International Workshop on Mathematical Statistics

IWMS 2026

Book of Abstracts

Smolenice Castle, Smolenice, Slovakia

June 1–3, 2026

Contents

Welcome in Smolenice for IWMS 2026

The International Workshop on Mathematical Statistics – IWMS 2026 held at *Smolenice Castle* in Slovakia, brings together contributions from a wide spectrum of disciplines connected with the "*Art of Guessing*" — whether under the classical banner of Statistics, or within contemporary domains such as Teaching and Learning, Machine Intelligence, Applied Mathematics, Scientific Computing, and Artificial Intelligence.

The workshop embraces both foundational theoretical developments and practical applications, ranging from elegant abstract ideas to modern computational methodologies. In this spirit, IWMS 2026 aims to create an informal and stimulating environment where researchers from diverse backgrounds can exchange ideas, explore new perspectives, and strengthen existing collaborations across disciplines.

The motivation for this somewhat unconventional event follows a long-standing tradition associated with the retirements of faculty members from the Department of Mathematical and Statistical Sciences at the University of Alberta (Edmonton, Canada). This year, the workshop is dedicated to *Prof. Ivan Mizera*.

Ivan, our colleague, collaborator, mentor, co-author, and friend, spent over two decades building scientific and personal bridges across countries, institutions, and communities. In his own unique way, he significantly helped to reduce the geographical distance between the Canadian Rockies and the Slovak Carpathians, between Edmonton and Bratislava (or perhaps Prague?), between Banff and Smolenice. Through his scholarship, generosity, and unique sense of humor, he influenced generations of students and colleagues, while fostering collaborations that continue to connect people across continents.

We are delighted to welcome you to *Smolenice Castle* and we hope that the workshop will provide not only inspiring scientific discussions, but also an opportunity to enjoy the unique atmosphere of this historic place, reconnect with old friends, and establish new collaborations.

Welcome to **IWMS 2026**, and enjoy your stay!

Viktor Witkovský, Linglong Kong, Matúš Maciak
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Prof. Ivan Mizera

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Scientific Program Committee

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Abstracts

The International Workshop on Mathematical Statistics hosts 23 invited scientific talks and two poster contributions authored and co-authored by 41 scientists from 12 countries (Austria, Canada, China, Czech Republic, Germany, Italy, Japan, Poland, Sweden, Switzerland, United States of America, and Slovakia). The abstrats are ordered alphabetically, according to the last name of the presenting author. The authors's index is provided at the end.

Of penalties and plates

Vladimír Balek [1*]

Just like the thin-plate splines can be interpreted in terms of deformation of an elastic plate, with the penalty to be minimized equal to the deformation energy of the plate, one can relate the total-variation bivariate smoothing to deformation of plastic plates.

We will take a quick look at the physics behind the formula for deformation energy of the two kinds of plates and show how it works in simple settings.

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Nonparametric inference in Physics-Informed Spatial Regression

Michele Cavazzutti[1]** Eleonora Arnone[2]† Laura Sangalli[3]‡

Inference for semiparametric and nonparametric regression models is a classical yet challenging problem, extensively studied due to both its intrinsic complexity and the variety of available approaches. In this talk, we focus on a specific class of models, namely physics-informed spatial regression. These semiparametric models incorporate physics-based penalties defined through partial differential equations, encoding prior knowledge about the phenomenon under study coming, for instance, from physical, chemical, or biological laws governing the system dynamics.

Uncertainty quantification in this setting is particularly challenging, due to the complexity of both the penalties and the data structures involved. We propose nonparametric inference procedures based on sign-flipping of model scores, leveraging the resampling scheme of Hemerik et al. (2020). In particular, we introduce Eigen-Sign-Flip tests for both the linear and nonlinear components of the model. We show that the test for the linear parameter is asymptotically exact, while the test for the nonlinear component is exact in finite samples.

Acknowledgments

The work of M. Cavazzutti was supported by the ERC CZ grant LL2407 of the Ministry of Education, Youth and Sport of the Czech Republic.

