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Maximum likelihood estimation of the mixture of log-concave densities

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ABSTRACT

Finite mixture models are useful tools and can be estimated via the EM algorithm. A main drawback is the strong parametric assumption about the component densities. In this paper, a much more flexible mixture model is considered, which assumes each component density to be log-concave. Under fairly general conditions, the log-concave maximum likelihood estimator (LCMLE) exists and is consistent. Numeric examples are also made to demonstrate that the LCMLE improves the clustering results while comparing with the traditional MLE for parametric mixture models.

1. Introduction

The finite mixture model (McLachlan and Peel, 2000; Mcnicholas and Murphy, 2008) provides a flexible methodology for both theoretical and practical analysis. It has a density of the form

$$f(x) = \sum_{j=1}^{K} \lambda_j g_j(x; \theta_j) \quad x \in \mathbb{R}^d, \tag{1.1}$$

where $\lambda_1, \ldots, \lambda_K$ are the mixing proportions and $g_j(x; \theta_j)$'s are component densities. The unknown parameters in the mixture model (1.1) can be estimated by the EM algorithm, see e.g. Dempster et al. (1977) and McLachlan and Krishnan (2007). One major drawback of the traditional mixture model (1.1) is the strong parametric assumption about the component density g_j. It is often too restrictive and the density estimation may be inaccurate due to the model misspecification. Another drawback is that each model requires a specific EM algorithm based on the parametric assumption.

To relax the parametric assumption, nonparametric shape constraints are becoming increasingly popular. In this paper, we make one fairly general shape constraint for our mixture model. We assume that each component density is log-concave. A density g is log-concave if $\log g$ is concave. Examples of log-concave densities include normal, Laplace, logistic, as well as gamma and beta with certain parameter constraints. Log-concave densities have lots of nice properties as described by Balabdaoui et al. (2009). Their nonparametric maximum likelihood estimators were studied by Dümbgen and Rufibach (2009), Cule et al. (2010), Cule and Samworth (2010), Chen and Samworth (2013), Pal et al. (2007) and Dümbgen et al. (2011) (referred as [DSS 2011] thereafter). The convergence rates of these estimators for log-concave densities were studied by

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Doss and Wellner (2013) and Kim and Samworth (2014). Such estimators provide more generality and flexibility without any tuning parameters.

In our model, we assume that $\mathbf{x}_1, \ldots, \mathbf{x}_n$ are independent d-dimensional random variables with distribution Q_0 and the mixture density f_0. The mixture density f_0 belongs to a given class

$$\mathcal{F} = \left\{ f : f(x) = \sum_{j=1}^{K} f_j(x) = \sum_{j=1}^{K} \lambda_j \exp\{\phi_j(x)\}, \boldsymbol{\lambda} \in \Lambda, \boldsymbol{\phi} \in \Phi \right\}, \tag{1.2}$$

where $\boldsymbol{\lambda} = (\lambda_1, \ldots, \lambda_K)$, $\Lambda = \{(\lambda_1, \ldots, \lambda_K) : 0 < \lambda_j < 1, \sum_{j=1}^{K} \lambda_j = 1\}$, $\boldsymbol{\phi} = (\phi_1, \ldots, \phi_K)$, and $\Phi = \{(\phi_1, \ldots, \phi_K) : \phi_j \text{ is concave}\}$. We assume that each ϕ_j is continuous and is coercive in the sense that $\phi_j(x) \to -\infty$ as $\|x\| \to \infty$ $(j = 1, \ldots, K)$.

One issue for mixture models is that the likelihood might be unbounded in some cases. For example, the likelihood function for a normal mixture takes the form of $L(\boldsymbol{\theta}|x) = \sum_{i=1}^{n} (\lambda g(x_i|\mu_1, \sigma_1^2) + (1 - \lambda) g(x_i|\mu_2, \sigma_2^2))$, where $\boldsymbol{\theta} = \{(\lambda, \mu_1, \mu_2, \sigma_1^2, \sigma_2^2) : \sigma_1^2, \sigma_2^2 > 0, \lambda \in (0, 1)\}$ and g is the density function for the standard normal distribution. When $\mu_1 = x_1$ and $\sigma_1^2 \to 0$, $L(\boldsymbol{\theta}|x) \to \infty$ (see Section 3.10 of McLachlan and Peel, 2000 for detailed discussions). Many methods have been proposed to solve the unboundedness issue of mixture likelihood, see for example, Hathaway (1985), Chen et al. (2008), and Yao (2010). Note that, similar to traditional normal mixture models with unequal variances, the likelihood functions for mixtures of log-concave densities are unbounded as well. Thus, similar to Hathaway (1985), we will define LCMLE on a constrained parameter space. Let $M_j(\boldsymbol{\phi}) = \max_{x \in \mathbb{R}^d} \{\phi_j(x)\}$, $M_{(1)}(\boldsymbol{\phi}) = \min_j \{M_j(\boldsymbol{\phi})\}$, and $M_{(K)}(\boldsymbol{\phi}) = \max_j \{M_j(\boldsymbol{\phi})\}$. We further define the ratio $\mathcal{S}(\boldsymbol{\phi}) = M_{(1)}(\boldsymbol{\phi}) / M_{(K)}(\boldsymbol{\phi})$. Here, we borrow the idea of Hathaway (1985) by restricting our interest to a constrained subspace $\boldsymbol{\Phi}_\eta$ such that $\boldsymbol{\Phi}_\eta = \{\boldsymbol{\phi} \in \boldsymbol{\Phi} : |\mathcal{S}(\boldsymbol{\phi})| \geq \eta > 0\}$ for some $\eta \in (0, 1]$. This restriction avoids estimating the case that the modes of different components differ a lot. By restricting on $\boldsymbol{\Phi}_\eta$, we focus our interest on $f \in \mathcal{F}_\eta$, where

$$\mathcal{F}_\eta = \left\{ f : f(x) = \sum_{j=1}^{K} f_j(x) = \sum_{j=1}^{K} \lambda_j \exp\{\phi_j(x)\}, \boldsymbol{\lambda} \in \Lambda, \boldsymbol{\phi} \in \Phi_\eta \right\}. \tag{1.3}$$

Let Q_n be the empirical distribution of $X_1, \ldots, X_n$. The (restricted) log-concave maximum likelihood estimator (LCMLE) is

$$f_n = f(\cdot|Q_n) = \operatorname*{argmax}_{f \in \mathcal{F}_\eta} \int \log(f) dQ_n. \tag{1.4}$$

In practice, similar to Hathaway (1985), picking η can be tricky for some extreme case. If η is too small, there might be a chance that some boundary point $|\mathcal{S}(\boldsymbol{\phi})| = \eta$ maximizes the log-likelihood and the solution will depend on the choice of η. In this paper, we do not focus on the issue of choosing η. The constrained subspace $\boldsymbol{\Phi}_\eta$ is mainly used for theoretical development. Based on our empirical experience, if we start the algorithm from a reasonable initial value, such as the maximum likelihood estimate assuming all components are normal with equal variance, the unboundedness issue is very rare.

