Unsupervised Learning with discrete latent variable models

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Organization

Thursdays 8h30 - 11h45, this room.

$6 \times$ 3h classes

1h30 class + 1h30 practical session (except today)

Important: you need one computer/person for practical sessions

Evaluation

1. CC: assiduity, practical session
2. Final exam on Friday 12th January, 2024
3. $\max(\text{Exam}, \text{mean}(\text{Exam}, \text{CC}))$

Bibliography & relevant sources

- Kevin P. Murphy (2022). *Probabilistic Machine Learning: An introduction*. MIT Press
- Trevor Hastie et al. (2001). *The Elements of Statistical Learning*. Springer Series in Statistics. New York, NY, USA
- Christopher M. Bishop (2007). *Pattern Recognition and Machine Learning (Information Science and Statistics)*. Springer

Some relevant lecture/slides on the topic for a different point-of-view (⚠notations)

- S. Robin lectures
-

Introduction

Types of statistical learning

Supervised

Data $\mathcal{D} = \{(x_i, y_i)\}_{i=1}^n$ with y_i an output (*response*) and x_i some features (*covariates*).
The goal is to learn a good predictor $\hat{f}$ such that $y_i \approx \hat{f}(x_i)$ that generalizes well on new data.

Unsupervised (this course)

The data $\mathcal{D} = \{x_i\}_{i=1}^n$ The goal is to learn "interesting" and hidden structure in the data to

- partition the data, aka clustering
- visualize/compress the data, aka dimension reduction

Generative models: posit a statistical model on the distribution of (X_i)

Many flavors in modern ML

semi-supervised, self-supervised, reinforcement learning, multi-task, etc.

What this course is about...

(Discrete) latent variables models for unsupervised learning

$\rightsquigarrow$ we will assume the generative process of X involves an unobserved (latent) variable Z

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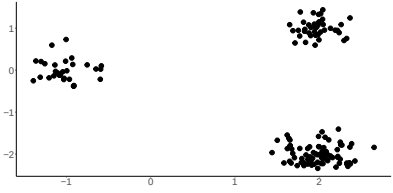
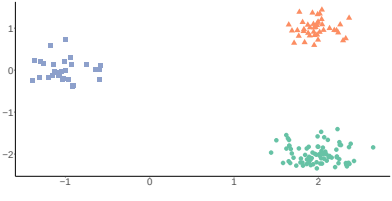
Clustering

X is an unlabeled observation and Z its group membership





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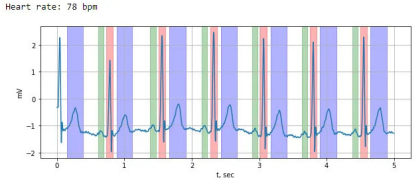
Time series segmentation

X is the temporal signal and Z the cardiac phase



Example of ECG annotation, source: `https://medium.com/data-analysis-center/56f8b9abd83a`

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(Discrete) latent variables models for unsupervised learning

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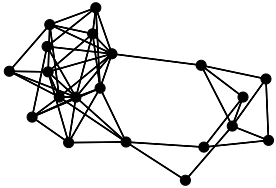
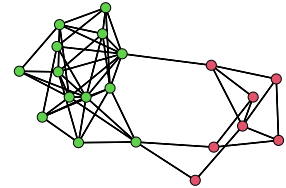
Node clustering in a network





X is the graph (connection between node) and Z the group of the node (community)

Course outline

1. **Fundamentals of Bayesian statistics**
2. **Clustering with mixture models**
3. **Inference in latent variable models: the EM algorithm**
4. **Hidden Markov Models (HMMs)**
5. **Stochastic Block Model: an introduction to variational inference**

Fundamentals of Bayesian statistics

Bayes formula

Frequentist inference

Assumption: the observation $\boldsymbol{x} = (x_1, \dots, x_n) \in \mathcal{X}^n$ is a realization of a random vector $\boldsymbol{X} = \{X_1, \dots, X_n\}$ with distribution $p_{\theta^\star}$.

Posit: a statistical model $\{p_\theta,\ \theta \in \Theta\}$, *i.e.* a family of parametric distribution on $\mathcal{X}^n$

Goal: Provide an estimate $\hat{\theta}$ of $\theta^\star$. [1]

Maximum-likelihood estimation

Find the model, hence θ, that maximizes the probability of having seen the data

$$\hat{\theta}_n \in \arg\max_{\theta \in \Theta} \log p_\theta(x_1, \dots, x_n) \qquad \text{(MLE)}$$

[1] and eventually derive theoretical guarantees such as convergence and confidence intervals on $\hat{\theta}_n(X_1, \dots, X_n)$ (*e.g.* via central limit theorem)

The Bayesian paradigm

Maximum-likelihood and frequentist statistics produces *point estimates*

Paradigm shift: random parameters

Parameters θ are no longer treated as deterministic but as *random* quantities. The *prior* distribution, denoted as $\pi(\theta)$, encodes knowledge & uncertainty we have on the parameters **before** seeing new data.
$\rightsquigarrow$ the goal is to update this a priori knowledge when new data comes: this is the essence of Bayes formula.

A bit of history...

The terminology *Bayesian* has been coined that way thanks to the work of Reverend Thomas Bayes (1701-1761) and his posthumous *essay in view of solving the doctrine of chance*. Pierre-Simon Laplace independently proposed a version in 1774.
N.B. : this course will not settle the somewhat sterile debate "Bayesian VS Frequentist".

Bayes formula

Equipped with a prior $\pi(\theta)$, we posit an observational model on $X \mid \theta \iff$ the likelihood. Bayesian modelization essentially adds one layer to frequentist models : the prior.

1. $\theta \sim \pi$, (prior)
2. $X \mid \theta \sim p(\cdot \mid \theta) = p_\theta$ (likelihood).

The posterior

Given a realization x, we update our prior via a new distribution called the *posterior*:

$$\pi(\theta \mid x) = \frac{p(x \mid \theta)\pi(\theta)}{Z}, \qquad \text{(Bayes formula)}$$

Here, $Z = \int_\Theta p(x \mid \theta)\pi(\theta)\,\mathrm{d}\theta$ is a normalization constant, independent of θ. Thus, it is common to write[a]

$$\pi(\theta \mid x) \propto p(x \mid \theta)\pi(\theta)$$

[a] Although computing this normalization constant is generally a challenging task in Bayesian statistics.

Choosing a prior

Expert knowledge

The prior π may be used to represent any available expert knowledge on θ.

Conjugate priors

When the prior π and the posterior $\pi(\cdot \mid x)$ belong to the same family of distributions (e.g. Gaussian, Beta, etc.), then we say that the prior is *conjugate* to the observational model $p(x \mid \theta)$. Skip to an example

Conjugate priors are widely used as they greatly simplify computations.

Uninformative prior

When the prior equally charges Θ we say that the prior is *uninformative*, noted $\pi(\theta) \propto 1$. Obviously, $\pi \propto 1$ does not always define a proper p.d.f. (consider $\Theta = \mathbb{R}$). Still, as long as the posterior is well defined (*i.e.* the normalization constant Z exists and is finite) then we can still use the posterior $\pi(\theta \mid x)$ and the prior is *improper*.

Example of conjugacy: the Beta-Binomial model (1)

Experiment & question Given a sequence of independent coin flips $\boldsymbol{x} = \{x_1, \ldots, x_n\}$, determine the probability of getting tail.

Observational model: the likelihood
Given a probability of tail θ, we model the random vector $\boldsymbol{X} = (X_1, \ldots, X_n)$ as *i.i.d.* Bernoulli $X_i \sim Ber(\theta)$ so that

$$p(\boldsymbol{X} \mid \theta) = \prod_{i=1}^{n} Ber(x_i \mid \theta) = \theta^{\sum_i x_i}(1-\theta)^{\sum_i 1-x_i}.$$

Choice of a prior
We use Beta distribution with support $\Theta = [0, 1]$

$$\pi(\theta) = Beta(a, b) \propto \mathbf{1}_{[0,1]}(\theta)\theta^{a-1}(1-\theta)^{b-1}.$$

a and b are called *hyper-parameters* and they control our level of a priori

- $a = b = 1$: uniform on $[0, 1]$ (uninformative)
- $a = b > 1$: in favor of a balanced coin, the greater a, the stronger the prior
- $a > b$ (resp. $a < b$): in favor of tail (resp. head).

