

# THE ANNALS *of* STATISTICS

AN OFFICIAL JOURNAL OF THE  
INSTITUTE OF MATHEMATICAL STATISTICS

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THE ANNALS OF STATISTICS

Vol. 54, No. 1, pp. 1–541 February 2026

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*The Annals of Statistics* [ISSN 0090-5364 (print); ISSN 2168-8966 (online)], Volume 54, Number 1, February 2026. Published bimonthly by the Institute of Mathematical Statistics, 9760 Smith Road, Waite Hill, OH 44094, USA. Periodicals postage paid at Cleveland, Ohio, and at additional mailing offices.

**POSTMASTER:** Send address changes to *The Annals of Statistics*, Institute of Mathematical Statistics, Dues and Subscriptions Office, PO Box 729, Middletown, MD 21769, USA.

# DUALIZING LE CAM’S METHOD FOR FUNCTIONAL ESTIMATION I: GENERAL THEORY

BY YURY POLYANSKIY<sup>1,a</sup> AND YIHONG WU<sup>2,b</sup>

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Le Cam’s method (or the two-point method) is a commonly used tool for obtaining statistical lower bound and especially popular for functional estimation problems. This work aims to explain and give conditions for the tightness of Le Cam’s lower bound in functional estimation from the perspective of convex duality. Under a variety of settings, it is shown that the maximization problem that searches for the best two-point lower bound, upon dualizing, becomes a minimization problem minimizing an upper bound on the quadratic risk over a family of estimators. Since by the minimax theorem two problems have the same value, this value also characterizes (up to a universal factor) the optimal estimation rate. For estimating linear functionals of a distribution, our work strengthens prior results of Donoho–Liu (*Ann. Statist.* **19** (1991) 633–667) (for quadratic loss) by dropping the Hölderian assumption on the modulus of continuity. For exponential families, our results extend those of Juditsky–Nemirovski (*Ann. Statist.* **37** (2009) 2278–2300) by characterizing the minimax risk for the quadratic loss under weaker assumptions on the exponential family. We also provide an extension to the high-dimensional setting for estimating separable functionals.

An application of our methodology to the area of “estimating the unseens” is provided in the companion paper (Polyanskiy and Wu (2023)), resolving the optimal rates (within logarithmic factors) of the distinct elements problem and Fisher’s species problem.

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*MSC2020 subject classifications.* Primary 62G05; secondary 62C20, 62G86, 62G07.

*Key words and phrases.* Functional estimation, minimax optimality, convex optimization and duality, modulus of continuity, linear programming.

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# ON THE STRUCTURAL DIMENSION OF SLICED INVERSE REGRESSION

BY DONGMING HUANG<sup>1,a</sup> , SONGTAO TIAN<sup>2,b</sup> AND QIAN LIN<sup>3,c</sup>

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In this work, we address the longstanding puzzle that Sliced Inverse Regression (SIR) often performs poorly for sufficient dimension reduction when the structural dimension  $d$  (the dimension of the central space) exceeds 4. We first show that in the multiple index model  $Y = f(\mathcal{P}X) + \epsilon$  where  $X$  is a  $p$ -standard normal vector,  $\epsilon$  is an independent noise, and  $\mathcal{P}$  is a projection operator from  $\mathbb{R}^p$  to  $\mathbb{R}^d$ , if the link function  $f$  follows the law of a Gaussian process. Then with high probability, the  $d$ th eigenvalue  $\lambda_d$  of  $\text{Cov}[\mathbb{E}(X|Y)]$  satisfies  $\lambda_d \leq Ce^{-\theta d}$  for some positive constants  $C$  and  $\theta$ . We then focus on the low signal regime where  $\lambda_d$  can be arbitrarily small and not larger than  $d^{-8.1}$ , and prove that the minimax risk of estimating the central space is lower bounded by  $\frac{dp}{n\lambda_d}$ . Combining these two results, we provide a convincing explanation for the poor performance of SIR when  $d$  is large, a phenomenon that has perplexed researchers for nearly three decades. The technical tools developed here may be of independent interest for studying other sufficient dimension reduction methods.

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*MSC2020 subject classifications.* Primary 62J02; secondary 62C20, 62H12.