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Empirical Bayes for Compound Adaptive Experiments

Karun Adusumilli* Jiaying Gu† Junfan Tao‡

We investigate Empirical Bayes methods in the context of compound adaptive experiments, where the arm distribution inin each experiment follows a normal distribution with an unknown mean that we seek to estimate. There are two main EB strategies: g-modeling, which estimates the prior by maximizing the marginal likelihood, and f-modeling, which derives posterior means directly from the empirical distribution of the observations. We show that g-modeling continues to be a valid EB procedure even when it incorrectly assumes that data are collected exogenously; its validity does not depend on the particular sampling algorithm or on whether sample sizes are endogenous. In practice, one can apply standard g-modeling techniques by acting as though the data were exogenously sampled. Strikingly, we prove that risk guarantees established for g-modeling under i.i.d. sampling can be extended to data generated adaptively, without requiring any prior knowledge of the sampling rule, even when it differs across experiments. By contrast, f-modeling yields biased estimators. We corroborate the robustness of g-modeling through simulations with widely used adaptive algorithms and demonstrate its applicability using a real-world dataset consisting of multiple sequential experiments.

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On a possible improvement of the D'Agostino test

Zdeněk Hlávka[1*] Muhammad Nauman Khan[2†]

Using optimal transport theory and the so-called empirical center-outward distribution function [1], we propose a bivariate Monte Carlo critical region for transformed skewness and kurtosis underlying the D'Agostino test of normality [3]. Similarly as [2], we show that the p-value of the improved D'Agostino test corresponds to a naturally defined nonnormality score admitting a decomposition in terms of skewness and kurtosis deviations from normality. Moreover, the value of the empirical center-outward distribution function corresponding to the observed skewness and kurtosis provides a simple and easily interpretable graphical representation of the test result.

In a simulation study, we show that the improved D'Agostino test has almost the same power as the celebrated Shapiro-Wilk test in all simulation setups and that it clearly outperforms the Shapiro-Wilk test against a platykurtic alternative. We conclude by observing that the proposed method, with a multivariate "Monte Carlo mosaic" critical region, can be used as a general goodness-of-fit test also for other uni- and multivariate distributions with only minimal and straightforward modifications.

Acknowledgments

This work was supported by the Czech Science Foundation project GAČR No. 25-15844S.

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Achieving Fairness-Utility Trade-off with Fair Synthetic Data

Bei Jiang[1*]

Artificial intelligence and machine learning increasingly inform decisions in hiring, lending, healthcare, and justice. Yet real-world datasets often encode historical bias, and models trained on them can reproduce or amplify inequities. Pre-processing via fair synthetic data is a promising: if we can generate data that mitigates bias at the source while preserving signal, downstream models can be both fair and useful.

This talk introduces fDA (Fair synthetic data via Data Augmentation), a statistically principled framework that makes the fairness–faithfulness trade-off explicit and controllable. FDA jointly models a fair submodel and a faithful submodel, coupled by a single parameter $\alpha \in [0, 1]$ that quantifies the fraction of bias removed. We prove clear operating points: $\alpha = 0$ yields maximal fairness (with larger deviation from the original distribution), $\alpha = 1$ recovers the original data in probability (hence in distribution), and intermediate α values guarantee calibrated compromises with interpretable bounds. Practically, fDA samples directly from simple predictive distributions, avoiding heavy black-box training. We further provide theory connecting FDA's α to fairness of downstream models.

Together, these results deliver a transparent, efficient, and deployable path to generating fair synthetic data without sacrificing essential statistical structure.

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Test for covariance matrix under multivariate t distribution with uncorrelated observations

Katarzyna Filipiak* Daniel Klein† Stepan Mazur‡
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In many applied fields such as, for example, macro and financial economics the distribution of variables is skewed and heavy tailed. Multivariate t-distribution assumption provides a better solutions than multivariate normality when variables are heavy tailed. In the multivariate normal case uncorrelated observations are independent which is not the case for any other distribution. Two types of matrix-variate t distributions are discussed. The estimators of unknown parameters are derived and their basic statistical properties are investigated. These estimators are then applied to test hypotheses concerning the covariance structure of a multivariate t distribution associated with a collection of uncorrelated, though not necessarily independent, observation vectors, using two types of matrix- variate t distributions. Distributional properties of a likelihood ratio test under the null hypothesis are studied for the hypothesis of sphericity or identity of the covariance matrix.

