Statistical Methods in AI (CSE/ECE 471)

Lecture-12: Nonparametric Density Estimation



Ravi Kiran (ravi.kiran@iiit.ac.in)

Vineet Gandhi (v.gandhi@iiit.ac.in)





Center for Visual Information Technology (CVIT)

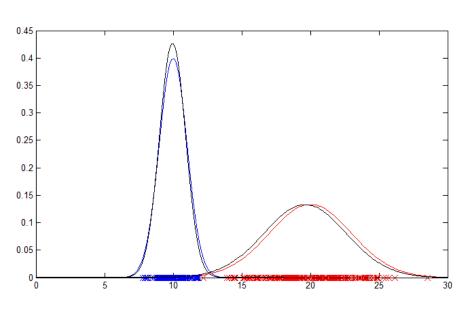
IIIT Hyderabad

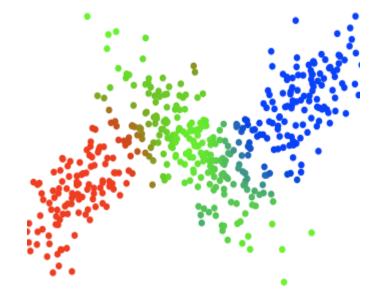
Unsupervised Learning → Density Estimation

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

Gaussian Mixture Model

$$p(\mathbf{x}) = \sum_{k=1}^{K} \pi_k \mathcal{N}(\mathbf{x}|\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)$$

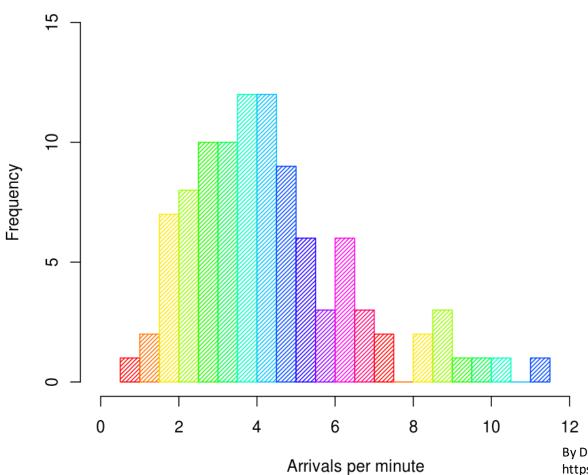




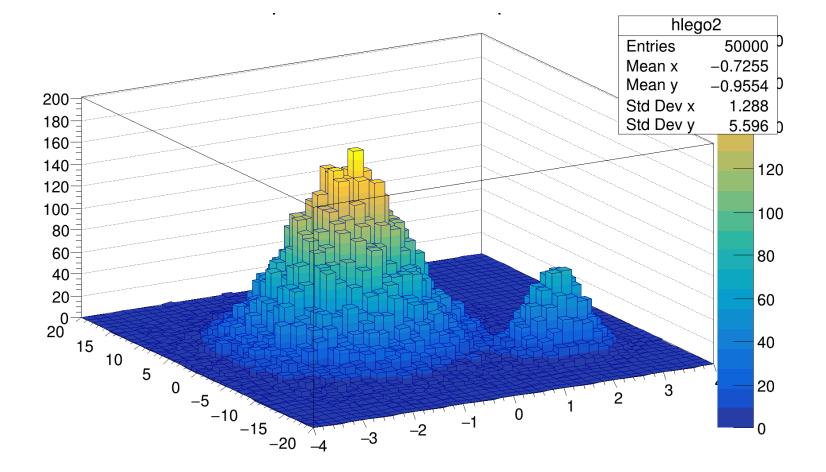
- What if component densities are not unimodal Gaussian?
- Can we get rid of K?

Non-parametric density estimation

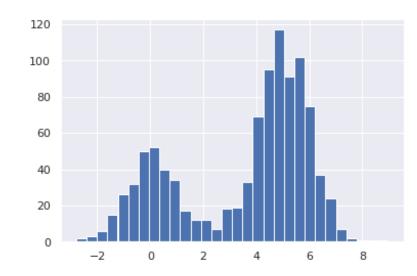
Histogram of arrivals



By DanielPenfield - Own work, CC BY-SA 3.0, https://commons.wikimedia.org/w/index.php?curid=9401898