Example of conjugacy: the Beta-Binomial model (2)

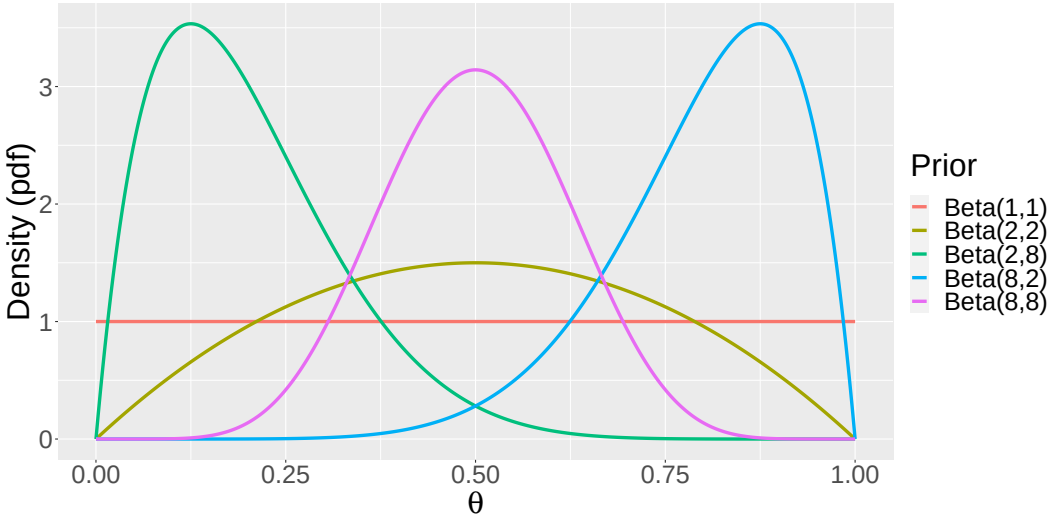


Figure: Graph of the p.d.f. $Beta(\cdot \mid a, b)$ for different values of a and b.

Example of conjugacy: the Beta-Binomial model (3)

We seek to derive the posterior, and we directly have

$$\begin{aligned}\pi(\theta \mid \boldsymbol{X}) &\propto p(\boldsymbol{X} \mid \theta)\pi(\theta), \\ &\propto \theta^{\sum_i x_i}(1-\theta)^{\sum_i 1-x_i}\theta^{a-1}(1-\theta)^{b-1}\mathbf{1}_{[0,1]}(\theta), \\ &\propto \theta^{a+\sum_i x_i-1}(1-\theta)^{b+n-\sum_i x_i-1}\mathbf{1}_{[0,1]}(\theta).\end{aligned}$$

We recognize the p.d.f of a Beta distribution

$$\theta \mid \boldsymbol{X} \sim Beta\left(a+\sum_i X_i, b+n-\sum_i X_i\right)$$

Remarks :

1. a and b act as *pseudo-counts* for head and tails, smoothing the estimates when n is small.
2. This conjugacy between the Beta prior and the binomial model always hold : property of the model (prior + likelihood) and not our specific experiment.

Bayesian decision theory

Bayesian point estimates

Having derived the posterior: how do we provide point estimates $\hat{\theta}$?

Cost function

A *cost function* is a function $C : \Theta \times \Theta \in \mathbb{R}_+$ where $C(\eta, \theta)$ is the "cost of predicting η for a parameter θ. Some examples

- $C(\eta, \theta) = (\eta - \theta)^p$ (L^p-loss)
- $C(\eta, \theta) = \mathbf{1}_{\eta \neq \theta}$ (0-1 loss)

Bayesian estimator

Remember that θ is random. For a given model and observation x, the Bayesian estimator is the one that minimizes the average cost under the posterior distribution:

$$\hat{\theta} \in \arg\min_{\eta} \left\{ \mathbb{E}_{\theta \sim \pi(\cdot|x)} \left[C(\eta, \theta) \right] = \int_{\Theta} C(\eta, \theta) \pi(\theta \mid x) \, \mathrm{d}\theta \right\}. \qquad \text{(Bayes estimator)}$$

Posterior Mean, Median & Mode

Different cost functions leads to different Bayes estimator among which

1. posterior mean $\hat{\theta} = \mathbb{E}[\theta \mid x]$ corresponds to the L^2-loss
2. posterior median $\hat{\theta}$ such that $\pi(\theta \geq \hat{\theta} \mid x) = \pi(\theta \leq \hat{\theta} \mid x) = 0.5$ (L^1-loss)
3. **posterior mode (aka MAP)**: $\hat{\theta} \in \arg\max_\theta \pi(\theta \mid x)$ (0-1 loss)

Maximum a posteriori is one of the most popular

- reduces to an optimization problem
- log-prior can be interpreted in a frequentist setting as a regularizer for MLE

$$\log \pi(\theta \mid x) = cte + \underbrace{\log p_\theta(x)}_{\text{likelihood}} + \underbrace{\log \pi(\theta)}_{\text{regularizer}}$$

Credibility regions

The posterior may also be used for uncertainty quantification by computing regions $\mathcal{R} \subset \Theta$ s.t. $\pi(\theta \in \mathcal{R} \mid x) = \int_{\mathcal{R}} \pi(\theta \mid x)\, \mathrm{d}\theta = 1 - \alpha$

Latent variable models

Incomplete data models

Most often, the observations are involved in complicated (biological, ecological, physical) processes, with many unobserved variables and complex dependency structure.

- $\boldsymbol{X}$ observed random variables
- $\boldsymbol{Z}$ unobserved (latent/hidden) variables
- θ unknown parameters

An attempt at defining latent variables (creds. to S. Robin)

- Frequentist setting:

$$\text{latent variables} = \text{random but unobserved}, \quad \text{parameters} = \text{fixed}$$

- Bayesian setting:

$$\text{both latent variables and parameters} = \text{random}$$

but

$$\#\text{ latent variable} \simeq \#\text{ data}, \quad \#\text{ parameters} \ll \#\text{ data}$$

Different types of likelihoods

In this course, we place ourselves in the frequentist setting, using MLE inference. Although Bayesian extension of the proposed models are common.

Complete data likelihood

Joint likelihood of the whole random process $(\boldsymbol{X}, \boldsymbol{Z})$ with given parameters θ.

$$p_\theta(\boldsymbol{X}, \boldsymbol{Z}) = p_\theta(\boldsymbol{X} \mid \boldsymbol{Z}) p_\theta(\boldsymbol{Z}).$$

$\rightsquigarrow$ tractable in many models, but we do not observe $\boldsymbol{Z}$!

Observed data likelihood

Marginal likelihood of the observed random variables $\boldsymbol{X}$

$$p_\theta(\boldsymbol{X}) = \int_{\mathcal{Z}} p_\theta(\boldsymbol{X}, \boldsymbol{z}) \, \mathrm{d}\boldsymbol{z}^a$$

$\rightsquigarrow$ only involves the observed $\boldsymbol{X}$, but not always tractable.

[a] When $\mathcal{Z}$ is discrete, replace $\int$ by $\sum$

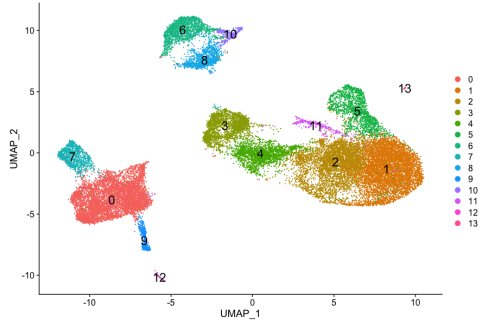
Clustering with mixture models

Motivation

Sometimes our data is organized in sub-population: groups of individuals we call *clusters*.