Acknowledgments

This work was supported by the Slovak Research and Development Agency under the Contract No. APVV-21-0369, and grant VEGA No. 1/0585/24.

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An adaptive weighted mean for multivariate location estimation and depth

Keith Knight[1*]

Given multivariate observations $\boldsymbol{x}_1, \cdots, \boldsymbol{x}_n$ from some distribution, we consider location estimates that are weighted means: $\widehat{\boldsymbol{\mu}} = w_1\boldsymbol{x}_1 + \cdots + w_n\boldsymbol{x}_n$ where the weights $\{w_i\}$ are non-negative and sum to 1. For each $(w_i, \boldsymbol{x}_i)$, we define a measure of proximity $\text{prox}(w_i, \boldsymbol{x}_i)$ for $(w_i, \boldsymbol{x}_i)$ to the other observations $\{(w_j, \boldsymbol{x}_j) : j \neq i\}$; $\{\text{prox}(w_i, \boldsymbol{x}_i)\}$ are proportional to the diagonal elements of a projection matrix. The weights $\{w_i\}$ are defined so that

$$\text{prox}(w_1, \boldsymbol{x}_1) = \cdots = \text{prox}(w_n, \boldsymbol{x}_n),$$

It can be shown that the points $\{w_i^{1/2}(\boldsymbol{x}_i - \widehat{\boldsymbol{\mu}})\}$ lie within an ellipsoid where the points with smaller weights lie closer to its boundary. The resulting estimate $\widehat{\boldsymbol{\mu}}$ is affine equivariant and the weights $\{w_i\}$ can be interpreted as measures of depth of $\{\boldsymbol{x}_i\}$. The weights $\{w_i\}$ can be computed using an iterative algorithm that computes a QR decomposition at each step. The method also has a dimension reduction feature: If a sufficient number of observations lie in or close to a lower dimensional subspace, these observations will receive the highest weights.

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Choquet Risk and Portfolio Choice

Roger Koenker [1*]

Abstract

An alternative to the classical mean-variance portfolio proposal of Markowitz will be described. In place of variance as a measure of risk, a pessimistic notion of expected return is employed together with an arbitrary concave utility function. It will be shown that the new proposal can improve upon the performance of Markowitz portfolios in both the lower and upper tails of returns.

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Ivan Mizera: A scholar of depth, a mentor of independence, and a colleague of quiet generosity

Linglong Kong [1*]

This short talk celebrates Professor Ivan Mizera's retirement by reflecting on his contributions to statistical science, his distinctive scholarly style, and his lasting influence as a mentor and colleague.

Speaking as both a former PhD student and former colleague at the University of Alberta, I will highlight Ivan's intellectual depth, independence, and generosity, and the lasting legacy he has built through his research, mentorship, and service to the academic community.

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On Guessing Without a Model

Matúš Maciak[1*]

A personal reflection on long-term collaboration with Ivan, spanning different periods, roles, and settings: from an initially unknown compatriot, through postdoctoral mentorship at the University of Alberta, scientific collaboration and co-authored manuscripts, to mountain adventures and recent interactions as colleagues at Charles University—occasionally resembling a Sherlock–Dr. Watson–like relationship.

The talk aims to highlight how ideas emerge, evolve, and persist across contexts—scientific, geographical, and personal. It seeks to illustrate how collaboration in statistics, understood also as the "art of guessing," is shaped not only by practical questions, technical limitations, or theoretical challenges, but also by shared experiences, conversations, and friendships.

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Discrete probability distributions as models for phoneme frequencies

Ján Mačutek[1]** Michaela Koščová[2]†

Frequency and length of linguistic units are often at the beginning of mathematical modelling of language properties. In our contribution, we will present some results on discrete distribution models for frequencies of phonemes.

