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Problem 1 Gaussian Mixture Model and EM (30 points)

1.1 In the lecture we applied EM to learn Gaussian Mixture Models (GMMs) and showed the M-Step without a proof. Now it is time that you prove it. Consider a GMM with the following PDF of \mathbf{x}_n :

$$p(\mathbf{x}_n) = \sum_{k=1}^K \omega_k \mathcal{N}(\mathbf{x}_n \mid \boldsymbol{\mu}_k, \Sigma_k) = \sum_{k=1}^K \frac{\omega_k}{(\sqrt{2\pi})^D |\Sigma_k|^{\frac{1}{2}}} \exp\left(-\frac{1}{2}(\mathbf{x}_n - \boldsymbol{\mu}_k)^T \Sigma_k^{-1} (\mathbf{x}_n - \boldsymbol{\mu}_k)\right)$$

where $K \in \mathbb{N}$ is the number of Gaussian components, $D \in \mathbb{N}$ is dimension of a data point \mathbf{x}_n . This GMM has K tuples of model parameters $(\mu_k, \Sigma_k, \omega_k)$, which standards for the mean vector, covariance matrix, and component weight of the k -th Gaussian component. $|\Sigma|$ denotes the determinant of matrix Σ .

For simplicity, we further assume that all components are isotropic Gaussian, i.e., $\Sigma_k = \sigma_k^2 I$. Find the MLE of *the expected complete log-likelihood*. Equivalently, find the optimal solution to the following optimization problem.

$$\begin{aligned} \arg \max_{\omega_k, \boldsymbol{\mu}_k, \Sigma_k} \quad & \sum_n \sum_k \gamma_{nk} \ln \omega_k + \sum_n \sum_k \gamma_{nk} \ln \mathcal{N}(\mathbf{x}_n \mid \boldsymbol{\mu}_k, \Sigma_k) \\ \text{s.t.} \quad & \omega_k \geq 0 \\ & \sum_{k=1}^K \omega_k = 1 \end{aligned}$$

where γ_{nk} is the posterior of latent variables computed from the E-Step. (20 points)

$$\gamma_{nk}$$

is derived from E step.

$$\begin{aligned} \log(N(x_i, \mu_k, \Sigma_k)) &= -\log(2\pi^{-d/2}) - 0.5 \log(\det(\sum_k)) - 0.5(x_i - \mu_k)' \Sigma_k^{-1} (x_i - \mu_k) \\ &= \sum_i \gamma_{ik} \log(N(x_i, \mu_k, \Sigma_k)) \\ &= \sum_i \gamma_{ik} (-0.5 \log(\det(\sum_k)) - 0.5(x_i - \mu_k)' \Sigma_k^{-1} (x_i - \mu_k)) \\ &= \frac{\partial \sum_i -0.5 \gamma_{ik} (x_i - \mu_k)' \Sigma_k^{-1} (x_i - \mu_k)}{\partial \mu_k} \\ &= \sum_i -\gamma_{ik} \Sigma_k^{-1} (x_i - \mu_k) = 0 \\ \mu_k \sum_i \gamma_{ik} &= \sum_i \gamma_{ik} x_i \\ \mu_k &= \frac{\sum_i \gamma_{ik} x_i}{\sum_i \gamma_{ik}} \\ -0.5 \sum_i \gamma_{ik} \log(\det(\Sigma_k)) - 0.5 \sum_i \gamma_{ik} (x_i - \mu_k)' \Sigma_k^{-1} (x_i - \mu_k) \\ &= 0.5 \sum_i \gamma_{ik} \log(\det(\Sigma_k^{-1})) - 0.5 \sum_i \gamma_{ik} (x_i - \mu_k)' \Sigma_k^{-1} (x_i - \mu_k) \\ \frac{\partial(\text{above})}{\Sigma_k^{-1}} &= 0.5 \sum_i \gamma_{ik} \Sigma_k - 0.5 \sum_i \gamma_{ik} (x_i - \mu_k) (x_i - \mu_k)' = 0 \\ \Sigma_k &= \frac{\sum_i \gamma_{ik} (x_i - \mu_k) (x_i - \mu_k)'}{\sum_i \gamma_{ik}} \end{aligned}$$

1.2 The posterior probability of z in GMM can be seen as a *soft* assignment to the clusters; In contrast, K-means assign each data point to one cluster at each iteration (*hard* assignment). Describe how to set the model parameters such that the GMM in the previous question reduces to a K-means; please also derive $p(z_n = k | \mathbf{x}_n)$ in this case. (10 points)

GMM is soft labels, while KMeans is hard labels, to make a GMM model KMeans, after we finish the E step and get a new assignment, we set the one with largest probability to 1 and all others to 0.

$$p(z_n=k|x_n) = 1 \text{ if } x_n\text{'s closest centroid is } k \text{ else } p=0$$

