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Book of Abstracts

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This booklet contains about 90 abstracts submitted to the 9th International Workshop on Simulation. These abstracts reflect almost all main directions of the elaboration of mathematical techniques for stochastic simulation and experimental designs. Responsibility for the accuracy of all statements in each paper rests solely with the author(s).

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THE BOOKLET OF ABSTRACTS OF THE 9th INTERNATIONAL WORKSHOP ON SIMULATION
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Preface

The booklet contains abstracts of the 9th International Workshop on Simulation.

The Workshop is a regular international conference devoted to advanced mathematical techniques in applied probability and statistics, especially in stochastic simulation, experimental designs, queueing systems and extremums of random processes. The 1st- 6th Workshops took place in St. Petersburg (Russia) in 1994, 1996, 1998, 2001, 2005 and 2009, the 7th workshop was in Rimini in June 2013, and the 8th workshop was in Vienna in September 2015. The present workshop and the previous ones were organized by Stochastic Simulation Department of the St. Petersburg State University and the INFORMS college on Simulation (USA) in cooperation with other institutions.

It should be noted that the authors are entirely responsible for the final form of the abstracts.

The editors would like to thank all colleagues collaborated with them in the organization of the Workshop. Especially we would like to thank the following people for their excellent work: Josep Casanovas, Jordi Ocaña and Sonia Navarro

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Contents

Computable Simulated Transformations of the Cartesian Coordinates for Random Vectors

Abdrazakova A.R., Voytishek A.V.[1]

With the development of computer technology, there is the increasing interest in numerical algorithms for solving applied problems, with special importance of the computational schemes, which can be implemented on modern multiprocessor computers. From this point of view, the numerical statistical modelling algorithms (or the Monte Carlo methods) are sufficiently perspective (see, for example, [1]). One of the main elements of the algorithms of the Monte Carlo method is the numerical simulation (the generating of the sample values on a computer) of random variables and vectors (random points, multidimensional random variables). In this talk we introduce the notion of the computable simulated transformation of the Cartesian coordinates for a "non-simulated" (in the Cartesian coordinates) random vector. This notion is based on the lemma on the transformation of random variables. As the examples of such transformations we consider: - polar and spherical coordinates for the simulating uniformly distributed random points in a circle and in a three-dimensional ball, - cylindrical coordinates (three-dimensional case) for the simulating uniformly distributed random points in a cylinder, - parabolic coordinates for a special distribution of a random point in a two-dimensional curvilinear domain with "parabolic" boundaries. In addition, we give examples of algorithms of numerical statistical modelling for solving informative problems of mathematical physics in which computable simulated transformations of Cartesian coordinates are used.

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A New Branch and Bound Algorithm for the D-optimal Design Problem

Selin Damla Ahipasaoglu[1] and Benjamin Tan

Calculating an exact D-optimal design over a finite set of points remains a very challenging task, even though approximate designs can be found efficiently. We develop a new branch and bound framework for solving the Exact D-optimal Design problem and discuss how it can be implemented efficiently. Our approach is based on a first-order algorithm for solving the Minimum Volume Enclosing Ellipsoid problem, the dual problem to the approximate design problem, and on a simple technique to generate bounds on the objective function value of the subproblems in the search tree. We provide promising computational results.

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On new results for different record schemes

M. Ahsanullah[1], I.V. Belkov[2], V.B. Nevzorov[3],

Some non-classical record constructions are considered.

1) The representations of record ranges via sums of independent identically distributed exponential random variables are obtained for asymmetrical Laplace distributions. This result generalizes the corresponding relations for record values in the cases of exponential and negative exponential distributions.

2) The representation of record values based on sequences of non-identically distributed random variables in terms of independent summands is also obtained.

3) It is discussed, using the examples of exponential and geometrical distributions, how the process of discretization (up to seconds, up to meters or up to thousands of individuals) of observed results can vary the numbers of records in the sequences of random variables.

4) Independent random variables $X_1, X_2, \ldots, X_n$ having the standard uniform distribution and the upper and lower record values in this set are considered. The problem how to maximize (taking into account some consecutively observed values $x_1, x_2, \ldots, x_k$ of these X-s) the expectation of sums of records in this sequence under the optimal choice of the corresponding variable X_k (instead of X_1) as the initial record value is under consideration.

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Testing for serial independence in vector autoregressive models

J.S. Allison, S.G. Meintanis and J. Ngatchou-Wandji

We consider tests for serial independence of arbitrary finite order for the innovations in vector autoregressive models. The tests are expressed as L2–type criteria involving the difference of the joint empirical characteristic function and the product of corresponding marginals. Asymptotic as well as MonteCarlo results are presented.

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Multivariate small sample tests for two-way designs with applications to industrial statistics

Arboretti Rosa[1], Ceccato Riccardo[2], Corain Livio[2], Ronchi Fabrizio[2] and Salmaso Luigi[2]

In this paper, we present a novel nonparametric approach for multivariate analysis of two-way crossed factorial design based on NonParametric Combination applied to Synchronized Permutation tests. This nonparametric hypothesis testing procedure not only allows to overcome the shortcomings of MANOVA test like violation of assumptions such as multivariate normality or covariance homogeneity, but, in an extensive simulation study, reveals to be a powerful instrument both in case of small sample size and many response variables. The case of small sample size reflects the frequent needs of practitioners in the industrial environment where there are constraints or limited resources for the experimental design. Furthermore, an increase in rejection rate can be observed under alternative hypothesis when the number of response variables increases with fixed number of observed units. This could lead to a strategical benefit considering that in many real problems it could be easier to collect more information on a single experimental unit than adding a new unit to the experimental design. An application to industrial thermoforming processes is useful to illustrate and highlight the benefits of the adoption of the herein presented nonparametric approach.

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A stochastic model for the MHD-Burgers system

Yana Belopolskaya[1]

The aim of this article is to construct a stochastic representation of the Cauchy problem solution for a class of systems of nonlinear parabolic equations. In other words we aim to reduce the original Cauchy problem to a certain stochastic problem and moreover to construct the required solution via this stochastic system. The systems under consideration can be treated as systems of conservation laws arising in physics, chemistry, biology and other fields and were studied by many authors (see [1] – [3] and references there). We suggest an alternative interpretation for systems of this class and consider them as systems of nonlinear forward Kolmogorov equations for some nonlinear Markov processes. At the first step we find generators of these Markov processes. Unfortunately it appears that we need not these processes but their time reversal and their multiplicative functionals. We illustrate our approach studying as an example the Cauchy problem of the MHD-Burgers system.

Consider a PDE system which describe hydrodynamics in magnetic field including the MHD equation

$$\frac{\partial u_1}{\partial t}+\frac{\partial(u_1u_2)}{\partial x}=\frac{\sigma^2}{2}\frac{\partial^2 u_1}{\partial x^2},\quad u_1(0,x)=u_{10}(x) \tag{1}$$

and the Burgers equation with pressure provided by the magnetic field

$$\frac{\partial u_2}{\partial t}+\frac{1}{2}\frac{\partial(u_1^2+u_2^2)}{\partial x}=\frac{\mu^2}{2}\frac{\partial^2 u_2}{\partial x^2},\quad u_2(0,x)=u_{20}(x). \tag{2}$$

We construct a probabilistic representation of a weak solution $u=(u_1,u_2)$ to (1), (2) that is of a solution u which satisfy the integral identities

$$\int_0^T\int_R u_m(\theta,x)\left[\frac{\partial h_m(\theta,x)}{\partial\theta}+(\mathcal{A}_m^u+B_m^u)h_m(\theta,x)\right]dxd\theta+$$

$$+\int_R u_{m0}(x)h_m(0,x)dx=0,\quad m=1,2,$$

for any test function $h\in C_0^\infty([0,T)\times R)$. Here $\sigma_1=\sigma,\sigma_2=\mu$,

$$\mathcal{A}_m^u h_m=\frac{1}{2}\sigma_m^2\frac{\partial^2 h_m}{\partial x^2},\quad B_1^u h_1(x)=u_2\frac{\partial h_1}{\partial x},\quad B_2^u(x)h_2(x)=\left[\frac{u_1^2}{2u_2}+\frac{1}{2}u_2\right]\frac{\partial h_2}{\partial x}.$$

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Along with PDE system (1),(2) we consider a stochastic system of the form

$$d\hat{\xi}^m(\theta) = -\sigma_m dw(\theta), \quad \hat{\xi}^m(0) = x, \tag{3}$$

$$\tilde{\eta}^m(t) = exp\left\{\int_0^t C_m^u(\psi_{\theta,t}(x))dw(\theta) - \frac{1}{2}\int_0^t [C_m^u]^2(\psi_{\theta,t}(x))d\theta\right\} \tag{4}$$

$$u_m(t,x) = E[\tilde{\eta}^m(t)u_{0m}(\hat{\xi}^m(t))], \quad m = 1,2. \tag{5}$$

where $\hat{\xi}_{0,x}(t) = \psi_{0,t}(x)$ and

$$C_1^u(x) = \frac{1}{\sigma_1}u_2(\theta,x), \quad C_2^u(x) = \frac{1}{2\sigma_2}\left[u_2(\theta,x) + \frac{u_1^2(\theta,x)}{u_2(\theta,x)}\right].$$

Connections between (1),(2) and (3)–(5) are described in the following assertions.

Theorem 1. *Assume that there exists a unique weak solution $u = (u_1, u_2)$ to (1), (2) which is strictly positive, bounded and differentiable. Then functions $u_m(t,x)$ admit a representation of the form (5).*

We can prove as well an alternative statement.

Theorem 2. *Assume that there exists a unique solution $\hat{\xi}^m(\theta), \tilde{\eta}(\theta), u_m(t,x)$ to (3)– (5) and u_m are strictly positive, bounded and differentiable. Then functions $u_m(t,x)$ of the form (5) satisfy (1), (2) in a weak sense.*

Finally we can prove one more assertion.

Theorem 2. *Assume that u_{m0}, $m = 1,2$ are strictly positive, bounded and differentiable. Then there exists a solution to the stochastic system (3)– (5), functions $u_m(s,x)$ are strictly positive, bounded and differentiable and thus they satisfy (1), (2) in a weak sense.*

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Identifying and representing clusters of spatial defects in microelectronics planar artefacts

Riccardo Borgoni[1], Chiara Galimberti[2], Diego Zappa[3]

Statistical process control (SPC) charts are routinely adopted to monitor the stability of different processes over time mainly in manufacturing industries but also in other fields. Control charts detect a process distributional shift when the charting statistic is beyond the control limits. Amongst the different types of control charts, the cumulative sum (CUSUM) charts [2] are widely used in practice. However, practitioners would also be interested in knowing how strong the signal is in order to plan subsequent actions appropriately. For this reason, several authors have suggested control charts based on the p-value [1]. Following this approach the in-control distribution of the charting statistic is preliminarily computed and the p-value is obtained at any given time point. If the p-value is smaller than a pre-specified significance level α, the chart points out a process distributional shift. This approach has some benefits if compared to conventional control charts. Firstly, a p-value based control chart always has a vertical axis in the range [0, 1] and, hence, a unique control limit corresponding to α. Secondly, it provides a measure of how the data suggest a potential out-of-control state even if it is not detected.

Defects that tend to show systematic patterns over the wafer area, can be usually ascribed to specific causes of the production process. A prompt identification of these patterns allows to reduce discards and the need of reworking production items, hence improving the yield. Hereafter, it is assumed that a defect can be represented by a random point occurring in the wafer area, W, and the spatial dynamics of defectivity is thought as governed by a spatial point process over W. The lack of interaction among points is named complete spatial randomness (CSR) property. Being $N(W)$ the (random) number of events occurring in W and supposing that $N(W) = n$, the conditional property of CSR states that these n points are independent and uniformly distributed in W. If the CSR condition holds true, no structures are present in the defectivity process and defects are somehow a physiological result of the fabrication process. Testing the CSR condition consists in identifying a suitable test statistic that summarises

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the "discrepancy between the data and the CSR hypothesis". Being r_i the distance of the i-th event of the observed point pattern to its nearest event in the sample, we consider the Euclidean norm between the empirical cumulative distribution function (ecdf), $\hat{G}(r) = n^{-1} \sum_{i=1}^{n} \mathbb{1}(r_i \leq r)$ and the cdf, $G(r)$, of the nearest neighbour distance (NND) expected under the CSR condition denoted by $D = D(\hat{G}, G)$ hereafter. A large value of D observed on the data is not favourable to the CSR hypothesis. The p-value is obtained by approximating the distribution of D under the null hypothesis via Monte Carlo simulations. A large number B of point patterns under CSR are simulated and for the b-th simulated point pattern the ecdf $\hat{G}_b^*(r)$ and D_b^* are calculated. Finally, the p-value is obtained as $p = (B+1)^{-1}[1 + \sum_{b=1}^{B} \mathbb{1}(D_b^* \leq D_{obs})]$ where $D_{obs} = D(\hat{G}_{oss}, G)$ and $\hat{G}_{oss}$ is the ecdf calculated on the actual sample. A p-value control chart for structured spatial defectivity can be naturally based on a statistical test for CSR. Following the CUSUM approach, the defects occurred up to time t are cumulated and the ecdf of the NND is calculated on the cumulated point patterns. Hence, the test statistics, D_t, and the p-value, p_t, at time t are worked out as described above. In order to construct the chart, p_t values are reported on the y axis whereas time values are reported on the x axis as in usual control charts. A horizontal line is also added to the chart at the value of significance level α one wants to consider in the statistical test. In order to control the variability induced by the simulations that are necessary to estimate the distribution of the test statistics under the null hypothesis, we suggest to calculate a confidence interval of the p-value by bootstrapping the values $D_{tb}^*, b = 1, ..., B$ simulated at a given time t. The confidence interval is displayed on the chart and the process is considered out of control when this interval is below the α level adopted for the test.

Once an out-of-control state is detected it is relevant to assess the shape of the clusters occurring on the wafer areas in order to understand the defectivity process and to plan remediation actions. To this end, a clustering algorithm has been implemented to highlight those areas of the wafer more prone to high defectivity. We propose to reconstruct the structure and the shape of the cluster using the alpha-shape and principal curve methodologies.

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Asymptotics for High-Dimensional Covariance Matrices of Factor Models

Monika Bours[1]

In this talk we consider high dimensional vector time series $Y_1, ..., Y_n$ with a factor model structure

$$Y_i \;=\; BF_i + E_i, \quad i = 1, ..., n,$$

where the vector F_i contains all factors at time i, for $i = 1, ..., n$. It is assumed that the number of factors is allowed to go to infinity. The matrix B contains the corresponding factor loadings and E_i is the error component.

Factor models are widely used in various areas including psychometrics, marketing, finance as well as natural sciences and technology. For example, factor models are a key tool for financial risk analysis and macroeconomic forecasting of indicators such as the GDP (Gross Domestic Product) and inflation. Since large datasets are becoming increasingly available in many disciplines the analysis of high dimensional time series has become an highly active area. The estimation of high-dimensional variance-covariance matrices is of particular interest, but often only an intermediate step, since interest focuses on the behavior of functions of the sample variance-covariance matrix, especially bilinear forms which naturally arise when studying projection type statistics.

We establish new results on distributional approximations for bilinear functions of sample variance-covariance matrices in terms of Brownian motions. In the high dimensional setting, where also the dimension is allowed to go to infinity, these approximations by Gaussian processes hold true without any constraints on the dimension, the sample size or their ratio. Our results are valid for uniformly ℓ_1-bounded projection vectors which arise either naturally or by construction in many statistical problems like change-point analysis, sparse financial portfolio selection and shrinkage estimation.

A simulation study illustrates the performance of this theory. For example we will use our results to detect changes in the variance of a projection.

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Modeling and Asymptotic Analysis of Insurance Company Performance

Ekaterina Bulinskaya[1]

1 Introduction

It is well known that in order to study any real-life process or system one needs a mathematical model. Description of the new models which became important in modern actuarial sciences during the last twenty years one can find in the paper by Bulinskaya [1]. We mention only the strong interaction of insurance and finance and employment of sophisticated mathematical tools for investigation of complex stochastic systems. This paper deals with modeling of insurance company performance and its analysis continuing the research started in [2] - [7]. Thus, we are going to deal with models involving reinsurance, dividends payment and investment.

2 Formulation of the problem

One of our aims is to evaluate the functioning of an insurance company and study the sensitivity of optimal decisions to small fluctuations of parameters and perturbation of underlying distributions. The methods useful for this purpose one can find in the books by Saltelli at al. [11] and Rachev et al. [10], respectively. It is possible to perform this investigation in the framework of reliability and cost approaches. In other words, one can choose either the ruin probability as objective function or costs incurred by implementation of the optimal control. The solvency problems (see, e.g., [12]) demanded consideration of the so-called Parisian ruin and Omega models (for definitions see, e.g., [1] or [9] and references therein, as well as, [1]). We are interested in calculation and asymptotic analysis of these characteristics. Moreover, we introduce a new indicator of insurance company performance, namely, the first time η_l^X when the interval of the surplus staying above zero (before the Parisian ruin) becomes greater than l. For the Cramér-Lundberg model the explicit form of the Laplace transform of η_l^X is calculated as a function of the model's parameters. This enables us to carry out the sensitivity analysis of the new characteristic and establish the model stability.

Another problem treated in our presentation is the choice of dividends payment strategy in dual Sparre Andersen models which can arise in life-insurance or investigation of investment company performance.

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Run-length performance estimation of the functional regression control chart

Fabio Centofanti[1], Antonio Lepore[1], Alessandra Menafoglio[2], Biagio Palumbo[1] and Simone Vantini[2]

Because of advances in data acquisition technologies, it is increasingly common, in diverse fields of science, to gather data that are functional in nature. *Profile monitoring* is an expanding area of statistical process control (SPC) whose methods allow monitoring and controlling process quality characteristics which can be modelled as *functional data*. In many practical situations, measures of the quality characteristic are available jointly with those of other functional covariates. In this context, we propose a new control chart that takes into account additional information contained in those functional covariates to better monitoring the quality characteristic. This chart is referred to as *functional regression control chart* (FRCC) and is an extension of the *regression*, or *cause-selecting*, *control chart* which is used in the multivariate context.

Let $Y(t)$ represent the functional quality characteristic (hereinafter referred to as *response*) and $\boldsymbol{X}(t) = (X_1(t), \ldots, X_p(t))^\top$ be the functional covariates (hereinafter referred to as *predictors*) with $t \in \mathcal{S}$, a compact set in $\mathbb{R}$. We model the predictors as influencing the response according to the following multivariate non-concurrent (i.e., the response at time t is explained by the functional covariate values in $\mathcal{S}$ and not only at the same time t) functional-on-functional (i.e., functional response on functional covariates) linear regression model

$$Y^Z(t) = \int_{\mathcal{S}} (\boldsymbol{\beta}(s,t))^\top \boldsymbol{X}^Z(s)\, ds + \varepsilon(t), \tag{1}$$

with $Y^Z(t)$ and $\boldsymbol{X}^Z(t) = \left(X_1^Z(t), \ldots, X_p^Z(t)\right)^\top$ the point-wise standardized response and predictor variables, respectively, and $\boldsymbol{\beta}(s,t) = (\beta_1(s,t), \ldots, \beta_p(s,t))^\top$ the vector of the regression functional parameters.

The FRCC monitors the functional residuals of the model (1) adotpting the approach used in , where the coefficients from the Karhunen-Loève decomposition of the residual are monitored by means of the Hotellings T^2 and the squared prediction error (SPE) control charts.

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A simulation study is performed to quantify the FRCC performance, in terms of average run length (ARL), in identifying mean shifts in the functional response. Simulated data are generated using pre-specified covariance structure and means reference model for the response and predictors, similar to another simulation studies. Two different scenarios are considered: Scenario 1, where shifts affect only the conditional mean of the response given the predictors by means of changes in the response mean; Scenario 2, where both shifts in response and predictor means occurred. FRCC performance are compared with those of other two charts widely used to monitor profiles in the industrial context. Results show that the proposed control chart outperforms the competitor ones in both Scenario 1 and Scenario 2. However, in Scenario 2 shifts in the predictor means affect the FRCC performance, and conclusions about response mean shift must be drawn with caution.

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Nonparametric Permutation-based Testing on Multivariate Paired Preference Sensorial Evaluations

Livio Corain[1], Luigi Salmaso[1]

Suppose that several assessors are evaluating two or more attributes of a set of sensorial stimuli, i.e. fragrances or foods/beverages etc., by testing their smell or taste or in general by sensorial evaluations. Quite often those stimuli are not presented all in a row but in pairs of two at time [1]; when the response variables are defined by ordered scores, this design is known as the Degree of Difference (DOD) test [2]. By emphasizing that the order in which the two stimuli are submitted to assessors is definitely relevant, the purpose of this paper is to propose a novel DOD data representation modelling that was inspired the so-called dyadic data modelling [3]. As hypothesis testing solution, permutation and combination-based tests [4] were compared to univariate traditional testing proposed in this field [5], and a novel method of combination of traditional tests was also proposed. Via an extensive Monte-Carlo simulation study we investigated the properties of the proposed novel testing methodology where we proved its validity under different random distributions.

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Abstracts of the Ninth Workshop on Simulation (2018) 17-17

The ϵ-complexity of finite dimensional continuous maps

Boris Darkhovsky[1], Alexandra Piryarinska[2]

The concept of complexity for different mathematical objects is constantly in sight of many outstanding scientists. In our talk, we recall some basic ideas in approach to the problem of complexity, and then present our concept of the *ϵ-complexity* of continuous maps.

One of the first efforts to provide a quantitative approach to the concept of the "complexity of a physical system" was made in the 1870s by Boltzmann, who introduced the notion of entropy in equilibrium statistical physics. The greater the entropy, the more "complicated" the system is.

In the 1940s Shannon developed the concept of entropy to measure the uncertainty of a discrete random variable. He interpreted the entropy as a measure of the "degree of uncertainty" peculiar to a particular probability distribution. It can be shown that Shannon's entropy of stationary and ergodic random sequence is the coefficient in the asymptotic of the logarithm of the number of typical trajectories when time goes to infinity. Therefore, it is possible to use Shannon's entropy as the measure of "complexity" for stationary and ergodic random sequence.

In the 1950s Kolmogorov and Sinai introduced the entropy concept to the theory of dynamical systems. The entropy of a dynamical system is the coefficient of the asymptotic behavior of the logarithm of the number of different types of trajectories of a dynamical system when the time goes to infinity. Again, the entropy of a dynamical system may serve as a measure of "complexity": the more "complex" the system, the richer variety of its trajectories.

In the mid-sixties Kolmogorov has offered the general idea about "complexity of an object." At the semantic level, this idea can be described as follows: *a "complex" object requires a lot of information for its reconstruction and, for a "simple" object, little information is needed.* The "complexity" of an object should be measured by the length of its *"shortest description"*.

We show that neither Shannon's entropy, nor entropy of dynamic systems, nor Kolmogorov complexity are good tools for assessment of complexity of continuous maps. In this talk, we propose the concept of the *ϵ-complexity* for finite-dimensional continuous maps. This concept is in line with Kolmogorov's idea, but it is not confined to it. Our approach is based on a recovery of a continuous map by its values at some uniform grid. This approach allows receiving effective characterization of a complexity for Hölder maps. Employing the ϵ-complexity it was possible to offer *model-free* approach to the problems of classification and segmentation for data of arbitrary nature.

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Goodness of Fit Testing via fixed points of distributional transforms

Bruno Ebner

We propose new tests for the goodness of fit problem to parametric families of distributions. The new procedures are based on weighted L_2-distances of empirical distributional transforms to the empirical distribution function. The method will be illustrated for well-known goodness of fit problems as testing for normality or for gamma distributions. Weak convergence results are derived under the null hypothesis as well as under fixed and contiguous alternatives. A comparative finite sample power study shows the competitiveness to classical procedures.

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Some properties of quasi random numbers and their randomizations

Ermakov S. M[1], Leora S.N.[2]

A sequence of vectors $X_1, X_2, ..., X_N, ...$ in the unit s-dimensional hypercube is called quasi-random (low discrepancy) sequence, if its star-discrepancy has the best order $O(ln^S N/N)$. The well-known Koksma-Hlawka inequality [1] in this case gives the estimation of discrepancy decreasing of numeral integration error in the class of functions of bounded variation in the sense of Hardy and Krause also as $O(ln^S N/N)$. Since the logarithm is a function growing as N^S at an arbitrarily small ϵ, this suggests that the quasi-Monte Carlo methods are significantly better than the Monte Carlo method. This is true at moderate values of s and large values of N. However at large s ($s \geq 10$, for example), good asymptotic can occur at the excessively large values of N, practically unrealized on a computer (compare $1/\sqrt{N}$ and $ln^S N/N$ at $N = 10000$ and $s = 10$). For moderate N, another asymptotic is valid. The paper gives a number of numeral examples that support these considerations. Thus, only randomization of sequences can be recommended for the method quasi-Monte Carlo error estimation. These methods have close connection with the theory of quadrature formulas with one free node [2]. In the paper, these connections are discussed and are illustrated by numeral examples. We also propose the reception of the Holton sequence [3] transformation taking into account the behavior of the integrand. Advantage of such approach is confirmed by numeral examples. Acknowledgments. This work was partially supported by Russian Foundation for Basic Research, project 17-01-00267-a.