1. The negative hypergeometirc distribution (see, e.g., [3, pp. 465–468]) is the model which achieves a good fit in general (see, e.g., [1]).

2. The Zipf-Mandelbrot distribution (see, e.g., [3, p. 666]) is a very common model for (not only) frequencies of higher language units (syllables, words,...). However, when the distribution is applied to model phoneme or grapheme frequencies, its parameters attain unrealistically high values (which, in addition, vary depending on a software tool used). We will show that this parameter behaviour can be explained by the convergence of the Zipf-Mandelbrot distribution to the geometric distribution (see [2]).

The results hint at different 'frequency regimes' of the lowest language units (graphemes, phonemes) and those positioned higher in the language unit hierarchy (words, clauses, sentences,...).

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Choquet Risk and Portfolio Choice

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The Art of Guessing Genes: Can AI Help Us Find the 1 in 10,000?

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International Workshop on Matrices and Statistics (IWMS 2026)
In honour of Prof. RNDr. Ivan Mizera, CSc. · Smolenice Castle, Slovakia, May 2026

In 2025, Prof. Ivan Mizera invited me to speak at the Advanced Statistical Seminar at the Department of Probability and Mathematical Statistics, Charles University, on explainable AI in drug discovery. I said I was too busy. A decision I immediately regretted, since it is statistically improbable that a better excuse to visit a Slovak castle will ever present itself. This abstract is the delayed fulfilment of that invitation.

Abstract

Explainable AI (XAI) asks whether a model's predictions can be traced back to interpretable causes. In drug discovery, this means identifying *which genes drive disease in which cell type*, at the resolution of individual cells. We present *Teddy* (Merck & Co. / BCG X AI Science Institute, arXiv:2503.03485, 2025), a family of Transformer-based **foundation models for single-cell RNA sequencing (scRNA-seq)**, and examine the statistical methodology and explainability evidence underlying them.

Pre-training as conditional imputation. Each cell is a sparse vector of ∼3,000 active genes (out of 20,000). We mask 15 % uniformly at random (MCAR) and train the model to recover them from context, fitting a non-parametric model for $P(\text{gene}_i \mid \text{all other genes})$ on 116 million cells spanning 122 diseases, 413 tissues, and 860 cell types (CELLxGENE corpus). Ontology supervision (disease, tissue, cell-type, sex labels) acts as domain regularisation, yielding +3–5 % F1 on downstream tasks. Scaling laws are regular: $\mathcal{L} \propto N^{-0.10}$ (parameters), $\mathcal{L} \propto D^{-0.07}$ (data).

Benchmark results. On a 14-way held-out donor classification task (82 donors), Teddy-G 400M achieves **0.72 accuracy** vs. 0.64 (scGPT/Nicheformer) and 0.39 (Geneformer base).

Explainability via zero-shot causal validation. We simulate a **GATA4 cardiac knockout** in silico ($n = 236$ fetal cardiomyocytes), rank genes as direct targets, indirect targets, or housekeeping, and apply **paired one-sided Wilcoxon signed-rank tests**. Teddy-G passes all four pairwise comparisons ($p_{\text{HK}\to\text{Dir}} = 9.45 \times 10^{-25}$, $p_{\text{Indir}\to\text{Dir}} = 1.27 \times 10^{-20}$); scGPT fails all four ($p_{\text{Indir}\to\text{Dir}} = 0.99$). The model has learned a causal hierarchy of gene regulation from pre-training alone, without any fine-tuning or labels. The practical implication: the model improves the prior over which 10 candidates out of 10,000 enter a clinical trial.

Open statistical problems: MNAR masking in scRNA-seq; loss specification (NB/Poisson vs. rank-value MSE); identifiability for unordered gene sets; GRN recovery from attention weights; conformal uncertainty on embeddings; multi-modal integration.

Keywords: explainable AI, foundation models, single-cell RNA sequencing, masked imputation, Transformer, Wilcoxon test, scaling laws, drug discovery.

Reference: T. Heimberg *et al.*, *TEDDY: A Family of Foundation Models for Understanding Single Cell Biology*, arXiv:2503.03485, 2025. Collaboration: Merck & Co. Inc. and BCG X AI Science Institute.

