21st European Young Statisticians meeting – Book of Abstracts

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21st European Young Statisticians Meeting

29 July-2 August 2019, Belgrade, Serbia

Book of Abstracts

Eds. Bojana Milošević, Marko Obradović





Preface

This booklet contains basic information about the 21st European Young Statisticians Meeting (21st EYSM) to be held at Hotel Palace, Belgrade, in the organization of the Faculty of Mathematics, University of Belgrade, from July 28 to August 2 2019.

There are twenty seven European countries participating at the 21st EYSM. The International Organizing Committee (IOC) was responsible for invitation of at most two young scientists from each country whose research interests are in the stochastic range, from pure probability theory to applied statistics. Here the term "young scientist" refers to scientists who are less than thirty years of age or have two to eight years of research experience.

The scientific part of the Conference is organized as follows:

- [-] five eminent scientists from the field of mathematical statistics and probability will hold 60-minutes keynote lectures
- [-] forty eight invited young scientists will hold 20-minutes lectures.

Following the tradition of European Young Statisticians Meetings, there are no parallel sections. The lectures of invited young scientists are divided into eight sessions, six of them having six lectures, and two of them seven lectures each. Sessions were set in such manner that lectures inside one session belong roughly to the same research area, or at least have something in common. However, the sessions were not named since in some cases it was unlikely to find a title that would suit all the lectures within the session.

The topics to be presented include, but are not limited to

- Applied statistics in biology, medicine, ...
- Bayesian inference
- Characterizations of probability distributions
- Extreme and record value theory
- Functional statistics

- Goodness-of-fit testing
- High-dimensional statistics
- Regression models
- Robust estimation
- Spatial statistics
- Stochastic processes
- Survival analysis
- Time series analysis

All invited young scientists have an opportunity to publish a short paper, i.e. extended abstract of their lectures, in the Proceedings of the 21st EYSM. The review process for short papers is organized by the IOC, in the way that the IOC representatives propose reviewers for papers of participants they invited or personally act as a referee.

This booklet, beside all important information about the Conference, contains the scientific program, abstracts of all lectures to be given at the 21st EYSM and the list of participants together with their affiliations and contact information. Abstracts of all contributors are given in order following the schedule of lectures from the scientific program.

More details about the 21st European Young Statisticians Meeting could be found at the website www.eysm2019.matf.bg.ac.rs

21st European Young Statisticians Meeting

Organized by

Faculty of Mathematics, University of Belgrade

Under the auspices of

Bernoulli Society for Mathematical Statistics and Probability

Ministry of Education, Science and Technological Development of the Republic of Serbia

International Organizing Committee

Apostolos Batsidis, University of Ioannina, Greece Bettina Porvázsnyik, University of Debrecen, Hungary Bojana Milošević, University of Belgrade, Serbia Bruno Ebner, Karlsruher Institut für Technologie (KIT), Germany David Preinerstorfer, Université libre de Bruxelles, Belgium Deniz İnan, Marmara University, Turkey Eduardo García-Portugués, Carlos III University of Madrid, Spain Johanna Ärje, Tampere University of Technology, Finland Juan-Juan Cai, Delft University of Technology, Netherlands Laetitia Teixeira, University of Porto, Portugal Måns Thulin, Uppsala University, Sweden Marko Obradović, University of Belgrade, Serbia Nenad Šuvak, University of Osijek, Croatia Nina Munkholt Jakobsen, Technical University of Denmark, Denmark Radim Navrátil, Masaryk University, Czech Republic Riccardo De Bin, University of Oslo, Norway Tobias Fissler, Imperial College London, United Kingdom Wiktor Ejsmont, Mathematical Institute University of Wroclaw, Poland

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Keynote speakers

Ana Colubi, Justus-Liebig University of Giessen, Germany Igor Pruïster, Bocconi University, Milan, Italy M. Dolores Jiménez Gamero, University of Seville, Spain Pavle Mladenović, University of Belgrade, Serbia Peter Rousseeuw, KU Leuven, Belgium

Conference structure: keynote lectures, invited lectures.

Conference language: English

Scientific Program

Monday - July 29, 2019

9:05 - 9:30 **Opening ceremony**

9:30 - 11:10	Session 1 Chairman: Theodoros Nicoleris	
	9:30 - 9:55	Alisa Kirichenko
		Function estimation on large graphs
	9:55 - 10:20	Jure Vogrinc
		Anomalous scaling of the Metropolis Adjusted
	10.00 10.45	Langevin Algorithm
	10:20 - 10:45	Federico Cameriengni
	10.45 - 11.10	Alexandro Mösching
	10.40 11.10	Estimating Conditional Distributions under a
		Stochastic Ordering Constraint
11:10 - 11:30	Coffee break	
11:30 - 12:30	Keynote lectu	ıre
	Peter J. Rous	SSEEUW
	Department of l	Mathematics, KU Leuven, Belgium
	Detecting Devia	ting Data Cells
12:30 - 12:40	Break	
12:40 - 13:30	Session $1 - co$	ntinued

Chairman: Peter J. Rousseeuw

 12:40 - 13:05 Nikita Zhivotovskiy Robust covariance estimation for vectors with bounded kurtosis
 13:05 - 13:30 Arshak Minasyan On the Convergence and Robustness of Mean Estimation

$13{:}30-15{:}00 \quad \textbf{Lunch}$

15:00 - 16:15	Session 2 Chairman: Je	lena Stanojević
	15:00 - 15:25	Stanislav Lohvinenko Statistical analysis of parameter estimators in the fractional Vasicek model
	15:25 - 15:50	Michele Nguyen From theory to application: a spatio-temporal modelling perspective
	15:50 - 16:15	Ashish Kumar Impact of Stochastic Correlation on Wrong Way risk

16:15 – 16:35 **Coffee break**

16:35 - 17:50 Session 2 – continued Chairman: Fatih Kizilaslan

16:35 - 17:00	Ayça Pamukcu
	Risk Prediction in the Presence of Multivari-
	ate Repeated Measurements
17:00 - 17:25	Morten Overgaard
	The pseudo-observation method
17:25 - 17:50	Blanka Szietl
	Controlling Unit-Nonresponse Bias During
	Within-Household Selection With Optimal Al-
	location and New Specification of Kish Grid

Tuesday - July 30, 2019

9:05 - 11:10	Session 3 Chairman: Al	lex Karagrigoriou
	9:05 - 9:30	Jenni Niku
		Generalized linear latent variable models with applications
	9:30 - 9:55	Nuriye Sancar
		Liu-type Logistic Estimator based on Particle
		Swarm Optimization
	9:55 - 10:20	Vera Djordjilović
		Global test for high-dimensional mediation:
		testing groups of potential mediators
	10:20 - 10:45	Dario Azzimonti
		Bayesian excursion set estimation with Gaus- sian process models
	10:45 - 11:10	Una Radojičić
	-	Algorithms for Initialization of Gaussian Mix- ture Models

- 11:10 11:30 **Coffee break**
- 11:30 12:30 **Keynote lecture**

PAVLE MLADENOVIĆ University of Belgrade Extreme values in samples from stationary sequences and some combinatorial problems

12:30 - 12:40 Break

12:40 - 13:30 Session 3 – continued Chairman: Vladimir Božin

12:40 - 13:05	Helene Charlotte Rytgaard Generalized random forests for survival anal-
13:05 - 13:30	ysis Claudia Di Caterina Fast and efficient selection of high- dimensional graphical models through sparse combination of pairwise scores

13:30 – 15:00 Lunch

15:00 - 16:15	Session 4 Chairman: M.	. Dolores Jiménez Gamero
	15:00 - 15:25	Christian Zwatz
		Size and Power Properties of Autocorrelation
		and Heteroskedasticity Robust Tests in Spatial
		Error Models
	15:25 - 15:50	Daniela Correia
		GAMLSS with Random Effects: A Tool to Es-
		timate Usual Intake
	15:50 - 16:15	Mariusz Kubkowski
		Selection consistency of two-step selection method for misspecified binary model

16:15 – 16:35 **Coffee break**

16:35 - 17:50 Session 4 – continued Chairman: Jasmina Đorđević

Busenur Kızılaslan
Intuitionistic Fuzzy Liu-Type Regression
Functions
Łukasz Rajkowski
A note on the geometry of the MAP partition
in some conjugate Normal Bayesian Mixture
Models
Luísa Novais
Order selection in mixtures of linear mixed
models

Wednesday - July 31, 2019

9:30 - 11:10	Session 5 Chairman: Vlad Stefan Barbu	
	9:05 - 9:30	Andreas Makrides Semi-Markov Processes in Reliability: Theory and Applications
	9:30 - 9:55	Céline Cunen Survival and Competing Risk Models via Gamma Processes
	9:55 - 10:20	Thomas Kuenzer Snatial PCA for functional random fields
	10:20 - 10:45	Anne van Delft Frouwnau domain based informase of (non
	10:45 - 11:10	stationary) functional time series Julien Remy Testing for Principal Component Directions under Weak Identifiability
11:10 - 11:30	Coffee break	
11:30 - 12:30	Keynote lecture	
	Ana Colubi Justus-Liebig-U On functional re	niversity Giessen epresentations to deal with (fuzzy) set-valued data
12:30 - 12:40	Break	
12:40 - 13:30	Session 5 – continued Chairman: Bojana Milošević	
	12:40 - 13:05	Javier Álvarez Liébana A Goodness-of-Fit test for the functional lin-
	13:05 - 13:30	ear model with functional response Daniela Kuruczova Performance of principal component analysis through conditional expectation on longitudi- nal data
13:30 - 15:00	Lunch	
16:00 - 19:00	Excursion	

Thursday – August 1, 2019

9:30 - 11:10	Session 6
	Chairman: Marko Obradović

9:30 - 9:55	Christina Parpoula
	Distribution-Free Change-Point Outbreak De-
	tection Control Charts in Biosurveillance
9:55 - 10:20	Ilia Ragozin
	Goodness-of-fit tests for the logistic distribu-
	tion based on some characterization
10:20 - 10:45	Slađana Babić
	Optimal tests for elliptical symmetry against
	skew-elliptical alternatives
10:45 - 11:10	Viktor Skorniakov
	On asymptotic normality of certain linear
	rank statistics

11:10 - 11:30 **Coffee break**

11:30 - 12:30 **Keynote lecture**

M. DOLORES JIMÉNEZ GAMERO Departamento de Estadística e Investigación Operativa, Universidad de Sevilla Goodness-of-fit tests based on the characteristic function

- 12:30 12:40 Break
- 12:40 13:30 Session 6 continued Chairman: Bojana Milošević

12:40 - 13:05	Marija Cuparić New class of suprem-type exponentiality tests based on V-empirical Laplace transforms and Puri-Rubin characterization
13:05 - 13:30	Steffen Betsch Distributional Characterizations for Non- normalized Density Functions and Their Ap- plications

13:30 - 15:00 Lunch

15:00 - 16:15 Session 7 Chairman: Jasmina Đorđevic

Gilles Nisol
Factor Models for Functional Time Series in
High Dimensions: Representation Theory and
Consistent Estimation
Yolanda Larriba
Order Restricted Inference in Chronobiology
Vít Kubelka
Linear filtering of Gaussian processes in the
space of continuous functions

