

# Shape-Adaptive Kernel Density Estimation

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## Abstract

Kernel density estimation has gained popularity in the past few years. Generally the methods use symmetric kernels, even though the data of which the density is estimated are not necessarily spread equally in all dimensions. To account for this asymmetric distribution of data we propose the use of shape adaptive kernels: kernels whose shape changes to fit the spread of the data in the local neighborhood of the point whose density is estimated. We compare the performance of the shape adaptive kernels on both artificial and real world datasets with the performance of symmetric kernels on the unprocessed datasets and on the whitened datasets.

Results

Conclusion

## 1 Introduction

Estimating densities with kernels has been fairly popular of late; in the medical field this approach has been used to predict dose-volume histograms, which are instrumental in the determination of radiation doses [6]. Ecologists have applied it to explore the habitats of seabirds [5]. Ferdosi et al. [3] have described it as “a critical first step in making progress in many areas of astronomy.” Within this discipline density estimation is, among other things, used to estimate the density of the cosmic density field, which is required for the reconstruction of the large-scale structure of the universe.

Formally the aim of density estimation is to find the probability density  $f(\mathbf{x})$  in  $d$ -dimensional Euclidean space underlying  $N$  points  $\mathbf{x}_1, \dots, \mathbf{x}_N$ , that have been selected independently from  $f(\mathbf{x})$ .

Kernel density estimation methods approximate  $f(\mathbf{x})$  by placing bumps, referred to as kernels, on the different observations and summing them to arrive at a final density estimate. This paper is concerned with a method to make the shape of these bumps adaptive to the local neighborhood of  $\mathbf{x}$ . Before introducing the process used to determine the shape of the kernel we first review the different symmetric kernel density estimation methods that our approach is based on.

The Parzen approach [7] is one of the most simple kernel density estimation methods. It estimates the

density of  $\mathbf{x}$  according to:

$$\hat{f}(\mathbf{x}) = \frac{1}{N} \sum_{i=1}^N h^{-d} K\left(\frac{\mathbf{x} - \mathbf{x}_i}{h}\right), \quad (1)$$

where  $d$  denotes the dimensionality of the data points. The shape of the placed bumps is determined by the kernel function  $K$ . The Parzen approach requires the kernel to be a probability density function, i.e.  $K(\mathbf{x}) \geq 0$  and  $\int K(\mathbf{x}) = 1$ . The width of the kernels is controlled by the bandwidth  $h$  [8]. Choosing this bandwidth too small, results in a density estimate with spurious fine structures, whereas kernels that are too wide can oversmooth the density estimate. Kernel estimators, such as the Parzen approach, that use kernels of the same width for all  $\mathbf{x}_j$ , are called fixed-width estimators.

One downside of fixed-width methods is that they cannot respond appropriately to variations in the magnitude of the density function, i.e. the peakedness of the kernel is not data-responsive. Consequently in low density regions the density estimate will have peaks at the few sample points and be too low elsewhere. In areas with high density, the sample points are more densely packed together, which causes the Parzen estimate to spread out [1]. Adaptive-width methods address this disadvantage of the fixed-width methods by allowing the width of the kernel to vary per data point. For example the estimator we refer to as the Breiman estimator, introduced by Breiman, Meisel, and Purcell, uses the distance between  $\mathbf{x}_i$  and the  $k$ -nearest neighbors of

$\mathbf{x}_i$ , denoted by  $D_{i,k}$ , to adapt the width of the kernel:

$$\hat{f}(\mathbf{x}) = \frac{1}{N} \sum_{i=1}^N (\alpha \cdot D_{i,k})^{-d} K_G \left( \frac{\mathbf{x} - \mathbf{x}_i}{\alpha \cdot D_{i,k}} \right). \quad (2)$$

In Equation (2)  $K_G$  is used to represent a Gaussian kernel, and  $\alpha$  is a multiplicative constant. The values of both  $\alpha$  and  $k$  can be determined with a minimization algorithm on a goodness of fit statistic. Comparing Equation (1) with (2) one finds that the bandwidth  $h$  of the Breiman estimator is defined as  $\alpha D_{i,k}$ . The second factor of this bandwidth depends on the local neighborhood of  $\mathbf{x}_i$ . In low density regions  $D_{i,k}$  is large, and the kernel spreads out due to its high bandwidth. In areas with relatively many data points the converse occurs.

