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A NONASYMPTOTIC DISTRIBUTIONAL THEORY OF APPROXIMATE MESSAGE PASSING FOR SPARSE AND ROBUST REGRESSION

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Characterizing the distribution of high-dimensional statistical estimators is a challenging task, due to the breakdown of classical asymptotic theory in high dimension. This paper makes progress towards this by developing nonasymptotic distributional characterizations for approximate message passing (AMP)—a family of iterative algorithms that prove effective as both fast estimators and powerful theoretical machinery—for both sparse and robust regression. Prior AMP theory, which focused on high-dimensional asymptotics for the most part, failed to describe the behavior of AMP when the number of iterations exceeds $o(\log n/\log\log n)$ (with n the sample size). Our AMP theory is further leveraged to derive a refined rate for the Lasso estimator, built upon a nonasymptotic convergence of AMP to Lasso. To the best of our knowledge, this is the first result of its kind, breaking the rate barrier resulting from the widely adopted Gaussian min-max theorem. Our results establish approximate accuracy of Gaussian approximation of the AMP iterates, which improves upon prior results and implies enhanced distributional characterizations for both optimally tuned Lasso and robust M-estimator.

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LOCAL GEOMETRY OF HIGH-DIMENSIONAL MIXTURE MODELS: EFFECTIVE SPECTRAL THEORY AND DYNAMICAL TRANSITIONS

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We study the local geometry of empirical risks in high dimensions via the spectral theory of their Hessian and information matrices. We focus on settings where the data, $(Y_\ell)_{\ell=1}^n \in \mathbb{R}^d$, are i.i.d. draws of a k-Gaussian mixture model, and the loss depends on the projection of the data into a fixed number of vectors, namely $\mathbf{x}^\top Y$, where $\mathbf{x} \in \mathbb{R}^{d\times\mathcal{C}}$ are the parameters, and $\mathcal{C}$ need not equal k. This setting captures a broad class of problems such as classification by one and two-layer networks and regression on multi-index models. We provide exact formulas for the limits of the empirical spectral distribution and outlier eigenvalues and eigenvectors of such matrices in the proportional asymptotics limit, where the number of samples and dimension $n, d \to \infty$ and $n/d = \phi \in (0, \infty)$. These limits depend on the parameters $\mathbf{x}$ only through the summary statistic of the $(\mathcal{C}+k)\times(\mathcal{C}+k)$ Gram matrix of the parameters and class means, $\mathbf{G} = (\mathbf{x}, \boldsymbol{\mu})^\top(\mathbf{x}, \boldsymbol{\mu})$.

It is known that under general conditions, when $\mathbf{x}$ is trained by online stochastic gradient descent, the evolution of these same summary statistics along training converges to the solution of an autonomous system of ODEs, called the *effective dynamics*. This enables us to connect the training dynamics to the spectral theory of these matrices generated with test data. We demonstrate our general results by analyzing the *effective spectrum* along the effective dynamics in the case of multiclass logistic regression. In this setting, the empirical Hessian and information matrices have substantially different spectra, each with their own static and dynamical spectral transitions.

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HIGH-ORDER ACCURATE INFERENCE ON MANIFOLDS

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We present a new framework for statistical inference on Riemannian manifolds that achieves high-order accuracy, addressing the challenges posed by non-Euclidean parameter spaces frequently encountered in modern data science. Our approach leverages a novel and computationally efficient procedure to reach higher-order asymptotic precision. In particular, we develop a bootstrap algorithm on Riemannian manifolds that is both computationally efficient and accurate for hypothesis testing and confidence region construction. Although locational hypothesis testing can be reformulated as a standard Euclidean problem, constructing high-order accurate confidence regions necessitates careful treatment of manifold geometry. To this end, we establish high-order asymptotics under an appropriate coordinate representation induced by a second-order retraction, thereby enabling precise expansions that incorporate curvature effects. We demonstrate the versatility of this framework across various manifold settings, including spheres, the Stiefel manifold, fixed-rank matrix manifolds, and rank-one tensor manifolds; for Euclidean submanifolds, we also introduce a class of projection-like coordinate charts with strong consistency properties. Finally, numerical studies confirm the practical merits of the proposed procedure.