Example

In modern biology, discovering cell-types via their gene expression profile is an important task.



When the groups are unknown, we call the task of discovering them *clustering*[2]

[2] as opposed to classification in a supervised context

Mathematical context

We search for an optimal partition of $\boldsymbol{x} = \{x_1, \ldots, x_n\}$ into K groups.

Definition: partition

A partition $\boldsymbol{C} = \{C_1, \ldots, C_K\}$ of $\{1, \ldots, n\}$ is a set of sets s.t.

$$\bigcup_k C_k = \{1, \ldots, n\}, \qquad \forall k \neq l, \quad C_k \cap C_l = \emptyset.$$

Alternative encoding of the partition

For each individual $i = 1, \ldots, n$, we define its *cluster membership* $z_i \in \{0, 1\}^K$

$$k = 1, \ldots, K, \quad z_{ik} = \begin{cases} 1 & \text{if i belongs to cluster k,} \\ 0 & \text{otherwise} \end{cases}.$$

The set $\boldsymbol{Z} = \{z_1, \ldots, z_n\}$ represents a partition of $\{1, \ldots, n\}$. This particular encoding is sometimes referred to as one-hot encoding.

Clustering criteria

"Optimality" implies the definition of some criterion $L \iff$ assumptions on the nature of clusters. Methods can be roughly split in two

Similarity-based methods

Design L via geometric notions of similarity between x_i's, favoring *e.g.*

- elliptic clusters
- convex clusters
- connected clusters

Statistical methods

Consider the partition $\boldsymbol{Z}$ as a latent variable and posit a generative model $p_\theta(\boldsymbol{X}, \boldsymbol{Z})$

$\rightsquigarrow$ Clustering becomes an inference problem of finding $\hat{\boldsymbol{Z}}$.

There are connections between both !

K-means

The K-means problem

K-means seeks clusters well concentrated around their centroids $\mu_k \coloneqq \frac{1}{|C_k|} \sum_{i \in C_k} x_i$ by minimizing

$$\arg\min_{\boldsymbol{C}} \left\{ L(\boldsymbol{C}, \boldsymbol{X}) = \sum_{k=1}^{K} \sum_{i \in C_k} \|x_i - \mu_k\|_2^2 \right\} \qquad \text{(K-means problem)}$$

- Good news: discrete problem $\rightsquigarrow$ there exists an optimum $\boldsymbol{C}^\star$.
- **Bad news**: there are K^n possible partitions $\rightsquigarrow$ enumeration is not an option.

In fact, K-means problem is a **nonconvex NP-hard** problem and one need to resort to fast heuristics.
⚠With a slight abuse, we drop distinction between K-means problem and heuristics to solve it.

The K-means algorithm (MacQueen 1967)

Draw centroids $\mu_1, \ldots, \mu_K$ at random among the sample $\boldsymbol{X}$ and

1. Assign each point to its closest centroid

$$C_k \leftarrow \left\{ i \,:\, \|x_i - \mu_k\|_2^2 = \min_j \|x_j - \mu_k\|_2^2 \right\}$$

2. recompute centroids as the barycenter of each center

$$\mu_k := \frac{1}{|C_k|} \sum_{i \in C_k} y_i$$

3. Go to 1 until clusters (hence barycenters) are unchanged

Properties of the algorithm

K-means is a greedy algorithm which

- monotonically decreases the criterion
- converges in a finite number of iterations
- will get stuck in local minima of L (non-convex)

$\rightsquigarrow$ In practice, we try several restarts with different random inits.

Extensions

Kmeans++ initialization matter ! $\rightsquigarrow$ stop drawing centroids at random

- Choose μ_1 uniformly among the sample
- then sequentially do for each $k = 2, \ldots, K$
  - compute weight $w_i := \min_{j<k} \|x_i - \mu_j\|_2^2$
  - Choose μ_k among the sample with proba $\propto w_i$

Optimality bounds can be obtained (Arthur et al. 2007)

Sparse K-means include variable selection, useful when x_i in dimension $d \gg n$

Kernel K-means compute distance between $\phi(x_i)$ with $\phi : \mathcal{X} \to \mathcal{H}$ a *feature map*.

Mixture models

Probabilistic view on clustering

The partition is now seen as a set of discrete latent variables $\boldsymbol{Z} = \{z_1, \ldots, z_n\}$

Denote $\pi = (\pi_1, \ldots, \pi_K)$ the (unknown) cluster proportions, we have

$$p_\pi(z_{ik} = 1) = \pi_k \iff z_i \sim \mathcal{M}(1, \pi)$$

Mixture models

For all $i = 1, \ldots, n$, mixture models suppose that (z_i, x_i) are drawn *i.i.d.* according to the two-stage hierarchical model

1. $Z_i \sim \mathcal{M}_K(1, \pi)$
2. $X_i \mid \{z_{ik} = 1\} \sim p_{\gamma_k}$

The model parameters are $\theta = \{\pi_k, \gamma_k\}_{k=1}^K$ and p_γ can be any parametric distribution over X_i.

Clusters are sometimes called *components*

$\rightsquigarrow$ **general** and **flexible** framework, adapt to nature of the data (discrete, continuous, mixed-type)via p_γ

Observed (marginal) likelihood

Properties: independence

In a mixture model, $(Z_i)_i$ are *i.i.d.* and $(X_i)_i$ also are *i.i.d.*

Observed likelihood

$$
\begin{aligned}
p_\theta(\boldsymbol{X}) &= \sum_{z_1,\dots,z_n} p_\theta(\boldsymbol{Z}, \boldsymbol{X}) = \sum_{z_1,\dots,z_n} \prod_{i=1}^{n} p_\theta(X_i \mid z_i) p_\theta(z_i), \\
&= \prod_{i=1}^{n} \sum_{z_i} p_\gamma(X_i \mid z_i) p_\theta(z_i), \\
&= \prod_{i=1}^{n} \left(\sum_{k=1}^{K} \pi_k p_{\gamma_k}(X_i) \right).
\end{aligned}
$$

$\rightsquigarrow$ the marginal distribution of X_i is a convex combination (*mixture*) of the K base distributions $(p_{\gamma_k})_k$, with weights π_k.

Complete likelihood

Properties: conditional independence

In a mixture model, $(X_i)_i \perp\!\!\!\perp \boldsymbol{Z}$ and $(Z_i)_i \perp\!\!\!\perp \boldsymbol{X}$, **but not** identically distributed

Complete log-likelihood

$$\log p_\theta(\boldsymbol{X}, \boldsymbol{Z}) = \log p_\theta(\boldsymbol{Z}) + \log p_\theta(\boldsymbol{X} \mid \boldsymbol{Z}) = \sum_{i=1}^{n} \log p_\pi(Z_i) + \log p_\gamma(X_i \mid Z_i),$$

$$= \sum_{k=1}^{K} \sum_{i=1}^{n} Z_{ik} \left[\log \pi_k + \log p_{\gamma_k}(X_i) \right].$$

Posterior distribution of $Z \mid X$

For $i = 1, \ldots, n$, $Z_i \mid X_i \sim \mathcal{M}_K(1, \tau_i)$ with

$$\tau_{ik} \coloneqq p_\theta(z_{ik} = 1 \mid X_i) \propto \pi_k p_{\gamma_k}(X_i)$$

Notice that τ_i also depends on the parameters θ.

A note on identifiability

Definition: identifiability

A statistical model p_θ is said to be identifiable iff the mapping $\theta \mapsto p_\theta$ is injective.

