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TWO-STEP SEMIPARAMETRIC EMPIRICAL LIKELIHOOD INFERENCE

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In both parametric and certain nonparametric statistical models, the empirical likelihood ratio satisfies a nonparametric version of Wilks' theorem. For many semiparametric models, however, the commonly used two-step (plug-in) empirical likelihood ratio is not asymptotically distribution-free, that is, its asymptotic distribution contains unknown quantities, and hence Wilks' theorem breaks down. This article suggests a general approach to restore Wilks' phenomenon in two-step semiparametric empirical likelihood inferences. The main insight consists in using as the moment function in the estimating equation the influence function of the plug-in sample moment. The proposed method is general; it leads to a chi-squared limiting distribution with known degrees of freedom; it is efficient; it does not require undersmoothing; and it is less sensitive to the first-step than alternative methods, which is particularly appealing for high-dimensional settings. Several examples and simulation studies illustrate the general applicability of the procedure and its excellent finite sample performance relative to competing methods.

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THE PHASE TRANSITION FOR THE EXISTENCE OF THE MAXIMUM LIKELIHOOD ESTIMATE IN HIGH-DIMENSIONAL LOGISTIC REGRESSION

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This paper rigorously establishes that the existence of the maximum likelihood estimate (MLE) in high-dimensional logistic regression models with Gaussian covariates undergoes a sharp "phase transition." We introduce an explicit boundary curve h_{MLE}, parameterized by two scalars measuring the overall magnitude of the unknown sequence of regression coefficients, with the following property: in the limit of large sample sizes n and number of features p proportioned in such a way that $p/n \to \kappa$, we show that if the problem is sufficiently high dimensional in the sense that $\kappa > h_{\mathrm{MLE}}$, then the MLE does not exist with probability one. Conversely, if $\kappa < h_{\mathrm{MLE}}$, the MLE asymptotically exists with probability one.

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RERANDOMIZATION IN 2^K FACTORIAL EXPERIMENTS

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With many pretreatment covariates and treatment factors, the classical factorial experiment often fails to balance covariates across multiple factorial effects simultaneously. Therefore, it is intuitive to restrict the randomization of the treatment factors to satisfy certain covariate balance criteria, possibly conforming to the tiers of factorial effects and covariates based on their relative importances. This is rerandomization in factorial experiments. We study the asymptotic properties of this experimental design under the randomization inference framework without imposing any distributional or modeling assumptions of the covariates and outcomes. We derive the joint asymptotic sampling distribution of the usual estimators of the factorial effects, and show that it is symmetric, unimodal and more "concentrated" at the true factorial effects under rerandomization than under the classical factorial experiment. We quantify this advantage of rerandomization using the notions of "central convex unimodality" and "peakedness" of the joint asymptotic sampling distribution. We also construct conservative large-sample confidence sets for the factorial effects.

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SPARSE SIR: OPTIMAL RATES AND ADAPTIVE ESTIMATION

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Sliced inverse regression (SIR) is an innovative and effective method for sufficient dimension reduction and data visualization. Recently, an impressive range of penalized SIR methods has been proposed to estimate the central subspace in a sparse fashion. Nonetheless, few of them considered the sparse sufficient dimension reduction from a decision-theoretic point of view. To address this issue, we in this paper establish the minimax rates of convergence for estimating the sparse SIR directions under various commonly used loss functions in the literature of sufficient dimension reduction. We also discover the possible trade-off between statistical guarantee and computational performance for sparse SIR. We finally propose an adaptive estimation scheme for sparse SIR which is computationally tractable and rate optimal. Numerical studies are carried out to confirm the theoretical properties of our proposed methods.