*Key words and phrases.* Central space, sufficient dimension reduction, sliced inverse regression, structural dimension, minimax lower bound, multiple-index model.

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# OPTIMAL AND EXACT RECOVERY ON THE GENERAL NONUNIFORM HYPERGRAPH STOCHASTIC BLOCK MODEL

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Consider the community detection problem in random hypergraphs under the nonuniform hypergraph stochastic block model (HSBM), where each hyperedge appears independently with some given probability depending only on the labels of its vertices. We establish, for the first time in the literature, a sharp threshold for exact recovery for the nonuniform, multiple-community case, subject to only minor constraints. One crucial point here is that, by aggregating information from all the uniform layers, we may obtain exact recovery, even in cases when this is impossible if each layer were considered alone. In addition, for the almost exact recovery regime, we prove a wide-ranging, information-theoretic lower bound on the number of misclassified vertices for any algorithm. The bound depends on a *generalized Chernoff–Hellinger* divergence involving model parameters. We provide two efficient algorithms (one for the minimal information case, another for the full information case) which successfully achieve exact recovery when above the threshold and attain the lowest possible mismatch ratio when the exact recovery is impossible. The theoretical analysis of our algorithms relies on the concentration and regularization of the adjacency matrix for nonuniform random hypergraphs, which could be of independent interest. We also address some open problems regarding parameter knowledge and estimation.

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*MSC2020 subject classifications.* Primary 60B20; secondary 05C80.

*Key words and phrases.* Random matrices, random hypergraphs, stochastic block model, strong consistency.

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# PSEUDO-LIKELIHOOD-BASED $M$ -ESTIMATION OF RANDOM GRAPHS WITH DEPENDENT EDGES AND PARAMETER VECTORS OF INCREASING DIMENSION

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An important question in statistical network analysis is how to estimate models of discrete and dependent network data with intractable likelihood functions, without sacrificing computational scalability and statistical guarantees. We demonstrate that scalable estimation of random graph models with dependent edges is possible, by establishing convergence rates of pseudo-likelihood-based  $M$ -estimators for discrete undirected graphical models with exponential parameterizations and parameter vectors of increasing dimension in single-observation scenarios. We highlight the impact of two complex phenomena on the convergence rate: phase transitions and model near-degeneracy. The main results have possible applications to discrete and dependent network, spatial, and temporal data. To showcase convergence rates, we introduce a novel class of generalized  $\beta$ -models with dependent edges and parameter vectors of increasing dimension, which leverage additional structure in the form of overlapping subpopulations to control dependence. We establish convergence rates of pseudo-likelihood-based  $M$ -estimators for generalized  $\beta$ -models in dense- and sparse-graph settings.

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*MSC2020 subject classifications.* Primary 05C80; secondary 62B05, 62F10, 91D30.

*Key words and phrases.* Markov random fields, graphical models, conditional independence, statistical exponential families, phase transitions, model near-degeneracy.

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# NEAR OPTIMAL SAMPLE COMPLEXITY FOR MATRIX AND TENSOR NORMAL MODELS VIA GEODESIC CONVEXITY

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The matrix normal model, that is, the family of Gaussian matrix-variate distributions whose covariance matrices are the Kronecker product of two lower-dimensional factors, is frequently used to model matrix-variate data. The tensor normal model generalizes this family to Kronecker products of three or more factors. We study the estimation of the Kronecker factors of the covariance matrix in the matrix and tensor normal models.

For the above models, we show that the maximum likelihood estimator (MLE) achieves *nearly optimal nonasymptotic sample complexity* and *nearly tight error rates* in the Fisher–Rao and Thompson metrics. In contrast to prior work, our results do not rely on the factors being well conditioned or sparse, nor do we need to assume an accurate enough initial guess. For the matrix normal model, all our bounds are minimax optimal up to logarithmic factors, and for the tensor normal model our bounds for the largest factor and for overall covariance matrix are minimax optimal up to constant factors provided there are enough samples for any estimator to obtain constant Frobenius error. In the same regimes as our sample complexity bounds, we show that the flip-flop algorithm, a practical and widely used iterative procedure to compute the MLE, converges linearly with high probability.