Intuition: the labels of the clusters $1, \ldots, K$ should have no impact on the marginal likelihood

$$\pi_1 p_{\gamma_1}(x) + \pi_2 p_{\gamma_2}(x) = \pi_2 p_{\gamma_2}(x) + \pi_1 p_{\gamma_1}(x)$$

Label switching

Let σ be a permutation of $[\![1, K]\!]$, then for a mixture model with parameters π, γ we have

$$p(\boldsymbol{X} \mid \pi, \gamma) = p(\boldsymbol{X} \mid \sigma(\pi), \sigma(\gamma))$$

Hence, there are $K!$ equivalent formulations of a mixture model.

$\rightsquigarrow$ conceptually not a problem, it simply states that there are $K!$ different encoding $\boldsymbol{Z}$ of a given partition $C = \{C_1, \ldots, C_K\}$.

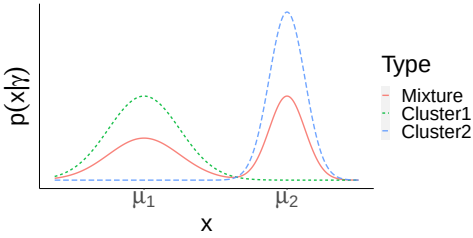
$\rightsquigarrow$ can cause problems in Bayesian inference procedure since the posterior is highly multimodal.

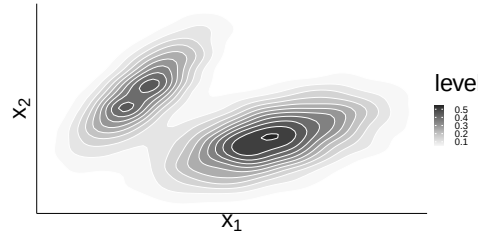
Gaussian Mixture Models (GMM)

Continuous data: $\boldsymbol{x} = \{x_1, \ldots, x_n\} \subset \mathbb{R}^d$

Model: Mixture of Gaussians $p_{\gamma_k}(x) = \mathcal{N}(x \mid \mu_k, \Sigma_k)$, with $\gamma_k = (\mu_k, \Sigma_k)$

Multimodal marginal density around the $(\mu_k)_k$'s





Number of free parameters: $K - 1 + Kd + K\frac{d(d+1)}{2} = \mathcal{O}(Kd^2)$ to estimate

Maximum-likelihood estimation

Non-convex MLE problem

$$\arg\max_{\pi_k, \mu_k, \Sigma_k} \sum_{i=1}^{n} \log \left(\sum_{k=1}^{K} \pi_k \log \mathcal{N}(x_i \mid \mu_k, \Sigma_k) \right).$$

- Much more complex to maximize than in standard Gaussian models ($K = 1$)
- No closed-form solution, gradients can be derived but
  1. they are not cheap to compute at each iteration (although one could resort to stochastic optimization to leverage this issue).
  2. Requires re-projecting on the cone of p.d. matrices $\Sigma_k \succ 0$.

By contrast, the complete log-likelihood is much simpler to handle

$$\log p_\theta(\boldsymbol{x}, \boldsymbol{Z}) = \sum_{k=1}^{K} \sum_{i=1}^{n} Z_{ik} \left[\log \pi_k + \log \mathcal{N}(x_i \mid \mu_k, \Sigma_k) \right].$$

$\rightsquigarrow$ **But we do not observe the $\boldsymbol{Z}$!**

Maximum-likelihood estimation (cont'd)

A chicken-and-egg problem

1. If we knew $\boldsymbol{Z}$ we could maximize $p_\theta(\boldsymbol{X}, \boldsymbol{Z}) \rightsquigarrow$ amount to compute MLE $\hat{\gamma}_k$ in each cluster. In the Gaussian case we'd have cluster's empirical means and covariance

$$n_k = \sum_i z_{ik}, \qquad \hat{\mu}_k = \sum_i z_{ik} x_i / n_k, \qquad \hat{\Sigma}_k = \sum_i z_{ik} \frac{(x_i - \hat{\mu}_k)(x_i - \hat{\mu}_k)^\top}{n_k}$$

2. If we knew $\theta^\star$, we could find the best estimate of $\boldsymbol{Z}$ via the posterior distribution

$$\tau_{ik}(\theta) = p_\theta(z_{ik} = 1 \mid x_i) = \frac{\pi_k \mathcal{N}(x_i \mid \mu_k, \Sigma_k)}{\sum_l \pi_l \mathcal{N}(x_i \mid \mu_l, \Sigma_l)}$$

$\rightsquigarrow$ this suggest an iterative scheme between 1) & 2) to solve MLE.

Inference in latent variable models: the EM algorithm

Some tools from information theory

Jensen's inequality

Quizz ! Which is larger: $\mathbb{E}[Z^2]$ or $\mathbb{E}[Z]^2$?

Jensen's inequality

Quizz ! Which is larger: $\mathbb{E}[Z^2]$ or $\mathbb{E}[Z]^2$? $\quad \rightsquigarrow \mathbb{E}[Z^2] - \mathbb{E}[Z]^2 = \mathbb{V}(Z) \geq 0$

Jensen's inequality

Quizz ! Which is larger: $\mathbb{E}[Z^2]$ or $\mathbb{E}[Z]^2$? $\quad \rightsquigarrow \mathbb{E}[Z^2] - \mathbb{E}[Z]^2 = \mathbb{V}(Z) \geq 0$

General result: Jensen's inequality

Let Z be a random vector in $\mathcal{Z} \subset \mathbb{R}^d$ and $\phi : \mathbb{R}^d \to \mathbb{R}$ a convex function, then

$$\mathbb{E}_Z\left[\phi(Z)\right] \geq \phi\left(\mathbb{E}_Z[Z]\right). \qquad \text{(Jensen)}$$

$\rightsquigarrow$ the inequality is reversed with ϕ concave ($\phi \leftarrow -\phi$)

Proof:

- ϕ convex $\implies$ it is above its tangents, hence at any point $z_0 \in \mathbb{R}^d, \exists a$ s.t.

$$\forall z \in \mathbb{R}^d, \quad \phi(z) \geq \phi(z_0) + a(z - z_0).$$

- Take $z_0 = \mathbb{E}_Z[Z]$, since the above inequality is true for all z, it generalizes to $\mathbb{E}_Z$

$$\mathbb{E}_Z\left[\phi(Z)\right] \geq z_0 + a\underbrace{(\mathbb{E}_Z[Z] - z_0)}_{=0} = z_0 = \phi\left(\mathbb{E}_Z[Z]\right)$$

Entropy of a random variable

Definition: entropy

For a discrete random variable Z with distribution $q(Z = z)$ we define its entropy as

$$\mathcal{H}(Z) = \mathcal{H}(q) = -\mathbb{E}\left[\log q(Z)\right] = -\sum_{z \in \mathcal{Z}} q(z) \log q(z)$$

with the convention that $0 \times \log 0 = 0$

Properties

- $\mathcal{H}(q) \geq 0$
- **Continuous formulation:** Let Z be a r.v. with distribution Q. If there exist a measure μ such that $\mathrm{d}Q = q\,\mathrm{d}\mu$ then we can define

$$\mathcal{H}(Q) = \mathcal{H}_\mu(q) = -\int \log q(z) q(z)\,\mathrm{d}\mu(z)$$

  Now depends on the base measure μ.