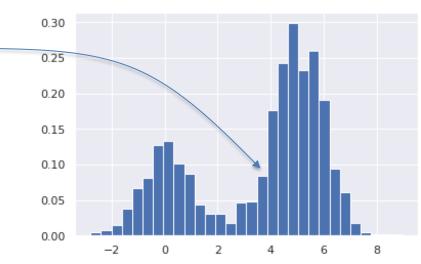


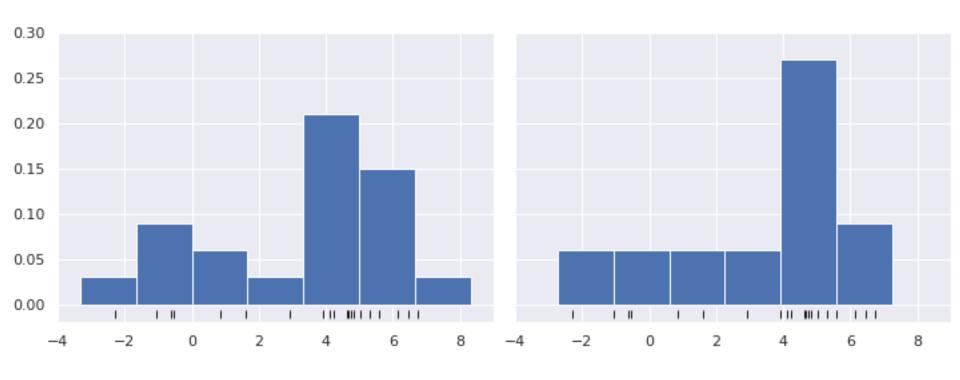
Normalizing a histogram → probability density



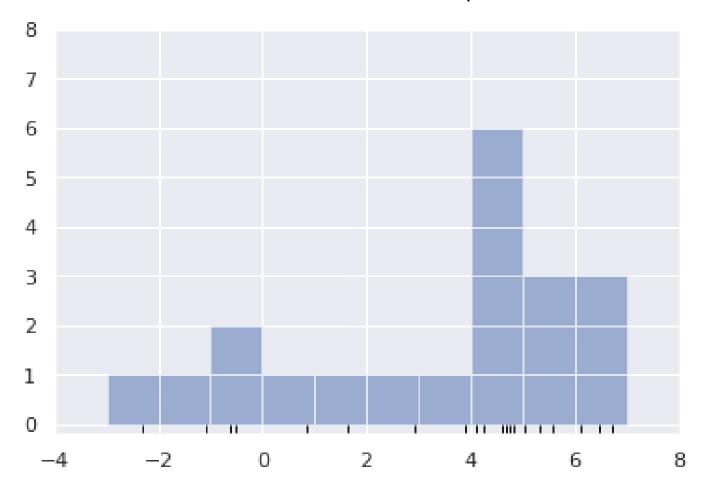
Probability that a random sample x will fall in this bin

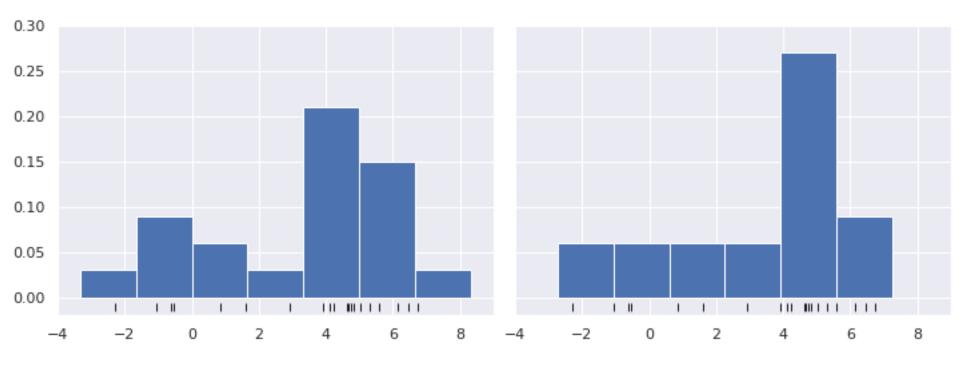
$$p_H(x) = \frac{1}{N} \frac{\left[\# \ of \ x^{(k} \ in \ same \ bin \ as \ x \right]}{\left[width \ of \ bin \right]}$$





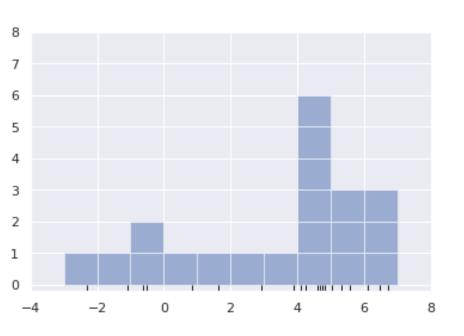
Histogram as a stack of unit sized blocks. Each data sample contributes towards a block.