Our main technical insight is that, given enough samples, the negative log-likelihood function is *strongly geodesically convex* in the geometry on positive-definite matrices induced by the Fisher information metric. This strong convexity is determined by the expansion of certain random quantum channels.

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*MSC2020 subject classifications.* Primary 62F12; secondary 62F30.

*Key words and phrases.* Covariance estimation, matrix normal model, tensor normal model, maximum likelihood estimation, geodesic convexity, operator scaling, quantum expansion.

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# SCALABLE INFERENCE IN FUNCTIONAL LINEAR REGRESSION WITH STREAMING DATA

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Traditional static functional data analysis is facing new challenges due to streaming data, where data constantly flows in. A major challenge is that storing such an ever-increasing amount of data in memory is nearly infeasible. In addition, existing inferential tools in online learning are mainly developed for finite-dimensional problems, while inference methods for functional data are focused on the offline settings. In this paper, we focus on the online estimation of functional linear regression with a scalar response and a functional covariate. To tackle these issues in this setting, we develop a functional stochastic gradient descent algorithm and propose an online bootstrap resampling procedure that enables us to perform the local (and global) inference for the slope function in functional linear regression. In particular, the proposed estimation and inference procedures use only one pass over the data; thus they are easy to implement and suitable to the situation where data arrive in a streaming manner. Furthermore, we establish the convergence rate and the asymptotic distribution for the proposed slope function estimator. The proposed perturbed estimator from the bootstrap procedure is shown to enjoy the same theoretical properties, which provide the theoretical justification for our online inference tool. As far as we know, this is the first inference result on functional linear regression with streaming data. Numerical studies are conducted to demonstrate the finite-sample performance of our proposed procedure.

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*MSC2020 subject classifications.* Primary 62R10; secondary 62G20.

*Key words and phrases.* Online learning, reproducing kernel Hilbert space, functional data, bootstrap, stochastic gradient descent.

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# POISSON EMPIRICAL BAYES ESTIMATION: WHEN DOES $g$ -MODELING BEAT $f$ -MODELING IN THEORY (AND IN PRACTICE)?

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Empirical Bayes (EB) is a popular framework for large-scale inference that aims to find data-driven estimators to compete with the Bayesian oracle that knows the true prior. Two principled approaches to EB estimation have emerged over the years:  $f$ -modeling, which constructs an approximate Bayes rule by estimating the marginal distribution of the data, and  $g$ -modeling, which estimates the prior from data and then applies the learned Bayes rule. For the Poisson model, the prototypical examples are the celebrated Robbins estimator and the nonparametric MLE (NPMLE), respectively. It has long been recognized in practice that the Robbins estimator, while being conceptually appealing and computationally simple, lacks robustness and can be easily derailed by “outliers” (data points that were rarely observed before), unlike the NPMLE which provides more stable and interpretable fit thanks to its Bayes form. On the other hand, not only do the existing theories shed little light on this phenomenon, but they all point to the opposite, as both methods have recently been shown optimal in terms of the *regret* (excess over the Bayes risk) for compactly supported and subexponential priors with exact logarithmic factors (Brown, Greenshtein and Ritov (2013) *J. Amer. Statist. Assoc.* **108** 741–749; Polyanskiy and Wu (2021) [arXiv:2008.08244](https://arxiv.org/abs/2008.08244)).

In this paper we provide a theoretical justification for the superiority of  $g$ -modeling over  $f$ -modeling for heavy-tailed data by considering priors with bounded  $p$ th moment, a class previously studied for the Gaussian model (Jiang and Zhang (2009) *Ann. Statist.* **37** 1647–1684). For the Poisson model with sample size  $n$ , assuming  $p > 1$  (for otherwise triviality arises), we show that with mild regularization, any  $g$ -modeling method that is Hellinger rate-optimal in density estimation achieves a total regret  $\tilde{\Theta}(n^{\frac{3}{2p+1}})$ , which is minimax optimal within logarithmic factors; in particular, the special case of NPMLE succeeds without regularization. In contrast, there exists an  $f$ -modeling estimator whose density estimation rate is optimal but whose EB regret is suboptimal by a polynomial factor. These results show that the proper Bayes form provides a “general recipe of success” for optimal EB estimation that applies to all  $g$ -modeling (but not  $f$ -modeling) methods. As by-products of our analysis, we also obtain: (a) the minimax Hellinger rate of estimating Poisson mixture over the moment class, (b) the characterization of the regret suboptimality of the Robbins estimator, (c) an extension to the compound setting.