Many methods have been proposed to relax the parametric assumption of (1.1). Hunter et al. (2007), Bordes et al. (2006b), Butucea and Vandekerkhove (2014), and Chee and Wang (2013) considered the extension of (1.1) by assuming all component densities are symmetric but unknown. Bordes et al. (2006a), Bordes and Vandekerkhove (2010), Hohmann and Holzmann (2013), Xiang et al. (2014), and Ma and Yao (2015) considered the extension of (1.1) when $K = 2$ and one of the component densities is symmetric but unknown. Mixtures of log-concave densities have been studied by Chang and Walther (2007), Cule et al. (2010) and Balabdaoui and Doss (2014). Chang and Walther (2007) provided an EM-type algorithm and demonstrated sound numerical results in the simulation study. Cule et al. (2010) applied the log-concave mixture model to the Wisconsin breast cancer data set. Balabdaoui and Doss (2014) considered a special case when all components have the same symmetric log-concave densities but with different location parameters, and proved the $\sqrt{n}$-consistency of their proposed M-estimators for mixing proportion as well as location parameters. Note that these models are special cases from the family of $\mathcal{F}$. Therefore, their estimators and asymptotic results cannot be applied here. For example, the mixture of normal distributions with different component means and variances belongs to $\mathcal{F}$ but does not belong to the model family considered by Balabdaoui and Doss (2014).

To the best of our knowledge, none of the existing works has studied the theoretical properties of the estimator for the log-concave mixture model (1.2) under such general conditions. This paper aims to fill in this gap. We show that theoretically, the LCMLE (in the restricted subset $\mathcal{F}_\eta$) exists, and is consistent under fairly general conditions. However, we want to point out that the extension of the properties of the log-concave density to mixtures of log-concave densities is not trivial. The log-density $l_n = l(\cdot|Q_n) = \log f_n$ is no longer guaranteed to be a concave function. Consequently, many nice theoretical properties stated in DSS 2011 no longer hold for our mixture model.

The rest of the paper is organized as follows. Section 2 introduces the basic setup, model details, and notations. Section 3 states the theoretical properties. We review the EM-type algorithm for log-concave mixture models in Section 4. Simulation and real data studies are conducted in Sections 5 and 6. We end the article with a short conclusion in Section 7. The proofs and lemmas are presented in the Appendix.

2. Log-concave maximum likelihood estimator

Let $\mathcal{Q} = \mathcal{Q}(d)$ be the family of all distributions Q on $\mathbb{R}^d$. Our goal is to maximize a log-likelihood-type functional:

$$L(\boldsymbol{\phi}, \boldsymbol{\lambda}, \boldsymbol{\pi}, Q) = \int \log\left[\sum_{j=1}^{K} \lambda_j \exp\{\phi_j(x)\}\right] dQ(x) - \sum_{j=1}^{K} \pi_j \left(\int \exp\{\phi_j(x)\}dx - 1\right), \tag{2.1}$$

where π_j's are Lagrange multipliers to incorporate the constraint $\int \exp\{\phi_j(x)\}dx = 1$ $(j = 1, \ldots, K)$. We define a profile log-likelihood:

$$L(Q) = \sup_{\boldsymbol{\phi}\in\Phi_\eta, \boldsymbol{\lambda}\in\Lambda, \boldsymbol{\pi}} L(\boldsymbol{\phi}, \boldsymbol{\lambda}, \boldsymbol{\pi}, Q). \tag{2.2}$$

If, for fixed Q, $(\boldsymbol{\psi}, \boldsymbol{\lambda}^*, \boldsymbol{\pi}^*)$ maximizes $L(\boldsymbol{\phi}, \boldsymbol{\lambda}, \boldsymbol{\pi}, Q)$, it will automatically satisfy that:

$$\pi_j^* = E(\pi(j|x)) = \int \frac{\lambda_j^* \exp\{\psi_j(x)\}}{\left(\sum_{h=1}^{K} \lambda_h^* \exp\{\psi_h(x)\}\right)} dQ(x); \tag{2.3}$$

$$\int \exp\{\psi_j(x)\}dx = 1 \quad (j = 1, 2, \ldots, K). \tag{2.4}$$

Note that differing from the non-mixture setting in DSS 2011, π_j^* is not equal to 1.

To verify this, note that $\boldsymbol{\phi} + \boldsymbol{c} \in \Phi$ for any fixed vector of functions $\boldsymbol{\phi} \in \Phi$ and arbitrary $\boldsymbol{c} = (c_1, \ldots, c_K)^T \in \mathbb{R}^K$, and

$$\left.\frac{\partial L(\boldsymbol{\psi} + \boldsymbol{c}, \boldsymbol{\lambda}, \boldsymbol{\pi}, Q)}{\partial c_h}\right|_{\boldsymbol{c}=0} = \left(\int \frac{\lambda_h \exp\{\psi_h(x)\}}{\sum_{j=1}^{K} \lambda_j \exp\{\psi_j(x)\}} dQ(x) - \pi_h \int e^{\psi_h(x)}dx\right) = 0,$$

$$\frac{\partial L(\boldsymbol{\psi}, \boldsymbol{\lambda}, \boldsymbol{\pi}, Q)}{\partial \pi_h} = 1 - \int \exp\{\psi_h(x)\}dx = 0.$$

The maximizer $(\boldsymbol{\psi}, \boldsymbol{\lambda}^*)$ forms the log-likelihood maximizer $l^*(x) = \log \sum_{j=1}^{K} \lambda_j^* e^{\psi_j(x)}$.

3. Theoretical properties

Before we state the main theories, we first define the convex support of a distribution.

Definition. For any distribution Q, let $Q(C)$ be the probability measure of the set C. The convex support of Q is the set such that:

$$csupp(Q) = \bigcap\{C : C \subseteq \mathbb{R}^d \text{ closed and convex}, Q(C) = 1\}.$$

The convex support is itself closed and convex with $Q(csupp(Q)) = 1$.

In the following text. we define:

$\mathcal{Q}^1 = \{Q \in \mathcal{Q} : \int \|x\| dQ < \infty\}$, (we define $\|x\|$ as Euclidean norm in our paper).
$\mathcal{Q}^0 = \{Q \in \mathcal{Q} : interior(csupp(Q)) \neq \emptyset\}$.

