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TESTING NONPARAMETRIC SHAPE RESTRICTIONS

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We describe and examine a test for a general class of shape constraints, such as signs of derivatives, U-shape, quasi-convexity, log-convexity, among others, in a nonparametric framework using partial sums empirical processes. We show that, after a suitable transformation, its asymptotic distribution is a functional of a Brownian motion index by the c.d.f. of the regressor. As a result, the test is distribution-free and critical values are readily available. However, due to the possible poor approximation of the asymptotic critical values to the finite sample ones, we also describe a valid bootstrap algorithm.

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CARVING MODEL-FREE INFERENCE

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Complex studies involve many steps. Selecting promising findings based on pilot data is a first step. As more observations are collected, the investigator must decide how to combine the new data with the pilot data to construct valid selective inference. Carving, introduced by Fithian, Sun and Taylor (2014), enables the reuse of pilot data during selective inference and accounts for overoptimism from the selection process. However, currently, carving is only justified for parametric models such as the commonly used Gaussian model. In this paper, we develop the asymptotic theory to substantiate the use of carving beyond Gaussian models. Our results indicate that carving produces valid and tight confidence intervals within a model-free setting, as demonstrated through simulated and real instances.

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OPTIMAL SUBGROUP SELECTION

BY HENRY W. J. REEVE[1,a], TIMOTHY I. CANNINGS[2,b] AND RICHARD J. SAMWORTH[3,c]

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In clinical trials and other applications, we often see regions of the feature space that appear to exhibit interesting behaviour, but it is unclear whether these observed phenomena are reflected at the population level. Focusing on a regression setting, we consider the subgroup selection challenge of identifying a region of the feature space on which the regression function exceeds a pre-determined threshold. We formulate the problem as one of constrained optimisation, where we seek a low-complexity, data-dependent selection set on which, with a guaranteed probability, the regression function is uniformly at least as large as the threshold; subject to this constraint, we would like the region to contain as much mass under the marginal feature distribution as possible. This leads to a natural notion of regret, and our main contribution is to determine the minimax optimal rate for this regret in both the sample size and the Type I error probability. The rate involves a delicate interplay between parameters that control the smoothness of the regression function, as well as exponents that quantify the extent to which the optimal selection set at the population level can be approximated by families of well-behaved subsets. Finally, we expand the scope of our previous results by illustrating how they may be generalised to a treatment and control setting, where interest lies in the heterogeneous treatment effect.

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ADJUSTED CHI-SQUARE TEST FOR DEGREE-CORRECTED BLOCK MODELS

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We propose a goodness-of-fit test for degree-corrected stochastic block models (DCSBM). The test is based on an adjusted chi-square statistic for measuring equality of means among groups of n multinomial distributions with $d_1, \dots, d_n$ observations. In the context of network models, the number of multinomials, n, grows much faster than the number of observations, d_i, corresponding to the degree of node i, hence the setting deviates from classical asymptotics. We show that a simple adjustment allows the statistic to converge in distribution, under null, as long as the harmonic mean of $\{d_i\}$ grows to infinity. When applied sequentially, the test can also be used to determine the number of communities. The test operates on a compressed version of the adjacency matrix, conditional on the degrees, and as a result is highly scalable to large sparse networks. We incorporate a novel idea of compressing the rows based on a $(K+1)$-community assignment when testing for K communities. This approach increases the power in sequential applications without sacrificing computational efficiency, and we prove its consistency in recovering the number of communities. Since the test statistic does not rely on a specific alternative, its utility goes beyond sequential testing and can be used to simultaneously test against a wide range of alternatives outside the DCSBM family. In particular, we prove that the test is consistent against a general family of latent-variable network models with community structure. We show the effectiveness of the approach by extensive numerical experiments with simulated and real data. In particular, applying the test to the Facebook-100 data set, a collection of one hundred social networks, we find that a DCSBM with a small number of communities (say < 25) is far from a good fit in almost all cases.

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LOCAL WHITTLE ESTIMATION OF HIGH-DIMENSIONAL LONG-RUN VARIANCE AND PRECISION MATRICES

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This work develops nonasymptotic theory for estimation of the long-run variance matrix and its inverse, the so-called precision matrix, for high-dimensional time series under general assumptions on the dependence structure including long-range dependence. The estimation involves shrinkage techniques, which are thresholding and penalizing versions of the classical multivariate local Whittle estimator. The results ensure consistent estimation in a double asymptotic regime where the number of component time series is allowed to grow with the sample size as long as the true model parameters are sparse. The key technical result is a concentration inequality of the local Whittle estimator for the long-run variance matrix around the true model parameters. In particular, it handles simultaneously the estimation of the memory parameters, which enter the underlying model. Novel algorithms for the considered procedures are proposed, and a simulation study and a data application are also provided.

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S-ESTIMATION IN LINEAR MODELS WITH STRUCTURED COVARIANCE MATRICES

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We provide a unified approach to S-estimation in balanced linear models with structured covariance matrices. Of main interest are S-estimators for linear mixed effects models, but our approach also includes S-estimators in several other standard multivariate models, such as multiple regression, multivariate regression and multivariate location and scatter. We provide sufficient conditions for the existence of S-functionals and S-estimators, establish asymptotic properties such as consistency and asymptotic normality, and derive their robustness properties in terms of breakdown point and influence function. All the results are obtained for general identifiable covariance structures and are established under mild conditions on the distribution of the observations, which goes far beyond models with elliptically contoured densities. Some of our results are new and others are more general than existing ones in the literature. In this way, this manuscript completes and improves results on S-estimation in a wide variety of multivariate models. We illustrate our results by means of a simulation study and an application to data from a trial on the treatment of lead-exposed children.

