \) are consistent and asymptotically normally distributed:

\[
L \left\{ \sqrt{T}(\hat{\theta} - \theta^0) \right\} \to N_{n(n+1)} (0, G^{-1}) .
\]

where \( G \) is determined by (10).

Theorems 2-4 are used to construct statistical tests on the values of true unknown parameters \( \{ \theta^0_s \} \) and statistical forecasting statistics for future values \( \{ x_{t,s} : t = T + 1, ..., T + \tau \} \).

Results of computer experiments on simulated and real data illustrate the theoretical results.

**References**


Forest fire model on configuration graphs with random node degree distribution

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Abstract: We consider configuration graphs with node degrees being i.i.d. random variables following the power-law distribution. The distribution parameter is a random variable following the uniform distribution on a predefined interval.

We consider a destructive process which could be interpreted as a fire spreading over the graph links, and could be used for modeling forest fires as well as banking system defaults. This process is often referred to as a “forest fire model”. The probability of fire transfer over a graph link either possess a predefined value and is fixed for all the graph links or is a random variable following the standard uniform distribution. By computer simulation we study the robustness of such graphs from a viewpoint of node survival in the two cases of starting a fire propagation process: the “random ignition” and the “targeted lightning-up”. The results on finding the optimal interval of the node degree distribution parameter that would ensure maximum survival of trees in case of a fire are presented. A comparative analysis of various graph models in terms of their robustness to various fire propagation processes was performed.

Power-law random graph

We consider random graphs the number of nodes in which is equal to $N$. Node degrees $\xi_1,\xi_2,\ldots,\xi_N$ are independent identically distributed random variables drawn from the following power-law distribution:

$$
P\{\xi \geq k\} = k^{-\tau}, \quad k = 1, 2, \ldots, \tau > 1. \quad (1)
$$

Node degrees form stubs, numbered in an arbitrary order. Then all stubs are joined one to another equiprobably to form links. If the sum of
node degrees appears to be odd, one stub is added to a randomly chosen node to form a lacking connection. In our work we consider power-law graphs with the parameter \( \tau \) of distribution (1) following the uniform distribution on a predefined interval \([a, b]\). The studies of the power-law random graphs has been attracting consistent interest because of the wide use of these models for representing massive data networks (see e.g. \([3, 4, 6]\)).

**Forest fires**

An interesting trend in the studies of random graphs is the aspect connected to the transmission of various destructive influences through graph links. In particular, we consider the process which could be interpreted as spreading of a fire over the graph links \([2]\), and might have some other applications, for example, modeling of banking system defaults \([1]\).

To study a forest fire model we view graph nodes as trees growing in a certain area of a real forest. Since we consider this area to be limited, the number of trees on it also has to be limited. For this purpose we proposed to use auxiliary square lattice graphs sized \(100 \times 100\) (see \([5]\)). If a real fire can be transferred from one tree to another, corresponding graph nodes are connected by a link. Thus, under a full packing every inner auxiliary graph node has 8 adjacent neighbours. Knowing that \( i = \zeta(\tau) \) (where \( \zeta(x) \) is the Riemann zeta function), we derived a regression relation between graph size \( N \leq 10000 \) and the parameter \( \tau \) of node degree distribution (1):

\[
N = 9256\tau^{-1.05}, \quad R^2 = 0.97.
\]  

The relation (2), where \( \tau = \tau = \frac{a+b}{2} \) confines the number of nodes in the graph \( N \). Thus, we study a fire propagation process on power-law configuration graphs with \( N \) nodes, where \( N \) is calculated from (2) for various intervals \([a, b]\). The probability of fire transition \( p \) over the graph links is either a predefined value and is fixed for all the graph links or is a random variable following the standard uniform distribution. The purpose is to find the optimal interval for the node degree distribution parameter \( \tau \) that would ensure maximum survival of graph nodes in case of a fire.
In our work we consider the three intervals $[a, b]$: $(1, 2]$, $[2, 3]$, $(1, 3]$ with the $N$ values obtained from (2) being equal to 6046, 3536 and 4470, respectively. The two considered cases of starting a fire propagation process are the “targeted lightning-up” when the fire starts from the node with the highest degree and the “random ignition” starting from an equiprobably chosen node. For both cases we found the relations between the average number of trees surviving in a fire $n$ and the probability of fire transition $p$. Figures 1 and 2 show how the percentage of nodes $\frac{n}{N}$ in % depends on the probability $p$ for the two cases of starting a fire.

![Fig.1](image1) ![Fig.2](image2)

**Fig.1** Relation between $\frac{n}{N}$ % and the probability of fire transition $p$ (“targeted lightning-up”).

**Fig.2** Relation between $\frac{n}{N}$ % and the probability of fire transition $p$ (“random ignition”).

Obviously, the number of remaining nodes $n$ as well as the proportion $\frac{n}{N}$ is decreasing with the increase of $p$. The results show that graphs with the parameter $\tau \in [2, 3]$ are more fire resistant, whereas graphs with $\tau \in (1, 2]$ are the most vulnerable to the fire in both fire start cases.

Furthermore, we study a case when the probability of fire transition $p$ is a random variable drawn from the standard uniform distribution. The obtained results are presented in the following Table 1.

<table>
<thead>
<tr>
<th>$\tau \in [a, b]$</th>
<th>“targeted lightning-up”</th>
<th>“random ignition”</th>
</tr>
</thead>
<tbody>
<tr>
<td>$(1, 2]$</td>
<td>52.03</td>
<td>81.6</td>
</tr>
<tr>
<td>$[2, 3]$</td>
<td>97.96</td>
<td>99.92</td>
</tr>
<tr>
<td>$(1, 3]$</td>
<td>65.26</td>
<td>87.85</td>
</tr>
</tbody>
</table>

The results show a similar picture where in both cases of fire ignition graphs with the node degree distribution parameter $\tau \in [2, 3]$ will ensure a better survival of nodes in case of a fire.

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References


Markov branching process with immigration

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Abstract: In the talk we consider critical Markov branching process with infinite variance and non-homogeneous Poisson immigration. The asymptotic of the probability for non extinction and limit theorems are proved in a particular case when the probability generating function of the process without immigration has an explicit representation.

Introduction and definitions

A Markov branching process can be described as follows: The particles of a given type evolve in a broad-media. Each particle, independently of the others, lives random time $\tau$ with exponential distribution function $G(t) = P\{\tau \leq t\} = 1 - e^{-t/\mu}$, $t \geq 0$ and at the end of its life the particle produces random number $\xi \geq 0$ of new particles of the same type. Each of them evolves in the same way.

If we assume that this evolution started at time $t = 0$ with one new particle, then the number of particles at every moment $t \geq 0$, $Z(t)$ form the stochastic process, known as Markov branching process (see [1]).