Theorem 1. *For any $Q \in \mathcal{Q}^1 \cap \mathcal{Q}^0$, the value of $L(Q)$ is real and there exists a maximizer:*

$$(\boldsymbol{\psi}, \boldsymbol{\lambda}^*, \boldsymbol{\pi}^*) = \operatorname*{argmax}_{\boldsymbol{\phi}\in\Phi_\eta, \boldsymbol{\lambda}\in\Lambda, \boldsymbol{\pi}} L(\boldsymbol{\phi}, \boldsymbol{\lambda}, \boldsymbol{\pi}, Q) \text{ such that } \int e^{\psi_j(x)}dx = 1 \quad \text{for } j = 1, \ldots, K.$$

Next, we establish the consistency of the estimated mixture density. In the following, we refer to the concept of convergence of distribution as converging with respect to Mallows distance D_1 : $D_1(Q, Q') = \inf_{(X,X')} E\|X - X'\|$, where Q and Q' are two distributions and the infimum is taken over all pairs of (X, X') such that $X \sim Q$ and $X' \sim Q'$. The convergence of Q_n to Q_0 with respect to Mallows distance, i.e. $\lim_{n\to\infty} D_1(Q_n, Q) = 0$, is equivalent to assuming that Q_n weakly converges to Q_0, denoted by $Q_n \to^w Q$, and $\int \|x\| dQ_n(x) \to \int \|x\| dQ(x)$ as $n \to \infty$.

Theorem 2. *Let Q_n be a sequence such that $\lim_{n\to\infty} D_1(Q_n, Q_0) = 0$ for some $Q_0 \in \mathcal{Q}^1 \cap \mathcal{Q}^0$. Then,*

$$\lim_{n\to\infty} L(Q_n) = L(Q_0).$$

Let ϕ_{nj}'s and λ_{nj}'s be the maximizer corresponding to profile log-likelihood $L(Q_n)$, i.e., $f_n(x) = \sum \lambda_{nj} \exp\{\phi_{nj}(x)\} = f(\cdot|Q_n) \in \mathcal{F}_\eta$. For $f_0(x) = f(\cdot|Q_0) \in \mathcal{F}_\eta$, we have:

$$\lim_{n\to\infty, x\to y} f_n(x) = f_0(y) \quad \text{for all } y \notin \partial\{f_0 \geq 0\}, \tag{3.1}$$

$$\lim_{n\to\infty, x\to y} f_n(x) \leq f_0(y) \quad \text{for all } y \in \mathbb{R}^d, \tag{3.2}$$

$$\lim_{n\to\infty} \int |f_n(x) - f_0(x)|dx = 0. \tag{3.3}$$

The above theorem showed the consistency of the estimated mixture density. If we further assume that the true mixture density $f_0(x)$ is identifiable, then each estimated component density and mixing proportions are also consistent. We will discuss more about the identifiability issue in Section 7.

4. EM-type algorithm

The EM algorithm for estimating log-concave mixture densities has already been developed by Chang and Walther (2007). Here we briefly summarize it. First we randomly generate initial values for the normal mixture EM-algorithm and run the normal mixture EM-algorithm until convergence, which will provide a good initial value. Then we use the outcome as the starting values for our EM-type algorithm. We assume the observed data $\mathbf{X} = (\mathbf{x}_1, \ldots, \mathbf{x}_n)^T \in \mathbb{R}^{n\times d}$ to be incomplete and define the missing value $\mathbf{Z} = (\mathbf{z}_1, \ldots, \mathbf{z}_n)^T$, where $\mathbf{x}_i = (x_{i,1}, \ldots, x_{i,d})^T$ and $\mathbf{z}_i$ is a K-dimension vector with its jth element given by:

$$z_{ij} = \begin{cases} 1 & \text{if } x_i \text{ belongs to } j\text{th group,} \\ 0 & \text{otherwise.} \end{cases}$$

So the complete log-likelihood is:

$$\log f(\boldsymbol{\phi}, \boldsymbol{\lambda}; \mathbf{X}, \mathbf{Z}) = \log \prod_{i=1}^{n}\prod_{j=1}^{K} [\lambda_j e^{\phi_j(\mathbf{x}_i)}]^{z_{ij}} = \sum_{i=1}^{n}\sum_{j=1}^{K} z_{ij}[\log \lambda_j + \phi_j(\mathbf{x}_i)].$$

In E-step, we replace z_{ij} by

$$z_{ij}^{(t+1)} = \frac{\lambda_j^{(t)} e^{\widehat{\phi}_j^{(t)}(\mathbf{x}_i)}}{\sum_{h=1}^{K} \lambda_h^{(t)} e^{\widehat{\phi}_h^{(t)}(\mathbf{x}_i)}}.$$

In M-step, first we update λ by $\lambda_j^{(t+1)} = \frac{1}{n}\sum_{i=1}^{n} z_{ij}^{(t+1)}, j = 1, \ldots, K$. Then we update ϕ_j by maximizing $\sum_{i=1}^{n} z_{ij}^{(t+1)} \phi_j(\mathbf{x}_i)$ with respect to ϕ_j through the function called `mlelcd` in the R package `LogConcDEAD` (Cule et al., 2009) and get estimator $\widehat{\phi}_j^{(t+1)}$ for $j = 1, \ldots, K$. The estimation of $\widehat{\phi}_j$ has been studied by Walther (2002) and Rufibach (2007). Given i.i.d. data $X_1, \ldots, X_n$ from distribution f, the Log-concave Maximum Likelihood Estimator (LCMLE) $\widehat{f}_n$ exists uniquely and has support on the convex hull of the data (by Theorem 2 of Cule et al., 2010). The log-likelihood estimator $\log\widehat{f}_n$ is a piecewise linear function with knots which are a subset of $\{X_1, \ldots, X_n\}$. Walther (2002) and Rufibach (2007) provided algorithms for computing $\widehat{f}_n(X_i), i = 1, \ldots, n$. The entire log-density $\log\widehat{f}_n$ can be computed by linearly interpolating between $\log\widehat{f}_n(X_{(i)})$ and $\log\widehat{f}_n(X_{(i+1)})$. Walther (2002) and Rufibach (2007) also pointed out that it is natural to apply weights for an EM-type algorithm. The $z_{1j}^{(t+1)}, \ldots, z_{nj}^{(t+1)}$ can be viewed as weights for $\mathbf{x}_1, \ldots, \mathbf{x}_n$ when estimating the log-concave density ϕ_j in our algorithm for $j = 1, \ldots, K$. The algorithm stops once the increasing increment $\ell^{(t+1)} - \ell^{(t)}$ is below 10^{-7}, where $\ell^{(t)} = \sum_{i=1}^{n} \log \sum_{j=1}^{k} \lambda_j^{(t)} \exp\{\phi_j^{(t)}(x_i)\}$.

To avoid the local maximum, we restart the algorithm 20 times and choose the result with the highest log-likelihood. As we discussed in Section 1, the unboundedness issue of the log-likelihood does happen infrequently, mostly due to an inappropriate initial. In our algorithm, we borrow the idea of restarting process in many existing EM-algorithms for parametric mixture models, e.g. Benaglia et al. (2009). If the log-likelihood goes to infinity in any iteration, our EM-type algorithm will be forced to restart from the beginning with a new randomly chosen initial.

5. Simulation results

5.1. Copula procedure to generate multivariate log-concave mixtures

As we do not have a tuning issue for LCMLE, the most attractive application of LCMLE is the density estimation with dimensionality higher than 1. To generate data from a multivariate log-concave mixture model, we borrow the idea of

Table 1
The simulation setups of Model II–IV.