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ROBUST SPARSE COVARIANCE ESTIMATION BY THRESHOLDING TYLER'S M-ESTIMATOR

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Estimating a high-dimensional sparse covariance matrix from a limited number of samples is a fundamental task in contemporary data analysis. Most proposals to date, however, are not robust to outliers or heavy tails. Toward bridging this gap, in this work we consider estimating a sparse shape matrix from n samples following a possibly heavy-tailed elliptical distribution. We propose estimators based on thresholding either Tyler's M-estimator or its regularized variant. We prove that in the joint limit as the dimension p and the sample size n tend to infinity with $p/n \to \gamma > 0$, our estimators are minimax rate optimal. Results on simulated data support our theoretical analysis.

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MODEL ASSISTED VARIABLE CLUSTERING: MINIMAX-OPTIMAL RECOVERY AND ALGORITHMS

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The problem of variable clustering is that of estimating groups of similar components of a p-dimensional vector $X = (X_1, \dots, X_p)$ from n independent copies of X. There exists a large number of algorithms that return data-dependent groups of variables, but their interpretation is limited to the algorithm that produced them. An alternative is model-based clustering, in which one begins by defining population level clusters relative to a model that embeds notions of similarity. Algorithms tailored to such models yield estimated clusters with a clear statistical interpretation. We take this view here and introduce the class of G-block covariance models as a background model for variable clustering. In such models, two variables in a cluster are deemed similar if they have similar associations will all other variables. This can arise, for instance, when groups of variables are noise corrupted versions of the same latent factor. We quantify the difficulty of clustering data generated from a G-block covariance model in terms of cluster proximity, measured with respect to two related, but different, cluster separation metrics. We derive minimax cluster separation thresholds, which are the metric values below which no algorithm can recover the model-defined clusters exactly, and show that they are different for the two metrics. We therefore develop two algorithms, COD and PECOK, tailored to G-block covariance models, and study their minimax-optimality with respect to each metric. Of independent interest is the fact that the analysis of the PECOK algorithm, which is based on a corrected convex relaxation of the popular K-means algorithm, provides the first statistical analysis of such algorithms for variable clustering. Additionally, we compare our methods with another popular clustering method, spectral clustering. Extensive simulation studies, as well as our data analyses, confirm the applicability of our approach.

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NEW *G*-FORMULA FOR THE SEQUENTIAL CAUSAL EFFECT AND BLIP EFFECT OF TREATMENT IN SEQUENTIAL CAUSAL INFERENCE

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In sequential causal inference, two types of causal effects are of practical interest, namely, the causal effect of the treatment regime (called the sequential causal effect) and the blip effect of treatment on the potential outcome after the last treatment. The well-known G-formula expresses these causal effects in terms of the standard parameters. In this article, we obtain a new G-formula that expresses these causal effects in terms of the point observable effects of treatments similar to treatment in the framework of single-point causal inference. Based on the new G-formula, we estimate these causal effects by maximum likelihood via point observable effects with methods extended from single-point causal inference. We are able to increase precision of the estimation without introducing biases by an unsaturated model imposing constraints on the point observable effects. We are also able to reduce the number of point observable effects in the estimation by treatment assignment conditions.

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ENVELOPE-BASED SPARSE PARTIAL LEAST SQUARES

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Sparse partial least squares (SPLS) is widely used in applied sciences as a method that performs dimension reduction and variable selection simultaneously in linear regression. Several implementations of SPLS have been derived, among which the SPLS proposed in Chun and Keleş (*J. R. Stat. Soc. Ser. B. Stat. Methodol.* **72** (2010) 3–25) is very popular and highly cited. However, for all of these implementations, the theoretical properties of SPLS are largely unknown. In this paper, we propose a new version of SPLS, called the envelope-based SPLS, using a connection between envelope models and partial least squares (PLS). We establish the consistency, oracle property and asymptotic normality of the envelope-based SPLS estimator. The large-sample scenario and high-dimensional scenario are both considered. We also develop the envelope-based SPLS estimators under the context of generalized linear models, and discuss its theoretical properties including consistency, oracle property and asymptotic distribution. Numerical experiments and examples show that the envelope-based SPLS estimator has better variable selection and prediction performance over the SPLS estimator (*J. R. Stat. Soc. Ser. B. Stat. Methodol.* **72** (2010) 3–25).