Let us suppose that along the Markov branching process $Z(t)$ there is a sequence of random vectors $(S_k, I_k), k = 0, 1, 2, \ldots$, independent of $Z(t)$, where

$$0 = S_0 < S_1 < S_2 < S_3 < \ldots$$

are the jump points of a non-homogeneous Poisson process $\nu(t)$ independent of $Z(t)$. Denote by $r(t)$ the intensity of $\nu(t)$ and by $R(t) = \int_0^t r(u)du$. Assume that at every jump-point $S_k$, $I_k$ new particles immigrate into the
process $Z(t)$ and they participate in the evolution as the other particles. Let us denote the new process by $Y(t)$. It can be represent as follows

$$Y(t) = \begin{cases} \sum_{k=1}^{\nu(t)} Z_{(k)}(t - S_k), & \nu(t) > 0; \\ Y(t) = 0, & \nu(t) = 0, \end{cases}$$

where $Z_{(k)}(t)$ have the same branching mechanism as $Z(t)$ but they started with random number of ancestors at random time, i.e. $Z_{(k)}(t-S_k)$ starts with $I_k$ ancestors at the moment $S_k$. The process $Y(t)$, $t \geq 0$ is a Markov branching process with non-homogeneous Poisson immigration (MBPNPI).

In the talk we assume that $I_k = 1$ almost surely.

**Assumptions and results**

We assume that the probability generating function of the offspring of one particle is $h(s) = Es^k = s + (1-s)^{1+\gamma}$, $0 < \gamma < 1$ and $G(t) = 1 - e^{-t/\mu}$, $t \geq 0$. Then the probability generating function of the the process $Z(t), t \geq 0$ has the following form

$$F(t; s) = 1 - \frac{1 - s}{(1 + ct(1 - s)\gamma)^{1/\gamma}}, \quad t > 0, \quad s \in [0, 1]. \quad (1)$$

where $\gamma \in (0, 1)$ and $c = \frac{\gamma}{(1 + \gamma)\mu} \in (0, \infty)$. See Sevastyanov’s book [1] or the recent paper of Sagitov and Lindo [2]).

Under these assumptions the process is critical, that is the number of the offspring of one particle is a random variable with mean one and infinite variance.

Such processes in general settings were first studied by V.M.Zolatarev [4].

The probability generating function of the process $Y(t)$ has the following form (see Yakovlev and Yanev[3]),

$$\Phi(t; s) := E(s^{Y(t)}) = \exp \left\{ - \int_0^t \frac{(1-s)r(t-u)}{(1 + cu(1-s)\gamma)^{1/\gamma}} du \right\}. \quad (2)$$

For the intensity of the Poisson process we assume one of the following
conditions

\[ r(t) \downarrow 0, r(t) = t^{-\theta} L_R(t), t \to \infty, \theta > 0, \quad (3) \]
\[ r(t) \uparrow r > 0, \quad t \to \infty, \quad (4) \]
\[ r(t) \uparrow \infty, \quad r(t) = t^{\theta} L_R(t), \quad t \to \infty, \theta > 0, \quad (5) \]

where \( L_R(.) \) is a slowly varying function at infinity.

From (1) we get

\[ Q(t) = 1 - F(t; 0) = \frac{1}{(1 + ct)^{1/\gamma}}, \quad t \geq 0. \]

It is not difficult to calculate that \( Q = \int_0^\infty Q(t)dt = \frac{\gamma}{c(1-\gamma)} \in (0, \infty). \) Therefore, \( Q(t)/Q, t \geq 0 \) is a density on \([0, \infty).\)

Depending on the rate of change of \( r(t) \) we obtain the following results:

1. Assume that (1) and (3) with \( \theta > 1 \) hold.

   In this case \( R = \lim_{t \to \infty} R(t) = \int_0^\infty r(u)du \in (0, \infty) \) and \( r(t)/R \) is also density on \([0, \infty).\) Then we have

\[ P(Y(t) > 0) \sim \frac{\gamma}{c(1-\gamma)}r(t) + R \times (1 + ct)^{-1/\gamma}, \quad t \to \infty. \]

Depending on the asymptotic of \( Q(t)/r(t) \) we have three different limit distributions.

1.A. If \( Q(t) = \frac{1}{(1 + ct)^{1/\gamma}} = o(r(t)), \quad t \to \infty \) then

\[ \lim_{t \to \infty} P(Y(t) = k|Y(t) > 0) = p_k, k = 1, 2, \ldots, \]
\[ \sum_{k=1}^\infty p_k s^k = 1 - (1 - s)^{1-\gamma}. \]

1.B. If \( r(t) = o(Q(t)), \quad t \to \infty \) then

\[ \lim_{t \to \infty} P(Y(t)Q(t) \leq x|Y(t) > 0) = D_\gamma(x), x \geq 0. \]

where \( D_\gamma(x) \) has Laplace transform \( \hat{D}_\gamma(\lambda) = 1 - \frac{\lambda}{(1+\lambda^\gamma)^{1/\gamma}}, \quad \lambda > 0. \)
1. C. If \( \frac{r(t)}{Q(t)} \to d \in (0, \infty) \) then

\[
\lim_{t \to \infty} P(Y(t) = k | Y(t) > 0) = p_k,
\]

\[
\sum_{k=1}^{\infty} p_k s^k = \frac{Q}{Q + R/d}(1 - (1 - s)^{1-\gamma}),
\]

and

\[
\lim_{t \to \infty} P(Y(t)Q(t) \leq x | Y(t) > 0) = \frac{Qd}{R + Qd} + \frac{R}{R + Qd} D_\gamma(x), \quad x \geq 0.
\]

2. Assume that (1) and (3) with \( \theta \in (0, 1) \) hold. Then

\[
P(Y(t) > 0) \sim \frac{\gamma}{c(1 - \gamma)} r(t), \quad t \to \infty.
\]

\[
\lim_{t \to \infty} P(Y(t) = k | Y(t) > 0) = p_k, \quad k = 1, 2, \ldots,
\]

\[
\sum_{k=1}^{\infty} p_k s^k = 1 - (1 - s)^{1-\gamma}.
\]

3. Assume that (1) and (4) hold. Then

\[
P(Y(t) > 0) \to 1 - e^{-\frac{\gamma}{c(1 - \gamma)}}, \quad t \to \infty.
\]

\[
\lim_{t \to \infty} P(Y(t) = k) = p_k, \quad k = 1, 2, \ldots,
\]

\[
\sum_{k=1}^{\infty} p_k s^k = \exp\left(-\frac{\gamma(1 - s)^{1-\gamma}}{c(1 - \gamma)}\right),
\]

4. Assume that (1) and (5) hold. Then

\[
P(Y(t) > 0) \to 1, \quad t \to \infty.
\]

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On the effect of lifespan distribution on mutation times in continuous-time branching models

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Abstract: Recently branching stochastic models have been intensively used as models of mutations in cancer research (see [1]). On the other side, it turned out that the lifespan of a cell is not deterministic but random by nature (see [2, 3]). This is our motivation of considering the cellular life time as a continuous random variable. That is why we choose the so-called Bellman–Harris branching process (BHBP) or age-dependent BP as a model in which every cell has a continuously distributed lifespan and at the end of its life it reproduces or dies.