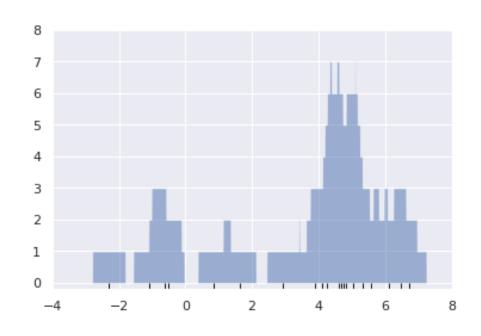




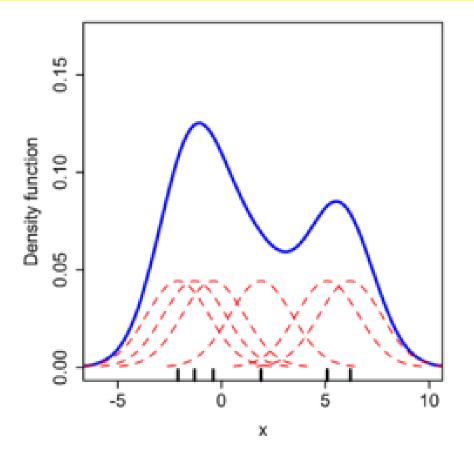
Why be at the mercy of binning parameters which are decided in a "data-blind" manner?

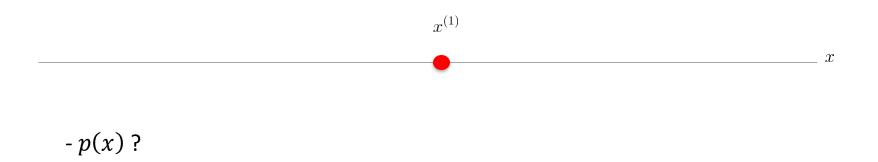
Alternative: Let data determine bin locations (and density at a location x).

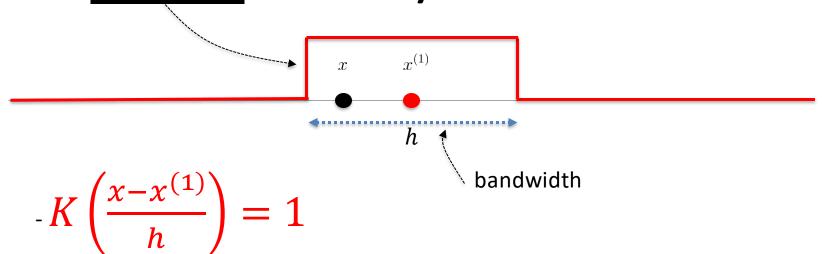




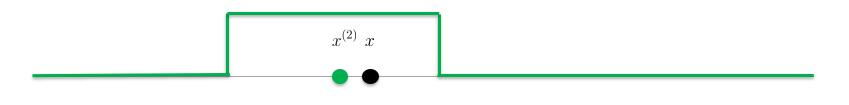
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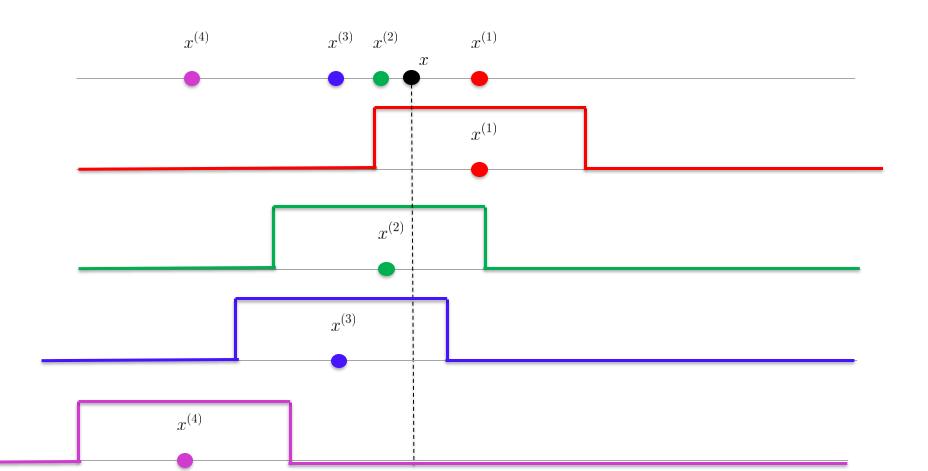