16:15 – 16:35 **Coffee break**

16:35 - 17:50 Session 7 – continued Chairman: Lenka Glavaš

16:35 - 17:00	Andrej Gajdoš
	Forecasting time series in the light of recent
	$advances \ in \ linear \ mixed \ modeling \ and \ convex$
	optimization
17:00 - 17:25	Panagiota Tsamtsakiri
	Bayesian model selection for a family of dis-
	crete valued time series models
17:25 - 17:50	Petra Laketa
	On random environment integer-valued au-
	$to regressive \ models - a \ survey$

20:00 - Conference dinner

Friday - August 2, 2019

9:30 - 11:10	Session: 8 Chairman: Ja	asmina Đorđevic
	9:30 - 9:55	Hrvoje Planinić Record times of station

$3.00 \ \ 3.00$	
	Record times of stationary regularly varying
	time series
9:55 - 10:20	Niko Leitzén
	On blind source separation under martingales:
	A probability theoretic perspective
10:20 - 10:45	Kaloyan Vitanov
	On decomposable multi-type Bellman-Harris
	branching process for modeling cancer cell pop-
	ulations with mutations
10:45 - 11:10	Lívia Leššová
	Limit Distribution for Some Iterated Partial
	Summations

- 11:10 11:30 Break
- 11:30 12:30 **Keynote lecture**

IGOR PRÜNSTER Bocconi University, Milan Bayesian nonparametric models derived from completely random measures

- 12:45 13:15 Closing ceremony
- 13:30 Lunch

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Keynote lectures

Detecting Deviating Data Cells

Peter J. Rousseeuw¹ and Wannes Van den Bossche¹

¹Department of Mathematics, KU Leuven, Belgium

Monday July 29th 11:30–12:30

Abstract

A multivariate dataset consists of n cases in d dimensions, and is often stored in an n by d data matrix. It is well-known that real data may contain outliers. Depending on the situation, outliers may be (a) undesirable errors which can adversely affect the data analysis, or (b) valuable nuggets of unexpected information. In statistics and data analysis the word outlier usually refers to a row of the data matrix, and the methods to detect such outliers only work when at least half the rows are clean. But often many rows have a few contaminated cell values, which may not be visible by looking at each variable (column) separately. We propose the first method to detect deviating data cells in a multivariate sample which takes the correlations between the variables into account. It has no restriction on the number of clean rows, and can deal with high dimensions. Other advantages are that it provides predicted values of the outlying cells, while imputing missing values at the same time. We illustrate the method on several real data sets, where it uncovers more structure than found by purely columnwise methods or purely rowwise methods. The proposed method can help to diagnose why a certain row is outlying, e.g. in process control. It also serves as an initial step for estimating multivariate location and scatter matrices.

Keywords: Cellwise outlier, Missing values, Multivariate data, Robust estimation, Rowwise outlier.

AMS subject classifications: 62G35.

Acknowledgements: The research of P. Rousseeuw has been supported by projects of Internal Funds KU Leuven. W. Van den Bossche obtained financial support from the EU Horizon 2020 project SCISSOR: Security in trusted SCADA and smart-grids 2015–1017. Thanks go to Jakob Raymaekers for assistance with including this method in the CRAN package *cellWise*.

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Extreme values in samples from stationary sequences and some combinatorial problems

Pavle Mladenović¹

Tuesday July 30th 11:30–12:30

¹ University of Belgrade, Serbia, paja@matf.bg.ac.rs

Abstract

The basic results related to extreme values in iid sequences of random variables and stationary sequences that satisfy weak dependence conditions will be introduced in the first part of the talk. The second part of the talk will be devoted to extreme values in the incomplete samples from stationary sequences. In the third part of the talk we shall use extreme value theory approach to discuss some combinatorial problems (coupon collector's problem, some extremal properties of random permutations, ...). The possibilities for statistical applications of extreme value theory will be indicated at the end of the talk.

Keywords: Extreme value distributions, Stationary sequences, Weak dependence conditions, Missing observations, Uniform AR(1) processes, Point processes. **AMS subject classifications:** 60G70.

Acknowledgements: Research was supported by a grant by Ministry of Education, Science and Technological Development of the Republic of Serbia, Grant No. 174012.

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On functional representations to deal with (fuzzy) set-valued data

Ana Colubi¹

¹Justus-Liebig-University Giessen, Germany

Wednesday July 31st 11:30-12:30

Abstract

Numerous experimental studies involve semi-quantitative expert information, or measured in a non-precise way, which can be modeled with interval (fluctuations, grouped data, etc.) or fuzzy (ratings, opinions, perceptions etc.) data. A general framework to analyze these kinds of inexact data with statistical tools developed for Hilbertian random variables will be presented. The space of nonempty convex and compact (fuzzy) subsets of R^p , has been traditionally used to handle this kind of imprecise data. Mathematically, these elements can be characterized via the support function, which agrees with the usual Minkowski addition, and naturally embeds the considered into a cone of a separable Hilbert space. The support function embedding holds interesting properties, but it lacks of an intuitive interpretation for imprecise data. Moreover, although the Minkowski addition is very natural when p = 1, if p > 1 the shapes which are obtained when two sets are aggregated are apparently unrelated to the original sets, because it tends to convexity. An alternative and more intuitive functional representation will be introduced in order to circumvent these difficulties. The imprecise data will be modeled by using star-shaped sets on \mathbb{R}^p . These sets will be characterized through a center and the corresponding polar coordinates, which have a clear interpretation in terms of location and imprecision, and lead to a natural directionally extension of the Minkowski addition. The structures required for a meaningful statistical analysis from the socalled ontic perspective are introduced, and how to determine the representation in practice is discussed.

Goodness-of-fit tests based on the characteristic function

M. Dolores Jiménez-Gamero¹

11:30–12:30 ¹Departamento de Estadística e Investigación Operativa, Universidad de Sevilla

Abstract

A classical problem in Statistics is that of checking if the law of the data belongs to a certain parametric family of distributions (the null hypothesis), which is usually called the goodness-of-fit (GoF) problem. A usual strategy to test GoF consists in comparing a nonparametric estimator of a function characterizing the data distribution with a parametric estimator of such function, constructed by assuming that the null hypothesis is true. A common choice for that function is the distribution function, although other choices are possible. In this talk, we review GoF tests based on the characteristic function, putting special emphasis on testing normality.

Keywords: Goodness-of-fit, characteristic function, parametric bootstrap. AMS subject classifications: 62G09, 62G10.

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Thursday

August 1st

Bayesian nonparametric models derived from completely random measures

Igor Prünster¹

¹ Department of Decision Sciences and Bocconi Institute for Data Science & Analytics, Bocconi University, Milan, Italy

Friday August 2nd 11:30–12:30

Abstract

The Dirichlet process represents the cornerstone of Bayesian Nonparametrics and is used as main ingredient in a wide variety of models. The many generalizations of the Dirichlet proposed in the literature aim at overcoming some of its limitations and at increasing the models' flexibility. In this talk we provide an overview of a large set of such generalizations by using completely random measures as a unifying concept. All the considered models can be seen as suitable transformations of completely random measures and this allows to highlight interesting distributional structures they share a posteriori in several statistical problems ranging from density estimation and clustering to survival analysis and species sampling. Furthermore, we discuss some natural approaches, which rely on additive, hierarchical and nested structures, to derive dependent versions of Bayesian nonparametric models derived from completely random measures.

Keywords: Bayesian Nonparametrics, Completely random measure, Dirichlet process, Normalized random measure, Posterior distribution. **AMS subject classifications:** 62F15; 60G57.

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Abstracts

Function estimation on large graphs

Alisa Kirichenko¹ and Harry van Zanten²

¹Centrum Wiskunde en Informatica (CWI) ²University of Amsterdam Monday July 29th 9:30–9:55

Abstract

In recent years there has been substantial interest in high-dimensional estimation and prediction problems in the context of relational data. These can in many cases be viewed as high-dimensional or nonparametric regression or classification problems in which the goal is to learn a "smooth" function on a given graph. We present a mathematical framework that allows to study the performance of nonparametric function estimation methods on large graphs and derive the minimax convergence rates within the framework. We consider graphs that satisfy an assumption on their "asymptotic geometry", formulated in terms of the graph Laplacian. We also introduce a Sobolev-type smoothness condition on the target function using the graph Laplacian to quantify smoothness. Finally, we present Bayesian estimation procedures and show how they achieve (asymptotically) optimal regularization.

Keywords: Networks, Bayesian statistics, Asymptotic statistics, Inference on graphs

Anomalous scaling of the Metropolis Adjusted Langevin Algorithm

Jure Vogrinc¹ and Wilfrid Kendall¹

¹ University of Warwick

Monday July 29th 9:55–10:20

Abstract

Metropolis Adjusted Langevin Algorithm (MALA) is a Markov Chain Monte Carlo (MCMC) method that improves on Random walk Metropolis (RWM) algorithm by also using information about the derivatives of the target. For sufficiently smooth targets of product form it can be respectively shown the variance of a single coordinate of proposals in RWM and MALA should optimally scale as d^{-1} and as $d^{-1/3}$ with dimension [1]. Heuristically, the complexity of RWM and MALA grows as d and $d^{1/3}$ with dimension. This leads to the famous guidelines of tuning the

acceptance ratio of RWM and MALA respectively to 0.234 [2] and 0.576 [3]. The work presented will address the open question: to what extent is the requirement of smoothness of the target necessary and how much is it a consequence of the proof? For MALA at least three derivatives of the target are indeed required for the mentioned scaling. I will present a class of generic random targets that are in $C^2(\mathbb{R})$ but not in $C^3(\mathbb{R})$, for which the optimal scaling of MALA proposal is almost surely worse than $d^{-1/3}$.

Keywords: Metropolis algorithm, Langevin algorithm, Markov chain Monte Carlo, optimal scaling AMS subject classifications: 60F05, 60J22, 65C05

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Hierarchical nonparametric processes

Monday 29th July 10:20–10:45 Federico Camerlenghi¹

¹University of Milano - Bicocca & Collegio Carlo Alberto

Abstract

Hierarchical processes are extremely popular Bayesian nonparametric models, which have been successfully applied in linguistics, information retrieval, topic modeling and genetics, among others. They are particularly suited for inducing dependence across different and related samples. We define and investigate suitable classes of hierarchical processes which are useful to face prediction in the context of species or feature models, to estimate random dependent densities or dependent survival functions. More specifically we first focus on hierarchical random probability measures recently introduced and investigated in [2] (see also [3]). Exploiting the results in [2], we are able to devise suitable computational methods to face prediction in the context of species sampling models, when one is provided with multiple populations of animals and wish to predict specific characteristics of additional and unobserved samples. We then move to the context of feature models, which generalize species sampling models by allowing every observation to belong to more than one species, now called features. We discuss a class of hierarchical priors tailored for such a setting and we introduce all the necessary distributional properties to develop full Bayesian inference (see [1]).