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*MSC2020 subject classifications.* Primary 62C12; secondary 62H30.

*Key words and phrases.* Empirical Bayes, Poisson distribution, mixture model, density estimation, nonparametric MLE, Robbins, heavy tail, regret.

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# AVERAGE PARTIAL EFFECT ESTIMATION USING DOUBLE MACHINE LEARNING

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Single-parameter summaries of variable effects in regression settings are desirable for ease of interpretation. However, (partially) linear models, for example, which would deliver these, may fit poorly to the data. On the other hand, an interpretable summary of the contribution of a given predictor is provided by the so-called average partial effect—the average slope of the regression function with respect to the predictor of interest. Although one can construct a doubly robust procedure for estimating this quantity, it entails estimating the derivative of the conditional mean and also the conditional score of the predictor of interest given all others, tasks which can be very challenging in moderate dimensions: in particular, popular decision tree based regression methods cannot be used.

In this work, we introduce an approach for estimating the average partial effect whose accuracy depends primarily on the estimation of certain regression functions, which may be performed by user-chosen machine learning methods that produce potentially nondifferentiable estimates. Our procedure involves resmoothing a given first-stage regression estimator to produce a differentiable version, and modelling the conditional distribution of the predictor of interest through a location–scale model. We show that with the latter assumption, surprisingly the overall error in estimating the conditional score is controlled by a sum of errors of estimating the conditional mean and conditional standard deviation, and the estimation error in a much more tractable univariate score estimation problem. Our theory makes use of a new result on the sub-Gaussianity of Lipschitz score functions that may be of independent interest. We demonstrate the attractive numerical performance of our approach in a variety of settings including ones with misspecification. An R package `drape` implementing the methodology is available on CRAN.

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*MSC2020 subject classifications.* 62G20.

*Key words and phrases.* Asymptotic properties of nonparametric inference, average partial effect, average derivative effect, incremental causal effect, double/debiased machine learning, score estimation.

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# SOLVING THE POISSON EQUATION USING COUPLED MARKOV CHAINS

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This article shows how coupled Markov chains that meet exactly after a random number of iterations can be used to generate unbiased estimators of the solutions of the Poisson equation. Through this connection, we re-derive known unbiased estimators of expectations with respect to the stationary distribution of a Markov chain and provide conditions for the finiteness of their moments. We further construct unbiased estimators of the asymptotic variance of Markov chain ergodic averages, and provide conditions for the finiteness of the estimators' moments of any order. If their second moment is finite, the average of independent copies of such estimators converges to the asymptotic variance at the Monte Carlo rate, comparing favorably to known rates for batch means and spectral variance estimators. The results are illustrated with numerical experiments.

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*MSC2020 subject classifications.* Primary 65C40, 65C05, 60F05; secondary 60J22, 60J05, 62F15.

*Key words and phrases.* Markov chain Monte Carlo, coupling, Poisson equation, asymptotic variance.

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# A COMPUTATIONAL TRANSITION FOR DETECTING CORRELATED STOCHASTIC BLOCK MODELS BY LOW-DEGREE POLYNOMIALS

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Detection of correlation in a pair of random graphs is a fundamental statistical and computational problem that has been extensively studied in recent years. In this work, we consider a pair of correlated (sparse) stochastic block models  $\mathcal{S}(n, \frac{\lambda}{n}; k, \epsilon; s)$  that are subsampled from a common parent stochastic block model  $\mathcal{S}(n, \frac{\lambda}{n}; k, \epsilon)$  with  $k = O(1)$  symmetric communities, average degree  $\lambda = O(1)$ , divergence parameter  $\epsilon$ , and subsampling probability  $s$ .