Silverman [8] shows that the minimization procedure used by Breiman, Meisel, and Purcell implicitly uses a  $k$ -NN pilot estimate. If pilot estimates are used explicitly the density estimation process becomes:

- (i) Compute pilot densities with some estimator that ensures that  $\forall i \hat{f}(\mathbf{x}_i) > 0$ .
- (ii) Define local bandwidth factors  $\lambda_i$  as

$$\lambda_i = \left( \frac{\tilde{f}(\mathbf{x}_i)}{\text{GM}(\tilde{f}(\mathbf{x}_0), \dots, \tilde{f}(\mathbf{x}_N))} \right)^{-\beta}, \quad (3)$$

where GM denotes the geometric mean and the sensitivity parameter  $\beta$  must lie in the range  $[0, 1]$ .

- (iii) Compute the adaptive kernel estimate as

$$\hat{f}(\mathbf{x}) = \frac{1}{N} \sum_{i=1}^N (h \cdot \lambda_i)^{-d} K \left( \frac{\mathbf{x} - \mathbf{x}_i}{h \cdot \lambda_i} \right) \quad (4)$$

with  $K$  integrating to unity.

Since the pilot densities computed in step (i) do not need to be sensitive to the fine details of the pilot estimate a convenient method, e.g. the Parzen approach, can be used to estimate them [8]. The local bandwidths computed in (ii) depend on the exponent  $\beta$ . The higher this value is the more sensitive the local bandwidths are to variations in the pilot densities. Choosing  $\beta = 0$  reduces Equation (4) to a fixed-width method. In the literature two values of  $\beta$  are prevalent. Breiman, Meisel, and Purcell [1] argue that choosing  $\beta = 1/d$  will ensure that the number of observations covered by the kernel will be approximately the same in all parts of the data. Whereas Silverman favors  $\beta = 1/2$  independent of

the dimension of the data points, as this value results in a bias that can be shown to be of a smaller order than that of the fixed-width kernel estimate.

One disadvantage of the Breiman estimator is its computational complexity. This is partially due to its use of a Gaussian kernel. Because of the infinite base of this kernel an exponential function has to be evaluated  $N$  times to estimate the density of one data point. The Modified Breiman Estimator (MBE), introduced by Wilkinson and Meijer [9], reduces this computational complexity in two ways. Firstly they replace the infinite base Gaussian kernel with a spherical Epanechnikov kernel in both the computation of the pilot densities and the final density estimate. They define this kernel as:

$$K_E(\mathbf{x}) = \begin{cases} \frac{d+2}{2c_d} (1 - \mathbf{x} \cdot \mathbf{x}) & \text{if } \mathbf{x} \cdot \mathbf{x} < 1 \\ 0 & \text{otherwise} \end{cases} \quad (5)$$

where  $c_d$  denotes the volume of the  $d$ -dimensional unit sphere. It should be noted that the kernel defined in Equation (5) does not have unit variance. This can be corrected by multiplying the bandwidth,  $h$ , with the square root of the variance of  $K_E$ . There are two advantages to using this kernel, firstly it is computationally much simpler than the Gaussian kernel, in part due to its finite base and secondly it is optimal in the sense of the Mean Integrated Square Error (MISE) [2]. A disadvantage of this kernel is that it is not continuously differentiable. This does not matter when computing the pilot densities, as they are only used to determine the local bandwidths. In the computation of the final densities it is a trade off between a continuously differentiable  $\hat{f}$  and a low computational complexity.