Model	d	Marginal distribution of component 2
II	2	$N(0, 1)$, and $Gamma(2, 1) + 2$
III	3	$N(0, 1)$, $Gamma(2, 1) - 1$, and $Beta(4, 1)$
IV	4	$N(0, 1)$, $Gamma(2, 1) + 2$, $Beta(4, 1)$, $Laplace(0, 1) + 1$

Table 2
Simulation results of Model I–IV.

Model	d	AMN_1	AMN_2	MSE_1	MSE_2	$AvARI$
I	1	17.56	**10.86**	0.0016	**0.0007**	0.91
II	2	30.35	**13.28**	0.0085	**0.0013**	0.86
III	3	12.43	**4.79**	0.0010	**0.0005**	0.93
IV	4	7.97	**3.21**	0.0006	**0.0004**	0.95

the copula procedure from Chang and Walther (2007). For a d-dimensional log-concave mixture density, we observe n observations $\mathbf{x}_1, \ldots, \mathbf{x}_n$, where $\mathbf{x}_i = (x_{i,1}, \ldots, x_{i,d})^T \in \mathbb{R}^d$. To simplify our simulation, we focus on the model whose univariate marginal distributions are log-concave. We model the dependence structure with a normal copula. Suppose $(N_1, \ldots, N_d)^T$ are multivariate normal with mean $\mathbf{0}$ and covariance matrix Σ. Let $F_1, \ldots, F_d$ be the CDFs of the desired univariate log-concave distributions. Then,

$$\mathbf{x}_i = (x_{i,1}, \ldots, x_{i,d})^T = (F_1^{-1}(\Phi(N_1)), \ldots, F_d^{-1}(\Phi(N_d)))^T.$$

5.2. Significant Improvement when densities are log-concave mixtures

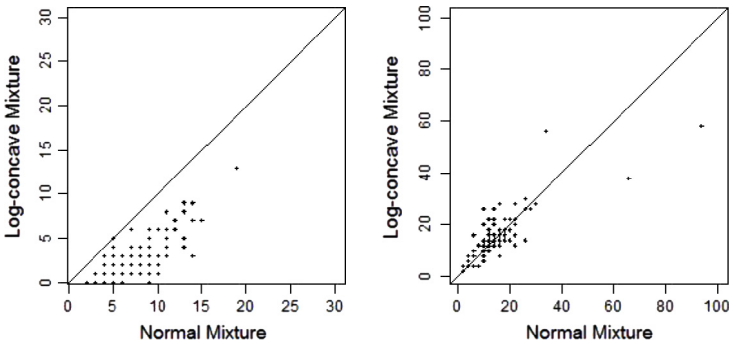
We first generate 500 observations from a univariate log-concave mixture model: $0.3Logistic(0, 1) + 0.7Laplace(5, 1)$ (referred as Model I). This setup is a more general form of Chang and Walther (2007), as Chang and Walther (2007) only considered the case that one component is a location shift of the other. For the multivariate cases, we generate 500 observations based on the copula procedure as we discussed in Section 5.1 for Model II through IV, which are multivariate log-concave mixture models with dimensionality d from 2 to 4. For each model, component 1 (with probability 0.3) is generated as a joint normal distribution $N(0, \mathbf{I}_d)$; component 2 (with probability 0.7) is generated through a normal copula $N(0, 0.5\mathbf{I}_d + 0.5\mathbf{1}_d)$, where $\mathbf{I}_d$ is a $d \times d$ identity matrix and $\mathbf{1}_d$ is a $d \times d$ matrix of ones. The marginal distributions of component 2 are summarized in Table 1.

We repeat the simulation 100 times for each model. When evaluating the simulation results for mixture models, there is a well-known *label switching* issue when sorting the labels for mixture models (Stephens, 2000; Yao and Lindsay, 2009). In this paper, we adopt the method of Yao (2015) to find labels by minimizing the distance between the estimated classification probabilities and the true labels over different permutations. After sorting the labels, we compute the mean square errors obtained by the log-concave EM algorithm (MSE_2) and compare them with the parametric normal EM-algorithm (MSE_1) to compare the accuracy of the estimated λ's. As mixture models also serve as methods of classification, we compute the average misclassification number (denoted as AMN_2 for the log-concave EM-algorithm and AMN_1 for the normal EM-algorithm) among the 100 replicates. We are also interested in the difference between two classification methods. One of many possible measurements to summarize the similarity between two clusterings is the Adjusted Rand Index (ARI), which ranges from -1 to 1, see Hubert and Arabie (1985) for detailed description of ARI. In this paper, we compute the average Adjusted Rand Index ($AvARI$) among the 100 replicates.

We report results over the 100 replicates in Table 2. We observe significant smaller MSEs for the estimated λ obtained by log-concave mixture models. Especially for Model I and II, the mean square errors obtained by log-concave mixture model are less than half of those obtained by normal mixture model. In terms of classification, the average misclassification number among the 500 observations are significantly reduced as well. The $AvARI$ indicates that the classification results of the log-concave mixture model and the normal mixture model are quite different, especially for Model I and II.

To compare the classification result for each replicate, we take $d = 4$ as an example and show the clustering results in Fig. 1. In Fig. 1(a), each point represents a single replicate from Model IV's setup. The x-axis represents the number of misclassification by the Normal mixture EM-algorithm. The y-axis represents the number of misclassification by our log-concave mixture EM-algorithm. We observe significant improvement in the misclassification rates, as all the points for our 100 replicates are below the identity line.

To better illustrate the finite sample performance of the LCMLE, we pick one replicate from Model I. To compare the fitted densities with the true densities, in Fig. 2, we plot the true component densities in the solid lines and the fitted densities in the dashed line. Even for a finite sample size of 500, the LCMLE for the log-concave mixture model approximates the true component densities well.



(a) Model IV. (b) Model VIII.

Fig. 1. Four-dimensional clustering result: normal mixture EM-algorithm vs. log-concave mixture EM-algorithm by number of misclassifications. The solid lines represent the identity.

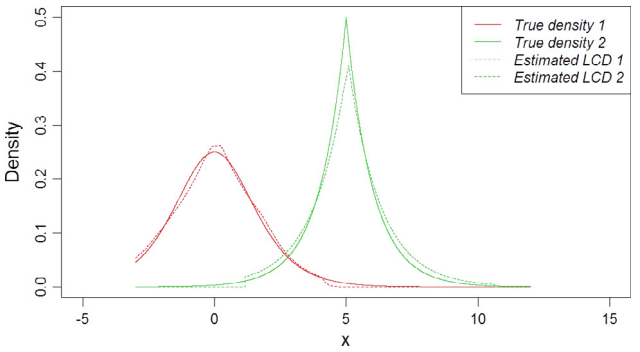


Fig. 2. EM-type algorithm estimation for log-concave mixtures for a single replicate of Model I. Solid line represents the truth and dashed line represents the estimation results. The fitted $\hat{\lambda} = 0.3076$.

