Combining Population Density Estimates in Line Transect Sampling Using the Kernel Method

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SUMMARY

Line transect methods that are "pooling robust" (Buckland et al, 1993;Burnham et al, 1980) allow data from different transects or locations to be pooled for estimation of population density. This is particularly important in situations where data from individual transects are sparse and pooling is done out of necessity. In this study we investigate a method for combining estimates from individual transects when each transect has sufficient data to support estimation with the kernel method. It is based on a minimizer of the asymptotic mean squared error of a linear combination of the individual population density estimators. The asymptotic mean squared error of the simple pooled estimator is always at least as large as the optimally combined estimator. We apply this combination to two estimates from data on a real population of mussels. Using a variety of simulations, we demonstrate the better finite sample efficiency for combining unbalanced cases. In practice, if the detection functions were identical, it can be better to pool; but the gains are modest. On the other hand, when the detection functions are different, it can be substantially better to combine. This recommends the new linear combination.

Key words: ecology, environmental survey, nonparametric, pooling

1. Introduction

Line transect sampling methods are commonly used by biologists to estimate population density. Here perpendicular distances from selected transect lines are used to construct an estimate of population density. This involves estimating the probability density of sighting distances on the transect line, i.e. at distance = 0. Recent work has focused on employing kernel methods to estimate the probability density (Mack and Quang, 1998; Chen, 1996). This method does not require a parametric form of the probability density to be specified, but does require specification of the amount of smoothing through a parameter often known as a bandwidth.

It has been suggested by some authors (Buckland et al, 1993; Burnham et al, 1980) that line transect estimators be "pooling robust." That is, the estimators should yield consistent estimates of population density when distances from different transects or groups of transects are pooled and treated as one dataset. This quality is especially pertinent in those situations where individual transects or naturally grouped transects do not yield sufficient sightings to provide adequate individual estimates. Hence the data are pooled out of necessity. In situations where individual transects have adequate data to form individual estimates, more efficient estimates may be formed by combining these estimators in some way other than simple pooling.

In this paper we propose and investigate an alternative method of combining kernel based population density estimates from different sources under the assumption that the underlying true population density is constant. The estimator is based on the minimizer of the asymptotic mean square error of a linear combination of the individual population density estimates and is similar in nature to the estimators studied in Gerard and Schucany (1996,1997) for combining nonparametric regression estimates. Different transect line lengths can be accommodated as can different detection functions, which is simply the probability of detecting on object as a function

of its distance from the transect line, so long as the probability of detection on the transect line is 1.0. Differences in detection functions could be caused by a variety of factors including differences in observers or weather conditions. For a good overview, see Buckland et al (1993). We now examine an actual ecological survey.

Consider distance data for a common species of mussels from two transects. The first transect was 42 meters in length and yielded distances for 53 mussels while the second was 52 meters in length and yielded 233 sighting distances. The data for each transect are displayed along the horizontal axes in Figure 1a and 1b, respectively, with the corresponding kernel density estimate of sighting distances. Each kernel estimate uses a quadratic weight function and global bandwidths of 25 and 15 centimeters, respectively. The goal is to combine the individual estimators based on these kernel estimators of probability density to form a single estimate of population density.