The second change Wilkinson and Meijer [9] introduce is the indirect computation of the pilot densities. They first compute the pilot densities for the vertices of a grid that covers all data points, before determining the actual pilot densities by multi-linear interpolation. The bandwidth of the kernel used in the computation of the pilot densities is defined as

$$h = \sigma \cdot N^{-1/(d+4)} \left( \frac{8(d+4) \cdot (2\sqrt{\pi})^d}{c_d} \right)^{\frac{1}{d+4}}, \quad (6)$$

where  $\sigma$  represents the square root of the average of the variances of the different dimensions. The final densities are estimated with Equation (4) using the general and local bandwidths estimated with Equation (6) and (3), respectively.

Ferdosi et al. [3] consider the application of density estimation on large datasets, i.e. sets with more than 50 000 points with the dimension of the data

points ranging from ten to hundreds of elements. They use the MBE, but introduce a computationally less complex method to estimate the bandwidth. First they determine an intermediate bandwidth for each dimension  $l$  of the data:

$$h_l = \frac{P_{80}(l) - P_{20}(l)}{\log N}, l = 1, \dots, d, \quad (7)$$

where  $P_{20}(l)$  and  $P_{80}(l)$  are the twentieth and eightieth percentile of the data in dimension  $l$ , respectively. To avoid oversmoothing the pilot window width is then defined as:

$$h = \min_l h_l.$$

Although the widths of the kernels used in the estimators proposed by Breiman, Meisel, and Purcell, Wilkinson and Meijer are sensitive to the data, the shapes of the kernels are dependent on the kernel itself not the data. To further increase the responsiveness of the estimator to the data we propose the use of shape-adaptive kernels in density estimation. Not only the width but also the shape of these kernels is steered by the local neighborhood of the data.

A possible disadvantage of these shape-adaptive kernels is that in regions where the density of sample points is low, the number of data points is insufficient to reliably compute the shape of the kernel. Therefore we let the amount of influence exerted by the local data on the shape of the kernel depend on the number of data points in the local neighborhood.

This paper is organized as follows. Section 2 introduces the proposed shape-adaptive kernels. The experiments used to investigate the performance of these kernels are discussed in Section 3, their results are presented in Section 4. The discussion of these results can be found in Section 5. Section 6 concludes the this paper.

## 2 Method

We use shape adaptive kernels in combination with the Modified Breiman Estimator introduced by Wilkinson and Meijer [9] with the general bandwidths computed according to the method introduced by Ferdosi et al. [3] for its lower complexity. The pilot densities are computed on a  $20 \times \dots \times 20$  grid that covers all data points. We have empirically determined that using  $\beta$  works best in our case.

The final densities are estimated according to Equation (4) with a reshaped and scaled Epanechnikov kernel. The shape of the kernel is determined by the

bandwidth matrix  $\mathbf{H}$ . Which is incorporated in the estimation of the densities by using

$$\hat{f}(\mathbf{x}) = \frac{1}{N} \sum_{i=1}^N \frac{1}{\det(\mathbf{H})} K(\mathbf{H}^{-1}(\mathbf{x} - \mathbf{x}_i)) \quad (8)$$

instead of Equation (1) [4]. If  $\mathbf{H} = h \cdot \mathbb{I}_{d \times d}$  Equation (8) reduces to the fixed-width Parzen estimator defined in Equation (1).