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UNIFORM ESTIMATION AND INFERENCE FOR NONPARAMETRIC PARTITIONING-BASED M-ESTIMATORS

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This paper presents uniform estimation and inference theory for a large class of nonparametric partitioning-based M-estimators. The main theoretical results include: (i) uniform consistency for convex and nonconvex objective functions; (ii) rate-optimal uniform Bahadur representations; (iii) rate-optimal uniform (and mean square) convergence rates; (iv) valid strong approximations and feasible uniform inference methods; and (v) extensions to functional transformations of underlying estimators. Uniformity is established over both the evaluation point of the nonparametric functional parameter and a Euclidean parameter indexing the class of loss functions. The results also account explicitly for the smoothness degree of the loss function (if any), and allow for a possibly nonidentity (inverse) link function. We illustrate the theoretical and methodological results in four examples: quantile regression, distribution regression, L_p regression, and logistic regression. Many other possibly nonsmooth, nonlinear, generalized, robust M-estimation settings are covered by our results. We provide detailed comparisons with the existing literature and demonstrate substantive improvements: we achieve the best (in some cases optimal) known results under improved (in some cases minimal) requirements in terms of regularity conditions and side rate restrictions. The Supplementary Material reports complementary technical results that may be of independent interest, including a novel uniform strong approximation result based on Yurinskii's coupling.

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DIPMIND: DISTANCE PROFILE BASED MUTUAL INDEPENDENCE TESTING FOR RANDOM OBJECTS

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This paper develops a novel unified framework for testing mutual independence among random objects residing in possibly different metric spaces. The framework generalizes existing methodologies and introduces new measures of mutual independence, and proposes associated tests that achieve minimax rate optimality and exhibit strong empirical power. The foundation of the proposed tests is the new concept of joint distance profiles, which uniquely characterize the joint law of random objects under a mild condition on either the joint law or the metric spaces. Our test statistics quantify the difference of the joint distance profiles of each data point with respect to the joint law and the product of marginal laws of the vector of random objects. To enhance power, we consider integrating this difference with respect to different measures and incorporate flexible data-adaptive weight profiles in the test statistics. We derive the limiting distribution of the test statistics under the null hypothesis of mutual independence and show that the proposed tests with certain weight profiles are asymptotically distribution-free if the marginal distance profiles are continuous. Furthermore, we establish the consistency of the tests under sequences of alternative hypotheses converging to the null. For practical implementations, we employ a permutation scheme to approximate the p-values and provide theoretical guarantees that the permutation-based tests maintain type I error control under the null and achieve consistency under alternatives. We demonstrate the power of the proposed tests across various types of data objects through simulations and real data applications, where the new tests exhibit better performance compared with popular existing approaches.

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ESTIMATING THE FALSE DISCOVERY RATE OF VARIABLE SELECTION

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We introduce a generic estimator for the false discovery rate of any model selection procedure, in common statistical modeling settings including the Gaussian linear model, Gaussian graphical model, and model-X setting. We prove that our method has a conservative (nonnegative) bias in finite samples under standard statistical assumptions, and provide a bootstrap method for assessing its standard error. For methods like the Lasso, forward-stepwise regression, and the graphical Lasso, our estimator serves as a valuable companion to cross-validation, illuminating the tradeoff between prediction error and variable selection accuracy as a function of the model complexity parameter.

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IMPROVED THRESHOLDS FOR E-VALUES

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The rejection threshold used for e-values and e-processes is by default set to $1/\alpha$ for a guaranteed type-I error control at α, based on Markov's and Ville's inequalities. This threshold can be wasteful in practical applications. We discuss how this threshold can be improved under additional distributional assumptions on the e-values; some of these assumptions are naturally plausible and empirically observable, without knowing explicitly the form or model of the e-values. For small values of α, the threshold can roughly be improved (divided) by a factor of 2 for decreasing or unimodal densities, and by a factor of e for decreasing or unimodal-symmetric densities of log-transformed e-values. Moreover, we propose to use the supremum of comonotonic e-values, which is shown to preserve the type-I error guarantee. We also propose some preliminary methods to boost e-values in the e-BH procedure under some distributional assumptions while controlling the false discovery rate. Through a series of simulation studies, we demonstrate the effectiveness of our proposed methods in various testing scenarios, showing enhanced power.

