# MO433 - Unsupervised Learning Probability Density Functions (PDFs)

Alexandre Xavier Falção

Institute of Computing - UNICAMP

afalcao@ic.unicamp.br

# Bayes' theorem for classification

Let  $x = (x_1, x_2, ..., x_n) \in \mathbb{R}^n$  be a continuous random variable vector (a feature vector) and  $y \in \{1, 2, ..., K\}$  be a discrete random variable of the class label of each sample x in a dataset.

### Bayes' theorem

$$P(y = k|x) = \frac{p(x|y = k)P(y = k)}{p(x)}$$

#### Where:

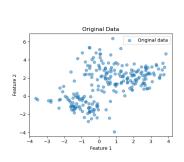
- ▶ P(y = k|x) is the **posterior probability** of class k given features x.
- ightharpoonup p(x|y=k) is the **class-conditional PDF** (likelihood).
- ightharpoonup P(y=k) is the **prior probability** of class k.
- $p(x) = \sum_{k=1}^{K} p(x|y=k)P(y=k)$  is the **marginal PDF** (evidence).

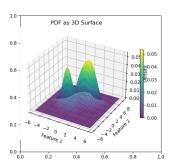
In this case, the **joint distribution** is p(x, y).



# Geometric interpretation

- $\times = (x_1, \dots, x_n)^T \in \mathbb{R}^n$  continuous feature vector.
- ightharpoonup p(x) defines a surface (manifold) in  $\mathbb{R}^{n+1}$ .
- ▶ The (n+1)-th dimension represents density values.





# From classification to generation

- For classification tasks, we want to determine P(y = k|x) the probability that a feature vector x belongs to class k.
- ▶  $p(x) = \sum_{j=1}^{K} p(x|y=j)P(y=j)$  is our main challenge to estimate.
- ▶ The techniques could also be applied to p(x|y = k), if you use only samples from a class k.
- Nowledge of p(x) combined with labeled **representative** samples enables semi-supervised classification (pseudo-labeling) of unlabeled data.

We will be interested in using p(x) to generate new representative samples.

# Agenda

Goal: PDF estimation from finite data samples, challenges, and applications.

- 1. Non-parametric methods make minimal assumptions about p(x).
- 2. Parametric methods Assume p(x) follows a known family (e.g., Gaussian).
- 3. Manifolds and curse of dimensionality.
- 4. Applications: KL divergence, model comparison, and a real example.

# Non-parametric PDF estimation

For a dataset with N samples, the methods usually rely on a region R of volume V around each sample x.

$$p(\mathbf{x}) = \lim_{V \to 0} \frac{\mathsf{Number of points in region } R \mathsf{ around } \mathbf{x}}{\mathit{N} \cdot \mathit{V}}$$

The region R may be:

- ▶ A hypercube of side h (bandwidth) and volume  $V = h^n$ .
- A hypersphere of radius h (bandwidth) and volume

$$V = \frac{\pi^{n/2}}{\Gamma(\frac{n}{2} + 1)} h^n$$

where  $\Gamma$  is Euler's gamma function (preferred).

### Kernel-based methods

An exponential kernel is used around each sample x in both approaches:

$$\phi\left(\frac{\mathsf{x}_i - \mathsf{x}}{h}\right) = \exp\left(-\frac{\|\mathsf{x}_i - \mathsf{x}\|^2}{2h^2}\right)$$

The density estimate becomes:

$$p(x) = \frac{1}{N \cdot V} \sum_{i \in S} \phi\left(\frac{x_i - x}{h}\right)$$

where S is the set of samples to consider.

- 1. **Parzen Window:**  $S = \{1, 2, ..., N\}$  (all samples), V is fixed hypersphere volume (see code1-parzen\_window.py).
- 2. **k-NN:**  $S = \{k \text{ nearest neighbors}\}, V \text{ adapts to contain exactly } k \text{ samples (see code2-knn_density.py)}.$

# Curse of Dimensionality

Let R be a hypersphere with radius h = 1, its volume  $V_n$  shrinks dramatically as the dimension n increases.