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EFFICIENT SHAPE-CONSTRAINED INFERENCE FOR THE AUTOCOVARIANCE SEQUENCE FROM A REVERSIBLE MARKOV CHAIN

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In this paper, we study the problem of estimating the autocovariance sequence resulting from a reversible Markov chain. A motivating application for studying this problem is the estimation of the asymptotic variance in central limit theorems for Markov chains. We propose a novel shape-constrained estimator of the autocovariance sequence, which is based on the key observation that the representability of the autocovariance sequence as a moment sequence imposes certain shape constraints. We examine the theoretical properties of the proposed estimator and provide strong consistency guarantees for our estimator. In particular, for geometrically ergodic reversible Markov chains, we show that our estimator is strongly consistent for the true autocovariance sequence with respect to an ℓ_2 distance, and that our estimator leads to strongly consistent estimates of the asymptotic variance. Finally, we perform empirical studies to illustrate the theoretical properties of the proposed estimator as well as to demonstrate the effectiveness of our estimator in comparison with other current state-of-the-art methods for Markov chain Monte Carlo variance estimation, including batch means, spectral variance estimators, and the initial convex sequence estimator.

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GAUSSIAN PROCESS REGRESSION IN THE FLAT LIMIT

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Gaussian process (GP) regression is a fundamental tool in Bayesian statistics. It is also known as kriging and is the Bayesian counterpart to the frequentist kernel ridge regression. Most of the theoretical work on GP regression has focused on a large-n asymptotics, characterising the behaviour of GP regression as the amount of data increases. Fixed-sample analysis is much more difficult outside of simple cases, such as locations on a regular grid.

In this work, we perform a fixed-sample analysis that was first studied in the context of approximation theory by Fornberg and Driscoll (2002), called the "flat limit". In flat-limit asymptotics, the goal is to characterise kernel methods as the length-scale of the kernel function tends to infinity, so that kernels appear flat over the range of the data. Surprisingly, this limit is well-defined, and displays interesting behaviour: Driscoll and Fornberg showed that radial basis interpolation converges in the flat limit to polynomial interpolation, if the kernel is Gaussian. Subsequent work showed that this holds true in the multivariate setting as well, but that kernels other than the Gaussian may have (polyharmonic) splines as the limit interpolant.

Leveraging recent results on the spectral behaviour of kernel matrices in the flat limit, we study the flat limit of Gaussian process regression. Results show that Gaussian process regression tends in the flat limit to (multivariate) polynomial regression, or (polyharmonic) spline regression, depending on the kernel. Importantly, this holds for both the predictive mean and the predictive variance, so that the posterior predictive distributions become equivalent.

For the proof, we introduce the notion of prediction-equivalence of semi-parametric models, which lets us state flat-limit results in a compact and unified manner. Our results have practical consequences: for instance, they show that optimal GP predictions in the sense of leave-one-out loss may occur at very large length-scales, which would be invisible to current implementations because of numerical difficulties.

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PROJECTIVE, SPARSE AND LEARNABLE LATENT POSITION NETWORK MODELS

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When modeling network data using a latent position model, it is typical to assume that the nodes' positions are independently and identically distributed. However, this assumption implies the average node degree grows linearly with the number of nodes, which is inappropriate when the graph is thought to be sparse. We propose an alternative assumption—that the latent positions are generated according to a Poisson point process—and show that it is compatible with various levels of sparsity. Unlike other notions of sparse latent position models in the literature, our framework also defines a projective sequence of probability models, thus ensuring consistency of statistical inference across networks of different sizes. We establish conditions for consistent estimation of the latent positions, and compare our results to existing frameworks for modeling sparse networks.

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NONLINEAR NETWORK AUTOREGRESSION

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We study general nonlinear models for time series networks of integer and continuous-valued data. The vector of high-dimensional responses, measured on the nodes of a known network, is regressed nonlinearly on its lagged value and on lagged values of the neighboring nodes by employing a smooth link function. We study stability conditions for such multivariate process and develop quasi-maximum likelihood inference when the network dimension is increasing. In addition, we study linearity score tests by treating separately the cases of identifiable and nonidentifiable parameters. In the case of identifiability, the test statistic converges to a chi-square distribution. When the parameters are not identifiable, we develop a supremum-type test whose p-values are approximated adequately by employing a feasible bound and bootstrap methodology. Simulations and data examples support further our findings.

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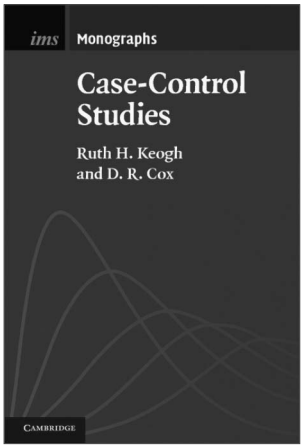

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