Kullback-Leibler (KL) divergence

Definition: KL divergence (discrete case)

Let p and q be two distribution over discrete set $\mathcal{Z}$, we define the KL-divergence as

$$\mathrm{KL}(p \parallel q) \coloneqq \mathbb{E}_{Z\sim p}\left[\log \frac{p(Z)}{q(Z)}\right] = \sum_{z\in\mathcal{Z}} p(z) \log \frac{p(z)}{q(z)}$$

Properties

- $\mathrm{KL}(p \parallel q) \geq 0$ with equality iff $p = q$ (*proof:* Jensen on $\frac{q}{p}(Z)$ with convex $\phi(x) = -\log x$)
- Diverges if $\exists z_0$ such that $q(z_0) = 0$ when $p(z_0) = 0$
- Not a distance (not symmetric)
- **Continuous formulation:** For two distribution P and Q, if there exists a measure μ such that $\mathrm{d}P = p\,\mathrm{d}\mu$ and $\mathrm{d}Q = q\,\mathrm{d}\mu$, then

$$\mathrm{KL}(P \parallel Q) = \int \log \frac{\mathrm{d}P}{\mathrm{d}Q}\,\mathrm{d}P = \int \log \frac{p(z)}{q(z)} p(z)\,\mathrm{d}\mu(z).$$

  $\rightsquigarrow$ invariant w.r.t. the choice of (p, q, μ) since the ratio $\mathrm{d}P/\,\mathrm{d}Q$ is invariant.

The evidence lower bound (ELBO)

Minorizer of the observed-likelihood

Evidence lower bound

Let q be a distribution over $\mathcal{Z}$ absolutely continuous with respect to $p_\theta(X, Z)$. Then,

$$\log p_\theta(\boldsymbol{X}) \geq \mathcal{L}(q, \theta) \coloneqq \mathbb{E}_q \left[\log p_\theta(X, Z)\right] + \mathcal{H}(q). \qquad \text{(ELBO)}$$

The quantity $\mathcal{L}$ is called *the evidence lower-bound*, moreover the gap is expressed as

$$\log p_\theta(X) - \mathcal{L}(q, \theta) = \mathrm{KL}(q \parallel p_\theta(\cdot \mid X)).$$

Proof: $\log p_\theta(X) = \log \int p_\theta(X, z)\, \mathrm{d}z = \log \mathbb{E}_q \left[\frac{p_\theta(X,Z)}{q(Z)}\right] \overset{\text{Jensen}}{\geq} \mathbb{E}_q \left[\log \frac{p_\theta(X,Z)}{q(Z)}\right] = \mathcal{L}(q, \theta)$

Comments

- The ELBO holds for any distribution q on $\boldsymbol{Z}$
- For a given θ, the gap is 0 iff

$$q(z) = p_\theta(z \mid X)$$

Expectation-maximization (EM, Dempster et al. 1977)

EM: a universal algorithm for latent variables

Intuition: chicken-and-egg

1. *if we knew* $\boldsymbol{Z}$, we could easily work with $f(\theta) = \log p_\theta(\boldsymbol{X}, \boldsymbol{Z})$
2. *if we knew* θ, the best representation of $\boldsymbol{Z}$ is via its posterior $p_\theta(\boldsymbol{Z} \mid \boldsymbol{X})$

Expectation-Maximization algorithm

Starting from $\theta^{(0)}$, iterate between

Expectation step

Use $q^{(t+1)}(\boldsymbol{Z}) = p_{\theta^{(t)}}(\boldsymbol{Z} \mid \boldsymbol{X})$ to form the objective function

$$f(\theta) = Q(\theta, \theta^{(t)}) = \mathbb{E}_{\boldsymbol{Z} \sim q^{(t+1)}} \left[\log p_\theta(\boldsymbol{X}, \boldsymbol{Z}) \right].$$

It involves (generalized) moments of $\boldsymbol{Z}$ under $q^{(t+1)}$.

Maximization step

Solve $\theta^{(t+1)} \in \arg\max_\theta Q(\theta, \theta^{(t)})$

In practice, EM stop after likelihood gaps fall below a given threshold ϵ

$$|\mathcal{L}(q^{(t+1)}, \theta^{(t)}) - \mathcal{L}(q^{(t)}, \theta^{(t-1)})| = |\log p_{\theta^{(t)}}(\boldsymbol{X}) - \log p_{\theta^{(t-1)}}(\boldsymbol{X})| < \epsilon$$

Rewriting EM: coordinate ascent on the ELBO

EM algorithm (equivalent formulation)

Starting from $\theta^{(0)}$, iterate between

$$q^{(t+1)} = \arg\max_q \mathcal{L}(q, \theta^{(t)}), \qquad \text{(E-step)}$$

$$\theta^{(t+1)} = \arg\max_\theta \mathcal{L}(q^{(t+1)}, \theta). \qquad \text{(M-step)}$$

- E-step is equivalent to $\min_q \mathrm{KL}(q \,\|\, p_{\theta^{(t+1)}}(\cdot \mid X)) \implies q^{(t+1)} = p_{\theta^{(t+1)}}(\cdot \mid X)$
- basis of inference in latent variable models, many extensions: see *e.g.* Peel et al. (2000) for mixture models

Monotonic increase of the observed likelihood

Property of EM algorithm

The sequence of iterates $\{\theta^{(t)}\}_t$ returned by EM verifies

$$\forall t \geq 0, \quad \log p_{\theta^{(t+1)}}(\boldsymbol{X}) \geq \log p_{\theta^{(t)}}(\boldsymbol{X})$$

Proof:

$$\log p_{\theta^{(t+1)}}(\boldsymbol{X}) \underbrace{\geq}_{\text{ELBO}} \mathcal{L}(q^{(t+1)}, \theta^{(t+1)}) \underbrace{\geq}_{\text{M-step}(t+1)} \mathcal{L}(q^{(t+1)}, \theta^{(t)}) \underbrace{=}_{\text{E-step}(t)} \log p_{\theta^{(t)}}(\boldsymbol{X})$$

- Guarantees EM converges with the likelihood gaps criterion
- In general, only converges to local maxima of the likelihood
- Does not guarantee convergence of the sequence of parameters $\{\theta^{(t)}\}_t$ itself.

A graphical illustration of EM algorithm (cred: G. Obozinski)

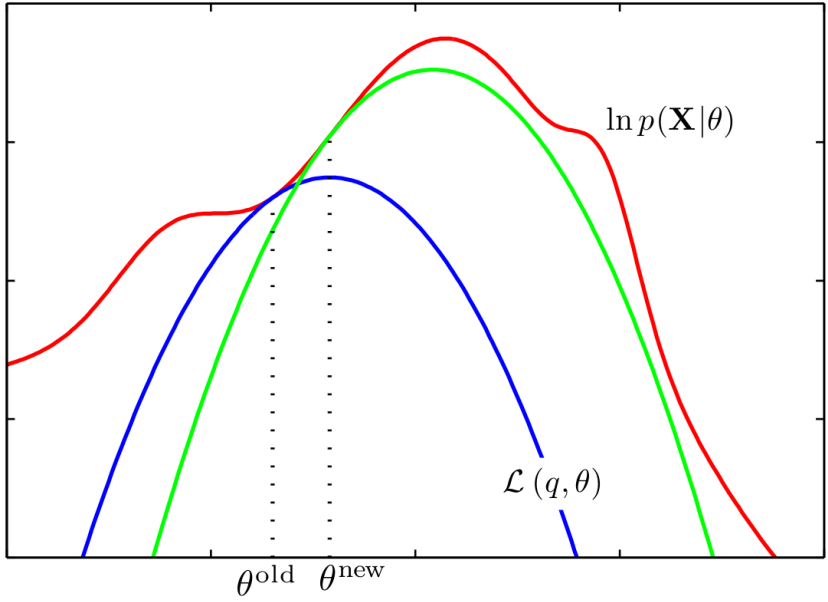


Illustration with Gaussian mixture

Expected complete log-likelihood

Denote $\tau_{ik}^{(t)} := p_{\theta^{(t-1)}}(Z_{ik} = 1 \mid x_i) \underset{\text{Multinomial}}{=} \mathbb{E}_{q^{(t)}}[Z_{ik}]$, then

$$
\begin{aligned}
f(\theta) =& \mathbb{E}_{q^{(t)}} \left[\log p_\theta(\boldsymbol{X}, \boldsymbol{Z}) \right], \\
=& \mathbb{E}_{q^{(t)}} \left[\sum_{i=1}^{n} \log p_\theta(x_i, Z_i) \right], \\
=& \mathbb{E}_{q^{(t)}} \left[\sum_{k=1}^{K} \sum_{i=1}^{n} Z_{ik} \left[\log \pi_k + \log \mathcal{N}_q(x_i \mid \mu_k, \Sigma_k) \right] \right], \\
=& \sum_{k=1}^{K} \sum_{i=1}^{n} \mathbb{E}_{q_i^{(t)}} [Z_{ik}] \left[\log \pi_k + \log \mathcal{N}_d(x_i \mid \mu_k, \Sigma_k) \right], \\
=& \sum_{k=1}^{K} \sum_{i=1}^{n} \tau_{ik}^{(t)} \left[\log \pi_k + \log \mathcal{N}_d(x_i \mid \mu_k, \Sigma_k) \right],
\end{aligned}
$$

It involves $\tau_{ik}^{(t)}$: (first) moments of Z under $q^{(t)}$.