Keywords: Bayesian nonparametrics, prediction, hierarchical processes, species sampling models, feature models AMS subject classifications: 62F15

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Estimating Conditional Distributions under a Stochastic Ordering Constraint

Alexandre Mösching¹ and Lutz Dümbgen¹

¹University of Bern

Monday July 29th 10:45–11:10

Abstract

For a fixed set $\mathcal{X} \subset \mathbb{R}$, consider $n \geq 1$ pairs

$$(X_1, Y_1), (X_2, Y_2), \dots, (X_n, Y_n) \in \mathcal{X} \times \mathbb{R},$$

such that, conditional on $\mathbf{X} := (X_i)_{i=1}^n$, the responses Y_1, Y_2, \ldots, Y_n are independent with respective distribution functions $F_{X_1}, F_{X_2}, \ldots, F_{X_n}$. That means $\mathbb{P}(Y_i \leq y | \mathbf{X}) = F_{X_i}(y)$, for all $y \in \mathbb{R}$ and $1 \leq i \leq n$. We focus here on a stochastic ordering constraint over the unknown family of distribution functions $(F_x)_{x \in \mathcal{X}}$:

For any fixed
$$y \in \mathbb{R}$$
, $F_x(y)$ is decreasing in $x \in \mathcal{X}$. (1)

Such a constraint appears natural on several occasions. For example, an employee's income Y presumably increases with his or her age X. In forecasting, the measured cumulative precipitation amount Y is expected to increase with the numerical predictions X of the same quantity.

The estimation of $(F_x)_{x \in \mathcal{X}}$ under constraint can be done via nonparametric monotone least squares, as discussed in [1], and is often computed with the pool-adjacentviolators algorithm.

One can also consider minimal and maximal β -quantiles of F_x , respectively defined for each $x \in \mathcal{X}$ by $F_x^{-1}(\beta) := \min\{y \in \mathbb{R} : F_x(y) \geq \beta\}$ and $F_x^{-1}(\beta+) := \inf\{y \in \mathbb{R} : F_x(y) > \beta\}$. Then, constraint (1) is equivalent to $F_x^{-1}(\beta)$ and $F_x^{-1}(\beta+)$ being increasing in x, for any fixed $\beta \in (0, 1)$. Nonparametric monotone regression quantiles provide estimators for $(Q_x)_{x \in \mathcal{X}}$, with $Q_x(\beta)$ being any β -quantile of F_x , see [2] and [4].

In our manuscript [3], we give a detailed description of the aforementioned estimators. We prove that quantiles of $(\hat{F}_x)_{x \in \mathcal{X}}$ yield a large family of estimated quantile curves containing the estimators $(\hat{Q}_x)_{x \in \mathcal{X}}$, but also smoother ones. Finally, under some regularity conditions on \boldsymbol{X} and $(F_x)_{x \in \mathcal{X}}$, we provide rates of convergence for $\hat{F}_x(y)$ and $\hat{Q}_x(\beta)$, uniformly over some rectangles.

Keywords: Regression quantiles, stochastic order, uniform consistency.

AMS subject classifications: 62G08, 62G20, 62G30.

Acknowledgements: This work was supported by Swiss National Science Foundation.

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Robust covariance estimation for vectors with bounded kurtosis

Monday July 29th 12:40–13:05 Nikita Zhivotovskiy¹

¹ This work was prepared while the author was a postdoctoral fellow at the department of Mathematics, Technion I.I.T. and researcher at National University Higher School of Economics. Now visiting researcher at Google.

Abstract

Let X be a centered random vector taking values in \mathbb{R}^d and let $\Sigma = \mathbb{E}(X \otimes X)$ be its covariance matrix. We show that if X satisfies an $L_4 - L_2$ norm equivalence (sometimes referred to as the bounded kurtosis assumption), there is a covariance estimator $\hat{\Sigma}$ that given a sequence $X_1, ..., X_N$ of independent random vectors distributed according to X exhibits the optimal performance one would expect had X been a gaussian vector. The procedure also improves the current state-of-the-art regarding high probability bounds in the subgaussian case [1] (sharp results were only known in expectation or with constant probability).

In both scenarios the new bound does not depend explicitly on the dimension d, but rather on the effective rank of the covariance matrix Σ . The talk is based on [2].

Keywords: Robust statistics, Covariance estimation, Matrix Bernstein inequality **AMS subject classifications:** Primary 60K35, 60K35; secondary 60K35

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On the Convergence and Robustness of Mean Estimation

Arshak Minasyan¹

Monday July 29th 13:05–13:30

¹Yerevan State University, Yerevan

Abstract

In [2] the problem of common p-dimensional mean vector estimation of inliers among n independent Gaussian vectors is studied by iteratively using soft-thresholding operator. The presented method is the approximation of the solution of a non-convex optimization problem involving Huber function (see [3]). We simplify this problem and reduce it to Fermat-Weber location problem [1] using Huber function instead of Euclidean distance. Iteratively re-weighted least squares (IRLS) [4] method was modified for minimizing the resulting objective function and the global convergence property was proved given that the starting point is chosen accordingly. We illustrate the robustness of the resulting estimator through numerical experiments and examples, which are nicely consistent with theoretical results.

Keywords: Huber function, Iteratively Re-weighted Least Squares (IRLS), Fermat-Weber problem, Robustness. **AMS subject classifications:** 62F35.

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Statistical analysis of parameter estimators in the fractional Vasicek model

Monday July 29th 15:00–15:25

Stanislav Lohvinenko¹

¹Taras Shevchenko National University of Kyiv

Abstract

The fractional Vasicek model, which is described by the following stochastic differential equation

$$X_t = x_0 + \int_0^t \left(\alpha - \beta X_s\right) ds + \gamma B_t^H, t \ge 0,$$

where B^H is a fractional Brownian motion, is studied. It is assumed that the parameters $x_0 \in \mathbb{R}, \gamma > 0$ and $H \in (0, 1)$ are known and a problem of estimating α and β is considered.

First, applying the analog of the Girsanov formula for a fractional Brownian motion ([1, Theorem 3]), maximum likelihood estimators (MLEs) for the parameters α and β are obtained for the case H > 1/2. The problem is investigated in three variants: (i) when β is known, then the MLE for α is derived and it is proved that it is unbiased, strongly consistent and normal ([3, Theorem 3.1]); (ii) when α is known, then the MLE for β is described and it is proved that it is strongly consistent and asymptotically normal ([3, Theorem 3.2]); (iii) when both parameters are unknown, then the MLEs for α and β are presented and it is proved that they are consistent and asymptotically normal ([3, Theorem 3.3]). Moreover, in the last case, asymptotic distribution of the MLE of vector parameter (α , β) is studied
and its asymptotic normality for $\beta > 0$ is proved ([2, Theorem 4.2]). It is worth noting that the estimators of α and β turned out to be asymptotically independent. Next, the least squares estimators of the unknown parameters are introduced and their strong consistency in the case $H \ge 1/2$ is proved ([4, Theorem 2.1]). Since the discretization and simulation of above estimators are quite difficult, alternative estimators and their discretized versions, which are more useful for practical applications, are presented and their strong consistency for any $H \in (0, 1)$ is proved ([4, Theorems 2.2 and 2.3]).

Keywords: Fractional Brownian motion, fractional Vasicek model, parameter estimation, consistency, asymptotic normality.

AMS subject classifications: 60G22, 62F10, 62F12.

Acknowledgements: I would like to thank Kostiantyn Ralchenko for an invaluable constant support throughout whole my research and Olga Zhuchenko for the theorem about discretized estimators.

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From theory to application: a spatio-temporal modelling perspective

Michele Nguyen¹

Monday July 29th 15:25–15:50

¹Malaria Atlas Project, Oxford Big Data Institute, Nuffield Department of Medicine, University of Oxford, Oxford, UK.

Abstract

Increasingly, data are being collected at higher frequencies and spatial resolutions. To address the inherent complexity, researchers have been developing spatiotemporal models and related methodologies. The most popular ingredient of these models is the Gaussian random field (RF) with a Matérn covariance. This has been shown to be a solution of a linear fractional stochastic partial differential equation (SPDE) [5].

Recently, there has been renewed interest in viewing the solutions of SPDEs as RFs as well as investigating their probabilistic and statistical properties. Of special mention is the work on ambit fields, a family of non-Gaussian spatio-temporal stochastic integrals, which were introduced in the context of turbulence modelling [1]. We present two fundamental sub-classes of ambit fields: the spatio-temporal Ornstein-Uhlenbeck (STOU) process and the mixed STOU process [3, 4]. By focusing on shape of the integration set and the Lévy basis, we show how these ambit fields are able to model clusters in space-time as well as bridge between short-range and long-range dependence.

In addition to paving the way to more interesting spatio-temporal models, the link between Gaussian Matérn RFs and SPDEs has been used to make inference and prediction with such models computationally feasible [2]. We illustrate this using a study of the seasonality characteristics of malaria cases in Madagascar. A log-linear spatio-temporal regression model is used to predict monthly proportions and fits to von Mises distributions are used to determine useful features such as the start, peak and length of malaria transmission.

Keywords: Spatio-temporal Statistics, random fields, statistical modelling. AMS subject classifications: 62M30, 62M40, 62M86, 62F10, 62F12, 62F15, 62H11, 62H12.

Acknowledgements: My gratitude goes to Imperial College for my PhD scholarship and the Bill & Melinda Gates Foundation for supporting my current research. I would also like to thank Almut Veraart for the fruitful discussions during my PhD as well as Daniel Weiss, Rosalind Howes and the rest of the Malaria Atlas Project team for their useful feedback on the seasonality work.

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Impact of Stochastic Correlation on Wrong Way risk

Ashish Kumar¹, László Márkus¹ and Norbert Hari²

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²Széchenyi István University, Győr, Hungary,
² Morgan Stanley, Budapest, Hungary

Monday July 29th 15:50–16:15

Abstract

A positive correlation between exposure and counterparty credit risk gives rise to the so called Wrong-Way Risk (WWR). Even after a decade of financial crisis, addressing WWR in a both sound and tractable way remains challenging [1]. Academicians have proposed arbitrage-free set-ups through copula methods but those are computationally expensive and hard to use in practice. Resampling methods are proposed by the industry but they lack in mathematical foundations. This is probably the reason why WWR is not explicitly handled in the Basel III regulatory framework inspite of its acknowledged importance. The purpose of this article is to bridge this gap between the approaches used by academics and industry. To this end, we propose a new method to handle WWR: a stochastic correlation approach in modeling WWR. All the methods proposed post financial crisis more often than not use constant correlation to model the dependency between exposure and counterparty credit risk, i.e. assumes a linear dependency, thus fails to capture the tail dependence. Using a stochastic correlation [3] we move further away from Gaussian copula [2] and can capture the tail risk. This can be achieved by modelling the stochastic correlation as a proper transformation of a diffusion process. For our study we calculate the credit valuation adjustment (CVA) by taking a cross currency swap into account which is prone to wrong way risk because of an additional FX risk other than interest rate risk and credit risk. The performance of our approach is illustrated by a thorough comparison with the case when constant correlation model is used. The results show that even supposing perfect correlation between exposure and credit risk the wrong way risk may be underestimated leading to a wrong calculation of CVA. Given the uncertainty inherent to CVA, the proposed method is believed to provide a promising way to handle WWR in a sound and tractable way.