5.3. Insignificant penalty when the parametric assumptions are correct

We are also interested in the price that we have to pay for the flexibility while the data actually are from normal mixtures. For Model V–VIII, we generate $n = 500$ observations from a joint normal mixture distribution, in which the first component (with probability 0.4) is a d-dimensional normal distribution with mean $\mathbf{0}_d$ and covariance matrix $0.5\mathbf{I}_d + 0.5\mathbf{1}_d$, and the second component (with probability 0.6) is a d-dimensional normal distribution with mean $\boldsymbol{\mu}_d$ and the same covariance matrix, where $\mu_1 = 5$, $\boldsymbol{\mu}_2 = (3, 2)^T$, $\boldsymbol{\mu}_3 = (3, 2, 2)^T$, and $\boldsymbol{\mu}_4 = (3, 1, 3, 1)^T$. We also repeat the simulation 100 times and compare the same criteria.

From Table 3, we observe no significant penalty for applying log-concave mixture models instead of normal mixture models. The MSEs and average misclassification numbers for log-concave mixture models are either almost the same or only a little bit higher than those for the multivariate normal mixture model. The classification results of the log-concave mixture model and the normal mixture model are quite similar to each other, as we observe the *AvARI*'s are close to 1 in Table 3. This phenomena is further supported in Fig. 1(b), which shows the classification results for Model VIII ($d = 4$). We observe no significant difference in terms of misclassifications, as most points in Fig. 1(b) are around the identity line. Consequently, we conclude that the log-concave mixture model is a more flexible methodology without significant penalties if the data are actually from normal mixtures.

6. Real data application

To further illustrate the performance of log-concave mixture models, we apply the log-concave EM algorithm to the crab data set of Campbell and Mahon (1974), which contains two types of crabs in the data set: 100 blue crabs and 100 orange crabs. We focus on these blue crabs, which include $n_1 = 50$ males and $n_2 = 50$ females referred to as groups G_1 and G_2, respectively. For each crab, there are five measurements. We are only interested in two of them: *RW* (rear width) and *BD* (body depth), both in unit of mm. In Fig. 3, we give the scatter plot of *RW* and *BD*.

Fitting a 2-dimensional two component log-concave mixture model results in 18 observations misclassified. Fifteen observations from G_1 are misclassified into G_2 and three observations from G_2 are misclassified into G_1. The normal mixture model results in 20 observations misclassified in total. Two additional observations from G_1 are misclassified into G_2.

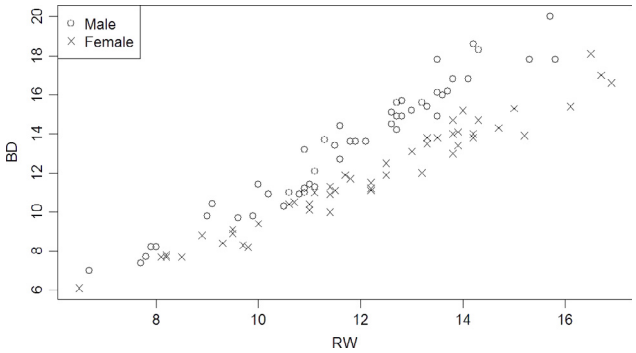


Fig. 3. Scatter plot of *RW* (rear width) and *BD* (body depth) of the Blue Crab data set.

Table 3
Simulation results of Model V–VIII.

Model	d	AMN_1	AMN_2	MSE_1	MSE_2	*AvARI*
V	1	3.17	3.51	0.0004	0.0005	0.99
VI	2	33.95	37.12	0.0018	0.0020	0.91
VII	3	21.95	23.57	0.0008	0.0008	0.94
VIII	4	17.71	18.20	0.0018	0.0020	0.96

7. Conclusion

The log-concave maximum likelihood estimator (LCMLE) provides more flexibility to estimate mixture densities, when compared to the traditional parametric mixture models. The estimation of LCMLE for log-concave mixtures can be achieved by an EM-type algorithm. The LCMLE is not sensitive to the model mis-specification and consequently, only one implementation of the EM-type algorithm is necessary. Through simulation studies, we observed significant improvements in the sense of classification and no significant penalties when the parametric assumption is indeed correct.

In this paper, we proved the existence of the LCMLE for log-concave mixture models. The consistency is also proved for the estimated mixture density. If the true mixture density is identifiable, then the estimated component densities are also identifiable. However, it is not an easy task to prove the overall identifiability for the most general family of mixtures of log-concave distributions in (1.2) from a nonparametric point of view. Some restrictive conditions, such as symmetry, are needed to ensure identifiability. Hunter et al. (2007) and Bordes et al. (2006b) proved the identifiability of (1.1) if $K = 2$ and both component densities are symmetric but with different location parameters. Balabdaoui and Doss (2014) have considered a special case of (1.2), when $\phi_j(x;\theta_j) = \phi(x-\theta_j)$ and ϕ is a symmetric concave function about 0, and the identifiability of (1.2) follows from Hunter et al. (2007) and Bordes et al. (2006b) when $K = 2$.

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Appendix A. Lemmas

Lemma 1 is taken from Cule and Samworth (2010). Lemmas 2–5 are taken from DSS 2011. Lemma 6 is the extension of Lemma 2.13 of DSS 2011.

Lemma 1. *For any log-concave distribution Q with density f, there exist finite constants $B_1 = B_1(Q) > 0$ and $B_2 = B_2(Q) > 0$ such that $f(x) \le B_1 \exp(-B_2\|x\|)$ for all $x \in \mathbb{R}^d$.*

Lemma 2. *The following properties of Q are equivalent:*

(a) *csupp(Q) has non-empty interior.*
(b) *$Q(H) < 1$ for any hyperplane $H \subset \mathbb{R}^d$.*
(c) *With Leb denoting Lebesgue measure on $\mathbb{R}^d$,*

$$\lim_{\delta \downarrow 0} \sup\{Q(A) : A \subset \mathbb{R}^d \text{ closed and convex}, Leb(A) \le \delta\} < 1.$$

Lemma 3. *Let ϕ be the function such that for any $x, y \in interior(dom(\phi))$ and $t \in (0,1)$, if $tx+(1-t)y \in interior(dom(\phi))$, $\phi(tx+(1-t)y) \geq t\phi(x)+(1-t)\phi(y)$ and for $C \subseteq \mathbb{R}^d$, $\int_C e^{\phi(x)}dx \leq 1$. We define $D_q = \{x \in C : \phi(x) \geq q\}$. For any $r < M \leq \max_{x\in\mathbb{R}^d}\phi(x)$,*

$$Leb(D_r) \leq (M-r)^d e^{-M} \Big/ \int_0^{M-r} t^d e^{-t}dt.$$

Lemma 4. *Let $\overline{\phi}, \phi_1, \phi_2, \ldots$ be concave functions and $\phi_n \leq \overline{\phi}$. Further we assume the set $H = \{x : \liminf_{n\to\infty}\phi_n(x) > -\infty\}$ is not empty. Then there exist a subsequence $(\phi_{n(k)})_k$ of $(\phi_n)_n$ and a function ϕ such that $H \subset dom(\phi) \overset{d}{=} \{\phi > -\infty\}$:*

$$\lim_{k\to\infty, x\to y}\phi_{n(k)}(x) = \phi(y) \quad \text{for all } y \in interior(dom(\phi)),$$

$$\lim_{k\to\infty, x\to y}\phi_{n(k)}(x) \leq \phi(y) \quad \text{for all } y \in \mathbb{R}^d.$$

