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Asymptotic Optimality of Likelihood-Based Cross-Validation

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May 12, 2003

Abstract

Likelihood-based cross-validation is a statistical tool for selecting a density estimate based on n i.i.d. observations from the true density among a collection of candidate density estimators. General examples are the selection of a model indexing a maximum likelihood estimator, and the selection of a bandwidth indexing a nonparametric (e.g. kernel) density estimator. In this article, we establish a finite sample result for a general class of likelihood-based cross-validation procedures (as indexed by the type of sample splitting used, e.g. V -fold cross-validation). This result implies that the cross-validation selector performs asymptotically as well (w.r.t. to the Kullback-Leibler distance to the true density) as a benchmark model selector which is optimal for each given dataset and depends on the true density. Crucial conditions of our theorem are that the size of the validation sample converges to infinity, which excludes leave-one-out cross-validation, and that the candidate density estimates are bounded away from zero and infinity. We illustrate these asymptotic results and the practical performance of likelihood-based cross-validation for the purpose of bandwidth selection with a simulation study. Moreover, we use likelihood-based cross-validation in the context of regulatory motif detection in DNA sequences.

Key words: Likelihood cross-validation, maximum likelihood estimation, Kullback-Leibler divergence, density estimation, bandwidth selection, model selection, variable selection.

1 Introduction

Density estimation arises in important and common problems in the statistical literature. As discussed below, bandwidth selection in kernel density estimation, selecting the number of components in mixture models, and variable selection in regression (e.g., logistic and linear regression with normal error), are three examples of problems that involve explicitly or implicitly some form of density estimation.

Let X_1, \dots, X_n be n independent and identically distributed (i.i.d.) random variables with distribution P and corresponding density f with respect to a dominating measure μ . Let $f_k(\cdot \mid P_n)$ be an estimator of f , $k = 1, \dots, K(n)$, where P_n denotes the empirical distribution function. For example, $f_k(\cdot \mid P_n)$ can be the maximum likelihood estimator of f according to a model \mathcal{M}_k , that is,

$$f_k(\cdot \mid P_n) = \max_{f \in \mathcal{M}_k}^{-1} \int \log(f(x)) dP_n(x).$$

A fundamental and practical problem is the selection of a \hat{k} in such a manner that $f_{\hat{k}}(\cdot \mid P_n)$ converges to the true density f optimally. For mixture modeling, \mathcal{M}_k could denote the mixture model with k components. In the case of variable selection in regression, \mathcal{M}_k could be a model for the conditional density of a continuous (regression with normal error) or discrete (multinomial regression) outcome Y , given a set of covariates Z , corresponding with a regression model $\mu_k(Z)$ for the conditional mean $E(Y \mid Z)$. Here k could index a particular set of variables in the regression model. Alternatively, in the regression context, k could index a forward selection algorithm $f_k(\cdot \mid P_n)$ applied to the empirical distribution P_n which stops after having selected k variables. For kernel density estimation, the parameter k could correspond to the bandwidth of the kernel density estimator.

Implicit in this selection problem is the notion of distance between two distributions. Here, we focus on the Kullback-Leibler divergence as a measure of distance between two densities. The Kullback-Leibler divergence between densities f and g is defined as

$$DKL(f, g) = \int \log \left(\frac{f(x)}{g(x)} \right) f(x) d\mu(x)$$

and has the following two basic properties: $DKL(f, g) \geq 0$ and $DKL(f, g) = 0$ if and only if $f = g$ a.s. Ideally, given P_n , one seeks $f_k(\cdot \mid P_n)$ that is closest

to the true f . With the Kullback-Leibler criterion, one would choose

$$\tilde{k}_n \equiv \min_{k \in \{1, \dots, K(n)\}}^{-1} DKL(f, f_k) = \min_{k \in \{1, \dots, K(n)\}}^{-1} - \int \log(f_k(x | P_n)) dP(x). \quad (1)$$

This selector, \tilde{k}_n , chooses the density closest to the true density for each given dataset. However, P is unknown. One could envisage using the empirical distribution, P_n , in place of the true P but this could lead to over-fitting. Instead, we turn to cross-validation. In this setting, the learning sample X_1, \dots, X_n is split (repeatedly) at random into two sets, a training set and a validation set. A density f_k is estimated for each $k \in \{1, \dots, K(n)\}$ using the training set only and the empirical distribution for the validation set is used in place of the true P in the distance criterion.

This article considers the class of likelihood-based cross-validation procedures in which the size of the validation samples converges to infinity with sample size, which thus excludes the leave-one-out scheme. We establish a finite sample result, which shows that, if the density is bounded away from zero and infinity, then the cross-validation selector for k performs as well as the benchmark selector \tilde{k}_n . We illustrate this asymptotic result and the practical performance of likelihood-based cross-validation for the purpose of bandwidth selection in kernel density estimation with a simulation study. Moreover, we apply likelihood-based cross-validation in the context of regulatory motif detection in DNA sequences. Our results complement the current literature on likelihood-based cross-validation, which has focussed on the computationally intensive leave-one out scheme. For example, (Stone, 1984; Hall, 1987) provide asymptotic optimality results for leave-one-out cross-validation.

We will now provide an overview of the previous work on likelihood-based cross-validation. Leave-one-out likelihood cross-validation in density estimation is discussed in Silverman (1986) who refers to Stone (1974a) and Geisser (1975) for its general applicability to model fitting as well. Silverman (1986) refers to Scott & Factor (1981) to indicate that for densities with infinite support this leave-one-out likelihood cross-validation method for bandwidth selection in density estimation is sensitive to outliers, and to Schuster & Gregory (1981) to point out that leave-one-out cross-validation can result, in fact, into inconsistent density estimators under non-pathological conditions. Stone (1984) provides an asymptotically optimal bandwidth selection rule for kernel density estimation, which has a leave-one-out cross-validation interpretation. Moreover, Hall (1987) investigates the leave-one-out cross-

validation with Kullback-Leibler loss in the context of nonparametric kernel density estimation and shows that its asymptotic properties are affected by tail probabilities of the kernel and of the unknown density with infinite support. Hall (1987) also shows that if the kernel is chosen appropriately, then the leave-one-out likelihood-based cross-validation asymptotically minimizes the Kullback-Leibler loss.

Recent work on (V -fold or Monte-Carlo) cross-validated likelihood methods for choosing the number of components in mixture models is found in Smyth (2000) and Pavlic & van der Laan (2003). In particular, the simulation studies of Pavlic & van der Laan (2003) showed that likelihood-based cross-validation performed well compared to common approaches based on validity functionals such as Akaike's information criterion (Akaike (1973), Bozdogan (2000)), Bayesian Information criterion BIC (Schwartz (1978)) or Minimum description length (Rissanen (1978), see Hansen & Yu (2001), for an overview) and ICOMP (Bozdogan (1993)).