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MEASURING EVIDENCE AGAINST EXCHANGEABILITY AND GROUP INVARIANCE WITH E-VALUES

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We study e-values for quantifying evidence against exchangeability and general invariance of a random variable under a compact group. We start by characterizing such e-values, and explaining how they nest traditional group invariance tests as a special case. We show they can be easily designed for an arbitrary test statistic, and computed through Monte Carlo sampling. We prove a result that characterizes optimal e-values for group invariance against optimality targets that satisfy a mild orbit-wise decomposition property. We apply this to design expected-utility-optimal e-values for group invariance, which include both Neyman–Pearson-optimal tests and log-optimal e-values. Moreover, we generalize the notion of rank- and sign-based testing to compact groups, by using a representative inversion kernel. In addition, we characterize e-processes for group invariance for arbitrary filtrations, and provide tools to construct them. We also describe test martingales under a natural filtration, which are simpler to construct. Peeking beyond compact groups, we encounter e-values and e-processes based on ergodic theorems. These nest e-processes based on de Finetti's theorem for testing exchangeability.

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PRIVACY GUARANTEES IN POSTERIOR SAMPLING UNDER CONTAMINATION

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In recent years, differential privacy has been adopted by tech-companies and governmental agencies as the standard for measuring privacy in algorithms. In this article, we study differential privacy in Bayesian posterior sampling settings. We begin by considering differential privacy in the most common privatisation setting in which Laplace or Gaussian noise is injected into the output. In an effort to achieve better differential privacy, we consider adopting *Huber's contamination model* for use within privacy settings, and replace at random data points with samples from a heavy-tailed distribution (*instead* of injecting noise into the output). We derive bounds for the differential privacy level (ϵ, δ) of our approach, without requiring bounded observation and parameter spaces, a restriction commonly imposed in the literature. We further consider for our approach the effect of sample size on the privacy level and the rate at which (ϵ, δ) converges to zero. Asymptotically, our contamination approach is fully private with no information loss. We also provide examples of inference models for which our approach applies, with theoretical convergence rate analysis and simulation studies.

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UNBIASED KINETIC LANGEVIN MONTE CARLO WITH INEXACT GRADIENTS

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We present an unbiased method for Bayesian posterior means based on kinetic Langevin dynamics that combines advanced splitting methods with enhanced gradient approximations. Our approach avoids Metropolis correction by coupling Markov chains at different discretization levels in a multilevel Monte Carlo approach. Theoretical analysis demonstrates that our proposed estimator is unbiased, attains finite variance, and satisfies a central limit theorem. It can achieve accuracy $\epsilon > 0$ for estimating expectations of Lipschitz functions in d dimensions with $\mathcal{O}(d^{1/4}\epsilon^{-2})$ expected gradient evaluations, without assuming warm start. We exhibit similar bounds using both approximate and stochastic gradients, and our method's computational cost is shown to scale independently of the size of the dataset. The proposed method is tested using a multinomial regression problem on the MNIST dataset and a Poisson regression model for soccer scores. Experiments indicate that the number of gradient evaluations per effective sample is independent of dimension, even when using inexact gradients. For product distributions, we give dimension-independent variance bounds. Our results demonstrate that in large-scale applications, the unbiased algorithm we present can be 2–3 orders of magnitude more efficient than the "gold-standard" randomized Hamiltonian Monte Carlo.

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ASSOCIATION AND INDEPENDENCE TEST FOR RANDOM OBJECTS

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We develop a unified framework for testing independence and quantifying association between random objects that are located in general metric spaces. Special cases include functional and high-dimensional data as well as networks, covariance matrices and data on Riemannian manifolds, among other metric space-valued data. A key concept is the profile association, a measure based on distance profiles that intrinsically characterize the distributions of random objects in metric spaces. We establish a connection between Hoeffding's D statistic and the profile association and derive a permutation test with theoretical guarantees for consistency and power under alternatives to the null hypothesis of independence (equivalently, no association). We extend this framework to the conditional setting, where the independence between random objects given a Euclidean predictor is of interest. In simulations across various metric spaces, the proposed profile independence test is found to outperform existing approaches. The practical utility of this framework is demonstrated with applications to brain connectivity networks derived from magnetic resonance imaging and age-at-death distributions for males and females obtained from human mortality data.