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Abstracts of the Ninth Workshop on Simulation (2018) 20-20

On Numerical Calculations of Stochastic Integrals

Ermakov S.M[1], Pogosian A[2]

The majority of numerical methods for calculation of stochastic integrals and stochastic differential equations (SDEs) are well-known to have both systematic and random errors [1]. Theres been a number of research works that are focused on systematic error reduction [2]. This paper considers a method that estimates Ito and Stratonovich integrals using Monte Carlo methods that have virtually no systematic error [3]. These methods may also be used for the numerical solution of SDEs: linear and polynomial. For the more general case of SDE local polynomial approximation is possible. Various numerical examples are given. The aforementioned methods are believed to extend to integrals over a martingale which could be of importance when dealing with problems in applied finance.

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Abstracts of the Ninth Workshop on Simulation (2018) 21-21

On quasirandom search

Ermakov Sergey M[1], Semenchikov Dmitriy N[2]

This paper looks at a combination of methods for finding the global extremum of a function of several variables: the simulated annealing method[1] and the stochastic gradient descent method[2]. The simulated annealing method gives an initial approximation for the global extremum and the stochastic gradient descent method yields its more precise value. For a more complete study (given the same number of calculations) of the function's domain, quasirandom numbers are used instead of pseudorandom numbers[3]. A modified method of simulated annealing, as it's described in [4], is also used. This modification uses the fact that a function $f^n(x)/\int f^n(x)$, as $n \to \infty$, converges to a function concentrated at the global extremum of f(x); where f(x) can have several equivalent extrema. To illustrate this algorithm's operation, a problem of regression experiment planning was chosen finding the D-optimal experimental designs.

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Abstracts of the Ninth Workshop on Simulation (2018) 22-23

Simulation of Branching Random Walks on Multidimensional Lattices

Ekaterina Ermishkina and Elena Yarovaya[1]

The processes with generation and transport of particles on the lattice $\mathbf{Z}^d$, $d \geq 1$, are usually called *branching random walks* (BRWs). It is convenient to describe such processes in terms of birth, death, and walks of particles on $\mathbf{Z}^d$. We assume that the structure of an environment is defined by the offspring reproduction law at a finite number of particle generation centers, *branching sources*, situated at points of $\mathbf{Z}^d$. The spatial dynamics of particles is considered under different assumptions about underlying random walks that may be simple symmetric, symmetric or non-symmetric. Such processes are used in numerous applications [1], in particular, in statistical physics, population dynamics, chemical kinetics.

In the last decade, for various models of branching random walks, a series theoretical results were obtained among which the limit theorems about behavior of the process for large times has been obtained, see, e.g. [1]. However, as it is often the case, much more difficult or almost impossible to analyze analytically branching random walks on finite time intervals. So, in this paper we generalize an algorithm for simulating branching random walks introduced in [1] and give new examples of its numerical realization.

In the BRW models with one branching source, the exponential growth of the population may occur when the intensity of the source β surpasses the critical value β_c [2]. The situation when $\beta > \beta_c$ is close to β_c (weakly supercritical BRWs) considered in [3] is of keen interest for the study, for example, of cell evolution [1]. The effect of phase transitions on the asymptotic behavior of a particle population in BRWs was studied analytically in detail by many authors, see, e.g., [4, 5, 6, 7] and the bibliography therein.

In [1], simulation of BRWs with one branching source is applied for numerical estimation of a threshold value of the parameter on finite time intervals. In the present work we propose an approach to simulation of the mean number of particles over the lattice and at every lattice point for BRWs with several sources. Simulation of the process is based on queue data structures, see, e.g., [8], and the Monte Carlo method described, e.g., in [9]. This approach allows to simulate BRWs with sources of different intensities and random walks with jumps not only to neighbor lattice points.

The evolution of particle system in BRWs is carried out in accordance with the rules used for constructing the algorithm for the BRW simulation. Some necessary theoretical results for an interpretation of the simulation are given.

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The simulation is illustrated by an example of a BRW with a few sources of equal intencities, which demonstrates how the space configuration of the sources affects the behavior of the mean numbers of particle. An analytical investigations of the same BRW can be found in [3, 10]. In conclusion, more general BRWs with a finite number of sources of different intensities and finite variance of jumps considered in [7] are simulated.

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Abstracts of the Ninth Workshop on Simulation (2018) 24-25

Modelling count time series in a state-dependent under-reporting scheme

A. Fernandez, A. Cabaña[1], H. Joe, D. Moriña, P.Puig

Since the introduction of the Integer-Valued AutoRegressive (INAR) models in [1], the interest in the analysis of count time series has been growing. The main reason for this increasing popularity is the limited performance of the classical time series analysis approach when dealing with discrete valued time series. With the introduction of discrete time series analysis techniques, several challenges appeared such as unobserved heterogeneity, periodicity, under-reporting, ... Many efforts have been devoted in order to introduce seasonality in these models [2] and also coping with unobserved heterogeneity. However, the problem of under-reported data is still in a quite early stage of study in many different fields. This phenomenon is very common in many contexts such as epidemiological and biomedical research. It might lead to potentially biased inference and may also invalidate the main assumptions of the classical models. For instance, in [3] the author explores a Markov chain Monte Carlo based method to study worker absenteeism where sources of under-reporting are detected. Also in the context of public health , it is well known that several diseases have been traditionally under-reported (occupational related diseases, food exposures diseases, ...).

The model we will present here considers two discrete time series: the observed series of counts Y_t which may be under-reported, and the underlying series X_t with an INAR(1) structure

$$X_t = \alpha \circ X_{t-1} + W_t$$

where $0 < \alpha < 1$ is a fixed parameter and W_t is Poisson(λ). The *binomial thinning* operator is defined as $\alpha \circ X_{t-1} = \sum_{i=1}^{X_{t-1}} Z_i$, where Z_i are i.i.d Bernoulli random variables with probability of success equal to α.

The way we allow Y_t to be under-reported is by defining that $Y_t = X_t$ with probability $1 - \omega$ or it is $q \circ X_t$ with probability ω. This process $\{Y_n\}$ represents an under-reported phenomenon coming from the latent INAR(1) process, where parameters ω and $q$are the frequency and the intensity of under-reporting, respectively.

For a more general model, suppose now that the states of under-reporting follow a binary discrete-time Markov chain. This new situation only adds one further parameter to the previous situation, and is more flexible for modelling.

We derive the autocorrelation structure of both models, and compute maximum likelyhood estimators for the parameters via a modification of Viterbi algorithm.

Several examples of application of the models in the field of public health will be discussed, using real data.

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Abstracts of the Ninth Workshop on Simulation (2018) 26-27

Ascent with Quadratic Assistance for the Construction of Exact Experimental Designs

Lenka Filová[1], Radoslav Harman[2]

In the area of experimental design, there is a large body of theoretical knowledge and computational experience concerning so-called optimal approximate designs. However, for an approximate design to be executed in a practical setting, it must be converted into an exact design, which is usually done via rounding procedures.

The first notable rounding method was suggested by Kiefer [3], who formulated the rounding problem as the minimization of the maximum of the difference between the exact and approximate design weights. By using techniques similar to those applied in voting apportionment, the authors of [4] arrived at a criterion-independent rounding algorithm known as efficient rounding (ER). More recent proposals include randomized rounding heuristics (see [1] and [5]); however, these methods are only applicable if the criterion function is submodular (e.g., D-optimality). Although generally rapid, rounding procedures have several drawbacks; in particular, they often yield worse exact designs than heuristics that do not require approximate designs at all.

In the talk, we will present a model- and criterion-based hill-climbing method, which we call ascent with quadratic assistance (AQuA), based on a quadratic simplification of the optimality criterion in the neighborhood of the optimal approximate information matrix, extending the approach of [2]. AQuA overcomes almost all of the disadvantages of ER and similar methods. In particular, the proposed method does not depend on the choice of the optimal approximate design (if the approximate design is not unique), it is not restricted to the support of the optimal approximate design, and the resulting designs are usually significantly more efficient than the designs computed via ER and somewhat more efficient than the results produced via heuristic methods that do not use approximate designs. Unlike the method proposed in [2], AQuA does not require advanced integer quadratic solvers; moreover, it is generally more efficient, and its applicability is not restricted to problems of D-optimality but rather extends to a much broader spectrum of criteria.

We numerically demonstrate the generally superior performance of AQuA relative to both rounding procedures and standard heuristics for a problem of optimal mixture experimental design.

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Abstracts of the Ninth Workshop on Simulation (2018) 28-28

Pretesting Assumptions for the validity of two sample Mean Tests

Pablo Flores M[1] and Jordi Ocaña[2]

Traditional pretests to prove homoscedasticity should be avoided because they induce an alteration in Type I Error Probability. In conjunction with an adequate irrelevance limits, a test of dispersion equivalence is a more affordable pretesting strategy indepedently of heteroscedasticity, but only if normality is ensured or for mild and moderate contaminations from this distribution. For high and severe non-normality there is not an adequate robust procedure that can be recommended.

Keywords— homoscedasticity, equivalence test, indifference zone, pretest, robustness

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Statistical Implications of Informative Dose Allocation in Binary Regression

Nancy Flournoy[1] and Assaf Oron[2]

In many fields such acute toxicity studies, Phase I cancer trials, sensory studies and psychometric testing, binomial regression techniques are used to analyze data following informative dose allocation. We assume the simplest general case in which a univariate binary response Y has a monotone positive response probability $P(Y = 1|X = x) = F(x)$ to a stimulus or treatment X; X values are sequentially selected from a finite discrete set $\{d_1, d_2, \ldots d_M\}$ of M values to concentrate treatments in a region of interest under $F(x)$. We call a positive response a toxicity and the stimulus a dose. From first principles, we describe dependencies that are introduced by sequentially choosing informative doses.

Suppose n subjects receive treatments that were sequentially selected according to some rule using data from prior subjects. Let N_m and T_m denote the final number of subjects allocated to dose d_m and the number of toxicities observed there, respectively, $m = 1, \ldots, K$. We remind the reader that the *joint likelihood* of treatment and response data is a function of the final set of observed allocation and toxicity rates $\{N_m, T_m, m = 1, \ldots, K\}$ [1] that is similar to likelihood for binomial random variables but with random sample sizes, and without the combinatorial constants. That is, under mild conditions that typically hold:

$$\mathcal{L}_n = \prod_{m=1}^{M} F(d_m)^{T_m}[1 - F(d_m)]^{N_m - T_m}.$$

We refute the prevailing notion that T_m given N_m is a binomial random variable; and characterize, at finite sample sizes, the bias of the observed toxicity rate T_m/N_m for $F(x)$ at dose x. We show that

$$E[T_m/N_m] = F_m - Cov[T_m/N_m, N_m]/E[N_m].$$

So, the observed toxicity rate is biased for F_m when adaptive allocations, by design, induce a correlation between toxicity and allocation rates. Commonly used variance formulae are also first-order linear approximations.

Understanding this is important for small to moderately sized designs because isotonic regression methods use the toxicity rates $\{T_m/N_m, m = 1, \ldots M\}$ directly;

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and standard likelihood methods indirectly as first-order linear approximations. We study these biases using isotonic and likelihood-based regression methods in some commonly used (small sample size) adaptive methods including some up-and-down designs, interval designs, and the continual reassessment method.

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Abstracts of the Ninth Workshop on Simulation (2018) 31-32

Inference under a two-stage adaptive design for non-linear regression models with normal errors

Nancy Flournoy[1], Caterina May[2], Chiara Tommasi[3]

In this work, we assume that a response variable is explained by several controlled explanatory variables through a non-linear regression model with normal errors. The unknown parameter is the vector of coefficients, and thus it is multidimensional.

To collect the responses, we consider a two-stage experimental design; in the first-stage data are observed at some fixed initial design; then the data are used to estimate an optimal design at which the second-stage data are observed. Therefore, first- and second-stage responses are dependent. At the end of the study, the whole set of data is used to estimate the unknown vector of coefficients through maximum likelihood.

In practice it is quite common to take a small pilot sample to demonstrate feasibility. This pilot study provides an initial estimate of unknown parameters which are then used to build a second-stage design and add additional data to improve the estimate. See, for instance, [1] and [2] for a scalar case. Accordingly, we obtain the asymptotic behaviour of the maximum likelihood estimator under the assumption that only the second-stage sample size goes to infinity, while the first-stage sample size is assumed to be fixed. This contrasts with the classical approach in which both the sample sizes are assumed to become large and standard results maintain for the asymptotic distribution of the maximum likelihood estimator.

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Abstracts of the Ninth Workshop on Simulation (2018) 33-34

Performance measures in dose-finding experiments

Nancy Flournoy[1], José A. Moler[2], Fernando Plo[3]

Consider binary responses indicating toxicity for which the probability of toxicity is assumed to increase with dose. In the first phase of pharmaceutical development in oncology, the main statistical goal is to estimate a given target percentile from such binary responses. In this work, we present tools for studying the performance of adaptive designs in this context, taking measures of inferential precision and toxic exposure into account simultaneously. Finally, these tools are used in a simulation study that evaluates the performance of selected phase I procedures.

1 Introduction

In this work, we study combined measures of ethical treatment and quality estimation to clarify their tradeoff and to quantify the global performance of a design. Then, selected competing designs are compared with each other with respect to these measures. Of course, these measures depend on the method of quantile estimation and/or dose-selection used.

By simulation, summary ethical and inferential measures are obtained for each n, as n increases over a preset range. The Pareto frontier is graphically obtained from a plot of a selected ethical and inferential measure. Such graphs are shown to be useful for studying the performance of various allocation rules with respect to both criteria simultaneously.

For an ethical criterion, many papers in the literature use some measure of how close dose allocations are to the target dose. These measures are surrogates for patients' toxic exposure. In a simulation study, toxic exposure can be measured directly. Therefore, we measure the ethics of a design in terms of the (simulated) observed toxicity rates. Measures of how close doses are to the target dose we call *allocation criteria*. Procedures can perform identically with respect to studies overall toxicity rates while having quite distinct dose-allocation patterns.

We study several measures of the quality of estimators. First, the root mean square error is measured on the dose scale, that is, using the distance of each quantile estimator from the target dose. It is also measured on the toxicity scale, that is, using the distance between the simulated toxicity rate and actual toxicity

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rate at the target dose. Finally, in order to provide a performance measure in terms of patients (to match the ethical criterion), the classical optimal design concept of efficiency is included.

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Aberrations of Orthogonal Arrays with removed runs

Roberto Fontana[1] and Fabio Rapallo[2]

1 Introduction

In this work, we consider multilevel Orthogonal arrays (OAs) under the Generalized Minimum Aberration (GMA) criterion, and we focus on the following problem. In several situations, it is hard to define *a priori* a fixed sample size. For example, budget constraints or time limitations may occur after the definition of the design, or even when the experiments are running, thus leading to an incomplete design. In such a situation, it is relevant not only to choose an OA with good properties, but also to define an order of the design points, so that the experimenter can stop the sequence of runs and loose as less information as possible. While OAs with added runs are well studied, see for instance [1] and the references therein, less has been done in the case of OAs with removed runs. Some results in this direction can be found in [3]. For a general reference on OAs, see [2].

2 Removing points from an OA

Let $\mathcal{D}$ be a full factorial design and $\mathcal{F}$ be a fraction. We use for each factor the complex coding of the levels. Moreover, denote with $\{X^\alpha, \alpha \in L\}$ the monomial basis of all complex functions defined on $\mathcal{D}$.

The counting function R of $\mathcal{F}$ is a polynomial defined over $\mathcal{D}$ so that for each $x \in \mathcal{D}$, $R(x)$ equals the number of appearances of x in the fraction. A $0-1$ valued counting function is called an indicator function of a single-replicate fraction $\mathcal{F}$. We denote by c_α the coefficients of the representation of R on $\mathcal{D}$ using the monomial basis $\{X^\alpha,\ \alpha \in L\}$:

$$R(x) = \sum_{\alpha \in L} c_\alpha X^\alpha(x),\ x \in \mathcal{D},\ c_\alpha \in \mathbf{C}\,.$$

The Generalized Word-Length Pattern (GWLP) of a fraction $\mathcal{F}$ of the full factorial design $\mathcal{D}$ is a the vector $A_\mathcal{F} = (A_0(\mathcal{F}), A_1(\mathcal{F}), \ldots, A_m(\mathcal{F}))$, where

$$A_j(\mathcal{F}) = \sum_{|\alpha|_0 = j} a_\alpha \quad j = 0, \ldots, m\,,$$

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$$a_\alpha = \left(\frac{\|c_\alpha\|}{c_0} \right)^2 , \tag{1}$$

$|\alpha|_0$ is the number of non-null elements of α, and $c_0 := c_{(0,\dots,0)} = \#\mathcal{F}/\#\mathcal{D}$.

The number a_α in Eq. (1) is the aberration of the term X^α. The GMA criterion consists in the lexicographic minimization of the GWLP $A_\mathcal{F}$.

In order to see how the GWLP changes when one or more design points are removed from an OA, we prove a general formula for the GWLP of the union of two or more fractions.

Given k fractions $\mathcal{F}_1, \dots, \mathcal{F}_k$ with $n_1, \dots, n_k$ runs respectively, consider their union $\mathcal{F} = \mathcal{F}_1 \cup \dots \cup \mathcal{F}_k$. The j-th element of the GWLP of $\mathcal{F}$ is

$$A_j(\mathcal{F}) = \sum_{i=1}^{k} \frac{n_i^2}{n^2} A_i(\mathcal{F}_i) + 2\frac{(\#\mathcal{D})^2}{n^2} \sum_{i_1<i_2} \sum_{|\alpha|_0=j} \mathrm{Re}(c_\alpha^{(i_1)} \overline{c}_\alpha^{(i_2)}), \quad j = 0, \dots, m\,. \tag{2}$$

The formula in Eq. (2) can be applied with two different strategies to study the fractions obtained by deletion of runs:

- first, Eq. (2) ca be used to compute the aberrations of a fraction obtained by an OA by removing a few points;
- second, we can consider the decomposition of a large OA into smaller fractions.

Several examples concerning both approaches will be discussed.

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A Quasi-Newton Algorithm for Optimal Approximate Linear Regression Design

Norbert Gaffke[1]

1 Introduction

Given a linear regression model and an experimental region for the independent variable, a problem of optimal approximate design leads to minimizing a convex criterion function $\Phi(M)$ over the set of all information matrices $M(\xi)$ of feasible approximate designs ξ. The set $\mathcal{M} = \big\{M(\xi) : \xi \text{ any approximate design}\big\}$ is typically given as a convex hull of the set of all information matrices of elementary designs,

$$\mathcal{M} = \operatorname{Conv}\big\{M(x) : x \in \mathcal{X}\big\}, \tag{1}$$

where $\mathcal{X}$ denotes the experimental region and $M(x)$ is the elementary information matrix at the design point x which is a nonnegative definite $p \times p$ -matrix. The optimization problem reads as

$$\text{minimize} \quad \Phi(M) \quad \text{over} \quad M \in \mathcal{M} \cap \mathcal{A}\,, \tag{2}$$

where $\mathcal{A}$ is a given 'feasibility cone' constituting the domain of Φ, i.e., $\mathcal{A}$ is a convex cone of symmetric $p \times p$ -matrices containing all positive definite $p \times p$ -matrices. It is assumed that the generating set $\{M(x) : x \in \mathcal{X}\}$ is compact, its convex hull $\mathcal{M}$ contains some positive definite matrix, and the (convex) criterion function Φ is twice continuously differentiable on $\operatorname{int}(\mathcal{A})$, the interior of $\mathcal{A}$. Moreover, the algorithm requires that linear minimization over $\mathcal{M}$, or equivalently over its generating set, can easily be done, i.e., a subroutine is available to solve the problem

$$\text{minimize} \quad \operatorname{tr}\big(A\,M(x)\big) \quad \text{over} \quad x \in \mathcal{X}\,, \tag{3}$$

for any given symmetric $p \times p$ -matrix A. Note that for a finite experimental region $\mathcal{X}$ linear minimization is trivial, unless $\mathcal{X}$ is tremendously large. The quasi-Newton algorithm for solving (2) was originally established in [2]. The recent paper [3] has demonstrated new possibilities of applications of the algorithm.

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2 Outline of the algorithm

As a main tool the algorithm employs a subroutine which provides minimization over $\mathcal{M}$ of any given convex quadratic function via repeatedly solving linear minimization problems (3). The subroutine is an adaptation of a more general method in [4] and therefore we call it the 'Higgins-Polak subroutine'. The outline given next of the quasi-Newton algorithm for solving (2) employs $p(p+1)/2$-dimensional column vectors m obtained by vectorization of symmetric $p \times p$ -matrices M which is convenient in view of quadratic approximations and BFGS-updates. By $g(m)$ we denote the gradient of Φ at $m \in \mathcal{M} \cap \mathrm{int}(\mathcal{A})$.

Quasi-Newton algorithm:
(o) *Initialization*: choose any $m_1 \in \mathcal{M} \cap \mathrm{int}(\mathcal{A})$; compute $g_1 = g(m_1)$; choose any $B_1 \in \mathrm{PD}\big(p(p+1)/2\big)$; set $t = 1$. Go to step (i).
(i) *Quasi-Newton step*: apply the Higgins-Polak subroutine to compute an optimal solution $\overline{m}_t \in \mathcal{M}$ to the convex quadratic minimization problem

$$\text{minimize} \quad (g_t - B_t m_t)^{\mathrm{T}} m + \tfrac{1}{2} m^{\mathrm{T}} B_t m \quad \text{over} \quad m \in \mathcal{M}.$$

Go to step (ii).
(ii) *Line search*: apply an adaptation of Fletcher's line search procedure ([1], Chapter 2.6) which computes a suitable $\alpha_t \in (\,0\,,\,\alpha_{\max}]$, where $\alpha_{\max}$ is a predefined constant in $(0\,,\,1)$ usually close to 1, e. g., $\alpha_{\max} = 0.99$. Set $m_{t+1} = (1-\alpha_t)m_t + \alpha_t \overline{m}_t$ and compute the gradient $g_{t+1} = g(m_{t+1})$. Go to step (iii).
(iii) *BFGS update*: let $\delta_t = m_{t+1} - m_t$ and $\gamma_t = g_{t+1} - g_t$. Set

$$B_{t+1} = B_t + (\gamma_t^{\mathrm{T}} \delta_t)^{-1} \gamma_t \gamma_t^{\mathrm{T}} - (\delta_t^{\mathrm{T}} B_t \delta_t)^{-1} B_t \delta_t \delta_t^{\mathrm{T}} B_t, \quad \text{if } \gamma_t^{\mathrm{T}} \delta_t > 0,$$

and set $B_{t+1} = B_t$ otherwise, i. e., if $\gamma_t^{\mathrm{T}} \delta_t = 0$.
Go to step (i) with t replaced by $t+1$.

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The Hellinger dependence measure and its root-n estimation

Gery Geenens, Pierre Lafaye de Micheaux[1] and Spiridon Penev

Testing for the independence between two or more random variables or vectors is a very active topic of statistical research; see for example [1] for a recent survey.

In his seminal paper [2], Rényi formulated 7 axioms that an ideal dependence measure should satisfy. However, these axioms are too strong for general use. In this work, we give a list of reasonable properties that any dependence measure between two random variables should satisfy.

This leads us to propose the following new dependence measure between two random variables X_1 and X_2:

$$\Delta(X_1, X_2) = 1 - \int\int_{\mathcal{I}} \sqrt{c_{12}}(u_1, u_2) du_1 du_2,$$

where $\mathcal{I} = [0,1] \times [0,1]$. This dependence measure is based on the Hellinger distance. It involves the square root of the joint copula density of X_1 and X_2.

We show how to obtain a root-n consistent estimator of our new Hellinger dependence measure by borrowing ideas from the k-nearest neighbours technique. This estimator is then used to build a new test of independence between two random variables. Empirical simulations show the good performance of our new approach against several competitors, such as [3] and [4].

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Goodness-of-fit tests for compound distributions with applications in insurance

Pierre-O. Goffard[1]

Goodness of fit procedures are provided to test for specified compound models for the total claims, as well as for the constituent components namely the claim frequency distribution, as well as distribution of individual claims. This is done without the need for observations on these two component variables. Goodness-of-fit tests that utilize the Laplace transform as well as classical tools based on the distribution function, are proposed and compared. These methods are validated by extensive simulations and then applied to a real data example.

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Excess of D-optimal Designs for Cobb-Douglas model

Yu.D. Grigoriev[1], V.B. Melas[2], P.V. Shpilev[3]

1 Introduction

The problem of searching nonsingular optimal designs with the minimal number of support points is quite important since the use of such designs allows to decrease experimental expenses. Many works were devoted to the study of this problem, see [7], [8] and [1]). In pioneer paper [2] was shown that D-optimal designs are always saturated for polynomial regression models, i. e. the number n of support points of these designs coincides with the number p of unknown parameters $\theta \in \Theta \subseteq R^p$ of the model $\eta(x, \theta)$. In [6], this result is called the de la Garza phenomenon. On the other hand, for nonlinear in parameters models, cases in which optimal designs arise with the number of support points $n > p$ are not rare. In our recent paper [4] we proposed to call such cases the *excess phenomenon*, and the corresponding designs *excess* designs. The series of papers [9], [10], [11] and [3] consider the question on transferring de la Garza result to nonlinear models. For example, in [9] and [11] it was provided an approach allowing to decrease the upper estimate for the number of support points which is equal to $\frac{p(p+1)}{2}$ for D-optimal designs following from the Caratheodori theorem. In some cases, the Yang method directly leads to the conclusion that the locally optimal design $\xi = \xi(\theta)$ for the model in question is saturated. One manages to decrease the upper estimate for the number of support points in the Yang-Stufken method due to analysis of the structure of the information matrix elements. It is evident that, if there are equal elements among them or if they possess certain specific properties, then the account for this information leads to reducing the upper estimate.