Keywords: CVA, Wrong Way Risk, Stochastic correlation, Tail dependence, Copulas AMS subject classifications: 91G40. Acknowledgements: Széchenyi István University

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Risk Prediction in the Presence of Multivariate Repeated Measurements

Monday July 29th 16:35–17:00 Ayça Pamukcu¹ and Özgür Asar¹

¹ Acıbadem Mehmet Ali Aydınlar University, Biostatistics and Medical Informatics, İstanbul, Turkey

Abstract

Main objective in many clinical studies is typically to derive accurate prediction of patients' prognosis. For this purpose, generally repeated measurements of a single biomarker are used [1] In the study, we investigate added gains of repeated measurements of additional biomarkers for risk prediction. Joint models for a survival and multivariate longitudinal outcomes under a Bayesian paradigm are used [2]. A real dataset from a randomised clinical trial on primary biliary cirrhosis of the liver patients is analysed. Univariate and bivariate analyses of two biomarkers are considered. Model performances are compared through calibration and discrimination measures. For the specific application, bivariate analysis gave better results.

Keywords: Joint models, Multivariate data, Risk Prediction **AMS subject classifications:** 62N99 **Acknowledgements:** Your acknowledgements.

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The pseudo-observation method

Morten Overgaard¹

¹Department of Public Health, Aarhus University, Bartholins Allé 2, DK-8000 Aarhus C, Denmark Monday July 30th 17:00–17:25

Abstract

This talk will be about the pseudo-observation method. Here, pseudo-observations are jack-knife pseudo-values and are related to the influence of an observation on an estimator. Such pseudo-observations can, under some assumptions, successfully replace incompletely observed outcomes in a regression analysis. This approach is the so-called pseudo-observation method, which is useful in survival analysis where outcomes may be missing due to censoring. The talk will touch upon two challenges in establishing appropriate asymptotic properties. Firstly, unbiasedness of the method relies on the pseudo-observations having, asymptotically, the correct conditional expectation and a challenge is to find out under which circumstances this will be the case. Secondly, the pseudo-observations are clearly correlated and a challenge is to handle this correlation. The correlation of the pseudo-observations turns out to have an impact on the variance of regression parameter estimates which complicates variance estimation.

Controlling Unit-Nonresponse Bias During Within-Household Selection With Optimal Allocation and New Specification of Kish Grid

Blanka Szeitl 1 and Tamás Rudas 2

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Bolyai Institute, Faculty of Science University of Szeged

Monday July 29th 17:25–17:50

Abstract

Several techniques exist to measure and adjust for non-response bias such as propensity models, or post-stratification. All of them can be applied only after the data collection, and require reliable data for the entire population regarding unit nonresponse patterns however, currently only estimates are available. In this paper, we demonstrate a new procedure controlling unit non-response during the sampling stage, preceding the actual data collection by combining classical techniques as Neyman's optimal allocation and the Kish grid.

The main finding is that the new sampling algorithm leads to lower SE then the usually applied post stratification.

Keywords: Survey sampling, Unit-Nonresponse, Household selection, Optimal allocation

AMS subject classifications: 62D05

Generalized linear latent variable models with applications

 $Jenni Niku^1$

¹ Department of Mathematics and Statistics, University of Jyväskylä, Finland

Abstract

Tuesday July 30th 9:05–9:30

> In many studies in community ecology, multivariate abundance data are often collected. Such data are characterized by two main features. First, the data are high-dimensional in that the number of species often exceeds the number of sites. Second, the data almost always cannot be suitably transformed to be normally distributed. Instead, the most common types of responses recorded include presenceabsence records, overdispersed species counts, biomass, and heavily discretized percent cover data. One promising approach for modelling data described above is generalized linear latent variable models. By extending the standard generalized linear modelling framework to include latent variables, we can account for covariation between species not accounted for by the predictors, species interactions an correlations driven by missing covariates.

> We consider the challenges with computationally efficient estimation and inference and introduce methods to overcome these issues, such as the variational approximation and the Laplace approximation method. Using illustrative examples we introduce applications of GLLVMs, eg. constrained or unconstrained ordination, studying species correlation patterns, fourth corner models and making inferences about environmental associations. An R package gllvm for fitting the models is also introduced.

> **Keywords:** Community analysis, ecological data, multivariate data, ordination, variational approximation.

AMS subject classifications: 62H12, 62J12, 62P12.

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Liu-type Logistic Estimator based on Particle Swarm Optimization

Nuriye Sancar¹ and Deniz Inan²

¹Near East University, Nicosia, Cyprus ²Marmara University, Istanbul, Turkey Tuesday July 30th 9:30–9:55

Abstract

The logistic regression model is the popular method of regression analysis when the response variable is binary. However, maximum likelihood estimations of the logistic model are severely affected by multicollinearity since this problem causes the inflation of the variance of the maximum likelihood estimator. The Liu-type logistic estimator was introduced as an alternative to the ridge logistic estimator to overcome multicollinearity problem in logistic regression, especially severe multicollinearity problem [2]. In the existing studies for the Liu-type logistic estimator, the pair of shrinkage parameter, k and biasing parameter, d is obtained in two stages [3],[1]. The parameter d is identified after identifying the parameter k, such that the mean squared error of the parameters is minimized. Since it is not feasible to evaluate the mean square error of the parameters numerically, an optimum value of the biasing parameter d is obtained in the terms of parameters. Estimations of different parameters are used to estimate the optimum value of d. Therefore, the pair of the parameters k and d chosen in this way is not optimal. In this study, a new simultaneous approach based on particle swarm optimization is proposed for the estimation of the shrinkage and biasing parameters (k,d) of Liu-type logistic estimator, instead of two stage procedure. Evaluation of the performance of the proposed method is performed by simulation studies and real data sets.

Keywords: Liu-type estimator, Logistic Regression, Particle Swarm Optimization, Multicollinearity **AMS subject classifications:** 62J12.

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Global test for high-dimensional mediation: testing groups of potential mediators

Tuesday July 30th 9:55–10:20 Vera Djordjilović¹

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Abstract

Over the last years, we have witnessed an increased interest for causal mediation analysis in genetic epidemiology, genomics, epigenomics, and neuroscience. For instance, researchers in epidemiology investigate whether epigenetic alterations mediate the effect of smoking on lung cancer [2], while in neuroscience, researchers investigate whether brain response measured at thousands of voxels mediates the effect of temperature on reported pain [1].



Figure 1: Mediation model with an exposure X, an outcome Y, and a vector $\boldsymbol{M} = (M_1, \ldots, M_p)^{\top}$ of potential mediators.

What these problems have in common is that instead of a single variable M on the path between an exposure X and an outcome Y, there is a high-dimensional vector M (Figure 1). In this work, we address the problem of testing whether Macts as a mediator between X and Y. We propose a global test for mediation, which combines a global test [3] with the intersection-union principle [4]. We derive theoretical properties of our approach and conduct simulation studies which demonstrate that it performs equally well or better than its competitor. We also propose a multiple testing procedure, Screen-Min, that provides asymptotic control of either familywise error rate or false discovery rate when multiple groups of potential mediators are tested simultaneously. We apply our approach to data from a large Norwegian cohort study, where we look at the hypothesis that smoking increases the risk of lung cancer by modifying the level of DNA methylation.

Keywords: global test, mediation analysis, FWER, FDR **AMS subject classifications:** 62G10, 62H15, 62F03, 62P10

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Bayesian excursion set estimation with Gaussian process models

Dario Azzimonti¹

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Tuesday July 30th 10:20–10:45

Abstract

We consider the problem of estimating the set of points where an unknown realvalued function is above a certain threshold in the setting where only few function evaluations are available. In a Bayesian framework, we estimate the function with a Gaussian process (GP) regression model and we study the excursion set of the posterior GP distribution. By exploiting random closed set properties, we are able to provide estimates for the excursion set and to quantify their uncertainty. In particular we review sequential design of experiments techniques that reduce the uncertainty on set estimates and we provide a method to explore excursion sets in higher dimensions. We apply the methods to test cases from reliability engineering where the function is an expensive computer experiment and the set of interest represents safe configurations for the system. **Keywords:** Gaussian process, excursion set estimation, active learning, experimental design, visualization.

AMS subject classifications: 62M30, 60G15, 62L05, 62P12

Acknowledgements: Dario Azzimonti acknowledges support from the SNSF, grant number 167199. The topic presented is the result of joint works with: D. Ginsbourger, C. Chevalier, J. Bect, and Y. Richet, J. Rohmer and D. Idier.

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Algoritms for Initialization of Gaussian Mixture Models

Tuesday July 30th 10:45–11:10 Una Radojičić¹

¹University of J. J. Strossmayer in Osijek - Department of Mathematics

Abstract

Gaussian mixture models are used for modeling data in cases where the data set is heterogeneous, in a sense that it consists of multiple underlying populations, where each population comes from a certain Gaussian distribution. Gaussian distribution naturally arises as an appropriate distribution for modeling various natural phenomena such as attributes of individuals in a certain population, temperature at certain area and time of the year, errors that occur because of the imperfect instruments etc. Therefore, data set that consists of observations coming from multiple such populations, is naturally modeled with a Gaussian mixture model. Furthermore, it a Gaussian mixture model is a universal approximator of densities, in the sense that any smooth density can be approximated with any specific nonzero amount of error by a Gaussian mixture model with enough components. The question arises, how to estimate the parameters of such model? While the problem is rather trivial in dimensions one, two and even three, in high-dimensional setting, this problem can be arbitrary hard. A typical approach for parameter estimation in statistical models is a maximization of the likelihood function. The idea of the maximum likelihood estimation is to estimate the model parameters as those for which the observed data is the most likely. The problem in such approach in the case of Gaussian mixture model is that the likelihood function of the model is not convex. Not only that it is not convex, but it can have a huge number of local maxima and saddle points. Therefore, it is easy for numerical local optimization methods, such as for example Expectation Maximization algorithm, especially in high-dimensional problems, to get stuck in one of them, and therefore, fail in attempt of finding a global maximum. The key in solving this problem is finding a good initial approximation to such method. Therefore, we place a focus on algorithms for finding an initial approximation for parameter estimation in Gaussian mixture models.

Keywords: Gaussian Mixture Models, EM Algorithm, Internal Annealing, MCMC, Parameter Estimation AMS subject classifications: 62G07

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Generalized random forests for survival analysis

Helene Charlotte Rytgaard¹

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Tuesday July 30th 12:40–13:05

Abstract

Random forests [2] is a machine learning method used for non-parametric prediction in a large variety of problems, including regression analysis, classification and also survival analysis. Generalized random forests (GRFs) [1] are a more recent extension applicable for inference in more general problems including estimation of average treatment effects. Based on honesty and subsampling, a large sample theory has been developed for GRFs establishing that the estimators are consistent and asymptotically normal.

This talk is concerned with an adaption of the GRF framework to the survival analysis setting where a time-to-event outcome of interest is observed subject to right-censoring. We define our target parameter as the average treatment effect on survival beyond some prespecified time-point, defined as the solution to a martingale estimating equation. In the formulation of treatment effects, potential outcomes already induce a missing data structure to the estimation problem, and the rightcensoring of the outcome adds to this missingness in a slightly more complicated way. To customize the partitioning scheme which is central for the GRF algorithm we derive the influence function for our target parameter, written as a functional of the node-specific Kaplan-Meier estimator stratified on the treatment variable. The final estimate of the time-point specific average treatment effect on survival is obtained by using the similarity weights produced by the forest to solve the martingale estimating equation.

Keywords: Survival analysis, random forests, causal inference, treatment effects, influence function.