Likelihood-based cross-validation covers in particular squared error-loss cross-validation for prediction. Specifically, let \mathcal{M}_k be a regression model $Y = \mu_k(Z) + N(0, \sigma^2)$, with μ_k ranging over a family of curves indexed by k , and let $f_k(X | P_n)$ be the corresponding (least squares estimator (i.e., maximum likelihood estimator) . There is a rich literature on leave-one-out cross-validation in nonparametric univariate regression. For example, Silverman (1984) proposes a fast approximation of the leave-one-out cross-validation method in spline regression. We refer to Härdle (1993) for an overview on the leave-one-out cross-validation method in kernel regression. In particular, Härdle & Marron (1985a) and Härdle & Marron (1985b) prove that leave-one-out cross-validation is asymptotically optimal for choosing the smoothing parameter in nonparametric kernel regression (see page 158, Härdle (1993)). In the general prediction literature involving covariate and model selection cross-validation is commonly used for estimation of the risk for squared error loss (e.g., Breiman et al. (1984), Breiman (1996), Burman (1989), Shao (1993), Zhang (1993)), Hastie et al. (2001), Ripley (1996), Stone (1974b), Stone (1977)). The main procedures include: leave-one-out cross-validation, V -fold cross-validation (i.e., random division of the learning set into V mutually exclusive and exhaustive sets), Monte Carlo cross-validation (i.e., repeated random splits of the learning set into a training and a validation set), and the bootstrap. Györfi et al. (2002) recently proved that for bounded outcomes, the single-split cross-validation for the squared error loss function is asymptotically optimal in selecting predictors based on the training sample

in the same sense as in our Theorem 1 below.

2 Method and Results

2.1 Framework.

To formalize the cross-validated likelihood method, we introduce a binary random vector $S_n \in \{0, 1\}^n$, independent of P_n . A realization of S_n defines a particular split of the sample of n observations into a training sample $\{i \in \{1, \dots, n\} : S_n(i) = 0\}$ and a validation sample $\{i \in \{1, \dots, n\} : S_n(i) = 1\}$. Let P_{n,S_n}^1, P_{n,S_n}^0 be the empirical distributions of the validation and training samples, respectively. Let the proportion $p = \sum_{i=1}^n S_n(i)/n \in (0, 1)$ of observations in the validation sample be constant (but possibly depend on n). We define the cross-validated likelihood criterion as:

$$\hat{\theta}_{n(1-p)}(k) = -E_{S_n} \int \log(f_k(x | P_{n,S_n}^0)) dP_{n,S_n}^1(x).$$

This criterion defines an optimal choice \hat{k} given by

$$\hat{k} = \min_{k \in \{1, \dots, K(n)\}}^{-1} \hat{\theta}_{n(1-p)}(k).$$

We note that different choices of the random variable S_n cover many types of cross-validation such as V -fold cross-validation, Monte-Carlo (repeated random splits) cross-validation, and resampling (bootstrap) cross-validation. The latter corresponds with resampling n observations with replacement from the original data set and setting $S_{n,i}$ equal to the number of times the observation i is sampled. In this case, P_{n,S_n}^0, P_{n,S_n}^1 denote the empirical distributions of the resampled observations, and the excluded observations, respectively. Our proof of Theorem 1 below straightforwardly generalizes to random p , and therefore our results apply to bootstrap cross-validation as well.

To obtain a benchmark for the selected \hat{k} we also define

$$\tilde{\theta}_{n(1-p)}(k) = -E_{S_n} \int \log(f_k(x | P_{n,S_n}^0)) dP(x)$$

and its minimizer

$$\tilde{k} = \min_{k \in \{1, \dots, K(n)\}}^{-1} \tilde{\theta}_{n(1-p)}(k).$$

Note that \tilde{k} corresponds to an optimal selector since it indexes the minimizer over k of the expectation over S_n of the Kullback-Leibler distance of the

density estimator $f_k(\cdot \mid P_{n,S_n}^0)$ based on the training sample to the true distribution P :

$$k \rightarrow E_{S_n} \int \log \left(\frac{f(x)}{f_k(x \mid P_{n,S_n}^0)} \right) dP(x).$$

If necessary, we will also refer to \tilde{k} as $\tilde{k}_{n(1-p)}$ to distinguish it from the minimizer \tilde{k}_n for the whole sample of n observations, as defined in (1), of

$$k \rightarrow \tilde{\theta}_n(k) = - \int \log(f_k(x \mid P_n)) dP(x).$$

The theorem below shows that asymptotically, the cross-validation selector \hat{k} performs as well as the optimal benchmark selector $\tilde{k}_{n(1-p)}$ in the sense that the ratio $(E\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}) / (E\tilde{\theta}_{n(1-p)}(\tilde{k}_{n(1-p)}) - \theta_{opt})$ of mean conditional Kullback-Leibler distances converges to 1. The theorem implies also an interesting result for the Hellinger distance between $f_{\hat{k}}(\cdot \mid P_{n(1-p)})$ and the true density f since the Kullback-Leibler distance bounds, in particular, the Hellinger distance (see e.g. van der Vaart (1998), page 62):

$$\int (\sqrt{f}(x) - \sqrt{g}(x))^2 d\mu(x) \leq \int \log \left(\frac{f(x)}{g(x)} \right) f(x) d\mu(x).$$

Finally, we define the minimum of $g \rightarrow - \int \log(g(x)) dP(x)$ among all densities g :

$$\theta_{opt} = - \int \log(f(x)) dP(x).$$

Note that $\tilde{\theta}_{n(1-p)}(\hat{k}) \geq \tilde{\theta}_{n(1-p)}(\tilde{k}) \geq \theta_{opt}$.

Before we state the theorem we will present two regression examples. We refer to our simulation study in section 3 for a detailed treatment of a bandwidth selection example in kernel density estimation.

Example 1 (Regression for continuous outcome) Suppose $X = (Y, Z)$, where Y is a continuous outcome and Z is a vector of covariates. Given a regression model $\mu_k(Z \mid \beta_k)$ for the conditional mean $E(Y \mid Z)$, let

$$\mathcal{M}_k = \left\{ f_k(Y; Z \mid \beta_k) = \frac{1}{\sqrt{2\pi}\sigma^2} \exp \left(-\frac{(Y - \mu_k(Z \mid \beta_k))^2}{2\sigma^2} \right) : \beta_k \right\}$$

be the Gaussian regression model for the conditional density of Y , given Z : that is, $Y = \mu_k(Z \mid \beta_k) + N(0, \sigma^2)$. Suppose $f_k(\cdot \mid P_n) = f_k(\cdot \mid \beta_k(P_n))$

is the maximum likelihood estimator according to this model, where $\beta_k(P_n)$ is the corresponding maximum likelihood estimator of β_k . Then $\beta_k(P_n) = \min_{\beta_k}^{-1} \sum_{i=1}^n (Y_i - \mu_k(Z_i | \beta_k))^2$ is the least squares estimator. In addition, we have that up till a multiplicative and additive constant

$$\hat{\theta}_{n(1-p)}(k) = E_{S_n} \int (y - \mu_k(z | \beta_k(P_{n,S_n}^0)))^2 dP_{n,S_n}^1(y, z)$$

is the standard residual sum of squares of the predictor $\mu_k(z | \beta_k(P_{n,S_n}^0))$ based on the training sample over the validation sample, averaged across all S_n -specific sample splits. Consequently, $\hat{k} = \min_k^{-1} \hat{\theta}_{n(1-p)}(k)$ denotes the squared-error loss cross-validation selector. Finally, we note that up till a multiplicative and additive constant

$$\tilde{\theta}_{n(1-p)}(k) = E_{S_n} \int (y - \mu_k(z | \beta_k(P_{n,S_n}^0)))^2 dP(y, z)$$

is the average over S_n of the true conditional risk of the predictor $\mu_k(z | \beta_k(P_{n,S_n}^0))$ based on the S_n -specific training sample, so that \tilde{k} indexes the predictor with minimal true conditional risk.