For the detection problem of distinguishing this model from a pair of independent Erdős–Rényi graphs with the same edge density  $\mathcal{G}(n, \frac{\lambda s}{n})$ , we focus on tests based on *low-degree polynomials* of the entries of the adjacency matrices, and we determine the threshold that separates the easy and hard regimes. More precisely, we show that this class of tests can distinguish these two models if and only if  $s > \min\{\sqrt{\alpha}, \frac{1}{\lambda\epsilon^2}\}$ , where  $\alpha \approx 0.338$  is the Otter’s constant and  $\frac{1}{\lambda\epsilon^2}$  is the Kesten–Stigum threshold. Combining a reduction argument in (Li (2025)), our hardness result also implies low-degree hardness for partial recovery and detection (to independent block models) when  $s < \min\{\sqrt{\alpha}, \frac{1}{\lambda\epsilon^2}\}$ . Finally, our proof of low-degree hardness is based on a conditional variant of the low-degree likelihood calculation.

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*MSC2020 subject classifications.* Primary 62M20; secondary 68Q87, 68Q17.

*Key words and phrases.* Random graph matching, correlated stochastic block models, computation transition, low-degree polynomials.

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# PSEUDO-LABELING FOR KERNEL RIDGE REGRESSION UNDER COVARIATE SHIFT

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We develop and analyze a principled approach to kernel ridge regression under covariate shift. The goal is to learn a regression function with small mean squared error over a target distribution, based on unlabeled data from there and labeled data that may have a different feature distribution. We propose to split the labeled data into two subsets, and conduct kernel ridge regression on them separately to obtain a collection of candidate models and an imputation model. We use the latter to fill the missing labels and then select the best candidate accordingly. Our nonasymptotic excess risk bounds demonstrate that our estimator adapts effectively to both the structure of the target distribution and the covariate shift. This adaptation is quantified through a notion of effective sample size that reflects the value of labeled source data for the target regression task. Our estimator achieves the minimax optimal error rate up to a polylogarithmic factor, and we find that using pseudo-labels for model selection does not significantly hinder performance.

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# CHANGE POINT ESTIMATION FOR A STOCHASTIC HEAT EQUATION

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We study a change point model based on a stochastic partial differential equation (SPDE) corresponding to the heat equation governed by the weighted Laplacian  $\Delta_{\vartheta} = \nabla \vartheta \nabla$ , where  $\vartheta = \vartheta(x)$  is a space dependent diffusivity. As a basic problem, the domain  $(0, 1)$  is considered with a piecewise constant diffusivity with a jump at an unknown point  $\tau$ . Based on local measurements of the solution in space with resolution  $\delta$  over a finite time horizon, we construct a simultaneous M-estimator for the diffusivity values and the change point. The change point estimator converges with rate  $\delta$ , while the diffusivity constants can be recovered with convergence rate  $\delta^{3/2}$ . Furthermore, when the diffusivity parameters are known and the jump height vanishes as the spatial resolution tends to zero, we derive a limit theorem for the change point estimator and identify the limiting distribution. For the mathematical analysis, a precise understanding of the SPDE with discontinuous  $\vartheta$ , tight concentration bounds for quadratic functionals in the solution and a generalization of classical M-estimators are developed.

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*MSC2020 subject classifications.* Primary 60H15, 62F12; secondary 60F05.

*Key words and phrases.* Change point detection, stochastic heat equation, local measurements.

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# MULTIVARIATE ROOT- $n$ -CONSISTENT SMOOTHING PARAMETER-FREE MATCHING ESTIMATORS AND ESTIMATORS OF INVERSE DENSITY WEIGHTED EXPECTATIONS

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Expected values weighted by the inverse of a multivariate density or, equivalently, Lebesgue integrals of regression functions with multivariate regressors occur in various areas of applications, including estimating average treatment effects, nonparametric estimators in random coefficient regression models or deconvolution estimators in Berkson errors-in-variables models. The frequently used nearest-neighbor and matching estimators suffer from bias problems in multiple dimensions. By using polynomial least squares fits on each cell of the  $K$ th-order Voronoi tessellation for sufficiently large  $K$ , we develop novel modifications of nearest-neighbor and matching estimators, which again converge at the parametric  $\sqrt{n}$ -rate under mild smoothness assumptions on the unknown regression function and without any smoothness conditions on the unknown density of the covariates. We stress that in contrast to competing methods for correcting for the bias of matching estimators, our estimators do not involve nonparametric function estimators and in particular do not rely on sample-size dependent smoothing parameters. We complement the upper bounds with appropriate lower bounds derived from information-theoretic arguments, which show that some smoothness of the regression function is indeed required to achieve the parametric rate. Simulations illustrate the practical feasibility of the proposed methods.