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LINEAR METHODS FOR NONLINEAR INVERSE PROBLEMS

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We consider the recovery of an unknown function f from a noisy observation of the solution u_f to a partial differential equation that can be written in the form $\mathcal{L}u_f = c(f, u_f)$, for a differential operator $\mathcal{L}$ that is rich enough to recover f from $\mathcal{L}u_f$. Examples include the time-independent Schrödinger equation $\Delta u_f = 2u_f f$, the heat equation with absorption term $(\partial_t - \Delta_x/2)u_f = fu_f$ and the Darcy problem $\nabla \cdot (f\nabla u_f) = h$. We transform this problem into the linear inverse problem of recovering $\mathcal{L}u_f$ under the Dirichlet boundary condition, and show that Bayesian methods with priors placed either on u_f or $\mathcal{L}u_f$ for this problem yield optimal recovery rates not only for u_f, but also for f. We also derive frequentist coverage guarantees for the corresponding Bayesian credible sets. Adaptive priors are shown to yield adaptive contraction rates for f, thus eliminating the need to know the smoothness of this function. The results are illustrated by numerical experiments on synthetic data sets.

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ON THE EFFICIENCY OF HIGHLY STRATIFIED EXPERIMENTS

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This paper studies the use of highly stratified designs for the efficient estimation of a large class of treatment effect parameters that arise in the analysis of experiments. By a "highly stratified" design, we mean experiments in which units are divided into blocks of a fixed size and a proportion within each block is assigned to a binary treatment uniformly at random. The class of parameters considered are those that can be expressed as the solution to a set of moment conditions constructed using a known function of the observed data. They include, among other things, average treatment effects, quantile treatment effects and local average treatment effects as well as the counterparts to these quantities in experiments in which the unit is itself a cluster. In this setting, we establish three results. First, we show that under a highly stratified design, the naïve method of moments estimator achieves the same asymptotic variance as what could typically be attained under alternative treatment assignment mechanisms only through *ex post* covariate adjustment. Second, we argue that the naïve method of moments estimator under a highly stratified design is asymptotically efficient by deriving a lower bound on the asymptotic variance of regular estimators of the parameter of interest in the form of a convolution theorem. In this sense, highly stratified experiments are attractive because they lead to efficient estimators of treatment effect parameters "by design." Finally, we strengthen this conclusion by establishing conditions under which a "fast-balancing" property of highly stratified designs is in fact necessary for the naïve method of moments estimator to attain the efficiency bound.

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GENERALIZED MULTIVARIATE THRESHOLD AUTOREGRESSIVE MODELS WITH LINEARLY PARTITIONED THRESHOLD SPACE

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We consider a k-dimensional multiple-regime vector threshold autoregressive model, in which the regime-switching mechanism is governed by a bivariate threshold variable. Specifically, the regimes are induced by a partition of the threshold space by an unknown number of threshold lines. Within each regime, the process follows a specific vector autoregressive (VAR) model. We formulate the model selection and parameter estimation into a minimization problem based on the Minimum Description Length (MDL) principle and estimate the number of threshold lines, parametric forms of threshold lines and VAR model parameters in each regime simultaneously. Theoretically, we show that the MDL estimators of threshold lines are n-consistent and characterize their limiting distribution. This requires novel proving techniques of introducing a new functional space $\mathbb{G}$ for the local MDL difference functions and establishing weak convergence results therein. Finally, we conduct some empirical studies with simulated datasets and perform real data analyses on U.S. interest rates and U.S. GNP Data.

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PSEUDO-MAXIMUM LIKELIHOOD THEORY FOR HIGH-DIMENSIONAL RANK ONE INFERENCE

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We develop a pseudo-likelihood theory for rank one matrix estimation problems in the high-dimensional limit. We prove a variational principle for the limiting pseudo-maximum likelihood, which also characterizes the performance of the corresponding pseudo-maximum likelihood estimator. We show that this variational principle is universal and depends only on four parameters determined by the corresponding null model. Through this universality, we introduce a notion of equivalence for estimation problems of this type and, in particular, show that a broad class of estimation tasks, including community detection, sparse submatrix detection and nonlinear spiked matrix models, are equivalent to spiked matrix models. As an application, we obtain a complete description of the performance of the least-squares (or "best rank one") estimator for any rank one matrix estimation problem.