Example 2 (Logistic regression) Suppose $X = (Y, Z)$, where Y is a Bernoulli random variable, Z is a vector of covariates. Given a regression model $\mu_k(Z | \beta_k)$ for the conditional mean $E(Y | Z) = P(Y = 1 | Z)$, let

$$\mathcal{M}_k = \left\{ f_k(Y; Z | \beta_k) = \mu_k(Z | \beta_k)^Y \{1 - \mu_k(Z | \beta_k)\}^{1-Y} : \beta_k \right\}.$$

Suppose $f_k(\cdot | P_n) = f_k(\cdot | \beta_k(P_n))$ is the maximum likelihood estimator according to this model, where $\beta_k(P_n)$ is the corresponding maximum likelihood estimator of β_k . In this case $\hat{\theta}_{n(1-p)}(k)$ equals

$$E_{S_n} \int y \log\{\mu_k(z | \beta_k(P_{n,S_n}^0))\} + (1 - y) \log\{1 - \mu_k(z | \beta_k(P_{n,S_n}^0))\} dP_{n,S_n}^1(y, z)$$

and $\tilde{\theta}_{n(1-p)}(k)$ equals

$$= E_{S_n} \int y \log\{\mu_k(z | \beta_k(P_{n,S_n}^0))\} + (1 - y) \log\{1 - \mu_k(z | \beta_k(P_{n,S_n}^0))\} dP(y, z).$$

2.2 Finite sample result and asymptotic implications.

We will now present our main result.

Theorem 1 Suppose that there exist $\epsilon > 0$ and $L < \infty$ so that $\epsilon < f_k(X | P_n) < L$ a.s. for all $k \in \{1, \dots, K(n)\}$. Let $M_1 = 2\log(L/\epsilon)$ and $M_2 = 4L/\epsilon$. For any $\delta > 0$ we have

$$E\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt} \leq (1+2\delta) \left\{ E\tilde{\theta}_{n(1-p)}(\tilde{k}) - \theta_{opt} \right\} + 2c(M_1, M_2, \delta) \frac{1 + \log(K(n))}{np},$$

where

$$c(M_1, M_2, \delta) = 2(1 + \delta)^2 \left(\frac{M_1}{3} + \frac{M_2}{\delta} \right).$$

This finite sample result has the following asymptotic implications: If

$$\frac{\log(K(n))}{(np)\{E\tilde{\theta}_{n(1-p)}(\tilde{k}) - \theta_{opt}\}} \rightarrow 0 \text{ for } n \rightarrow \infty, \quad (2)$$

then

$$\frac{E\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}{E\tilde{\theta}_{n(1-p)}(\tilde{k}) - \theta_{opt}} \rightarrow 1 \text{ for } n \rightarrow \infty.$$

Similarly, if

$$\frac{\log(K(n))}{(np)\{\tilde{\theta}_{n(1-p)}(\tilde{k}) - \theta_{opt}\}} \rightarrow 0 \text{ in probability for } n \rightarrow \infty, \quad (3)$$

then

$$\frac{\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}{\tilde{\theta}_{n(1-p)}(\tilde{k}) - \theta_{opt}} \rightarrow 1 \text{ in probability for } n \rightarrow \infty.$$

The final convergence in probability statement follows from the fact that, given a sequence of random variables X_1, X_2, \dots , $E | X_n | = O(g(n))$ for a positive function $g(n)$ implies $X_n = O_P(g(n))$, which itself is a direct consequence of Markov's inequality. We note that our conditions for the asymptotic optimality statements exclude leave-one-out cross-validation, since it is required that the validation sample size np converges to infinity.

2.3 Asymptotic equivalence with the optimal benchmark selector

Theorem 1 provides a finite sample bound for the expected value of $\tilde{\theta}_{n(1-p)}(\hat{k}) - \tilde{\theta}_{n(1-p)}(\tilde{k})$, which compares the performance of the cross-validated selector \hat{k} to the benchmark \tilde{k} in terms of the conditional Kullback-Leibler distances. $\tilde{\theta}_{n(1-p)}(k)$ based on $n(1-p)$ training observations. This bound is used to prove that the ratio $(\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt})/(\tilde{\theta}_{n(1-p)}(\tilde{k}) - \theta_{opt})$ converges to one in probability, or equivalently $\tilde{\theta}_{n(1-p)}(\hat{k}) - \tilde{\theta}_{n(1-p)}(\tilde{k})/(\tilde{\theta}_{n(1-p)}(\tilde{k}) - \theta_{opt})$ converges to zero in probability.

However, one would like the cross-validated selector \hat{k} to perform as well as a benchmark selector \tilde{k}_n based on the whole sample of size n , rather than only $n(1-p)$ as above. The following is an immediate corollary of Theorem 1, which relates $\tilde{\theta}_{n(1-p)}(\hat{k})$ to that of a benchmark selector based on n observations, $\tilde{\theta}_n(\tilde{k}_n)$. In this corollary, we use the notation $p = p_n$ to emphasize the dependence of the validation set proportion p on n . It shows that if $p = p_n$ converges slowly enough to zero when the sample size n converges to infinity, then, given a mild condition (4) below, the wished asymptotic optimality of the selector \hat{k} follows.

Corollary 1 *Suppose that there exist $\epsilon > 0$ and $L < \infty$ so that $\epsilon < f_k(X | P_n) < L$ a.s. for all $k \in \{1, \dots, K(n)\}$.*

If $p = p_n \rightarrow 0$, (3) holds, and for $n \rightarrow \infty$

$$\frac{\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}}{\tilde{\theta}_{n(1-p_n)}(\tilde{k}_{n(1-p_n)}) - \theta_{opt}} \rightarrow 1 \quad \text{in probability} \quad (4)$$

then

$$\frac{\tilde{\theta}_{n(1-p_n)}(\hat{k}) - \theta_{opt}}{\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}} \rightarrow 1 \quad \text{in probability.} \quad (5)$$

A sufficient condition for (4) to hold is that

$$\left(n^\gamma (\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}), (n(1-p_n))^\gamma (\tilde{\theta}_{n(1-p_n)}(\tilde{k}_{n(1-p_n)}) - \theta_{opt}) \right) \xrightarrow{D} (Z, Z)$$

for some $\gamma > 0$ and random variable Z with $\Pr(Z > a) = 1$ for some $a > 0$. In particular, if $\Pr(S_n = s) = 1$ for some $s \in \{0, 1\}^n$ (i.e., single split cross-validation), then it suffices to assume $n^\gamma (\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}) \xrightarrow{D} Z$ for some $\gamma > 0$ and $\Pr(Z > a) = 1$ for some $a > 0$.