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OPTIMAL RATES FOR COMMUNITY ESTIMATION IN THE WEIGHTED STOCHASTIC BLOCK MODEL

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Community identification in a network is an important problem in fields such as social science, neuroscience and genetics. Over the past decade, stochastic block models (SBMs) have emerged as a popular statistical framework for this problem. However, SBMs have an important limitation in that they are suited only for networks with unweighted edges; in various scientific applications, disregarding the edge weights may result in a loss of valuable information. We study a weighted generalization of the SBM, in which observations are collected in the form of a weighted adjacency matrix and the weight of each edge is generated independently from an unknown probability density determined by the community membership of its endpoints. We characterize the optimal rate of misclustering error of the weighted SBM in terms of the Renyi divergence of order 1/2 between the weight distributions of within-community and between-community edges, substantially generalizing existing results for unweighted SBMs. Furthermore, we present a computationally tractable algorithm based on discretization that achieves the optimal error rate. Our method is adaptive in the sense that the algorithm, without assuming knowledge of the weight densities, performs as well as the best algorithm that knows the weight densities.

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ADAPTIVE RISK BOUNDS IN UNIVARIATE TOTAL VARIATION DENOISING AND TREND FILTERING

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We study trend filtering, a relatively recent method for univariate nonparametric regression. For a given integer $r \geq 1$, the rth order trend filtering estimator is defined as the minimizer of the sum of squared errors when we constrain (or penalize) the sum of the absolute rth order discrete derivatives of the fitted function at the design points. For $r = 1$, the estimator reduces to total variation regularization which has received much attention in the statistics and image processing literature. In this paper, we study the performance of the trend filtering estimator for every $r \geq 1$, both in the constrained and penalized forms. Our main results show that in the strong sparsity setting when the underlying function is a (discrete) spline with few "knots," the risk (under the global squared error loss) of the trend filtering estimator (with an appropriate choice of the tuning parameter) achieves the *parametric* n^{-1}-rate, up to a logarithmic (multiplicative) factor. Our results therefore provide support for the use of trend filtering, for every $r \geq 1$, in the strong sparsity setting.

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SPECTRAL AND MATRIX FACTORIZATION METHODS FOR CONSISTENT COMMUNITY DETECTION IN MULTI-LAYER NETWORKS

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We consider the problem of estimating a consensus community structure by combining information from multiple layers of a multi-layer network using methods based on the spectral clustering or a low-rank matrix factorization. As a general theme, these "intermediate fusion" methods involve obtaining a low column rank matrix by optimizing an objective function and then using the columns of the matrix for clustering. However, the theoretical properties of these methods remain largely unexplored. In the absence of statistical guarantees on the objective functions, it is difficult to determine if the algorithms optimizing the objectives will return good community structures. We investigate the consistency properties of the global optimizer of some of these objective functions under the multi-layer stochastic blockmodel. For this purpose, we derive several new asymptotic results showing consistency of the intermediate fusion techniques along with the spectral clustering of mean adjacency matrix under a high dimensional setup, where the number of nodes, the number of layers and the number of communities of the multi-layer graph grow. Our numerical study shows that the intermediate fusion techniques outperform late fusion methods, namely spectral clustering on aggregate spectral kernel and module allegiance matrix in sparse networks, while they outperform the spectral clustering of mean adjacency matrix in multi-layer networks that contain layers with both homophilic and heterophilic communities.

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STATISTICAL INFERENCE FOR MODEL PARAMETERS IN STOCHASTIC GRADIENT DESCENT

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The stochastic gradient descent (SGD) algorithm has been widely used in statistical estimation for large-scale data due to its computational and memory efficiency. While most existing works focus on the convergence of the objective function or the error of the obtained solution, we investigate the problem of statistical inference of true model parameters based on SGD when the population loss function is strongly convex and satisfies certain smoothness conditions.