Problem 2 Hidden Markov Model (30 points)

Recall that an HMM is parameterized as follows:

- initial state distribution $P(X_1 = s) = \pi_s$
- transition distribution $P(X_{t+1} = s' \mid X_t = s) = a_{s,s'}$
- emission distribution $P(O_t = o \mid X_t = s) = b_{s,o}$

2.1 Suppose we observe a sequence of outcomes o_1, \dots, o_T and wish to predict the next state X_{T+1}

$$P(X_{T+1} = s \mid O_{1:T} = o_{1:T}).$$

Denote the forward message as

$$\alpha_s(T) = P(X_T = s, O_{1:T} = o_{1:T}).$$

Please derive how $P(X_{T+1} = s \mid O_{1:T} = o_{1:T})$ can be represented using $\alpha_s(T)$. (10 points)

$$\begin{aligned} &P(X_{T+1} = s | O_{1:T} = o_{1:T}) \\ &= \frac{P(X_{T+1} = s, O_{1:T} = o_{1:T})}{P(O_{1:T} = o_{1:T})} \\ &= \frac{\sum_{s'} P(X_T = s', O_{1:T} = o_{1:T}) P(X_{T+1} = s | X_T = s', O_{1:T} = o_{1:T})}{\sum_{s'} P(X_T = s', O_{1:T} = o_{1:T})} \\ &= \frac{\sum_{s'} \alpha_{s'}(T) P(X_{T+1} = s | Z_T = s')}{\sum_{s'} \alpha_{s'}(T)} \\ &= \frac{\sum_{s'} \alpha_{s'}(T) a_{s',s}}{\sum_{s'} \alpha_{s'}(T)} \end{aligned}$$

2.2 Describe how to set the model parameters such that an HMM reduces to the GMM described in Problem 1. In addition, derive the posterior probability $P(X_2 = s \mid O_1 = o_1, O_2 = o_2)$ using the parameters you set to show that the HMM really reduces to GMM. (20 points)

α_s becomes the soft assignment γ in GMM $a_{s,s'}$ becomes the x_i (data) in GMM

$$\begin{aligned} P(X_2 | O_1 = o_1, O_2 = o_2) &= \frac{P(O_2 = o_2 | X_2 = s, O_1 = o_1) P(X_2 = s, O_1 = o_1)}{P(O_1 = o_1, O_2 = o_2)} \\ &= \frac{P(O_2 = o_2) P(X_2 = s, O_1 = o_1)}{P(O_1 = o_1, O_2 = o_2)} \\ &= \frac{b_{s,o_2} \sum_{s'} P(X_2 = s, X_1 = s', O_1 = o_1)}{P(O_1 = o_1, O_2 = o_2)} \\ &= \frac{b_{s,o_2} \sum_{s'} P(X_2 = s | X_1 = s') P(X_1 = s', O_1 = o_1)}{P(O_1 = o_1) P(O_2 = o_2)} \\ &= \frac{b_{s,o_2} \sum_{s'} a_{s',s} \alpha_{s'}(1)}{P(O_1 = o_1) P(O_2 = o_2)} \end{aligned}$$

Problem 3 Viterbi Algorithm (40 points)

In this problem, we want to fit DNA sequence data with a generative model. In particular, we assume that they are generated by a hidden Markov model (HMM). Let $O_{1:N}$ which denote the sequence $[O_1 O_2 \dots O_N]$ be random variables corresponding to a DNA sequence of length N , controlled by hidden states $X_{1:N} = [X_1, X_2 \dots X_N]$. Each O_n takes a value in $\{A, C, G, T\}$ and each X_n takes one of the two possible states $\{s_1, s_2\}$. This HMM has the following parameters:

$$\theta = \{\pi_i, a_{ij}, b_{ik}\} \text{ for } i \in \{1, 2\}, j \in \{1, 2\}, \text{ and } k \in \{A, C, G, T\}$$

- Initial state distribution π_i for $i \in \{1, 2\}$:

$$\pi_1 = P(X_1 = s_1) = 0.6; \pi_2 = P(X_1 = s_2) = 0.4$$

- Transition probabilities $a_{ij} = P(X_{n+1} = s_j | X_n = s_i)$ for any $n \in N^+, i = \{1, 2\}$ and $j = \{1, 2\}$:

$$a_{11} = 0.7, a_{12} = 0.3, a_{21} = 0.2, a_{22} = 0.8$$

- Emission probabilities $b_{ik} = P(O_n = k | X_n = s_i)$ for any $n \in N^+, i \in \{1, 2\}$ and $k \in \{A, C, G, T\}$:

$$b_{1A} = 0.4, b_{1C} = 0.1, b_{1G} = 0.4, b_{1T} = 0.1$$

$$b_{2A} = 0.2, b_{2C} = 0.3, b_{2G} = 0.2, b_{2T} = 0.3$$

We observe a sequence $o_{1:4} = [o_1, o_2 \dots o_4] = [\text{AGCT}]$, please answer the following questions with step-by-step computations:

