

Statistical Methods in AI (CS7.403)

Lecture-23: Non-parametric density estimation (KDE)

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Unsupervised Learning → Density Estimation

Aka “learning without a teacher”

Feature Space \mathcal{X}



Word distribution
(Probability of a word)

Task: Given $X \in \mathcal{X}$, learn $f(X)$.

Parametric Density Estimation (GMM)

- Initialize the means μ_k , covariances Σ_k and mixing coefficients π_k

- Iterate until convergence:

- ▶ E-step: Evaluate the responsibilities given current parameters

$$\gamma_k^{(n)} = p(z^{(n)}|\mathbf{x}) = \frac{\pi_k \mathcal{N}(\mathbf{x}^{(n)}|\mu_k, \Sigma_k)}{\sum_{j=1}^K \pi_j \mathcal{N}(\mathbf{x}^{(n)}|\mu_j, \Sigma_j)}$$

- ▶ M-step: Re-estimate the parameters given current responsibilities

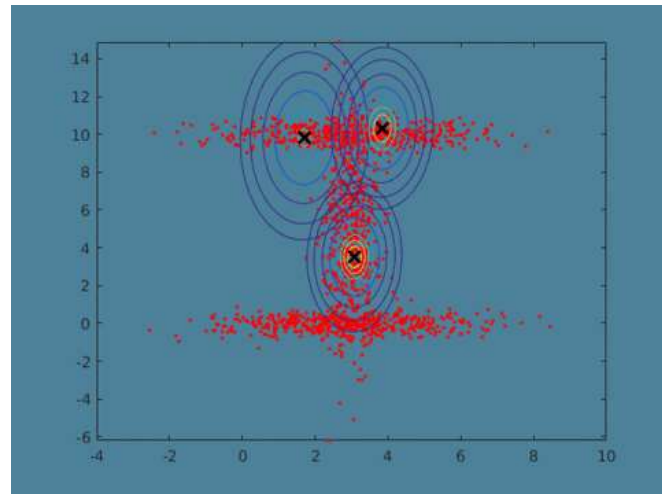
$$\mu_k = \frac{1}{N_k} \sum_{n=1}^N \gamma_k^{(n)} \mathbf{x}^{(n)}$$

$$\Sigma_k = \frac{1}{N_k} \sum_{n=1}^N \gamma_k^{(n)} (\mathbf{x}^{(n)} - \mu_k)(\mathbf{x}^{(n)} - \mu_k)^T$$

$$\pi_k = \frac{N_k}{N} \quad \text{with} \quad N_k = \sum_{n=1}^N \gamma_k^{(n)}$$

- ▶ Evaluate log likelihood and check for convergence

$$\ln p(\mathbf{X}|\pi, \mu, \Sigma) = \sum_{n=1}^N \ln \left(\sum_{k=1}^K \pi_k \mathcal{N}(\mathbf{x}^{(n)}|\mu_k, \Sigma_k) \right)$$



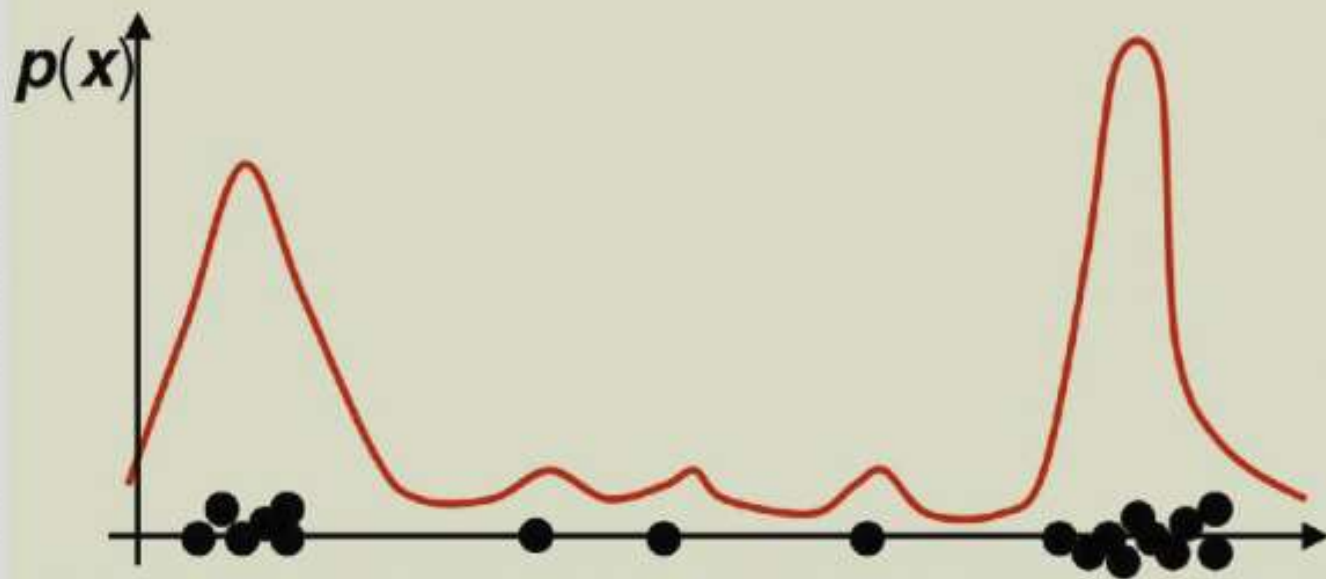
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 - Assuming that its shape takes a special form (e.g. Gaussian) is also mostly unrealistic – this results in a mismatch between the real and the assumed distribution, which we shortly called as the “modelling error”
- Today: methods that do not use a parametric curve (such as a Gaussian), to describe the shape of the distribution
 - This is why they are called “non-parametric methods”