- ► n = 2:  $V_2(1) = \pi \approx 3.14$
- ▶ n = 5:  $V_5(1) \approx 5.26 \leftarrow Peak$
- ▶ n = 10:  $V_{10}(1) \approx 2.55 \leftarrow Declining$
- ► n = 20:  $V_{20}(1) \approx 0.026 \leftarrow \text{Tiny!}$
- ▶ n = 100:  $V_{100}(1) \approx 10^{-40} \leftarrow \text{Negligible!}$

Neighbors are far away as n increases, making the data points isolated and so the density estimates become unreliable.

Conversely, to maintain unit volume, radius must grow drastically (see code3-curse\_dimensionality.py).

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### Bottom Line

Parzen window and k-NN methods may fail for n > 10 dimensions.



### Parametric PDF estimation

Assuming that p(x) belongs to a known parametric family, the problem is to estimate its parameters  $\theta$  from the data samples.

**Example:** A multivariate Gaussian distribution.

$$p(\mathsf{x}) = \mathcal{N}(\mathsf{x}|\boldsymbol{\mu},\boldsymbol{\Sigma}) = \frac{1}{(2\pi)^{n/2}|\boldsymbol{\Sigma}|^{1/2}} \exp\left(-\frac{1}{2}(\mathsf{x}-\boldsymbol{\mu})^T\boldsymbol{\Sigma}^{-1}(\mathsf{x}-\boldsymbol{\mu})\right)$$

where  $x, \mu \in \mathbb{R}^n$  and  $\Sigma \in \mathbb{R}^{n \times n}$  is positive definite (i.e.,  $x^T \Sigma x > 0$ ).

#### Parameters $\theta$ :

- $\mu = (\mu_1, \dots, \mu_n)^T$ : mean vector.
- $\triangleright \Sigma$ :  $n \times n$  covariance matrix.

# Parameter estimation by maximum likelihood

Given N data samples  $\{x_1, \dots, x_N\}$ , the maximum likelihood estimates

$$\hat{oldsymbol{\mu}} = rac{1}{N} \sum_{i=1}^{N} \mathsf{x}_i \ \hat{oldsymbol{\Sigma}} = rac{1}{N} \sum_{i=1}^{N} (\mathsf{x}_i - \hat{oldsymbol{\mu}}) (\mathsf{x}_i - \hat{oldsymbol{\mu}})^T$$

# Whitening Transform: Data decorrelation

For  $\mathsf{x} \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Sigma})$ , let

- ightharpoonup Q be the eigenvectors of  $\Sigma = Q\Lambda Q^T$ , which define the principal axes of the data distribution, and
- $\Lambda = \text{diag}(\lambda_1, \dots, \lambda_n)$  be its eigenvalues that define spread.

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The whitening transform defines the latent

$$\mathsf{z} = \mathbf{\Sigma}^{-1/2}(\mathsf{x} - oldsymbol{\mu}) \sim \mathcal{N}(\mathsf{0}, \mathsf{I})$$

where

$$egin{aligned} \mathbf{\Sigma}^{-1/2} &= \mathsf{Q} \mathbf{\Lambda}^{-1/2} \mathsf{Q}^{\mathcal{T}} \ \mathbf{\Lambda}^{-1/2} &= \mathsf{diag}(1/\sqrt{\lambda_1}, \dots, 1/\sqrt{\lambda_n}) \ p(\mathsf{z}) &= rac{1}{(2\pi)^{n/2}} \exp\left(-rac{1}{2}\|\mathsf{z}\|^2
ight) \end{aligned}$$

**Applications:** Generative models and dimensionality reduction. See code4-whitening\_transform.py and code5-gaussian\_analysis.py.