E-step for GMM

Compute the posterior given $\theta^{(t-1)}$, $q^{(t)} = p_{\theta^{(t-1)}}(\boldsymbol{Z} \mid \boldsymbol{X})$

As seen previously, the posterior for mixture model always writes

$$p_\theta(\boldsymbol{Z}) = \prod_{i=1}^{n} \mathcal{M}_K(1, \tau_i(\theta)), \quad \text{with: } \tau_{ik}(\theta) \propto \pi_k p_{\gamma_k}(x_i).$$

So that

$$\tau_{ik}^{(t)} = \tau_{ik}(\theta^{(t-1)}) = \frac{\pi_k \mathcal{N}_d(x_i \mid \mu_k^{(t-1)}, \Sigma_k^{(t-1)})}{\sum_{l=1}^{K} \pi_l \mathcal{N}_d(x_i \mid \mu_l^{(t-1)}, \Sigma_l^{(t-1)})}.$$

Careful with numerical underflow $\rightsquigarrow$ better to work with in log-space with $\log \tau$.

M-step for GMM

Solve

$$(\pi_k^{(t)}, \mu_k^{(t)}, \Sigma_k^{(t)})_{k=1}^K \in \arg\max_\theta \left\{ f(\theta) = \mathbb{E}_{q^{(t)}}[\log p_\theta(\boldsymbol{X}, \boldsymbol{Z})] \right\}$$

For GMM, the updates are

$$\begin{cases} \tilde{n}_k^{(t)} = & \sum_{i=1}^n \tau_{ik}^{(t)}, \\ \pi_k^{(t)} = & \frac{\tilde{n}_k^{(t)}}{n}, \\ \mu_k^{(t)} = & \frac{1}{\tilde{n}_k^{(t)}} \sum_{i=1}^n \tau_{ik}^{(t)} x_i, \\ \Sigma_k = & \frac{1}{\tilde{n}_k^{(t)}} \sum_{i=1}^n \tau_{ik}^{(t)} (x_i - \mu_k^{(t)})(x_i - \mu_k^{(t)})^\top \end{cases}$$

We recognize standard Gaussian MLE in each cluster, using soft probability memberships τ in place of unknown $\boldsymbol{Z}$.

Link with K-means algorithm

The K-means algorithm can be interpreted as an EM algorithm for a constrained GMM with equal proportions $\pi_k = 1/K$, known isotropic covariance $\Sigma_k = \sigma^2 \, \mathrm{Id}_d$. Dropping the known quantities, the criterion is

$$\underset{\mu_1,\ldots,\mu_K,\boldsymbol{Z}}{\arg\min} \; -\log p_\mu(\boldsymbol{X}, \boldsymbol{Z}) = cte + \sum_k \sum_{i \in C_k} \|x_i - \mu_k\|_2^2.$$

Rewriting K-means (Classification-EM for GMM)

1. *Hard E-step:* set partition $C^{(t+1)}$ via MAP $\arg\max_l \tau_{il}^{(t+1)} = \arg\min_l \|x_i - \mu_l^{(t)}\|_2^2$
2. *M-step:* update the centroids $\mu_k^{(t+1)} \leftarrow (1/n_k) \sum_{i \in C_k^{(t+1)}} x_i$

Comments

- highlight connections between similarity-based and probabilistic methods
- unveil hypothesis behind K-means criterion: spherical, equal-volume and equal-size clusters.

Choosing the number of components K

Challenge: how to choose the number of clusters K ?

Intuition: the larger the likelihood, the better our model fits the data $\boldsymbol{X}$

Caveat: complex models tend to provide larger likelihood, for example

- mixture models with $K-1$ components are nested in models with K components.
- models with constraints (diagonal, spherical) are nested in unconstrained ones.

$\rightsquigarrow$ we need to account for "model complexity"

Definition: dimension/size of a model

Let $\mathcal{M} = \{p_\theta, \theta \in \Theta_\mathcal{M}\}$, we denote $d_\mathcal{M}$ the number of free parameters in the model.
For unconstrained mixtures, it is $d_K = K - 1 + Kd_\Gamma$, $\gamma_k \in \Gamma$.

Penalized likelihood criterion

For a mixture model with K components, denote $\hat{\theta}_K = \arg\max_{\theta \in \Theta_K} \log p_\theta(\boldsymbol{X})$. A *penalized likelihood* estimate of K is given by

$$\hat{K} = \arg\max_K \left\{ \log p_{\hat{\theta}_K} - pen(K) \right\}.$$

Different penalties leads to different criterion

Definitions: AIC, BIC, ICL

For a model $\mathcal{M}$ and observations $\boldsymbol{X}$, we have several choice of penalize likelihood criteria

$$\begin{aligned} AIC(K) &\coloneqq \log p_{\hat{\theta}_K}(\boldsymbol{X}) - d_K, \\ BIC(K) &\coloneqq \log p_{\hat{\theta}_K}(\boldsymbol{X}) - \frac{d_K}{2}\log(n), \\ ICL(K) &\coloneqq \mathbb{E}_{Z\sim p_{\hat{\theta}_K}(\cdot|\boldsymbol{X})}\left[\log p_{\hat{\theta}_K}(\boldsymbol{X}, \boldsymbol{Z})\right] - \frac{d_K}{2}\log(n) \end{aligned}$$

Note: the ELBO property gives

$$ICL(K) = BIC(K) - \mathcal{H}(p_{\hat{\theta}_K}(\cdot \mid \boldsymbol{X})).$$

Hence, ICL is more focused on models with strongly separable clusters (peaked posterior $\implies$ low entropy), while BIC is more focused on fitting the marginal density of $\boldsymbol{X}$.

Focus on BIC: Bayesian information criterion

Put a prior $p(K)$ on K, and the model: $p(\theta \mid K)$ and $p(\boldsymbol{X} \mid \theta)$. Bayes rule suggests choosing

$$\begin{aligned}\hat{K} &= \arg\max_K \left\{ p(K \mid \boldsymbol{X}) \propto p(K) p(\boldsymbol{X} \mid \theta) \right\}, \\ &= \arg\max_K \log p(K) + \log p(\boldsymbol{X} \mid K), \\ &= \arg\max_K \log p(K) + \log \int p(\boldsymbol{X} \mid \theta, K) p(\theta \mid K) \, \mathrm{d}\theta.\end{aligned}$$

Dropping the prior term $\log p(K)$ which is constant with n, we need to compute the integral in the second term $\rightsquigarrow$ difficult in general !

Under regularity assumptions (see Lebarbier et al. 2004, for details), we have

$$\log p(\boldsymbol{X} \mid K) = \log p_{\hat{\theta}_K}(\boldsymbol{X}) - \frac{d_K}{2} \log(n) + \mathcal{O}_P(1).$$

This justifies the formula of BIC.

Hidden Markov Models (HMMs)

Motivations

What if observations $\boldsymbol{X} = \{x_i\}_i$ are ordered ? *e.g.*

- time series
- genomic data: observations collected at precise locations in the genome
- etc.