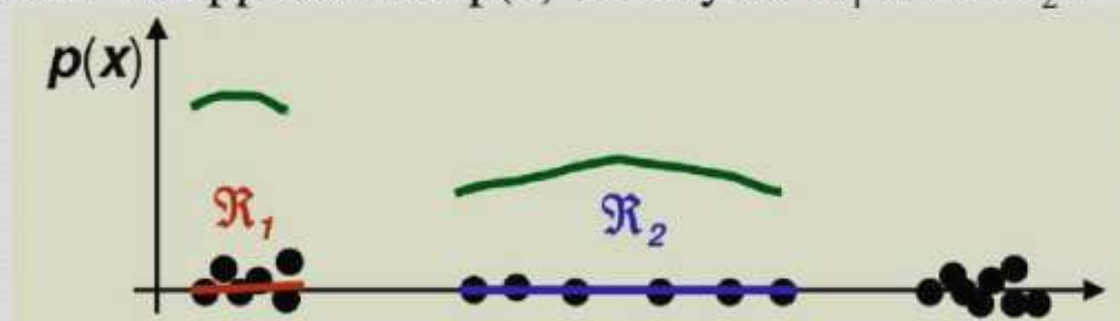
Basic idea

- In a given point we will estimate $p(x)$ from the density of the data points falling into a small region R around x
 - More samples \rightarrow larger probability



Example

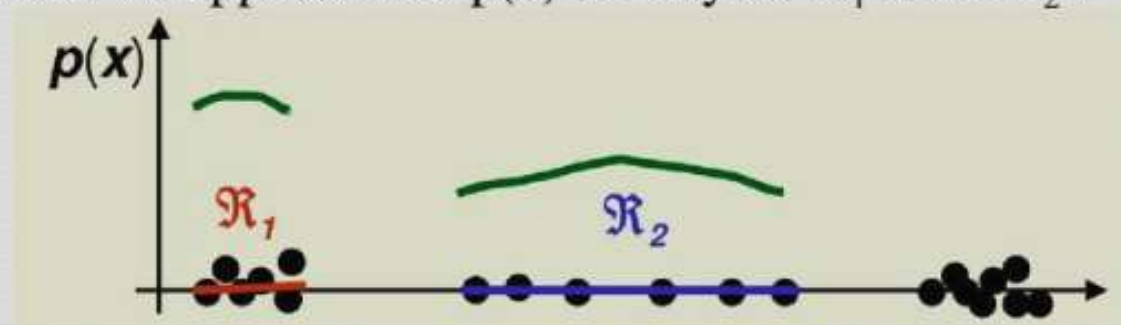
- How can we approximate $p(x)$ for any $x \in R_1$ or $x \in R_2$?



- To estimate $P[x \in R_1]$ and $P[x \in R_2]$, we divide the number k of the samples that fall in the given region R with the total number n of all samples

Example

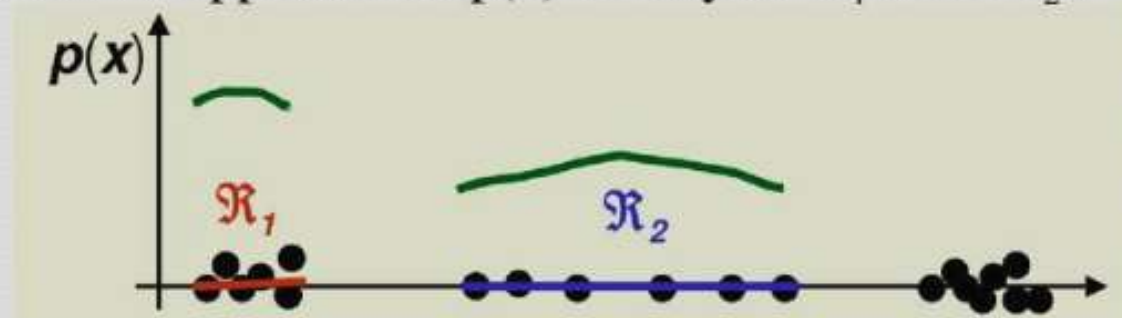
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 - $P[x \in R_1] = 6/20$ $P[x \in R_2] = 6/20$
- Should our estimates for $p(x)$ be equal?

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- To estimate $P[x \in R_1]$ and $P[x \in R_2]$, we divide the number k of the samples that fall in the given region R with the total number n of all samples
 - $P[x \in R_1] = 6/20$ $P[x \in R_2] = 6/20$
- Should our estimates for $p(x)$ be equal?
 - No, because R_2 is wider than R_1
- So the estimate will be inversely proportional to the region size V
 - Altogether, our estimate will be $p(x) \approx k/nV$

Non-parametric density estimation : preliminaries

- The probability that a vector x , drawn from a distribution $p(x)$, will fall in a given region \mathfrak{R} of the sample space is

$$P = \int_{\mathfrak{R}} p(x') dx'$$

Non-parametric density estimation : preliminaries

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- It can be shown (from the properties of the binomial p.m.f.) that the mean and variance of the ratio k/N are

$$E \left[\frac{k}{N} \right] = P \quad \text{and} \quad \text{var} \left[\frac{k}{N} \right] = E \left[\left(\frac{k}{N} - P \right)^2 \right] = \frac{P(1-P)}{N}$$

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- Therefore, as $N \rightarrow \infty$ the distribution becomes sharper (the variance gets smaller), so we can expect that a good estimate of the probability P can be obtained from the mean fraction of the points that fall within \mathfrak{R}

$$P \cong \frac{k}{N}$$

[Bishop, 1995]

Non-parametric density estimation : preliminaries

- On the other hand, if we assume that \mathfrak{R} is so small that $p(x)$ does not vary appreciably within it, then

$$\int_{\mathfrak{R}} p(x') dx' \cong p(x)V$$

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- Merging with the previous result we obtain

$$\left. \begin{array}{l} P = \int_{\mathfrak{R}} p(x') dx' \cong p(x)V \\ P \cong \frac{k}{N} \end{array} \right\} \Rightarrow p(x) \cong \frac{k}{NV}$$