Proof of Corollary. Firstly, note that

$$\frac{\tilde{\theta}_{n(1-p_n)}(\hat{k}) - \theta_{opt}}{\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}} \frac{\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}}{\tilde{\theta}_{n(1-p_n)}(\tilde{k}_{n(1-p_n)}) - \theta_{opt}} \rightarrow 1$$

by Theorem 1. This proves the first statement of the corollary. We now show that (4) holds under the given sufficient condition. Define

$$\begin{aligned} Z_{1,n} &= n^\gamma (\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}) \\ Z_{2,n} &= (n(1-p_n))^\gamma (\tilde{\theta}_{n(1-p_n)}(\tilde{k}_{n(1-p_n)}) - \theta_{opt}) \end{aligned}$$

If $(Z_{1,n}, Z_{2,n}) \xrightarrow{D} (Z, Z)$ then by the continuous mapping theorem we have $\frac{Z_{1,n}}{Z_{2,n}} \rightarrow 1$. However, note that

$$\frac{Z_{1,n}}{Z_{2,n}} = \frac{1}{(1-p_n)^\gamma} \frac{\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}}{\tilde{\theta}_{n(1-p_n)}(\tilde{k}_{n(1-p_n)}) - \theta_{opt}}.$$

Thus, if $p_n \rightarrow 0$, then we have

$$\frac{\tilde{\theta}_n(\tilde{k}_n) - \theta_{opt}}{\tilde{\theta}_{n(1-p_n)}(\tilde{k}_{n(1-p_n)}) - \theta_{opt}} \rightarrow 1,$$

and thus (4) holds. If there is only one split i.e. $P(S_n = s) = 1$ for some s , then $Z_{1,n} = Z_{2, \frac{n}{1-p_n}}$, and hence $Z_{1,n} \xrightarrow{D} Z$ implies $(Z_{1,n}, Z_{2,n}) \xrightarrow{D} (Z, Z)$. This completes the proof. \square

An important and practical issue is the impact of the cross-validation proportion p on the estimators $\tilde{\theta}_{n(1-p)}(k)$ in relation to $\tilde{\theta}_n(k)$. The following discussion provides some intuition regarding the behavior of $\tilde{\theta}_{n(1-p)}(k)$ compared to $\tilde{\theta}_n(k)$ for a density estimator $f_k(\cdot | P_n)$ based on the entire empirical distribution P_n . One can argue that, due to the expectation w.r.t. S_n in the definition of $\tilde{\theta}_{n(1-p)}(k)$, for each fixed $p \in (0, 1)$, the first order linear approximation of $\tilde{\theta}_{n(1-p)}(k) - \tilde{\theta}_n(k)$ equals zero. This is formalized by the following argument. Let $\theta_k = -\int \log(f_k(x | P))dP(x)$ be the parameter corresponding with the "estimator" $\tilde{\theta}_n(k) = \int \log(f_k(x | P_n))dP(x)$. Suppose

$$\tilde{\theta}_n(k) - \theta_k = \frac{1}{n} \sum_{i=1}^n IC_k(X_i | P) + R_k(P_n, P)$$

for some function $IC_k(\cdot | P)$ of X and remainder term $R_k(P_n, P)$. Application of this expansion to $\int \log(f_k(x | P_{n,S_n}^0))dP(x)$ and taking the expectation w.r.t. S_n yields

$$\tilde{\theta}_{n(1-p)}(k) - \theta_k = E_{S_n} \frac{1}{n(1-p)} \sum_{i=1}^n IC_k(X_i | P) I(S_n(i) = 0) + E_{S_n} R_k(P_{n,S_n}^0, P).$$

Now, we note that, the first term on the right-hand side actually equals $\frac{1}{n} \sum_{i=1}^n IC_k(X_i | P)$. Consequently,

$$\tilde{\theta}_n(k) - \tilde{\theta}_{n(1-p)}(k) = R_k(P_n, P) - E_{S_n} R_k(P_{n,S_n}^0, P).$$

In words, the difference between $\tilde{\theta}_n(k)$ and $\tilde{\theta}_{n(1-p)}(k)$ is driven by the second order terms. Due to this fact, that is, even for a fixed $p \in (0, 1)$, $\tilde{\theta}_{n(1-p)}(k)$ can be viewed as a decent approximation of $\tilde{\theta}_n(k)$, one expects that the sensitivity of the likelihood cross-validation selector $\hat{k}(p)$ to the choice of p (i.e., the choice of distribution for S_n), is significantly less than it would be for single split cross-validation.

In fact, in our bandwidth selection simulation study we have the remarkable practical result that, for each choice of V defining the V -fold likelihood-based cross-validation procedure (e.g., $V = 2$, which corresponds with $p = 0.5$), $(E\tilde{\theta}_n(\hat{k}) - \theta_{opt}) / (E\tilde{\theta}_n(\hat{k}_n) - \theta_{opt}) \approx 1$ for large sample size.

3 Simulation for bandwidth selection

3.1 Fixed p optimality result.

In this subsection, we illustrate the result of Theorem 1 in the context of kernel density estimation with a simulation study. In particular, the studied likelihood-based cross-validation method is used to choose the optimal bandwidth in a density estimation problem using a gaussian kernel. The gaussian kernel density estimate for a sample x_1, \dots, x_n is given by

$$\hat{f}_b(x) = \frac{1}{nb} \sum_{i=1}^n K\left(\frac{x - x_i}{b}\right),$$

where $K(\cdot)$ is the standard normal density function and b is the bandwidth of this kernel. We generated 20 replicate data sets from the standard normal

distribution enforcing the compact support in the interval $[-2, 2]$ at each of the following six samples sizes: $n = 50, 100, 200, 400, 800, 1600$. $K(n) = 100$ different bandwidth values b are generated from the interval $[0.02, 2]$ so that the difference between any two consecutive bandwidth values is 0.02. We set the proportion of the validation set to $p = 0.1$ and perform 10-fold likelihood-based cross-validation to select the optimal bandwidth. For this choice of the kernel, the integral θ_{opt} is given by

$$\theta_{opt} = - \int_{-2}^2 \log \left(\frac{\phi(x)}{\Phi(2) - \Phi(-2)} \right) \frac{\phi(x)}{\Phi(2) - \Phi(-2)} dx$$

where $\phi(x)$ and $\Phi(x)$ denote the density and the cumulative distribution function of the standard normal distribution, respectively. We performed the simulations in R and used the R-function `integrate()` to compute θ_{opt} and $\tilde{\theta}_{n(1-p)}(\cdot)$ with numerical integration. Figure 1 shows the ratio $\frac{\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}{\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}$ for each of the 20 replicate data sets at each of the six sample sizes. As predicted by Theorem 1, we observe from this plot that this ratio converges to 1 in probability as n increases. In Table 1 we report $\frac{\hat{E}\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}{\hat{E}\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}$ at each sample size where $\hat{E}\tilde{\theta}_n(\cdot)$ is the averaged $\tilde{\theta}_n(\cdot)$ over 20 replicate data sets.

n	50	100	200	400	800	1600
$\frac{\hat{E}\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}{\hat{E}\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}$	1.542497	1.400015	1.150882	1.139386	1.068780	1.033064

Table 1: $\frac{\hat{E}\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}{\hat{E}\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}$ based on 20 replicate data sets at each of the six different sample sizes.