In Section 2 we will review kernel estimation of population density and describe the two estimators to be compared. We then evaluate the asymptotic relative efficiency of the optimally combined estimator to the pooled estimator by comparing their asymptotic mean squared errors. In Section 3, these two estimators are compared using Monte Carlo simulation techniques. We will revisit the example introduced in the previous paragraph in Section 4 and then provide some discussion in Section 5. Technical details about the estimators and a proof of a theorem concerning the dominance of the optimally combined estimator over the simple pooled estimator are in the Appendix.
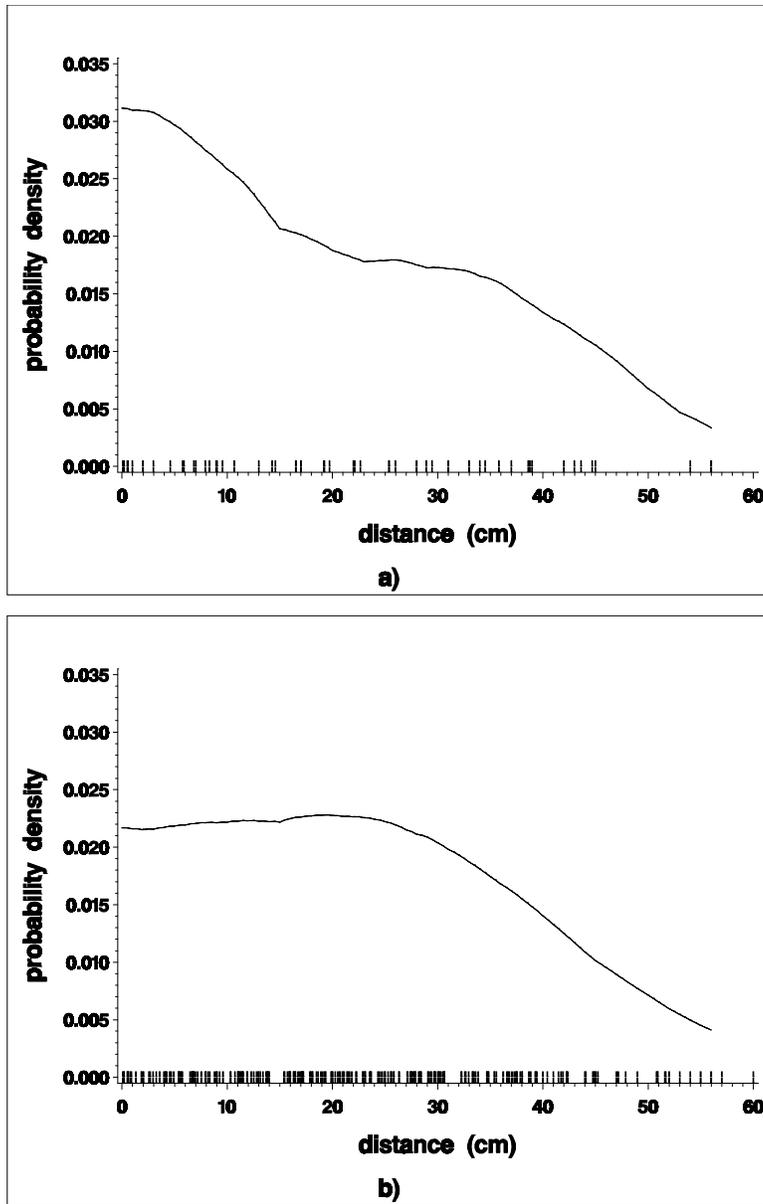
Figure 1. Estimated Kernel Densities of Sighting Distances of Mussel Line
Transect Sightings using Global Bandwidths of a) 25 centimeters and b) 15 centimeters
and the Quadratic Weight Function.

2. Kernel Estimation of Population Density

The typical estimate of population density is

$$\hat{D} = n\hat{f}(0)/(2L), \tag{2.1}$$

where n is the number of objects detected, L is the length of the transect line, and $\hat{f}(0)$ is an estimate of the probability density of perpendicular sighting distances evaluated right on the line.

For kernel estimates $\hat{f}(0) = n^{-1} \sum_{i=1}^{n} K_h^*(x_i)$, where h is a bandwidth that governs the amount of smoothness, x_i is the ith perpendicular distance from the object to the transect line, and $K_h^*(u) = h^{-1} K^*(u/h)$ is a kernel function adapted for estimation at the edge of a region, so that $K^*(\cdot) = 2K(\cdot)$. Here $K(\cdot)$ is a symmetric kernel function as in Silverman (1986) or Wand and Jones (1995).