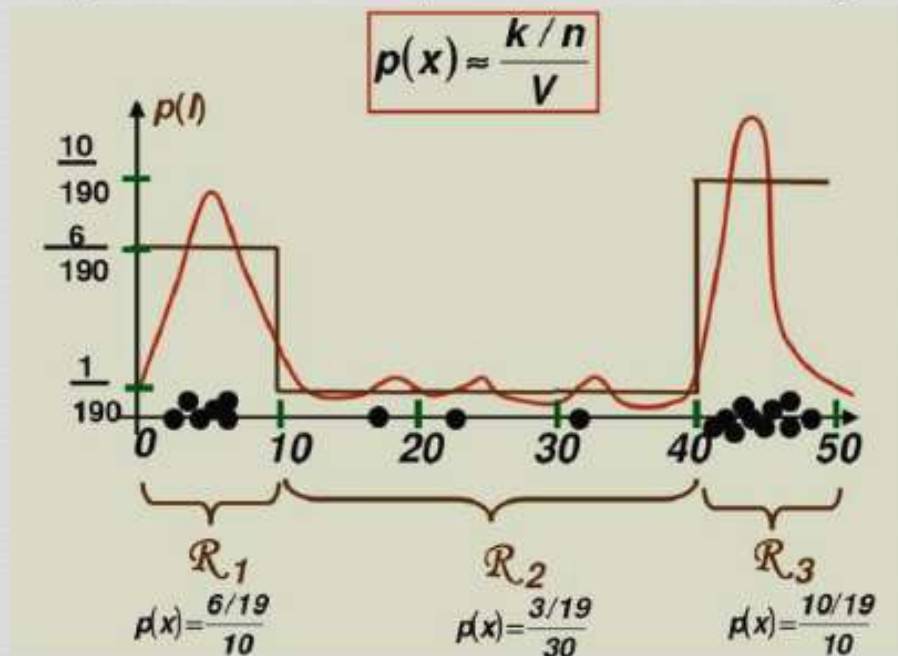
Non-parametric density estimation : preliminaries

- In conclusion, the general expression for non-parametric density estimation becomes

$$p(x) \cong \frac{k}{NV} \text{ where } \begin{cases} V & \text{volume surrounding } x \\ N & \text{total \#examples} \\ k & \text{\#examples inside } V \end{cases}$$

Interpretation as a histogram

- Our probability estimate is very similar to a histogram:



- If the regions do not overlap and cover the whole range of the values then our estimate is basically a (normalized) histogram

The histogram

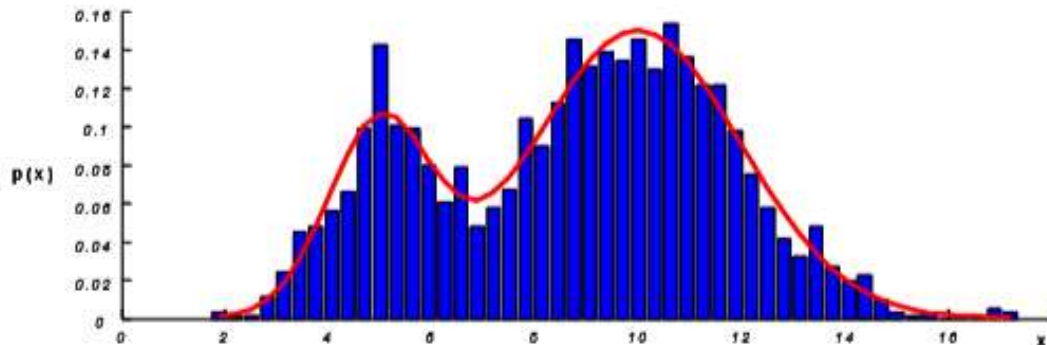
The simplest form of non-parametric DE is the histogram

- Divide the sample space into a number of bins and approximate the density at the center of each bin by the fraction of points in the training data that fall into the corresponding bin

$$p(x) \cong \frac{k}{NV}$$

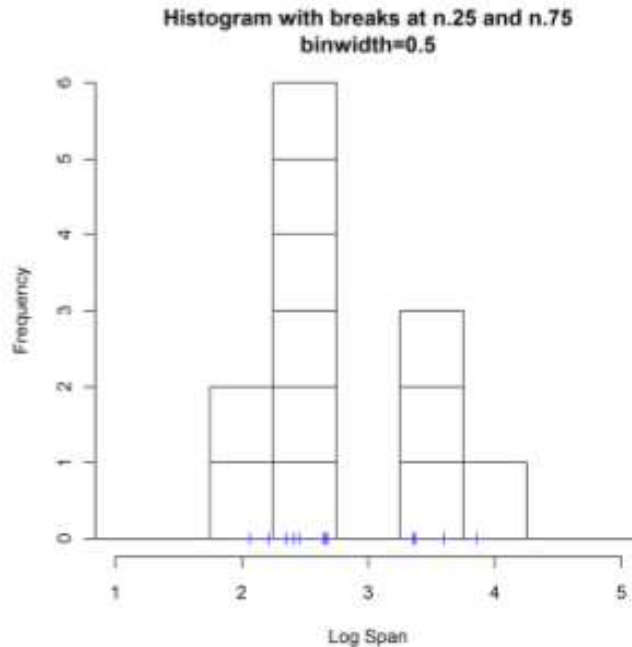
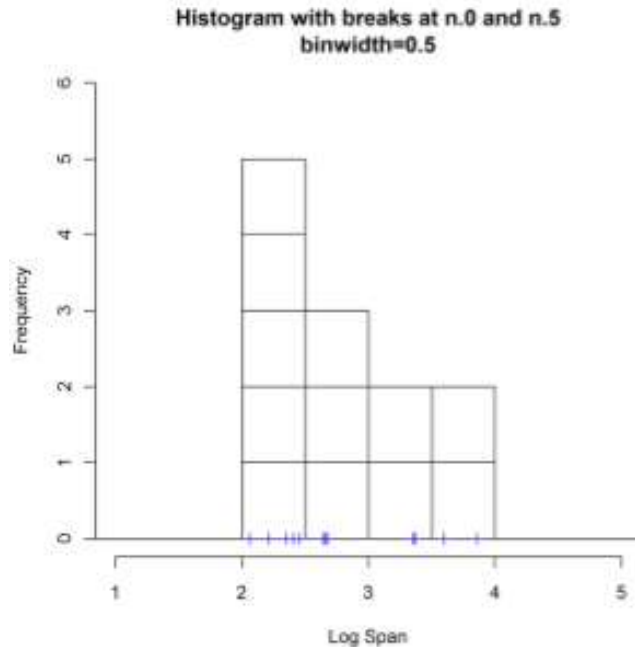
$$p_H(x) = \frac{1}{N} \frac{[\# \text{ of } x^{(k)} \text{ in same bin as } x]}{[\text{width of bin}]}$$

- The histogram requires two “parameters” to be defined: bin width and starting position of the first bin