More precisely, we consider two-type BHBP in which subcritical type cells could mutate into supercritical cells. Our conjecture is that the time to appearance of a mutant depends strongly on the chosen lifespan distribution of the cells. We study this relationship in terms of BHBP and find out the most probable times for these mutants to appear in different model settings. Several types of lifespan distributions are considered, including non-exponential, and a possible application of the results in medicine is discussed.

Introduction

We consider two types of cells – type 1, which is subcritical, and type 0, which is supercritical. The type 0 cells produce cells of both types at the end of their life, but the cells of type 0 produce only cells of the same type. If the BP is subcritical, then we know the cells will extinct with probability 1, but if it is supercritical there is a positive probability that the cells will never extinct. We will call the supercritical type 0 cells - mutants. We will call “successful mutant” the first cell of type 0 that leads to exponential growth, i.e. it escapes extinction. The
waiting times for appearance of mutants and “successful mutants” are of interest in medicine where they model cancer cell development and possible appearance of metastasis. This paper studies the distribution of these waiting times and their dependence on the type and parameters of cellular lifespan distribution.

**Preliminary theoretical results**

The theorems presented in this section are the key results needed to calculate the distribution of the time to appearance of a “successful mutant” and the corresponding hazard function. Let the random variable $T$ denote the time to appearance of “successful mutant”, $q_0$ denote the probability the mutant type to extinct, $u$ denote the probability for a mutation to occur in the offspring of type 1, $G_1(t)$ be the distribution of the cellular lifespan and $f_1$ - the probability generating function (p.g.f.) of type 1 cells.

**Theorem 1.** (see Slavtchova–Bojkova [4])

The distribution of $T$ satisfies the following integral equation:

$$
P(T > t) = 1 - G_1(t) + \int_0^t f_1(uq_0 + (1 - u)P(T > t - y)) dG_1(y). \quad (1)
$$

**Remark.** Notice the solution of equation (1) neither depends on the life length distribution of mutant type cells, nor of the particular form of the offspring generating function of mutant type cells. It depends only on the probability of extinction of mutant cells - $q_0$.

**Theorem 2.** The joint probability that successful mutant has not been born yet and there are not cells of type 1 (with subcritical reproduction, $m_1 < 1$) satisfies the following integral equation:

$$
P(T > t, Z^1(t) = 0) = \int_0^t f_1(uq_0 + (1 - u)P(T > t - y, Z^1(t - y) = 0)) dG_1(y). \quad (2)
$$

By definition the hazard function $g(t)$ is defined by $g(t)dt = P(T \in [t, t + dt] | T > t, Z^1(t) > 0)$, which can be written also in the form

$$
g(t) = \frac{F_T(t)}{P(T > t, Z^1(t) > 0)}, \quad (3)
$$
where $F_T'(t)$ is the probability density function (PDF) of $T$. The denominator $P(T > t, Z^1(t) > 0)$ in equation (3) satisfies

$$
P(T > t, Z^1(t) > 0) = P(T > t) - P(T > t, Z^1(t) = 0)$$

$$= F_T(t) - P(T > t, Z^1(t) = 0).$$

(4)

Using Theorem 1 and Theorem 2 we can calculate numerically $P(T > t)$ and $P(T > t, Z^1(t) = 0)$ and by substituting equation (4) in equation (3) we can also calculate the hazard function $g(t)$. The results from the calculations are presented in the next Section.

**Results and applications**

To illustrate the importance of the choice of lifespan distribution we consider several examples with normal, exponential, uniform, chi squared and beta distribution. The parameters of the distributions are chosen so that the life expectancy is equal to 10 time units in all of the cases. This makes the lifespan distributions comparable on a single plot and allows to study how the PDFs of the time to appearance of successful mutant depends on the “shape” of the distribution that we choose for the model. All other parameters of the model are kept the same in the simulations. We consider the probability for mutation to type 0 to be $u = 20\%$, the offspring p.g.f. for type 1 cells to be $f_1(s) = 0.625 + 0.375s^2$ and the extinction probability of BP, starting with a type 0 cell, to be $q_0 = 30\%$. On Figure 1 are shown the calculated PDFs of the waiting time $T$ for appearance of “successful mutant” and the hazard function $g(t)$.

**Conclusions**

The simulation results reveal the importance of the distribution of the life length of type 1 cells as the time to the appearance of “successful mutant” depends on it. There are certain times at which the probability for appearance of a mutant is at its highest. In cancer treatment context this means we can target these moments to control the risk of metastasis and develop a better schedule for the therapy. We can also calculate the probability if a person has not yet developed mutant type of cancer, what are the chances he does not develop it in the future, namely $P(T = \infty |$
Figure 1: Probability density function of $T$ (left) and the hazard function $g(t)$ (right).

$T > t$). The approach developed also allows to find the probability of a person who decided not to get treated again does not develop mutant type of cancer – $\mathbb{P}(T = \infty)$.

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Distribution of the Order in Some Classes of Random Mappings

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Abstract: This is the short review on limit theorems for the logarithm of the order in random mappings of different classes obtained earlier.

Key words: random mappings, random permutations, cyclic points, order of a mapping.

Description of a problem

Let $\mathfrak{S}_n$ be a semigroup of all mappings of a finite set $X$ with $n$ elements into itself and a mapping $\sigma$ belongs to $\mathfrak{S}_n$. The number of different elements in a sequence $\{\sigma, \sigma^2, \sigma^3, \ldots\}$ of powers (i.e., iterations) of $\sigma$ is called as an order of this mapping. Set an arbitrary probability distribution on $\mathfrak{S}_n$ (in the majority of the cited articles it is uniform distribution on some subset $B_n \subseteq \mathfrak{S}_n$, having sufficiently large power). Let $\sigma_n$ be a random mapping from $\mathfrak{S}_n$ with this distribution and $M_n = M(\sigma_n)$ is it’s order. The limit theorems received for $\ln M_n$ as $n \to \infty$ known to the author are given here.