 $x^{(2)}$

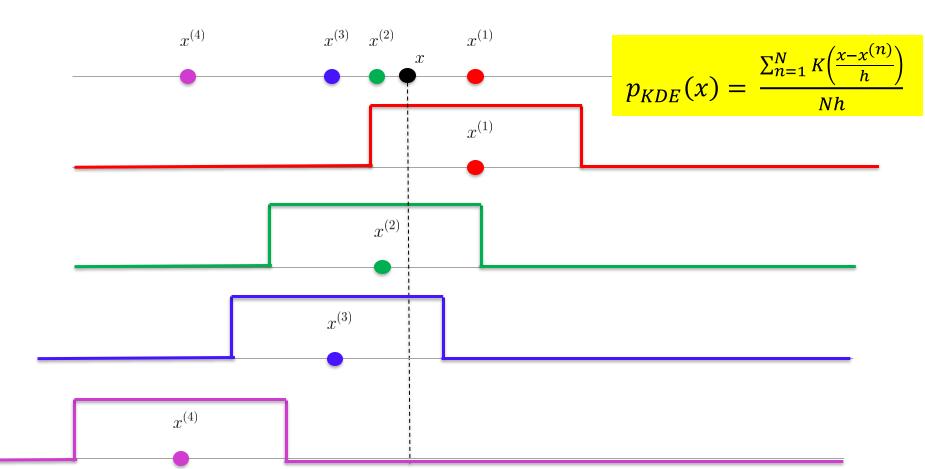


$$-K\left(\frac{x-x^{(2)}}{h}\right) = 1$$

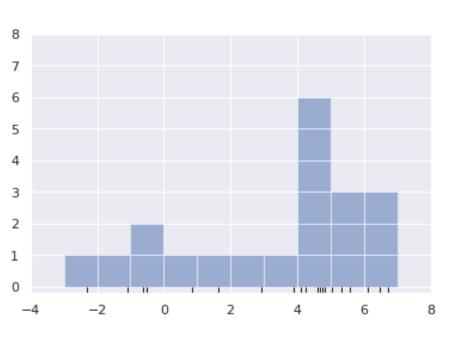
Parzen Window Density Estimation

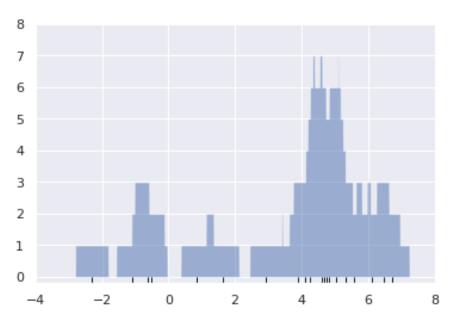


Parzen Window Density Estimation



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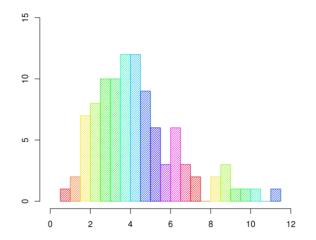


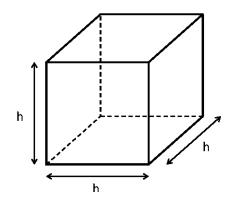


$$p_{KDE}(x) = \frac{\sum_{n=1}^{N} K\left(\frac{x-x^{(n)}}{h}\right)}{Nh}$$

Parzen Window Density Estimation

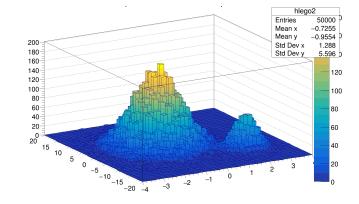
$$V = h^D$$





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

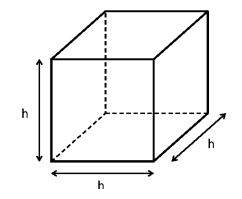
$$p_{KDE}(x) = \frac{1}{N} \frac{\sum_{n=1}^{N} K\left(\frac{x - x^{(n)}}{h}\right)}{V}$$

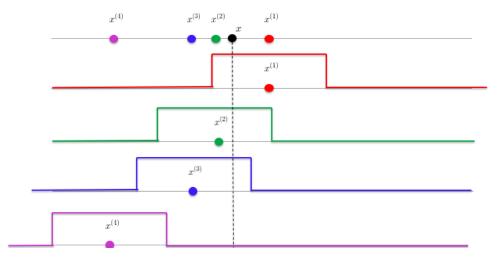


Parzen Window Density Estimation

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

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

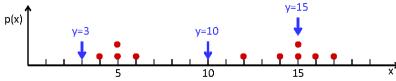




$_{KDE}(x) = \frac{1}{N} \frac{\sum_{n=1}^{N} K\left(\frac{x-x^{(n)}}{h}\right)}{V}$