Most authors are concentrated their attention on models with one explaining variable whereas many regression models used in practice are multidimensional. These models are much more difficult to study and methods that work good enough for one dimensional models (such as Yang-Stufken method and its specifications for example) usually can't be generalized to a multidimensional case. To a large extent, this is related to the fact that Chebyshev systems of functions do not exist in this case, see [3].

Excess phenomenon also takes place for the locally optimal design for multidimensional models. The analytical solution of the problem of finding the dependence between the number of the locally optimal design support points and the

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lengths of the design intervals could be a very useful instrument which allows the investigator to choose the most suitable design space to reduce experimental expenses. In our recent paper [4] we got some results for Ayen-Peters model but to our best knowledge no other analytical solutions of this problem for multidimensional models are available in the literature. The purpose of the present paper is to study excess phenomenon on the example of the two-dimensional Cobb-Douglas model which is used in microeconomics [5]. In our work, we show that, for some homotheties $T\colon \mathcal{X} \to \mathcal{X}'$ of the design space $\mathcal{X}$, saturated locally D-optimal designs for two-dimensional model can become excess and vice versa. We find saturated designs in the explicit form. In our paper we provide an analytical solution of the problem we've discussed.

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A Nonhomogeneous Risk Model

Alice Gross[1]

Introduction

This paper deals with the problem of ruin in the compound binomial model that describes the temporal evolution of the surplus of an insurance company at fixed dates. The premium income process is deterministic, and the successive claim amounts are independent and nonidentically distributed. Our purpose is to evaluate the probability of ruin over any finite time horizon under the assumption of the model where the claim sizes are distributed as a discrete phase-type distribution.

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T-Optimal Designs for Discrimination between Rational and Polynomial Models

R.A. Guchenko[1] and V.B. Melas[1]

This paper considers the problem of the analytical construction of T-optimal experimental designs for discrimination between the simplest rational and polynomial regression models. It is shown how the classical results from approximation theory can be used to derive explicit formulas describing the behavior of support points and weights of T-optimal designs for different fixed parameter values. The problem of discrimination between Michaelis–Menten model and quadratic model is considered as an example. The text is based on the paper [1].

Let experimental results $\{y_i\}$ be described by the equation:

$$y_i = \eta(x_i, \theta) + \varepsilon_i, \qquad i = 1, \ldots, n,$$

where $x_1, \ldots, x_n$ are experimental conditions that belong to a certain compact set $\mathcal{X}$ and are such that $x_i \neq x_j$ if $i \neq j$, $\theta = (\theta_1, \ldots, \theta_d)^T \in \Theta$ is the vector of unknown parameters, $\eta(x, \theta)$ is a real-valued regression function, and $\{\varepsilon_i\}$ are independent normally distributed random errors with zero mean and fixed variance.

Suppose that we have two competing regression functions for $\eta(x, \theta)$: $\eta_1(x, \theta_1)$ and $\eta_2(x, \theta_2)$ that are both continuous over x. Besides we know a certain approximate value of $\overline{\theta}_1$ for the first model parameters θ_1 a priori and we also assume that η_2 is continuously differentiable over θ_2 on compact Θ_2. The discrete probability measure ξ^*, which maximizes the criterion

$$T_{1,2}(\xi, \overline{\theta}_1) = \inf_{\theta_2 \in \Theta_2} \int_{\mathcal{X}} \left[\eta_1(x, \overline{\theta}_1) - \eta_2(x, \theta_2)\right]^2 \xi(dx),$$

is called T-optimal experimental design (see [2]).

It is known that the problem of finding T-optimal designs is related to the best Chebyshev approximation problem (see, e.g., [3]) in the sense that the equality

$$\sup_{\xi} \inf_{\theta_2 \in \Theta_2} \int_{\mathcal{X}} \left[\eta_1(x, \overline{\theta}_1) - \eta_2(x, \theta_2)\right]^2 \xi(dx) = \inf_{\theta_2 \in \Theta_2} \sup_{x \in \mathcal{X}} \left|\eta_1(x, \overline{\theta}_1) - \eta_2(x, \theta_2)\right|, \quad (1)$$

holds, and the support points of a T-optimal design for discrimination between $\eta_1(x, \theta_1)$ and $\eta_2(x, \theta_2)$ coincide with the alternance points for the problem of the best Chebyshev approximation of the function $\eta_1(x, \overline{\theta}_1)$ with function $\eta_2(x, \theta_2)$.

Let us consider the following pair of regression models:

$$\eta_1(x, \theta_1) = \sum_{i=0}^{m} \theta_{1,i} x^i + \frac{1}{x - a}, \qquad \eta_2(x, \theta_2) = \sum_{i=0}^{m} \theta_{2,i} x^i, \quad (2)$$

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that are defined for $x \in [-1,1]$. Due to (1) the problem of finding the T-optimal design for discrimination between this models is reduced to the classical problem of Chebyshev approximation theory, i.e., the search for a polynomial providing the best fit to the function $1/(x-a)$. It is natural to assume that $a \notin [-1,1]$. Without loss of generality, we will assume that $a > 1$.

In the paper we prove that T-optimal design for discrimination between models (2) is concentrated at $(m+2)$ points from the interval $[-1,1]$, becides the points ± 1 always belong to this design's support for every m and the support points from the interval $(-1,1)$ are the roots of polynomials

$$\begin{aligned} \Psi_1(x) &= U_m(x) - 2\alpha U_{m-1}(x) + \alpha^2 U_{m-2}(x), && m \geq 2, \\ \Psi_2(x) &= \left(\alpha^2 - 1\right) T_m(x) + \left(2\alpha - x - \alpha^2 x\right) U_{m-1}(x), && m \geq 1, \end{aligned}$$

where $\alpha = a - \sqrt{a^2-1}$. For $m \leq 4$ the roots of this polynomials can be easily found.

The similar result also holds for the following pairs of competing models:

$$\eta_1(x,\theta_1) = \sum_{i=0}^{m} \theta_{1,i} x^i + \frac{1}{x^2 - a}, \qquad \eta_2(x,\theta_2) = \sum_{i=0}^{m} \theta_{2,i} x^i; \tag{3}$$

$$\eta_1(x,\theta_1) = \sum_{i=0}^{m} \theta_{1,i} x^i + \frac{x}{x^2 - a}, \qquad \eta_2(x,\theta_2) = \sum_{i=0}^{m} \theta_{2,i} x^i; \tag{4}$$

on the interval $x \in [-1,1]$ with $a > 1$.

It is shown that T-optimal designs for models (3) and (4) are concentrated at $(m+2)$ points. If m is odd, the support points from the interval $(-1,1)$ of the design for pair (3) coincide with the roots of polynomials

$$\begin{aligned} \Psi_1(x) &= U_m(x) - 2\alpha^2 U_{m-2}(x) + \alpha^4 U_{m-4}(x), && m \geq 4, \\ \Psi_2(x) &= 2x\left(\alpha^4 - 1\right) T_{m-1}(x) + \left(\alpha^4 + 2\alpha^2 + 1 - 2x^2[\alpha^4 + 1]\right) U_{m-2}(x), && m \geq 2, \end{aligned}$$

and if m is even, this is true for pair (4). The points ± 1 always belong to an optimal designs support for every m. As earlier, $\alpha = a - \sqrt{a^2-1}$ here.

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Computing optimal experimental designs with respect to a compound Bayes risk criterion

Radoslav Harman[1] and Maryna Prus[2]

1 Introduction

We will consider the problem of computing optimal experimental designs with respect to a compound Bayes risk criterion, which includes various specific criteria, such as a linear criterion for prediction in a random coefficient regression model. We will prove that this problem can be converted into a problem of constrained A-optimality in an artificial model, which allows us to directly use existing theoretical results and software tools. We will demonstrate the application of the proposed method for the optimal design in a random coefficient regression model with respect to an integrated mean squared error criterion. The talk is based on [2].

2 Formulation of the problem

Let $\mathcal{X}$ be a finite design space. For an experimental design ξ, let $\mathbf{M}(\xi)$ denote the information matrix. The aim is to propose a method for computing optimal approximate and exact designs on $\mathcal{X}$ with respect to the criterion Φ defined by

$$\Phi(\xi) = \sum_{j=1}^{s} \mathrm{tr}((\mathbf{M}(\xi) + \mathbf{B}_j)^{-1}\mathbf{H}_j) \tag{1}$$

for all designs ξ such that the matrices $\mathbf{M}(\xi)+\mathbf{B}_j$ are non-singular for $j = 1, \ldots, s$, and is defined by $\Phi(\xi) = +\infty$ for all other designs ξ. In (1), $\mathbf{B}_1, \ldots, \mathbf{B}_s$ are given non-negative definite $p \times p$ matrices, and $\mathbf{H}_1, \ldots, \mathbf{H}_s$ are given positive definite $p \times p$ matrices.

We will call (1) the compound Bayes risk criterion (CBRC) because for $s = 1$, it is equivalent to the standard Bayes risk criterion; see [1]. The class of CBRC criteria includes the recently proposed criterion for the prediction of individual parameters in random coefficient regression models ([3]) which is our main motivation for studying optimality criteria of this form.

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We will show that it is possible to convert any problem of CBRC-optimality into a problem of linearly constrained A-optimality in an auxiliary linear model. This enables computing CBRC-optimal designs by existing methods of mathematical programming, such as second-order cone programming and mixed-integer second-order cone programming ([4]).

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Optimal Design for Growth Curve Models

Heinz Holling[1], Fritjof Freise[2], Rainer Schwabe[3]

In educational and psychological testing repeated measurement of cognitive abilities leads to considerable gains in ability scores. To efficiently analyze these gains we will develop an optimal test design for growth curve models based on item response models. Item difficulties are assumed to be known in order to efficiently estimate individual growth curves for the abilities due to retesting or learning.

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Bayesian optimal designs for the Michaelis-Menten Model

Guillermo Juliá[1], Jesús López-Fidalgo[1]

The Michaelis-Menten model describes the velocity rate in many enzymatic reactions. This model is used in cases when the concentration of the substrate is higher than enzyme concentration, and when the concentration of the substrate-enzyme compound stays constant. Biochemical reactions involving a single substrate are also often modelled with this equation. Using the optimal experiment design theory for non-linear regression models, like the Michaelis-Menten model (e.g. [3, 4, 5], we have applied the D-optimal criteria and the pseudo Bayesian D-optimal criteria and found the optimal design for each case. The so called General Equivalence Theorem provides a fantastic tool for checking whether a particular design is optimal or not with respect to a convex criterion. When applying Bayesian optimality (e.g. [1, 2]) a closed-form expression for the optimal design is not always available for this model. Therefore, numerical computations have performed for different cases. Two different Bayesian approaches have been used. On the one hand the expectation of any criterion according to the prior distribution has been used. This is sometimes called pseudo-Bayesian and it is very much used in the literature. A more sophisticated version considers an information matrix which depends on the sample size and the prior covariance matrix. We have compared different optimal designs for both approaches and different values of the sample size. Adapted equivalence theorems allow for computation and measuring the efficiency of the designs obtained. Keywords: Bayesian Optimal Designs; D-optimality; Equivalence Theorem; Fisher Information Matrix.

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Abstracts of the Ninth Workshop on Simulation (2018) 51-51

Monte Carlo simulation of air temperature, pressure and relative humidity joint non-stationary time-series

Kargapolova N.A[1],Khlebnikova E.I.[2], Ogorodnikov V.A.[3]

A stochastic model of air temperature, relative humidity and atmospheric pressure joint time-series is presented. The model is based on long-term observations at meteorological stations, where weather elements were measured every 3 hours. Month-long time-series are considered as a periodically correlated random process, the period of which is equal to 1 day. To describe the correlation structure of time-series, sample correlation matrices are used. Instead of sample one-dimensional distributions mixtures of Gaussian, beta and gamma-distributions are used. Parameters of the mixtures are time-dependent periodic functions whose values are determined from real data. On the basis of simulated trajectories, some statistical properties of rare meteorological events were studied. This work was supported by the Russian Foundation for Basis Research (grant No 18-01-00149-a), Russian Foundation for Basis Research and Government of Novosibirsk region (grants No 18-41-540003-r_a, 18-41-543006-r_mol_a), the President of the Russian Federation (grant No MK-659.2017.1).

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Monte Carlo Simulation of Optical Radiation Transfer Process in Stochastic Scattering Media

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The talk deals with a number of aspects related to statistical modeling of processes of optical radiation transfer in scattering and absorbing media. Space-time variations of optic parameters of these media are assumed to have a random character. Algorithms of the Monte Carlo method and a set of programs, which allow construction of numerical models of the electromagnetic radiation field in such media have been developed. The set is mainly intended for solving stochastical problems of the cloudy atmosphere optics. Some issues connected with construction of the 3D random fields of continuous and broken cloudiness are discussed. The main emphasis is being given to the discussion of algorithms of simulation of radiation fields in clouds and cloudy atmosphere. A special attention has been paid to solving the problem of optimization of Monte Carlo algorithms. The optimization is based on the method of dependent trials.

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Statistical Modelling of the Optical Radiation Transfer in Ocean-Atmosphere System

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In the geometric optics approximation a statistical model of the optical radiation transfer process in the form of an integral equation for collision density in the ocean-atmosphere system for both the complete and simplified "facet" model of the random agitated ocean surface is described. Some variations of the transfer equation for collision density corresponding to different problems of remote optical probing of the ocean are written out. This work is carried out in connection with the task of substantiation of analogue and weight algorithms of statistical modeling of direct problems of passive and active aerospace probing of the ocean. Alongside the Monte-Carlo method, the considered models may be useful for the analysis of the optical radiation field with other numerical or analytical methods connected to the integral transfer equation.

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Stochastic Mesh Method for Non-Linear Functionals on Paths

Yuri Kashtanov[1]

Let x_s be a diffusion process $dx_s = a(x_s)dw_s + b(x_s)ds$, $y_t = \int_0^t h_s(x_s)ds$ be integrals on trajectories and $f_t = f_t(x_t, y_t)$ be some "reward" functions. The optimal stopping problem connected with f_t is formulated as calculation of

$$C_T = \sup_{\tau<T} \mathbf{E} f_\tau, \tag{1}$$

where τ are Markov moments.

Examples. It is shown in [1] that a problem of optimal stopping of resource extraction is described with "reward" functions $f_t = \int_0^t \alpha_u S_u du + \beta_t S_t$, where $S_t = \exp(x_t)$ is the resource price. If f_t has the form

$$f_t = \left(e^{\frac{1}{t}\int_0^t x_u du} - K \right)^+$$

then C_T is a price of geometrical average Asian option [2]. The latter gives an example of non-linear functional.

After discretization we receive the chain $z_n = (x_n, y_n)$ which approximates the process (x_t, y_t). The problem is reduced to the solution in the form of backward induction:

$$Y_N(z) = f_N(z), \quad Y_n(z) = \max\left(f_n(z), \mathbf{E}_{n,z} Y_{n+1}(z_{n+1})\right). \tag{2}$$

Mark Broadie and Paul Glasserman in [3] suggested a stochastic mesh method for the sequence (2) which does not depend on the dimension. But conditions for consistency of the method for the above problem are not fulfilled directly because transitional densities for z_n have singularities. It was shown in [4] that in the linear case the component y_n may be randomized and consistency of the method under some conditions was proved.

Here we consider the case when functions f_n are not linear, then this randomization does not work but we can get rid of singularity in a different way.

Let ξ_n be a sequence of independent standard normal variables, define

$$\begin{aligned} x_{2n+1} &= x_{2n} + a(x_{2n})\xi_{2n+1}\sqrt{\Delta} + b(x_{2n})\Delta, \\ x_{2n+2} &= x_{2n+1} + a(x_{2n})\xi_{2n+2}\sqrt{\Delta} + b(x_{2n})\Delta, \\ y_n &= \sum_{i=1}^{n} x_i \Delta. \end{aligned}$$

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We can consider the process $z_n = (x_{2n}, y_{2n})$. Transitional probabilities $p(z, z'')$ for the chain z_n have the form

$$p(z, z'') \quad = \quad \frac{1}{\Delta}\varphi\left(x + b(x)\Delta - x',\, a^2(x)\Delta\right)\varphi\left(x' + b(x)\Delta - x'',\, a^2(x)\Delta\right).$$

where $z = (x, y)$, $z'' = (x'', y'')$, $x' = (y'' - y)/\Delta - x''$, $\varphi(\cdot, \sigma^2)$ being the normal density with variance σ^2. These transitional probabilities are not singular but now conditions from [4] are not fulfilled because the "drift" component in $p(z, z'')$ is unbounded.

It is shown in the present investigation that inequalities from [4] needed for consistency are fulfilled, and thus stochastic mesh method works.

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Optimal Design for a Causal Structure

Zaher Kmail[1], and Kent Eskridge[2]

Linear models and linear mixed models are important statistical tools. But in many natural phenomena, there is more than one dependent (endogenous) variable involved and these variables are related in a sophisticated way. Structural Equation Modeling (SEM) is often used to model the relationship between the endogenous (dependent) variables and the exogenous (independent) variables. SEM allows us to estimate the parameters that explain the relationships among the variables [1]. It was first implemented in research to not only separate, but also demonstrate the direction of direct and indirect effects [5], and measure the relative magnitude of each causal factor [3]. Traditional optimal design theory and literature focuses on optimal design for univariate linear and univariate mixed models. There are four objectives for our research. First, we will use the modified Federov search algorithm to produce a D-optimal design for a causal structure for both the 3SLS and FIML estimators. Next, we will obtain a D-optimal design for the estimate of the endogenous and exogenous parameters of a mixed random causal structure. Then, we will use Composite criteria [6] to produce an optimal design for the estimate of the endogenous, exogenous, and random parameters (variance components) of a mixed random causal structure. Finally, we will develop a search algorithm that produces a D-optimal design for the estimates of the endogenous and exogenous parameters of a causal structure with fixed blocks. We then compare the efficiency of each of the optimal designs for causal structures with the optimal design for the univariate case. In each of the four cases above, the causal relationship changed the optimal designs dramatically. The new optimal designs were much more efficient. Even orthogonal designs, which are universally optimal in the univariate case [2][4], are not optimal with causal structural models. The new optimal designs for causal structures were much more efficient than orthogonal designs.

Keywords: Optimal design, D-optimality criteria, causal structure modeling, three-stage least squares, orthogonal design, endogenous variables, exogenous variables

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Numerical statistical study of reconstruction algorithms of the aerosol scattering matrix elements

A.S. Korda[1], S.A. Ukhinov[2]

The variations of the sky brightness are defined mainly by the volatility of the aerosol part of the atmosphere, which posesses strong scattering ability. Theoretical study of the radiation transfer problems is impossible without knowing it's optical parameters. In this work is considered the problem of reconstructing the aerosol scattering matrix by using observations of polarized radiation in the solar almucantar, i.e., in various directions that make the same angle θ_s with the zenith as the line of sight to the Sun [1, 3, 4].

The first component of the matrix is scattering phase function or indicatrix of the atmosphere, the second component is responsible for the polarization of radiation. Under the "single-scattering" approximation the observed values of the Stokes vector are proportional to the corresponding values of the matrix components.

Several iterative algorithms for estimation of the indicatrix are constructed in [1, 3, 4]. In this algorithms the values of the indicatrix are successively refining by mathematical modeling based on the information of the angle distribution of the radiation intensity on the underlying surface and under the assumption that the contribution of the single-scattered radiation is rather large. The polarization of radiation by air molecules is taken into account by using the well-known matrix of Rayleigh scattering. Reconstruction of the scattering matrix is carried out in several steps. On the first step we reconstruct the first component of the matrix assuming that the second component is null, after that we reconstruct the second component using the estimate of the first component. In this work the predictor-corrector modification of the method is suggested, i.e. on the third step we are looking for more precise estimate for the indicatrix using the estimate for the second component received on the second step..

In [2] is given theoretical substantiation of the convergence of the reconstruction methods for the indicatrix for specific parameters of the atmosphere. In order to

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numerically substantiate the convergence of these methods, an algorithm of Jacobi matrices calculation for the iteration operators of the methods was developed, and calculations were carried out for various parameters of the atmosphere. The objective of this work is to numerically substantiate the convergence of the methods of reconstructing the scattering matrix and suggested modification. Also a study of the influence of measurement errors on the reconstruction of the scattering matrix was carried out. Test calculations showed the stability of algorithms to errors in the initial data.

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Some Applications of Evolution Modelling for Multi-Particle Systems in the Kinetic Model Framework[1]

M.A. Korotchenko[2], A.V. Burmistrov[3]

In this paper, we will describe our experience in application of kinetic models in the rarefied gas dynamics, as well as in some other areas: coagulation of particles, vehicular traffic flows, and prices formation in the market. In all these cases, the use of the integral equations and the corresponding Markov chains allows to extend the well-developed theory of weighted Monte Carlo methods to the problems under consideration. Moreover, this makes it possible to estimate the parametric derivatives of the solution. This is especially important when one studies the influence of various parameters on the solution of the nonlinear kinetic equations.

1 Introduction

A number of mathematical physics problems could be reduced to the estimation of some linear functionals of solutions to integral equations. This is mainly because a mathematical model of such problems is constructed based on the corresponding stepwise Markov process, which terminates with probability one. The transition density of the latter process is the substochastic kernel of the integral operator, which describs the evolution of the system during single a step. The first example of such equation is the nonlinear kinetic Boltzmann equation, which remains the basis of the kinetic theory of gases. This integro-differential equation describes the dynamics of a rarefied gas and was derived by Ludwig Boltzmann in 1872. The nonlinearity of this equation lies in the collision integral, which describes the pair interactions of particles.

Though the kinetic equation was first obtained for the homogeneous relaxation of a single component ideal gas, the range of its applications turned out to be much wider. Boltzmann type equations are used to study the radiation transfer in matter, neutrons transfer in a nuclear reactor, electrons transfer in solids and plasmas, and also to study the growth of droplets in clouds, defects in materials, gas pores in metals, etc.

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2 Applications

In this paper, we summarize our approaches earlier developed in the field of multi-particle systems modelling for various problems such as: rarefied gas relaxation (see, for example, [1]), particle coagulation [1, 3, 5], vehicular traffic flow [2, 4] and price formation [6]. All these problems are described by the Boltzmann type equations. To solve them numerically, we propose to use the integral equation of the second kind and the weighted modelling using the Markov chain, which is uniquely determined by the coefficients of this integral equation.

For some problems we construct "value" modifications of the weighted statistical modelling to solve numerically the kinetic equation (for details see [1, 3, 5]), which leads to a considerable reduction of computational costs.

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Adaptive Designs for Optimal Observed Fisher Information

Adam Lane[1]

Expected Fisher information can be found a priori and as a result its inverse is the primary variance approximation used in the design of experiments. This is in contrast to the common claim that the inverse of observed Fisher information is a better approximation of the variance of the maximum likelihood estimator. Observed Fisher information cannot be known a priori ; however, if an experiment is conducted sequentially (in a series of runs) the observed Fisher information from previous runs is known. In the current work two adaptive designs are proposed that use the observed Fisher information from previous runs to design the future runs. The results of a simulation study using a generalized linear model (gamma regression with log link) is used to illustrate the performance of the adaptive designs proposed in this work. It is found that the adaptive designs significantly increase efficiency compared to alternative designs. This is most pronounced when the sample size is small to moderate. For large samples the improvement is still present; however, it is reduced.

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Block tensor train decomposition for missing data estimation

Namgil Lee[1], Jong-Min Kim[2]

We propose a new method for imputation of missing values in large scale matrix data based on a low-rank tensor approximation technique called the block tensor train (TT) decomposition. Given sparsely observed data points, the proposed method iteratively computes the soft-thresholded singular value decomposition (SVD) of the underlying data matrix with missing values. The SVD of matrices is performed based on a low-rank block TT decomposition, by which storage and time complexities can be reduced dramatically for large scale data matrices with a low-rank tensor structure. We implemented an iterative soft-thresholding algorithm for missing data estimation [6], and the SVD with block TT decomposition was computed based on alternating least squares iteration. Experimental results on simulated data demonstrate that the proposed method can estimate a large amount of missing values accurately compared to a matrix-based standard method.

1 Introduction

A tensor refers to a multi-dimensional array, which can be considered as a generalization of vectors and matrices. Tensor decomposition, like matrix SVD, has been developed for a wide scope of applications in signal processing, machine learning, chemometrics, and neuroscience [3]. Traditional tensor decompositions include Candecomp/Parafac (CP) decomposition and Tucker decomposition; see, e.g., [3]. Modern tensor decompositions have been developed more recently to cope with the problem called as the curse-of-dimensionality, which means an exponential rate of increase in the storage and computational costs as the dimensionality of tensors increases [2]. The tensor train (TT) decomposition is one of the modern tensor decompositions which generalize the matrix SVD to higher-order (i.e., multi-dimensional) tensors [7]. Modern tensor decompositions such as the TT decomposition applies not only to higher order tensors, but also to large scale vectors and matrices, by transforming the vectors and matrices into higher-order tensors via a tensorization process [1]. Once the large scale vectors and matrices have been decomposed by TT decomposition, algebraic operations such as the matrix-by-vector multiplication can be performed much efficiently with logarithmically scaled computational costs [7].