Our main contributions are twofold. First, in the fixed dimension setup, we propose two consistent estimators of the asymptotic covariance of the average iterate from SGD: (1) a plug-in estimator, and (2) a batch-means estimator, which is computationally more efficient and only uses the iterates from SGD. Both proposed estimators allow us to construct asymptotically exact confidence intervals and hypothesis tests.

Second, for high-dimensional linear regression, using a variant of the SGD algorithm, we construct a debiased estimator of each regression coefficient that is asymptotically normal. This gives a one-pass algorithm for computing both the sparse regression coefficients and confidence intervals, which is computationally attractive and applicable to online data.

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BOOTSTRAP CONFIDENCE REGIONS BASED ON M-ESTIMATORS UNDER NONSTANDARD CONDITIONS

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Suppose that a confidence region is desired for a subvector θ of a multidimensional parameter $\xi = (\theta, \psi)$, based on an M-estimator $\hat{\xi}_n = (\hat{\theta}_n, \hat{\psi}_n)$ calculated from a random sample of size n. Under nonstandard conditions $\hat{\xi}_n$ often converges at a nonregular rate r_n, in which case consistent estimation of the distribution of $r_n(\hat{\theta}_n - \theta)$, a pivot commonly chosen for confidence region construction, is most conveniently effected by the m out of n bootstrap. The above choice of pivot has three drawbacks: (i) the shape of the region is either subjectively prescribed or controlled by a computationally intensive depth function; (ii) the region is not transformation equivariant; (iii) $\hat{\xi}_n$ may not be uniquely defined. To resolve the above difficulties, we propose a one-dimensional pivot derived from the criterion function, and prove that its distribution can be consistently estimated by the m out of n bootstrap, or by a modified version of the perturbation bootstrap. This leads to a new method for constructing confidence regions which are transformation equivariant and have shapes driven solely by the criterion function. A subsampling procedure is proposed for selecting m in practice. Empirical performance of the new method is illustrated with examples drawn from different nonstandard M-estimation settings. Extension of our theory to row-wise independent triangular arrays is also explored.

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SPARSE HIGH-DIMENSIONAL REGRESSION: EXACT SCALABLE ALGORITHMS AND PHASE TRANSITIONS

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We present a novel binary convex reformulation of the sparse regression problem that constitutes a new duality perspective. We devise a new cutting plane method and provide evidence that it can solve to provable optimality the sparse regression problem for sample sizes n and number of regressors p in the 100,000s, that is, two orders of magnitude better than the current state of the art, in seconds. The ability to solve the problem for very high dimensions allows us to observe new phase transition phenomena. Contrary to traditional complexity theory which suggests that the difficulty of a problem increases with problem size, the sparse regression problem has the property that as the number of samples n increases the problem becomes easier in that the solution recovers 100% of the true signal, and our approach solves the problem extremely fast (in fact faster than `Lasso`), while for small number of samples n, our approach takes a larger amount of time to solve the problem, but importantly the optimal solution provides a statistically more relevant regressor. We argue that our exact sparse regression approach presents a superior alternative over heuristic methods available at present.

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TESTING FOR PRINCIPAL COMPONENT DIRECTIONS UNDER WEAK IDENTIFIABILITY