Exercise

- Given dataset $X = \{4, 5, 5, 6, 12, 14, 15, 15, 16, 17\}$, use Parzen windows to estimate the density p(x) at y = 3,10,15; use h = 4
- Solution
 - Let's first draw the dataset to get an idea of the data

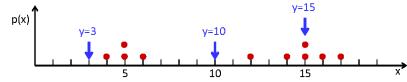


• Let's now estimate p(y = 3)

 $V = h^D$

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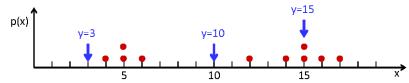


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$$p(y = 3) = \frac{1}{Nh^D} \sum_{n=1}^{N} K\left(\frac{x - x^{(n)}}{h}\right)$$

Exercise

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$$p(y=3) = \frac{1}{Nh^D} \sum_{n=1}^{N} K\left(\frac{x-x^{(n)}}{h}\right) = \frac{1}{10 \times 4^1} \left[K\left(\frac{3-4}{4}\right) + K\left(\frac{3-5}{4}\right) + \cdots + K\left(\frac{3-17}{4}\right) \right] = 0.0025$$

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Similarly

$$p(y = 10) = \frac{1}{10 \times 4^{1}} [0 + 0 + 0 + 0 + 0 + 0 + 0 + 0 + 0 + 0] = 0$$

$$p(y = 15) = \frac{1}{10 \times 4^{1}} [0 + 0 + 0 + 0 + 0 + 1 + 1 + 1 + 1 + 0] = 0.1$$

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

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 $K(\boldsymbol{u})$

$$\int_{PD} K(x) dx = 1$$

- 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

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

$$-1/2$$

$$-1/2$$

$$-1/2$$

$$-1/2$$

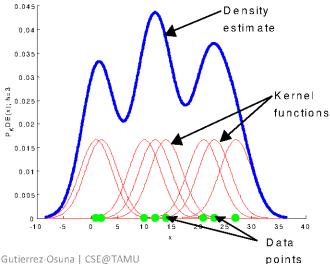
$$-1/2$$

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Interpretation

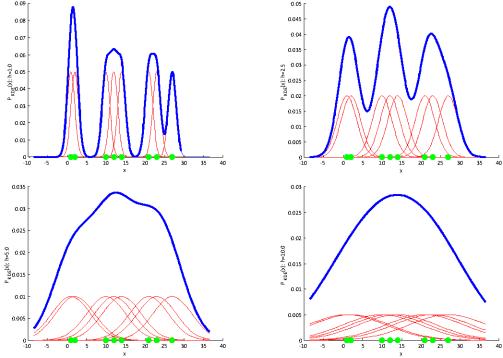
- Just as the Parzen window estimate can be seen as a sum of boxes centered at the data, the smooth kernel estimate is a sum of "bumps"
- The kernel function determines the shape of the bumps
- The parameter h, also called the <u>smoothing parameter</u> or <u>bandwidth</u>, determines their width

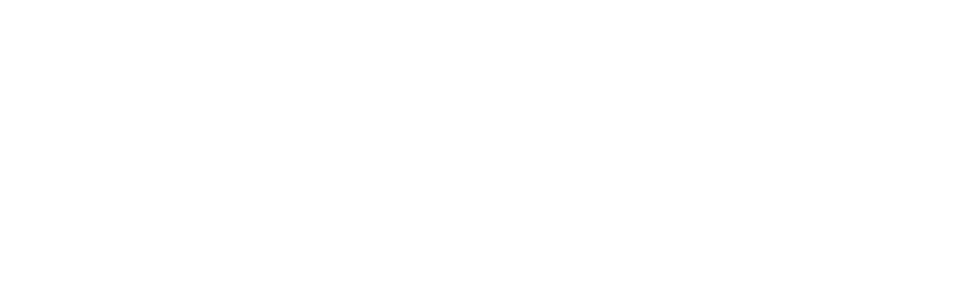


Bandwidth selection

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

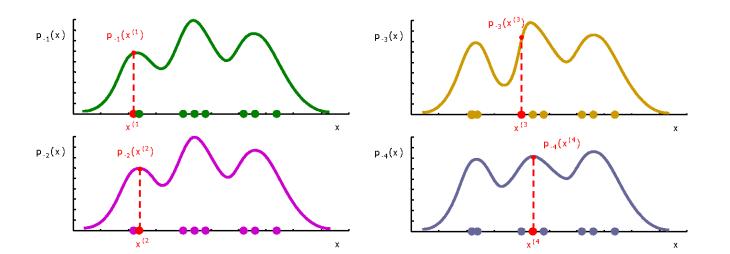
Maximum likelihood cross-validation

- 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

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

$$h^* = \arg\max\left\{\frac{1}{N} \sum_{n=1}^{N} log p_{-n}(x^{(n)})\right\}$$
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