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In this work, we consider the singular value decomposition (SVD) of a large matrix $\widehat{\mathbf{Y}} \in \mathbb{R}^{I \times J_1 J_2 \cdots J_N}$, where the goal is to compute the R_X largest singular values and the corresponding left/right singular vectors as

$$\widehat{\mathbf{Y}} \approx \mathbf{U}\mathbf{S}\mathbf{V}^\top, \tag{1}$$

where $\mathbf{U} \in \mathbb{R}^{I \times R_X}$, $\mathbf{S} = \mathrm{diag}(s_1, \ldots, s_{R_X})$, and $\mathbf{V} \in \mathbb{R}^{J_1 \cdots J_N \times R_X}$. We consider that a large "tall-and-skinny" matrix $\mathbf{V} \in \mathbb{R}^{J_1 \cdots J_N \times R_X}$ is reshaped and permuted into a tensor $\mathcal{V}$ of size $J_1 \times \cdots \times J_n \times R_X \times J_{n+1} \times \cdots \times J_N$. The block-$n$ tensor train (TT) decomposition of $\mathbf{V}$ is defined by a product of a series of low-order tensors as

$$\mathbf{V} \approx \mathcal{V} = \mathcal{V}_1 \bullet \mathcal{V}_2 \bullet \cdots \bullet \mathcal{V}_N, \tag{2}$$

where $\mathcal{V}_m \in \mathbb{R}^{R_{m-1} \times J_m \times R_m}$ $(m \neq n)$ are third-order tensors, $\mathcal{V}_n \in \mathbb{R}^{R_{n-1} \times J_n \times R_X \times R_n}$ is a fourth-order tensor. The tensors $\mathcal{V}_1, \ldots, \mathcal{V}_N$ are called the TT-cores and $R_1, \ldots, R_{N-1}$ are called the TT-ranks. We assume that $R_0 = R_N = 1$. Note that when the large matrix $\mathbf{V}$ is decomposed by the block TT decomposition, the storage cost reduces from $\mathcal{O}(J^N R)$ to $\mathcal{O}(NJR^2)$, where $J = \max(\{J_m\})$ and $R = \max(\{R_m\}, R_X)$. See, e.g., [4,5,7], for further properties of TT decomposition and algebraic operations.

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The accuracy and convergence of spectral models for the sea surface and rogue waves simulation

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The sea surface roughness is sufficiently well described by a random Gaussian field, which is stationary with respect to time and homogeneous with respect to space. Spectral models of the sea surface were used to solve series of applied problems by Monte Carlo method, including the simulation and research into the rogue or freak waves. We use conditional spectral models of random fields for the numerical simulation of rogue waves [1, 2, 3]. A realization of a conditional spectral model of the sea surface with a rogue wave is presented in Figure 1. Figure 1: An example of the simulated topography of the rogue wave (a realization of conditional spectral model). The values on the axes are given in meters. n this paper, we study sufficient conditions for the convergence in various function spaces of the sea surface undulation models based on the spectral decomposition of the stochastic field of the water level. We analyze numerical errors for the functionals of spectral models of the sea surface roughness in order to estimate the accuracy of the stochastic models. This research was supported by the Russian Foundation for Basic Research (Project 18-31-00159).

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Supercomputer simulation of electron avalanches in gases with calculation of diffusive characteristics

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1 Introduction

We consider the problem of electron transfer in a gas under the action of a strong external electric field. Electrons started at the initial (zero) time moment from the cathode move with an acceleration to the anode. For the sake of simplicity, we assume that the anode and cathode are plane-parallel. Electrons move, collide with gas molecules, and then are absorbed, or diffused elastically or non-elastically, or ionize the gas "beating out" secondary electrons. Thus, the number of charged particles grows exponentially, that forms ionized gas particles and an electron avalanche (or electron cloud). The basic transport characteristics of an avalanche are diffusion coefficients (longitudinal D_L and transversal D_T ones), the drift velocity of the cloud, mobility of electrons, frequency of ionization, mean kinetic energy, primary ionization coefficient (see, e.g., [1]). This work is focused on calculations of D_L and D_T by the Monte Carlo method.

2 Formulation of the problem

The mathematical model of transfer of charger particles in an external electric field is described by the following transfer equation (see, e.g., [9]):

$$\frac{\partial f}{\partial t} + \mathbf{v}\frac{\partial f}{\partial \mathbf{r}} + \frac{q\mathbf{E}}{m}\frac{\partial f}{\partial \mathbf{v}} = \nu_c \int\limits_{\Omega'} [f(\mathbf{r}, \mathbf{v}', t) - f(\mathbf{r}, \mathbf{v}, t)] w(\omega, \omega') d\omega'. \qquad (1)$$

Here $f(\mathbf{r}, \mathbf{v}, t)$ is the electron distribution density, $\mathbf{r} = (x, y, z)$, t is the time, $\mathbf{v}$ is the velocity vector, q is the charge of a particle, $\mathbf{E}$ is the electric field vector, m is the mass of a particle, ν_c is the frequency of collision of articles with elements of the medium, $\omega = \mathbf{v}/V$, $\omega' = \mathbf{v}'/V'$ are the motion direction vectors before collision and after it, V is the absolute value of the velocity.

Special algorithms of statistical modelling are constructed to solve this equation by Monte Carlo method. Since (1) admits reduction to an integral equation, it is possible to construct motion trajectories of particles by the usual technique, which corresponds to a probabilistic physical model of electron transfer process (see, e.g., [1]).

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It is possible to calculate diffusion coefficients in several ways. One of them was proposed within the framework of diffusion approximation, i.e., for Gaussian approximation of the density. However, it can be also used for more accurate estimates of the required functionals. In this method the diffusion coefficients are obtained using the "radii" of transversal and longitudinal diffusion $R_T = \sqrt{4D_T t}$ and $R_L = \sqrt{4D_L t}$, respectively. Let the electrons begin their motion at the point with the coordinates $(x, y, z) = (0, 0, 0)$ and the electric field intensity equal $\mathbf{E} = (0, 0, -E_z)$. Thus, the electron cloud moves along the axis OZ. For the distribution density of particles $\rho(x, y, z, t)$ we obtain

$$\rho(0, y, z, t)/\rho(R_T, y, z, t) = e^{R_T^2/(4D_T t)} = e^1,$$

$$\rho(x, y, z_{max}, t)/\rho(x, y, z_{max} + R_L, t) = e^{R_L^2/(4D_L t)} = e^1.$$

Therefore, to calculate the diffusion radii we have to construct the graph of the distribution density of particles, determine the point of its maximal value ("top" point) and the point where the value of the graph is e times less than at the top point. It is clear that the sufficiently accurate calculation of the diffusion coefficients requires construction of sufficiently accurate global estimators of the density. A histogram and a polygon of frequencies with especially chosen steps were used previously for that purpose (see [1, 2]). In this work we construct more precise estimators for the diffusion radius based on the smoothed estimators of particles distribution density, namely, kernel estimators of ParzenRosenblatt [3] using a grouped sample and randomized projection method utilizing Laguerre and Hermite polynomials.

The calculations were performed by ELSHOW package in the Siberian Supercomputer Center of SB RAS with the use of PARMONC package for parallel computations [4].

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Simulation of the interaction of solitons by the Monte Carlo method

Vitaliy Lukinov[1]

The rapidly increasing demand on communication speed is exerting great pressure on the network's infrastructure at every scale, which explains the real motivation behind all optical communications research. Since the introduction of fiber-optic communications in the late 1970s, many technological advances, such as erbium-doped fiber amplifiers, wavelength division multiplexing (WDM), dispersion management, forward error correction, and Raman amplification, have been developed to enable the exponential growth of data traffic. However, the continuing bandwidth demand is pushing the required capacity close to the theoretical limit of the standard single-mode fiber (SSFM), which is imposed by the fiber's nonlinearity effects (Kerr effect) [1]. In recent years, there have been extensive efforts in attempting to surpass the Kerr nonlinearity limit through various nonlinearity compensation techniques. However, there are still many limitations and challenges in applying the aforementioned nonlinear compensation methods, because the transmission technologies utilized in optical fiber communication systems were originally developed for linear (radio or open space) communication channels. Therefore the true limits of nonlinear fiber channels are yet to be found.

The interaction and propagation of optical signals in fiber can be accurately modelled by the nonlinear Schrodinger equation (NLSE) [1], which describes the continuous interplay between dispersion and nonlinearity. It is well known that the NLSE (without perturbation) belongs to the class of integrable nonlinear systems. In particular, this means that the NLSE allows the existence of a special type of solutions: highly robust nonlinear waves, called solitons. Solitons were proposed as the information carriers for the high-capacity fiber-optic communications. In this article we use super(multicore) computing to modell the soliton interaction where the number of nuclei runs into hundreds of thousands puts forward Monte Carlo methods (MCM) the most adapted to parallel calculations, both from the point of view of the simplicity of parallelizing the algorithms and the necessity of carrying out a huge number of identical calculations. The highest efficiency of using MCM in parallel calculations is achieved on modeling long term random processes, in particular, the solutions of stochastic differential equations. By modeling on supercomputer independent from each other trajectories of the solutions of SDE, one can evaluate any required functionals from the solutions with an assigned

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accuracy. We present the investigation of pulse power of solitons at distances of 6-10 km when a random heterogeneous medium passes through and the results of high-frequency interactions of solitons arising at maximum loads of optical fiber lines.

The calculations were carried out on the cluster of NCC-30T of Siberian Supercomputer Center at the ICM&MG SB RAS.

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On the interval right censored data with unobserved status after censoring

Irina Yu. Malova[1], Alexandre Berred[2], Sergey V. Malov[3]

We consider the interval censoring approach for right-censored survival data. Right-censored event times are not observed exactly, but at some random inspection times. Status of each individual becames not observable just after censoring. We discuss crucial properties of the maximum likeihood estimator and investigate asymptotic properties of the estimator.

1 Introduction

Let T and U be independent failure and censoring times respectively, having distribution functions F and G respectively. Right censored observation is given by the event time $X = T \wedge U$ and the indicator $\delta = \mathbb{1}_{\{T \le U\}}$. In practice often the event time is not observed exactly, but at some random observation times $0 = W_0 < W_1 < \ldots < W_k < \infty$, having common distribution $\boldsymbol{J}$, which divide the time line into a fixed number of r disjoint finite intervals $I_1, \ldots, I_s$: $I_1 = [0, W_1]$, $I_k = (W_{k-1}, W_k]$, $k = 2, \ldots, s$, and the infinite interval (W_k, ∞). We use notation $\boldsymbol{J}$ for the common distribution function of $\boldsymbol{W} = (W_1, \ldots, W_k)$. The intrval right censored observation is given by the set of dummy variables $\eta_i = \mathbb{1}_{\{T \in I_i; U > W_i\}}$ and $\nu_i = \mathbb{1}_{\{T > W_{i-1}; U \in I_i\}}$, $i = 1, \ldots, k$. Interval right censored data is a sample from the distribution $(\boldsymbol{W}, \nu, \eta)$.

The Kaplan–Meier estimator [3] is the nonparametric maximum likelihood estimator (NPMLE) in this case. Asymptotic properties of the Kaplan–Meier estimator are well developed [1]. The iterative convex minorant algorithm to create NPMLE from interval censored data and the asymptotic behavior of the NPMLE due to [2]. The nonparametric estimate from interval right censored data with observed status after censoring was developed by [M], the particular case of the life time data was considered in [5]. The particular case of the interval right censored data with unknown status after censoring under fixed observation times and the corresponding categorical survival tests was given in [6]. We consider NPMLE from a sample of interval right censored data with unobserved status after censoring under random observation times and discuss its asymptotic properties.

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2 Formulation of the problem

Assume that (T_j, U_j) be a sample from the distribution of (T, U) and $(\boldsymbol{W}_1, \ldots, \boldsymbol{W}_n)$: $\boldsymbol{W}_j = (W_{1j}, \ldots, W_{kj})$, $0 < W_{1j} < \ldots < W_{kj}$ be a sample from $\boldsymbol{J}$; $I_{1i} = [0, W_{1i}]$ and $I_i = (W_{i-1}, W_i]$, $j = 2, \ldots, k$, $i = 1, \ldots, n$. The observed data are W_{ij} η_{ij} and ν_{ij}, where $\eta_{ij} = \mathbb{1}_{\{T_j \in I_{ij}; U_j > W_{ij}\}}$, $\nu_{ij} = \mathbb{1}_{\{T_j > W_{j-1}; U_j \in I_{ij}\}}$, $j = 1, \ldots, s$, $i = 1, \ldots, n$. The log likelihood function can be written as the sum $LL(F, G) = LL^f(F) + LL^c(G)$ with

$$LL^f(F) = \sum_{j=1}^{n} \sum_{i=1}^{k} \big\{ \eta_{ij} \log(F(W_{ij}) - F(W_{i-1j})) + \nu_{ij} \log(1 - F(W_{i-1j})) \big\} + (1 - \eta_{\bullet j} - \nu_{\bullet j}) \log(1 - F(W_k))$$

and

$$LL^c(G) = \sum_{j=1}^{n} \sum_{i=1}^{k} \big\{ \nu_{ij} \log(G(W_{ij}) - G(W_{i-1j})) + \eta_{ij} \log(1 - G(W_{ij})) \big\} + (1 - \eta_{\bullet j} - \nu_{\bullet j}) \log(1 - G(W_k)),$$

where $\eta_{\bullet j} = \sum_{i=1}^{k} \eta_{ij}$ and $\nu_{\bullet j} = \sum_{i=1}^{k} \nu_{ij}$, $j = 1, \ldots, n$. In the particular case of $k = 1$, $LL^f(F) = \sum_{j=1}^{n} \eta_j \log F(W_j) + (1 - \eta_j - \nu_j) \log(1 - F(W_j))$ and $LL^c(G) = \sum_{j=1}^{n} \nu_j \log G(W_j) + (1 - \nu_j) \log(1 - G(W_j))$ and the maximum likelihood estimators (MLE) for the distribution functions F and G can be obtained from LL^f and LL^c using convex minorant algorithm. In general case of $k > 1$, the MLE can be created using a special case of the iterative convex minorant algorithm.

Consistency and a rate of convergence as well as some problems in obtaining of weak convergence will be discussed. Some features of the case of fixed observation times will be discussed too.

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Testing for Structural Breaks in Factor Copula Models

Hans Manner [1], Florian Stark[2] and Dominik Wied[2]

1 Introduction

We propose new fluctuation tests for detecting structural breaks in factor copula models and analyze the behavior under the null hypothesis of no change. In the model, the joint copula is given by the copula of random variables, which arise from a factor model. Parameters are estimated with the simulated method of moments (SMM). Due to the discontinuity of the SMM objective function, it is not trivial to derive a functional limit theorem for the parameters.

2 Test and Behavior under the Null Hypothesis

The dynamic dependence implied by the copula $C(.,\theta_t^0)$ is determined by the unknown parameters θ_t^0 for $t = 1,\dots,T$. We are interested in estimating the $p \times 1$ vectors $\theta_t^0 \in \Theta$ of the copula, by information from the data and information generated by simulations from the factor copula model $C(.,\theta_t)$ for all t, implied by the following factor structure

$$X_{it} = \sum_{k=1}^{K} \beta_{ik}^t Z_{kt} + q_{it}, \quad i = 1,\dots,N,$$

where $q_{it} \overset{iid}{\sim} F_{\boldsymbol{q}_t}(\alpha_{\boldsymbol{q}_t})$ and $Z_{kt} \overset{init}{\sim} F_{\boldsymbol{Z}_{kt}}(\gamma_{kt})$ for $t = 1,\dots,T$. Note that Z_{kt} and $\boldsymbol{q}_{it}$ are independent $\forall i,k,t$ and the Copula for $\boldsymbol{X}_t = [X_{1t},\dots,X_{Nt}]'$ is given by $\boldsymbol{X}_t \sim \boldsymbol{F}_{\boldsymbol{X}_t} = C(G_{1t}(x_{1t};\theta_t),\dots,G_{Nt}(x_{Nt};\theta_t);\theta_t)$, with marginal distributions $G_{it}(.,\theta_t)$ and
$\theta_t = \left[\{\{\beta_{ik}^t\}_{i=1}^N\}_{k=1}^K, \alpha_{\boldsymbol{q}_t}', \gamma_{1t}', \dots, \gamma_{Kt}'\right]'$. For the estimation, we use the simulated method of moments (SMM) to receive estimators $\theta_{sT,S}$ of $\theta_{\lfloor sT \rfloor} = \theta_t$. The estimators are defined as $\theta_{sT,S} := \underset{\theta\in\Theta}{\arg\min}\ Q_{sT,S}(\theta)$, where $Q_{sT,S}(\theta) := g_{sT,S}(\theta)'\hat{W}_{sT}g_{sT,S}(\theta)$, $g_{sT,S}(\theta) := \hat{m}_{sT} - \tilde{m}_S(\theta)$ and $\hat{W}_{sT}$ a positive definite weight matrix. $\hat{m}_{sT}$ are $k \times 1$ vectors of averaged pairwise dependence measures computed

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from the data and $\tilde{m}_S(\theta)$ is the corresponding vector of dependence measures using simulations from $\boldsymbol{F}_{\boldsymbol{X}_t}$. We are interested in testing

$$H_0 : \theta_1 = \theta_2 = \cdots = \theta_T \qquad H_1 : \theta_t \neq \theta_{t+1} \text{ for some } t = \{1, \ldots, T-1\}.$$

with the test statistic S, defined as

$$S := \max_{1 \leq t \leq T} \frac{\left(\frac{t}{T}\right)^2}{1/T + 1/S} (\theta_{t,S} - \theta_{T,S})'(\theta_{t,S} - \theta_{T,S}),$$

where $\theta_{sT,S}$ is the SMM estimator up to the information at time point $t = \lfloor sT \rfloor$ and $\varepsilon > 0$. Under suitable assumptions we receive the following limit distribution result for our test statistic

Theorem 1. Under the null hypothesis $\theta_1 = \theta_2 = \cdots = \theta_T$ and suitable assumptions, we have for $\varepsilon > 0$

$$\frac{s}{\sqrt{1/T + 1/S}} (\theta_{sT,S} - \theta_0) \xrightarrow{d} A^*(s), \qquad T, S \to \infty, \quad \forall s \in [\varepsilon, 1], \varepsilon > 0,$$

with $A^*(s) = (G'WG)^{-1} G'WA(s)$ and $A(s)$ a certain Gaussian process, where G is the approximated derivative of $g_{sT,S}(\theta_0)$ and W a weighting matrix.

Corollary 1. Under the null hypothesis $\theta_1 = \theta_2 = \cdots = \theta_T$ and suitable Assumptions, we receive for our test statistic

$$\sup_{s \in [\varepsilon, 1]} \frac{s^2}{1/T + 1/S} (\theta_{sT,S} - \theta_{T,S})'(\theta_{sT,S} - \theta_{T,S}) \xrightarrow{d} \sup_{s \in [\varepsilon, 1]} (A^*(s) - sA^*(1))'(A^*(s) - sA^*(1)).$$

as $T, S \to \infty$

For the computation of the p-values we use a multiplier resampling scheme that takes the serial dependence into account. We then test the finite-sample performance of the procedure under the null using simulations and provide an empirical application.

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Finding Optimal Designs for Nonlinear Models Using the Imperialist Competitive Algorithm

Ehsan Masoudi[1], Heinz Holling[2] and Weng Kee Wong[3]

Finding optimal designs for nonlinear models is complicated because the optimality criterion usually depends on the model parameters. The simplest approach is to replace the unknown parameters by some initial estimates from a similar study or a pilot study so that the criterion is free of the unknown parameters and can be directly optimized. Such an approach results in optimal designs that depend on the initial estimates, so are called *locally* optimal designs. Locally optimal designs may be inefficient when the initial estimates are far away from the true values of the parameters. if a plausible region for the unknown parameters is available, a *minimax* optimal design may be obtained by minimizing the maximum inefficiency that may arise due to mis-specification in the parameters. Another approach is to elicit a prior distribution for the unknown parameters and optimize the criterion averaged over the prior distribution. The resulting designs are termed *Bayesian* optimal designs.

In this talk, we introduce different versions of the imperialist competitive algorithm [1] (ICA) to find locally, Bayesian and minimax optimal designs in a general framework. ICA is a metaheuristic evolutionary algorithm inspired from the socio-political process of human. Finally, we demonstrate the application of the ICAODR package [2] to solve different types of optimal design problems for nonlinear models.

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Inference on the Second Moment Structure of High-Dimensional Sensor-Type Data in a K - Sample Setting

Nils Mause[1]

In this talk we consider K high-dimensional vector time series $\mathbf{Y}_{T,1}, \ldots, \mathbf{Y}_{T,K}$ generated by independently working stations $j = 1, \ldots, K$ of sensors within a time interval $[0, T]$ for some $T > 0$. Here the sensors located in different stations may collect and transmit data at distinct sampling frequencies $\omega_j \in [0, 1]$, such that the resulting sample sizes given by $N_j = \lfloor \omega_j T \rfloor$ may also be different.
Projections $\mathbf{w}_T' \mathbf{Y}_{T,j}$ based on such high-dimensional time series with some appropriate weighting vector $\mathbf{w}_T$ appear naturally in many statistical procedures and applications, such as the Principal Component Analysis and Portfolio Optimization, and are a common method of dealing with high-dimensional data sets. Taking the data of all K stations into account, quadratic forms (and more generally bilinear forms) based on the pooled sample variance-covariance matrix need to be analyzed in order to draw inference on the variance of these projections.
Within the high-dimensional framework where not only the time horizon T shall go to infinity but also the dimension d_T of the data is allowed to grow with the time horizon we establish a new strong approximation result for the cdlg process

$$\mathcal{D}_T(t_1, \ldots, t_K) = \frac{1}{\sum_{l=1}^K N_l} \boldsymbol{v}_T' \left(S_{T,\lfloor t_1 N_1 \rfloor, \ldots, \lfloor t_K N_K \rfloor} - E(S_{T,\lfloor t_1 N_1 \rfloor, \ldots, \lfloor t_K N_K \rfloor}) \right) \boldsymbol{w}_T,$$

for $t_1, \ldots, t_K \in [0, 1]$, where $S_{T,k_1,\ldots,k_K} = \sum_{j=1}^K \sum_{i=1}^{k_j} \boldsymbol{Y}_{T,j} \boldsymbol{Y}_{T,j}', k_j \leq N_j, j = 1, \ldots, K$, and $\boldsymbol{v}_T, \boldsymbol{w}_T$ are uniformly ℓ_1 - bounded weighting vectors. In particular, without any constraints on the ratio of dimension and sample sizes, we receive the strong approximation

$$\sup_{t_1,\ldots,t_K \in [0,1]} \left| \mathcal{D}_T(t_1, \ldots, t_K) - \sum_{j=1}^K \alpha_{T,j} B_T^{(j)} \left(\frac{\lfloor t_j N_j \rfloor}{\sum_l N_l} \right) \right| = o(1), \quad T \to \infty,$$

by the scaled sum of independent Brownian motions $\{B_T^{(j)}(t_j) : t_j \in [0, 1]\}$ with variances $\alpha_{T,j}^2, j = 1, \ldots, K$. Moreover, we will show that a similar result also holds for an increasing (and possibly infinite) amount, L_T, of bilinear forms based on the pooled sample variance-covariance matrix. These approximation results are

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therefore also applicable in situations where the dimension d_T grows much faster than the sample sizes N_j and the time horizon T.
As an application of the strong approximation results we will deal with a change in variance problem, where, under the null hypothesis of no change, the data $\mathbf{Y}_{T,j,1}, \ldots, \mathbf{Y}_{T,j,N_j}$ is supposed to form a stationary d_T - dimensional vector time series with mean zero and variance - covariance matrix $\mathbf{\Sigma}_{T,0}^{(j)}$, which can either be known or unknown.
Lastly, we conduct a simulation study in order to illustrate the finite sample performance of our change-point test statistic.

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Universal modification of vector weighted method of correlated sampling with finite computation cost

Ilia Medvedev[1]

Consider the system of the 2nd kind integral equations with parameter λ:

$$\phi_i(x,\lambda) = \sum_{j=1}^{m} \int_X k_{ij}(x,y,\lambda)\phi_j(y,\lambda)dy + h_i(x,\lambda), \quad i = 1,...,m, \tag{1}$$

or $\Phi_\lambda = \mathbf{K}_\lambda \Phi_\lambda + H_\lambda$, in the vector form, where $\lambda \in \Lambda = \{\lambda_1, ..., \lambda_s\}$, $H_\lambda^{\mathrm{T}} = (h_1(\lambda), \ldots, h_m(\lambda)) \in L_\infty$, $\mathbf{K}_\lambda \in [L_\infty \to L_\infty]$, $||H_\lambda||_{L_\infty} = \text{vrai} \sup\limits_{i,x} |h_i(x,\lambda)|$. We assume that the spectral radius is $\rho(\mathbf{K}_{\lambda,1}) < 1$ where $\mathbf{K}_{\lambda,1}$ is the operator obtained from the operator $\mathbf{K}_{\lambda,1}$ by replacement $k_{ij}(x,y,\lambda) \to |k_{ij}(x,y,\lambda)|$ and $\rho(\mathbf{K}_{\lambda,1}) = \underline{\lim} ||\mathbf{K}_{\lambda,1}^n||_{L_\infty}^{1/n} = \inf ||\mathbf{K}_{\lambda,1}^n||_{L_\infty}^{1/n}$. The Neumann series for (1) converges if the inequality $||\mathbf{K}_{\lambda,1}^{n_0}|| < 1$ holds for some $n_0 \geq 1$ and $\forall \lambda \in \Lambda$ where $||\mathbf{K}_{\lambda,1}|| = \sup\limits_{x,i} \sum\limits_{j=1}^{m} \int |k_{ij}(x,y,\lambda)|dy$.