Robust regression and data depth – a personal review

Christine H. Müller*

A review of the work of Ivan in connection with my work is given. Starting from our works Mizera (1996) and Müller (1996) presented at PROBASTAT '94 in Smolenice, I show how it led to the publications (Mizera and Müller 1999, 2001, 2002) concerning breakdown points of robust regression via M-estimators. Later we considered robust regression based on regression depth introduced by Rousseeuw and Hubert (1999). Mizera (2002) extended this approach to global and tangent depth based on general quality measures and derived breakdown points. This general approach can be used in particular for quality measures given by likelihood functions providing likelihood depth and yielded the common paper Mizera and Müller (2004) on location-scale depth. But likelihood depth can also be used for testing as considered in Müller (2005) and led to sign-depth tests in Leckey et al. (2023) and Müller et al. (2025).

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Improving AI Explainability through Design of Experiments

Alexandra Stadler[1*] Werner G. Müller[1*†]
Radoslav Harman[2‡]

In artificial intelligence (AI), the complexity of many models and processes surpasses human understanding, making it challenging to determine why a specific prediction is made. This lack of transparency is particularly problematic in critical fields like healthcare, where trust in a model's predictions is paramount. As a result, the explainability of machine learning (ML) and other complex models has become a key area of focus. Efforts to improve model explainability often involve experimenting with AI systems and approximating their behavior through interpretable surrogate mechanisms. However, these procedures can be resource-intensive. Optimal design of experiments, which seeks to maximize the information obtained from a limited number of observations, offers promising methods for improving the efficiency of these explainability techniques.

To demonstrate this potential, we explore Local Interpretable Model-agnostic Explanations (LIME), a widely used method introduced by [1]. LIME provides explanations by generating new data points near the instance of interest and passing them through the model. While effective, this process can be computationally expensive, especially when predictions are costly or require many samples. LIME is highly versatile and can be applied to a wide range of models and datasets. In this work, we focus on models involving tabular data, regression tasks, and linear models as interpretable local approximations.

By utilizing optimal design of experiments' techniques, we reduce the number of function evaluations of the complex model, thereby reducing the computational effort of LIME by a significant amount. We consider this modified version of LIME to be energy-efficient, and thus preferable.

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MIZERA: Multi-changepoint Inference with Zero-tuning Eigenbootstrap Resampling for Alcoholics

Michal Pešta[1*] Barbora Peštová[2†] Martin Romaňák[3‡]

Tensor data consisting of multivariate outcomes over the items and across the subjects with longitudinal and cross-sectional dependence are considered. A completely distribution-free and tweaking-parameter-free detection procedure for changepoints at different locations is designed, which does not require training data. A CUSUM type test statistic is employed, and its asymptotic properties are derived for a large number of available individual profiles. The considered test is shown to be consistent. We propose an eigenbootstrap superstructure that overcomes the computational curse of dimensionality without any loss of information, while it preserves all the dependencies within and between the panels. The validity of this new and fast resampling algorithm is proved in this general setting. The empirical properties of the detection technique are investigated through a simulation study. The fully data-driven test is applied to real-world data from alcoholics.

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Designing networks using design of experiments

Samuel Rosa[1]** Radoslav Harman[2†]

There has been significant interest in recent years in designing networks to optimize robustness and other performance metrics. Many of these metrics are based on the Laplacian spectrum, such as total effective resistance, the number of spanning trees, and algebraic connectivity. It was established more than forty years ago that designing graphs or networks to optimize Laplacian spectra is equivalent to designing block experiments to optimize the spectra of information matrices. However, many of the results and approaches from optimal experimental design that can be translated to network design settings have not yet been fully developed in that field. Moreover, many results known in the network design community have been independently derived in multiple subareas of the network design field.