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*MSC2020 subject classifications.* Primary 62H12; secondary 62G05.

*Key words and phrases.* Average treatment effects, Berkson errors in variables models, bias correction, inverse density weighted expectations, matching estimators, random coefficients, Voronoi tessellation.

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# BERRY–ESSEEN BOUNDS FOR DESIGN-BASED CAUSAL INFERENCE WITH POSSIBLY DIVERGING TREATMENT LEVELS AND VARYING GROUP SIZES

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Neyman (1923/1990) introduced the randomization model, which contains the notation of potential outcomes to define causal effects and a framework for large-sample inference based on the design of the experiment. However, the existing theory for this framework is far from complete, especially when the number of treatment levels diverges and the treatment group sizes vary. We provide a unified discussion of statistical inference under the randomization model with general treatment group sizes. We formulate the estimator in terms of a linear permutation statistic and use results based on Stein’s method to derive various Berry–Esseen bounds on the linear and quadratic functions of the estimator. These new Berry–Esseen bounds serve as the basis for design-based causal inference with possibly diverging treatment levels and a diverging number of causal parameters of interest. We also fill an important gap by proposing novel variance estimators for experiments with possibly many treatment levels without replications. Equipped with the newly developed results, design-based causal inference in general settings becomes more convenient with stronger theoretical guarantees.

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*MSC2020 subject classifications.* 62K15, 62J05, 62G05.

*Key words and phrases.* Central limit theorem, permutation, potential outcome, Stein’s method, randomized experiment.

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# NEURAL NETWORKS GENERALIZE ON LOW COMPLEXITY DATA

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We show that feedforward neural networks with ReLU activation generalize on low complexity data, suitably defined. Given i.i.d. data generated from a simple programming language, the minimum description length (MDL) feedforward neural network which interpolates the data generalizes with high probability. We define this simple programming language, along with a notion of description length of such networks. We provide several examples on basic computational tasks, such as checking primality of a natural number. For primality testing, our theorem shows the following and more. Suppose that we draw an i.i.d. sample of  $n$  numbers uniformly at random from 1 to  $N$ . For each number  $x_i$ , let  $y_i = 1$  if  $x_i$  is a prime and 0 if it is not. Then the interpolating MDL network accurately answers, with probability  $1 - O((\ln N)/n)$ , whether a newly drawn number between 1 and  $N$  is a prime or not. Note that the network is not *designed* to detect primes; minimum description learning *discovers* a network which does so. Extensions to noisy data are also discussed, suggesting that MDL neural network interpolators can demonstrate tempered overfitting.

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*MSC2020 subject classifications.* Primary 68T07, 62H30; secondary 68Q32.

*Key words and phrases.* Neural networks, supervised learning, generalization error, minimum description length, Kolmogorov complexity.

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# SEMIPARAMETRIC BERNSTEIN–VON MISES PHENOMENON VIA ISOTONIZED POSTERIOR IN WICKSELL’S PROBLEM

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In this paper, we propose a novel Bayesian approach for nonparametric estimation in Wicksell’s problem. This has important applications in astronomy for estimating the distribution of the positions of the stars in a galaxy given projected stellar positions and in materials science to determine the 3D microstructure of a material, using its 2D cross-sections. We deviate from the classical Bayesian nonparametric approach, which would place a Dirichlet Process (DP) prior on the distribution function of the unobservables, by directly placing a DP prior on the distribution function of the observables. Our method offers computational simplicity due to the conjugacy of the posterior and allows for asymptotically efficient estimation by projecting the posterior onto the  $\mathbb{L}_2$  subspace of increasing, right-continuous functions. Indeed, the resulting Isotonized Inverse Posterior (IIP) satisfies a Bernstein–von Mises (BvM) phenomenon with minimax asymptotic variance  $g_0(x)/2\gamma$ , where  $\gamma > 1/2$  reflects the degree of Hölder continuity of the true cdf at  $x$ . Since the IIP gives automatic uncertainty quantification, it eliminates the need to estimate  $\gamma$ . Our results provide the first semiparametric Bernstein–von Mises theorem for projection-based posteriors with a DP prior in inverse problems.