For each data point  $\mathbf{x}$  the bandwidth matrix is determined according to these steps:

- (i) Find  $C_{\mathbf{x}}$ , the  $k$ -nearest neighbors of  $\mathbf{x}$ .
- (ii) Compute  $\Sigma$ , the biased covariance matrix of local neighborhood  $C_{\mathbf{x}}$ .
- (iii) To determine  $\mathbf{H}$ , scale  $\Sigma$  with

$$s = h \left( \prod_{l=1}^d \lambda_l \right)^{-\frac{1}{d}} \quad (9)$$

Step (i) determines the local neighborhood of  $\mathbf{x}$  with the  $k$  nearest neighbors algorithm ( $k$ -NN) with Euclidean distance. We use this approach rather than a fixed-radius neighborhood to ensure that, independent of the sparsity of the data, the kernel shape is always based on a reasonable number of data points. We follow Silverman's [8] recommendation of choosing  $k = \sqrt{N}$ . To ensure that  $\Sigma$  is nonsingular we also need  $k > d$ , therefore

$$k = \max \left( \left\lceil \sqrt{N} \right\rceil, d \right) + 1.$$

Step (ii) determines the basic shape of the bandwidth covariance matrix.

Step (iii) ensures that the kernels used in the density estimation of different patterns have the same domain, modulo the local bandwidths. Equation (9) scales the bandwidth matrix in such a way that the volume of the eigenellipse of  $\mathbf{H}$  is equal to that of the eigenellipse of the bandwidth matrix that is implicitly used in Equation (1). It should be noted that  $\mathbf{H}$  is scaled with the local bandwidth if an adaptive-width method is used.

## 3 Experiment

We compare the performance of the shape-adaptive with that of the adaptive-width method it is based on, i.e. the Modified Breiman Estimator. Section 3.1 introduces the datasets we use for our experiments. The metrics used to compare the performance of the different estimators are introduced in Section 3.2.

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### 3.1 Datasets

The performance of the estimators is investigated with two groups of datasets: a number of simulated datasets with known density fields and a real world dataset with an unknown density field. The simulated datasets allow us to test how well a method can recover simple density distributions. Whereas the real world dataset make it possible to compare the performance of the estimators in the context in which they would be applied.

#### Simulated Datasets

The simulated datasets are based on the simulated datasets used by Ferdosi et al. [3]. Figure 1 presents scatter plots of the data sets. The definitions of these simulated data sets are shown in Table 1.

Dataset 1, shown in Figure 1a, is the most simple set in this group. It is an unimodal Gaussian distribution with random noise added.

The second dataset, depicted in Figure 1b, contains two Gaussian distributions with different covariance matrices and uniform noise. The means and covariance matrices of the Normal distributions are such that the two distributions are very unlikely to overlap.

Dataset 3, represented in Figure 1c, consists of four different normal distributions and uniformly distributed noise. The four Gaussian distributions are placed in such a way that it is unlikely that among them any overlap occurs.

Figure 1d illustrates dataset 4. This set consists of a horizontal wall-like structure and a vertical filament-like structure.

The fifth dataset, shown in Figure 1e, contains three intersecting walls. For each point in these walls its position in two of the three dimensions is drawn from a uniform distribution, the third coordinate is sampled from a Gaussian distribution.

We expect comparable performance from all estimators on dataset one through three, as other than the randomly sampled noise these sets only contain data sampled from a Gaussian distribution with a diagonal covariance matrix. Which results in an equal spread of the data in all dimensions for the non-noise data. Dataset four and five are clearly spread more in one dimension than in others, thus we expect the shape adaptive estimator to outperform the MBE estimator.

The increasing complexity of these datasets allows us to investigate the performance of the classifier on simple situations, one cluster of data with some noise, to complex density fields that should

better approximate real world data. The advantage of using simulated data is that the true densities of the data points are known, which allows us to test how well the different methods estimate the densities.

#### Real World Datasets

Iets over real world data

### 3.2 Error Measures

To quantify the performance of the estimators on the simulated datasets we use the Mean Squared Error (MSE):

$$\text{MSE}(\hat{f}(\bullet)) = \frac{1}{N} \sum_{j=0}^N (\hat{f}(\mathbf{x}_j) - f(\mathbf{x}_j))^2.$$

Iets over het quantificeren van de resultaten op real world data.