Let us consider a Markov chain of collisions $\{x_n\}, (n = 0, \ldots, N)$ with the transition density $p(x,y)$ and $\rho(B_p) < 1$, where B_p is an integral operator with the kernel $p(x,y)$ (in particular, for $p(x) \geq \varepsilon > 0$). A standard vector Monte Carlo collision estimator is constructed for the value $\Phi_\lambda(x) = \mathrm{E}\boldsymbol{\xi}_x(\lambda)$ on the base of relations

$$\boldsymbol{\xi}_x(\lambda) = H_\lambda(x) + \delta_y Q(x,y,\lambda)\boldsymbol{\xi}_y(\lambda), \tag{2}$$

where $Q(x,y,\lambda) = K(x,y,\lambda)/p(x,y)$ is the matrix weight and δ_x is the indicator of chain non-breaking in the transition $x \to y$. The variance $\mathrm{V}\boldsymbol{\xi}_x(\lambda)$ depends on the matrix of second moments $\Psi(x,\lambda) = \mathrm{E}(\boldsymbol{\xi}_x(\lambda)\boldsymbol{\xi}_x^{\mathrm{T}}(\lambda))$ which satisfies the following equation ([2])

$$\Psi(x,\lambda) = \chi(x,\lambda) + \int_X \frac{K(x,y,\lambda)\Psi(y,\lambda)K^{\mathrm{T}}(x,y,\lambda)}{p(x,y)}dy, \tag{3}$$

or $\Psi_\lambda = \chi_\lambda + \mathbf{K}_{\lambda,p}\Psi_\lambda$, where $\chi_\lambda = H_\lambda\Phi_\lambda^{\mathrm{T}} + \Phi_\lambda H_\lambda^{\mathrm{T}} - H_\lambda H_\lambda^{\mathrm{T}}$. This equation is considered in the space $\mathbf{L}_\infty$. Denote the operator obtained from $\mathbf{K}_{\lambda,p}$ by replacing the kernels by their absolute values by $\mathbf{K}_{\lambda,p,1}$. It is known ([2]) that if $\rho(\mathbf{K}_{\lambda,p,1}) < 1$ then $\Psi(x,\lambda) = \mathrm{E}(\boldsymbol{\xi}_x(\lambda)\boldsymbol{\xi}_x^{\mathrm{T}}(\lambda))$ is a solution of the equation (3) and $\Psi_\lambda \in \mathbf{L}_\infty$. The corresponding Monte Carlo algorithms (see (2)) were naturally named the method of similar trajectories (MST) [1] or the weighted method of correlated sampling

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[2]. The use of such methods allows one to construct estimators of functionals on a single Markov chain simultaneously for a given range of parameters (Λ) and to study effectively the results dependence on the parameters of the system, in particular, for their small variations [1].

If the spectral radius is $\rho(\mathbf{K}_{\lambda,p,1}) > 1$, then the elements of $\mathrm{V}\boldsymbol{\xi}(\lambda)$ can be infinitely large and the use of the weight estimator $\boldsymbol{\xi}_x(\lambda)$ for the calculation of the $\Phi(x,\lambda)$ is not expedient. Note that the estimation of the value $\rho(\mathbf{K}_{\lambda,p,1})$ for real problems demands a separate and labor-consuming theoretical study. The standard way to decrease the value $\mathrm{V}\boldsymbol{\xi}_x(\lambda)$ is the use of the following modification of the estimator $\boldsymbol{\xi}_x(\lambda)$ with additional trajectory branching (randomized splitting)

$$\boldsymbol{\zeta}_{x_0}(\lambda) = H_\lambda(x_0) + \delta_{x_1}\frac{Q^{(1)}(x_0,x_1,\lambda)}{\mathrm{E}\nu_1}\sum_{i=1}^{\nu_1}\boldsymbol{\zeta}_{x_1}^{(i)}(\lambda), \tag{4}$$

$$\boldsymbol{\zeta}_{x_{n-1}}(\lambda) = H_\lambda(x_{n-1}) + \delta_{x_n}\frac{Q^{(1)}(x_{n-1},x_n,\lambda)}{\mathrm{E}\nu_n}\sum_{i=1}^{\nu_n}\boldsymbol{\zeta}_{x_n}^{(i)}(\lambda), \tag{5}$$

where $\boldsymbol{\zeta}_{x_n}^{(\cdot)}(\lambda)$ are independent realizations of $\boldsymbol{\zeta}_{x_n}(\lambda)$ and $Q^{(1)}(x_{n-1},x_n)$ corresponds to $\boldsymbol{K}$ with $|k_{ij}(x,y,\lambda)|$.

If we introduce $\{A\}_{ij} = a_{ij}$ for an arbitrary element of the matrix A and

$$\mathrm{E}\nu_1 = \max_\lambda \sup_i \sum_{j=1}^m \{Q^{(1)}(x_0,x_1,\lambda)\}_{ij},\ \mathrm{E}\nu_n = \max_\lambda \sup_i \sum_{j=1}^m \left\{\frac{Q_{n-1}^{(1)}Q^{(1)}(x_{n-1},x_n,\lambda)}{\mathrm{E}\nu_1 ... \mathrm{E}\nu_{n-1}}\right\}_{ij}, \tag{6}$$

then, as in [3] it is easy to check that $\mathrm{E}\boldsymbol{\zeta}_x(\lambda) = \Phi_\lambda(x)$ and $\mathrm{E}(\boldsymbol{\zeta}_x(\lambda)\boldsymbol{\zeta}_x^{\mathrm{T}}(\lambda)) \in \mathbf{L}_\infty$ if only $\rho(\mathbf{K}_{\lambda,1}) < 1$ and $\rho(B_p) < 1$. The last inequalities also ensure that the mean computer simulation time for calculation of one sample value of $\boldsymbol{\zeta}_x$ is also bounded.

Numerical study of the efficiency of the presented weighted method of correlated sampling with branching in comparison with "analog" modelling for every parameter $\lambda \in \Lambda$ was carried out on the example of the standard problem of transfer theory with allowance for polarization.

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Approximate spectral model of periodically correlated air temperature time-series

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The article is devoted to the issues related to the use of periodically correlated processes for the simulation of real time series. Two types of models of the periodically correlated processes are considered. The first model is based on the representation of the periodically correlated process of a discrete argument in the form of a vector stationary process with a given matrix correlation function. The second model is based on the one special spectral representation of a periodically correlated process. Each of these models has its advantages and disadvantages. For example, the first model is convenient for modeling long Gaussian sequences with a constant time step. And the second model is, in general case, approximately Gaussian, but this model allows constructing processes both in equidistant and not equidistant points in time. We used six-hour measurement observations data of surface air temperature for the month of May with the period 1938-1984 at the meteorological "Sverdlovsk" station in Russia to construct models for real processes. The Gaussian periodically correlated process being interpreted as vector stationary processes with a given matrix correlation function is considered as the first model. For a process with discrete time on a limited interval $\xi_1, ..., \xi_t, ..., \xi_m$ matrix correlation function $R_0, R_1, ..., R_m - 1$ corresponds to the block-Toeplitz correlation matrix and the process is constructed on the basis of the conditional distributions method. The vector models of autoregression of a fixed order are used to model long-length vector sequences. In this model, a sample matrix correlation function of time series of air temperature evaluated by real data is used as the matrix correlation function.

As the second model of a periodically correlated process, a nonrandomized spectral model of a random process in the form:

$$\eta_n(t) = \sum_{i=1}^{n} p_i^{1/2}(t)(\zeta_i sin(\lambda_i t) + \xi_i cos(\lambda_i t))$$

is considered , where ζ_i and ξ_i - are independent standard normal values,

$$p_i(t) = \int_\Lambda S(\lambda, t) d\lambda,$$

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where Λ_i is partition of the spectral space, $\lambda_i \in \Lambda_i$, and spectral densities $S(\lambda, t) = S(\lambda, t + P)$ are periodic functions of time .

In this paper, we proposed an approach to estimate the input characteristics of this model on the basis of real temperature data. The approach is based on the Fourier transformation of the correlation functions obtained by means of a special approximation of the sample correlation functions of stationary processes for each observation period. The correlation functions for each observation period are used as the input characteristics when constructing the spectral model, but cross-correlation is determined by the model under consideration. However, a periodically correlated process with all the correlations taken into account can be constructed with the help of the first model. We constructed the time dependencies on the process correlations based on the sample models for various time shifts based on the first and second models. 1 000 000 simulated trajectories were used for modeling. Comparison of the model correlations with the actual ones has shown that the first model reproduces the real character of the correlation dependence on time more accurately than the second one. This is because cross-correlation is not the input parameters of the second model. So, it is expedient to use the first model for a realistic description of the time series of the surface air temperature. The second model can be useful for modeling such time series for which the correlation structure is well described by the class of correlation functions corresponding to the given model.

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Goodness-of-Fit Tests with Survival Data

Simos G. Meintanis[1]

Tests of fit are proposed for the baseline hazard under the Cox proportional hazards model and the accelerated failure time model. The tests are based on the empirical characteristic function and make use of the specifics of these models so that the final distribution being tested is the unit exponential. The new methods are compared with classical methods based on the empirical distribution function.

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New algorithms of Monte Carlo method for investigation of criticality of particle scattering process with multiplication in random media

G.A. Mikhailov, G.Z. Lotova[1]

A Monte Carlo algorithm admitting parallelization is constructed for estimation of probability moments of the spectral radius of the operator of the integral equation describing transfer of particles with multiplication in a random medium. A randomized homogenization method is developed with the same aim on the base of the theory of small perturbations and diffusive approximation. Test calculations performed for a one-group spherically symmetric model system have shown a satisfactory concordance of results obtained from two models.

1 Introduction

This work is focused on development of numerical statistical modelling algorithms for studying fluctuations of the criticality of particles transfer with multiplication in a random medium. For the sake of simplicity, we consider a one-velocity transfer process with isotropic indicatrices of scattering and splitting (replication), however, the structure of proposed algorithms does not practically change in the passage to more complex many-velocity and anisotropic models of the process. For the variant of the process presented here, it is expedient to consider the following homogeneous integro-differential transfer equation:

$$(\omega, grad\Phi) + \sigma\Phi = \frac{1}{k}\Big[\sigma_s\Phi_0 + \nu\sigma_f\Phi_0\Big].$$

Here $\Phi \equiv \Phi(r,\omega)$ is the density of the flow of particles (radiation intensity), $\sigma \equiv \sigma(r)$ is the total cross-section (attenuation coefficient), and $\sigma = \sigma_s + \sigma_c + \sigma_f$, where σ_s is the cross-section of scattering, σ_f is the cross-section of fission, σ_c is the cross-section of capture, ν is the mean number of particles emitted from the points of fission, $r \in R^3$ is a spatial point, ω is a unit direction vector, $\Phi_0(r) \equiv \int \Phi_0(r,\omega)d\omega$.

2 Formulation of the problem

If the parameters of the problem are random, then k is random as well and, in particular, it is practically important to estimate the probability $P(k > 1)$,

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i.e., the probability of over-criticality of the transfer problem of particles with multiplication in a random medium. This can be performed by estimating the probability moments Ek and Dk, i.e., the mean value and the variance of k. Using the approximate Gaussian property of the distribution of the random variable k, one can estimate the probability $P(k > 1)$ sufficiently well. Test numerical statistical modelling allows us to check the adequacy of this technique.

The value k is an effective coefficient of particle multiplication in generations of scattering acts. It can be estimated (see, e.g., review in [1]) by direct simulation of the transfer process. It is clear that this estimator is not very efficient for solving stochastic problems because it does not admit the use of double randomization. Therefore, we formulate Monte Carlo algorithms related to the limit relation [2]

$$k = \lim_{n\to\infty} k_n, \quad k_n = \sqrt[n]{\|K^n\|},$$

and

$$\|K^n\| = \sup_{x\in X} \int \dots \int k(x, x_1)k(x_1, x_2) \dots k(x_{n-1}, x_n)\, dx_1 \dots dx_n. \qquad (1)$$

According to the definition of the substochastic density $k(x', x)$, the value $\|K^n\|$ equals to the mean number of collisions of the n-th number under the condition that the source normalized by one collision is positioned at the point x_0. Thus, we actually formulate an iterative algorithm of direct statistical modelling for estimation of the value $\|K^n\|$ with the special initial density function in the expression (1). Performing calculations simultaneously for different values of n according to (1), we can construct estimators for Ek and Dk based on approximation of the function $x^{1/n}$ and the corresponding double randomization [3].

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Vector Monte-Carlo algorithms for polarized radiative transfer process

G.A. Mikhailov[12], S.M. Prigarin[12],S.A. Rozhenko[1]

There are two versions of weighted vector algorithms for the statistical modeling of polarized radiative transfer: a "standard" one, which is convenient for parametric analysis of results, and an "adaptive" one, which ensures finite variances of estimates [1, 2, 3]. The application of the adaptive algorithm is complicated by the necessity of modeling the previously unknown transition density. An optimal version of the elimination algorithm used in this case is presented in this talk. A new combined algorithm with a finite variance and an algorithm with a mixed transition density are constructed. The comparative efficiency of the latter is numerically studied as applied to radiative transfer with a molecular scattering matrix. Statistical kernel estimates were constructed for the angular distributions of the vector intensity.

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Monte Carlo simulation of laser pulse propagation in clouds and water media

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The receiver of a monostatic wide-angle CCD lidar should record an expanding luminous ring in the case of sensing cloud layer of an optical thickness less than 4 in visible range of the spectrum [1, 2]. The brightness of the ring rapidly decreases with respect to time. The radial speed measured by the brightness ring area decreases for optical thicker cloud layers.

This paper being a continuation of the research presented in [3], deals with stochastic simulation of short laser pulses scattering in atmospheric clouds and water media. We analyze peculiarities of photons distribution in thin cloud layers. Simulation results show that the smaller luminous ring may appear for a short time in addition to the primary ring of light expanding in the cloud layer. The second ring appears because of local maxima of the cloud phase functions in the neighborhood of 180 and 140 degrees. Existence of such local maxima is typical for the most cloud phase functions. Moreover, under certain conditions the effects similar to expanding ring may be observed in water media.

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Analytics on Mobility Data from new technologies: a Simulation-based Assessment

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Analytics on mobility data are proliferating due to the low-cost wireless data communications and the pressures of traffic authorities for reducing deployment and maintenance costs of traditional sensors. Several new sources of data from Information and Communication Technologies (ICT) can be used to derive traffic and mobility data, such as Bluetooth measurements of travel times between detection antennas, GPS measurements locations, timestamps for large samples of vehicles GPS equipped (Tom-Tom, INRIX, HERE could be examples of that) or Call Detail Records (CDR) from cellular phone tracking. This paper presents a particular case study that analyzes and evaluates by microscopic traffic simulation how the use of data provided by probe vehicles can provide travel times estimates from network segments and how navigation strategies can be defined based on those estimates for a set of connected cars. A set of city scale KPIs (Key Performance Indicators) and drivers KPI are presented for different scenarios defined by an experimental design. The case study adopts a microscopic simulation approach to emulate real size fleets of probe data cars providing positions and speed data every simulation step. As a remarkable modeling behavior, drivers are segmented according to network conditions knowledge as experts, regular drivers and tourists. The paper discusses the modeling approach and experimental design for simulation in a medium size traffic simulation model of Barcelona CBD. Emulated real-time probe car data for the evaluation of connected car guidance under different levels of probe car penetration and navigation strategies is the aim of the current work,

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a reduced set of sensors for probe cars has been assumed allowing data for vehicle position and speed at each simulation step. AIMSUN [1] is the simulation platform that supports the case study. Factors considered in the design of the simulation experiments are: Driver Type (drivers are split into six groups according to the knowledge of network and traffic conditions and guidance availability), Guidance Penetration, Congestion Level (referred to basic historical demand), Probe Vehicle fleet Size and Interval length for segment travel time estimation. A factorial design leading to identify non aliased factor main effects is considered. The average trip travel time is the target KPI used to select the number of replications that fulfils on the base scenario a global 5A set of 15 network KPIs are collected, these are numeric variables with different scales and internal correlation, Data Science procedures are applied to understand the underlying structure of network KPIs and to reveal hidden variables. Drivers KPI are also defined. One of the objectives of the study is to show how network KPIs are affected by design factors, either when gross effects or net effects are considered. The same applies to drivers KPIs. The research contribution relies of a detailed simulation of driver classes, travel time estimates from new ICT probe vehicle data and the implementation off several navigation strategies that have been shown to be advantageous for guided and non-guided cars up to a certain level around 30

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Symbolic method of cumulants for subordinated Brownian motions: the variance gamma case

Elvira Di Nardo[1], Patrizia Semeraro[2]

With symbolic calculus we mean a set of manipulation techniques aiming at performing algebraic calculation [4]. Symbolic calculus applies to Lévy processes since we can represent a Lévy process through its time one moment generating function, which has the following expression:

$$M(z) = \exp\{(K(z) - 1)\}. \tag{1}$$

In the ring of formal power series $\mathbb{R}[[z]]$, equation (1) is well defined independently of convergence radius [9]. Moreover if $M(z)$ and $K(z)$ have the following formal power series expansions:

$$M(z) = 1 + \sum_{i=1}^{\infty} \frac{a_i}{i!} z^i \quad K(z) = 1 + \sum_{i=1}^{\infty} \frac{c_i}{i!} z^i. \tag{2}$$

then $\{c_i\}$ are said the formal cumulants of $\{a_i\}$. Comparing (2) with (1), $\{c_i\}$ result to be cumulants of the time one distribution of the Lévy process and the moments of the Lévy process are sequence of binomial type whose coefficients are $\{c_i\}$.

Using this approach subordination of Lévy processes (see [1] and [8] as references on Lévy processes and subordination) becomes a formal series composition of cumulant generating functions. Therefore, using Faà di Bruno formula [4] we can calculate the cumulants of a subordinated Lévy process starting from the cumulants of the subordinand and of the subordinator.

Our aim is to develop an estimation procedure of the parameters of subordinated Brownian motions based on polykays. Polykays are corrected estimators of cumulant products with minimum variance [7]. We propose to apply this methodology in financial applications. In fact, subordinated Brownian motions are widely used to model asset returns, having the subordinator the appealing interpretation of economic time. In this framework, a famous subordinated Brownian motion is the variance gamma process [5], which is constructed using a gamma subordinator. Its time one moment generating function is therefore the composition of the moment generating function of a gamma process and a Brownian motion:

$$\log M(z) = \frac{1}{\nu} \log \frac{1}{1 - \nu\left(\mu z + \sigma^2 \frac{z^2}{2}\right)} \quad \nu > 0 \quad \mu \in \mathbb{R}, \quad \sigma > 0. \tag{3}$$

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Since the estimate of the variance gamma parameters is still an open issue ([2], [3] and [6]), we apply our procedure to this model.

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Analysis of Multicast Queuing Systems with Random Requirements of Overlapping Resources

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In this paper we consider queueing system designed for the performance analysis of multicast telecommunication systems [1]. During each busy period system transmits a stream of media data. Busy periods are separated by idle periods. Busy period starts when the first customer connects to the stream. Later more customers may connect to the stream. When the stream transmission ends all customers get disconnected and the idle period starts. Let the sequence of idle and busy periods of the system form the alternating renewal process [2] with the cumulative distribution functions of the length of idle and busy periods given by and respectively. We assume that during transmission of the stream customers arrive according Poisson arrival process with the rate and no more than N customers may be connected to the stream. Arriving customers switch up to the highest available quality within their network bandwidth, which are independent random variables with the cumulative distribution function (CDF) . A newcomer never decreases the amount of resources occupied in the system but it can increase this amount. So the total amount of occupied resources is equal to the maximum of these random variables each with CDF . In such a system blocking may occur if and only if at the instant of a new customer arrival there are N customers in the system.

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Abstracts of the Ninth Workshop on Simulation (2018) 92-94

Approximations of the boundary crossing probabilities for the maximum of moving weighted sums - Abstract

Jack Noonan[1] , Anatoly Zhigljavsky[2]

1 Introduction

We study approximations of boundary crossing probabilities for the maximum of moving weighted sums of i.i.d. random variables. We demonstrate that the approximations based on classical results of extreme value theory, see [1-3], provide some scope for improvement, particularly for a range of values required in practical applications.

2 Formulation of the problem

Let $\varepsilon_1, \varepsilon_2, \ldots$ be a sequence of independent identically distributed random variables with finite mean μ and variance σ^2 and some c.d.f. F. Define the moving weighted sum as

$$\mathcal{S}_{n;L,Q} = \sum_{s=n+1}^{n+L+Q-1} w_{L,Q}(s-n)\varepsilon_t \quad (n = 0, 1, \ldots) \tag{1}$$

where the weight function $w_{L,Q}(\cdot)$ is defined by

$$w_{L,Q}(t) = \begin{cases} t & \text{for } 0 \le t \le Q, \\ Q & \text{for } Q \le t \le L, \\ L+Q-t & \text{for } L \le t \le L+Q-1. \end{cases} \tag{2}$$

where L and Q are positive integers with $Q \le L$.

The weight function $w_{L,Q}(\cdot)$ is depicted in Figure 1. In the special case $Q = 1$, the weighted moving sum (1) becomes an ordinary moving sum.

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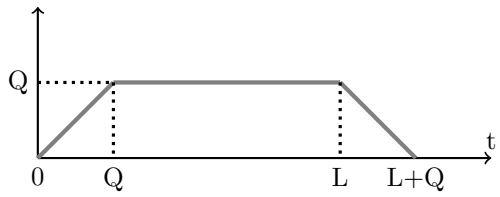

Figure 1: The weight function $w_{L,Q}(\cdot)$, $1 \leq Q \leq L$.

The main aim of this paper is to study precision of different approximations of boundary crossing probabilities for the maximum of the moving weighted sum; that is,

$$P\left(\max_{n=0,1,\ldots,M} \mathcal{S}_{n;L,Q} > H\right), \tag{3}$$

where H is a given threshold, M is reasonably large and L, Q are fixed parameters.

3 Application

The particular weight function defined in (2) is directly related to the SSA change point algorithm described in [4] (for an extensive introduction to SSA, we point the reader towards [5-6]. More precisely, if we let $\varepsilon_j = \xi_j^2$, where $\xi_1, \xi_2, \ldots$ are i.i.d. random variables with zero mean, variance δ^2 and finite fourth moment $\mu_4 = E\xi_i^4$, then $\mathcal{S}_{n;L,Q}$ can be seen as a moving weighted sum of squares; we have $\mu = E\varepsilon_j = \delta^2$ and $\sigma^2 = \mathrm{var}(\varepsilon_j) = \mu_4 - \delta^4$. In this particular setting, a good approximation for (3) is needed in the theory of sequential change-point detection because the boundary crossing probability defines the significance levels for the SSA change-point detection statistic.

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Abstracts of the Ninth Workshop on Simulation (2018) 95-95

Stochastic models of atmospheric clouds

V. A. Ogorodnikov[1], S. M. Prigarin[2], E. G. Kablukova[3]

This paper deals with the development of numerical stochastic models of Status and Cirrus. The statistical analysis of cloud optical thickness horizontal fields was made. These two-dimensional fields were retrieved from the ground-based and the aircraft measurements of the downward and the upward solar spectral radiances [1]. It is shown that the marginal distribution density of the fields slightly deviates from a truncated Gaussian density or a mixture of truncated Gaussian densities. Assuming the homogeneity of the optical thickness fields, the correlation functions of the fields were estimated. The numerical stochastic models of the cloud optical thickness fields were constructed on the basis of the inverse distribution function method from the Gaussian fields. The Gaussian fields were simulated using the two-dimensional autoregressive method [2],[3]. The optimal order of the autoregressive method for attaining of a sufficient accuracy in approximating the correlation function within an acceptable time was estimated.