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Fast and efficient selection of high-dimensional graphical models through sparse combination of pairwise scores

Tuesday July 30th 13:05–13:30 Claudia Di Caterina¹, Davide La Vecchia² and Davide Ferrari¹

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Abstract

Undirected graphical models have become important analysis tools in many areas of applied research, including bioinformatics and genetics [1]. For high-dimensional graphs consisting of a large number of potentially meaningful edges, however, both model selection and inference are challenging due to the computational intractability of the full likelihood. We introduce a new methodology for simultaneous model selection and parameter estimation in large graphical models. Within a pairwise likelihood framework [2], our proposal is to build estimating equations by including only the most informative pairwise likelihood scores selected from a great variety of candidates. Selection is carried out by minimizing an approximate distance between the composite and the full likelihood score functions, subject to a ℓ_1 -constraint. Differently from other approaches based on penalized likelihoods with penalties for model parameters [3, 4, 5], here penalization occurs on coefficients for the pairwise likelihood scores. This strategy discourages the construction of overly complex likelihoods, thus reducing the computing burden while retaining unbiasedness of the resulting parameter estimator. The performance of our method is illustrated through numerical simulations and real data examples.

Keywords: composite likelihood estimation, lasso penalty, model selection, regularization.

AMS subject classifications: 62H12, 62M40, 62P10. **Bibliography**

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Size and Power Properties of Autocorrelation and Heteroskedasticity Robust Tests in Spatial Error Models

Christian Zwatz¹

Tuesday July 30th 15:00–15:25

¹University of Vienna

Abstract

A typical approach for testing linear hypotheses on the regression parameters in regression models with autocorrelated and/or heteroskedastic disturbances is to modify the conventional F-test statistic by using a heteroskedasticity and autocorrelation consistent (HAC) estimator for the covariance matrix. These are nonparametric estimators designed to take the heteroskedasticity and autocorrelation in the data into account. HAC estimators for models where heteroskedasticity and autocorrelation is due to spatial interdependence among the observational units have been, e.g., proposed in [1] and [2].

We consider heteroskedasticity and autocorrelation robust testing in spatial error models, i.e. models where the disturbances follow a spatial autoregressive or spatial moving average process. It is well known that tests based on HAC estimators in the case of time series regression models suffer from substantial size and power problems. Based on a general theory developed in [3], [4] and [5], we show that similar problems also occur in the spatial error model. In particular, we give conditions under which the size of the resulting test is in fact one. We also give conditions under which the size of the test can be controlled by an appropriate choice of critical value.

Keywords: Size distortion, power deficiency, HAC, spatial models AMS subject classifications: 62F03, 62F05, 62J05, 62M30, 91B72

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GAMLSS with Random Effects: A Tool to **Estimate Usual Intake**

Daniela Correia^{1,2,3}, Milton Severo^{2,3} and Óscar Felgueiras^{1,4}

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Portugal

Abstract

Generalized Additive Models for Location, Scale and Shape (GAMLSS) are an extension of Generalized Additive Models (GAM) that allow parametric distributions from outside the exponential family for the response variable as well as modeling location, scale and shape parameters as linear or smooth functions of explanatory variables. It is a versatile yet simple method that allows regression predictors to be placed on any parameter of a potentially complex response distribution. While GAMLSS was originally designed for independent observations, the fact that smoothing can be represented as a random effect model facilitates the idea of introducing random effects within GAMLSS.

The usual intake of a food or nutrient of an individual is defined as the long-run average daily intake focusing on the long-term patterns rather than consumption on any given day. It is extremely relevant to some chronic phenomena such as inadequate dietary intake or long-term exposure to food contaminants. Its direct observation is unpractical since it would require participants to complete dietary intake questionnaires over a long period of time such as a year, depending on the foods/nutrient to be measured. Hence, each participant is asked to report dietary intakes of a few randomly selected days, so that usual intake can be estimated at the population level, as a repeated measurements distribution. However, it is necessary to consider that individuals day-to-day variability in consumption produces large within-person variance, heterogeneous across subjects. For that reason, the population usual intake distribution is the result distribution of average daily intakes recorded after removing within-person variability. Therefore, GAMLSS with random effects can be used to estimate the distribution of usual intake of foods/nutrients in a population. Thus, with this work we aim to explain how random effects models can be used within GAMLSS and explain the advantages and disadvantages of such modeling. Also, we use these models to estimate usual intake distributions and compare it to the results obtained using the standard approaches to estimate usual intake. We use data from the National Food, Nutrition, and Physical Activity Survey of the Portuguese General Population, IAN-AF 2015-2016.

Keywords: gamlss, random effects, usual intake.

Wednesday July 30th 15:25-15:50

AMS subject classifications: 62P10, 92D30.

Acknowledgements: Data used throughout the present study are retrieved from the IAN-AF databank, developed in the context of the National, Food, Nutrition and Physical Activity Survey funded by the EEAGRANTS programme-initiatives in Public Health (EEAGRANTS PT06_00088SI3). The project is coordinated by the University of Porto. The author is solely responsible for the contents of the document. The opinions expressed do not represent the opinions of the Consortium and the Consortium is not responsible for any use that might be made of the information included.

Selection consistency of two-step selection method for misspecified binary model

Mariusz Kubkowski¹² and Jan Mielniczuk¹²

¹ Warsaw University of Technology
² Institute of Computer Science Polish Academy of Sciences

Abstract

We consider two-stage selection method of predictors $\mathbf{X} \in \mathbb{R}^p$ when the underlying random binary regression model:

$$\mathbb{P}(Y=1|\mathbf{X}=\mathbf{x}) = q(\mathbf{x}) \tag{2}$$

is misspecified. We discuss a problem of finding consistent estimator $\hat{\beta}$ of β^* , where β^* minimizes risk function:

$$R(\mathbf{b}) = \mathbb{E}\rho(\mathbf{b}^T \mathbf{X}, Y)$$

for $\mathbf{b} \in \mathbb{R}^p$ and $\rho: \mathbb{R} \times \{0, 1\} \to \mathbb{R}$ is convex function. We call model (2) misspecified, when $q(\mathbf{x}) = q(\boldsymbol{\beta}^T \mathbf{x})$ and corresponding minus log-likelihood is not equal ρ . In this case an aim of selection is to find $\hat{\boldsymbol{\beta}}$ which recovers the support of $\boldsymbol{\beta}^*$ with high probability. The proposed procedure consists of screening and ordering predictors by Lasso and then selecting a subset of predictors which minimizes Generalized Information Criterion on the nested family pertaining to them.

In the contribution we discuss sufficient conditions in [1] on the parameters of the method and distribution of (X, Y) under which the above procedure is consistent. In numerical experiments we discuss performance of several modifications of the above procedure, in particular its net version when the nested family \mathcal{M} is replaced by the sum of such families constructed for a net of λ s.

Tuesday July 30th 15:25–15:50 Keywords: misspecification, binary regression, consistent selection, subgaussianity, Generalized Information Criterion AMS subject classifications: Primary 62J05, 62J07, secondary 90C25

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Intuitionistic Fuzzy Liu-Type Regression Functions

Busenur Kızılaslan¹, Erol Egrioglu² and Atif Ahmet Evren³

¹Department of Statistics, Marmara University, Istanbul, Turkey ²Department of Statistics, Giresun University, Giresun, Turkey ³Department of Statistics, Yildiz Technical University, Istanbul, Turkey Tuesday July 30th 16:35–17:00

Abstract

Developing technology shows how useful fuzzy inference systems in lots of applications. Fuzzy functions approach [3] which is one of the important fuzzy inference system for time series forecasting. In fuzzy functions approach, the membership values and their non-linear transformations are used together with original input variables to increase the prediction power. However, multicollinearity problem can be occured because of using these correlated variables. Purpose of the paper is to propose a new fuzzy forecasting method with intuitionistic fuzzy sets [1] which has addition information known as hesitation degree. In this case, both intuitionistic fuzzy sets and their non-linear transformations is used to increase the prediction power. Liu-Type estimator [2] is preferred to obtain intuitionistic fuzzy functions without exposed to multicolinearity problem. To demonstrate the performances of proposed method, some real world time series data are used and the results have shown that the effectiveness of the proposed method in conrast to other methods.

Keywords: forecasting, intuitionistic fuzzy sets, liu-type regression, multicollinearity, ridge regression

AMS subject classifications: 62J07, 62M10, 94D05

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A note on the geometry of the MAP partition in some conjugate Normal Bayesian Mixture Models

Łukasz Rajkowski¹ and John Noble¹

¹Faculty of Mathematics, Informatics and Mechanics, University of Warsaw

Abstract

Bayesian Mixture Models are increasingly popular among researchers for clustering problems. I will present the results of our research regarding the geometry of the maximal a posteriori (MAP) partition in the Bayesian Mixture Model where the component distribution is multivariate Normal with Normal-inverse-Wishart prior on the component mean and covariance ([2]). We prove that in this case the clusters in any MAP partition are quadratically separable. Basically this means that every two clusters are separated by a quadratic surface. In connection with results of [1], where the linear separability of clusters in the Bayesian Mixture Model with a fixed component covariance matrix was proved, it gives a nice Bayesian analogue of the geometric properties of Fisher Discriminant Analysis (LDA and QDA). Moreover, I will show how the first order approximation of the posterior probability gives an elegant formula which may serve as a score function in choosing the optimal clustering (for example) hierarchical clustering methods. This is the topic of our ongoing work.

Keywords: Bayesian Mixture Models, Maximal a Posteriori Partition **AMS subject classifications:** 62F15

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Order selection in mixtures of linear mixed models

Tuesday July 30th 17:25–17:50 Luísa Novais¹ and Susana Faria²

^{1,2}Department of Mathematics and Applications, University of Minho, Portugal

Tuesday July 30th 17:00–17:25

Abstract

Finite mixture models are one of the most widely used methods for modelling data that arise from a heterogeneous population, given that for these cases the estimation of a single linear model is not sufficient. In regression analysis, it has been a popular practice to model unobserved population heterogeneity through finite mixtures of regression models. Within the family of mixtures of regression models, finite mixtures of linear mixed models have also been applied in different areas of application since they not only take into account the correlations between observations from the same individual, but they also conveniently model unobserved heterogeneity between individuals at the same time.

One of the main difficulties in mixture models arises in the selection of the correct number of components for each case, an important and difficult research problem that has not yet been resolved. In this work we address the problem of determining the number of components for mixtures of linear mixed models by investigating the performance of various model selection methods, namely different information criteria and the likelihood ratio test.

In order to evaluate the methodologies developed we carry out a simulation study, in particular using resampling methodologies, and we apply these methodologies to a real data set. The results demonstrate that the criteria HQIC, AIC4 and aBIC, as well as the likelihood ratio test, are the best options to estimate the number of components for mixtures of linear mixed models.

Keywords: Mixture models, Model selection, Information criteria, Likelihood ratio test, Bootstrap

AMS subject classifications: 62J99

Acknowledgements: This research was financed by FCT - Fundação para a Ciência e a Tecnologia, through the PhD scholarship with reference SFRH/BD/139121/2018. The collection of data used in this study was partly supported by the National Institutes of Health under grant number R01 HD069609 and R01 AG040213, and the National Science Foundation under award numbers SES 1157698 and 1623684.