$\rightsquigarrow$ it is likely that "past" influences the "future".

Need to introduce **dependence** between observations/latent variables in the model

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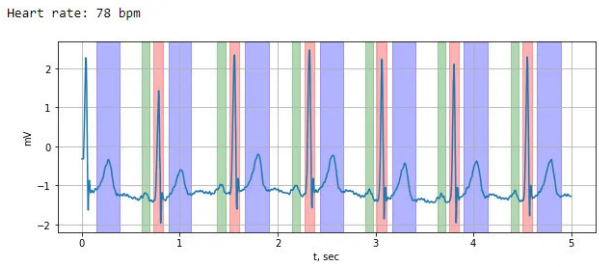
Example 1: time series segmentation



Source: https://medium.com/data-analysis-center/56f8b9abd83a

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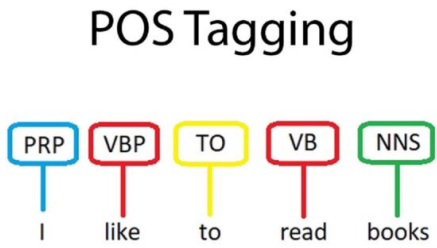
Example 2: part-of-speech tagging



Source: https://byteiota.com/pos-tagging/

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- genomic data: observations collected at precise locations in the genome
- etc.

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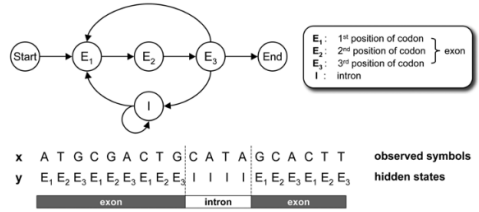
Example 3: protein coding



From Yoon (2009)

Reminder on discrete Markov chains

Markov Chains (discrete)

Suppose we observe a sequence $y_{1:n} :== \{y_1, \ldots, y_n\}$ at *discrete* time[3] steps $1, \ldots, n$, with discrete outcomes $y_i \in \{1, \ldots, K\}$

Markov chain (MC)

We say that the sequence $y_{1:n}$ is a Markov Chain if for all $i = 1, \ldots, n$,

$$p(y_{i+1} \mid y_{1:i}) = p(y_{i+1} \mid y_i)$$

"The future is independent from the past knowing the present."

Joint distribution of the sequence

$$p(y_{1:n}) = p(y_1)p(y_2 \mid y_1)p(y_3 \mid y_2) \ldots p(y_n \mid y_{n-1}) = p(y_1) \prod_{i=2}^{n} p(y_i \mid y_{i-1}).$$

Proof of the all the statements made about Markov Chains can be found in Sophie Lemaire's course.

[3] "Time" may also refer to locations within a sequence of words/genes/etc.

Vocabulary around MC

Homogeneous Markov chain

We say that a markov chain is homogeneous (or time invariant) if the transition probability $p(y_{i+1} \mid y_i)$ is independent time (of i).

Initial distribution

We denote as $\nu = (\nu_1, \dots, \nu_K)$ the vector $\nu_k \coloneqq p(y_1 = k)$

Marginal distribution

We denote as $\nu_i = (\nu_{i1}, \dots, \nu_{iK})$ the vector $\nu_{ik} \coloneqq p(y_i = k)$

Transition matrix

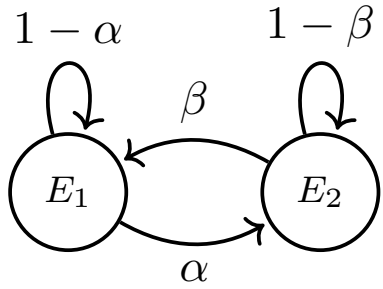
We denote A the $K \times K$ matrix with $A_{kl} = p(z_{i+1} = l \mid z_i = k)$ and properties:

- stochastic matrix: each row sum to 1 - $\sum_{l=1}^{K} A_{kl} = 1$
- eigenvalue 1 associated to the column vector $e = (1, \dots, 1)^\top$: $Ae = 1 \cdot e$
- For any $m, n \in \mathbb{N}$, $p(y_{n+m} = l \mid y_m = k) = A_{kl}^{(m)}$ (m-th matrix power)
- Moreover $\nu_i = \nu_1 A^{(i-1)}$

Notation: $y_{1:n} \sim MC(\nu, A)$

Diagram representation: a toy example

$$A = \begin{array}{c} \\ E_1 \\ E_2 \end{array} \begin{array}{c} \begin{array}{cc} E_1 & E_2 \end{array} \\ \begin{pmatrix} 1-\alpha & \alpha \\ \beta & 1-\beta \end{pmatrix} \end{array}$$

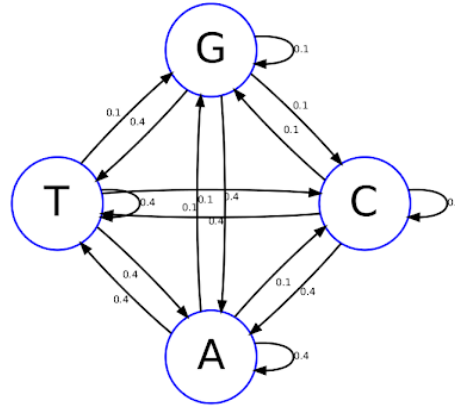


Graphical representation of a 2-state homogeneous Markov chain

A second example: modeling nucleotide transition

$$A = \begin{array}{c} \\ A \\ T \\ G \\ C \end{array} \begin{array}{c} \begin{array}{cccc} A & T & G & C \end{array} \\ \begin{pmatrix} & & & \\ & & p(y_t{=}G|y_{t-1}{=}T) & \\ & & & \end{pmatrix} \end{array}$$

$\rightarrow$



Source: https://www.r-bloggers.com/2012/04/introduction-to-markov-chains-and-modeling-dna-sequences-in-r/

A third example: Ehrenfest's urn model

- 4 balls distributed across 2 urns
- Each turn, we pick a ball and change its urn
- Let A be the transition of one urn (symmetric problem) :
  $\rightarrow$ State $=$ number of balls in this urn

A third example: Ehrenfest's urn model

- 4 balls distributed across 2 urns
- Each turn, we pick a ball and change its urn
- Let A be the transition of one urn (symmetric problem) :
  $\rightarrow$ State $=$ number of balls in this urn

$$A = \begin{array}{c} \\ 0 \\ 1 \\ 2 \\ 3 \\ 4 \end{array} \begin{array}{c} \begin{array}{ccccc} 0 & 1 & 2 & 3 & 4 \end{array} \\ \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ \frac{1}{4} & 0 & \frac{3}{4} & 0 & 0 \\ 0 & \frac{1}{2} & 0 & \frac{1}{2} & 0 \\ 0 & 0 & \frac{3}{4} & 0 & \frac{1}{4} \\ 0 & 0 & 0 & 1 & 0 \end{pmatrix} \end{array}$$

Stationary distribution & how to find them

Stationary distribution

Let A be a transition matrix over $[\![1, K]\!]$, we say that a vector π such that

$$\pi^\top A = \pi^\top \qquad \sum_{k=1}^{K} \pi_k = 1, \quad \pi_k \geq 0$$

is a **stationary** (or **invariant**) distribution for the homogeneous chain $MC(\nu, A)$.

Properties

1. π is a discrete probability vector & eigenvector of $A^\top$ associated to the eigenvalue $\lambda = 1$
2. if $y_1 \sim \pi$, then $\forall n \in \mathbb{N}$, $y_n \sim \pi$ (hence the name *stationary*)
3. **Existence:** for discrete MC it is an application of Perron-Frobenius theorem to A
4. **Uniqueness & convergence:** if there exists some power $q \in \mathbb{N}^\star$ such that $A^{(q)} > 0$ then
   - π is unique and $\pi_k > 0$.
   - $p(y_n = l \mid y_1 = k) = A^{(n)}_{kl} \xrightarrow[n \to +\infty]{} \pi_l$, whatever the initial distribution ν is.