In most instances, distance data are available from more than one transect or group of transects. Hence, the simple pooled estimator, $\hat{D}_p$, in the case where two transects are available is

$$\hat{D}_p = \sum_{i=1}^{2} \sum_{j=1}^{n_i} K_h^*(x_{ij}) \bigg/ \{2(L_1 + L_2)\}, \tag{2.2}$$

where n_i is the number of sightings for the ith transect, $i=1,2$; x_{ij} is the distance for the jth sighting in the ith group, $j=1 .. n_i$; and L_i is the transect length for the ith transect. Hence if we let $\hat{D}_i$ be the ith transect estimate as in (2.1), then $\hat{D}_p = p_L \hat{D}_1 + (1 - p_L)\hat{D}_2$, where $p_L = L_1/(L_1 + L_2)$. Note that the pooled estimator is a linear combination of the individual density estimates for each transect and that a single bandwidth is used for each individual estimator. The weighting factor involves only the length of the transect, with the longer transect receiving more weight. If the

detection function differs for the two transects, this estimator is not able to weight the individual estimators to account for this difference.

Evaluation of $\hat{D}_p$ and the estimator to be proposed here is facilitated by noting that the numerator of (2.1) is equivalent in form to an estimator of a varying Poisson intensity, λ, evaluated on the transect line (Diggle and Marron, 1985). Uniform true perpendicular distances of objects and the resulting uniform population density, μ_T, is a consequence of the underlying Poisson intensity of true distances being constant. Imperfect detection results in a non-constant Poisson intensity of sighting distances. As noted in Cowling, Hall, and Phillips (1996), consistent estimation of λ by $\hat{\lambda} = n\hat{f}(0)$ employing kernel methods requires that λ increase. In this application, the intensity of objects observed at a given distance is an increasing function of the length of the transect line, L. Hence it is natural that asymptotic arguments (as L increases) include the assumption that $\lambda = 2L\mu_T$, with μ_T the true underlying density to be estimated with $\hat{D}$. As with the intensity, the perceived population density, μ, is nonconstant.

The goal is to form a combined estimator, $\hat{D}_c$, as a weighted average of individual estimates of population density based on kernel methods,

$$\hat{D}_c = c\hat{D}_1 + (1-c)\hat{D}_2 . \tag{2.3}$$

Using $c = \tilde{c}$ and the bandwidths for the two estimators that minimize the asymptotic mean squared error of (2.3) yields the estimator $\hat{D}_{\tilde{c}}$. Details of the minimization can be found in the Appendix. The minimizing values for c (A.3) and the optimal bandwidths, (A.4) and (A.5), involve not only the lengths, L_i, but also the second derivatives of the perceived population densities, μ_i'', which depend on the respective detection functions. Extension to situations with more than two groups should be relatively straightforward.

It should be noted that if $\mu_1'' = \mu_2''$, then $\hat{D}_{\tilde{c}}$ is asymptotically equivalent to $\hat{D}_p$. However, if

the second derivatives differ, $\hat{D}_{\tilde{c}}$ weights the individual density estimates accordingly. For

example for equal transect lengths, if μ_2'' is large compared to μ_1'' the population density

estimate for the first transect is weighted more heavily. Hence, this estimator attempts to

simultaneously correct for differences in transect length and detection function. It should also be

noted that the bandwidths used, (A.4) and (A.5), yield density estimates for the two transects

with equal bias. Proof that this solution results in a local minimum asymptotic mean squared

error (A.2) follows from Theorem 1 of Gerard and Schucany (1996).