# Other computational simplification

Many generative models (VAEs, normalizing flows) assume diagonal covariance for computational efficiency, sometimes applying implicit whitening.

$$\boldsymbol{\Sigma} = \mathsf{diag}(\sigma_1^2, \dots, \sigma_n^2)$$

Simplified Gaussian with independent variables:

$$p(x) = p(x_1)p(x_2)\dots p(x_n)$$

$$p(x) = \prod_{i=1}^{n} \frac{1}{\sqrt{2\pi\sigma_i^2}} \exp\left(-\frac{(x_i - \mu_i)^2}{2\sigma_i^2}\right)$$

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### Computational simplification:

This simplification reduces from  $\frac{n(n+1)}{2}$  parameters in the full covariance to n parameters in the diagonal one.



### Mixture of Gaussians

Real data often exhibits multiple clusters/modes (components).

Solution: Mixture of Gaussians (MoG)

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

#### where:

- K is the number of components.
- $\bullet$   $\pi_k \ge 0$  are mixing weights with  $\sum_{k=1}^K \pi_k = 1$ .
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#### Parameters to estimate:

$$\boldsymbol{\theta} = \{\pi_1, \dots, \pi_K, \boldsymbol{\mu}_1, \dots, \boldsymbol{\mu}_K, \boldsymbol{\Sigma}_1, \dots, \boldsymbol{\Sigma}_K\}$$



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How do we estimate  $\theta$ ?



# KL Divergence: log-likelihood maximization

A PDF defined for the data samples only is

$$p_{data}(x) = \frac{1}{N} \sum_{i=1}^{N} \delta(x - x_i)$$

where  $\delta$  is the Kronecker's delta. The KL divergence:

$$D_{KL}(p_{data}(x)||p(x;\theta)) = \int_{\mathbb{R}^n} p_{data}(x) \log \frac{p_{data}(x)}{p(x;\theta)} dx$$
$$= \int_{\mathbb{R}^n} p_{data}(x) \log p_{data}(x) dx - \int_{\mathbb{R}^n} p_{data}(x) \log p(x;\theta) dx$$

$$= C - \frac{1}{N} \int_{\mathbb{R}^n} \sum_{i=1}^N \delta(\mathbf{x} - \mathbf{x}_i) \log p(\mathbf{x}; \boldsymbol{\theta}) d\mathbf{x} = C - \frac{1}{N} \sum_{i=1}^N \log p(\mathbf{x}_i; \boldsymbol{\theta})$$

where the term  $\ell(\theta) = \sum_{i=1}^{N} \log p(\mathbf{x}_i; \theta)$  is the log-likelihood.



# KL Divergence: log-likelihood maximization

Since  $p(x; \theta) = \sum_{k=1}^{K} \pi_k \mathcal{N}(x|\mu_k, \Sigma_k)$ , direct maximum likelihood estimation is intractable due to sum inside logarithm

$$\ell(oldsymbol{ heta}) = \sum_{i=1}^{N} \log \left( \sum_{k=1}^{K} \pi_k \mathcal{N}(\mathsf{x}_i | oldsymbol{\mu}_k, oldsymbol{\Sigma}_k) 
ight)$$

However, minimizing KL divergence is equivalent to maximizing  $\ell(\boldsymbol{\theta}).$ 

$$\min_{\boldsymbol{\theta}} D_{KL}(p_{data}(\mathbf{x})||p(\mathbf{x};\boldsymbol{\theta})) \equiv \max_{\boldsymbol{\theta}} \sum_{i=1}^{N} \log p(\mathbf{x}_{i};\boldsymbol{\theta})$$

See code6-kl\_divergence.py

**Key idea:** Introduce latent variables  $z_{ik} \in \{0,1\}$ 

- $ightharpoonup z_{ik} = 1$  if  $x_i$  belongs to component k, 0 otherwise
- ▶ Only one  $z_{ik} = 1$  per data sample  $x_i$