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*MSC2020 subject classifications.* Primary 62F15, 62C10, 62G20, 62G05; secondary 62C20, 62E20.

*Key words and phrases.* Semiparametric estimation, Bernstein–von Mises, Bayesian nonparametrics, inverse problems, isotonic estimation, efficiency theory.

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## OPTIMAL CONVEX $M$ -ESTIMATION VIA SCORE MATCHING

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In the context of linear regression, we construct a data-driven convex loss function with respect to which empirical risk minimisation yields optimal asymptotic variance in the downstream estimation of the regression coefficients. At the population level, the negative derivative of the optimal convex loss is the best decreasing approximation of the derivative of the log-density of the noise distribution. This motivates a fitting process via a nonparametric extension of score matching, corresponding to a log-concave projection of the noise distribution with respect to the Fisher divergence. At the sample level, our semiparametric estimator is computationally efficient, and we prove that it attains the minimal asymptotic covariance among all convex  $M$ -estimators. As an example of a non-log-concave setting, the optimal convex loss function for Cauchy errors is Huber-like, and our procedure yields asymptotic efficiency greater than 0.87 relative to the maximum likelihood estimator of the regression coefficients that uses oracle knowledge of this error distribution. In this sense, we provide robustness and facilitate computation without sacrificing much statistical efficiency. Numerical experiments using our accompanying R package `asm` confirm the practical merits of our proposal.

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# COMMUNICATION-EFFICIENT AND DISTRIBUTED-ORACLE ESTIMATION FOR HIGH-DIMENSIONAL QUANTILE REGRESSION

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In this article, we present a novel communication-efficient estimator for distributed high-dimensional quantile regression with folded-concave penalties. An Iterative Multi-Step Algorithm (IMSA) is employed to tackle the nonconvex challenge of the objective function, taking into account both the statistical accuracy and the communication constraints. We demonstrate that the proposed IMSA estimators share similar properties with the global folded-concave penalized estimator. To establish the theoretical results, we introduce a new concept called the *distributed-oracle estimator*. We prove that the proposed estimator converges to the distributed-oracle estimator with high probability. Compared to the  $\ell_1$ -penalized method, the IMSA estimator possesses a faster rate of convergence and requires milder conditions to achieve support recovery. Furthermore, we extend our framework to facilitate distributed inference for the preconceived low-dimensional components within the high-dimensional model. We derive the limiting distribution of the corresponding test statistic under the null hypothesis and the local alternatives. In addition, a new feature-splitting algorithm is devised to accommodate the high-dimensional data within the distributed system. Extensive numerical studies demonstrate the effectiveness and validity of our proposed estimation and inference methods. A real example is also presented for illustration.

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*MSC2020 subject classifications.* Primary 62F05, 62F12; secondary 62J07.

*Key words and phrases.* Communication efficiency, distributed statistical inference, partial penalization, SCAD.

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# OPTIMALITY OF APPROXIMATE MESSAGE PASSING FOR SPIKED MATRIX MODELS WITH ROTATIONALLY INVARIANT NOISE

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We study the problem of estimating a rank-one signal matrix from a noisy observed matrix corrupted by additive rotationally invariant noise. We develop a new class of approximate message passing algorithms for this problem and provide a simple and concise characterization of their dynamics in the high-dimensional limit. At each iteration, these algorithms leverage prior knowledge about the noise structure by applying a nonlinear matrix denoiser to the eigenvalues of the observed matrix, and utilize prior information regarding the signal structure by applying a nonlinear iterate denoiser to the previous iterates generated by the algorithm. We derive the optimal choices for both the matrix and iterate denoisers and demonstrate that the resulting algorithm achieves the lowest possible asymptotic estimation error among a broad class of iterative algorithms under a fixed iteration budget.