It can be shown that $AMSE\left(\hat{D}_{\tilde{c}}\right) \le AMSE\left(\hat{D}_p\right)$ (Theorem 1 in Appendix). A plot of the

asymptotic relative efficiency (*ARE*) of $\hat{D}_{\tilde{c}}$ relative to $\hat{D}_p$ is shown in Figure 2. The

$ARE = \left\{ AMSE\left(\hat{D}_p\right) / AMSE\left(\hat{D}_{\tilde{c}}\right) \right\}^{5/4}$ (see page 106, Wand and Jones, 1995) is evaluated as a

function of k_d in (A.5) and $k_L = L_1/L_2$. This plot provides contours of equal values of *ARE* in

increments of .2. It is evident from the plot that the effect due to differences in transect lengths

is not as pronounced as the effect due to differences in detection functions. For most values of

k_L, values of k_d between .4 and 1 yield *ARE* values less than 1.20. Values of k_d less than .2 yield

ARE values that increase sharply as k_d decreases. Of course in practice the weighting factors and

bandwidths involve quantities that are unknown and must be estimated. Hence, when adequate

sample sizes are available for each individual estimate, there is potential for greater efficiency by

combining rather than pooling. In Section 3 we compare the finite sample properties of these
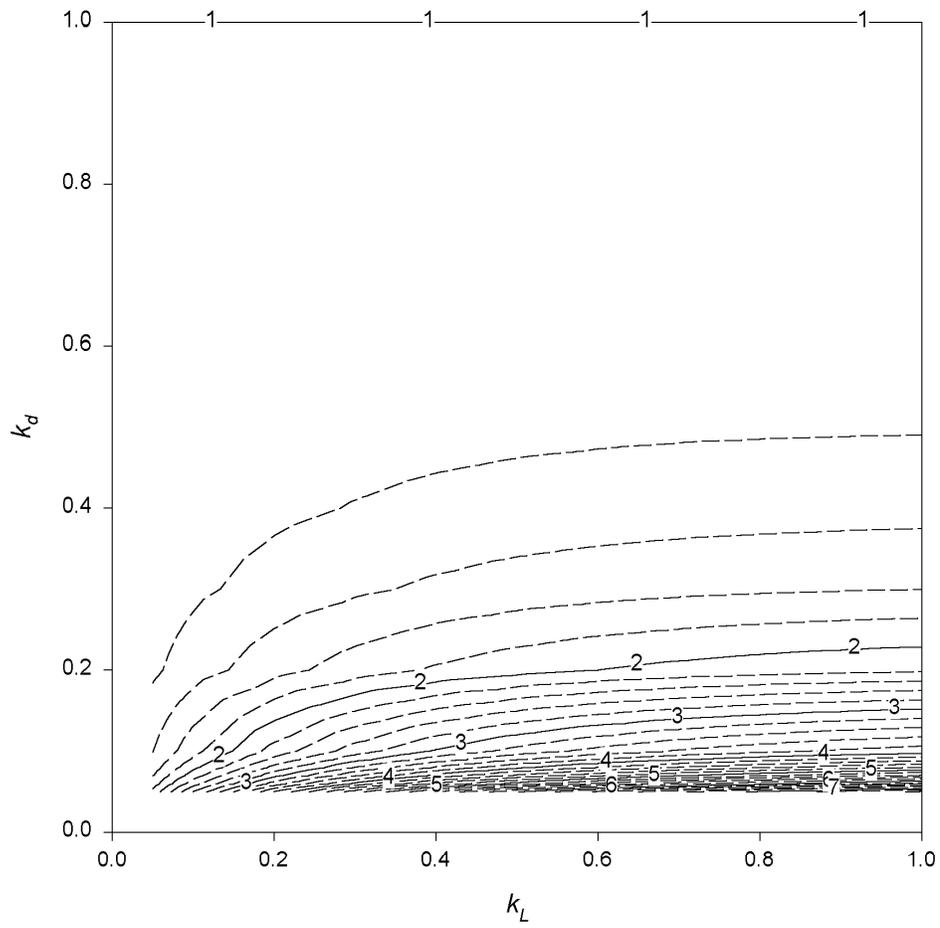
two estimators using Monte Carlo simulation.

Figure 2. Asymptotic Relative Efficiency of $\hat{D}_{\tilde{c}}$ relative to $\hat{D}_p$.