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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 $\boldsymbol{\theta}_1^0$ is a fixed unit p-vector. In the classical setup where eigenvalues $\lambda_1 > \lambda_2 \geq \cdots \geq \lambda_p$ are fixed, the Anderson (*Ann. Math. Stat.* **34** (1963) 122–148) likelihood ratio test (LRT) and the Hallin, Paindaveine and Verdebout (*Ann. Statist.* **38** (2010) 3245–3299) Le Cam optimal test for this problem are asymptotically equivalent under the null hypothesis, hence also under sequences of contiguous alternatives. We show that this equivalence does not survive asymptotic scenarios where $\lambda_{n1}/\lambda_{n2} = 1 + O(r_n)$ 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 severely overrejects the null hypothesis. 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's asymptotic theory of statistical experiments, we study the non-null and optimality properties of the Le Cam optimal test in the aforementioned asymptotic scenarios and show that the null robustness of this test is not obtained at the expense of power. Our asymptotic investigation is extensive in the sense that it allows r_n to converge to zero at an arbitrary rate. While we restrict to single-spiked spectra of the form $\lambda_{n1} > \lambda_{n2} = \cdots = \lambda_{np}$ to make our results as striking as possible, we extend our results to the more general elliptical case. Finally, we present an illustrative real data example.

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THE MULTI-ARMED BANDIT PROBLEM: AN EFFICIENT NONPARAMETRIC SOLUTION

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Lai and Robbins (*Adv. in Appl. Math.* **6** (1985) 4–22) and Lai (*Ann. Statist.* **15** (1987) 1091–1114) provided efficient parametric solutions to the multi-armed bandit problem, showing that arm allocation via upper confidence bounds (UCB) achieves minimum regret. These bounds are constructed from the Kullback–Leibler information of the reward distributions, estimated from specified parametric families. In recent years, there has been renewed interest in the multi-armed bandit problem due to new applications in machine learning algorithms and data analytics. Nonparametric arm allocation procedures like ϵ-greedy, Boltzmann exploration and BESA were studied, and modified versions of the UCB procedure were also analyzed under nonparametric settings. However, unlike UCB these nonparametric procedures are not efficient under general parametric settings. In this paper, we propose efficient nonparametric procedures.

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CONCENTRATION AND CONSISTENCY RESULTS FOR CANONICAL AND CURVED EXPONENTIAL-FAMILY MODELS OF RANDOM GRAPHS

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Statistical inference for exponential-family models of random graphs with dependent edges is challenging. We stress the importance of additional structure and show that additional structure facilitates statistical inference. A simple example of a random graph with additional structure is a random graph with neighborhoods and local dependence within neighborhoods. We develop the first concentration and consistency results for maximum likelihood and M-estimators of a wide range of canonical and curved exponential-family models of random graphs with local dependence. All results are nonasymptotic and applicable to random graphs with finite populations of nodes, although asymptotic consistency results can be obtained as well. In addition, we show that additional structure can facilitate subgraph-to-graph estimation, and present concentration results for subgraph-to-graph estimators. As an application, we consider popular curved exponential-family models of random graphs, with local dependence induced by transitivity and parameter vectors whose dimensions depend on the number of nodes.

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THE NUMERICAL BOOTSTRAP

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This paper proposes a numerical bootstrap method that is consistent in many cases where the standard bootstrap is known to fail and where the m-out-of-n bootstrap and subsampling have been the most commonly used inference approaches. We provide asymptotic analysis under both fixed and drifting parameter sequences, and we compare the approximation error of the numerical bootstrap with that of the m-out-of-n bootstrap and subsampling. Finally, we discuss applications of the numerical bootstrap, such as constrained and unconstrained M-estimators converging at both regular and nonstandard rates, Laplace-type estimators, and test statistics for partially identified models.

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CONSISTENT SELECTION OF THE NUMBER OF CHANGE-POINTS VIA SAMPLE-SPLITTING

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In multiple change-point analysis, one of the major challenges is to estimate the number of change-points. Most existing approaches attempt to minimize a Schwarz information criterion which balances a term quantifying model fit with a penalization term accounting for model complexity that increases with the number of change-points and limits overfitting. However, different penalization terms are required to adapt to different contexts of multiple change-point problems and the optimal penalization magnitude usually varies from the model and error distribution. We propose a data-driven selection criterion that is applicable to most kinds of popular change-point detection methods, including binary segmentation and optimal partitioning algorithms. The key idea is to select the number of change-points that minimizes the squared prediction error, which measures the fit of a specified model for a new sample. We develop a cross-validation estimation scheme based on an order-preserved sample-splitting strategy, and establish its asymptotic selection consistency under some mild conditions. Effectiveness of the proposed selection criterion is demonstrated on a variety of numerical experiments and real-data examples.