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There are two basic alternatives to solve the scaling problem without having to use a more general KDE

- Pre-scaling each axis (normalize to unit variance, for instance)
- <u>Pre-whitening</u> the data (linearly transform so $\Sigma = I$), estimate the density, and then transform back [Fukunaga]
 - The whitening transform is $y = \Lambda^{-1/2} M^T x$, where Λ and M are the eigenvalue and eigenvector matrices of Σ
 - Fukunaga's method is equivalent to using a hyper-ellipsoidal kernel

Product kernels

A good alternative for multivariate KDE is the product kernel

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

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

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 $K(x, x^{(n)}, h_1, ... h_D)$ uses kernel independence features are independent

Product kernels

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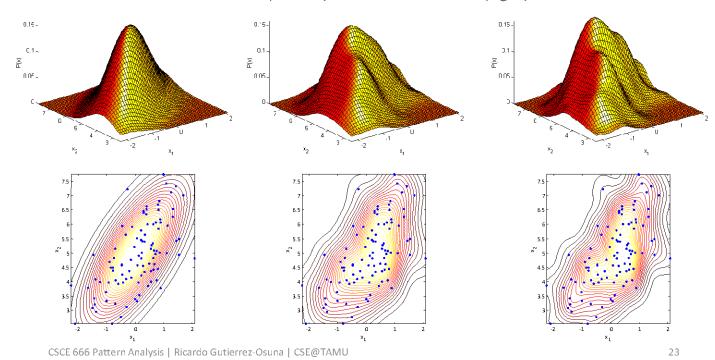
- The product kernel consists of the product of one-dimensional kernels
 - Typically the same kernel function is used in each dimension $(K_d(x) = K(x))$, and only the bandwidths are allowed to differ
- Note that although $K(x, x^{(n)}, h_1, ... h_D)$ uses kernel independence does not imply we assume the features are independent
 - If we assumed feature independence, the DE would have the expression

$$p_{FEAT-IND}(x) = \prod_{d=1}^{D} \frac{1}{Nh^{D}} \sum_{i=1}^{N} K_{d} \left(\frac{x_{d} - x_{d}^{(n)}}{h_{d}} \right)$$