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ESTIMATION BEYOND MISSING (COMPLETELY) AT RANDOM

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We study the effects of missingness on the estimation of population parameters. Moving beyond restrictive missing completely at random (MCAR) assumptions, we first formulate a missing data analogue of Huber's arbitrary ϵ-contamination model. For mean estimation with respect to squared Euclidean error loss, we show that the minimax quantiles decompose as a sum of the corresponding minimax quantiles under a heterogeneous, MCAR assumption and a robust error term, depending on ϵ, that reflects the additional error incurred by departure from MCAR.

We next introduce natural classes of *realisable ϵ-contamination models*, where an MCAR version of a base distribution P is contaminated by an arbitrary missing not at random (MNAR) version of P. These classes are rich enough to capture various notions of biased sampling and sensitivity conditions, yet we show that they enjoy improved minimax performance relative to our earlier arbitrary contamination classes for both parametric and nonparametric classes of base distributions. For instance, with a univariate Gaussian base distribution, consistent mean estimation over realisable ϵ-contamination classes is possible even when ϵ and the proportion of missingness converge (slowly) to 1. We extend our results to the setting of departures from missing at random (MAR) in normal linear regression with a realisable missing response, and also demonstrate that our methods can be made adaptive to the case of unknown ϵ.

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FAST MIXING OF DATA AUGMENTATION ALGORITHMS: BAYESIAN PROBIT, LOGIT AND LASSO REGRESSION

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We propose using a modified conductance-based method to study the mixing time of an important class of two-block Gibbs samplers, the data augmentation (DA) algorithm. Using this method, we prove the first non-asymptotic polynomial upper bounds on mixing times of three important DA algorithms: DA algorithms for Bayesian Probit regression (ProbitDA) and Bayesian Logit regression (LogitDA), and Bayesian Lasso Regression (LassoDA). Concretely, for ProbitDA and LogitDA, we demonstrate a tight bound that explicitly depends on the design matrix and prior covariance matrix. Under the assumption that data are independently generated from either a sub-Gaussian or log-concave distribution and properly scaled, the bound implies that with η-warm start, parameter dimension d, and sample size n, with high probability over data, the two algorithms require $\mathcal{O}(n\log(\frac{\log\eta}{\epsilon}))$ steps to obtain samples with at most ϵ error in TV, KL or χ^2 distance. Meanwhile, we show that under minimal data assumptions, LassoDA requires $\mathcal{O}(d^2(d\log d + n\log n)^2\log(\frac{\eta}{\epsilon}))$ steps to achieve ϵ-accuracy in TV distance. The results are generally applicable to settings with large n and large d, including settings with highly imbalanced response data in Probit and Logit regression. We compare them with the best known guarantees of Langevin Monte Carlo and Metropolis Adjusted Langevin Algorithm. We evaluate our theoretical results using numerical examples, and discuss the mixing times of the three algorithms under feasible initialization.

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STATISTICAL IMPOSSIBILITY AND POSSIBILITY OF ALIGNING LLMS WITH HUMAN PREFERENCES: FROM CONDORCET PARADOX TO NASH EQUILIBRIUM

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Aligning large language models (LLMs) with diverse human preferences is critical for ensuring fairness and informed outcomes when deploying these models for decision-making. In this paper, we seek to uncover fundamental statistical limits concerning aligning LLMs with human preferences, with a focus on the probabilistic representation of human preferences and the preservation of diverse preferences in aligned LLMs. We first show that human preferences can be represented by a reward model if and only if the preference among LLM-generated responses is free of any Condorcet cycle. Moreover, we prove that Condorcet cycles exist with probability converging to one exponentially fast under a general probabilistic preference model called the Luce model, thereby demonstrating the *impossibility* of fully aligning human preferences using reward-based approaches such as reinforcement learning from human feedback. Next, we explore the conditions under which LLMs would employ mixed strategies—meaning they do not collapse to a single response—when aligned in the limit using a nonreward-based approach, such as Nash learning from human feedback. We identify a necessary and sufficient condition for mixed strategies: the *absence* of a response that is preferred over all others by a majority. As a blessing, we prove that this condition holds with high probability under the Luce model, thereby highlighting the statistical *possibility* of preserving minority preferences without explicit regularization in aligning LLMs.