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*MSC2020 subject classifications.* Primary 62H99; secondary 62F15, 62E20, 68Q17.

*Key words and phrases.* Statistical-computational gap, low-rank matrix estimation, approximate message passing.

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# INFORMATION THEORETIC LIMITS OF ROBUST SUB-GAUSSIAN MEAN ESTIMATION UNDER STAR-SHAPED CONSTRAINTS

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We obtain the minimax rate for a mean location model with a bounded star-shaped set  $K \subseteq \mathbb{R}^n$  constraint on the mean, in an adversarially corrupted data setting with Gaussian noise. We assume an unknown fraction  $\epsilon \leq 1/2 - \kappa$  for some fixed  $\kappa \in (0, 1/2]$  of  $N$  observations are arbitrarily corrupted. We obtain a minimax risk up to proportionality constants under the squared  $\ell_2$  loss of  $\max(\eta^{*2}, \sigma^2 \epsilon^2) \wedge d^2$  with

$$\eta^* = \sup \left\{ \eta \geq 0 : \frac{N\eta^2}{\sigma^2} \leq \log \mathcal{M}_K^{\text{loc}}(\eta, c) \right\},$$

where  $\log \mathcal{M}_K^{\text{loc}}(\eta, c)$  denotes the local entropy of the set  $K$ ,  $d$  is the diameter of  $K$ ,  $\sigma^2$  is the variance and  $c$  is some sufficiently large absolute constant. A variant of our algorithm achieves the same rate for settings with known or symmetric sub-Gaussian noise, with a smaller breakdown point, still of constant order. We further study the case of unknown sub-Gaussian noise and show that the rate is slightly slower:  $\max(\eta^{*2}, \sigma^2 \epsilon^2 \log(1/\epsilon)) \wedge d^2$ . We generalize our results to the case when  $K$  is star-shaped but unbounded.

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*MSC2020 subject classifications.* Primary 62F35, 62F30; secondary 62B10, 62C20.

*Key words and phrases.* Robustness, adversarial corruption, star-shaped, convex, shape constraints, sub-Gaussian noise.

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# CONFOUNDER SELECTION VIA ITERATIVE GRAPH EXPANSION

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Confounder selection, namely choosing a set of covariates to control for confounding between a treatment and an outcome, is arguably the most important step in the design of an observational study. Previous methods, such as Pearl's back-door criterion, typically require prespecifying a causal graph, which can often be difficult in practice. We propose an interactive procedure for confounder selection that does not require prespecifying the graph or the set of observed variables. This procedure iteratively expands the causal graph by finding what we call “primary adjustment sets” for a pair of possibly confounded variables. This can be viewed as inverting a sequence of marginalizations of the underlying causal graph. Structural information in the form of primary adjustment sets is elicited from the user, bit by bit, until either a set of covariates is found to control for confounding or it can be determined that no such set exists. Other information, such as the causal relations between confounders, is not required by the procedure. We show that if the user correctly specifies the primary adjustment sets in every step, our procedure is both sound and complete.

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*MSC2020 subject classifications.* Primary 62A09; secondary 62D20.

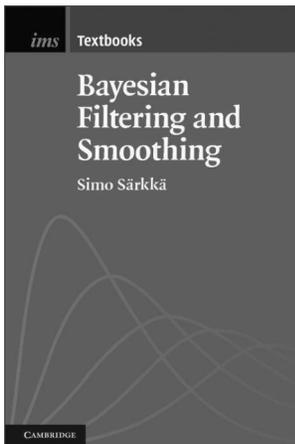
*Key words and phrases.* Causal inference, observational study, back-door criterion, background knowledge, adjustment, marginalization.

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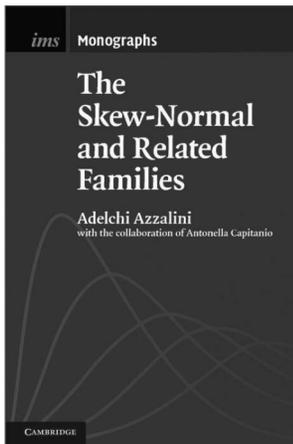
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