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

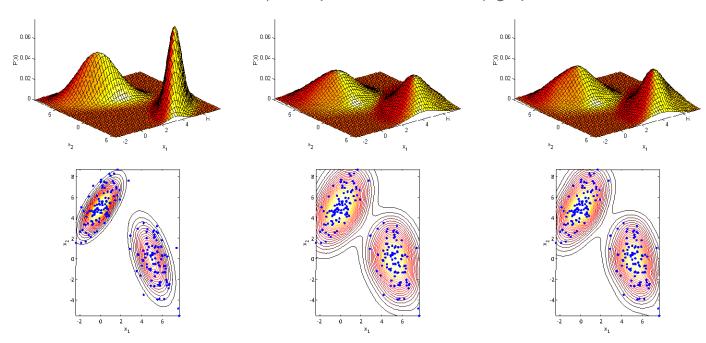
Example I

- This example shows the product KDE of a bivariate <u>unimodal</u> 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 <u>bimodal</u> 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, -0.41075698, -0.41075698, -0.41075698, -0.41076071])
```

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

- 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



— The probability that a vector x, drawn from a distribution p(x), will fall in a given region \Re of the sample space is

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

a given region \Re of the sample space is

$$P = \int p(x')dx$$

- The probability that a vector x, drawn from a distribution p(x), will fall in

- Suppose now that N vectors $\{x^{(1)}, x^{(2)}, ..., x^{(N)}\}$ are drawn from the distribution; the probability that k of these N vectors fall in \Re is given by

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

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

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

- Suppose now that N vectors $\{x^{(1)}, x^{(2)}, ..., x^{(N)}\}$ are drawn from the distribution; the probability that k of these N vectors fall in \Re is given by

 $P(k) = \binom{N}{k} P^k (1 - P)^{N-k}$

distribution; the probability that
$$k$$
 of these N vectors fall in \Re is given by the binomial distribution

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$$P(k) = {N \choose k} P^k (1 - P)^{N-k}$$
- It can be shown (from the properties of the binomial p.m.f.) that the mean

and variance of the ratio k/N are

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

the binomial distribution

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

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- Suppose now that N vectors $\{x^{(1)}, x^{(2)}, ..., x^{(N)}\}$ are drawn from the distribution; the probability that k of these N vectors fall in \Re is given by the binomial distribution

$$P(k) = \binom{N}{k} P^{k} (1 - P)^{N-k}$$

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

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

— Therefore, as $N \to \infty$ 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 \Re

$$P \cong \frac{\kappa}{N}$$
 [Bishop, 1995]

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

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

• where V is the volume enclosed by region \Re