3.1 Compute probability of the observed sequence, i.e. compute $P(O_{1:4} = o_{1:4}; \theta)$. (10 points)

Init:

$$\alpha_1^k = P(o_1 | \pi_1 = S_k) P(\pi_1 = S_k)$$

iter:

$$\alpha_i^k = p(x_i | \pi_i = S_k) \sum_i \alpha_{i-1}^i a_{i,k}$$

\alpha	S1	S2
1	0.6*0.4=0.24	0.4*0.3=0.12
2	0.0768	0.0504
3	6.384e-3	0.019
4	4.24e-4	5.13e-3

$$P(O_{1:4} = o_{1:4}) = \sum_s \alpha_s(T) = 5.59e - 3$$

3.2 Find out the most likely explanation i.e. compute $s_{1:4}^* = [s_1^*, s_2^* \dots s_4^*] = \arg \max_{s_{1:4}} P(X_{1:4} = s_{1:4} | O_{1:4} = o_{1:4}; \theta)$. (20 points)

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In [5]: from hmm import HMM
import numpy as np

def hmm_test(data):
    A = np.array(data['A'])
    B = np.array(data['B'])
    pi = np.array(data['pi'])
    obs_dict = data['observations']
    states_symbols = dict()
    for idx, item in enumerate(data['states']):
        states_symbols[item] = idx
    Osequence = np.array(data['Osequence'])
    N = len(Osequence)
    model = HMM(pi, A, B, obs_dict, states_symbols)
    delta = model.forward(Osequence)
    print("Your forward function output:", delta)
    gamma = model.backward(Osequence)
    print("Your backward function output:", gamma)
    prob1 = model.sequence_prob(Osequence)
    print("Your sequence_prob function output:", prob1)
    prob2 = model.posterior_prob(Osequence)
    print("Your posterior_prob function output:", prob2)
    prob3 = model.likelihood_prob(Osequence)
    print("Your likelihood_prob function output:", prob3)
    viterbi_path = model.viterbi(Osequence)
    print('Your viterbi function output: ', viterbi_path)
    return model

model = hmm_test({"A": [[0.7, 0.3], [0.2, 0.8]],
                  "pi": [0.6, 0.6],
                  "states": ["1", "2"],
                  "B": [[0.4, 0.1, 0.4, 0.1], [0.2, 0.3, 0.3, 0.3]],
                  "observations": {"A": 0, "C": 1, "T": 3, "G": 2},
                  "Osequence": ["A", "G", "C", "T"]})

Your forward function output: [[0.24      0.0768      0.006384      0.00082704]
 [0.12      0.0504      0.019008      0.00513648]]
Your backward function output: [[0.015592 0.0346      0.16      1.          ]
 [0.018512 0.0656      0.26      1.          ]]
Your sequence_prob function output: 0.00596352
Your posterior_prob function output: [[0.62749517 0.44558918 0.17128139 0.13868319]
 [0.37250483 0.55441082 0.82871861 0.86131681]]
Your likelihood_prob function output: [[[0.38989053 0.14423696 0.07493561]
 [0.23760464 0.30135222 0.09634578]]

 [[0.05569865 0.02704443 0.06374759]
 [0.31680618 0.52736639 0.76497102]]
Your viterbi function output: ['2', '2', '2', '2']
the state is ['2', '2', '2', '2'] from above running result.
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3.3 Predict most likely observation for the next step i.e. compute $o^* = \arg \max_{o_5} P(O_5 = o_5 | O_{1:4} = o_{1:5}; \theta)$. (10 points)

$$\begin{aligned} &P(O_5 = o_5 |_{1:4} = o_{1:4}; \theta) \\ &= \frac{P(O_{1:4} = o_{1:4}, O_5 = o_5 | \theta)}{P(O_{1:4} = o_{1:4})} \end{aligned}$$

the denominator is independent of O_5 so that we need to argmax $P(O_{1:4} = o_{1:4}, O_5 = o_5 | \theta)$

Based on the following likelihood, 'T' is the predition

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In [14]: cand = ['A','T','G','C']
for i in cand:
    prob3 = model.likelihood_prob(["A","G","C","T"]+[i])
    print(i, 'likelihood')
    print(prob3[:,i,-1])
    print()

A likelihood
[[0.15295841 0.0327768 ]
 [0.2714216  0.54284319]]

T likelihood
[[0.03944158 0.05071061]
 [0.06998829 0.63985951]]

G likelihood
[[0.11877405 0.03817737]
 [0.21076214 0.63228643]]

C likelihood
[[0.03944158 0.05071061]
 [0.06998829 0.63985951]]

In [ ] :
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