A toy example

- (the log of) wing spans of aircraft built from 1956 – 1984
- Wing-spans: 2, 22, 42, 62, 82, 102, 122, 142, 162, 182, 202, 222



Issues with Histograms

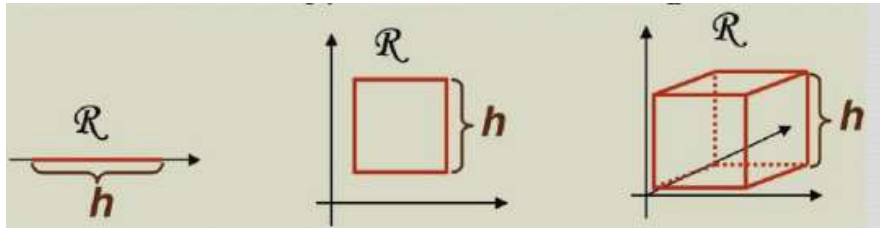
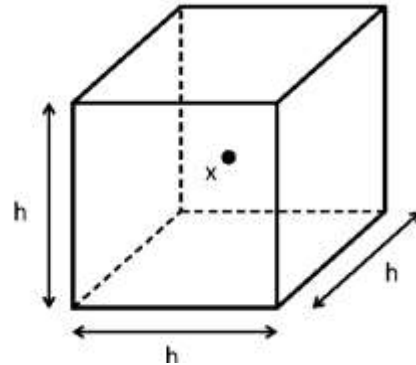
- Not smooth
- Depend on end points of bins
- Depend on width of bins

Characterizing density – a data-driven perspective

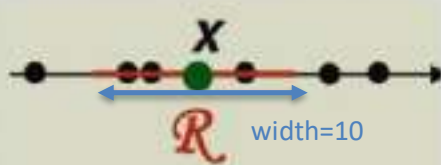
Parzen windows

Problem formulation

- Assume that the region \mathcal{R} that encloses the k examples is a hypercube with sides of length h centered at x
 - Then its volume is given by $V = h^D$, where D is the number of dimensions



Example:

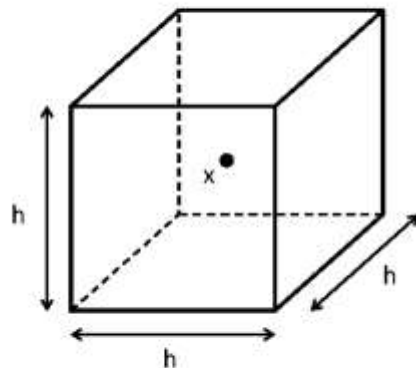


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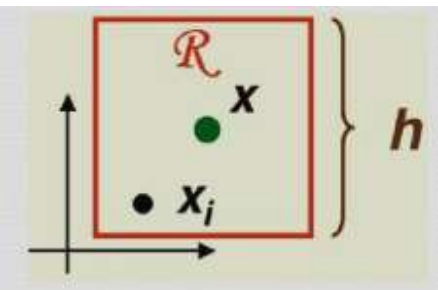


- To find the number of examples that fall within this region we define a kernel function $K(u)$

$$K(u) = \begin{cases} 1 & |u_j| < 1/2 \quad \forall j = 1 \dots D \\ 0 & \text{otherwise} \end{cases}$$

- This kernel, which corresponds to a unit hypercube centered at the origin, is known as a Parzen window or the naïve estimator
- The quantity $K((x - x^{(n)})/h)$ is then equal to unity if $x^{(n)}$ is inside a hypercube of side h centered on x , and zero otherwise

[Bishop, 1995]



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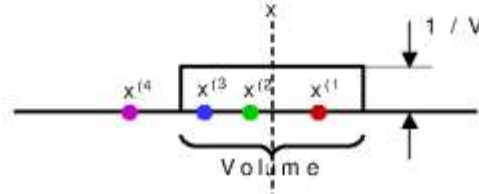
- The total number of points inside the hypercube is then

$$k = \sum_{n=1}^N K\left(\frac{x - x^{(n)}}{h}\right)$$

Substituting back into the expression for the density estimate

$$p_{KDE}(x) = \frac{1}{Nh^D} \sum_{n=1}^N K\left(\frac{x - x^{(n)}}{h}\right)$$

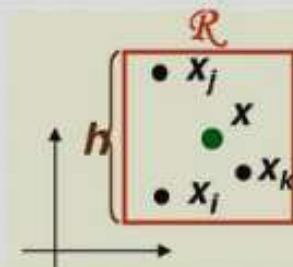
Still has to be a valid distribution



Parzen window – another interpretation

- So far, we fixed x and varied i to see which of the x_i samples fall within the hypercube centered on x , so that

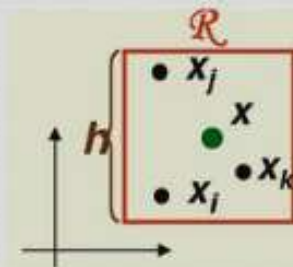
$$\phi\left(\frac{x - x_i}{h}\right) = 1$$



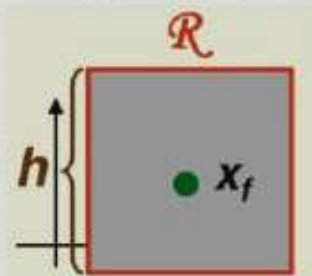
Parzen window – another interpretation

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$$\varphi\left(\frac{x - x_i}{h}\right) = 1$$



- Let's turn it around and analyze how a given x_i contributes to the estimate of $p(x)$
- We see that $\varphi\left(\frac{x - x_i}{h}\right) = 1$ is simply a function that gives 1 for all x values that are close enough to x_i , and 0 otherwise



Parzen window as a sum of functions

- Now, if we look at our estimate again

$$p_{\varphi}(x) = \frac{1}{n} \sum_{l=1}^{l=n} \frac{1}{h^d} \varphi\left(\frac{x - x_l}{h}\right) = \sum_{l=1}^{l=n} \underbrace{\frac{1}{nh^d} \varphi\left(\frac{x - x_l}{h}\right)}$$