A case of random permutations

In this section, we discuss the most investigated case when $P\{\sigma_n \in S_n\} = 1$, where $S_n$ is a group of one-to-one mappings from $\mathfrak{S}_n$, i.e., various permutations of a set $X$. Note that for the first time such problem (together with some other problems of the statistical theory of groups) was studied by P. Erdős and P. Turán 1965 - 1969 [6] with uniform distribution at $B_n = S_n$. In their researches, in particular, it was shown
that, for any fixed $x \in \mathbb{R}$

$$
P \left\{ \ln M_n \leq \frac{\ln^2 n}{2} + x\sqrt{\frac{\ln^3 n}{3}} \right\} \to \Phi(x)$$

as $n \to \infty$ where $\Phi(x)$ is the standard normal distribution function. It is curious to note that, according to E. Landau [12] (1909)

$$
\max_{\sigma_n \in S_n} \ln M(\sigma_n) \sim \sqrt{n \ln n}.
$$

Thus, we see that "typical" permutation from $S_n$ has much a smaller order, than that at which the maximum in the last expression is reached. The proof of this result of P. Erdős and P. Turán was rather difficult. Probably, therefore the present limit theorem drew to itself close attention of many researchers: it was proved again many times (see, for instance, the articles of Best [3] (1970), Kolchin [11] (1977), Pavlov [16] (1980), Bovey [4] (1980), DeLaurentis and Pittel [13] (1985), Arratia and Tavare [1] (1992)). Proofs became simpler step by step, but as a result of them nevertheless it was impossible to call simple. In 1985, Nicolas [15] showed that the error in Erdős-Turán law with a mean shift of $-\ln n \ln \ln n$ is of order at most $O(\ln^{1/2} n \ln \ln n)$. Barbour and Tavare [2] obtained in 1994 the estimation of correct order in this law. Note that they considered more general model of random permutation $\sigma_n(\varrho)$, having so called Ewens sampling distribution with parameter $\varrho > 0$ [7], i.e., for any $\sigma \in S_n$ with $k$ cycles $P\{\sigma_n(\varrho) = \sigma\} = \frac{\varrho^k}{\varrho(n)}$ where $\varrho(n) = \varrho(\varrho + 1) \cdots (\varrho + n - 1)$ (the uniform distribution on $S_n$ turns out for $\varrho = 1$). In particular, Barbour and Tavare showed in [2] that

$$
\sup_{x \in \mathbb{R}} \left| P \left\{ \frac{\ln M(\sigma_n(\varrho)) - \frac{\varrho \ln^2 n}{2} - \varrho \ln n \ln \ln n}{\sqrt{\frac{\varrho \ln^3 n}{3}}} \leq x \right\} - \Phi(x) \right| = O \left( \frac{1}{\sqrt{\ln n}} \right).
$$

A.I. Pavlov [17] (1981) considered a random permutation $\sigma_n = \sigma_{nk}$, having uniform distribution on the set $S_{nk} = \{a : a = x^k|x \in S_n\}$ and proved the next limit theorem for the logarithm of the order $\zeta_{nk}$ of $\sigma_{nk}$:

$$
\lim_{n \to \infty} P \left\{ \frac{\zeta_{nk} - E\zeta_{nk}}{\sqrt{D\zeta_{nk}}} \leq x \right\} = \Phi(x),
$$

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where \( k \in \mathbb{N} \) and \( x \in \mathbb{R} \) are fixed. Also he showed that \( \mathbb{E} \zeta_{nk} \sim \frac{\varphi(k)}{2k} \ln^2(n) \) and \( \mathbb{D} \zeta_{nk} \sim \frac{\varphi(k)}{3k} \ln^3(n) \) as \( n \to \infty \) and \( k \) is fixed, where \( \varphi(\cdot) \) is the Euler’s function. Note also curious fact (though it is beyond of the present review), that a weak limit for a number cycles \( \xi_{nk}(n) \) of fixed length \( s \) in this model of random permutation, have not, as usual, Poisson distribution, though the set of \( S_n^{(k)} \) has quite large power: \( |S_n^{(k)}| \sim An!n^{-1+\varphi(k)/k} \), nevertheless

\[
P\{\xi_{nk}(n) = \nu\} \to \frac{1}{\nu!s^\nu h_d^{-1} \left( \frac{1}{s} \right)}
\]
as \( n \to \infty \) for any fixed \( k \), where

\[
\bar{k} = \prod_{p | k} p, \quad d = (s, k), \quad d = \prod_{p | d} p^{\alpha_p} \mid k, \quad p^{\alpha_p+1} \nmid k, \quad h_d(z) = \sum_{m=0, d \mid m} \frac{z^m}{m!},
\]
p is a prime number and \( A \) depends only of \( k \). The similar effect for some class of random mappings has found L. Mutafchiev [14](1978). In 2004, Zacharovas [24] obtained a rate of convergence in Pavlov’s limit theorem:

\[
\sup_{x \in \mathbb{R}} \left| P \left\{ \frac{\zeta_{nk} - \mathbb{E} \zeta_{nk}}{\sqrt{\frac{\varphi(k)}{3k} \ln^3(n)}} \leq x \right\} - \Phi(x) - r_k(x) e^{-x^2/2} \sqrt{\ln n} \right| = O \left( \frac{\ln \ln n}{\ln n} \right)^{2/3}
\]
as \( n \to \infty \), where \( k \in \mathbb{N} \) is fixed and

\[
r_k(x) = \sqrt{\frac{3}{\beta}} \frac{(1 - 8c - x^2)}{8 \sqrt{2\pi}}, \quad c = \beta \int_0^1 \frac{(1 - y)^{\beta-1} - 1}{y} dy, \quad \beta = \frac{\varphi(k)}{k}.
\]

As we see, Zacharovas allocated the member having order \( \ln^{-1/2} n \) (see the result of Barbour and Tavare [2] specified earlier) and estimated an order of the corresponding difference. In the same work, Zacharovas specified mentioned above Pavlov’s result concerning an asymptotics of mean \( \zeta_{nk} \):

\[
\mathbb{E} \zeta_{nk} = \frac{\beta}{2} \ln^2 n - \beta \ln n (\ln \ln n + C(k)) + \sum_{\varrho} \Gamma(-\varrho)(\beta \ln n)^\varrho + O((\ln \ln n)^2),
\]

where

\[
C(k) = \ln \beta - 1 - \int_0^1 \frac{(1 - y)^{\beta-1} - 1}{y} dy - \sum_{p | k} \ln p - \frac{1}{p - 1}
\]
and $\sum_\rho$ means the sum on nontrivial zeros of Riemann’s zeta-function.