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Optimal Doubling Burn-in Policy Based on Tweedie Processes with Applications to Degradation Data

Chien-Yu Peng[1] and Kun-Hung Lin

In the current competitive marketplace, manufacturers need to screen weak products in a short period of time. It is a challenge for manufacturers to implement a burn-in test that can screen out the weak products quickly and efficiently. When selecting an approach to determine the duration of the burn- in, one could build a criterion aiming to minimize the burn-in cost. In practice, when the optimal burn-in time is unreasonable (e.g., time 0) due to minimizing the cost, this means that the burn-in procedure is unnecessary to perform for manufacturers. In this study, we propose an optimal doubling burn-in policy to improve the predicament without additional experiments. The advantage of the proposed policy is to simultaneously determine the optimal burn-in time and the optimal cutoff point for classifying weak and strong components from the production. In addition, a new degradation model based on a Tweedie mixture process is used for a burn-in test. The proposed burn-in procedure is applied to a real data

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Model-free classification of panel data via the ϵ-complexity theory

Alexandra Piryatinska[1], Boris Darkhovsky[2]

Success in solution of classification problem essentially depends on a right choice of a feature space. In majority of applications features spaces are constructed based on prior information on data generating mechanisms. However, such information is not always available. Typical example here is an electroencephalogram signal. According to most of experts, there are no generally accepted models of such signals and therefore it is difficult to analyze them. The same situation is typical in applications to financial time series, some biological problems, etc., where also there are no standard models. This circumstance significantly complicates creation of feature spaces for classification problems.

In this talk, we consider the problem of classification for so called *panel data*. In statistics and econometrics, panel data are multi-dimensional data involving measurements over time. Typically a problem to identify structural break in panel data is considered in the literature. For example, such phenomena may be produced by governmental policy changes, the introduction of a new technology, etc. We will classify different groups of simulated panel data which are generated by different mechanism. We use multidimensional linear model to simulate panel data. Such models are typical in econometrics. Different classes of the data generated by different matrices of states and noises. Such classification can be used further for detecting the moments of time at which these changes occurrences.

To perform such classification, we employ our theory of the *ϵ-complexity* of continuous map, in particular, continuous vector-functions. In the majority of applications, we deal with vector-functions given by their values at a discrete set of points (i.e., by a finite sample of finite-dimensional vectors). We will assume that this set of values is *the restriction of a continuous vector-functions on some uniform grid*. In our talk we generalized the main result of our theory to the case when a continuous map is given by its values on some uniform grid. We show that in this case the ϵ-complexity can be effectively characterized by two real numbers - *the complexity coefficients* - for "almost all" Hölder maps.

We describe our algorithm for calculation of the complexity coefficients and show that these coefficients can be used as features for classification of multivariate time series data including panel data. Therefore, complexity coefficients can be used also for detecting change-points in samples of panel data.

The results of simulations will be presented.

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Bootstrap confidence bounds: splitting the sample for higher-order accuracy

C Pretorius and JWH Swanepoel

Goodness of fit procedures are provided to test for specified compound models for the total claims, as well as for the constituent components namely the claim frequency distribution, as well as We propose a new method, based on sample splitting, for constructing bootstrap confidence bounds for a parameter appearing in the regular smooth function model. It has been demonstrated in the literature that the well-known percentile-t bootstrap confidence bounds are typically second-order accurate. Using our version of the bootstrap percentile-t method, confidence bounds of third- and even fourth-order accuracy can be obtained. Furthermore, whereas the standard percentile bounds are typically first-order accurate, the new bounds achieve second-order accuracy. In the case where the parameter of interest is the population mean, we derive for each confidence bound the exact coefficient of the leading term in an asymptotic expansion of the coverage error, although similar results may be obtained for other parameters such as the variance, the correlation coefficient, and the ratio of two means. We show that fourth-order accurate equal-tailed confidence intervals may be obtained from the newly proposed bounds, as opposed to the typical first-order accuracy of the standard intervals. It is also shown that the good properties of the new percentile-t bound carry over to regression problems. A small simulation study illustrates the behaviour of the confidence bounds for small to moderate sample sizes. of individual claims. This is done without the need for observations on these two component variables. Goodness- of-fit tests that utilize the Laplace transform as well as classical tools based on the distribution function, are proposed and compared. These methods are validated by extensive simulations and then applied to a real data example.

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Design of Experiments, Bayesian Quadrature and Sensitivity Analysis

Luc Pronzato[1]

A standard objective in computer experiments is to predict/interpolate the behaviour of an unknown function f on a compact domain from a few evaluations inside the domain. When little is known about the function, space-filling design is advisable: typically, points of evaluation spread out across the available space are obtained by minimizing a geometrical (for instance, minimax-distance) or a discrepancy criterion measuring distance to uniformity. We shall focus our attention to sequential constructions where design points are added one at a time. This work is in collaboration with Anatoly Zhigljavsky (Cardiff University) and is motivated by recent results [4] indicating that the sequence of design points generated by a vertex-direction algorithm applied to the minimization of a convex functional of a design measure can have better space filling properties than points generated by the greedy minimization of the corresponding supermodular set function.

We shall make a survey of some recent results on energy functionals, that can be used to measure distance to uniformity, based on [1, 5, 6]. In particular, we shall investigate connections between design for integration of f with respect to a measure μ (quadrature design), construction of the (continuous) BLUE for the location model, and minimization of energy (kernel discrepancy) for signed measures. Integrally strictly positive definite kernels define strictly convex energy functionals, with an equivalence between the notions of potential and directional derivative for smooth kernels, showing the strong relation between discrepancy minimization and more traditional design of optimal experiments. In particular, kernel herding algorithms are special instances of vertex-direction methods used in optimal design, and can be applied to the construction of point sequences with suitable space-filling properties.

Finally, when using a Gaussian-process prior for f, a suitable Karhunen-Loève decomposition of the process yields a Bayesian linear model. The machinery of optimal design theory can then be used to construct optimal design measures that minimize the integrated mean-squared prediction error (a Bayesian A-optimal design problem [2]), or the variance of estimators of Sobol' indices for sensitivity analysis (which corresponds to Bayesian L-optimal design [3]), or the variance of an unbiased estimator of the integral of f with respect to μ (Bayesian c-optimal design).

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Abstracts of the Ninth Workshop on Simulation (2018) 101-101

Optimal Designs for Minimax Criteria in Random Coefficients Regression Models

Maryna Prus[1]

In random coefficients regression (RCR) models observational units (individuals) are assumed to come from the same popularity and differ from each other by individual random parameters. These models have been introduced in biosciences for selection purposes and are now popular in many fields of statistical applications, for example in medical research and pharmacology. Optimal designs for the estimation of population (fixed) parameters are well discussed in the literature (see e. g. [2]). RCR models with known population (mean) parameters were investigated by [1]. [3] proposed solutions for optimal designs for the prediction of individual random parameters in models with given covariance matrix of random effects. However, the latter designs are locally optimal and depend on the covarince structure. Here, we present some results for minimax-optimal designs, which minimize the worst case for the criterion function over a specific region of reasonable values of the covariance matrix. We illustrate the results by a numerical example.

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Locally D-optimal Designs for Non-linear Models on the k-dimensional Ball

Martin Radloff[1] and Rainer Schwabe[2]

1 Introduction

We want to construct (locally) D-optimal designs for a wide class of linear and non-linear multiple regression models where the design region is a k-dimensional unit ball $\mathbb{B}_k$.
This class of regression models was already investigated, for example, in Konstantinou, Biedermann and Kimber [1]. But they only focused on a one-dimensional bounded interval. Schmidt and Schwabe [4] considered the same class of models, but with k covariates on a k-dimensional cuboid. They found a way to divide this problem into k marginal sub-problems with only one covariate in the form like Konstantinou et al. [1].
This special class of regression problems contains, for example, Poisson regression, negative binomial regression and regression models with censored data (see Schmidt and Schwabe [4]).
In linear multiple regression models on the k-dimensional unit ball $\mathbb{B}_k$ it is known (see Pukelsheim [2]) that the D-optimal design consists of the vertices of an arbitrarily rotated k-dimensional regular simplex, whose vertices lie on the surface of the design region – the unit sphere $\mathbb{S}_{k-1}$. Here "regular" means that all edges of the simplex have the same length.
In our case using invariance and equivariance (see Radloff and Schwabe [3]) the multidimensional problem can be reduced only to a one-dimensional marginal problem, which is analogous to Konstantinou et al. [1].

2 Problem and Result

The focus is on multiple regression models where the design region is a k-dimensional unit ball $\mathbb{B}_k$. This means for every design point $\boldsymbol{x} \in \mathbb{B}_k$ the regression function $\boldsymbol{f} : \mathbb{B}_k \to \mathbb{R}^{k+1}$ is considered to be $\boldsymbol{x} \mapsto (1, x_1, \ldots, x_k)^\top$. The parameter vector $\boldsymbol{\beta} = (\beta_0, \beta_1, \ldots, \beta_k)^\top$ is unknown and lies in the parameter space $\mathbb{R}^{k+1}$. This results in the linear predictor

$$\boldsymbol{f}(\boldsymbol{x})^\top \boldsymbol{\beta} = \beta_0 + \beta_1 x_1 + \ldots + \beta_k x_k \ .$$

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For the underlying model the one-support-point (or elemental) information matrix $\boldsymbol{M}(\boldsymbol{x}, \boldsymbol{\beta})$ is assumed to be in the form

$$\boldsymbol{M}(\boldsymbol{x}, \boldsymbol{\beta}) = \lambda\big(\boldsymbol{f}(\boldsymbol{x})^\top \boldsymbol{\beta}\big)\, \boldsymbol{f}(\boldsymbol{x}) \boldsymbol{f}(\boldsymbol{x})^\top$$

with an intensity (or efficiency) function λ which only depends on the value of the linear predictor.
As in Konstantinou et al. [1] and Schmidt and Schwabe [4] the intensity function λ is assumed to satisfy the following four conditions:

(A1) λ is positive on $\mathbb{R}$ and twice continuously differentiable.

(A2) λ' is positive on $\mathbb{R}$.

(A3) The second derivative u'' of $u = \frac{1}{\lambda}$ is injective on $\mathbb{R}$.

(A4) The function $\frac{\lambda'}{\lambda}$ is a non-increasing function.

Then the (locally) D-optimal design consists of a pole of the unit ball and the vertices of a $(k-1)$-dimensional regular simplex inscribed in the cut set of a plain, which is orthogonal to the polar axis, and the unit sphere.
For $(\beta_1, \ldots, \beta_k)^\top \neq (0, \ldots, 0)^\top$ the pole is the unique point on the sphere maximising the intensity, and the distance of the cutting plain to the pole depends on the magnitude of $||(\beta_1, \ldots, \beta_k)^\top||$.

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Abstracts of the Ninth Workshop on Simulation (2018) 104-105

Statistical modelling algorithm for solving the nonlinear Boltzmann equation on base of the projection method

S. V. Rogasinsky[1]

A statistical modelling algorithm is constructed for solution of the nonlinear kinetic Boltzmann equation based on the projection method. Hermite polynomials are used as an orthonormalized basis. The algorithm was tested on calculations for the problem of one-dimensional relaxation of gas with a known solution.

1 Introduction

In this report we consider solution of the Cauchy problem for a nonlinear kinetic Boltzmann equation in a spatially homogeneous case. It is well known that the approximate solution to this problem can be estimated by the Monte Carlo method simulating a Markov process of evolution of the corresponding N-particle ensemble whose phase states change due to pairwise interactions of particles (see, e.g., [1], [3], [4]).

The spatially homogeneous relaxation of a simple gas is described by the following Cauchy problem for the nonlinear Boltzmann equation (in dimensionless form) [2]:

$$\frac{\partial f(\mathbf{v},t)}{\partial t} = \int [f(\mathbf{v}',t)f(\mathbf{v}_1',t) - f(\mathbf{v},t)f(\mathbf{v}_1,t)]w(\mathbf{v}',\mathbf{v}_1' \to \mathbf{v},\mathbf{v}_1)d\mathbf{v}'d\mathbf{v}_1'd\mathbf{v}_1,$$

$$f(\mathbf{v},t) \Big|_{t=0} = f_0(\mathbf{v}),$$

where

$$w(\mathbf{v}',\mathbf{v}_1' \to \mathbf{v},\mathbf{v}_1) = 4\sigma(g,\cos\vartheta)\delta^{(3)}(\mathbf{v}'+\mathbf{v}_1'-\mathbf{v}-\mathbf{v}_1)\delta\Big(\frac{\mathbf{v}'^2+\mathbf{v}_1'^2}{2} - \frac{\mathbf{v}^2+\mathbf{v}_1^2}{2}\Big),$$

and $g = |\mathbf{v}' - \mathbf{v}_1'|$, $\sigma(g,\cos\vartheta)-$ is the differential cross-section of scattering of two particles, $\vartheta-$ is the angle of rotation of relative velocity in the system of the center of inertia of scattering particles.

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Here$f(\mathbf{v},t)$ is the distribution density of gas particles over velocities $\mathbf{v} \in \mathbf{R}^3$ at the time moment $t \geq 0$, and $\int f(\mathbf{v},t)d\mathbf{v} = 1$.

Let us pose the problem of calculation of the distribution density of particles over the absolute value of the velocity, i.e.,

$$\varphi(|\mathbf{v}|,t) = |\mathbf{v}|^2 \int f(\mathbf{v},t)d\omega, \quad \mathbf{v} = |\mathbf{v}| \cdot \omega.$$

For the sake of convenience, introduce the notation $x = |\mathbf{v}|$.

This report is focused on calculation of the solution to the problem formulated above by the Monte Carlo method based on the projection method.

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Abstracts of the Ninth Workshop on Simulation (2018) 106-106

Modeling the fair market price of Sukuk Mudharabah using monte carlo simulation approach

Dedi Rosadi[1], Heni Wahyuni[2], Sri Redjeki[3], Muslim[4]

We use design re-sampling framework, previously proposed in [1], for approximating Shariah financial products are currently developing in sharia financial market, including in Indonesia bond market. One of the most important products is called as Sukuk which is commonly referred to as "sharia compliant" bonds. The types of Sukuk that have been widely traded in Indonesia until now are Sukuk Ijarah and Sukuk Mudharabah. In this paper we consider the method to evaluate the fair market price of sukuk mudharabah based on monte carlo simulation approach. We provide the empirical studies using data from Indonesia Bonds market.

Keywords:

Sukuk mudharabah, sharia bond, fair market price, monte carlo simulation

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Geometry of Parameter Regions for Optimal Designs

Frank Röttger[1], Thomas Kahle, Rainer Schwabe

1 Introduction

Optimal design theory for nonlinear regression studies local optimality on a given design space. We identify the Bradley-Terry paired comparison model with graph representations and prove for an arbitrary number of parameters, that every saturated D-optimal design is displayed as a path in the graph representation. Via this path property we give a complete description of the optimality regions of saturated designs. Furthermore, we exemplify the unsaturated D-optimal designs with full support for 4 parameters.

2 Formulation of the problem

We consider pairs (i, j) of alternatives $i, j = 1, \ldots, n$. The preference for i over j is denoted in a binary variable $Y(i, j)$ with $Y(i, j) = 1$, if i is preferred over j and $Y(i, j) = 0$ otherwise. We assume, that there is a ranking for the alternatives via some constants π_i, so that the preference probability is

$$\mathbb{P}(Y(i,j) = 1) = \frac{\pi_i}{\pi_i + \pi_j}.$$

The model is transformed into a logistic model with $\beta_i := \log(\pi_i)$:

$$\mathbb{P}(Y(i,j) = 1) = \frac{1}{1 + \exp(-(\beta_i - \beta_j))} = \eta(\beta_i - \beta_j)$$

with $\eta(z) = (1 + \exp(-z))^{-1}$ as the inverse logit link function. As the preference probabilities only depend on the relation of the π_i, we are allowed to set $\pi_n = 1$ and therefore $\beta_n = 0$. The possibility to fix one of the parameters is known in general as the identifiability condition, the case with $\beta_n = 0$ as control coding. W.l.o.g. assume $i < j$. Furthermore, e_i is the $(n-1)$-dimensional unit vector. Then, we choose

$$f(i,j) = \begin{cases} e_i - e_j, & \text{for } i, j \neq n \\ e_i, & \text{for } (i, n) \end{cases}$$

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as the regression vector, so that

$$\mathbb{P}(Y(i,j)=1)=\eta(f(i,j)^\top\beta)$$

with $\beta^\top=(\beta_1,\ldots,\beta_{n-1})$. Then, the Information matrix of a design point (i,j) is

$$M((i,j),\beta)=\lambda_{ij}f(i,j)f(i,j)^\top$$

with the intensity $\lambda_{ij}:=\lambda_{i,j}(\beta)=\frac{e^{\beta_i-\beta_j}}{(1+e^{\beta_i-\beta_j})^2}$. The Information matrix of the model for a design ξ with weights w_{ij} is then given by

$$M(\xi,\beta)=\sum_{(i,j)}w_{ij}M((i,j),\beta)=\sum_{(i,j)}w_{ij}\lambda_{ij}f(i,j)f(i,j)^\top.$$

The celebrated equivalence theorem(compare for example [1]) states that a design ξ^* is locally D-optimal if and only if

$$\lambda_{ij}f(i,j)^\top M(\xi^*,\beta)^{-1}f(i,j)\leq n-1$$

for all $1\leq i<j\leq n$. So, the optimality regions of a design is given as a semialgebraic set, hence a set of polynomial equations and inequalities in the weights and the intensities. This enables us to apply tools from computer algebra to study the optimality regions of both saturated and unsaturated designs and to extend the results from [2] to 4 alternatives. Furthermore, we connect saturated designs with graph representations and proof the following theorem:

Theorem 2.1. *In the Bradley-Terry paired comparison model, every saturated optimal designs graph representation is a path, so a graph in which every node has at most two neighbours.*

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Abstracts of the Ninth Workshop on Simulation (2018) 109-110

Studying the resilience of communications in organizations using formal modelling and simulation

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After the nuclear accident at TEPCOs Fukushima Nuclear Power Plant (NPP) different studies pointed out that the emergency plan was not resilient [1]. After these analyses, we decided to ask ourselves: How can we design resilient emergency plans? To answer this question, since emergency plans can be considered a virtual organization, we started reviewing the concept of organizational resilience and how to measure it. We found a close relationship between resilient and viable organizations. Taking into account this relation, we proposed to apply the methodology to design viable organizations, introduced by Prez Rios [2], to the design of resilient organizations. This methodology, based on the Viable System Model (VSM), highlights the importance of the communications for the well-functioning of the organization. Due to the importance of the communications, we have focused on their study. The communications inside organizations can be studied as a diffusion process in multiplex networks. Researcher at the Laboratoire de l'Intgration du Matriau au Systme (IMS) at University of Bordeaux developed an architecture to simulate information diffusion processes in social networks [3]. We studied this architecture and we tested its applicability to study resilience of communications inside organizations. We used as case study a real Nuclear Emergency Plan (NEP) from Spain. We found that their architecture, although it was successfully proven to study the information diffusion process in social networks [4] and adapted to study business processes in the healthcare sector [5] was not suitable to include all the attributes specified in plan. For example, in our case, the behavior of the people is defined using complex rules that do not fit in a table format. Storing the properties in a table is a restriction of this architecture since it uses MySQL. We need structures that are more complex in order to store the behavior of the agents. Moreover, the Server-Proxy architecture does not allow us to include all the properties of our model. We are studying the diffusion of information between people, which use different devices, and these devices are connected through different networks. We are interested in studying different scenarios where both the devices and networks can fail. Therefore, it is crucial to include both of them in the model.

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Finally, to simulate dynamic networks, they use Dynamic DEVS (DS-DEVS). The use of DS-DEVS implies that we need to store all possible network configurations we want to simulate, which is not efficient in time of definition efforts and storage. Based on the architecture presented in [3], we propose an improved version that overcomes these issues. We also use Network Theory, ABM, and formal Modeling and Simulation (M&S), in our case we also use DEVS. A main difference is that this new architecture is general and can be used for any type of diffusion process in multiplex dynamic networks. There are many other aspects that differ. We introduce a development process (and a generic implementation of the architecture). We define a generic Diffusion Abstract Model (DAM) that can be modeled and implemented using other formal M&S methodologies different from DEVS. The design of the DAM is flexible and it allows modeling diffusion processes without storing all possible network configurations. It also provides several advantages such as including other properties of the network, as detail in the rest of the thesis. Using the proposed architecture, we were able to proposed improvements to the communications in the emergency plan.

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Abstracts of the Ninth Workshop on Simulation (2018) 111-113

On steady state probabilities of renewable systems with Marshal-Olkin failure model

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1. Stability of systems is a key problems in all natural sciences. For stochastic systems stability often means insensitivity or low sensitivity of their output characteristics to the shapes of some input distributions. There are some papers devoted to these problems (for the bibliography see, for example, [1]). Most of these investigations deal with system which components fail independently. In 1967 Marshall and Olkin [2] proposed bivariate distribution with depend components that can be used as a failure model for two-component reliability system. In the paper [1] the reliability function of the same system with Marshal-Olkin (MO) failure model for the its elements has been studied. In the present paper this investigations has been developed for the steady state probabilities (s.s.p) of the same system.

2. Consider a heterogeneous hot double redundant repairable system, the failure of which components satisfies to the MO model which can be represented by stochastic equation

$$(T_1, T_2) = (\min(A_1, A_3), \min(A_2, A_3)). \tag{1}$$

This means that there exists three reasons (shocks), which leads to the system failure. The first shock, time to which is a r.v. A_1, act only to the first component, the second one, time to which is a r.v. A_2, act only to the second one, while the third one, time to which is a r.v. A_1, act to both components and leads to the system failure. The r.v.'s A_1, A_2, A_3 are supposed to be independent exponentially distributed r.v.'s with parameters α_i $(i = 1, 2, 3)$.

In this paper it is supposed that after partial failure (when only one component fails) the partial repair begins, which means that the system prolong to work and the failed component begins to repair. But after the system failure the renewal of whole system begins that demand some random time, say B_3 with some c.d.f. $B_3(t)$, and after this time the system goes to the state 0. In any case the repair times B_i $(i = 1, 2, 3)$ of components and the whole system has absolute continuous distributions with cumulative distribution functions (c.d.f.) $B_i(x)$ $(i = 1, 2, 3)$ and probability density functions (p.d.f.) $b_i(x)$ $(i = 1, 2, 3)$ correspondingly. All repair times are independent. In further we will use the following notations.

- $\alpha = \alpha_1 + \alpha_2 + \alpha_3$ the summary intensity of the system failure;
- $\bar{\alpha}_k = \alpha_k + \alpha_3$ the intensity of the k-th and third shock;

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- $b_k = \int_0^\infty (1 - B_k(x))dx$ $(k = 1, 2, 3)$ k-th element repair time expectations;
- $\rho_k = b_k \alpha_i$;
- $\beta_k(x) = (1 - B_k(x))^{-1} b_k(x)$ $(k = 1, 2, 3)$ k-th element conditional repair intensity given elapsed repair time is x;
- $\tilde{b}_k(s) = \int_0^\infty e^{-sx} b_k(x)dx$ $(k = 1, 2, 3)$ Laplace transform (LT) of the k-th element repair time distribution.

Under considered assumptions the system state space can be represented as $E = \{0, 1, 2, (3,1), (3,2)\}$, which means: 0 — both components are working, 1 — the first component is repaired, and the second one is working, 2 — the second component is repaired, and the first one is working, $(3,1)$ — both components are in down states, and the first one is repaired, $(3,2)$ — both components are in down states, and the second is repaired.

For s.s.p. calculation we will use the method of additional variables introduction or so called markovization method that consists in introduction of some special additional variables in order to describe the system behavior with Markov processes. For our case as additional variables we use elapsed time of the failed component. Thus let us consider two-dimensional Markov process $Z = \{Z(t),\, t \geq 0)\}$, with $Z(t) = (J(t), X(t))$ where $J(t)$ is the system state in the time t, and $X(t))$ represents elapsed time of the failed component. The process phase space is $\mathcal{E} = \{0, (1,x), (2,x), (3,1,x), (3,2,x)\}$.

3. The main results are represented in the following theorems

Theorem 1. *The s.s.p.'s of the system under consideration has the form*

$$\begin{aligned}
\pi_1 &= \frac{\alpha_1}{\bar{\alpha}_2}(1 - \tilde{b}_1(\bar{\alpha}_2))\pi_0, \\
\pi_2 &= \frac{\alpha_2}{\bar{\alpha}_1}(1 - \tilde{b}_2(\bar{\alpha}_1))\pi_0, \\
\pi_3 &= [\alpha_1(1 - \tilde{b}_1(\bar{\alpha}_2)) + \alpha_2(1 - \tilde{b}_1(\bar{\alpha}_2)) + \alpha_3]b_3\pi_0
\end{aligned} \tag{2}$$

where π_0 is given by

$$\pi_0 = \left[1 + \alpha_1(1 - \tilde{b}_1(\bar{\alpha}_2))\left(b_3 + \frac{1}{\bar{\alpha}_2}\right) + \alpha_2(1 - \tilde{b}_2(\bar{\alpha}_1))\left(b_3 + \frac{1}{\bar{\alpha}_1}\right) + \alpha_3 b_3\right]^{-1}. \tag{3}$$

This theorem show an evident dependence of the system s.s.p. from the shapes of elements repair time distributions. However under rare failures this dependence became negligible.