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Semi-Markov Processes in Reliability: Theory and Applications

Wednesday Andreas Makrides¹, Alex Karagrigoriou² and Vlad Stefan Barbu¹

July 31st 9:05–9:30

¹University of Rouen ²University of the Aegean

Abstract

This work deals with multi state systems that we model by means of semi-Markov processes. The main characteristic of this work is that the sojourn times in a given state which are seen to be independent not identically distributed random variables are assumed to belong to two different general classes of distributions. The first class of distributions is closed under maxima and contains several distributions, like the Bernoulli distribution, the power function distribution and the extreme value Type I distribution. The second class of distributions is closed under minima and includes the exponential, the Weibull, the Pareto, the Rayleigh and the Erlang truncated exponential distribution [1]. For the above setting we obtain maximum likelihood estimators of the parameters of interest and investigate their asymptotic properties. Furthermore, plug-in type estimators are furnished for various reliability indices related to the system under study.

Conclusively, our main objective is the proposal of parsimonious modeling for multistate systems, considering also a semi-Markov framework. Thus, we introduce a useful and powerful tool with a reduced number of parameters, which can be of great importance from a practical point of view.

Keywords: multi-state system, reliability theory, survival analysis, semi-Markov processes, parameter estimation.

AMS subject classifications: 60J27, 60K15, 60K20, 62N02, 62N05, 90B25.

Acknowledgements: This work has been carried out during the post-doc appointment of the first author at the Laboratoire de Mathématiques Raphaël Salem, University of Rouen, France.

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Survival and Competing Risk Models via Gamma Processes

Céline Cunen¹ and Nils Lid Hjort¹

¹University of Oslo, Department of Mathematics

Wednesday July 31st 9:30–9:55

Abstract

We use gamma processes as a vehicle to construct biologically plausible models for survival and competing risk models. Our methods include both time-to-threshold perspectives, where an event takes place when the underlying process reaches such a threshold c (see for instance [1]), and sizes of shocks, where the event happens when a shock is above a different threshold d. These considerations lead to fruitful and flexible classes of survival distributions, also for the regression case with covariate information for the individuals under study. In addition, the time-to-threshold models are readily extended to the competing risk case, where one wishes to study different causes leading to the same event. Our models and methods are applied to real data.

Keywords: survival analysis, competing risk, gamma processes. AMS subject classifications: 62N99, 62P10

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Spatial PCA for functional random fields

Thomas Kuenzer¹, Siegfried Hörmann¹ and Piotr Kokoszka²

¹Institute of Statistics, Graz University of Technology, Austria ²Statistics Department, Colorado State University, Fort Collins, CO, USA Wednesday July 31st 9:55–10:20

Abstract

With the proliferation of remote sensing technology, functional spatial data is a subject of growing importance in statistics. The applications of such high-dimensional functional data on spatial grids range from climate data to hyperspectral imaging of the earth's surface. We propose a novel concept of functional principal components (FPCs) for spatial data. Ordinary functional principal component analysis ignores the information contained in the spatial dependence structure of a sample. By making use of this information, our method of spatial functional principal components (SFPC) provides a very efficient tool for dimension reduction.

We consider second-order stationary functional data on a spatial grid \mathbb{Z}^r for some $r \geq 1$, where in each grid point $\mathbf{t} \in \mathbb{Z}^r$, a random element $X_{\mathbf{t}} \in L^2([0,1])$ can be observed. Under mild assumptions on the functional random field $(X_{\mathbf{t}})_{\mathbf{t}\in\mathbb{Z}^r}$, we show that SFPCs provide both a quantitative and a qualitative improvement to the dimension reduction technique provided by the ordinary FPCs. That is, a given number of SFPCs explains a larger portion of the variance than the respective ordinary FPCs, while the SFPC scores exhibit a cross-covariance of zero at all spatial lags. The estimators of the SFPCs and their scores are shown to be consistent under the framework of increasing domain asymptotics. In empirical studies on real and simulated data, we show that SPFCs significantly outperform ordinary FPCs in terms of the mean squared error of the reconstructed data. We also briefly explore a possible statistical application of this method in the context of normality testing.

Keywords: Dimension reduction, Functional data analysis, Frequency domain analysis, Functional spatial data, Principal components.

AMS subject classifications: 62M30, 62H25 (primary) 62M15, 62G20, 62G05 (secondary)

Frequency domain-based inference of (non-stationary) functional time series

Wednesday July 31st 10:20–10:45 Anne van $Delft^1$

¹Ruhr University Bochum, Germany

Abstract

In the analysis of functional time series the objects of interest are ordered collection of random variables $\{X_t, t \in \mathbb{Z}\}\$ where each X_t takes values in some function space, often assumed to be L^2 . The setting is therefore high-dimensional where the intrinsic variation is inherently larger than the observation length. In order to extract information on the characteristics of such series, frequency domain-based inference techniques provide powerful tools: not only for optimal dimension reduction of stationary functional time series but also to model non-stationary functional time series as well as for hypothesis testing. We review some of the existing techniques and introduce some new results. **Keywords:** Functional data analysis, locally stationary processes, spectral analysis.

AMS subject classifications: Primary: 62HG99, 62M15, Secondary 62M10, 62H15.

Testing for Principal Component Directions under Weak Identifiability

Davy Paindaveine¹, Julien Remy¹ and Thomas Verdebout¹

¹Universit Libre de Bruxelles

Wednesday July 31st 10:45–11:10

Abstract

We consider the problem of testing, on the basis of a *p*-variate Gaussian random sample, the null hypothesis $\mathcal{H}_0: \boldsymbol{\theta}_1 = \boldsymbol{\theta}_1^0$ against the alternative $\mathcal{H}_1: \boldsymbol{\theta}_1 \neq \boldsymbol{\theta}_1^0$, where $\boldsymbol{\theta}_1$ is the "first" eigenvector of the underlying covariance matrix and $\pmb{\theta}_1^0$ is a fixed unit *p*-vector. In the classical setup where eigenvalues $\lambda_1 > \lambda_2 \geq \ldots \geq \lambda_p$ are fixed, the Anderson likelihood ratio test [1] and the Hallin, Paindaveine, Verdebout Le Cam optimal test [2] for this problem are asymptotically equivalent under the null, hence also under sequences of contiguous alternatives. We show that this equivalence does not survive asymptotic scenarios where $\lambda_{n1} - \lambda_{n2} = o(r_n)$ with $r_n = O(1/\sqrt{n})$. For such scenarios, the Le Cam optimal test still asymptotically meets the nominal level constraint, whereas the LRT becomes extremely liberal. Consequently, the former test should be favored over the latter one whenever the two largest sample eigenvalues are close to each other. By relying on the Le Cam theory of asymptotic experiments, we study in the aforementioned asymptotic scenarios the non-null and optimality properties of the Le Cam optimal test and show that the null robustness of this test is not obtained at the expense of efficiency. Our asymptotic investigation is extensive in the sense that it allows r_n to converge to zero at an arbitrary rate. To make our results as striking as possible, we not only restrict to the multinormal case but also to single-spiked spectra of the form $\lambda_{n1} > \lambda_{n2} = \ldots = \lambda_{np}$.

Keywords: Testing for directions, Weak identifiability, Le Cam, LAN, PCA **AMS subject classifications:** 62H11

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A Goodness-of-Fit test for the functional linear model with functional response

Wednesday July 31st 12:40–13:05

Javier Álvarez-Liébana¹, E. García-Portugués², G. Álvarez-Pérez³, W. González-Manteiga⁴ and M. Febrero-Bande⁴

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Abstract

The increasing availability of data for continuous processes has recently boosted the field of Functional Data Analysis (FDA). There is a large body of situations in which it is desirable to measure the relation between functional random variables $\mathcal Y$ and \mathcal{X} , by means of a linear regression $\mathcal{Y} = m(\mathcal{X}) + \mathcal{E}$, named as Functional Linear Model with Functional Response (FLMFR), where \mathcal{E} is a random error function, being m an unknown operator, admitting an integral representation in terms of a bivariate kernel β . Several authors have contributed to the Goodness-of-Fit (GoF) framework for scalar and multivariate regression models. Overcoming the poor empirical power of smoothing-based tests and tests based on the integrated regression function, a novel statistic, in the high-dimensional context, was proposed by [2], in terms of a residual marked empirical process based on projections. In contrast, the development of GoF test approaches in the FLMFR context is currently one of the challenges in FDA. Up to our knowledge, only proposals in [1] (just a residual diagnostic), [4, 5] (just tested the simple hypothesis) and [6] (only for concurrent models) can be found. In this work we will extend the GoF test in [3] for the FLMSR (FLM with Scalar Response) model (based on the proposal in [2]): we will present an easily computable Cramér-von-Mises statistic for the null composite hypothesis, being characterized in terms of an infinite-dimensional process by its two-sides projected version into functional directions, and the empirical estimator of the integrated regression function depending on empirical marked processes. Since β should be estimated, we also provide a novel estimator based on Lasso regression. The calibration of the test is performed by a wild bootstrap, applied to the functional residuals.

Keywords: CvM statistic, Functional linear model, Functional response, Goodness-of-Fit, Wild bootstrap.

AMS subject classifications: 62J02; 62M05; 62M10; 62M20

Acknowledgements: The work of J. Álvarez-Liébana was supported in part by project MTM2015-71839-P (co-funded by Feder funds), of the DGI, MINECO, Spain.

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Performance of principal component analysis through conditional expectation on longitudinal data

Daniela Kuruczová¹

Wednesday July 31st 13:05–13:30

¹Department of Mathematics and Statistics, Faculty of Science, Masaryk University

Abstract

Functional data analysis is a relatively novel approach in multivariate statistics which extends the concept of a random variable to the infinite dimensional setting. While the measurements of a functional random variable still have finite dimension, it is assumed, that the observed variable is in its nature infinitely dimensional. Natural examples of functional variables are time-dependent functions, but the notion can be extended to many other concepts, such as surfaces [1].

Longitudinal studies are a natural example of data suitable for the functional approach. Multiple variables are measured at several discrete points over time with the intention of estimating the underlying continuous function. The usual technique for analysing functional data is principal component analysis, which may be unsuitable in case of longitudinal data due to sparseness. To address this issue, a new method was developed – principal component analysis through conditional expectation (PACE). This method heavily relies on a non-parametric estimate of the mean and covariance function [2].

Via simulation study, we examined how the quality of these estimates affects the performance of the principal component analysis through conditional expectation, focusing on the choice of the smoothing parameter and its extremes such as overand undersmoothing. Then, using simulations as well as an actual dataset, we assessed the performance of this method as an option for dealing with missing data in longitudinal studies, addressing specific challenges of longitudinal data, such as drop-out effect.