To visualize this convergence result for a single data set as its size increases, we plot in Figure 2 the true density versus the kernel density estimate using the bandwidth selected by the likelihood-based cross-validation method.

3.2 Sensitivity to p .

In this subsection we investigate the effect of p with a simulation. We have

$$\hat{k}(p) = \min_{k \in \{1, \dots, K(n)\}}^{-1} \hat{\theta}_{n(1-p)}(k),$$

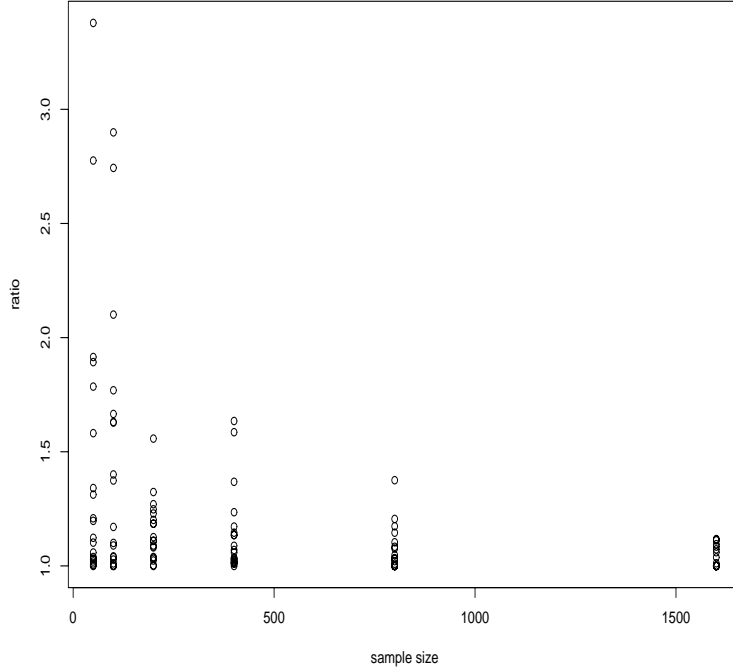


Figure 1: *Illustration of $\frac{\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}}{\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt}} \rightarrow 1$* : The ratios corresponding to various sample sizes are reported for 20 replicate data sets.

for a given p . For the k -th bandwidth value b_k the true conditional risk based on n observations is given by

$$\tilde{\theta}_n(k) = - \int \log \hat{f}_{b_k}(x) f(x) dx,$$

where the kernel density estimate $\hat{f}_{b_k}(x)$ uses all of the n observations. Then, $\hat{k}(p)$ for $p \in \{0.05, 0.1, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 0.45, 0.5\}$ are computed for 20 replicate data sets at each of the six different sample sizes: $n = 50, 100, 200, 400, 800, 1600$. Note that each choice of p corresponds to approximately a $1/p$ -fold cross validation scheme. Table 2 reports $\frac{\hat{E}\tilde{\theta}_n(\hat{k}(p)) - \theta_{opt}}{\hat{E}\tilde{\theta}_n(\hat{k}) - \theta_{opt}}$ based on 20 replicate data sets at each of the six different sample sizes. It is evident from this table that the likelihood-based cross-validation procedure is performing

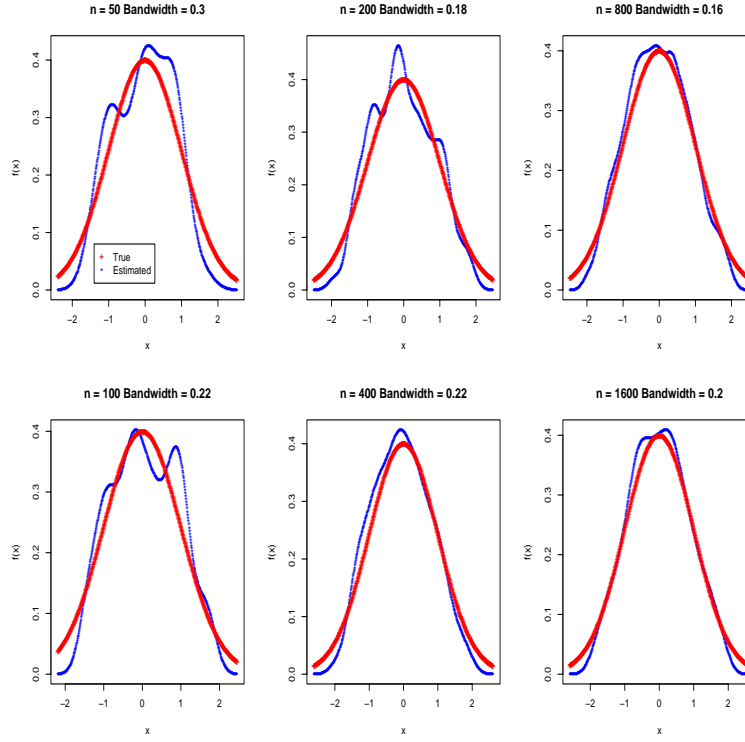


Figure 2: *True density versus estimated density based on a single data set:* The optimal bandwidth is selected by the 10-fold likelihood-based cross validation.

	n					
p	50	100	200	400	800	1600
1/ N	1.505519	1.490396	1.155552	1.165543	1.079040	1.049859
0.05	1.493594	1.465201	1.168274	1.115338	1.089441	1.047685
0.1	1.531736	1.391971	1.144236	1.136916	1.075563	1.048454
0.15	1.577241	1.473550	1.118831	1.117599	1.076197	1.061919
0.20	1.518429	1.417260	1.120498	1.100698	1.065835	1.064060
0.25	1.302580	1.443560	1.111674	1.182325	1.060759	1.100572
0.30	1.430726	1.388704	1.148916	1.119423	1.080356	1.083632
0.35	1.238741	1.414966	1.076628	1.093445	1.092477	1.112602
0.40	1.477980	1.617694	1.200306	1.123990	1.091412	1.091008
0.45	1.411283	1.483116	1.090528	1.142125	1.134810	1.143657
0.50	1.320979	1.398095	1.099359	1.136470	1.146952	1.167325

Table 2: *V-fold likelihood-based cross validation:* $\frac{\hat{E}\tilde{\theta}_n(\hat{k}(p)) - \theta_{opt}}{\hat{E}\theta_n(k) - \theta_{opt}}$ based on 20 replicate data sets at six different sample sizes for each $p \in \{0.05, 0.1, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 0.45, 0.5\}$. The first row reports the results for leave-one-out cross-validation.

equally well with any choice of p . The first row of Table 2 reports results for leave-one-out cross-validation. We observe that leave-one-out cross validation, which is computationally very intensive, is not performing better than the other cross-validation schemes. We also report the same quantity obtained performing likelihood based cross-validation with single split using various p -values in Table 3. As we commented in subsection 2.1, the likelihood-based cross-validation procedure with single split seems to be sensitive to the choice of p .