Theorem 2. *Under the rare components' failures, when $q = \max[\alpha_1, \alpha_2, \alpha_3] \to 0$ the s.s.p. of the considered system take the form*

$$\begin{aligned}
&\pi_0 \approx [1 + \rho_1 + \rho_2 + \rho_3 + b_3(\bar{\alpha}_1\rho_1 + \bar{\alpha}_2\rho_2)]^{-1}, \\
&\pi_i \approx \rho_i\pi_0 \quad (i = 1, 2), \\
&\pi_3 \approx [\rho_3 + b_3(\bar{\alpha}_1\rho_1 + \bar{\alpha}_2\rho_2)]\pi_0.
\end{aligned} \tag{4}$$

Remark. One can see that the part $b_3(\bar{\alpha}_1\rho_1 + \bar{\alpha}_2\rho_2)$ in probabilities π_0 and π_3 has the second order with respect to q, and therefore using only the first order of this value the above formulas can be rewrite as follows

$$\pi_0 \approx [1 + \rho_1 + \rho_2 + \rho_3]^{-1},$$
$$\pi_i \approx \rho_i \pi_0 \quad (i = 1, 2, 3).$$

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Abstracts of the Ninth Workshop on Simulation (2018) 114-114

Queueing Models for Performance Analysis of Future Wireless Networks

Konstantin Samouylov[1]

Over the past few years, there has been an increasing level of research activities worldwide to design and performance analysis for the future multiservice networks, namely M2M and D2D communications over the LTE networks, P2P live streaming networks. The talk outlines how mathematical models are being used to address current issues concerning quality of service and performance parameters of the modern and future networks, including wireless networks. We shall first show models based on the queuing theory and teletraffic theory and reflecting key features of admission control mechanisms in the LTE network. We also show the analysis for Licensed Shared Access (LSA) regulatory framework, and also resource allocation in wireless networks with random resource requirements. Then we discuss some stochastic geometry problems of the interference analysis in D2D wireless networks. Finally, we are discussing the problem of modelling users mobility in future wireless networks. There should be great opportunities for the scientific community to contribute to solution of these problems in the forthcoming decade.

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A nonparametric point estimation technique using the m-out-of-n bootstrap

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We investigate a method which can be used to improve an existing point estimator by a modification of the estimator and by using the m-out-of-n bootstrap. The estimation method used, known as bootstrap robust aggregating (or BRAGGing) in the literature, will be applied in general to the estimators that satisfy the smooth function model (for example, a mean, a variance, a ratio of means or variances, or a correlation coefficient), and then specifically to an estimator for the population mean. BRAGGing estimators based on both a naive and corrected version of the m-out-of-n bootstrap will be considered. We conclude with proposed data-based choices of the resample size, m, as well as Monte-Carlo studies illustrating the performance of the estimators when estimating the population mean for various distributions.

Key words:

BRAGGing, Cornish-Fisher expansion, m-out-of-n bootstrap, Monte-Carlo study, point estimation, resample size, smooth function model.

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Bounds on the Rate of Convergence for Constant Retrial Rate Queueing Model with Two Servers

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The paper deals with a $M/M/2/2$-type retrial queueing system with a constant retrial rate denoted as Σ. The exogenous (primary) customers arrive to the system according to a Poisson process with rate λ. The system has two stochastically identical servers with i. i. d. exponential service times, general service time S and rate $\mu := 1/ES$.

The system has the following special feature: if a primary customer finds both servers busy it goes to some kind of infinite-capacity repository (the so-called orbit that can be considered as a FIFO queue). Let us also assume that the orbit works as a single FIFS server, in which a head line (the oldest) secondary customer tries to enter the arbitrary server after an exponentially distributed time with (orbit) rate μ_0. (It returns to the orbit if both servers are busy). Since each secondary costumer has (potentially) an infinite number of attempts to enter servers, the system has no losses.

First, a single-server retrial queue with constant retrial rate was suggested in [5] and used to simulate a telephone exchange system. The authors of ([1, 2] extended the model with multiple servers and waiting places. The paper [2] deals with the performance and stability analysis of the model by means of matrix-analytical method for $c \geq 2$ servers. The authors found the stability criteria of the model in an explicit form depending on system parameters λ, μ, μ_0. In recent paper [3, 6]), the retrial model with constant retrial rate was considered in a general way and includes a multi-server case with general service times and multi-class customers. Nevertheless, the above mentioned researches assume the positive recurrence of the process (regenerative, not necessary Markovian) and as a result the existence of the stationary distribution. However, none of these papers analyze the rate of convergence to stationarity.

We extend the analysis of this type of systems by finding the rate of convergence to stationarity of the corresponding Markov process. We describe a two-server

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retrial model and thereby extend the similar analysis developed for the simplest $M/M/1$-type retrial model in [9]. The retrial queueing systems with constant retrial rate could be applied for a wide range of applications, e.g. for unslotted Carrier Sense Multiple Access with Collision Detection (CSMA/CD) protocol ([4]) or for the optical-electrical hybrid contention resolution scheme for Optical Packet Switching (OPS) networks ([7, 8]). In the paper, we derive the sufficient conditions for the null ergodicity and ergodicity of the corresponding process and obtain the upper bounds on the rate of convergence for the both situations. Numerical examples of bounding the rate of convergence for the corresponding models are also given.

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Abstracts of the Ninth Workshop on Simulation (2018) 118-119

Optimal Designs for Count Data with Random Parameters

Marius Schmidt[1], Rainer Schwabe[1]

1 Introduction

Count data arises in experiments, where the number of objects or occurrences of events of interest is observed. Frequently, the Poisson model is used to model such data, in which the expected value of the Poisson distributed response variable is linked to a linear predictor consisting of covariates and unknown model parameters. Assuming a Gamma distributed random effect for each statistical unit, we obtain the Poisson-Gamma model as a generalization of the Poisson model. We note that there may be repeated measurements for each statistical unit.
The estimates of the unknown model parameters depend on the choice of the covariates. In order to obtain the most accurate parameter estimates, we determine optimal designs, which specify the optimal values and frequencies of the covariates (see [4]). With such designs the number of experimental units can be reduced, leading to a reduction of experimental costs.
For the Poisson model Rodríguez-Torreblanca and Rodríguez-Díaz [2] determined D- and c-optimal designs for the case of one covariate and Russell et al. [3] derived D-optimal designs for the case of multiple covariates. In the context of intelligence testing Graßhoff et al. [1] considered the Poisson-Gamma model with one measurement per statistical unit and computed D-optimal designs for a binary design region.

2 Formulation of the problem

We consider n statistical units, for example groups or individuals, for each of which m experiments with response variables Y_{ij}, $i = 1, \dots, n$, $j = 1, \dots, m$, are performed. To each statistical unit a Gamma distributed block effect $\Theta_i \sim \gamma(a, b)$ is assigned. The probability density function of the Gamma distribution $\gamma(a, b)$, $a, b > 0$, is given by $f_\gamma(\theta) = \frac{b^a}{\Gamma(a)} \cdot \theta^{a-1} \cdot e^{-b\theta}$ for $\theta > 0$, where $\Gamma(a)$ denotes the Gamma function.
We assume that given $\Theta_i = \theta_i$ the random variables Y_{ij} are independent Poisson distributed with parameter λ_{ij}. The expected value λ_{ij} is related via the canonical

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link function to the linear predictor, which consists of a fixed effects term $\boldsymbol{f}(\boldsymbol{x}_{ij})^T\boldsymbol{\beta}$ and an additive random effect v_i:

$$\ln(\lambda_{ij}) = \boldsymbol{f}(\boldsymbol{x}_{ij})^T\boldsymbol{\beta} + v_i$$

The values of the covariates $\boldsymbol{x}_{ij}$ can be chosen from a design region $\mathscr{X} \subset \mathbb{R}^k$. The vector $\boldsymbol{f} = (1, f_1, \ldots, f_{p-1})$ consists of known regression functions and the vector $\boldsymbol{\beta} = (\beta_0, \ldots, \beta_{p-1})^T$ is the unknown parameter vector. The random effect is given by $v_i = \ln(\theta_i)$. It follows:

$$\lambda_{ij} = \theta_i \cdot e^{\boldsymbol{f}(\boldsymbol{x}_{ij})^T\boldsymbol{\beta}}$$

Since the Poisson and Gamma distribution are conjugate distributions, the probability density function of $\boldsymbol{Y_i} = (Y_{i1}, \ldots, Y_{im})$ and thus the information matrix can be derived analytically. Optimal designs are based on the optimization of a function of the information matrix, for example, for D-optimality the determinant of the information matrix is maximized with respect to the design. Since the model is nonlinear, the optimal designs depend on the unknown parameters and are therefore called locally optimal.
We investigate the relations between the information matrices for the Poisson and Poisson-Gamma model and show that the D-optimality criterion for the Poisson-Gamma model is equivalent to a combined weighted optimality criterion of D-optimality and D_s-optimality for $\beta_1, \ldots, \beta_{p-1}$ for the Poisson model. Moreover, we determine the D-optimal designs for the Poisson-Gamma model, obtaining the D_s-optimal designs for the Poisson model as a special case.
For linear optimality criteria like L- and c-optimality we show that the optimal designs in the Poisson and Poisson-Gamma model coincide, which facilitates the search for optimal designs.

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The Revival of Reduction Principles in the Generation of Optimal Designs for Non-standard Situations

Rainer Schwabe[1], Fritjof Freise[2], Osama I. O. Idais [1], Eric Nyarko [1], Martin Radloff [1], Dennis Schmidt [1]

1 General considerations

It is common sense that experimentation, when properly designed, yields the highest evidence in statistical reasoning. The backbones of experimentation are classical concepts like randomization, blinding and stratification. On top of that the quality of a statistical experiment may be improved by a suitable choice of the experimental settings and a suitable choice of the corresponding numbers of replications. This consideration constitutes essentially the concept of optimal design of statistical experiments.

Based on convex optimization the general theory of optimal design is well developed. However, in practice for every non-standard statistical situation an individual optimal solution still has to be computed which may be challenging in the case of high dimensions and/or nonlinear relationships. While a diversity of algorithmic approaches is available ranging from steepest descent, multiplicative, and quasi-Newton to generic and particle swarm optimization methods involving high computational efforts, there may be still interest in analytical solutions or in reduction of the complexity of the problem to decrease the computational burden or to obtain exact benchmarks on the quality of competing designs.

As reduction principles in the construction of optimal designs we revisit here

- invariance and equivariance,
- majorization, and
- reduction to lower-dimensional problems.

The concept of invariance allows for symmetrization of designs, which typically results in a large number of experimental settings, while the related pure equivariance may provide standardizations, which lead to canonical forms in nonlinear situations (see Radloff and Schwabe, 2016). By majorization the design region,

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i. e. the number of experimental settings, may be reduced either by the concept of Loewner ordering or by model embedding. Finally, in more-dimensional situations the optimal designs may be built from their univariate counterparts as product-type designs under factorization or as some star-type (polypod) designs in certain nonlinear additive models (see Schmidt and Schwabe, 2017). For a general treatment of these concepts in linear settings we refer to Schwabe (1996).

2 Applications

We will exhibit the applicability of these general concepts in a couple of examples.

1. For restricted design regions we characterize optimal designs in a K-factor experiment with binary predictors, when the number of active predictors is bounded. As a by-product we obtain irregular fractions of a 2^K full factorial experiment.

2. In paired comparisons we can derive optimal designs for models with interactions up to second order between binary attributes.

3. For nonlinear (or generalized linear) models, in which the information is based on the value of the linear predictor in K variates, optimal designs can be additively constructed from their counterparts in the corresponding univariate models, if the design region is a (potentially unbounded) hyperrectangle. For a spherical design region similar reductions are possible.

4. For the Gamma model of multiple regression majorization can be used to obtain optimal designs in the case that there is no constant term.

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Numerical stochastic model of time series of air heat content indicators with considering for diurnal and seasonal nonstationarity

Sereseva O.V[1], Khlebnikova E.I.[2], Ogorodnikov V.A[3]

The purpose of comfort air-conditioning is to provide an environment, which is comfortable for the majority of the occupants. Air conditioning is the process of treating air to control its temperature, humidity, cleanliness and distribution to meet the requirements of the conditioned space. When designing air-conditioning systems such climatic characteristics as temperature, atmosphere pressure and humidity are used. For the optimal functioning of air-conditioning systems, its desirable to have an idea of the detailed characteristics of the change and variability of the various atmospheric air indicators. In the first place, its desirable to know such characteristic as the enthalpy of moist air. The enthalpy is used when calculating cooling and heating processes. The enthalpy of moist air is the sum of the enthalpy of dry air and the enthalpy of water vapor associated with the same dry air:

$$J = C_c T + 0.622 R \frac{E(T)}{P}(L + C_E T),$$

where T – air temperature, R - relative humidity, P - atmosphere pressure, $E(T)$ - saturated water vapor pressure at a temperature T, $L = 2507$ - specific heat of vaporization, C_c - specific heat of dry air at constant pressure, C_E - specific heat of water vapor at constant pressure. The enthalpy is measured in kilojoule per kilogram (kJ/kg) of air.

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Abstracts of the Ninth Workshop on Simulation (2018) 123-124

The probability of the capital staying above zero long enough in the Cramér-Lundberg model

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We consider the classical Cramér-Lundberg model, in which the capital X_t of an insurance company at time t is represented by the stochastic process

$$X_t = x + ct - \sum_{n=1}^{N_t} Y_n,$$

where $x \geq 0$ is the initial capital, $c > 0$ is the constant premium rate, N_t is a standard Poisson process with intensity λ, $\{Y_n\}$ are independent random variables distributed exponentially with parameter α, which are independent of N_t.

Let τ_d^X be the time of Parisian ruin, i. e., the first time when the capital has stayed below zero for at least d. For this relatively simple model, there is an explicit formula for the probability of ultimate Parisian ruin $\mathsf{P}\left(\tau_d^X < \infty\right)$, it can be found in [1].

Let η_l^X be the first time when the capital has stayed above zero for at least l. Then $P(\eta_l^X < \tau_d^X)$ is the probability of this happening before ultimate Parisian ruin. Using an argument similar to one in [1], we have derived an explicit formula for this probability:

$$\mathsf{P}\left(\eta_l^X < \tau_d^X\right) = \bar{G}_{12}(l) + \frac{G_{12}(l)P_{21}(d)\bar{P}_{12}(l)}{1 - P_{21}(d)P_{12}(l)},$$

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where

$$g_{12}(t) = \frac{\lambda e^{-\alpha x} e^{-(c\alpha+\lambda)t}}{ct+x}\left(xI_0\left(2\sqrt{\alpha\lambda t(ct+x)}\right) + \frac{ct}{\sqrt{\alpha\lambda t(ct+x)}} I_1\left(2\sqrt{\alpha\lambda t(ct+x)}\right)\right), \quad t \geq 0,$$

$$G_{12}(l) = \int_0^l g_{12}(t)\, dt, \quad \bar{G}_{12}(l) = 1 - G_{12}(l),$$

$$P_{12}(l) = \sqrt{\frac{\lambda}{c\alpha}} \int_0^l e^{-(\lambda+c\alpha)t} t^{-1} I_1\left(2t\sqrt{\lambda c\alpha}\right)\, dt, \quad \bar{P}_{12}(l) = 1 - P_{12}(l),$$

$$P_{21}(d) = \sqrt{\frac{c\alpha}{\lambda}} \int_0^d e^{-(\lambda+c\alpha)t} t^{-1} I_1\left(2t\sqrt{\lambda c\alpha}\right)\, dt,$$

I_ν is the modified Bessel function.

We have also performed an analysis of the sensitivity of the function $P(\eta_l^X < \tau_d^X)$ to the parameters α, λ, x, c, d and l. Namely, large samples of these parameters were generated and the influence of each parameter was analyzed using scatterplots.

Also, another way of analyzing sensitivity was used. Applying an algorithm from the book [2], the numerical value of the first-order sensitivity index of the main function on each parameter was found, as well as the total-effect index.

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ON CONDITIONAL OPTIMIZATION OF THE RANDIMIZED PROJECTION AND PROJECTION-MESH FUNCTIONL ALGORITHMS FOR NUMERICAL SOLUTION OF THE FREDHOLM INTEGRAL EQUATIONS OF THE SECOND KIND

Shipilov N.M., Voytishek A.V.[1]

This talk continues the investigations of the paper [1], in which the systematization of numerical (implemented on a computer) randomized functional algorithms for approximation of a solution of Fredholm integral equation of the second kind is carried out. Wherein, three types of such algorithms are distinguished: the projection, the mesh and the projection-mesh methods. In the paper [1], the possibilities for usage of these algorithms for solution of practically important problems are investigated in detail. The disadvantages of the mesh algorithms, related to the necessity of calculation values of the kernels of integral equations in fixed points, are identified. On practice, these kernels have integrated singularities, and calculation of their values is impossible. Thus, for applied problems, related to solving Fredholm integral equation of the second kind, it is expedient to use not mesh, but the projection and the projection-mesh randomized algorithms. Nevertheless, as opposed to the mesh methods, the usage of the theory of conditional optimization (see, for example, [2]) for these algorithms is somewhat complicated. In this theory, the question is about the coordinated choice of the parameter M (the number of the nodes or the basic functions) and the parameter N (the number of the trajectories of the applied Markov chain, simulated on a computer) for the implemented functional algorithms. These parameters must provide the given error level (designate it as) by the minimal computing expenditures S. Construct the upper boundary UP(M,N) of the algorithm's error (M,N), which depends on the parameters M and N: (M,N)UP(M,N) (1) This function of the two variables is equated to the value . From the equation of the form UP(M,N)= (2) one of the parameters (for example, N) presents in terms of the other parameter: N=(M). This ratio is substituted into the expression for the expenditures S(M,N) (which is also depends on the parameters M and N; as a rule, S(M,N)=HMN;H=const). As

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the result, we get the function S (M) on the one variable M and investigate this function for minimum with the help of the well-known methods of mathematical or numerical analysis. The defined values $M_min(), N = (M_min())$ are named as the conditionally optimal parameters of the model (algorithm). The "conditionally" of this optimization technique is related to the fact that in the left-hand side of the equation of the form (2) we use not the algorithm's error (M,N) itself but it's upper boundary UP(M,N) (may be, this boundary is inexact, rough?!). The difficulties for the conducting of such reasoning for the projection methods are related to the existence of the "tails" of the infinite orthogonal function systems and the necessity of their estimation for construction of the error upper boundaries of the form (1). In this sense, it is rather more simple (and, possibly, effective) to use the projection-mesh methods, for which the search for the conditionally optimal parameters is not too complicated problem [3].

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Abstracts of the Ninth Workshop on Simulation (2018) 127-128

Effective coefficients in the electromagnetic logging problem with log-normal distribution, multi-scale conductivity and permittivity

Olga N. Soboleva[1], Mikhail I. Epov[2], Ekaterina P. Kurochkina [3]

The quasi-steady condition in a nomagnetic medium are $\omega\epsilon\rho_0 < 0.1$, where $\epsilon = \epsilon^*/\epsilon_0$, $\epsilon_0 = 8.85{\cdot}10^{-12}F/m$ and $\epsilon^* \leq 5{-}10$ is the relative permittivity, $\mu = 4\pi{\cdot}10^{-7}$ is the magnetic permeability, $\sigma = 1/\rho_0$, σ is the electric conductivity, ω is the cyclic frequency. For long probes of the well logging, the quasi-steady condition is satisfied with a high accuracy. However, in heterogeneous media, the quasi-steady condition may be violated. The permittivity affects a measured signal and ϵ^* may be equal to 40. In natural condition as a rule, the spatial geometry of small-scale heterogeneities is not exactly known, and the irregularity of electric conductivity and permittivity abruptly increases as the scale of measurements decreases. The numerical solution of the problem with variations of parameters at all the scales requires high computer costs. So, the small-scale heterogeneities are described by random fields with the joint probability distribution functions and they are taken into account with the help of the effective parameters. Many natural media are "scale regular" in the sense that they can be described by multifractals and hierarchical cascade models by Sahimi[1], Bekele[2]. In this paper, the effective coefficients for Maxwell's equations in the frequency domain for a multi-scale isotropic medium by using a subgrid modelling approach are calculated. The correlated fields of conductivity and permittivity are approximated by the Kolmogorov multiplicative continuous cascades with a lognormal probability distribution. The wavelength is assumed to be large as compared with the scale of heterogeneities of the medium. The equations for effective coefficients are obtained in the first order terms of $\omega\epsilon(x)/\sigma(x)$. The obtained effective parameters are frequency-independent, therefore it follows that they are also the effective parameters in the time domain. The theoretical results are compared with the results from the direct 3D numerical simulation. The permittivity also affects the results in a quasi-steady case if the parameters σ and ϵ are weakly correlated.

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Abstracts of the Ninth Workshop on Simulation (2018) 129-130

Inference and change detection for high-dimensional time series

Ansgar Steland[1]

New results about inference and change point analysis of zero mean high dimensional vector time series

$$\mathbf{Y}_{ni} = (Y_{ni}^{(1)}, \ldots, Y_{ni}^{(d)})', \qquad i = 1, \ldots, n,$$

are discussed. Here the dimension, $d = d_n$, of the time series is allowed to grow with the sample size n. The results deal with change-point procedures that can be based on an increasing number of bilinear forms of the sample variance-covariance matrix as arising, for instance, when studying change-in-variance problems for projection statistics and shrinkage covariance matrix estimation.

Contrary to many known results, e.g. from random matrix theory, the results hold true without any constraint on the dimension, the sample size or their ratio, provided the weighting vectors v_n, w_n, are uniformly ℓ_1-bounded. Extensions to ℓ_2-bounded projections are also discussed. The large sample approximations are in terms of (strong resp. weak) approximations by Gaussian processes for partial sum and CUSUM type processes, [1], such as

$$\mathbf{v}_n' \left(\sum_{i=1}^{k} \mathbf{Y}_{ni} \mathbf{Y}_{ni}' - \frac{k}{n} \sum_{j=1}^{n} \mathbf{Y}_{nj} \mathbf{Y}_{nj}' \right) \mathbf{w}_n,$$

which imply (functional) central limit theorems under certain conditions. It turns out that the approximations by Gaussian processes hold not only without any constraint on the dimension, the sample size or their ratios, but even without any such constraint with respect to the number of bilinear form. For the unknown variances and covariances of these bilinear forms nonparametric estimators are proposed and shown to be uniformly consistent.

We present related change-point procedures for the variance of projection statistics as naturally arising in principal component analyses, in financial portfolio management where the convex combination of asset returns matters, in signal processing where data from large sensor arrays has to be analyzed.

Further, we discuss how the theoretical results lead to novel distributional approximations and sequential methods for shrinkage covariance matrix estimators in the spirit of Ledoit and Wolf, given by convex combinations of the form

$$\widehat{\mathbf{\Sigma}}_n^s = (1 - W)\widehat{\Sigma}_n + W i_n \mathbf{I},$$

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where $W \in [0,1]$ is the shrinkage weight, $\mathbf{I}$ the d-dimensional identity matrix and $\widehat{i}_n$ is an estimator of the optimal shrinkage intensity $i_n = \mathrm{tr}(\mathrm{Var}(\mathbf{Y}_n))$. The estimator $\widehat{i}_n$ is obtained. Especially, we discuss an asymptotic confidence interval $[\widehat{i}_n - a_n, \widehat{i}_n + a_n]$ for the shrinkage intensity satisfying

$$\lim_{n\to\infty} P([\widehat{i}_n - a_n, \widehat{i}_n + a_n] \ni i_n) = 1 - \alpha.$$

and related lower and upper bounds for the covariance matrix.

A simulation studies is presented, which investigate the accuracy of the proposed confidence interval. Lastly, we discuss an application to NYSE asset returns over a 22-year period corresponding to $5,651$ trading days.

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Abstracts of the Ninth Workshop on Simulation (2018) 131-132

Comparing non-parametric bootstrap and subsampling batch means methods for confidence assessment of ranked list latent variable estimates

Vendula Švendová[1], Sereina A. Herzog[1], Michael G. Schimek[1]

1 Introduction

Data pooling, also called data fusion or meta analysis, is a standard approach for merging data in order to obtain robust results. A large number of methods use ranking as a means of data representation, as ranks have the advantage of being independent of data type, scale, normalisation or other transformations. One such pooling method which estimates the underlying signals in multiple ranked lists is proposed in [1]. This method takes lists of rankings and recovers the latent variables responsible for the observed ranks. The parameter optimisation is performed with a Markov chain Monte Carlo (MCMC) algorithm, using 10 independent chains. Naturally, there is a need for a certainty assessment of such estimated values. In [1], the standard errors (SEs) of the estimates are calculated via non-parametric bootstrap. Each bootstrap sample $b = 1, \ldots, B$ of the observed ranked lists requires an initialisation of 10 additional Markov chains, which has a dramatic impact on the algorithm's computational demand, with runtime being in the order of hours even for small datasets. In this work, the objective is to estimate the SEs directly from the 10 original chains available from the latent variable estimation, and hence speed up the SE calculation B times. We use a subsampling approach called batch means method, as explained in [3]. The bootstrap method proposed in [1] and the batch means method proposed in this work are compared in terms of speed and quality of the SE estimates.

2 Methods

In order to compare the behavior of the bootstrap method and the batch means method for SE estimation, we simulated two scenarios, each with $n = 20$ lists and $p = 10$ objects. In the first scenario, the lists were in high agreement (Kendall's τ correlation ~ 0.7), while in the second scenario they were in mild agreement (Kendall's τ correlation ~ 0.4). We simulated the datasets and their respective true latent variables $\theta \in \mathbf{R}^p$ in the same way as in [1]. The estimates $\hat{\theta} \in \mathbf{R}^p$ were obtained using Metropolis MCMC optimisation, 10 independent chains, each

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with 20 000 steps. Bootstrap SE estimates for each object were calculated from $B = 50$ bootstrap samples. For every sample, we initiated 10 chains with 20 000 steps each. The details of the data simulation and bootstrap SE estimation are explained in [1]. Batch means SEs were calculated using the R package `mcmcse` [4]. We applied the batch means method on a window of w multivariate points centred around the estimate $\hat{\theta}$. The final certainty intervals were determined as $\hat{\theta}\pm$ 2*SE for both methods. Each scenario was simulated multiple times in order to confirm the results.