Lemma 5. *Suppose Q_n is a sequence converged to some distribution Q and h be a nonnegative and continuous function, then*

$$\liminf_{n\to\infty}\int hdQ_n \geq \int hdQ.$$

If the stronger statement $\liminf_{n\to\infty}\int hdQ_n = \int hdQ < \infty$ holds, then for any function f such that $|f|/(1+h)$ is bounded,

$$\lim_{n\to\infty}\int fdQ_n = \int fdQ.$$

Lemma 6. *A point $x \in \mathbb{R}^d$ is an interior point of C if and only if*

$$h(Q,x) = \sup\{Q(E) : E \subset C, E \text{ closed and convex}, x \notin interior(E)\}/Q(C) < 1.$$

Proof. For $x \notin interior(E)$ and closed and convex E, there exists a unit vector $u_j \in R^d$ such that E is contained in the closed set H_C which is a subset of C:

$$C \supseteq H_C(x) = \{y \in C : u^T y \leq u^T x\} \supseteq E.$$

By the definition of $h(Q,x)$ we conclude $h(Q,x) \leq Q(H_C)/Q(C) \leq 1$. There are two cases: $E \subset H_C$ and $E = H_C(x)$. For the case $E \subset H_C$, by definition $h(Q,x) < 1$ strictly. For the case $E = H_C(x)$, as we have $x \notin interior(E)$ but $x \in H_C(x)$, we conclude $x \in \partial H_C(x)$. Now if $x \notin interior(C)$, by definition, $h(Q,x) = 1$. On the other hand, if $h(Q,x) = 1$, then $Q(H_C(x)) = Q(C)$, which leads to $C = H_C(x) = E$. Combined with $x \notin interior(H_C(x))$ we can conclude that $x \notin interior(C)$. Consequently, $x \notin interior(C) \iff h(Q,x) = 1$. Thus, $x \in interior(C) \iff h(Q,x) < 1$.

Appendix B. Proof of Theorem 1

The first thing is to prove the finiteness of the log-likelihood type function.

$L(Q)$ is the supreme of $L(\boldsymbol{\phi}, \boldsymbol{\lambda}, \boldsymbol{\pi}, Q)$ over all $\boldsymbol{\phi} \in \boldsymbol{\Phi}, \boldsymbol{\lambda} \in \boldsymbol{\Lambda}, \boldsymbol{\lambda} \in \mathbb{R}^K$. If we take a special case that $\phi_j^*(x) = -(\log\lambda_j^*) - \|x\|$, $L(\boldsymbol{\phi}^*, \boldsymbol{\lambda}^*, \boldsymbol{\pi}, Q) = \log K - \int \|x\|dQ > -\infty$. Consequently, $L(Q) > -\infty$.

Now we show $L(Q) < \infty$. As discussed at the end of Section 2, we do restrict our interest to the $\boldsymbol{\phi}$ such that $\int e^{\phi_j(x)}dx = 1$ for $j = 1, \ldots, K$. Consequently, we define the log-density as $l(x) = \log\sum_{j=1}^K \lambda_j e^{\phi_j(x)}$ and rewrite the log-likelihood-type function as $L(l, Q) = L(\boldsymbol{\phi}, \boldsymbol{\lambda}, \boldsymbol{\pi}, Q)$. For the convenience of the proof, we define an envelope function $\overline{\phi}(x) = \max_j\{\phi_j(x)\}$, i.e. $\overline{\phi}(x) \geq l(x)$ for every $x \in \mathbb{R}^d$. This function is continuous but not smooth on $d-1$ dimensional boundaries. These boundaries divide the $csupp(Q)$ into K sets: $C_1, \ldots, C_K$. Each set C_j is defined as $C_j = \{x \in \mathbb{R}^d : \overline{\phi}(x) = \phi_j(x)\}$. The sets $C_1, \ldots, C_K$ are disjoint except on the boundaries and $Leb(C_i \cap C_j) = 0$ for every $i \neq j$. For any $x, y \in C_j$ and $t \in (0,1)$, $\overline{\phi}(tx+(1-t)y) \geq t\overline{\phi}(x)+(1-t)\overline{\phi}(y)$ and $\int_{C_j} e^{\overline{\phi}(x)}dx \leq 1$. We define $M_j(\boldsymbol{\phi})$ and $\mathcal{S}(\boldsymbol{\phi})$ as stated in Section 1. As $L(l,Q) \leq \sum_{j=1}^K Q(C_j)M_j$, $M_j > -\infty$, and the restriction $|\mathcal{S}(\boldsymbol{\phi})| \geq \eta > 0$, we focus our interest on $M_j > 0$ and the only case which we have to worry about is all M_j's increasing to infinity. We define $D_q = \{x \in \mathbb{R}^d : \overline{\phi}(x) \geq q\}$. For any $c > 0$,

$$\begin{aligned} L(l,Q) &\leq \int \overline{\phi}(x)dQ = \int_{csupp(Q)\setminus D_{-cM_{(1)}}} \overline{\phi}(x)dQ + \int_{D_{-cM_{(1)}}} \overline{\phi}(x)dQ \\ &\leq -cM_{(1)}(1 - Q(D_{-cM_{(1)}})) + M_{(K)}Q(D_{-cM_{(1)}}) \\ &\leq (1+c\eta)\Big(Q(D_{-cM_{(1)}}) - \frac{c\eta}{c\eta+1}\Big)M_{(K)}. \end{aligned}$$

We can always find sufficient large c such that the set $D_{-cM_{(1)}}$ is a closed and convex subset of $\mathbb{R}^d$. We define the set $D_{j,q} = \{x \in C_j : \overline{\phi}(x) \geq q\} \subset C_j$. Obviously $Leb(D_{-cM_{(1)}}) = \sum_{j=1}^{K} Leb(D_{j,-cM_{(1)}})$. For any $c > 0$, applying Lemma 3 to set $D_{j,-cM_{(1)}}$ and letting $M = M_{(1)}$ yield $Leb(D_{j,-cM_{(1)}}) \leq (1+c)M_{(1)}^d e^{-M_{(1)}}/(d!+o(1)) \to 0$ as $M_{(1)} \to \infty$ for every $j = 1, \ldots, K$. Consequently, $Leb(D_{-cM_{(1)}}) \to 0$ as $M_{(1)} \to \infty$. By our definition, $\eta \in (0, 1]$. Thus, by Lemma 2, we can find sufficiently large c and small δ such that

$$\sup\{Q(D) : D \subset \mathbb{R}^d,\ Leb(D) \leq \delta\} < \frac{c\eta}{c\eta + 1}.$$

Thus, $L(l, Q) \to -\infty$ as $M_{(1)} \to \infty$, which indicates that when all modes of log-concave densities increase to infinity, the log-likelihood is poorly characterized. On the other hand, $L(l, Q) \leq M_{(K)}$. These considerations show that $L(Q)$ is finite and equals the supremum of $L(l, Q)$ for suitable finite M_j's such that $M_j \in [M_{*j}, M_j^*]$ $(j = 1, \ldots, K)$.