3. A Monte Carlo Comparison of $\hat{D}_p$ and $\hat{D}_{\tilde{c}}$

We investigated the finite-sample performance of these two estimators with a simulation study. The exponential power function, $g(x) = \exp\left\{-(bx)^a\right\}$, and a detection function based on the t distribution, $g(x) = \left(1 + x^2/k\right)^{-(k+1)/2}$ with $k = 4$, were used. These two functions adhere to the usual requirements for detection functions because they are nonincreasing and equal 1.0 at the origin. A population density of .15 was used in all simulation runs, with the length of the transect line and the number of objects placed in the study area altered to achieve this density. The effective width of the transect area was taken to be 10. The distances from the transect line for each object were independent uniform [0,10]. Next, objects were considered to be observed if the probability of detection, $g(x)$, at the generated distance was greater than an independent uniform [0,1]. Distances for two independent transect lines were generated, with possibly different detection functions and transect lengths. Five thousand replications were simulated under each set of conditions.

For each replication, both $\hat{D}_p$ and $\hat{D}_{\tilde{c}}$ were computed. In order to compute $\hat{D}_p$ as in (2.2), a single bandwidth was needed. Estimation of bandwidths for μ and μ_i'' is essentially equivalent to estimation of f and f_i'' (Diggle and Marron, 1985), as is evident from (2.1). The bandwidth used was a local normal scale rule that has been found to be as effective as (or even more than) some sophisticated local plug-in rules (Gerard and Schucany, 1999). For the local normal scale rule, the unknown quantities in the asymptotically optimal bandwidth are estimated by treating the underlying probability distribution of the sighting distances as the absolute value of a normal variable with mean zero. Hence, the bandwidth that is employed in estimation of f in the numerator of (2.1) treats the distances as absolute values of normal variables with mean zero.

Thus, one estimates σ^2 by $\hat{\sigma}^2 = n^{-1} \sum\limits_{i=1}^{n} x_i^2$, and substitutes this into either μ or μ_i'' in the

bandwidth estimator (Gerard and Schucany, 1999).

To compute $\hat{D}_{\tilde{c}}$, two bandwidths (A.4) and a weighting factor in (A.3) must be estimated.

Again, a normal scale rule was used to estimate the unknown quantities μ and μ_i''. Because we

have two sources to use when estimating μ in the bandwidth expressions, the normal scale

estimates from each source are averaged. It may also be noted that the normal scale rule

guarantees that our estimates of μ_i'' will have the same sign, as required for our asymptotic

results.

The results for ten combinations of n_i, L_i, and g_i are summarized in Table 1. For situations

where the estimators are asymptotically equivalent, where the detection functions are the same

for each transect, $\hat{D}_p$ performs better. Specifically, in Cases 1,2,4, and 7 the estimated

efficiencies range from 89% to 95% (similarly for Cases 3 and 5). It seems sensible to attribute

this penalty to the added variability due to estimation of the weighting factor (A.3). In Cases 6,

8, 9, and 10 the sizable improvements range from 1.22 to 1.60 to a dramatic case (8) in which

combining is 9 times more efficient. It follows that the new combination is the recommended

strategy, because these sizable payoffs are obtained for a small cost whenever pooling would

have been marginally better.

Table 1

Summary of Simulation Averages for Optimal and Pooled Estimators Based on 5000 Replications

	Transect 1			Transect 2			MSE x 10^4		
Case	g^1	L	n	g	**L**	n	$\hat{D}_c$	$\hat{D}_p$	**RE**^{2}
1	1	133	71	1	133	71	3.84	3.66	.94
2	1	133	71	1	67	35	4.76	4.53	.94
3	1	133	71	2	67	35	4.61	4.37	.94
4	2	67	36	2	67	36	6.08	5.84	.95
5	1	133	71	3	133	53	5.53	4.77	.83
6	4	133	35	1	133	71	4.97	5.81	1.22
7	4	133	35	4	67	18	9.06	8.29	.89
8	5	133	142	4	133	36	3.00	18.8	9.91
9	5	100	106	1	100	53	3.20	4.67	1.60
10	3	133	53	5	100	106	4.35	7.87	2.10

^{1}detection function, g =1 (Power(b=.5,a=2)), 2 (Power(b=.5,a=2.5)),
3 (t 4df), 4 (Power(b=1,a=1), 5 (Power(b=.25,a=2)).