Let $S_n^{(k)}$ be a set of permutations from $S_n$, having no more than $k$ cycles of identical length, and $\sigma_n^{(k)}$ be a random permutation uniformly distributed on $S_n^{(k)}$. In the paper [18] (1996), A.I. Pavlov obtained the next limit theorem:

$$\lim_{n \to \infty} P \left\{ \ln M \left( \sigma_n^{(k)} \right) - \frac{\ln^2 n}{2} \leq x \sqrt{\frac{\ln^3 n}{3}} \right\} = \Phi(x).$$

where $x \in R$ and $k \in N$ are fixed. As it is well known, every permutation decomposes into the cycles. Fix some set $A \subseteq N$. Permutation $\sigma \in S_n$ is called as $A$-permutation if all lengths of it’s cycles belong to a set $A$ [20]. By $T_n = T_n(A)$ we designate the set of all $A$-permutations of $n$-th degree. Let $\tau_n = \tau_n(A)$ be a random permutation uniformly distributed on $T_n(A)$. In 2010, it was shown by the author [23] that a sequence of random variables

$$\frac{\ln M(\tau_n(A)) - \sum_{i \in A, i \leq n} \ln(i)/i}{\sqrt{\frac{\varrho}{3} \ln^3 n}}$$

converges weakly to the standard normal r.v. if the next relations are valid:

$$\frac{|k : k \leq n, k \in A|}{n} \to \varrho > 0, \quad \frac{|k : k \leq n, k \in A, m - k \in A|}{n} \to \varrho^2$$

uniformly by $m \in [n, Cn]$ for an arbitrary constant $C \in (1, \infty)$ as $n \to \infty$. Since it is not evident, which sets $A$ satisfy assumptions (1), then some examples are given in the following section. More detailed analysis of examples is available in the book [22]. Here we note only that for $A = N$ Erdős-Turán result mentioned at the beginning of this section follows from here.

In the resent work [8] (2012), Gnedin, Iksanov and Marynych considered the next model of random permutation. Let a random variable $W$ has a distribution $D$ on $(0, 1)$ and let $W_1, W_2, \ldots$ be it’s independent copies. Set

$$Q_0 = 1, \quad Q_j = \prod_{i=1}^{j} W_i, \quad j \in N.$$
Suppose that \( U_1, \ldots, U_n \) be independent random variables uniformly distributed of \([0, 1]\) and not depending on \( W_1, W_2, \ldots \). We assume that permutation \( \Pi_n \in S_n \) has the cycle \( (i_1 \rightarrow \cdots \rightarrow i_l \rightarrow i_1) \) if \( U_{i_1} < \cdots < U_{i_l} \) and the points \( U_{i_1}, \ldots, U_{i_l} \) and only they from \( U_1, \ldots, U_n \) fall into interval \((Q_j, Q_{j+1}]\). It is clear that a permutation \( \Pi_n \) identically defines by it’s cycles. Let a distribution \( D \) is absolutely continuous with a density \( f \) and, for some \( \delta_1, \delta_2 \geq 0 \), a function \( f(x) \) is nondecreasing on \((0, \delta_1)\), is bounded on \([\delta_1, 1-\delta_2]\) and is nonincreasing on \((1-\delta_2, 1)\). In the article [8], it is shown that if r.v. \( |\ln W| \) is in domain of attraction of stable distribution with index \( \alpha \in (1, 2] \), then, for some sequences \( a_n \) and \( b_n \) (which are written out explicitly) distribution of r.v. \( (\ln M(\Pi_n) - a_n)/b_n \), weakly converges to a stable law with the same parameter \( \alpha \). In particular, if \( f(x) = \varrho x^{\varrho - 1} \), then the limit law is normal \( (\alpha = 2) \), and permutation \( \Pi_n \) has Ewens sampling distribution with parameter \( \varrho \), and, if \( \varrho = 1 \), we have the uniform distribution on \( S_n \).

**A case of random mappings**

Let, as earlier, \( \mathcal{G}_n \) be the set of all mappings of a finite set \( X \) with \( n \) elements into itself. For the first time, we consider the situation when a random mapping \( \sigma_n \) has uniform distribution on \( \mathcal{G}_n \). In the work [10] (1973), B. Harris proved, that, for an arbitrary fixed real \( x \),

\[
\lim_{n \to \infty} P \left\{ \ln M(\sigma_n) - \frac{\ln^2 n}{8} \leq x \sqrt{\frac{\ln^3 n}{24}} \right\} = \Phi(x).
\]

The mapping \( \sigma \in \mathcal{G}_n \) is called \( A \)-mapping, if all cycles of \( \sigma \) belong to the set \( A \subseteq N \). For more details on the \( A \)-mappings, see Sachkov’s book [20]. Let \( \sigma_n(A) \) be a random mapping uniformly distributed on the set \( V_n(A) \) of all \( A \)-mappings of the \( n \)th degree. Suppose that the relations (1) are valid (see the previous section). Recently the author proved (unpublished), that, under these assumptions, for an arbitrary fixed real \( x \)

\[
\lim_{n \to \infty} P \left\{ \frac{\ln M(\sigma_n(A)) - \sum_{i \in A, i \leq \sqrt{n}} \ln(i)/i}{\sqrt{\frac{\varrho}{24} \ln^3 n}} \leq x \right\} = \Phi(x). \tag{2}
\]
Now we give some examples of sets $A$ for which the relations (1) hold and therefore, the equality (2) takes place.

**Example 1.** Let a set $A$ has an asymptotic density 1 in the set of natural numbers. Then the relations (1) and hence (2) are valid with $\varrho = 1$. In particular, for $A = \mathbb{N}$ the just mentioned Harris result follows from here.

**Example 2.** Let a set $A$ be random and random variables $\eta_1 = \chi\{1 \in A\}, \eta_2 = \chi\{2 \in A\}, \ldots$ are independent and $P\{\eta_n = 1\} \to \varrho > 0$ as $n \to \infty$. Then the relations (1) hold for a set $A$ almost surely (a.s.) [22, section 3.6]. Thus, for an arbitrary fixed real $x$, as $n \to \infty$

$$P \left\{ \frac{\ln M(\sigma_n(A)) - \sum_{i \in A, \ i \leq \sqrt{n}} \ln(i)/i}{\sqrt{\frac{n}{24}} \ln^3 n} \leq x \right\} \to \Phi(x) \ a.s.$$

**Example 3.** Let an arbitrary finite union of intervals $\Delta$ from $[0, 1]$ and a function $g(t) = t^\alpha l(t), \forall t > 0$ are given, where function $l(t)$ slowly varies at infinity and number $\alpha$ is positive and noninteger. We include a number $n \in \mathbb{N}$ into a set $A$ if and only if $\{g(n)\} \in \Delta$. It is shown in the book [22, theorem 3.5.2, conclusion 3.5.1] that, if for an arbitrary $m = 1, 2, \ldots, [\alpha] + 3$

$$\frac{d^m}{dt^m} l(t) = o(t^{-m} l(t)) \quad (t \to \infty),$$

then the relations (1) are valid, therefore the equality (2) holds for $A$.