Keywords: functional data, principal component analysis, PACE, bandwidth selection, sparse data **AMS subject classifications:** 62H99

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Distribution-Free Change-Point Outbreak Detection Control Charts in Biosurveillance

Thursday August 1st 9:30–9:55 Christina Parpoula¹ and Alex Karagrigoriou¹

Lab of Statistics and Data Analysis, Department of Statistics and Actuarial-Financial Mathematics, University of the Aegean, Karlovasi, Samos 83200, Greece

Abstract

Epidemiological surveillance is a specific sector of Biosurveillance related solely to the human population and constitutes a dynamic scientific activity which progresses and requires systematic monitoring of developments in the field of health sciences and (bio)statistics. Epidemiological surveillance systems present various challenges regarding the source and quality of data, the statistical quality control, the monitoring (follow-up), the evaluation of statistical techniques used to detect outbreaks, anomalies and outliers in surveillance data, and extreme timeliness of detection [3]. Statistical process control (SPC) techniques have a long history of application to problems in health care monitoring and public health surveillance, and several proposed approaches for detecting outbreaks of infectious diseases are directly inspired by, or related to, methods of SPC [2]. This paper deals with the development of univariate distribution-free SPC charting methods based on change-point analysis [1], and discusses some of the statistical issues involved in the selection, construction and evaluation of such control charts for Phase I retrospective epidemiological surveillance purposes. Empirical study provides some guidelines for the implementation and effective use of Phase I univariate SPC charting methods for the very early and accurate outbreak detection. The interpretation of such SPC charts, from both a statistical and an epidemiological perspective, facilitates the better understanding of process variability in an epidemiological surveillance system and highlights important issues either for a health care or SPC practitioner.

Keywords: change-point analysis, statistical process control, distribution-free, control charts, outbreak detection.

AMS subject classifications: 62-07, 62-09, 62G05, 62G08, 62G10, 62P10. **Acknowledgements:** The work was carried out at the Lab of Statistics and Data Analysis of the University of the Aegean. The authors would like to thank the Department of Epidemiological Surveillance and Intervention of the Hellenic Centre for Disease Control and Prevention (HCDCP) for providing the influenza-like illness (ILI) rate data, collected weekly through the sentinel surveillance system.

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Goodness-of-fit tests for the logistic distribution based on some characterization

Ilia Ragozin¹

Thursday August 1st 9:55–10:20

¹ Department of Mathematics and Mechanics of Saint–Petersburg State University, Universitetsky pr. 28, Stary Peterhof 198504, Russia

Abstract

There were built two location-free goodness-of-fit tests for the logistic distribution based on a recent characterization by Hua and Lin [1]. The test statistics are based

on suitable functionals of U-empirical distribution functions. One of them has the integral structure, the second one is of Kolmogorov type. For every test statistic there was described the large deviation asymptotics under the null-hypothesis. Then the local Bahadur efficiency was calculated for some alternatives. For instance, in case of scale alternative this efficiency turned out to be 0.837 for the integral test and 0.353 for the Kolmogorov one. Conditions of local optimality in Bahadur sense were also studied.

Keywords: Bahadur efficiency, logistic distribution, large deviations, goodness-offit tests, U-statistics.

AMS subject classifications: 62G10, 62G20, 62G30, 62E10. **Acknowledgements:** I would like express my gratitude to my scientific advisor Prof. Ya. Yu. Nikitin for interesting problem statement and many useful advice.

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Optimal tests for elliptical symmetry against skew-elliptical alternatives

Thursday August 1st 10:20-10:45 Slađana Babić¹, Laetitia Gelbgras², Marc Hallin² and Christophe Ley³ ¹³ Ghent University

² Université libre de Bruxelles, ECARES

Abstract

New efficient tests for elliptical symmetry against skew-ellipticity are presented. The backbone of our construction is the Le Cam theory of asymptotic experiments, and optimality is to be understood in the Le Cam sense, namely asymptotically (in the sample size) and locally (against local generalized skew-elliptical deviations from elliptical symmetry). In each scenario (location specified and unspecified), we first build optimal parametric tests by assuming a given elliptical distribution. Then we render these tests semi-parametric so that they are valid under the entire family of elliptically symmetric distributions we are considering, yet each test will inherit optimal from its parametric antecedent under the parametric distribution the latter was built. We obtain quite astonishing and powerful results. When the location is specified, the optimal parametric tests all are of the same form, meaning that the test statistics do not involve the expression of the density. Consequently, they all lead to the same semi-parametric test, which thus happens to be uniformly optimal under the entire null hypothesis. This is an extremely rare setting, not only for testing elliptical symmetry, but in general when devising efficient tests. When the location is unspecified, the uniform optimality property logically gets lost, but we still obtain very simple and fast-to-compute test statistics that do not require estimating a density, as is often the case.

Keywords: Semi-parametric inference, elliptical symmetry, skewness, hypothesis testing

AMS subject classifications: 62H15, 62H10

On asymptotic normality of certain linear rank statistics

Viktor Skorniakov¹

Thursday July 30th 10:45–11:10

¹ Vilnius University, Faculty of Mathematics and Informatics, Naugarduko 24, LT-03225, Vilnius, Lithuania

Abstract

We consider asymptotic normality of linear rank statistics under binary randomization rules. Motivated by the set of open problems posed in [2] (see also [3]), our exposition is tightly attached to the context of randomized clinical trials (RCT). In particular, we show that the results obtained extend the ones given in [4] and [6], and apply to a wide class of randomization schemes considered in [1]. However, our derivations rely on some general limit theorem given in [5], and attachment to the RCT is just for the sake of a good demonstration. That is, the obtained results equally well apply to situations where randomization of similar kind takes place: optimal design theory, information theory, etc.

Keywords: Randomization, Asymptotic normality, Linear rank statistics, Clinical trial

AMS subject classifications: 62G10; 62G20; 62P10

Acknowledgements: This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors. Yet I would like to thank the managing stuff of my home department in the Faculty of Mathematics and Informatics of Vilnius University as well as the Organizing Committee of the 21st EYSM conference for providing me with an opportunity to participate in the event and present the result.

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New class of suprem-type exponentiality tests based on V-empirical Laplace transforms and Puri-Rubin characterization

Marija Cuparić¹, Bojana Milošević¹ and Marko Obradović¹

Thursday August 1st 12:40–13:05

¹Faculty of Mathematics, University of Belgrade

Abstract

We propose a new class of scale free goodness-of-fit tests for the exponential distribution based on Puri-Rubin characterization. For the construction of test statistics we employ weighted L^{∞} distance between V-empirical Laplace transforms of random variables that appear in characterization. We derive asymptotic properties, and to assess their quality, we calculate approximate Bahadur efficiency for common close alternatives. For small sample sizes, a simulated power study is performed. The tests are shown to be very efficient and powerful in comparison to many other competitors tests.

Keywords: asymptotic efficiency, Laplace transform, V-statistic with estimated parameters

AMS subject classifications: 62G10, 62G20 **Acknowledgements:** The work of M. Cuparić and B. Milošević is supported by the MNTRS, Serbia under Grant No. 174012

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Distributional Characterizations for Non-normalized Density Functions and Their Applications

Steffen Betsch¹ and Bruno Ebner¹

¹Institute of Stochastics, Karlsruhe Institute of Technology

Thursday August 1st 13:05–13:30

Abstract

A popular way to construct methods for statistical inference is to craftily employ functional characterizations of probability distributions. In this spirit, the mere fact that a distribution is uniquely determined by its distribution function is used to construct goodness-of-fit tests, like the Kolmogorov-Smirnov test, estimation methods, such as minimum-Crámer-von Mises-distance estimators, or scoring rules to evaluate probabilistic forecasts, like the continuous ranked probability score CRPS. Similar methods are based on characteristic functions, Laplace transforms, quantile functions, and their like. The corresponding procedures, however, fail in situations where only the functional shape of the statistical model is known, that is, if the normalization (or integration) constant of the density function, say, cannot be calculated or handled properly. Models of this type occur in such applied areas as image modeling, signal processing, and machine learning. Although some methods that tackle this problem, like the score matching approach for the estimation of parameters, are available, a broader framework for the construction of further tools seems beneficial.

In this regard, the distributional characterizations we establish in our work [2] provide a reasonable starting point. Extending the notion of the zero-bias distribution often encountered in the context of Stein's method, these characterizations facilitate the construction of suitable statistics, for they do not depend on the normalization constant of the underlying model. The transformations cover any univariate model which admits a continuously differentiable density function that satisfies some weak regularity conditions, and, both in their practical and theoretical handle, the resulting methods resemble classical ones. We already use this approach to construct goodness-of-fit tests (see [1], [3]), and we work on a method for the estimation of parameters. A promising feature of our approach is that even though it is meant to be applied to more complicated statistical models, and despite its wide range of applicability, it appears to perform quite as good as any other procedure even for simpler probability distributions.

Keywords: Distributional characterizations, Goodness-of-fit tests, Non-normalized models, Parameter estimation, Stein's method AMS subject classifications: 62E10, 60E10, 62F03, 62F10

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Factor Models for Functional Time Series in High Dimensions: Representation Theory and Consistent Estimation

Marc Hallin¹, Gilles Nisol² and Shahin³ Tavakoli

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Abstract

In this paper, we set up theoretical foundations for factor models for a panel of time series of functions. We first show that if the first r eigenvalues of the covariance operator of the cross-section of n FTS are unbounded as n diverges and if the (r + 1)th eigenvalue is bounded, then we can represent each FTS as a sum of a common component driven by r factors and an idiosyncratic component. We then turn to the estimation of the factors themselves. We show that under conditions weaker than commonly used, we can estimate the space spanned by the factors consistently, thus strengthening existing results for scalar factor models. We also show the consistency of our estimators of the factors perform on simulated data.

Keywords: Functional Time Series, factor models, high-dimensional statistics. **AMS subject classifications:** 62F02.

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Thursday August 1st 15:00–15:25

Order Restricted Inference in Chronobiology

Yolanda Larriba¹, Cristina Rueda¹, Miguel A. Fernández¹ and Shyamal D. Peddada²

Thursday August 1st 15:25–15:50

¹Departamento de Estadística e Investigación Operativa, Universidad de Valladolid, Spain ²Department of Biostatistics, Public School of Health, University of Pittsburgh,

USA

Abstract

Blood pressure, body temperature or circadian gene-expressions are just a few of the biological phenomena exhibiting oscillatory processes in nature. Such processes display periodic up-down-up patterns, or rhythms, along periods of time, usually of 24 hours length. The study of these temporal rhythms and how they change under different conditions is called chronobiology [1]. This work is motivated by applications in chronobiology, where researchers are typically interested in discovering the components (e.g. genes) of the oscillatory systems (e.g. circadian clock) that display temporal rhythmic patterns. The contributions of the work are twofold. First, a methodology is developed based on a *circular signal* plus error model that is defined using order restrictions [2]. This mathematical formulation of rhythmicity is simple, easily interpretable and very flexible, with the latter property derived from the non-parametric formulation of the signal. Second, we address various commonly encountered problems in the analysis of oscillatory systems data. Specifically, we propose solutions for the problems of detecting rhythmic signals in an oscillatory system [3], and for the question of estimating the timing of samples when this timing is unknown, such as when tissues are obtained from human biopsies [4]. The proposed methodology is computationally efficient, outperforms the already published ones and is broadly applicable to address a wide range of questions related to oscillatory systems.

Keywords: Constrained Inference, Circular Data, Rhythmicity Detection, Timing Estimation, Oscillatory Systems.

AMS subject classifications: 62P10.

Acknowledgements: The authors gratefully acknowledge the financial support received by the Spanish Ministerio de Ciencia e Innovación and European Regional Development Fund; Ministerio de Economía y Competitividad grant [MTM2015-71217-R to CR and MF] and Spanish Ministerio de Educación, Cultura y Deporte [FPU14/04534 to YL].