4 Application to regulatory motif detection in DNA sequences

Model selection is an important statistical topic in computational biology. It arises in problems such as microarray gene expression clustering, regulatory motif detection, linking microarray gene expression to clinical outcomes and single nucleotide polymorphism (SNP) analysis. One of the natural applica-

	n					
p	50	100	200	400	800	1600
0.05	21.778985	30.591547	5.366258	3.488738	2.147304	1.287172
0.1	4.969151	8.139912	3.709904	2.105173	1.948626	1.291611
0.15	1.972465	5.234631	2.283455	1.831317	1.628340	1.153562
0.20	1.836114	10.036376	2.465654	1.377272	1.370639	1.093183
0.25	2.495359	4.262036	1.246727	1.232388	1.209813	1.092931
0.30	2.260952	4.298054	1.410498	1.149826	1.215430	1.123646
0.35	1.553013	3.862468	1.511450	1.111143	1.165148	1.151871
0.40	1.446852	1.615702	1.276998	1.123451	1.146859	1.113719
0.45	1.583617	1.757668	1.263186	1.170124	1.112150	1.133443
0.50	1.333555	2.193936	1.258745	1.164263	1.149889	1.175700

Table 3: *Single split likelihood-based cross-validation:* $\frac{\hat{E}\tilde{\theta}_n(\hat{k}(p)) - \theta_{opt}}{\hat{E}\theta_n(k) - \theta_{opt}}$ based on 20 replicate data sets at six different sample sizes for each $p \in \{0.05, 0.1, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 0.45, 0.5\}$ using a single split.

tions of the likelihood-based cross-validation is the regulatory motif detection in DNA sequences. Regulatory motifs are short DNA segments (5-25 base pairs long) in the vicinity of the transcription start sites of the genes and they serve as attachment sites to transcription factors (DNA binding proteins). These elements have a crucial role in the regulation of gene expression. One of the challenging problems of computational biology is the identification of these short elements from a given set of sequences. Among the commonly used approaches is the modeling of the non-coding sequence data using a two component multinomial mixture model. In such models, the sites that do not contribute to the motif are assumed to be i.i.d with a multinomial distribution with 4 cell probabilities (corresponding to nucleotides A, C, G, T) and the sites that contribute to the motif are independent and have non-identical multinomial distributions. Such models represent the regulatory motifs by 4 by width of the motif matrix, called position weight matrix (PWM), where each column of the matrix has an independent multinomial distribution. We refer to Lawrence & Reilly (1990) and Bailey & Elkan (1994) for an introduction and overview of such models. The parameter estimation in these models is done with maximum likelihood estimation using the EM-algorithm (Dempster et al., 1977).

w	2-fold, $N = 20$	5-fold, $N = 20$	2-fold, $N = 100$	5-fold, $N = 100$
6	0	20	0	22
7	24	42	0	10
8	40	10	15	14
9	11	17	3	3
10	121	98	147	142
11	0	10	35	9
12	0	3	0	0
13	0	0	0	0
14	0	0	0	0
15	1	0	0	0

Table 4: *Simulations comparing 2-fold vs 5-fold likelihood-based cross-validation with sample sizes $N = 20$ and $N = 100$:* Number of simulations (out of 200) each width was selected in various fold-sample size setting. The true width is 10 base pairs, and each sequence is of length 600 base pairs.

In practice, using these models involve various model selection issues. Typically, the widths of the regulatory motifs (i.e. number of columns in the PWM) are unknown and variants of the simple two component mixture model might be appropriate. In the following subsections, we use likelihood-based cross-validation for motif width selection in the multinomial mixture models of the non-coding DNA sequences and illustrate its good performance by both simulations and real data analysis.

4.1 Simulation study

We have performed a simulation study to assess the practical performance of the likelihood-based cross validation in the mixture of multinomials context. The sequences are generated from a multinomial mixture model with i.i.d. background sites and a foreground site (motif site) of width 10 base pairs. Each sequence in the data set contains one copy of the motif. We estimate the model parameters using the EM-algorithm. We have tried a motif width range of $[6, 15]$ and selected among these widths using likelihood-based cross-validation. As cross-validation schemes, we used both 2-fold ($p = 0.5$) and 5-fold ($p = 0.2$) cross validation. Results of these simulations based on 200 replicates are summarized in Table 4 for different sample sizes. We observe

that 2-fold cross-validation performs well compared to 5-fold cross validation in selecting the correct motif width. We also observe that the over-fitting of the motif width is not an issue in the sense that cross-validation does not choose too wide of a motif. In general, estimation procedure in these mixture of multinomials is a time-wise expensive step. Hence observing that 2-fold cross validation performs well compared to 5-fold cross validation suggests using 2-fold cross-validation and saving computation time.

4.2 Data analysis

We have analyzed some of the transcription factor binding data of yeast by Simon et al. (2001) using a two component multinomial mixture model. These type of data sets are obtained with chromatin immunoprecipitation and microarray technology and are a good way of studying DNA-protein interactions and transcription regulation. Simon et al. (2001) data consist of genome-wide measurements for 9 of the transcription factors that take role in the transcription regulation of the cell cycle. For each transcription factor, we used the top 30 genes that have highest binding measurements and searched for motifs of width $[6, 15]$ in each of them. The motif width was selected by 2-fold likelihood-based cross-validation. The selected motif width agrees well with the motif width of the consensus reported in the literature (Spellman et al., 1998). In general, the overfitting and/or underfitting of the motif width is not larger than one base pairs. We refer to Keleş et al. (2003) for more applications of likelihood-based cross-validation in regulatory motif detection. In particular, Keleş et al. (2003) use likelihood-based cross-validation for both motif width selection and also motif structure selection.

5 Discussion

In this article 1) for a fixed $p \in (0, 1)$, we have established asymptotic equivalence of the likelihood cross-validation selector $\hat{k}(p)$ and the benchmark selector $\tilde{k}_{n(1-p)}$, and 2) for a sequence $p = p_n$ converging to zero slowly enough with sample size n , we showed asymptotic equivalence of $\hat{k}(p_n)$ and the optimal selector \tilde{k}_n . Here we use the notation $\hat{k}(p)$ to stress the dependence of the selector \hat{k} on p . We also argued, and illustrated this in our simulation study, that in many applications the asymptotic performance of $\hat{k}(p)$ for fixed p could be relatively insensitive to the choice p . Likelihood-based cross-

Factor	True Consensus	Consensus of the estimated PWM
Swi5	ACCAGC (6)	RCCAGCR (7)
Mbp1	ACGCGT (6)	ACGCGT (6)
Swi4	CACGAAA (7)	CACGAAAA (8)
Swi6	CGCGAAAA (8)	CGCGAAAA (8)
Mcm1	TTACCNAATTNGGTAA (16)	TTACCTAATTWGGT (14)

Table 5: *Analysis of the transcription factor binding data from Simon et al. (2001)*: The true consensus for each binding site is from Spellman et al. (1998). The width of each site is given in parenthesis. Estimated PWMs are converted to consensus sequences by reporting the most likely nucleotide at each position. The degenerate nucleotide representations are as follows: N={A,C,G,T}, W={A,T}, R={A,G}.

validation has many practical applications and regulatory motif detection in DNA sequences that we used in this paper is just one of them.