^{2} Estimated Relative Efficiency, RE = $\left\{ MSE\left(\hat{D}_p\right) \middle/ MSE\left(\hat{D}_{\tilde{c}}\right) \right\}^{5/4}$

In the next section we will use these two methods to calculate the population density of mussels.

4. Application to estimation of mussel population density

Consider the data from two transects displayed in Figure 1. Using a normal scale rule as described in Section 3 for bandwidth selection, $\hat{D}_p$ yields an estimate of population density of .000352/cm^2. Individual density estimates using the optimal bandwidths (A.4) estimated analogously as in Section 3 were .000167/cm^2 using a bandwidth of 25 centimeters for the first transect and .000486 using a bandwidth of 15 centimeters for the second transect. Optimally combining them yields $\hat{D}_{\tilde{c}}$ = .000300/cm^2. The pooled estimator weighs the individual

estimators in a very similar fashion because the transect lengths are nearly the same (42 meters and 52 meters, respectively). The optimally combined estimator weighs the second individual estimator more heavily because there is less curvature in the probability density of sighting distances on the line and therefore a smaller second derivative.

5. Discussion

In this paper we presented an alternative to the usual simple pooled estimator. It can be used in situations where sufficient sightings are available for each transect to yield reasonable individual estimates of population density. It adapts to differences in transect length as well as differences in detection functions for the two transects. Simulation studies show that in some situations where asymptotic results would suggest similar efficiency of the pooled and optimally combined estimators, the pooled estimator typically performs a little better (5-10%). This is quite reasonably attributable to the increased variability due to estimation of second derivatives in the weighting factor and bandwidths. In those situations where the detection functions are quite different, gains from using the optimally combined estimator are evident. Therefore combining can pay a large dividend in return for a modest premium whenever pooling would have been better.

In addition to the application of our proposed estimator to estimation of population density from two transects when the underlying population density is assumed to be the same for each transect, it also has potential use in hypothesis testing. Mack and Quang (1998) showed that estimates of population density using the kernel method are asymptotically normal. For example it may be desirable to use kernel based estimates to test whether population density differs for two locations in a study area. It may not be reasonable to assume that the detection function is the same for each area. An estimate of the variance of the difference between independent

kernel estimates of population density under the null hypothesis of equal density requires that

one compute an estimate of density under that assumption. Our proposed estimator does just

that. It has the added benefit of providing bandwidths that yield individual estimates of equal

bias. Equal bias simplifies testing because the numerator of the test statistic involves forming a

difference between the estimated population densities for the two locations, which essentially

cancels the bias terms.

Acknowledgements

Appendix

It follows directly from Cowling, Hall, and Phillips (1996) that the asymptotic mean squared

error is

$$AMSE\left[\hat{D}_p\right] = (1/4)k_2^{*2}h^4\{p_L\mu_1'' + (1 - p_L)\mu_2''\}^2 + \mu_T Q^* \big/ \{2(L_1 + L_2)h\}, \tag{A.1}$$

where $k_2^* = \int_0^\infty u^2 K^*(u)du$ and $Q^* = \int_0^\infty K^{*2}(u)du$. The first term in (A.1) is the squared

asymptotic bias and the second is the asymptotic variance. Although the underlying density, μ_T,

is assumed to be the same for each transect line, differing detection functions result in different

second derivatives, μ_i''. Differentiating (A.1) with respect to h leads to an asymptotically

optimal bandwidth. Substitution into (A.1) results in the minimum *AMSE* for $\hat{D}_p$, which is used

in Asymptotic Relative Efficiency (*ARE*) evaluations for Figure 2.