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UNIFORMLY VALID CONFIDENCE INTERVALS POST-MODEL-SELECTION

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We suggest general methods to construct asymptotically uniformly valid confidence intervals post-model-selection. The constructions are based on principles recently proposed by Berk et al. (*Ann. Statist.* **41** (2013) 802–837). In particular, the candidate models used can be misspecified, the target of inference is model-specific, and coverage is guaranteed for *any* data-driven model selection procedure. After developing a general theory, we apply our methods to practically important situations where the candidate set of models, from which a working model is selected, consists of fixed design homoskedastic or heteroskedastic linear models, or of binary regression models with general link functions. In an extensive simulation study, we find that the proposed confidence intervals perform remarkably well, even when compared to existing methods that are tailored only for specific model selection procedures.

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EFFICIENT ESTIMATION OF LINEAR FUNCTIONALS OF PRINCIPAL COMPONENTS

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We study principal component analysis (PCA) for mean zero i.i.d. Gaussian observations $X_1, \dots, X_n$ in a separable Hilbert space $\mathbb{H}$ with unknown covariance operator Σ. The complexity of the problem is characterized by its effective rank $\mathbf{r}(\Sigma) := \frac{\operatorname{tr}(\Sigma)}{\|\Sigma\|}$, where $\operatorname{tr}(\Sigma)$ denotes the trace of Σ and $\|\Sigma\|$ denotes its operator norm. We develop a method of bias reduction in the problem of estimation of linear functionals of eigenvectors of Σ. Under the assumption that $\mathbf{r}(\Sigma) = o(n)$, we establish the asymptotic normality and asymptotic properties of the risk of the resulting estimators and prove matching minimax lower bounds, showing their semiparametric optimality.

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OPTIMAL PREDICTION IN THE LINEARLY TRANSFORMED SPIKED MODEL

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We consider the *linearly transformed spiked model*, where the observations Y_i are noisy linear transforms of unobserved signals of interest X_i:

$$Y_i = A_i X_i + \varepsilon_i,$$

for $i = 1, \dots, n$. The transform matrices A_i are also observed. We model the unobserved signals (or regression coefficients) X_i as vectors lying on an unknown low-dimensional space. Given only Y_i and A_i how should we predict or recover their values?

The naive approach of performing regression for each observation separately is inaccurate due to the large noise level. Instead, we develop optimal methods for predicting X_i by "borrowing strength" across the different samples. Our linear empirical Bayes methods scale to large datasets and rely on weak moment assumptions.

We show that this model has wide-ranging applications in signal processing, deconvolution, cryo-electron microscopy, and missing data with noise. For missing data, we show in simulations that our methods are more robust to noise and to unequal sampling than well-known matrix completion methods.

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AVERAGES OF UNLABELED NETWORKS: GEOMETRIC CHARACTERIZATION AND ASYMPTOTIC BEHAVIOR

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It is becoming increasingly common to see large collections of network data objects, that is, data sets in which a network is viewed as a fundamental unit of observation. As a result, there is a pressing need to develop network-based analogues of even many of the most basic tools already standard for scalar and vector data. In this paper, our focus is on averages of unlabeled, undirected networks with edge weights. Specifically, we (i) characterize a certain notion of the space of all such networks, (ii) describe key topological and geometric properties of this space relevant to doing probability and statistics thereupon, and (iii) use these properties to establish the asymptotic behavior of a generalized notion of an empirical mean under sampling from a distribution supported on this space. Our results rely on a combination of tools from geometry, probability theory and statistical shape analysis. In particular, the lack of vertex labeling necessitates working with a quotient space modding out permutations of labels. This results in a nontrivial geometry for the space of unlabeled networks, which in turn is found to have important implications on the types of probabilistic and statistical results that may be obtained and the techniques needed to obtain them.