We compared the two methods based on the execution time and width of the certainty intervals.

3 Results

Both methods provided reliable SE estimates, succesfully covering the true signal values. With the number of bootstrap samples set to $B = 50$, the execution time of the batch means method was 50 times shorter. In our simulated scenarios with 20 lists and 10 objects, the runtime was reduced to 20.7 minutes using the batch means method, compared to 17.25 hours using the bootstrap method (benchmarked on a 4-core Intel(R) Core(TM) i7-6700 CPU@3.4GHz, running Win64bit). The width of the 2*SE intervals when using the batch means method depended heavily on the chosen window size w. Using a window size of $w = 500$, we obtained 2*SE intervals comparable to the bootstrap method, independently of the level of agreement between the lists. We conclude that the batch means method can be used as a much faster alternative to the bootstrap method.

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Blinded and Unblinded Sample-size Recalculation under Parametric Models

Sergey Tarima[1]

We use design re-sampling framework, previously proposed in [1], for approximating distributions of estimates of population parameters in the presence of nuisance parameters in pre-planned adaptive designs. We apply this re-sampling to likelihood ratio tests in Linear, Logistic and Poisson multiple regression models with sample size re-estimation (SSR). We consider estimation of nuisance parameter in blinded and unblinded manner. At the interim analysis, the sample size recalculation procedure resamples the whole study design to find a total sample size and a new critical value. As shown in our Monte-Carlo simulation studies this re-sampling method shows more accurate control of type I error and power when compared with naive sample size recalculation. This resampling procedure for SSR allows researchers to spend less resources than the naive SSR while it asymptotically secures the pre-determined type I error and power against a local alternative.

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Abstracts of the Ninth Workshop on Simulation (2018) 134-135

Linear generalized Kalman–Bucy filter

Tatiana M. Tovstik, Petr E. Tovstik[1], and Darya A. Shirinkina

1 Introduction

The linear generalized Kalman–Bucy filter problem [1] is studied. A signal and a noise are independent stationary auto-regressive processes with orders exceeding 1. In the frames of the recurrent algorithm, equations for the filter and its error are delivered. A direct algorithm is also proposed. The advantages and the locks of both algorithms are discussed. Numerical examples are given.

2 Statement of the problem

Let an observed process $\zeta_t = \theta_t + \eta_t$ be the sum of two independent processes consisting of a signal θ_t and a noise η_t. We assume that the processes θ_t and η_t are stationary autoregressive sequences of orders n and m, respectively,

$$\sum_{k=0}^{n} a_k \theta_{t-k} = \sigma_1 \varepsilon_1(t), \quad a_0 = 1, \qquad \sum_{k=0}^{m} b_k \eta_{t-k} = \sigma_2 \varepsilon_2(t), \quad b_0 = 1. \tag{1}$$

The random errors $\varepsilon_i,\ i,j = 1,2$ are such that $\mathbf{E}\varepsilon_i(t) = 0,\ \mathbf{E}\varepsilon_i(t)\varepsilon_j(s) = \delta_{ts}\delta_{ij}$ where δ_{kj} is the Kronecker delta. The moduli of the roots of the characteristic polynomials $a(z) = \sum_{k=0}^{n} a_k z^{n-k}$ and $b(z) = \sum_{k=0}^{m} b_k z^{m-k}$ are less than 1.

The Kalman–Bucy filter problem consists in the prognosis of the process θ_t at $t \geq 0$ by using observations of the process ζ_t at $t \geq 0$. In [2] the case $m = n = 1$ is studied. Here we investigate the more general case $n \geq 1,\ m \geq 1,\ n + m > 2$.

3 Recurrent relations of the Kalman-Bucy filter

We denote the process θ_t, estimate and its error with respect to the σ-algebra F_t^{ζ},

$$\mu_t = \mathbf{E}(\theta_t | F_t^{\zeta}), \quad \gamma_t = \mathbf{E}[(\theta_t - \mu_t)^2 | F_t^{\zeta}], \qquad F_t^{\zeta} = \sigma\{\omega : \zeta_0, \ldots, \zeta_t\}. \tag{2}$$

The recurrent relations are obtained in the following form

$$\mu_{t+1} = \sum_{k=0}^{w-1} A_{t,k}\mu_{t-k} + \sum_{k=0}^{m-1} B_{t,k}\zeta_{t-k}, \quad \gamma_{t+1} = C_t, \tag{3}$$

where $w = \max\{n, m\}$ and $A_{t,k}, B_{t,k}, C_t$ are the non-linear functions of the coefficients $a_j,\ b_j,\ \sigma_j$ in Eqs. (1), and of $\gamma_i,\ t + 1 - w \leq i \leq t$. Relations (3) are unacceptable at $0 \leq t \leq w - 2$, and for such t a direct algorithm shall be used.

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4 The direct algorithm

For $t \geq 0$ the Kalman–Bucy filter μ_t in the linear approximation is

$$\mu_t^d = \mathbf{E}(\theta_t | F_t^\zeta) = \sum_{k=0}^{t} \alpha_k^{(t)} \zeta_{t-k} \tag{4}$$

and we should choose the coefficients $\alpha_k^{(t)}$ so that the error $\gamma_t^d = \mathbf{E}(\theta_t - \mu_t^d)^2$ be minimum. That leads us to the equations

$$\sum_{p=0}^{t} \alpha_p^{(t)} R_\zeta(k-p) = R_\theta(t-k), \quad k = 0, 1, \ldots, t, \qquad R_\zeta(t) = R_\theta(t) + R_\eta(t), \tag{5}$$

and to the minimum value of $\gamma_t^d = R_\theta(0) - \mathbf{E}((\mu_t^d)^2) = R_\theta(0) - \sum_{k=0}^{t} \alpha_k^{(t)} R_\theta(t-k)$. Here $R_\theta(t)$ and $R_\eta(t)$ are to be found from the Yule–Walker equations [3].

5 Discussion

The direct algorithm may be used for all t, and not only for initial values of t.

It is proved that the direct algorithm converges as $t \to \infty$. By examples we show that the recurrent algorithm sometimes diverges.

For $n + m \leq 3$ the results of the recurrent and of the direct algorithm exactly coincide. In the remaining cases (excluding $t < w$) $\gamma_t^r > \gamma_t^d$, where γ_t^r and γ_t^d are the errors of the recurrent and of the direct algorithm, respectively.

The relations $\alpha_k^t \to \alpha_k^\infty < \infty$ for a fixed k, and $\alpha_k^\infty \to 0$ as $k \to \infty$ are valid. Therefore, if we want to use the direct algorithm for large values of t, it is possible to avoid the solution of Eqs. (5) of order t. We choose a small ε (say, $\varepsilon = 10^{-3}$), and find τ such that $|\alpha_k^{(t)}| < \varepsilon$ for all $t > \tau$. Then we may use the approximate equations (4) with summation from 0 to τ and with $\alpha_k^{(t)} = \alpha_k^{(\tau)}$.

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Abstracts of the Ninth Workshop on Simulation (2018) 136-137

On the evaluation of spatial-angular distributions of polarization characteristics of scattered radiation

Natalya Tracheva[1], Sergey Ukhinov[1]

In this talk, we present an algorithm of the Monte Carlo method for evaluation of spatial-angular characteristics of scattered polarized radiation. Suggested algorithm is constructed on the idea of projective expansion of the vector function of the angular distribution of the radiation flux in terms of hemispherical harmonics, which are based on associated Jacobi polynomials.

In previous works ([1], [2]) we proposed a randomized projective method for estimating the corresponding one-dimensional spatial-angular distribution for the particular axisymmetric case of the problem. This method is based on the expansion of the vector integral intensity of radiation in terms of modified Jacobi polynomials, orthonormalized with "Lambertian" weight $|\cos\theta|$. Here θ is the latitude reckoned from the normal to the surface. Now the challenge is to construct the similar algorithm of numerical statistical modeling for evaluation of two-dimensional angular characteristics of partially polarized radiation, transmitted and reflected by layers of the scattering and absorbing medium.

To do this, we consider the system of orthonormal with weight $\mu = |\cos\theta|$ on the set $(0,1) \times (0,2\pi)$ functions $\{H_{i,j}(\mu,\varphi),\ i = 0,...,\infty, j = -i,...,i\}$ in the Hilbert space $\mathcal{L}_{2,\mu}(\Omega_+)$ on the hemisphere of unit directions Ω_+. Here θ is the zenith angle, φ is the azimuth angle. The explicit form of the functions $H_{i,j}(\mu,\varphi)$ was obtained from the orthogonal system of hemispherical harmonics, first proposed in the paper [3]. In [4], the completeness of this system of hemispherical harmonics was proved.

After expansion of the vector function of the angular distribution of the radiation flux in terms of the orthonormal basis $\{H_{i,j}(\mu,\varphi),\ i = 0,...,\infty, j = -i,...,i\}$ and truncating it, we can get an estimator as a partial sum with coefficients that can be obtained with weighted vector Monte Carlo method [2].

We conclude by presenting some numerical results we have got for two-dimensional angular distributions of the intensity and the degree of polarization of radiation, transmitted and reflected by optically thick layers of a scattering and absorbing substance.

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Abstracts of the Ninth Workshop on Simulation (2018) 138-139

Algebraic views on classification problems

Gherardo Varando[1] and Eva Riccomagno[2]

1 Introduction

We study generative classifiers for binary class over categorical predictors, that is models of the joint probability distribution $\mathrm{P} > 0$ over the predictors $\mathbf{X} \in \boldsymbol{\mathcal{X}}$ and the class variable $C \in \{-1, +1\}$. Every generative classifier induce a discrimination function,

$$f_{\mathrm{P}} = \ln(\mathrm{P}(\mathbf{X}, C = +1)) - \ln(\mathrm{P}(\mathbf{X}, C = -1)),$$

such that the maximum a posteriori prediction $\arg\max_{c\in\{-1,+1\}} \mathrm{P}(C = c|\mathbf{X})$ is equal to the sign of f_{P}.

It is known that the form of the induced function f_{P} is connected to the conditional independece assumptions that hold in P [1, 2, 3]. For example the naive Bayes assumtpion $(X_i \perp\!\!\!\perp X_j | C)$ translates, for the discrimination functions, in the following decomposition,

$$f_{\mathrm{P}}(x_1, \ldots, x_n) = \sum_i f_i(x_i). \tag{1}$$

Complementarily we present a study of the set of generative classifier such that their induced functions satisfie the factorization in Equation (1).

$$\mathcal{P}_\emptyset = \{\mathrm{P} > 0 \text{ s.t. } f_{\mathrm{P}} = \sum_i f_i(x_i)\}.$$

2 Constant interactions models

Consider generative classifiers over two binary predictor variables X_1, X_2 and define the odds ratio of the conditional distribution of the predictors given the class variable,

$$\alpha[\mathrm{P}(X_1, X_2|C = c)] = \frac{\mathrm{P}(X_1 = 0, X_2 = 0|C = c)\,\mathrm{P}(X_1 = 1, X_2 = 1|C = c)}{\mathrm{P}(X_1 = 1, X_2 = 0|C = c)\,\mathrm{P}(X_1 = 0, X_2 = 1|C = c)}.$$

We can prove the following equivalence that characterize the set $\mathcal{P}_\emptyset$.

$$\mathrm{P} \in \mathcal{P}_\emptyset \Leftrightarrow \alpha[\mathrm{P}(X_1, X_2|C = +1)] = \alpha[\mathrm{P}(X_1, X_2|C = -1)].$$

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As Fienberg [4] we consider the manifold of costant interaction as the probabilities with odds ratios equal to $\alpha > 0$.

$$\mathcal{M}(\alpha) = \{\mathrm{Q} > 0 \text{ s.t. } \alpha[\mathrm{Q}] = \alpha\}.$$

If we parametrize a generative classifier $\mathrm{P} = \mathrm{P}(C)\,\mathrm{P}(X_1, X_2|C)$ we have that,

$$\mathrm{P} \in \mathcal{P}_\emptyset \Leftrightarrow \mathrm{P}(X_1, X_2|C = \pm 1) \in \mathcal{M}(\alpha),$$

for some $\alpha > 0$.

Obviously, naive Bayes classifiers belong to $\mathcal{P}_\emptyset$, in particular they correspond to the choice $\alpha = 1$ that reduces $\mathcal{M}(1)$ to the manifold of independence [5, 6].

The above characterization can be extended to more than two categorical predictors, and generalizing the odds ratios we can similarly consider more complex factorizations of the descrimination function f_P.

Moreover models in $\mathcal{P}_\emptyset$ can be seen as generative classifiers equivalent to the logistic regression and thus we investigate maximum-likelihood estimation over $\mathcal{P}_\emptyset$.

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Simulated Variogram-based Error Inspection of Manufactured Parts

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Industrial parts are routinely affected by dimensional and geometric errors originated in the course of manufacturing processes. These errors, whose pattern is typically related to a specific machining or forming process, are controlled in terms of dimensional and geometrical tolerances (such as e.g. straightness, roundness, flatness, profile) that require verification. In the present paper we focus on the inference on errors of different surfaces, whose tolerances are verified using a Coordinate Measuring Machine (CMM), commonly used for 3D measurement on account of both accuracy and flexibility. For this purpose, we have suggested to use the Kriging modelization for predicting the surfaces [1]. Kriging is a stochastic linear interpolation technique that predicts the response values at untried locations with weights assigned to the tried locations and the weights are selected so that the estimates are unbiased with minimum variance [2]. The fundamentals is the rate at which the variance between points changes over space. This can be expressed as a variogram [3] which shows how the average difference between values at points changes; it is a function of the distance and of the corresponding direction of any pair of points depicting their correlation extent. Theoretically, it is defined as the variance of the difference between the response values at two locations and it is equivalent to the correlation function for intrinsically stationary processes [4]. The use of the variogram for identifying the correlation structure is recommended by the geostatisticians even if the process is not stationary. In this paper we resort to variograms to detect possible manufacturing signatures, i.e. systematic pattern that characterizes all the features manufactured with a particular production process, and systematic errors of the CMM measurement process. We simulate different and typical manufacturing signatures of a planar surface and possible errors of a measurement process with CMM. The behavior of the omnidirectional variogram suggests the spatial correlations, giving evidence of possible non isotropy.

Keywords:

Kriging, Variogram, Anisotropy, Form Error, Measurement Errors, Technological Signature.

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More Efficient Estimation for Logistic Regression with Optimal Subsample

HaiYing Wang[1]

The Optimal Subsampling Method under the A-optimality Criterion (OSMAC) proposed in [1] samples more informative data points with higher probabilities. However, the original OSMAC estimator use inverse of optimal subsampling probabilities as weights in the likelihood function. This reduces contributions of more informative data points and the resultant estimator may lose efficiency. In this paper [2], we propose a more efficient estimator based on OSMAC subsample without weighting the likelihood function. Both asymptotic results and numerical results show that the new estimator is more efficient. In addition, our focus in this paper is inference for the true parameter, while [1] focuses on approximating the full data estimator. We also develop a new algorithm based on Poisson sampling, which does not require to approximate the optimal subsampling probabilities all at once. This is computationally advantageous when available random-access memory is not enough to hold the full data. Interestingly, asymptotic distributions also show that Poisson sampling produces more efficient estimator if the sampling rate, the ratio of the subsample size to the full data sample size, does not converge to zero. We also obtain the unconditional asymptotic distribution for the estimator based on Poisson sampling.

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Robust Sequential Designs for Approximate Inference in Generalized Linear Mixed Models

Xiaojian Xu

In this paper, we investigate the possible impact on the inference precision made when approximation appears in an assumed generalized linear mixed model (GLMM). We also discuss the relationships among various types of departures from the assumed GLMMs. The maximum likelihood estimation is adopted by fitting a given GLMM. We develop the methods of constructing the optimal robust sequential designs with protection on different types of model departures. Both I-optimality and D-optimality are employed. Although the design problems in a general setting of GLMMs are addressed, the commonly used logistic and Poisson mixed models are emphasized. A simulation study is carried and it has assessed both I- and D-optimal sequential designs in terms of integrated mean squared errors of the estimators for the parameters involved in the fixed effects in the link predictor (possibly misspecified). We conclude that the I-optimal designs outperform D-optimal designs for almost all the cases considered in the examples, and both I- and D-optimal designs developed in this paper are more efficient than the conventionally used uniform designs and the classical D-optimal designs obtained when assuming the fitted GLMMs are exactly correct.

Key Words:
Model-robust designs; Regression designs; Logistic mixed model; Poisson mixed model; Linear predictor; Integrated mean squared error.

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Information-Based Optimal Subdata Selection for LASSO regression

Min Yang

How to implement data reduction to draw useful information from big data is a hot spot of modern scientific research. Among all the data reduction techniques, subsampling-based methods are frequently used due to it's simplicity. However, sampling errors may affect the performance of subsampling based method and information carried by subsample is usually on scale of the subsample size, instead of the size of full data. In this talk, we consider linear model under LASSO with large p. Inspired by D-optimal criterion, optimal subsampling strategies are proposed to help us more efficiently pick informative subdata from the full data set. Performance of this new optimal subsampling strategy is tested in various simulations.

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The Markov decision process for adaptive design of clinical trials

Yanquing Yi[1]

An adaptive design uses information cumulated in a clinical trial to modify some aspect of the trial in order to save cost or to benefit patients from an ethics perspective. The information process can be formulated as a Markov process and the treatment allocation process be a Markov decision process. This talk will discuss optimal designs from the perspective of sequential decision making based on the formatted Markov process. The Bellman equation for optimality will be established and the iteration algorithm to achieve the optimal value thus optimal decision will be introduced. The properties of optimal designs will be discussed.

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Gradient Analysis of Markov-type Control Schemes and its Applications

Emmanuel Yashchin[1]

This paper discusses gradients by scheme parameters in the context of Markov Chain approach to analysis of Markov-type control schemes. Performance of control schemes is typically based on Run Length characteristics, and availability of efficiently computable gradients is helpful in design and analysis of schemes. Furthermore, gradients are useful in performing inference on Run Length characteristics based on Phase-1 data, in performance analysis for highly complex input data distributions, and other computational tasks associated with implementation of process control systems.

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Monte Carlo modelling of radiation angular distributions generated by laser beam in clouds

Yulia V.[1], Sergei M. Prigarin[2]

This paper, being a continuation of the research presented in [1-3], deals with studying time-stationary 3D distributions for a laser pulse multiply scattered in a comparatively dense medium. By Monte Carlo method for the scattered photons of a laser beam, we compute the concentration in space, order of scattering, fields of the preferable direction, angular distributions, and angular radiance distributions. We present numerical results for the laser sensing of water-drop clouds and water media, which show peculiarities of the 3D distributions of photons in space depending on geometrical and optical properties of the media. The research was supported by the Russian Foundation for Basic Research (project 16-01-00145).

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Combined nonparametric estimators of probability characteristics

Yury G. Dmitriev[1] and Gennady M. Koshkin[1]

Consider probability characteristics presented by the following functionals:

$$\theta = \theta(H) = \int_{R^s} \varphi(\vec{x}) dH(\vec{x}), \tag{1}$$

$$b_j = b_j(H) = \int_{R^s} \psi_j(\vec{x}) dH(\vec{x}), \quad j = \overline{1,m}, \tag{2}$$

where $\vec{x} = (x_1, \ldots, x_s)$, $H(\vec{x}) = \prod_{l=1}^{s} F(x_l)$, $dH(\vec{x}) = \prod_{l=1}^{s} dF(x_l)$, $F(x)$ is an unknown distribution function on R^1, $\varphi, \psi_j : R^s \to R^1$ are given functions.

Let us estimate θ under condition that b_j takes one of known values $\{\beta_{j,1}, \ldots, \beta_{j,k_j}\}$, $k_j \geq 1$, using independent sample $X_1, \ldots, X_N$ from $F(x)$. Thus, the problem can be formulated as follows: it is necessary to estimate (1) under the condition

$$\Delta_j(H) = \prod_{t=1}^{k_j} \Delta_{j,t}(H) = \prod_{t=1}^{k_j} (b_j(H) - \beta_{j,t}) = 0, \ j = \overline{1,m}. \tag{3}$$

The problem is to estimate (1) taking into account condition (3). In the special case $k_j = 1$, the problem was studied in [4] and [2]. With aim of using auxiliary information, several authors [1, 5, 6] have employed the empirical likelihood method. In all these works, it is shown that the estimators which take into account auxiliary information have smaller variances than the estimators without using auxiliary information.

Instead of unknown $H(\vec{x})$ in (1) and (3) substitute the estimates

$$\hat{H}_\tau(x_1, \ldots, x_s) = \frac{1}{|\omega_\tau|} \sum_{\{i_j\} \in \omega_\tau} \prod_{j=1}^{s} c(x_j - X_{i_j}), \tag{4}$$

where $c(t) = \{1 : t > 0;\ 0 : t \leq 0\}$, ω_τ is the set of index compositions $(i_1, \ldots, i_s)$, selected according to some rule with the index τ $(i_j = 1, \ldots, N;\ j = 1, \ldots, s)$, $|\omega_\tau|$ is the number of elements in the set ω_τ. Then, obtain $\hat{\theta}_\tau = \theta(\hat{H}_\tau)$, $\hat{\Delta}_{\tau,j} = \Delta_j(\hat{H}_\tau)$.

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Introduce the following class of estimators:

$$\hat{\theta}_{\lambda_\tau} = \hat{\theta}_\tau - \lambda_\tau^{\mathrm{T}} \hat{\boldsymbol{\Delta}}_{\boldsymbol{\tau}}, \tag{5}$$

where $\hat{\boldsymbol{\Delta}}_{\boldsymbol{\tau}} = (\hat{\Delta}_{\tau,1}, \ldots, \hat{\Delta}_{\tau,m})^{\mathrm{T}}$, $\lambda_\tau = V_\tau^{-1} C_\tau$, the matrix $V_\tau = E_F \hat{\boldsymbol{\Delta}}_{\boldsymbol{\tau}} \hat{\boldsymbol{\Delta}}_{\boldsymbol{\tau}}^{\mathbf{T}}$ is a non-degenerate matrix, V_τ^{-1} is the inverse matrix of V_τ, $C_\tau = E_F(\hat{\theta}_\tau - \theta)\hat{\boldsymbol{\Delta}}_{\boldsymbol{\tau}}$ is the matrix-column. Here, λ_τ minimizes MSE $E_F[\hat{\theta}_\lambda - \theta]^2$ for the given τ, and this minimum is equel to

$$E_F[\hat{\theta}_{\lambda_\tau} - \theta]^2 = E_F[\hat{\theta}_\tau - \theta]^2 - C_\tau^T V_\tau^{-1} C_\tau.$$

The non-negative quantity $C_\tau^T V_\tau^{-1} C_\tau$ determines the decrease of the MSE by attracting auxiliary information (3).

The estimator (5) combines (joins) the available empirical and prior information about the functionals (1) and (2). Statistical information about θ is contained by $\theta(\hat{H}_\tau)$, a priori information about b_j is given by $\{\beta_{j,1}, \ldots, \beta_{j,k_j}\}$, and statistical information is in $b_j(\hat{H}_\tau)$. Index τ corresponds to various methods of construction of an estimate, differing in the number of computational operations and the accuracy of estimation on the base of MSE.

It is important to note that the amount of this MSE's decrease depends on functionals (2), $\Delta_{j,t}$ in (3), τ, m, and k_j. For example, the increase of $|\Delta_{j,t}|$ and m reduces MSE, the increase of k_j increases MSE.

The statistic (5) can be used as an estimator for θ if you know λ_τ; otherwise you need to construct its estimate $\hat{\lambda}_\tau$. In the paper, adaptive estimators

$$\hat{\theta}_{\hat{\lambda}_\tau} = \hat{\theta}_\tau - \hat{\lambda}_\tau^{\mathrm{T}} \hat{\boldsymbol{\Delta}}_{\boldsymbol{\tau}} \tag{6}$$

are proposed. The asymptotic normality of all the proposed estimators is proved. Also, the mean square convergence for piecewise-smooth approximations [3] of estimators (6) is stated.

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Optimal design of sampling survey for efficient parameter estimation

Wei Zheng[1]

For many tasks of data analysis, we may only have the information of the explanatory variable and the evaluation of the response values are quite expensive. While it is impractical or too costly to obtain the responses of all units, a natural remedy is to judiciously select a good sample of units, for which the responses are to be evaluated. In this paper, we adopt the classical criteria in design of experiments to quantify the information of a given sample regarding parameter estimation. Then, we provide a theoretical justification for approximating the optimal sample problem by a continuous problem, for which fast algorithms can be further developed with the guarantee of global convergence. Our results have the following novelties: (*i*) The statistical efficiency of any candidate sample can be evaluated without knowing the exact optimal sample; (*ii*) It can be applied to a very wide class of statistical models; (*iii*) It can be integrated with a broad class of information criteria; (*iv*) It is much faster than existing algorithms. (*v*) A geometric interpretation is adopted to theoretically justify the relaxation of the original combinatorial problem to continuous optimization problem.

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