Let $\phi_{m,j}$'s and $\lambda_{m,j}$'s form a sequence $l_m(x) = \log \sum \lambda_{m,j} \exp\{\phi_{m,j}(x)\}$ such that $-\infty < L(l_m, Q) \uparrow L(Q)$ as $m \to \infty$. Next, we will prove that for every $j \in \{1, \ldots, K\}$, there exists a point, say, $x_{0,j} \in interior(csupp(Q))$, such that $\liminf_{m\to\infty} \phi_{m,j}(x_{0,j}) > -\infty$.

We define $\overline{\phi}_m(x) = \max_j\{\phi_{m,j}(x)\}$, $C_{m,j} = \{x \in \mathbb{R}^d : \overline{\phi}_m(x) = \phi_{m,j}(x)\}$, and $M_{m,j} = \max_{x\in\mathbb{R}^d} \phi_{m,j}(x)$. For any $j^* \in \{1, \ldots, K\}$, by picking any $x_{0,j^*} \in C_{m,j^*}$ such that $\phi_{m,j^*}(x_{0,j^*}) \in [M'_{m,j^*}, M_{m,j^*})$, where $M'_{m,j^*} = \max_{x\in\partial\{C_{m,j^*}\}} \phi_{m,j^*}(x)$, there exists a sufficient small $\epsilon \geq 0$ such that the set $E_{m,j^*} = \{x \in C_{m,j^*} : \phi_{m,j^*}(x) \geq \phi_{m,j^*}(x_{0,j^*}) + \epsilon\}$ is a closed and convex subset of C_{m,j^*} and x_{0,j^*} is not an interior point of E_{m,j^*}. Thus,

$$\begin{aligned} L(l_m, Q) &= \int l_m dQ \leq \int \overline{\phi}_m(x) dQ = \sum_{j\neq j^*} \int_{C_{m,j}} \phi_{m,j}(x) dQ + \int_{C_{m,j^*}} \phi_{m,j^*} dQ \\ &\leq \sum_{j\neq j^*} M_{m,j} Q(C_{m,j}) + \phi_{m,j^*}(x_{0,j^*}) Q(C_{m,j^*}) + (M_{m,j^*} - \phi_{m,j^*}(x_{0,j^*})) Q(E_{m,j^*}) \\ &\leq \sum_{j=1}^{K} \max(M_{m,j}, 0) + \phi_{m,j^*}(x_{0,j^*}) Q(C_{m,j^*})(1 - h_{j^*}(Q, x_{0,j^*})). \end{aligned}$$

These inequalities hold for the case of $\phi_{m,j^*}(x_{0,j^*}) = M_{m,j^*}$ as well ($\epsilon = 0$ accordingly). By Lemma 6, $h_{j^*}(Q, x_{0,j^*}) < 1$. Due to the fact that M_{m,j^*} is finite, $interior(C_{m,j^*})$ is not empty. Consequently, $\liminf_{m\to\infty} Q(C_{m,j^*}) > 0$, which yields

$$\begin{aligned} \phi_{m,j^*}(x_{0,j^*}) &\geq -\frac{\sum_{j=1}^{K} \max(M_{m,j}, 0) - L(l_m, Q)}{Q(C_{m,j^*})(1 - h_{j^*}(Q, x_{0,j^*}))} \\ &> -\frac{\sum_{j=1}^{K} \max(M_j^*, 0) - L(l_1, Q)}{Q(C_{m,j^*})(1 - h_{j^*}(Q, x_{0,j^*}))} > -\infty. \end{aligned}$$

Hence, the set $H_j = \{x : \liminf_{m\to\infty} \phi_{m,j}(x) > -\infty\}$ is not empty for every $j \in \{1, \ldots, K\}$. From Lemma 1 we conclude that for each ϕ_j, we can find suitable finite positive constants $a_j, b_j > 0$ such that $\phi_j(x) \leq a_j - b_j\|x\| \leq a - b\|x\|$, where $a = \max_j a_j > 0$ and $b = \min_j b_j > 0$. Then by Lemma 4, there exist a subsequence $(\phi_{1,m(k_1)})_{k_1}$ of $(\phi_{1,m})_m$ and a concave function ϕ_1 such that:

$$\begin{aligned} &\lim_{k_1\to\infty, x\to y} \phi_{1,m(k_1)}(x) = \phi_1(y) \quad \text{for all } y \in interior(dom(\phi_1)), \\ &\lim_{k_1\to\infty, x\to y} \phi_{1,m(k_1)}(x) \leq \phi_1(y) \quad \text{for all } y \in \mathbb{R}^d. \end{aligned}$$

If we define $\phi_1 = -\infty$ on $\mathbb{R}^d \setminus dom(\phi_1)$, then we can rewrite them as:

$$\begin{aligned} &\limsup_{k_1\to\infty} \phi_{1,m(k_1)}(x) \leq \phi_1(x) \quad \text{for all } x \in \partial\{dom(\phi_1)\}, \\ &\lim_{k_1\to\infty} \phi_{1,m(k_1)}(x) = \phi_1(x) \quad \text{for all } x \in \mathbb{R}^d \setminus \partial\{dom(\phi_1)\}. \end{aligned}$$

We can find a sub-subsequence in the original subsequence, which has the similar property for $\phi_{2,m(k_2)}$. Keeping doing this sequentially for all $\phi_{m,j}$'s and $\lambda_{m,j}$'s will yield the common subsequence $l_{m(k)}$ and a function $l^*(x) = \log \sum \lambda_j \exp\{\phi_j(x)\}$ such that:

$$\begin{aligned} &\limsup_{k\to\infty} l_{m(k)}(x) \leq l^*(x) \quad \text{for all } x \in \mathcal{P}, \\ &\lim_{k\to\infty} l_{m(k)}(x) = l^*(x) \quad \text{for all } x \in \mathbb{R}^d \setminus \mathcal{P}, \end{aligned}$$

where $\mathcal{P} = \cup_{j=1}^{K}\left(\partial\{dom(\phi_j)\}\right)$ and $Leb(\mathcal{P}) = 0$. The next step is to prove that $l^*(x)$ is the maximizer. Applying Fatou's lemma to the subsequence function $l_{m(k)}(x) \leq a - b\|x\|$ yields

$$\limsup_{k\to\infty} \int l_{m(k)} dQ \leq \int l^* dQ.$$

Hence,

$$L(Q) \geq l(l^*, Q) \geq \limsup_{k\to\infty} L(l_{m(k)}, Q) = L(Q),$$

from which we conclude $L(l^*, Q) = L(Q)$. The first inequality follows by the definition of $L(Q)$. The last equality follows by the definition that $l_{m(k)}$ is a sequence that maximizes $L(l_{m(k)}, Q)$ to $L(Q)$ as $k \to \infty$. Thus, it concludes the existence of the maximizer l^*, which indicates the existence of λ_j^*'s and ϕ_j^*'s.