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Linear filtering of Gaussian processes in the space of continuous functions

Thursday August 1st 15:50–16:15 Vít Kubelka¹ and Bohdan Maslowski²

¹ Charles University, Prague, Czech Republic ² Charles University, Prague, Czech Republic

Abstract This talk deals with an infinite - dimensional generalization of Kalman-

Bucy Filter which is a continuous time counterpart to the discrete time linear Kalman Filter. Therefore, it deals with dynamical system described by stochastic differential equations.

First, the continuous time linear filtering problem in finite - dimensional space will be introduced. Afterwards, an extension for Gaussian signal with values in the space of continuous functions and finite - dimensional observation process will be shown and some interesting examples will be discussed, e.g. the signal processes described by linear stochastic partial differential equations driven by Fractional Brownian motion.

Keywords: Kalman - Bucy filter, Stochastic evolution equations, Gaussian processes

AMS subject classifications: 60H05, 60H15, 60G35

Forecasting time series in the light of recent advances in linear mixed modeling and convex optimization

Thursday August 1st 16:35–17:00 Andrej Gajdoš¹ and Martina Hančová¹

¹P. J. Šafárik University, Košice, Slovakia

Abstract

Prediction of time series within the framework of kriging lays on the idea of the "plug-in" best linear unbiased predictor, the so-called empirical BLUP (EBLUP), where the unknown variance parameters of a chosen time series model are replaced by their estimates generally computed by numerical methods. In our case of kriging ([2]), we consider a class of finite discrete spectrum linear regression models of time series (FDSLRM) introduced by Štulajter ([4]), whose observations are given by a linear mixed model (LMM).

For purposes of real time-series data analysis, forecasting and computational research (Monte Carlo and bootstrap methods), we started to build our own R package (https://github.com/gajdosandrej/fdslrm) on current LMM R packages *nlme, sommer* available at https://cran.r-project.org/), and MATLAB package *mixed* (https://www.mathworks.com/). We also implemented diagnostic tools on the base of recent works ([3]) to improve model diagnostic checking.

Inspired by reference works on convex optimization ([1]), we derived important theoretical relations among the existing estimates of FDSLRM variance parameters. At the same time, in contrast to the nonlinear optimization used in noticed LMM packages, we were able to compute these estimates numerically by the latest convex optimization packages involving interior-point methods which are extremely reliable and time efficient. In addition, we also developed a new, very fast and accurate optimization algorithm for computing mentioned estimates of variances in FDSLRM.

In our conference talk, we will present the results of our research in the context of a real time-series data example from the area of cyber security using dynamic and reproducible documents created by open-source Jupyter technology (https://jupyter.org/).

Keywords: Time series, Linear mixed model, Variance components, EBLUP, Convex programming.

AMS subject classifications: 62M20, 62J05, 62J20, 91B84, 90C25, 65Y20.

Acknowledgements: We would like to thank Jozef Hanč for his technical support including the use of Jupyter technology and his principal help with numerical analysis using convex optimization.

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Bayesian model selection for a family of discrete valued time series models

Panagiota Tsamtsakiri¹ and Dimitris Karlis¹

Thursday August 1st 17:00–17:25

¹Department of Statistics, Athens University of Economics and Business

Abstract

Models for univariate count time series can be split into two main categories. The first one is known as parameter driven models where the time autocorrelation comes from an underlying latent process for the mean of the discrete process and the second category is the so called observation driven models where the current observations are related to the past observations in some way. This allows for easier construction and estimation of the model but due to the discreteness and the positivity of the counts special treatment is needed.

In this paper we consider the INARCH model, proposed by [1] and detailed in [3] and [2]. The models have a feedback mechanism for the mean process which is related deterministically with its past values together with past observations. Integer Autoregressive Heteroskedastic (INARCH) models belong to the class of observation driven models. While INARCH type models have gained interest, the problem of selecting the order of the terms in the specification of the models is not developed. We aim at contributing to this direction by proposing a Bayesian model selection approach for INARCH models.

In our study we consider that the conditional distribution of Y_t given the past values is a Poisson distribution and mean linked linearly or log-linearly with past values and past observations. We propose a Bayesian approach based on a transdimensional MCMC approach. At the same time we describe Bayesian estimation for INARCH models which has not been attempted so far. A real data application will be given. Simulation evidence to support the usage of the approach is also provided.

Keywords: discrete valued time series; transdimensional MCMC; model selection; **AMS subject classifications:** 62M10

Acknowledgements: This research is co-financed by Greece and the European Union (European Social Fund- ESF) through the Operational Programme \ll Human Resources Development, Education and Lifelong Learning \gg in the context of the project "Strengthening Human Resources Research Potential via Doctorate Research " (MIS-5000432), implemented by the State Scholarships Foundation (IKY).

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On random environment integer-valued autoregressive models – a survey

Petra Laketa¹

Thursday August 1st 17:25–17:50

¹University of Niš, Faculty of Sciences and Mathematics, Serbia

Abstract

A survey of random-environment INAR models is presented. There is a motivation for the introduction of the random environment into INAR models. Different models that are defined are considered, and also their mutual properties. Also, the description of problems that arise in estimation and application are given, as well as the approaches that overcome these problems.

Keywords: random environment; INAR

AMS subject classifications: 62M10

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Record times of stationary regularly varying time series

Bojan Basrak¹, Hrvoje Planinić¹ and Philippe Soulier²

Friday August 2nd 9:30–9:55

¹ University of Zagreb, Croatia
² Université Paris Nanterre, France

Abstract

In this talk we present a new type of the so-called complete point process convergence result for a stationary, regularly varying and weakly dependent time series $(X_i)_{i \in \mathbb{Z}}$. Due to dependence, extremal observations of (X_i) appear in clusters and the main novelty is that this convergence preserves the information about the temporal ordering of observations belonging to the same cluster. The key tool is the so-called tail process of (X_i) . As an application, we deduce the asymptotic behavior of rescaled record times of (X_i) , extending the well-known result in the i.i.d. case. These results are based on the joint work with Bojan Basrak and Philippe Soulier [1].

Keywords: Point process, Tail process, Record times **AMS subject classifications:** 60G55, 60G70

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On blind source separation under martingales: A probability theoretic perspective

Niko Lietzén¹

Friday August 2nd ns 9:55–10:20

¹Aalto University School of Science, Department of Mathematics and Systems Analysis, Helsinki, Finland

Abstract

In this work, we consider a blind source separation estimator that is suitable for a subclass of non-stationary processes. In particular, we consider linear blind source separation for martingales. The blind source separation problem is an occurring and a widely studied topic among especially the signal processing and statistics communities. Usually, the goal in blind source separation is to reverse the effects of an unknown mixing system and to recover some signals of interest. There exists a vast number of applications where blind source separation is utilized, e.g., audio applications, biomedical applications and telecommunications, see [1] for a collection.

Under processes that are not i.i.d., the study of asymptotic properties of different blind source separation estimators has received surprisingly little attention, when taking into account the popularity and the number of applications these estimators have. The asymptotic properties of non-i.i.d. blind source separation estimators have been previously considered under very specific classes of stationary processes in, e.g., [2, 3]. To our knowledge, limiting properties of blind source separation estimators have not yet been considered under non-stationary processes.

Our objective is to present some asymptotic properties for a blind source separation estimator under a subclass of non-stationary stochastic processes. We assume that the latent processes of interest have enough structure for us to employ the rich limiting theory of martingales. Martingales are widely applied in financial modeling. We hope to elevate the interest of the blind source separation community towards the financial applications by demonstrating that valid mathematical foundations can be constructed under models that have previously received little attention.

Keywords: blind source separation, convergence, joint diagonalization, martingales

AMS subject classifications: 60G42, 62H12, 94A12

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On decomposable multi-type Bellman-Harris branching process for modeling cancer cell populations with mutations

Friday August 2nd 10:20–10:45 Kaloyan Vitanov¹ and M. Slavtchova-Bojkova²

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Abstract

Metastasis, the spread of cancer cells from a primary tumour to secondary location(s) in the human organism, is the ultimate cause of death for the majority of cancer patients. That is why, it is crucial to understand metastases and their evolution in order to successfully combat the disease.

We consider a metastasized cancer cell population after some medical treatment (e.g. chemotherapy). Arriving in a different environment the cancer cells may change their characteristics concerning lifespan and reproduction, thus they may differentiate into different types. Even if the treatment is effective (resulting in subcritical reproduction of all cancer cell types), however, it is possible during cell division for mutations to occur. These mutations can produce a new cancer cell type that is adapted to the treatment (having supercritical reproduction). Cancer cells from this new type may lead to a non-extinction process.

As a continuation of [3] we model the above scenario with a decomposable multitype Bellman-Harris branching process. Expanding [1] and [2] we investigate relevant quantities such as the probability of extinction of the process until time tand as t approaches infinity, the number of occurred supercritical mutants until time t and as t approaches infinity, the time until the first occurrence of a mutant starting a non-extinction process and the immediate risk for the process to escape extinction. We also propose numerical schemes for performing calculations.

Keywords: Mutations, Decomposable multi-type branching process, Probability of extinction, Waiting time to escape mutant, Immediate risk of escaping extinction **AMS subject classifications:** 2010 Mathematics Subject Classification: Primary 60J80, Secondary 62P10

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Limit Distribution for Some Iterated Partial Summations

${f L}$ ívia ${f L}$ eššová 1	Friday
¹ Faculty of Mathematics, Physics and Informatics of the Comenius University in	August 2nd 10:45–11:10
Bratislava, Mlynská dolina, 842 48 Bratislava Slovakia	

Abstract

The univariate partial summations were defined in general in [3] as

$$P_x^{(1)} = c_1 \sum_{j=x}^{\infty} g(j) P_j^*, \qquad x = 0, 1, 2, ...,$$
(3)

where $\{P_j^*\}_{j=0}^{\infty}$ (parent) and $\{P_x^{(1)}\}_{x=0}^{\infty}$ (descendant) are univariate discrete distributions, g(j) is a real function and c_1 is a normalizing constant. Now we take the descendant of the first generation $\{P_x^{(1)}\}_{x=0}^{\infty}$ from the partial summation (3) as the parent of the second generation while function g(j) remains unaltered, with a proper normalizing constant c_2 . We obtain as the result another probability distribution - the descendant of the second generation $\{P_x^{(2)}\}_{x=0}^{\infty}$. Similarly the descendant of the *n*-th generation is obtained by applying summation (3) to the parent which is the descendant of the (n-1)-st generation, with the same function g(j) and with a proper normalizing constant c_n .

The question is whether there exists a limit distribution $\{P_x^{(\infty)}\}_{x=0}^{\infty}$ of such repeated summations for some given parent $\{P_i^*\}_{i=0}^{\infty}$ and some given function g(j). The

existence of this limit distribution in the univariate case for g(j) = c was proved in [4] (the limit distribution is geometric for a wide class of parent distributions). For some types of parental distributions defined on a finite support it is possible to find the limit distribution using the power method (see [1]). An extension to the bivariate case is possible. (see [2])

All extension to the bivariate case is possible. (see [2])

Keywords: Dicrete probability distributions, partial summations, limit distribution.

AMS subject classifications: 60E05. **Acknowledgements:** Supported by grant VEGA 2/0054/18.

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