*1 inside square centered at x_l
0 otherwise*

Parzen window as a sum of functions

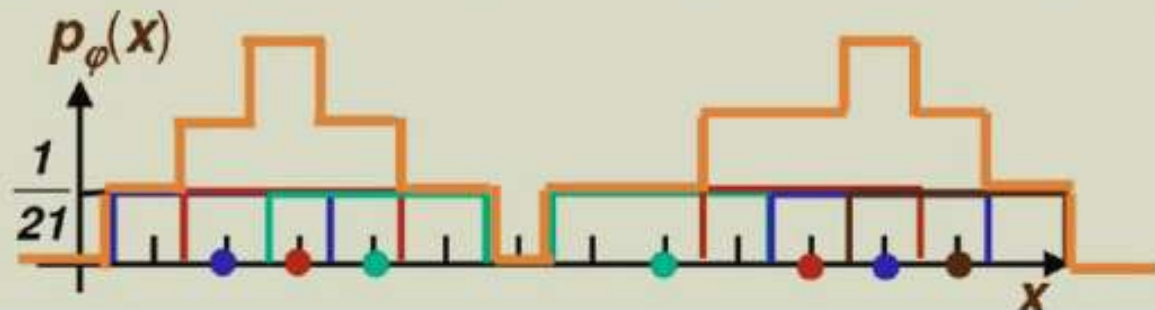
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- We see that we can easily calculate it by fitting hypercubes on all training instances x_1, \dots, x_n
- So $p(x)$ is just a sum of n box-like functions with height $\frac{1}{nh^d}$
- Let's see an example!

Parzen window - example

- We have seven samples $D=\{2,3,4,8,10,11,12\}$
- $n = 7, h = 3, d = 1$

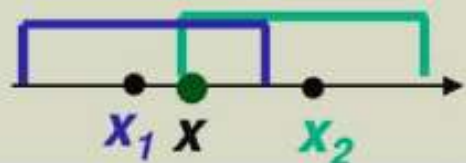


- To obtain our estimate we simply have to sum 7 boxes positioned on the seven points
- The height of the boxes is

$$\frac{1}{nh^d} = \frac{1}{21}$$

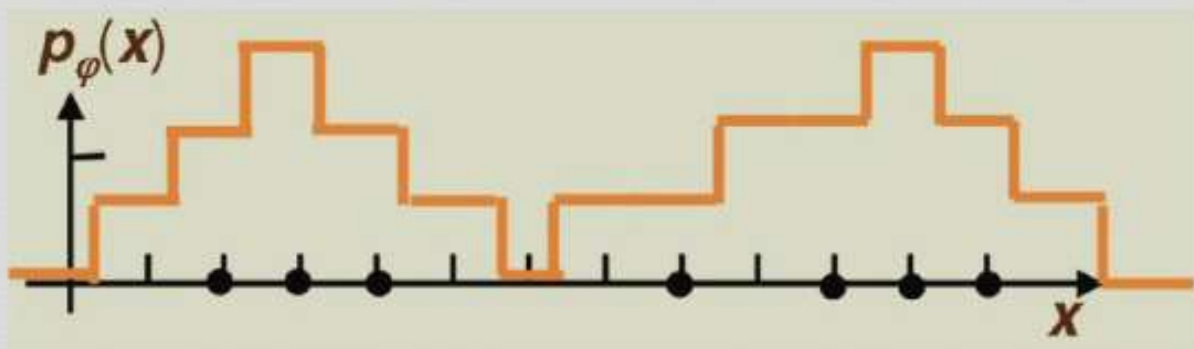
Drawbacks of the hypercube Parzen window

- As long as x_i is within the hypercube around x , its contribution to $p(x)$ will be the same, independent of its distance from x
 - The same is true for the samples outside the hypercube – they give a contribution of 0, no matter how far or close they are to x



$$\varphi\left(\frac{x - x_1}{h}\right) = \varphi\left(\frac{x - x_2}{h}\right) = 1$$

- The estimate of $p(x)$ is not smooth



Smooth kernels

The Parzen window has several drawbacks

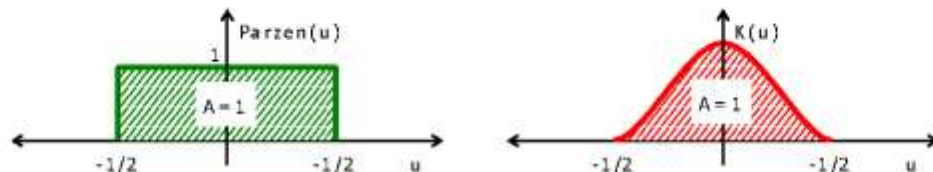
- It yields density estimates that have discontinuities
- It weights equally all points x_i , regardless of their distance to the estimation point x

For these reasons, the Parzen window is commonly replaced with a smooth kernel function $K(u)$

$$\int_{\mathbb{R}^D} K(x) dx = 1$$

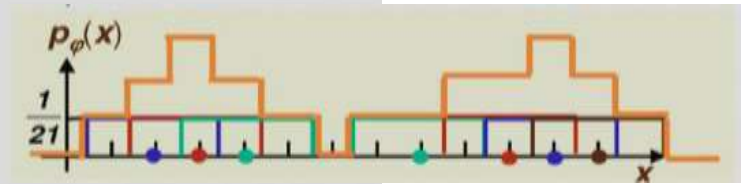
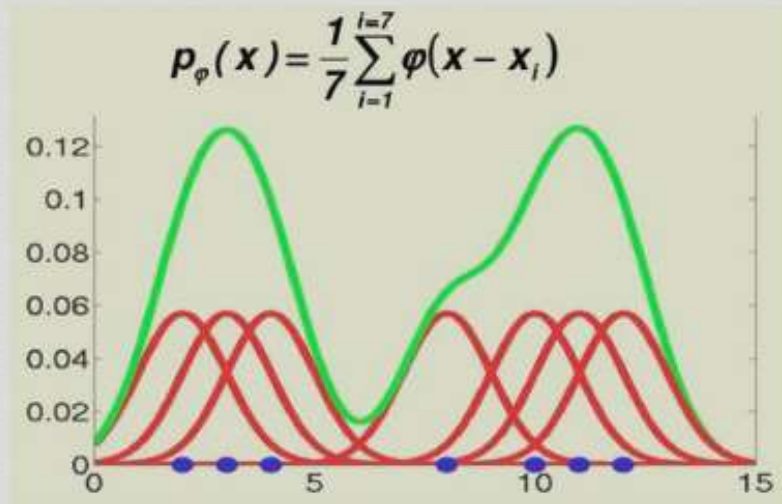
- Usually, but not always, $K(u)$ will be a radially symmetric and unimodal pdf, such as the Gaussian $K(x) = (2\pi)^{-D/2} e^{-\frac{1}{2}x^T x}$
- Which leads to the density estimate