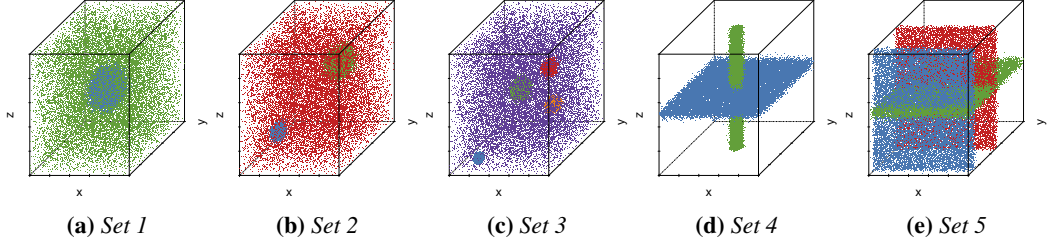
## 4 Results

## 5 Discussion

## 6 Conclusion

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**Figure 1:** Scatter plot representation of the simulated datasets defined in Table 1.

Set	Component	Fraction	Distribution
1	• Trivariate Gaussian	$2/3$	$(x, y, z) \sim \mathcal{N}([50, 50, 50], \text{diag}(30))$
	• Uniform random background	$1/3$	$(x, y, z) \sim \mathcal{U}([0, 0, 0], [100, 100, 100])$
2	• Trivariate Gaussian 1	$1/3$	$(x, y, z) \sim \mathcal{N}([25, 25, 25], \text{diag}(5))$
	• Trivariate Gaussian 2	$1/3$	$(x, y, z) \sim \mathcal{N}([65, 65, 65], \text{diag}(20))$
	• Uniform random background	$1/3$	$(x, y, z) \sim \mathcal{U}([0, 0, 0], [100, 100, 100])$
3	• Trivariate Gaussian 1	$1/6$	$(x, y, z) \sim \mathcal{N}([24, 10, 10], \text{diag}(2))$
	• Trivariate Gaussian 2	$1/6$	$(x, y, z) \sim \mathcal{N}([33, 70, 40], \text{diag}(10))$
	• Trivariate Gaussian 3	$1/6$	$(x, y, z) \sim \mathcal{N}([90, 20, 80], \text{diag}(1))$
	• Trivariate Gaussian 4	$1/6$	$(x, y, z) \sim \mathcal{N}([60, 80, 23], \text{diag}(5))$
	• Uniform random background	$1/3$	$(x, y, z) \sim \mathcal{U}([0, 0, 0], [100, 100, 100])$
4	• Wall-like structure	$1/2$	$(x, y) \sim \mathcal{U}([0, 0], [100, 100]), (z) \sim \mathcal{N}(50, 5)$
	• Filament-like structure	$1/2$	$(x, y) \sim \mathcal{N}([50, 50], \text{diag}(5)), (z) \sim \mathcal{U}(0, 100)$
5	• Wall-like structure 1	$1/3$	$(x, z) \sim \mathcal{U}([0, 0], [100, 100]), (y) \sim \mathcal{N}(10, 5)$
	• Wall-like structure 2	$1/3$	$(x, y) \sim \mathcal{U}([0, 0], [100, 100]), (z) \sim \mathcal{N}(50, 5)$
	• Wall-like structure 3	$1/3$	$(x, z) \sim \mathcal{U}([0, 0], [100, 100]), (y) \sim \mathcal{N}(50, 5)$

**Table 1:** The simulated datasets used to test the estimators. The column ‘Fraction’ indicates for each component of the dataset which fraction of the total number of points of the data set is part of that component.  $\mathcal{N}(\mu, \Sigma)$  denotes a Gaussian distribution with mean  $\mu$  and covariance matrix  $\Sigma$ . A diagonal matrix with the value  $x$  on the diagonal is represented as  $\text{diag}(x)$ .  $\mathcal{U}(a, b)$  denotes a uniform distribution with its minimum and maximum set to  $a$  and  $b$ , respectively. The colors shown in the second column correspond with the colors used for these components of the data set throughout the paper.

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