And one more new result. Let $\tau$ be some permutation. Set $\Theta(\tau) = (\xi_1, \xi_2, \ldots)$, where $\xi_i = \xi_i(\tau)$ is a number of cycles in permutation $\tau$ of lengths $i \in \mathbb{N}$. Suppose that, for some sequence of random permutations $\tau_n \in S_n$ and for positive sequences $a(n)$ and $b(n)$, the next relation

$$\frac{\ln M(\tau_n) - a(n)}{b(n)} \Rightarrow \eta \quad (n \to \infty)$$

holds, where $\eta$ is a r.v. with continuous distribution function. Let $\sigma_n \in S_n$ be an arbitrary sequence of random mappings such that

$$D(\Theta(\sigma^*_n)|\lambda_n = k) = D(\Theta(\tau_k)),$$
for any \(k, n \in \mathbb{N}, k \leq n\) where \(D(\cdot)\) denotes a distribution, \(\lambda_n\) is a number of cyclic points in a random mapping \(\sigma_n\), and \(\sigma^*_n\) is a reduction of \(\sigma_n\) into it's cyclic points. Suppose that \(\lambda_n / r(n) \Rightarrow \xi > 0\) for some positive sequence \(r(n) \to \infty\) such that \(r(n) \geq n^\varepsilon\) for any \(n \in \mathbb{N}\) and some \(\varepsilon > 0\). Assume that the inequality \(a(n) \geq c \ln n\) holds for some constant \(c > 0\) and all \(n \in \mathbb{N}\) and \(a(n)/b(n) \to \infty\) as \(n \to \infty\). Let there exists a positive function \(d(x) \to \infty\) such that

\[
\sup_{y \in (d^{-1}(x), d(x))} \frac{a(x) - a(xy)}{b(x)} \to 0 \quad (x \to \infty)
\]

(we set \(a(x) = a([x])\) and \(b(x) = b([x])\) for \(x > 0\)). Then

\[
\frac{\ln M(\sigma_n) - a(r(n))}{b(r(n))} \Rightarrow \eta \quad (n \to \infty).
\]

Using the sequences of random permutations from section 2, we can obtain from here the assertions for corresponding classes of random mappings \(\sigma_n\).

Nonuniform distributions on \(\mathfrak{S}_n\) were considered by different authors, for instance, by Cheplyukova [5], Hansen and Jaworski [9], Mutafchiev [14], Pavlov and Myllari [19], Timashëv [21] and others.

References


ABSTRACTS
Statistical analysis of interval-censored data in questionnaire surveys

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Interval-censored data arise in questionnaire surveys when, instead of being asked to provide an exact value, respondents are free to answer with any interval. Such a format is particularly suitable when asking questions that are difficult to answer with an exact amount (e.g. recall questions). In this context, the assumption of noninformative censoring is violated, and thus standard methods for interval-censored data can not be applied. We suggest a nonparametric maximum likelihood estimator of the underlying distribution function, based on a certain data collection scheme. The consistency of the estimator is established under general conditions and an iterative procedure for finding the estimate is proposed. The performance of the method is evaluated in a simulation study.

Animated Map of Mathematics

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Abstract: A graphical representation of connections between different areas of mathematics through the last 25 years of XX century.
Dave Rusin created his MathAtlass at the end of last age [1]. We present a replication of his idea. We made a graphical representation of connections between different areas of mathematics using MDS algorithm (realised in R [2]). The data (downloaded from [3]), contains the classifications of Mathematical Reviews according Mathematical Subject Classification through the last 25 years of XX century. Graphics are made by moving bubbles chart, a powerful visualization tool in Google spreadsheets.

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References


Modelling of epidemics with vaccination: stochastic monotonicity and continuity properties

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Vaccination is one of the key tools in controlling the spread of an epidemic and there have been numerous mathematical studies of its effect on disease dynamics. Recently, Ball et al. [1] have developed a framework for analyzing time-dependent vaccination policies for epidemics which are modelled by a Crump-Mode-Jagers branching process. 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. In this study we focus on expanding these properties in the framework of Sellke construction for SIR epidemic models [2].

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References


Stochastic Navier-Stokes equation on the 2D- Riemannian manifold (Sphere)

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We consider the stochastic Navier-Stokes equation on the unit sphere considered as a Riemannian manifold. Using the method of Galerkin approximations and the stochastic calculus, we prove the existence of the solution and the invariant measure for the discretized equation (finite dimensional case). We prove also the convergence of the discretized equation solutions to the stochastic Navier stokes solution on the sphere.

References:


Randomness uncertainty and ergodicity in nature and society: towards a sustainable society ethics in a non-ergodic world

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People live and take decisions under uncertainty in nature and society environment. Since ancient times they try to reduce randomness in nature by recognizing laws of nature as causal relationships among different events or processes. In society, laws and regulations are created by people’s mind according people’s value system beliefs. Randomness in society is incorporated in uncertainty of human’s behavior. Humans create institutions according a value system beliefs in order to reduce uncertainty and risk and to achieve stability and sustainability and they can make essential changes in society establishing a new value system of beliefs. It is difficult to predict occurrence of essential changes in society since processes in society are path-dependent and non-ergodic. This paper is concerned with problems of a transformation process towards a sustainable society value system of beliefs or secular ethics under the conditions of a non-ergodic world hypothesis.

A noisy drift forecast and trading policies for high-frequency markets

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We study the impact of the noise in predicting the near-future behavior of high-frequency markets. In contrast to the existing methods that smooth or neglect the noise, we assume that it contains an important information about the hidden news that drive the price dynamics. Thus, in case of high-frequency markets, we construct a trading policy by analysing not the whole time series, but only its noisy part. Making use of suitable neural networks and more than three year historical data for USD/JPY exchange rates, we show that market’s near-future behavior is partially predictable. A definition of a trading edge as a criterion for policy’s performance is also given.
On the successful and blocked calls in one finite queueing system with losses

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The paper deals with two important descriptors of any queueing system with losses and/or blocked calls: the number of successful and the number of lost (blocked) calls, made during a time interval (0,t). The system under consideration has one server that serves finite number of customers. The customer, arriving at a moment of a busy server is not allowed either to queue, or to repeat his/her attempts. He/she is blocked for an exponentially distributed time interval in the orbit of blocked customers. Formulas for computing the main characteristics of the system, including the number of successful and lost calls are obtained in previous papers. Objective of the present paper is to extend and generalize them, and on the basis of numerical results to investigate the influence of the system parameters on the behavior of these descriptors.