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MARKOV EQUIVALENCE OF MARGINALIZED LOCAL INDEPENDENCE GRAPHS

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Symmetric independence relations are often studied using graphical representations. Ancestral graphs or acyclic directed mixed graphs with m-separation provide classes of symmetric graphical independence models that are closed under marginalization. Asymmetric independence relations appear naturally for multivariate stochastic processes, for instance, in terms of local independence. However, no class of graphs representing such asymmetric independence relations, which is also closed under marginalization, has been developed. We develop the theory of directed mixed graphs with μ-separation and show that this provides a graphical independence model class which is closed under marginalization and which generalizes previously considered graphical representations of local independence.

Several graphs may encode the same set of independence relations and this means that in many cases only an equivalence class of graphs can be identified from observational data. For statistical applications, it is therefore pivotal to characterize graphs that induce the same independence relations. Our main result is that for directed mixed graphs with μ-separation each equivalence class contains a maximal element which can be constructed from the independence relations alone. Moreover, we introduce the directed mixed equivalence graph as the maximal graph with dashed and solid edges. This graph encodes all information about the edges that is identifiable from the independence relations, and furthermore it can be computed efficiently from the maximal graph.

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ASYMPTOTIC GENEALOGIES OF INTERACTING PARTICLE SYSTEMS WITH AN APPLICATION TO SEQUENTIAL MONTE CARLO

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We study weighted particle systems in which new generations are resampled from current particles with probabilities proportional to their weights. This covers a broad class of sequential Monte Carlo (SMC) methods, widely-used in applied statistics and cognate disciplines. We consider the genealogical tree embedded into such particle systems, and identify conditions, as well as an appropriate time-scaling, under which they converge to the Kingman n-coalescent in the infinite system size limit in the sense of finite-dimensional distributions. Thus, the tractable n-coalescent can be used to predict the shape and size of SMC genealogies, as we illustrate by characterising the limiting mean and variance of the tree height. SMC genealogies are known to be connected to algorithm performance, so that our results are likely to have applications in the design of new methods as well. Our conditions for convergence are strong, but we show by simulation that they do not appear to be necessary.

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ALMOST SURE UNIQUENESS OF A GLOBAL MINIMUM WITHOUT CONVEXITY

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This paper establishes the argmin of a random objective function to be unique almost surely. This paper first formulates a general result that proves almost sure uniqueness without convexity of the objective function. The general result is then applied to a variety of applications in statistics. Four applications are discussed, including uniqueness of M-estimators, both classical likelihood and penalized likelihood estimators, and two applications of the argmin theorem, threshold regression and weak identification.

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PENALIZED GENERALIZED EMPIRICAL LIKELIHOOD WITH A DIVERGING NUMBER OF GENERAL ESTIMATING EQUATIONS FOR CENSORED DATA

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This article considers simultaneous variable selection and parameter estimation as well as hypothesis testing in censored survival models where a parametric likelihood is not available. For the problem, we utilize certain growing dimensional general estimating equations and propose a penalized generalized empirical likelihood, where the general estimating equations are constructed based on the semiparametric efficiency bound of estimation with given moment conditions. The proposed penalized generalized empirical likelihood estimators enjoy the oracle properties, and the estimator of any fixed dimensional vector of nonzero parameters achieves the semiparametric efficiency bound asymptotically. Furthermore, we show that the penalized generalized empirical likelihood ratio test statistic has an asymptotic central chi-square distribution. The conditions of local and restricted global optimality of weighted penalized generalized empirical likelihood estimators are also discussed. We present a two-layer iterative algorithm for efficient implementation, and investigate its convergence property. The performance of the proposed methods is demonstrated by extensive simulation studies, and a real data example is provided for illustration.