   Such chains "forget their past" after enough steps.

Computing the stationary distribution

First strategy: eigenvector

We know that $A^\top \pi = 1 \cdot \pi$, so that π is an eigenvector associated to the unit[a] eigenvalue. **Careful**, most scientific softwares give eigenvector such that $\|v\|_2 = 1$, so we need to post process $\pi := v/(\sum_k v_k)$.
When K is big, there are efficient algorithms to find only largest eigenvector under conditions on A (*e.g.* Lanczos algorithm for symmetric matrices)

[a] Recall that eigenvalues (but not eigenvectors) of A and $A^\top$ are the same.

Second strategy: linear system

We have K unknown $\pi_1, \dots, \pi_K$ and $K+1$ equations $\pi^\top (A - I) = \mathbf{0}_{1\times K}$ & $\sum_k \pi_k = 1$
$\rightsquigarrow$ over-determined linear system.
Thus, we can create a new matrix M by arbitrarily replace a column (say last one) in $(A - I)$ by $\mathbf{1}_{K\times 1}$ and solve for $\pi^\top M = (0, \dots, 0, 1)$.

2-state example

Compute the stationary distribution of

$$A = \begin{pmatrix} 1-\alpha & \alpha \\ \beta & 1-\beta \end{pmatrix}$$

2-state example

Compute the stationary distribution of

$$A = \begin{pmatrix} 1-\alpha & \alpha \\ \beta & 1-\beta \end{pmatrix}$$

$$A^{-}I = \begin{pmatrix} -\alpha & \alpha \\ \beta - \beta & \end{pmatrix}$$

Replacing last column by $(1,1)^\top$ and solving the linear system when

$$\begin{pmatrix} \pi_1 & \pi_2 \end{pmatrix} \begin{pmatrix} -\alpha & 1 \\ \beta & 1 \end{pmatrix} = \begin{pmatrix} 0 & 1 \end{pmatrix}$$

leads to $\pi = (\frac{\beta}{\alpha+\beta}, \frac{\alpha}{\alpha+\beta})$ provided $\alpha + \beta \neq 0$.

Question (at home): when do we have convergence of A^n ? (Consider the matrix A on limit cases $\alpha = \beta = r$, $r \in \{0, 1\}$)

Numerical example

Find the stationary distribution of $A = \begin{pmatrix} 0 & 1 & 0 \\ 1/2 & 0 & 1/2 \\ 1 & 0 & 0 \end{pmatrix}$

```
A <- matrix(c(0, 1/2,1,1,0,0,0,1/2,0),3,3)
```

Eigenvector

```
eigen.res <- eigen(t(A))
Pi <- eigen.res$vectors[,1]
Pi/sum(Pi)
```

```
[,1]   [,2]   [,3]
[1,] 0.4+0i 0.4+0i 0.2+0i
```

Linear system

```
M<-diag(1, 3, 3) - A
M[,3] <- rep(1,3)
Pi <- solve(t(M),b=c(0,0,1))
Pi
```

```
[1] 0.4 0.4 0.2
```

Sanity check `> (pi - t(pi)%*%A) < 1e-15`

Hidden Markov Models (HMMs)

HMM: the model

Generative model

A general (discrete) hidden Markov model is defined as

1. $z_{1:n} \sim MC(\nu, A)$
2. $(x_i)_i$ independent $\mid$ $(z_i)_i$ and for all $i \in [\![1, n]\!]$, $x_i \mid \{z_{ik} = 1\} \sim p_{\gamma_k}(\cdot)$

The model parameters are $\theta = (\nu, A, \gamma)$.

Marginal likelihood of x_i

Denote $\nu_i = (\nu_{i1}, \ldots, \nu_{iK})$, such that $\nu_{ik} = p_\theta(z_{ik} = 1)$ [a]. Then,

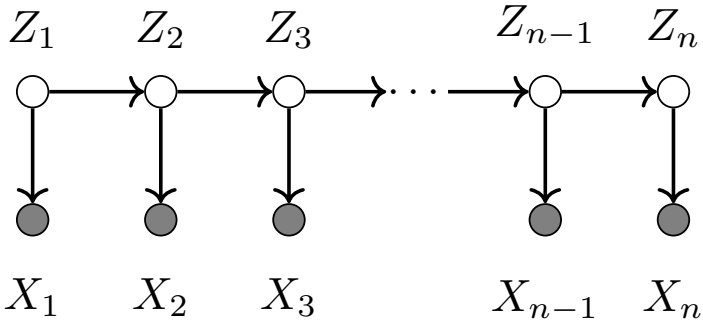
$$p_\theta(x_i) = \sum_k \nu_{ik} p_{\gamma_k}(x_i)$$

Moreover, if $\nu_1 = \pi$ (the chain's stationary distribution) then $p_\theta(x_i) = \sum_k \pi_k p_{\gamma_k}(x_i)$

$\rightsquigarrow$ HMMs can be thought of as a generalization of mixture with the introduction of dependency!

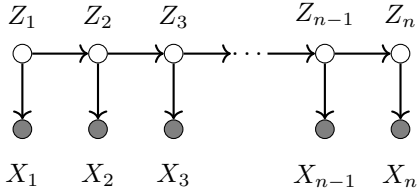
[a] For homogeneous MC we know that $\nu_i = \nu^\top A^{(i-1)}$.

Graphical model representation



- Empty circle ○ represents unobserved random variable
- Gray circles ● represents observed random variables

Conditional independence



Looking at the DAG, we have the three fundamental properties of HMM

1. $Z_{i+1} \perp\!\!\!\perp Z_{1:(i-1)} \mid Z_i$ (*i.e.* $Z_{1:n}$ is a MC)
2. $Z_{i+1} \perp\!\!\!\perp X_{1:i} \mid Z_i$
3. $X_{i+1} \perp\!\!\!\perp X_{1:i} \mid Z_{i+1}$ (and also $\mid Z_i$)

This basically states that knowing the hidden state at step i captures all relevant information about the past.

Complete-data likelihood

Complete-data log-likelihood for HMMs

$$
\begin{aligned}
\log p_\theta(\boldsymbol{X}, \boldsymbol{Z}) &= \log p_\theta(\boldsymbol{X} \mid \boldsymbol{Z}) \times p_\theta(\boldsymbol{Z}), \\
&= \log \left[\prod_{k=1}^{K} \prod_{i=1}^{n} p_{\gamma_k}(x_i)^{z_{ik}} \times \prod_{k=1}^{K} \nu_k^{z_{1k}} \prod_{k,l=1}^{K} \prod_{i=2}^{n} A_{k,l}^{z_{(i-1)k} z_{il}} \right], \\
&= \sum_{k=1}^{K} \sum_{i=1}^{n} z_{ik} \log p_{\gamma_k}(x_i) + \sum_{k=1}^{K} z_{1k} \log \nu_k + \sum_{k,l=1}^{K} \sum_{i=2}^{n} z_{(i-1)k} z_{il} \log A_{k,l}.
\end{aligned}
$$

Observed-data likelihood

Observed-data log-likelihood for HMMs

$$
\begin{aligned}
p_\theta(\boldsymbol{X}) &= \log \sum_{\boldsymbol{Z}} p_\theta(\boldsymbol{X} \mid \boldsymbol{Z}) \times p_\theta(\boldsymbol{Z}), \\
&= \log \left[\sum_{z_1,\ldots,z_n} \prod_{i=1}^{n} \prod_{k=1}^{K} p_{\gamma_k}(x_i)^{z_{ik}} \times \prod_{k=1}^{K} \nu_k^{z_{1k}} \prod_{k,l=1}^{K} \prod_{i=2}^{n} A_{k,l}^{z_{(i-1)k} z_{il}} \right].
\end{aligned}
$$

Brute force computation involves $\mathcal{O}(K^n)$ operations !