Randomly indexed central order statistics through examples and application

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In our paper from 2013, we have investigated the asymptotic behavior of central order statistics with random size, using regular time-space changes. Here, an example using the results of randomly indexed central order statistics is given and a survey on the possible applications in insurance is made.
A graph based methods for clustering a morphologically similar words

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In this paper we present a method for grouping a morphologically similar words. At first we use some metrics for measuring the distance between elements in nonempty finite sets. We use those metrics in order to create a similarity matrix between words. The distance between two words in our case depends only on their morphological similarity. This allow us to make word clustering without a dictionary and also help us to handle incorrectly written words (typos).

After this process we create a weight graph which represent the similarity between words. Words are represented as vertices and there is an edge between two of them if and only if the similarity between words are above some threshold. The weight of the edge presents similarity between words. On this graph we use some methods to extract only the most morphologically similar words. With those methods we practically do a graph clustering i.e. we make a grouping of similar words in a clusters. This approach should increase efficiency for words clustering and should give us a better way of clustering words which can be further used for making better bag of words, finding similar words etc.

Using data mining techniques for recognition of Macedonian national dances

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Nowadays there are numerous sensors and hardware devices that can be creatively used to solve a vast variety of problems. In our research we used the Microsoft Kinect sensor in order to collect data about the movement of different parts of the human body from individuals who perform Macedonian national dances. The main goal is to employ supervised learning techniques to create models of several traditional dance choreographies based on the built dataset. We discovered that, even by using simple data mining techniques and algorithms such as Naive Bayes, kNN, decision trees and classification rules, we obtained satisfactory results with accuracy values up to 95% for kNN and 93% for Naive Bayes on a randomly chosen test set. The potential applications of the proposed solution range from analyzing the constitutive elements of a particular traditional dance choreography, through implementing a dancing tutor, to digitizing and preserving the Macedonian cultural heritage.

**Compound power series distribution with negative multinomial summands**

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The class of Power Series Distributions is quite general. It contains the most important discrete distributions, e.g. Poisson, Binomial, Negative binomial, Logarithmic series etc. The paper considers a multivariate distribution which coordinates are dependent Compound Power Series Distributed random variables with Negative Multinomial summands. We show the relation between these distributions and Multinomial distribution. In the most important particular cases we found appropriate equivalent presentations. For example in geometric case the resulting vector is just stochastically equivalent to a product of independent Bernoulli random variable and Multivariate geometrically distributed random vector. Using these relations we obtain some additional properties of Compound Power Series Distribution with Negative Multinomial Summands and its particular cases.
Special application of Mellin transform to contingent claims pricing

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Obtaining the fair value of a contingent claim is a broadly explored area in financial mathematics. Based on the assumption of a Geometric Brownian Motion process for the underlying asset we need to solve a parabolic equation with the relevant special conditions depending on the contract structure. Mellin transform, under certain conditions, can be a useful tool for obtaining a price estimate. Moreover, it turns out that after applying an inverse technique based on maximum entropy principle, the solution remains smooth and positive. This effect is best illustrated when pricing path-dependent contracts.

Penalty functions for perturbed risk processes

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We study several penalty functionals of classical risk processes with two-sided jumps, perturbed by an alpha-stable process. We obtain a formula for the Laplace transform of such functionals, as well as a representation of the functionals as infinite series of convolutions of given known functions.
On the bivariate compound Pólya process

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Key words: Compound distributions, bivariate geometric distribution, Pólya process.

In this paper we define a bivariate counting process as a compound negative binomial process with bivariate geometric compounding distribution. The resulting process is called a Bivariate compound Pólya process. Then we consider a risk model in which the claim counting process is a Bivariate compound Pólya process and call it a Bivariate compound Pólya risk model. We also consider two types of ruin probability for this risk model and find the corresponding Laplace transforms. We discuss in detail the particular case of exponentially distributed claims.

Noncentral Pólya-Aeppli process and ruin probability

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In this paper we introduce a stochastic process which is a sum of homogeneous Poisson process and Pólya-Aeppli process and call it a non-central Pólya-Aeppli process (NPAP). The probability mass function, recursion formulas and some properties are derived. As application we consider a risk model with NPAP counting process. The joint distribution of the time to ruin and deficit at the time of ruin is defined. The differential equation of the ruin probability is given. As example we consider the case of exponentially distributed claims.
Noncentral Pólya-Aeppli of order $K$ risk model

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In this study we define the Pólya-Aeppli process of order $K$ as a compound Poisson process with truncated geometric compounding distribution with success probability $1 - \rho > 0$ and investigate some of its basic properties. Using simulation we provide a comparison between the sample paths of the Pólya - Aeppli process and the Poisson process. Also, we consider a risk model in which the claim counting process $N(t)$ is Pólya-Aeppli process of order $K$, and call it a Pólya-Aeppli of order $K$ risk model. For the Pólya-Aeppli of order $K$ risk model we derive the joint distribution of the time to ruin and the deficit at ruin as well as the ruin probability. We discuss in detail the particular case of exponentially distributed claims and provide simulation results for more general cases.

Two-sample tank tests based on Lee distance

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Let $X_1, X_2, \ldots, X_m$ and $Y_1, Y_2, \ldots, Y_n$ be two independent random samples with continuous distribution functions $F(x)$ and $G(x)$, respectively. We consider rank tests for the two-sample location problem of testing the null hypothesis $H_0$ against the alternative $H_1$

$$H_0 : F(x) \equiv G(x)$$
$$H_1 : F(x) \geq G(x),$$

with strict inequality for some $x$. 
For nonparametric testing problem there are various procedures to constructing rank tests via metrics on the permutation group. Critchlow proposed a unified approach based on distance defined by the minimum interpoint distance between appropriate sets of permutations. The test statistic for the above problem is derived by the distance between the class of equivalence $[\alpha]$ and the extremal set $E$

$$d ([\alpha], E) = \min_{\pi \in [\alpha], \sigma \in E} d(\pi, \sigma),$$

where $d$ is an arbitrary metric on the set $S_N$ of all permutations of $N$ integers. The set $[\alpha]$ consists of all permutations in $S_N$ which are equivalent to the observed permutation $\alpha$. The set $E$ of extremal permutations consists of all permutations in $S_N$ which are least in agreement with $H_0$ and most in agreement with $H_1$. The test rejects the null hypothesis for small values of $d([\alpha], E)$.

For two permutations $\alpha$ and $\beta$ from the set $S_N$, Lee distance is defined by

$$L(\alpha, \beta) = \sum_{i=1}^{N} \min (| \alpha(i) - \beta(i) |, N - | \alpha(i) - \beta(i) |).$$

The goal of this research is to derive the test statistic (1) induced by the Lee distance function and study the distribution under null hypothesis.
Stochastic model of the relationship pharmacological effect - drug plasma concentration for new Bulgarian antihypotensive agent

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In this work the mathematical models of pharmacokinetics are used for description of the pharmacological effect of the medicine as a function of experimental plasma concentration. Pharmacokinetics is a branch of medico-pharmaceutical sciences and its aim is to examine the qualitative changes of the medicine when it enters the body. Based on the experimental data the parameters of two stochastic models for the new Bulgarian antihypotensive agent are estimated. For the description of the relationships plasma concentration - time the compartment models are used. For the relationship pharmacological effect - plasma concentration, the model of enzyme kinetics Michaelis - Menten is applied.