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### Complete data log-likelihood

$$\ell_c(\boldsymbol{\theta}) = \sum_{i=1}^N \sum_{k=1}^K z_{ik} [\log \pi_k + \log \mathcal{N}(\mathsf{x}_i | \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)]$$

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### **EM Algorithm alternates:**

- 1. **E-step:** Compute  $\gamma_{ik}^{(t)} = E[z_{ik}|x_i, \theta^{(t)}] = P(z_{ik} = 1|x_i, \theta^{(t)})$
- 2. **M-step:** Maximize  $E[\ell_c(\theta^{(t)})]$  w.r.t.  $\theta^{(t)}$

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Guaranteed: Monotonic increase in likelihood until convergence

# EM Algorithm from $\boldsymbol{\theta}^{(0)} = \{\pi_k^{(0)}, \boldsymbol{\mu}_k^{(0)}, \boldsymbol{\Sigma}_k^{(0)}\}$

1: repeat

2: **E-step:** For each i, k:

$$\gamma_{ik}^{(t+1)} = \frac{\pi_k^{(t)} \mathcal{N}(\mathbf{x}_i | \boldsymbol{\mu}_k^{(t)}, \boldsymbol{\Sigma}_k^{(t)})}{\sum_{j=1}^K \pi_j^{(t)} \mathcal{N}(\mathbf{x}_i | \boldsymbol{\mu}_j^{(t)}, \boldsymbol{\Sigma}_j^{(t)})}$$

3: **M-step:** Update parameters:

$$egin{aligned} \mathcal{N}_k^{(t+1)} &= \sum_{i=1}^N \gamma_{ik}^{(t+1)} \ &\pi_k^{(t+1)} &= rac{\mathcal{N}_k^{(t+1)}}{\mathcal{N}}, \quad oldsymbol{\mu}_k^{(t+1)} &= rac{1}{\mathcal{N}_k^{(t+1)}} \sum_{i=1}^N \gamma_{ik}^{(t+1)} \mathbf{x}_i \ &\Sigma_k^{(t+1)} &= rac{1}{\mathcal{N}_k^{(t+1)}} \sum_{i=1}^N \gamma_{ik}^{(t+1)} (\mathbf{x}_i - oldsymbol{\mu}_k^{(t+1)}) (\mathbf{x}_i - oldsymbol{\mu}_k^{(t+1)})^T \end{aligned}$$

4:  $t \leftarrow t + 1$ 

5: until 
$$|\ell_c(\boldsymbol{\theta}^{(t+1)}) - \ell_c(\boldsymbol{\theta}^{(t)})| < \epsilon$$
.



### Model Selection: AIC and BIC

**Problem:** How many components K should we use in GMM?

- ► Too few → underfitting (high bias)
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Solution: Information criteria balance fit vs. complexity

Akaike Information Criterion (AIC)

$$AIC(K) = -2\ell(\theta) + 2r$$

Bayesian Information Criterion (BIC)

$$BIC(K) = -2\ell(\theta) + r \log N$$

where r is the number of parameters.

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**Strategy:** Choose K that minimizes AIC or BIC (code7-em\_algorithm.py).



## Real-world example

Let a store dataset with regular, premium, and occasional customers to study their behavior.

Customer vectors 
$$x = (x_1, x_2) \in \mathbb{R}^2$$

- $\triangleright$   $x_1$ : Monthly spending (\$).
- ► x<sub>2</sub>: Visit frequency (visits/month).

File: code8-customer\_analysis.py

### Preview of the next lecture

Real-world data often lives in high-dimensional spaces ( $n \gg 10$ ) where:

- Direct visualization is impossible.
- Traditional density estimation fails.
- We need dimensionality reduction techniques.

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### Fundamental questions

- ▶ How can we visualize PDFs in  $\mathbb{R}^{100+}$ ?
- What is the intrinsic dimensionality of real data?
- ▶ How do we preserve PDF structure when reducing dimension?