Appendix C. Proof of Theorem 2

We proof the theorem for a subsequence of Q_n. Let $L(Q_n) \to \Gamma$. As in the proof of Theorem 1, $l_n(x) \leq a - b\|x\|$ and $\inf \phi_{n,j}(x_0) > -\infty$ for some $x_0 \in interior(csupp(Q))$. Therefore, for a subsequence of $(Q_n)_n$, there exists a function l^* such that $l_n(y), l^*(y) \leq a - b\|y\|$, and

$$\limsup_{k\to\infty} l_{n(k)}(x) \leq l^*(x) \quad \text{for all } x \in \mathcal{P},$$
$$\lim_{k\to\infty} l_{n(k)}(x) = l^*(x) \quad \text{for all } x \in \mathbb{R}^d \setminus \mathcal{P}.$$

By Skorohod's theorem, there exists a probability space with random variables $X_n \sim Q_n, X \sim Q$ such that $X_n \to X$ almost surely. We define a random variable $H_n = a - b\|X_n\| - l_n(X_n) \geq 0$. Applying Fatou's lemma to H_n yields,

$$\begin{aligned}
\Gamma &= \lim_{n\to\infty} \int l_n dQ_n = \lim_{n\to\infty} \int (a - b\|x\|) dQ_n - E(H_n) = a - b\gamma - \liminf_{n\to\infty} E(H_n) \\
&\leq a - b\gamma - E\left(\liminf_{n\to\infty}(H_n)\right) \leq a - b\gamma - E\left(a - b\|X\| - l^*(X)\right) \\
&= b\left(\int \|x\| dQ_0 - \gamma\right) + \int l^*(X) dQ_0 = L(l^*, Q_0) \leq L(Q_0).
\end{aligned}$$

Let $l_0(x) = \log \sum \lambda_j \phi_j(x)$, i.e. λ_j's and ϕ_j's are the results corresponding with l_0. In the following proof we utilize a special approximation scheme. Let $l^{(\epsilon)}(x) = \log \sum \lambda_j^{(\epsilon)} \phi_j^{(\epsilon)}(x)$, $\lambda_j^{(\epsilon)} = \lambda_j$ and $\phi_j^{(\epsilon)} = \inf_{v,c}(v_j^T x + c_j)$ such that $\|v_j\| \leq \epsilon^{-1}$ and $\phi_j(y) \leq v_j^T y + c_j$. DSS 2011 shows that the approximation $\phi_j^{(\epsilon)}$ is real valued and Lipschitz continuous with constant ϵ^{-1}. Consequently, $l^{(\epsilon)}(x)$ is also Lipschitz-continuous with constant ϵ^{-1}. Moreover, $\phi_j^{(\epsilon)} \geq \phi_j$ and $\phi_j^{(\epsilon)} \downarrow \phi_j$ pointwise as $\epsilon \downarrow 0$. Thus, $l^{(\epsilon)} \downarrow l_0$ pointwise as $\epsilon \downarrow 0$ and $l^{(1)} \geq l^{(\epsilon)} \geq l_0$ for $\epsilon \in (0, 1)$. With this approximation, it follows from Lipschitz-continuity, $\int \|x\| dQ_0 = \gamma < \infty$, and the stronger version of Lemma 5 that

$$\begin{aligned}
\Gamma &= \lim_{n\to\infty} \int l_n dQ_n \geq \lim_{n\to\infty} L(l^{(\epsilon)}, Q_n) = \lim_{n\to\infty} \int l^{(\epsilon)} dQ_n - \sum \pi_j \int e^{\phi_j^{(\epsilon)}(x)} dx + 1 \\
&= \int l^{(\epsilon)} dQ_0 - \sum \pi_j \int \exp(\phi_j^{(\epsilon)}(x)) dx + 1.
\end{aligned}$$

Applying monotone convergence theorem to function $l^{(1)} - l^{(\epsilon)}$ and dominated convergence theorem to $\exp\{\phi_j^{(\epsilon)}\}$'s yields, $\lim_{\epsilon\to 0^+} L(l^{(\epsilon)}, Q_0) = L(l_0, Q_0)$. Hence, $\Gamma \geq L(Q_0)$. Combining with $\Gamma \leq L(l^*, Q_0) \leq L(Q_0)$ yields $\Gamma = L(Q_0) = L(l^*, Q_0)$, which indicates that l^* equals the maximizer $l_0 = l(\cdot|Q_0)$ that corresponds to $L(Q_0)$.

Applying to density $f_n = \exp\{l_n\}$ and $f_0 = \exp\{l_0\}$ yields,

$$\lim_{n\to\infty, x\to y} f_n(x) = f_0(y) \quad \text{for all } x \in \mathbb{R}^d \setminus \mathcal{P},$$
$$\lim_{n\to\infty, x\to y} f_n(x) \leq f_0(y) \quad \text{for all } y \in \mathcal{P},$$

where $\mathcal{P} = \cup_{j=1}^{K}\left(\partial\{f_{0j} > 0\}\right)$ and $Leb(\mathcal{P}) = 0$. Consequently, $(f_n)_n \to f_0$ almost everywhere with respect to Lebesgue measure. In addition, $|f_n(x)| \leq e^{a - b\|x\|}$, and $\int e^{a-b\|x\|} dx$ is finite. Applying Lebesgue's dominated convergence theorem yields,

$$\lim_{n\to\infty} \int |f_n(x) - f_0(x)| dx = 0.$$

Consequently, we claim Theorem 2 to be true for a subsequence of the original sequence $(Q_n)_n$. It remains to show it is true for the entire sequence.

Suppose any assertion about f_n is false, then one could replace the initial sequence $(Q_n)_n$ from the start with a subsequence such that one of the following three conditions is satisfied:

(i) $\lim_{n\to\infty} f_n(x_n) > f_0(y)$ for some sequence $(x_n)_n$ converge to point y;
(ii) $\lim_{n\to\infty} f_n(x_n) < f_0(y)$ for some sequence $(x_n)_n$ converge to point y;
(iii) $\lim_{n\to\infty} \int |f_n(x) - f_0(x)|dx > 0$.

Any of these three properties are transmitted to subsequence of $(Q_n)_n$, which would lead to a contradiction.

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