$$p_{KDE}(x) = \frac{1}{Nh^D} \sum_{n=1}^N K\left(\frac{x - x^{(k)}}{h}\right)$$



Gaussian window function - example

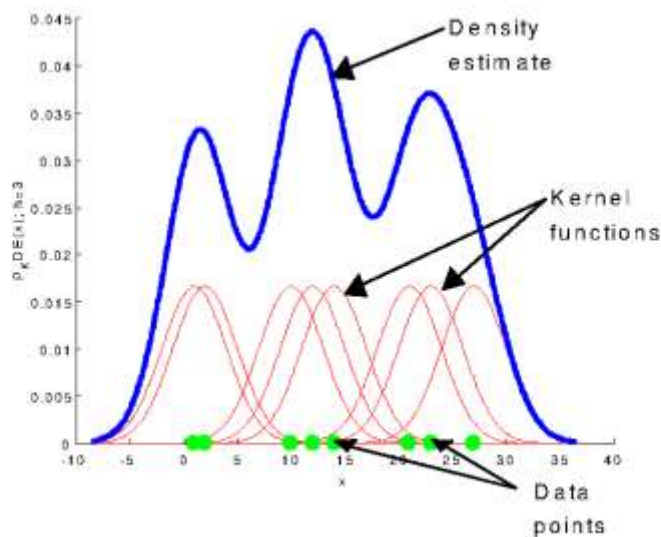
- Let's return to our previous example
- $D=\{2,3,4,8,10,11,12\}$, $n = 7$, $h = 1$, $d = 1$



- The estimate for $p(x)$ will be sum of 7 Gaussians, each centered on one of the sample points, each scaled by $1/7$

Interpretation

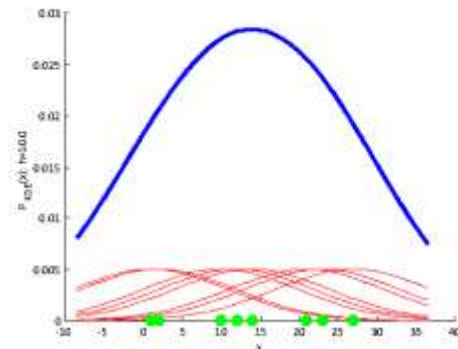
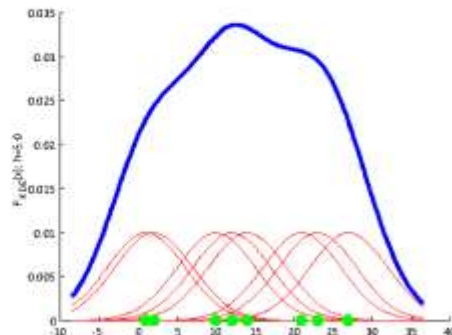
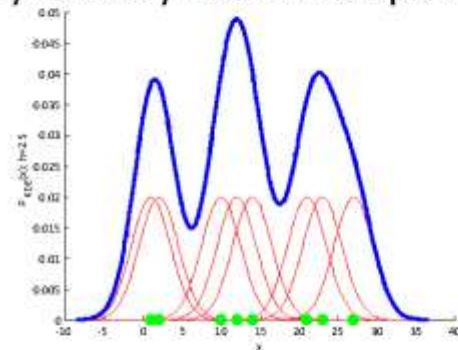
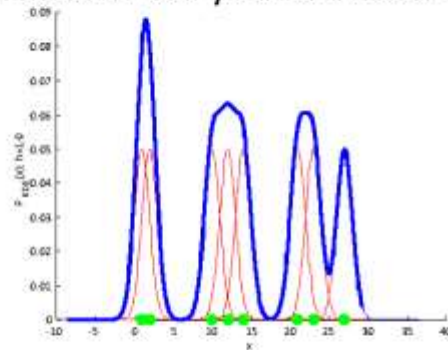
- Just as the Parzen window estimate can be seen as a sum of boxes centered at the data, the smooth kernel estimate is a sum of “bumps”
- The kernel function determines the shape of the bumps
- The parameter h , also called the smoothing parameter or bandwidth, determines their width



Bandwidth selection

The problem of choosing h is crucial in density estimation

- A large h will over-smooth the DE and mask the structure of the data
- A small h will yield a DE that is spiky and very hard to interpret



Maximum likelihood cross-validation

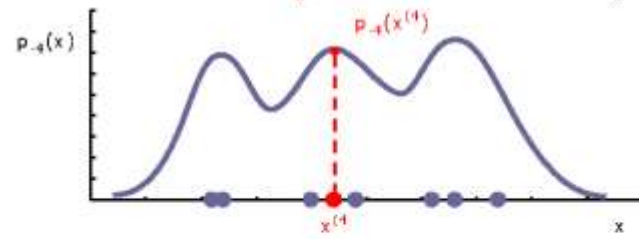
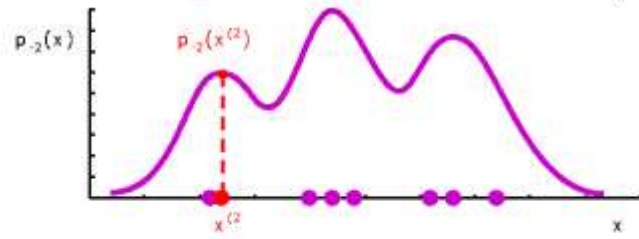
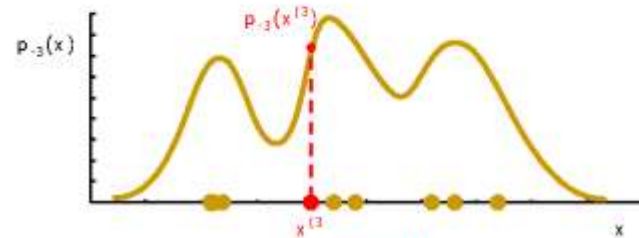
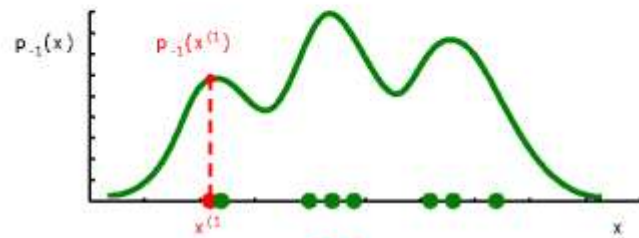
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- The ML estimate of h is degenerate since it yields $h_{ML} = 0$, a density estimate with Dirac delta functions at each training data point