Appendix: Proof of Theorem 1

We have

$$\begin{aligned}
0 &\leq \tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt} \\
&= -E_{S_n} \int \log \left(\frac{f_{\hat{k}}(x \mid P_{n,S_n}^0)}{f(x)} \right) dP(x) \\
&= -E_{S_n} \int \log \left(\frac{f_{\hat{k}}(x \mid P_{n,S_n}^0)}{f(x)} \right) dP(x) \\
&\quad + (1 + \delta) E_{S_n} \int \log \left(\frac{f_{\hat{k}}(x \mid P_{n,S_n}^0)}{f(x)} \right) dP_{n,S_n}^1(x) \\
&\quad - (1 + \delta) E_{S_n} \int \log \left(\frac{f_{\hat{k}}(x \mid P_{n,S_n}^0)}{f(x)} \right) dP_{n,S_n}^1(x) \\
&\leq -E_{S_n} \int \log \left(\frac{f_{\hat{k}}(x \mid P_{n,S_n}^0)}{f(x)} \right) dP(x) \\
&\quad + (1 + \delta) E_{S_n} \int \log \left(\frac{f_{\hat{k}}(x \mid P_{n,S_n}^0)}{f(x)} \right) dP_{n,S_n}^1(x)
\end{aligned}$$

$$\begin{aligned}
& -(1 + \delta)E_{S_n} \int \log \left(\frac{f_{\tilde{k}}(x \mid P_{n,S_n}^0)}{f(x)} \right) dP_{n,S_n}^1(x) \\
& = -(1 + 2\delta)E_{S_n} \int \log \left(\frac{f_{\tilde{k}}(x \mid P_{n,S_n}^0)}{f(x)} \right) dP(x) + T_{n,\hat{k}} + R_{n,\tilde{k}},
\end{aligned}$$

where

$$\begin{aligned}
T_{n,k} &= (1 + \delta)E_{S_n} \int \log \left(\frac{f_k(x \mid P_{n,S_n}^0)}{f(x)} \right) d(P_{n,S_n}^1 - P)(x) \\
&\quad + \delta E_{S_n} \int \log \left(\frac{f_k(x \mid P_{n,S_n}^0)}{f(x)} \right) dP(x)
\end{aligned}$$

and

$$\begin{aligned}
R_{n,k} &= -(1 + \delta)E_{S_n} \int \log \left(\frac{f_k(x \mid P_{n,S_n}^0)}{f(x)} \right) d(P_{n,S_n}^1 - P)(x) \\
&\quad + \delta E_{S_n} \int \log \left(\frac{f_k(x \mid P_{n,S_n}^0)}{f(x)} \right) dP(x).
\end{aligned}$$

Thus

$$0 \leq E\tilde{\theta}_{n(1-p)}(\hat{k}) - \theta_{opt} \leq (1 + 2\delta)\{E\tilde{\theta}_{n(1-p)}(\tilde{k}) - \theta_{opt}\} + ET_{n,\hat{k}} + ER_{n,\tilde{k}}.$$

In the sequel we will show that $\max(ET_{n,\hat{k}}, ER_{n,\tilde{k}}) \leq c(M_1, M_2, \delta) \frac{1+\log(K(n))}{np}$, which then completes the proof of the finite sample statement. The asymptotic implications are direct corollaries of this finite sample result.

We represent $T_{n,k}$ and $R_{n,k}$ as $T_{n,k} = E_{S_n} T_{n,k}(S_n)$ and $R_{n,k} = E_{S_n} R_{n,k}(S_n)$, respectively. We introduce the following notation for the relevant random variables

$$\begin{aligned}
\tilde{H}_k &\equiv \int \log \left(\frac{f_k(x \mid P_{n,S_n}^0)}{f(x)} \right) dP(x) \leq 0 \\
\bar{H}_k &\equiv \int \log \left(\frac{f_k(x \mid P_{n,S_n}^0)}{f(x)} \right) dP_{n,S_n}^1(x).
\end{aligned}$$

Note that

$$\begin{aligned}
T_{n,k}(S_n) &= -(1 + \delta) [\tilde{H}_k - \bar{H}_k] + \delta \tilde{H}_k \\
R_{n,k}(S_n) &= -(1 + \delta) [\bar{H}_k - \tilde{H}_k] + \delta \tilde{H}_k.
\end{aligned}$$

This gives us for $s \geq 0$

$$\begin{aligned} Pr(T_{n,\hat{k}}(S_n) \geq s \mid P_{n,S_n}^0, S_n) &= Pr\left(-(\tilde{H}_{\hat{k}} - \bar{H}_{\hat{k}}) \geq \frac{1}{1+\delta} \{s - \delta \tilde{H}_{\hat{k}}\} \mid P_{n,S_n}^0, S_n\right) \\ &\leq K(n) \max_{k \in \{1, \dots, K(n)\}} Pr\left(-(\tilde{H}_k - \bar{H}_k) \geq \frac{1}{1+\delta} \{s - \delta \tilde{H}_k\} \mid P_{n,S_n}^0, S_n\right). \end{aligned}$$

Similarly,

$$\begin{aligned} Pr(R_{n,\tilde{k}}(S_n) \geq s \mid P_{n,S_n}^0, S_n) \\ \leq K(n) \max_{k \in \{1, \dots, K(n)\}} Pr\left((\tilde{H}_k - \bar{H}_k) \geq \frac{1}{1+\delta} \{s - \delta \tilde{H}_k\} \mid P_{n,S_n}^0, S_n\right). \end{aligned}$$

We now proceed bounding $Pr\left(\pm(\tilde{H}_k - \bar{H}_k) \geq \frac{1}{1+\delta} \{s - \delta \tilde{H}_k\} \mid P_{n,S_n}^0, S_n\right)$, by using Bernstein's inequality, which we state here as a lemma for ease of reference. A proof is given in Lemma A.2, p. 564 in Györfi et al. (2002).

Lemma 1 Bernstein's inequality. *Let Z_i , $i = 1, \dots, n$, be independent real valued random variables such that $Z_i \in [a, b]$ with probability one. Let $0 < \sum_{i=1}^n \text{VAR}(Z_i)/n \leq \sigma^2$. Then, for all $\epsilon > 0$,*

$$Pr\left(\frac{1}{n} \sum_{i=1}^n (Z_i - EZ_i) > \epsilon\right) \leq \exp\left(-\frac{1}{2} \frac{n\epsilon^2}{\sigma^2 + \epsilon(b-a)/3}\right).$$

This implies

$$Pr\left(\frac{1}{n} \left| \sum_{i=1}^n (Z_i - EZ_i) \right| > \epsilon\right) \leq 2 \exp\left(-\frac{1}{2} \frac{n\epsilon^2}{\sigma^2 + \epsilon(b-a)/3}\right).$$

Conditional on P_{n,S_n}^0, S_n , we consider the random variable

$$Z_k = -\log\left(\frac{f_k(X \mid P_{n,S_n}^0)}{f(X)}\right),$$

and let Z_{ki} , $i = 1, \dots, np$, be the np i.i.d. copies of Z_k corresponding to X_i , given $S_n(i) = 1$. Note that $\bar{H}_k = -1/np \sum_{i=1}^{np} Z_{ki}$ and $\tilde{H}_k = -E(Z_k \mid P_{n,S_n}^0, S_n)$ so that $\tilde{H}_k - \bar{H}_k = 1/np \sum_{i=1}^{np} Z_{ki} - E(Z_k \mid P_{n,S_n}^0, S_n)$ represents a centered empirical mean of i.i.d. random variables. We will apply Bernstein's inequality to this centered empirical mean and exploit the following special property of Z_k to obtain an $\exp(-nps/c)$ tail probability instead of the usual $\exp(-nps^2/c)$ for some $c < \infty$. This will show that the centered empirical mean converges at an np rate instead of the usual $(np)^{0.5}$.