In this talk, based on [1], we first survey overlapping Laplacian optimization results from different subareas of network design. We then draw on ideas from experimental design to unify these results, and to advance the study of network design. In particular, we formalize desirable theoretical properties of performance measures, leading to the definition of information functions. We also use Kiefer's criteria from experimental design to connect the three most popular measures based on Laplacian spectra. We then use directional derivatives to provide a unified treatment of recurring quantities in Laplacian optimization, such as gradients and subgradients, and show that they are connected to Laplacian-based measures of node distance, which we call node dissimilarities. We apply the node dissimilarities to derive efficient rank-one update formulas for Kiefer's measures, and to develop a new edge-exchange method for network optimization. These update formulas enable greedy and exchange algorithms with reduced asymptotic time complexity.

Acknowledgments

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One Approach, Multiple Insights: Tensor Decomposition Applied to Two Cognitive Neuroscience Problems

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Tensor decomposition extends standard blind-source separation methods, such as Principal Component Analysis (PCA), to higher-order arrays known as tensors. Among these, Parallel Factor Analysis (PARAFAC) [1] remains the most prevalent approach, favored for its interpretability and theoretical properties. This study demonstrates the efficacy of two PARAFAC variants - Implicit Slice Canonical Decomposition (IMSCAND) and Parallel Profiles with Linear Dependencies (PARALIND) - when addressing challenges within cognitive neuroscience.

First, we apply tensor decomposition to detect narrowband oscillatory components in electroencephalogram (EEG) data, demonstrating how PARALIND effectively manages scenarios where latent components share characteristics across multiple modes. Furthermore, we establish a theoretical link between tensor decompositions and clustering by proving that IMSCAND is mathematically equivalent to polarity-invariant k-means approach. This equivalence provides a novel geometric interpretation of so-called EEG microstates and may enable the development of efficient algorithms for discovering latent structures in higher-order arrays in the future.

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The Pivotal Information Criterion

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We derive an information criterion that has three advantages over BIC: selection of λ is (asymptotically) pivotal, the information criterion is a continuous function of the parameters, and selection of λ allows to retrieve the correct input covariates with high probability. The Pivotal Information Criterion can be seen as the extension of square-root LASSO to the location scale [2] and exponential families [1] and to survival analysis [3]. PIC can be employed for a linear model or an artificial neural network.

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Small Data, Smart Tuning: Bayesian Optimization for Manufacturing Process Optimization

Sile Tao[1*]

Process parameter tuning in manufacturing is often constrained by high experimental cost, limited historical data, and a small number of allowable trials. This presentation introduces Bayesian optimization as a practical statistical tool for supporting such tuning tasks. Using process recipe optimization as a representative example, it explains how a surrogate model can be built from small-sample observations, how uncertainty is used to guide the next experiment, and how the balance between exploration and exploitation helps reduce inefficient trial-and-error.

The presentation also discusses the role of expert knowledge in defining feasible parameter spaces and engineering constraints, as well as practical ways to evaluate optimization performance by comparing recommended trials with historical expert experience. This talk focuses on how established statistical methods can be applied in real manufacturing workflows to improve tuning efficiency, shorten development cycles, and reduce experimental cost.

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One-Shot Weighted Ensemble Estimation for Federated Quantile Regression

Yafei Wang[1*]

Artificial intelligence and machine learning increasingly inform decisions in hiring, lending, healthcare, and justice. Yet real-world datasets often encode historical bias, and models trained on them can reproduce or amplify In this work, we propose a data-driven, one-shot weighted ensemble estimator for federated quantile regression that incorporates scalable weighting schemes to effectively leverage the partially observed features at each local agent. The proposed method enjoys both communication efficiency and estimation optimality.

We also study the estimator's sensitivity to perturbations introduced by local agents and derive conditions under which the estimator achieves stability and enjoys strong out-of-sample generalization. Extensive simulations and real data analysis under various scenarios validate the superior performance of the proposed method.

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Experimental design and M-estimation; robustness against dependence

Doug Wiens[1]** Rui Hu[2†]

Since retirement, my research has taken a rather self-indulgent turn. I have been investigating questions that were left unanswered at retirement but continued to interest me.