Maximum likelihood cross-validation

- The ML estimate of h is degenerate since it yields $h_{ML} = 0$, a density estimate with Dirac delta functions at each training data point
- A practical alternative is to maximize the “pseudo-likelihood” computed using leave-one-out cross-validation

$$h^* = \arg \max \left\{ \frac{1}{N} \sum_{n=1}^N \log p_{-n}(x^{(n)}) \right\}$$
$$\text{where } p_{-n}(x^{(n)}) = \frac{1}{(N-1)h} \sum_{\substack{m=1 \\ m \neq n}}^N K\left(\frac{x^{(n)} - x^{(m)}}{h}\right)$$



Multivariate density estimation

For the multivariate case, the KDE is

$$p_{KDE}(x) = \frac{1}{Nh^D} \sum_{n=1}^N K\left(\frac{x-x^{(n)}}{h}\right)$$

- Notice that the bandwidth h is the same for all the axes, so this density estimate will be weight all the axis equally
- If one or several of the features has larger spread than the others, we should use a vector of smoothing parameters or even a full covariance matrix, which complicates the procedure

Product kernels

A good alternative for multivariate KDE is the product kernel

$$p_{PKDE}(x) = \frac{1}{N} \sum_{i=1}^N K(x, x^{(n)}, h_1, \dots, h_D)$$

$$\text{where } K(x, x^{(n)}, h_1, \dots, h_D) = \frac{1}{h_1 \dots h_D} \prod_{d=1}^D K_d \left(\frac{x_d - x_d^{(n)}}{h_d} \right)$$

- The product kernel consists of the product of one-dimensional kernels
 - Typically the same kernel function is used in each dimension ($K_d(x) = K(x)$), and only the bandwidths are allowed to differ
 - Bandwidth selection can then be performed with any of the methods presented for univariate density estimation

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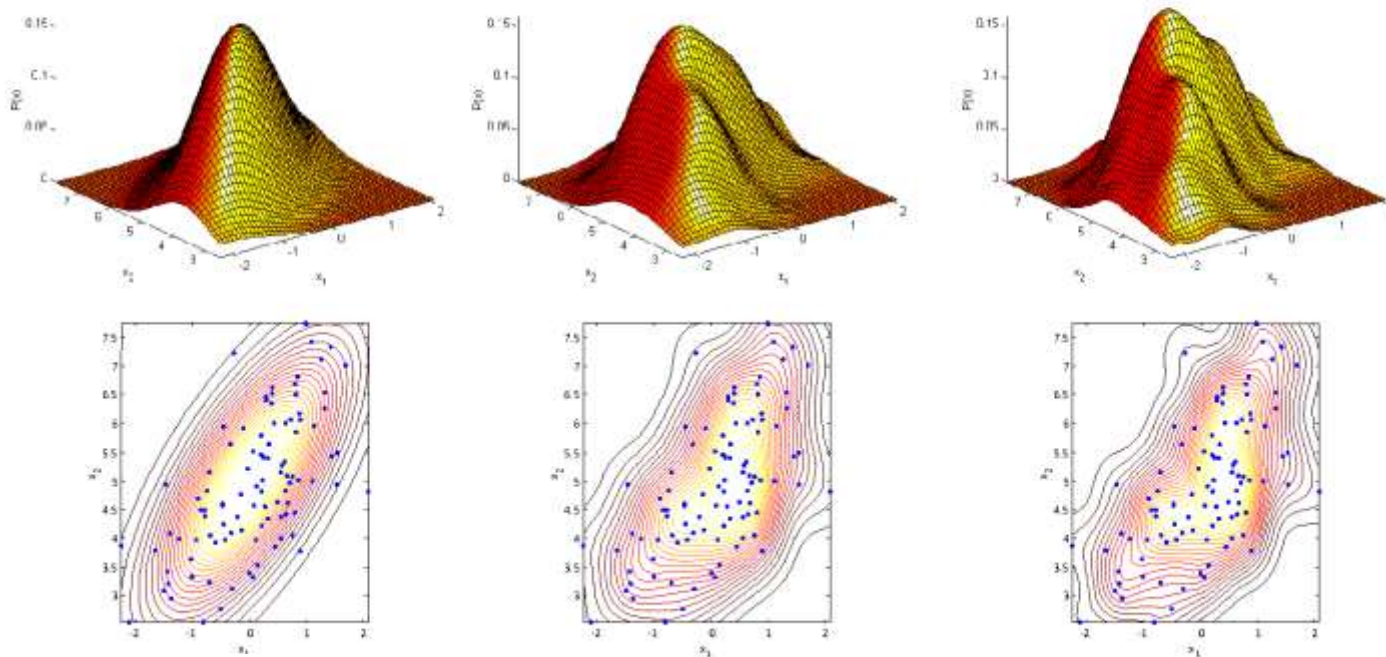
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 - Bandwidth selection can then be performed with any of the methods presented for univariate density estimation
- Note that although $K(x, x^{(n)}, h_1, \dots, h_D)$ uses kernel independence does not imply we assume the features are independent
 - If we assumed feature independence, the DE would have the expression

$$p_{FEAT-IND}(x) = \prod_{d=1}^D \frac{1}{N h_D} \sum_{i=1}^N K_d \left(\frac{x_d - x_d^{(n)}}{h_d} \right)$$

- Notice how the order of the summation and product are reversed compared to the product kernel