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HIGHER-ORDER GRAPHON THEORY: FLUCTUATIONS, DEGENERACIES AND INFERENCE

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Exchangeable random graphs, which include some of the most widely studied network models, have emerged as the mainstay of statistical network analysis in recent years. Graphons, which are the central objects in graph limit theory, provide a natural way to sample exchangeable random graphs. It is well known that network moments (motif/subgraph counts) identify a graphon (up to an isomorphism); hence, understanding the sampling distribution of subgraph counts in random graphs sampled from a graphon is pivotal for nonparametric network inference. Although there are a few results regarding the asymptotic normality of subgraph counts in graphon models, for many commonly appearing graphons this distribution is degenerate. This degeneracy phenomenon was overlooked until very recently and its consequences in network inference have remained unexplored. Toward this, we obtain the following results: We derive the joint asymptotic distribution of any finite collection of network moments in random graphs sampled from a graphon, which includes both the nondegenerate case (where the distribution is Gaussian) as well as the degenerate case (where the distribution has both Gaussian or non-Gaussian components). This provides the higher-order fluctuation theory for subgraph counts in the graphon model. Furthermore, we develop a novel multiplier bootstrap for graphons that consistently approximates the limiting distribution of the network moments (both in the Gaussian and non-Gaussian regimes). Using this and a procedure for testing degeneracy, we construct joint confidence sets for any finite collection of motif densities. This provides a general framework for statistical inference based on network moments in the graphon model. Examples and simulations are provided to validate the general theory. To illustrate the broad scope of our results, we also consider the problem of detecting global structure (i.e., testing whether the graphon is a constant function) based on small subgraphs. We propose a consistent test for this problem, invoking celebrated results on quasirandom graphs, and derive its limiting distribution both under the null and the alternative.

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GAUSSIAN AND BOOTSTRAP APPROXIMATION FOR MATCHING-BASED AVERAGE TREATMENT EFFECT ESTIMATORS

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We establish Gaussian approximation bounds for covariate and rank-matching-based Average Treatment Effect (ATE) estimators. By analyzing these estimators through the lens of stabilization theory, we employ the Malliavin–Stein method to derive our results. Our bounds precisely quantify the impact of key problem parameters, including the number of matches and treatment balance, on the accuracy of the Gaussian approximation. Additionally, we develop multiplier bootstrap procedures to estimate the limiting distribution in a fully data-driven manner, and we leverage the derived Gaussian approximation results to further obtain bootstrap approximation bounds. Our work not only introduces a novel theoretical framework for commonly used ATE estimators, but also provides data-driven methods for constructing nonasymptotically valid confidence intervals.

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SAMPLE SIZE AND POWER CALCULATIONS FOR CAUSAL INFERENCE IN OBSERVATIONAL STUDIES

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This paper investigates the theoretical foundation and develops analytical formulas for sample size and power calculations for causal inference with observational data. By analyzing the variance of an inverse probability weighting estimator of the average treatment effect, we decompose the power calculation into three components: propensity score distribution, potential outcome distribution and their correlation. We show that to determine the minimal sample size of an observational study, in addition to the standard inputs in the power calculation of randomized trials, it is sufficient to have two parameters: an overlap coefficient and a confounding coefficient, which quantify the strength of the confounder-treatment and the confounder-outcome association, respectively. For the overlap coefficient, we propose using the Bhattacharyya coefficient, which measures the covariate overlap and, together with the treatment proportion, leads to a uniquely identifiable and easily computable propensity score distribution. For the confounding coefficient, we propose a sensitivity parameter bounded by the R-squared statistic of the regression of the outcome on covariates. Our procedure relies on a parametric propensity score model and a semiparametric restricted mean outcome model, but does not require distributional assumptions on the multivariate covariates. We develop an associated R package `PSpower` and an online calculator.

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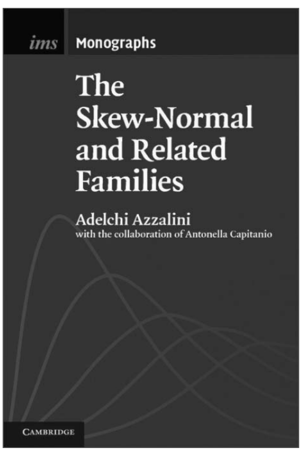

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