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

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- where V is the volume enclosed by region \Re
- Merging with the previous result we obtain

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$$P = \int_{-\infty}^{\infty} \frac{du'}{du'} du' = \frac{\partial u}{\partial u} du'$$

 $P = \int_{\Re} p(x')dx' \cong p(x)V$ $P \cong \frac{k}{N}$ $P \cong \frac{k}{N}$

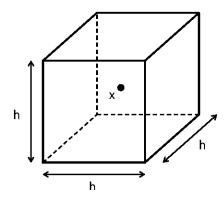
 In conclusion, the general expression for non-parametric density estimation becomes

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

Parzen windows

Problem formulation

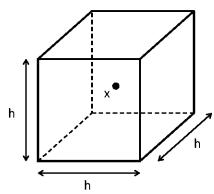
- Assume that the region \Re that encloses the k examples is a hypercube with sides of length h centered at x
 - Then its volume is given by $V = h^D$, where D is the number of dimensions



Parzen windows

Problem formulation

- Assume that the region \Re 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



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

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

- 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

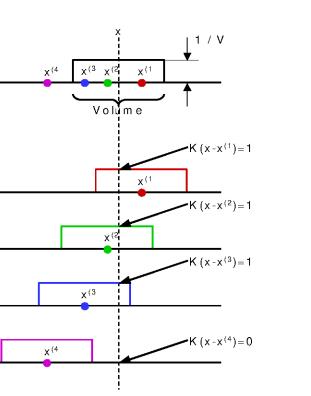
- The total number of points inside the hypercube is then $(x - x^{(n)})$

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

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

 Notice how the Parzen window estimate resembles the histogram, with the exception that the bin locations are determined by the data



Using KDE for visualization

Geographic distributions of recorded observations of two South American mammals, *Bradypus variegatus* (the Brown-throated Sloth) and *Microryzomys minutus* (the Forest Small Rice Rat)



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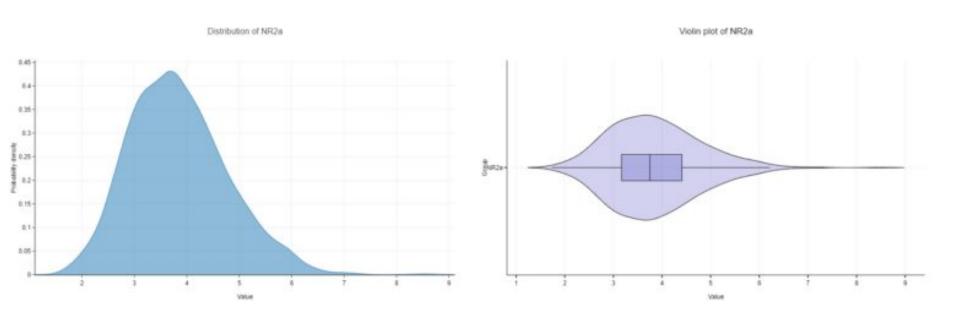
Forest Small Rice Rat)



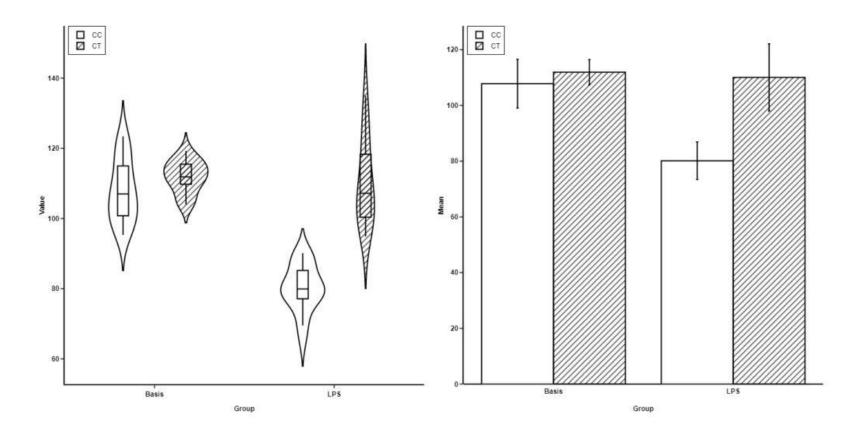




Using KDE for visualization – violin plot



Using KDE for visualization – violin plot



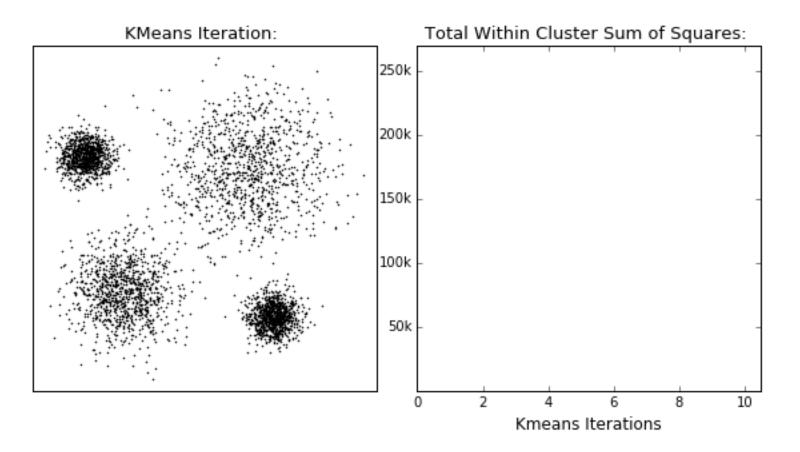
KDE

- Non-parametric density estimation → generative
- Advantage: Data-driven, Data-adaptive
- Disadvantage: Need to keep around all data samples to estimate the density, sensitive to bandwidth 'h' and choice of kernel

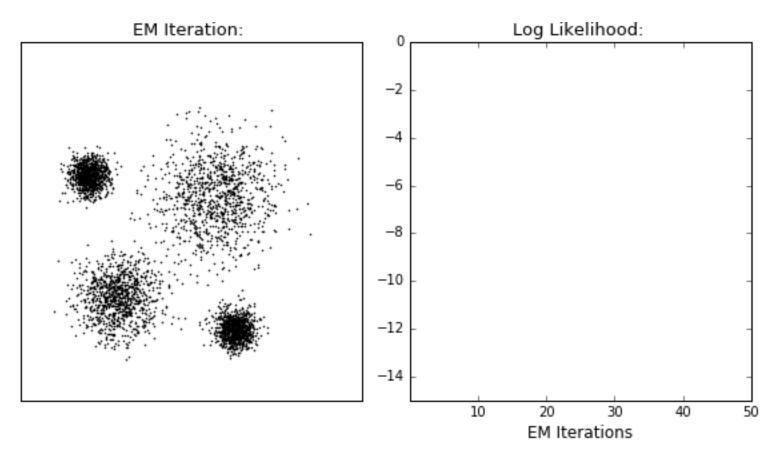
References

- Duda, Hart: 4.1, 4.2, 4.3.1 4.3.3, 4.4.1
- PRML (Bishop) : 2.5

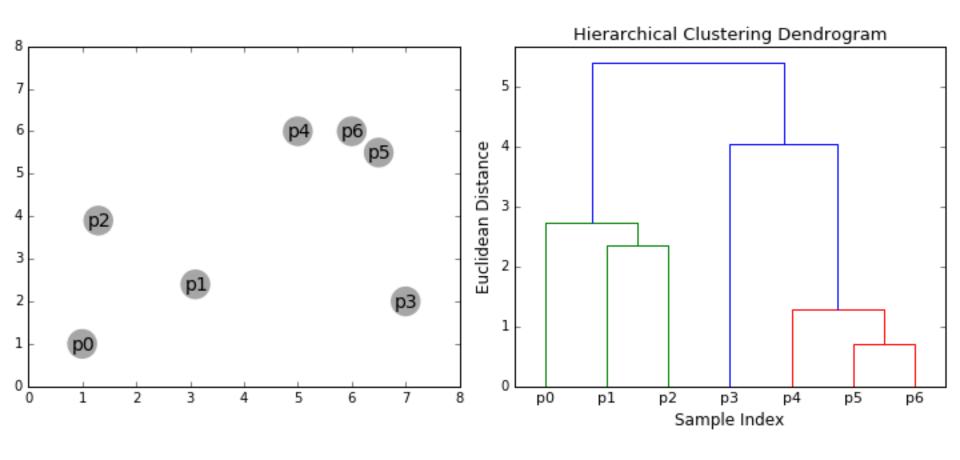
K-means



 GMM



Hierarchical Clustering



Application of KDE – mean shift clustering