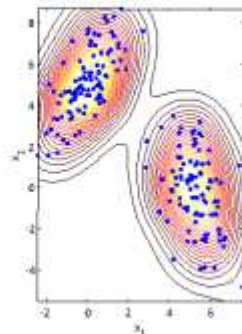
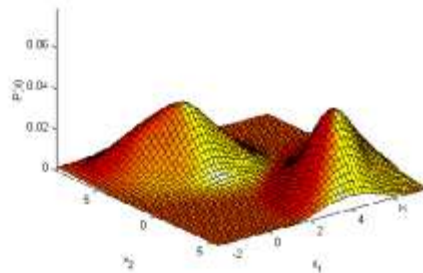
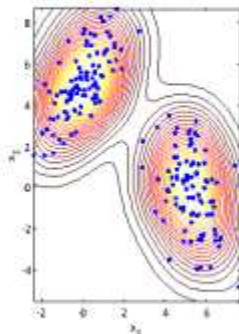
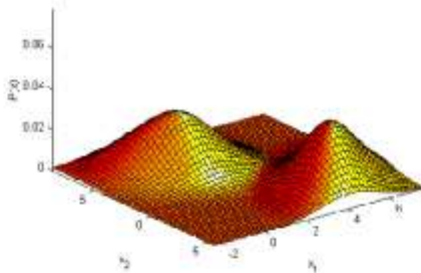
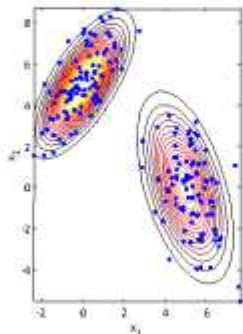
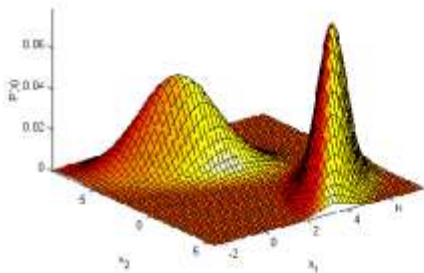
Example I

- This example shows the product KDE of a bivariate unimodal Gaussian
 - 100 data points were drawn from the distribution
 - The figures show the true density (left) and the estimates using $h = 1.06\sigma N^{-1/5}$ (middle) and $h = 0.9AN^{-1/5}$ (right)



Example II

- This example shows the product KDE of a bivariate bimodal Gaussian
 - 100 data points were drawn from the distribution
 - The figures show the true density (left) and the estimates using $h = 1.06\sigma N^{-1/5}$ (middle) and $h = 0.9AN^{-1/5}$ (right)



KDE

- <https://scikit-learn.org/stable/modules/density.html>

```
>>> from sklearn.neighbors.kde import KernelDensity
>>> import numpy as np
>>> X = np.array([[ -1, -1], [-2, -1], [-3, -2], [ 1,  1], [ 2,  1], [ 3,  2]])
>>> kde = KernelDensity(kernel='gaussian', bandwidth=0.2).fit(X)
>>> kde.score_samples(X)
array([-0.41075698, -0.41075698, -0.41076071, -0.41075698, -0.41075698,
       -0.41076071])
```

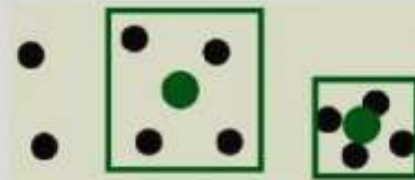
Connection between KDE and k-NN

$$p(x) \cong \frac{k}{NV} \text{ where } \begin{cases} V & \text{volume surrounding } x \\ N & \text{total \#examples} \\ k & \text{\#examples inside } V \end{cases}$$

- We can fix V and determine k from the data. This leads to **kernel density estimation** (KDE), the subject of this lecture
- We can fix k and determine V from the data. This gives rise to the **k-nearest-neighbor** (kNN) approach

Using k-NN for density estimation

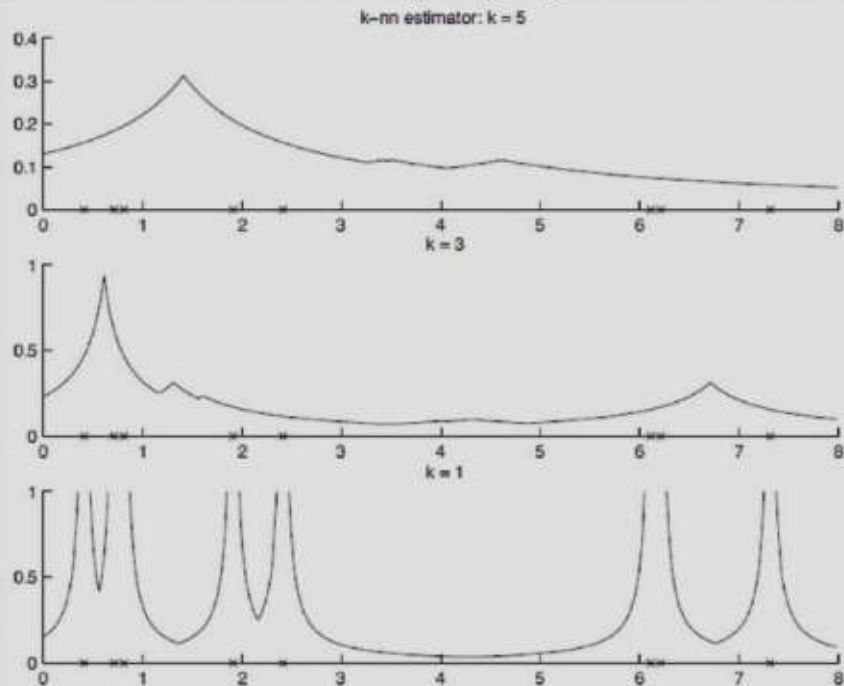
- The k-NN approach seems to be a good solution for the “optimal window size” problem
 - Center a cell on x and let it grow until it captures k samples
 - These k samples will be the k nearest neighbors of x
- The window size will change dynamically
 - If the samples are locally dense, then V will be small, and we obtain a more precise estimate
 - If the samples are sparse, then V is larger and the estimate is smoother



$$p(x) \cong \frac{k}{NV} \text{ where } \begin{cases} V & \text{volume surrounding } x \\ N & \text{total \#examples} \\ k & \text{\#examples inside } V \end{cases}$$

Using k-NN for density estimation

- For a larger k the estimate is better, but still not a valid distribution
- For small k the estimates are very “spiky”



References

- Duda-Hart: 4.1 – 4.6
- Bishop (PRML) : 2.5