Lemma 2 *We have*

$$\sigma_k^2 \equiv \text{VAR}(Z_k \mid P_{n,S_n}^0, S_n) \leq M_2 E(Z_k \mid P_{n,S_n}^0, S_n) = -M_2 \tilde{H}_k.$$

Proof of Lemma. Note $EZ_k^2 = \int \log^2(f_k(x)/f(x))f(x)d\mu(x)$ and $EZ_k = -\int \log(f_k(x)/f(x))f(x)d\mu(x)$, where we use the short-hand notation f_k for $f_k(\cdot \mid P_{n,S_n}^0)$. Firstly, (van der Vaart (1998), page 62) provides the following relation between the quadratic Hellinger distance and Kullback-Leibler distance for two densities f, g w.r.t. a dominating measure μ :

$$\int (\sqrt{g} - \sqrt{f})^2 d\mu \leq -\int \log(g/f) f d\mu.$$

This is shown as follows: Since $\log(x) \leq 2(\sqrt{x} - 1)$ we have

$$\begin{aligned} \int \log(g/f) f d\mu &\leq 2 \int (\sqrt{g/f} - 1) f d\mu \\ &= 2 \int \sqrt{g} \sqrt{f} d\mu - 2 \\ &= -\int (\sqrt{g} - \sqrt{f})^2 d\mu, \end{aligned}$$

where we used at the last equality that $-2 = -\int (\sqrt{f}^2 + \sqrt{g}^2) d\mu$. Secondly, we have

$$\int \log^2(g/f) f d\mu \leq 4 \left\| \frac{f}{\min(f, g)} \right\|_\infty \int (\sqrt{g} - \sqrt{f})^2 d\mu,$$

where the supremum is taken over a support of X . This is shown as follows: Applying $\log(x) \leq 2(\sqrt{x} - 1)$ to $\log(g/f)$ and $\log(f/g)$ yields:

$$|\log(g/f)| \leq 2 \frac{|\sqrt{f} - \sqrt{g}|}{\min(\sqrt{f}, \sqrt{g})}.$$

Thus

$$\int \log^2(g/f) f d\mu \leq 4 \left\| \frac{f}{\min(f, g)} \right\|_\infty \int (\sqrt{f} - \sqrt{g})^2 d\mu.$$

Combining the two inequalities proves the lemma. \square

We now proceed as follows. From Lemma 2 we have $-\tilde{H}_k \geq \sigma^2/M_2$, where $M_2 = 4L/\epsilon$. Thus,

$$\begin{aligned}
& Pr \left(-(\tilde{H}_k - \bar{H}_k) \geq \frac{1}{1+\delta} \left\{ s - \delta \tilde{H}_k \right\} \middle| P_{n,S_n}^0, S_n \right) \\
&= Pr \left(E(Z_k \mid P_{n,S_n}^0, S_n) - \frac{1}{np} \sum_{i=1}^n Z_{k,i} \geq \frac{1}{1+\delta} \left[s + \delta E(Z_k \mid P_{n,S_n}^0, S_n) \right] \middle| P_{n,S_n}^0, S_n \right) \\
&\leq Pr \left(E(Z_k \mid P_{n,S_n}^0, S_n) - \frac{1}{np} \sum_{i=1}^n Z_{k,i} \geq \frac{1}{1+\delta} \left[s + \delta \frac{\sigma_k^2}{M_2} \right] \middle| P_{n,S_n}^0, S_n \right) \\
&\leq \exp \left[-\frac{np}{2} \frac{1}{(1+\delta)^2} \frac{(s + \delta \sigma_k^2/M_2)^2}{\sigma_k^2 + \frac{M_1}{3(1+\delta)}(s + \delta \sigma_k^2/M_2)} \right],
\end{aligned}$$

where we applied Bernstein's inequality to the centered empirical mean $1/np \sum_i Z_{k,i} - E(Z_k \mid P_{n,S_n}^0, S_n)$, where we note that $|Z_k| < \log(L/\epsilon)$ so that we can set $b = a = M_1 = 2 \log(L/\epsilon)$. The same bound applies to $Pr \left((\tilde{H}_k - \bar{H}_k) \geq \frac{1}{1+\delta} \left\{ s - \delta \tilde{H}_k \right\} \middle| P_{n,S_n}^0, S_n \right)$.

We now note that for $s \geq 0$

$$\begin{aligned}
\frac{(s + \delta \sigma_k^2/M_2)^2}{\sigma_k^2 + \frac{M_1}{3(1+\delta)}(s + \delta \sigma_k^2/M_2)} &\geq \frac{(s + \delta \sigma_k^2/M_2)}{\frac{\sigma_k^2}{s + \delta \sigma_k^2/M_2} + \frac{M_1}{3}} \geq \frac{(s + \delta \sigma_k^2/M_2)}{\frac{M_2}{\delta} + \frac{M_1}{3}} \\
&\geq \frac{s}{\frac{M_2}{\delta} + \frac{M_1}{3}},
\end{aligned}$$

which is independent of k . This shows that

$$Pr(T_{n,\hat{k}}(S_n) \geq s \mid P_{n,S_n}^0, S_n) \leq K(n) \exp \left[-\frac{np}{c(M_1, M_2, \delta)} s \right]$$

with $c(M_1, M_2, \delta) = 2(1+\delta)^2(M_1/3 + M_2/\delta)$. The same bound applies to $Pr(R_{n,\hat{k}}(S_n) \geq s \mid P_{n,S_n}^0, S_n)$.

Since the bound is independent of P_{n,S_n}^0, S_n , this provides us also with

$$\begin{aligned}
Pr(T_{n,\hat{k}}(S_n) \geq s) &\leq K(n) \exp \left[-\frac{np}{c(M_1, M_2, \delta)} s \right] \\
Pr(R_{n,\hat{k}}(S_n) \geq s) &\leq K(n) \exp \left[-\frac{np}{c(M_1, M_2, \delta)} s \right].
\end{aligned}$$

Thus for each $u > 0$ we have

$$ET_{n,\hat{k}} = ET_{n,\hat{k}}(S_n)$$

$$\begin{aligned}
&\leq EI(T_{n,\hat{k}}(S_n) \geq 0)T_{n,\hat{k}}(S_n) \\
&= \int_0^\infty Pr(T_{n,\hat{k}}(S_n) > s)ds \\
&\leq u + \int_u^\infty K(n) \exp \left[-\frac{np}{c(M_1, M_2, \delta)}s \right] ds.
\end{aligned}$$

The minimum is attained at $u = c(M_1, M_2, \delta) \log(K(n))/np$ and is given by $c(M_1, M_2, \delta)(\log(K(n))+1)/np$. Similarly, $ER_{n,\hat{k}} \leq c(M_1, M_2, \delta)(\log(K(n))+1)/np$. This completes the proof of the theorem. \square

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