Suppose we now consider a general convex linear combination in (2.3) $\hat{D}_c = c\hat{D}_1 + (1-c)\hat{D}_2$

(0<c<1). The corresponding asymptotic mean squared error is

$$AMSE(\hat{D}_c) = (1/4)\{c(\mu_1'' h_1^2 k_2^*) + (1-c)(\mu_2'' h_2^2 k_2^*)\}^2 + \frac{c^2 \mu_T Q^*}{2L_1 h_1} + \frac{(1-c)^2 \mu_T Q^*}{2L_2 h_2}. \quad (A.2)$$

Define $\mu_c = \sqrt{\mu_2''/\mu_1''}\,\mu_T$ and $h_{2c} = \sqrt{\mu_2''/\mu_1''}\,h_2$ and assume that the second derivatives have the same sign. Inserting these into *AMSE* in (A.2) yields an expression of the same general form of Theorem 1 in Gerard and Schucany (1996). Hence, the values of c, h_1, and h_{2c} that minimize (A.3) are

$$\tilde{c} = (\mu_c/L_2)/(\mu/L_1 + \mu_c/L_2) = \left(|\mu_2''|^{1/2}/L_2\right)\Big/\left(|\mu_1''|^{1/2}/L_1 + |\mu_2''|^{1/2}/L_2\right) \quad (A.3)$$

and

$$\tilde{h}_1 = \tilde{h}_{2c} = \left[\left(|\mu_1''|^{1/2}/2L_1\right)\left(|\mu_2''|^{1/2}/2L_2\right)\mu Q^* \Big/ \left\{\left(|\mu_1''|^{1/2}/2L_1 + |\mu_2''|^{1/2}/2L_2\right)|\mu_1''|^{1/2}\left(k_2^* \mu_1''\right)^2\right\}\right]^{1/5}. \quad (A.4)$$

This leads to $\tilde{h}_2 = \tilde{h}_{2c} k_d$, where $k_d = |\mu_1''|^{1/2}\Big/|\mu_2''|^{1/2}$, $\qquad (A.5)$

which yields $\hat{D}_{\tilde{c}}$.

Theorem 1

If the signs of μ_1'' and μ_2'' are the same, then $AMSE(\hat{D}_p) \geq AMSE(\hat{D}_{\tilde{c}})$ with equality holding when $k_d = 1$.

Proof:

We can express $AMSE(\hat{D}_p) = AMSE(\hat{D}_2)\left\{\left(k_d^2 k_L + 1\right)/(k_L + 1)^3\right\}^{2/5}$, where k_d is as in (A.5) and

$k_L = L_1/L_2$. Similarly, the asymptotic mean squared error of $\hat{D}_{\tilde{c}}$ can be expressed

as $AMSE(\hat{D}_{\tilde{c}}) = AMSE(\hat{D}_2)\left\{k_d/(k_L + k_d)\right\}^{4/5}$. Form the ratio

$AMSE(\hat{D}_p)/AMSE(\hat{D}_{\tilde{c}}) = \left[\left(k_d^2 k_L + 1\right)(k_d + k_L)^2/\left\{(k_L + 1)^3 k_d^2\right\}\right]^{2/5}$, which reduces to

$\left\{\left(k_d^2 k_L^3 + k_d^2 + 2k_L^2 k_d^3 + k_d^4 k_L + k_L^2 + 2k_L k_d\right)/\left(k_d^2 k_L^3 + k_d^2 + 3k_L^2 k_d^2 + 3k_L k_d^2\right)\right\}^{2/5}$. Note that the

first two terms are the same in both numerator and denominator. Additionally,

$2k_L^2 k_d^3 + k_L^2 \geq 3k_L^2 k_d^2$, with equality when $k_d=1$ or $k_L=0$. Finally, $k_d^4 k_L + 2k_L k_d \geq 3k_L k_d^2$,

again with equality if $k_d=1$, $k_d=0$, or $k_L=0$. It follows that the ratio is greater than or equal to

unity.‖

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