Asymptotic normality of conditional distribution estimation in the single index model

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This work deals with the estimation of conditional distribution function based on the single-index model for functional time series data. The asymptotic normality of the conditional distribution estimator is established. Moreover, as an application, the asymptotic \((1 - \gamma)\) confidence interval of the conditional distribution function is given for \(0 < \gamma < 1\).
Consensus algorithms and Decompostion-Separation Theorem

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A classical dictionary definition describes consensus as general agreement about something: an idea or opinion that is shared by all the people in a group. Nowadays this definition is outdated. Numerous studies of the last 20-30 years have demonstrated that many particle (agents) systems exhibit cooperative behavior that can lead to a consensus, or to multiple consensuses. Examples of this kind can be found in biology, robotics and control, sociology, political science, physics, mechanics, computer science etc. Consensus algorithms are algorithms leading to consensus. The most studied of these algorithms are linear (averaging) defined by stochastic matrix transformation. This leads to the study of nonhomogeneous Markov chains in reversed time. The Decompostion-Separation theorem proved in a final form by I. Sonin about 30 years ago and started in the thirties by A. Kolmogorov, and continued by D. Blackwell and H. Cohn, is a general theorem describing the behavior of such arbitrary Markov chain. One of the current publications states that "D-S Theorem relates to and generalizes most of the existing results in the literature on convergence properties of linear consensus algorithms". I will give a brief survey of consensus algorithms and their relationship to the DS Theorem.

References:

Accelerated EM algorithm and statistical inference for multitype branching processes with multivariate power series offspring distributions

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In our work we use the Accelerated EM algorithm to estimate the individual parameters of the class of discrete-time multitype branching processes with power series offspring distributions.

We consider an observation scheme in which only the population sizes of each generation are known and there are unobservable data about the quantity of the children.

A possible iterative procedure for maximum likelihood estimation in this model is the regular EM algorithm. Previous work has shown that this algorithm is effective, but time consuming in case of statistical inference for multitype branching processes.

We propose an R-implementation of the Accelerated EM algorithm, simulations and computational results.

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Comparison of partially ranked lists with application to RNA-seq data

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In many situations, there are different methods for analyzing the same data. For example, several methods exist for finding differentially expressed genes using RNA-seq data. These methods tend to produce similar, but not identical significant genes and partial rankings of the gene list.

Here we consider partial rankings of all genes of a given species. The genes are split into several groups, so that there is a ranking between the groups and not necessarily within each group. An important special case is a setup in which the most significant \( k \) genes are ranked, with group \( k+1 \) consisting of the remaining genes.

When comparing different methods applied to the same data, we are interested in how close are their outputs. Prior studies have compared several RNA-seq differential expression methods using empirical results based on real and simulated data. Our approach is based on the statistical distribution of the distance on the set of partial rankings. This allows us not only to measure the relative similarities between different methods, but also to infer whether two methods are significantly different. The outputs of several RNA-seq differential expression methods are analyzed using this approach.
Computational assessments of multidimensional branching processes derived from cosmic rays cascades

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The cosmic rays cascades are one of the most famous examples of branching processes in physics. They consist of many different types of secondary high energy particles which are offsprings of leading primary one, usually high energy nucleon or gamma, after collision with atmosphere. The rate of expansion of cascade depends on multiple different conditional probabilities as the chance of survival in atmosphere without interactions, particle lifetime, the number of daughter particles and etc. The presentation demonstrates quantitative results of simulated in R procedures for parallel estimations of energy spectra distribution of multiple types of daughter particles. The models are based on simplified cascades with only most distributed particles. The probability dependencies on particle’s energy and free path in atmosphere are not constrained only to available experimental results. Moreover, for simplicity the scattering angles are not considered in this version of software.
The problem of the preservation of the distribution of compound mixed renewal processes under a change of measure

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Let \((\Omega, \Sigma, P)\) be a probability space, let \(N\) be a mixed renewal process with mixing parameter a random vector \(\Theta\), and let \(X\) a family of independent and identically distributed random variables (i.i.d. for short), such that \(X\) and \(N\) as well as \(X\) and \(\Theta\) are independent. Let \(S\) be the compound mixed renewal process with respect to the probability measure \(P\) induced by \(N\) and \(X\). We characterize all probability measures \(Q\) on \(\Sigma\) such that \(S\) remains a compound mixed renewal process with respect to \(Q\), and \(Q\) and \(P\) are progressively equivalent.

The fact that the interarrival process \(W\) is not i.i.d. but conditionally i.i.d. with respect to \(\Theta\) makes the problem more complicated and difficult than the one in the Classical Risk Theory which was posed and solved by F. Delbaen & J. Haezendock [1].

We provide a characterization of probability measures \(Q\) as above in terms of martingales and disintegrations. As a consequence we obtain as special cases well known results form F. Delbaen & J. Haezendock [1] and P. Embrechts & S. Meister [2]. Finally, we provide concrete examples of the calculation of the Radon-Nikodym derivative of \(Q\) with respect to \(P\).

References:


Generation of correlation matrices

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Correlation and covariance matrices representing the strength of the dependence for each pair of factors involved in a statistical experiment are always positive definite matrices. The article discusses ways to generate such matrices with or without restrictions on their elements and laws of distribution. Special attention is paid to the case when the resulting correlation matrix presents a weak correlation between pairs of factors involved in the experiment.

Limiting Distributions for Alternating Regenerative Branching Processes

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Three new classes of alternating regenerative branching processes (ARBP) are proposed and investigated applying renewal and regenerative methods developed in Mitov and Yanev [J. Appl. Prob. 2001], [Adv. Appl. Prob. 2001]. In this way new limiting distributions are obtained for AR Sevastyanov processes, for AR Sevastyanov processes with non-homogeneous Poisson immigration and for AR randomly indexed branching processes.
A Bayesian spatial analysis of mumps data in Bulgaria

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Bayesian spatial methods have been widely applied in different scientific areas such as epidemiological studies, image processing, fMRI data analysis and many others. We will apply Bayesian hierarchical model with conditionally autoregressive (CAR) prior to a collection of weekly mumps data from 2000–2008 in Bulgaria. We will generate a disease mapping of the crude standardized incidence ratio (SIR) across all regional centers. Similar mappings will also be produced for the smoothed relative risk. The combination of methods for estimates of the relative risk is a powerful tool to identify high risk regions and may be used to inform local authorities and programs.

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