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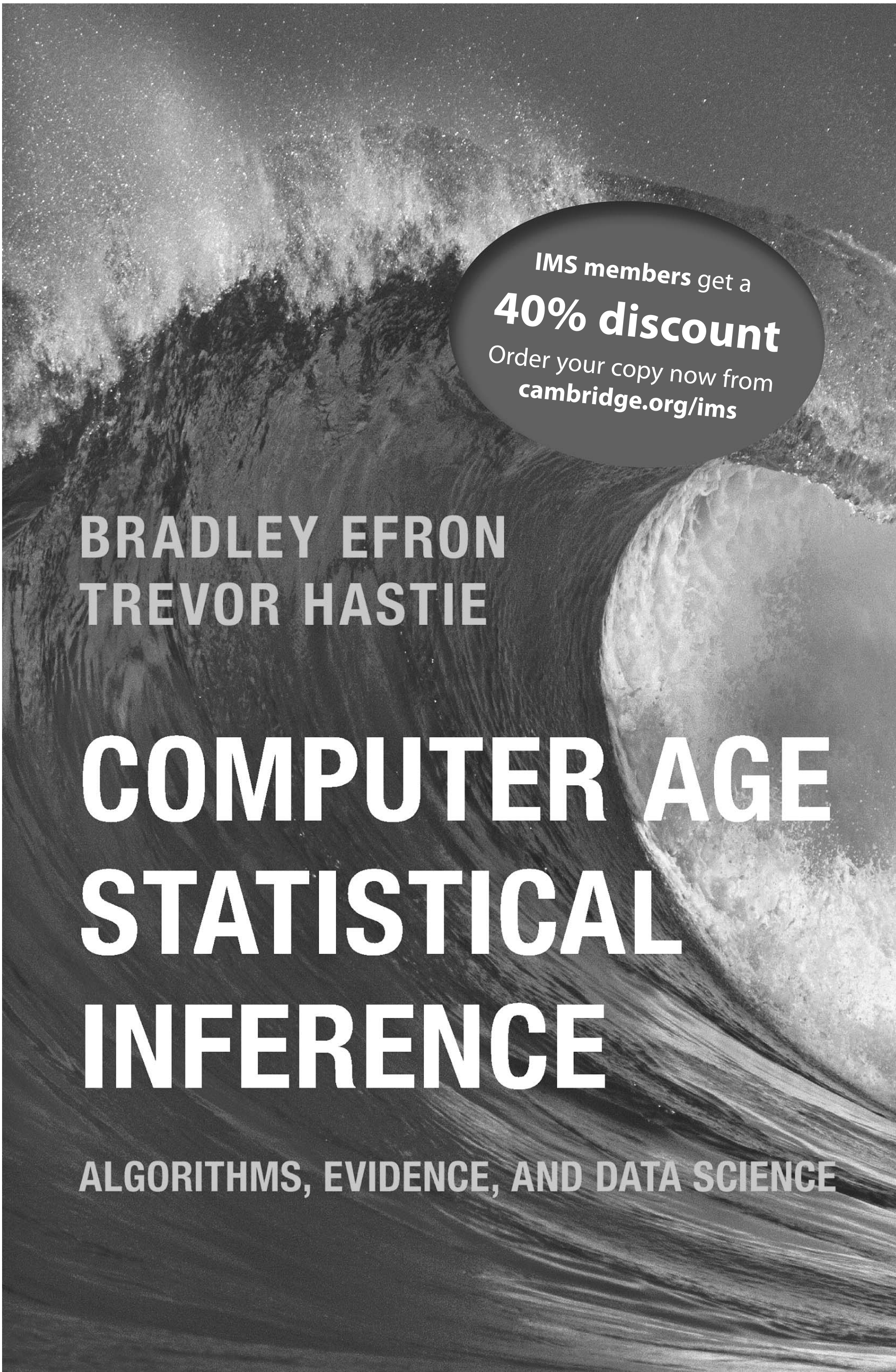
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