For years I had looked at the construction of experimental designs which are robust against misspecfied response functions. This was almost exclusively in the context of Least Squares estimation, and I had long wondered what might change under M-estimation. (Hard to talk about LS and robustness in the same breath, but note that this is a different kind of robustness.)

Another topic concerned the robustness of LS estimates and designs, constructed assuming i.i.d. errors, under dependence or heteroscedasticity. This resulted in some surprising results detailed in the *Biometrika* papers below, and I began to wonder if these could be extended to M-estimates.

It turns out that (i) replacing LS estimation by M-estimation has some, but not much, effect on the optimally robust designs, and even this should probably be ignored; and (ii) M-estimates do enjoy a property of being robust against broad classes of dependence structures, including those in which the errors are equicorrelated. So I guess this is what I'll talk about.

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Computing with Characteristic Functions: Numerical Techniques, Statistical Inference, and Practical Applications

Viktor Witkovsky*

Characteristic functions provide a powerful and flexible framework for modern computational statistics by transforming complex probabilistic and statistical problems into analytically and numerically tractable forms. This lecture presents a characteristic-function-based methodology as a unified computational paradigm for evaluating probability distributions, constructing exact and approximate solutions for stochastic models, and developing practical procedures for statistical inference. The presentation reviews key numerical inversion techniques for continuous, discrete, and multivariate distributions, including efficient algorithms to evaluate probability density functions, cumulative distribution functions, and quantiles. Particular emphasis is placed on computational tools for combining characteristic functions of sums, mixtures, products, and empirical distributions, as implemented in the CharFunTool ecosystem.

Recent advances include exact distribution theory for generalized logistic and q-Gaussian models, multivariate numerical inversion, and empirical characteristic function based inference, including goodness-of-fit testing for high-dimensional models using weighted L^2 discrepancy measures, radial Fourier transforms, and Hankel-transform techniques. Applications in metrology, uncertainty quantification, robust statistics, finance, and engineering demonstrate the broad practical relevance of the approach. By bridging classical probability theory with modern computational methodology, characteristic functions emerge not only as foundational theoretical objects but also as a versatile infrastructure for reproducible research, advanced statistical computing, and contemporary data-driven scientific applications.

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Functional Linear Regression: Linear Hypothesis Testing With Functional Response

Dengdeng Yu[1]**

Hypothesis testing is a fundamental aspect of functional data analysis, enabling inferential conclusions based on samples of functional observations. The inherent infinite-dimensional nature of functional data poses substantial challenges to the direct application of conventional hypothesis testing procedures. A common strategy is to project functional data onto a lower-dimensional subspace prior to testing; however, the choice of projection space can critically affect both the validity and power of the resulting test. In this paper, we propose a novel hypothesis testing procedure, the optimal functional projection test (OFPT). The method constructs an optimal projection space by leveraging the covariance structure of the error process, such that the projected hypothesis is equivalent to the original functional hypothesis while maximizing testing power. We establish both the optimality of the projection space and theoretical guarantees on the testing power of the proposed procedure. Extensive numerical studies under settings where the signal and noise processes exhibit complex dependence structures demonstrate strong finite-sample performance, with OFPT consistently outperforming existing methods for testing functional linear hypotheses. Furthermore, applications to the Autism Brain Imaging Data Exchange (ABIDE) and Human Connectome Project (HCP) datasets yield results that are not only consistent with existing and recent literature, but also reveal novel findings that warrant further investigation.

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Matrix mean testing in elliptical models with special variance structures

Ivan Žežula[1]** Daniel Klein[2]†

Many multivariate observation come naturally in matrix form. The biggest disadvantage in working with such data is the large number of parameters to be estimated, especially when the matrix dimensions are large. One possibility of coping with this problem is to consider special variance structures, which can naturally arise through the design of the experiment or be inherent in the subject under study.

Matrix multivariate models have until now relied on assumption of multivariate normality. This assumption allows in many cases derive explicit results, but is rather restrictive. All important tests for means in such models have been extensively studied in recent years. We will present extension of general results for mean testing in such models to the special class of elliptical models. These include e.g. multivariate t-distribution, thus providing solution also for many distribution with heavier tails.

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