Finite Mixture of Birnbaum-Saunders distributions using the $k$-bumps algorithm

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Abstract

Mixture models have received a great deal of attention in statistics due to the wide range of applications found in recent years. This paper discusses a finite mixture model of Birnbaum-Saunders distributions with $G$ components, as an important supplement of the work developed by Balakrishnan et al. (2011), who only considered two components. Our proposal enables the modeling of proper multimodal scenarios with greater flexibility, where the identifiability of the model with $G$ components is proven and an EM-algorithm for the maximum likelihood (ML) estimation of the mixture parameters is developed, in which the $k$-bumps algorithm is used as an initialization strategy in the EM algorithm. The performance of the $k$-bumps algorithm as an initialization tool is evaluated through simulation experiments. Moreover, the empirical information matrix is derived analytically to account for standard error, and bootstrap procedures for testing hypotheses about the number of components in the mixture are implemented. Finally, we perform simulation studies and analyze two real datasets to illustrate the usefulness of the proposed method.

Keywords: Birnbaum-Saunders distribution; EM algorithm; $k$-bumps algorithm; Maximum likelihood estimation; Finite mixture.

1 Introduction

Although most statistical applications are conceived to deal with unimodal data, in practice research data can exhibit heterogeneity due to skewness and multimodality. More importantly, skewness and non-distinctive shape variations can be due to intrinsic aspects of the data. Skew and distinctive shape variations that resemble multimodality can indicate not all observations come from the same parent population. In other words, if the data come from different sub-populations, and their identifications are not known, the mixture distribution can be used quite effectively to analyze the dataset (McLachlan & Peel, 2000). Although multimodal data can be modeled with a single distribution, the quality of the model is poor in general. Hence modeling based on finite mixture distributions plays a vital role in different data analysis situations. Finite mixture models are now applied in such diverse areas such as biology, biometrics, genetics, medicine, marketing,

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reliability, and pattern recognition problems, among others. Some examples of mixture models are based on gamma, exponential, inverse Gaussian and Weibull distributions.

The Birnbaum-Saunders (BS) distribution, originally introduced by Birnbaum & Saunders (1969), is a two parameter failure time distribution for modeling fatigue failure caused under cyclic loading, which is derived from the cumulative damage or Miner law. This distribution has been considered a more attractive alternative to the often-used Weibull, gamma, and log-normal models, because the BS model fits very well within the extremes of the distribution, even when the amount of fatigue life data is small. The BS distribution, also known as fatigue life distribution, was initially used to model failure times, but has since been extended to fields such as reliability, business, engineering, survival analysis, and medical sciences; see Leiva Leiva (2016) and Leiva et al. (2015).

A positive random variable $T$ is said to have a two-parameter BS distribution if its cumulative distribution function (cdf) can be written as

$$F_T(t; \alpha, \beta) = P(T \leq t) = \Phi(a_t(\alpha, \beta)), \quad t > 0, \quad \alpha > 0, \quad \beta > 0, \quad (1.1)$$

where $a_t(\alpha, \beta) = (\sqrt{t/\beta} - \sqrt{\beta/t})/\alpha$ and $\Phi(\cdot)$ is the cdf of the standard normal distribution. Clearly $\beta$ is the median of the BS distribution.

In the context of finite mixture distributions, if the sub-populations do not have symmetric distributions, then the finite mixture of BS distributions can be used to analyze these data, since BS distributions are positively skewed. This can make them, good alternatives to these based on skewed distributions. In reliability research, for example, populations can be heterogeneous due to at least two underlying sub-populations; one being the standard sub-population (also known as strong population) and the other being the defective sub-population. Data that arise from such heterogeneous populations are amenable to modeling by a mixture of two or more life distributions. Indeed, the mixture of BS distributions seems to be a suitable approach: multimodal distributions can be approximated very well by a mixture of distributions because sub-populations tend to not have symmetric distributions. Extensive work has been carried out regarding bimodal BS distributions; see Olmos et al. (2016) and Balakrishnan et al. (2009). However, not much work has been done on finite mixtures of BS distributions.

The aim of this paper is to consider a finite mixture model based on the BS distributions by extending the two-component mixture BS proposed by Balakrishnan et al. (2011). The maximum likelihood estimates are obtained via the EM algorithm, in which the $k$-bumps algorithm (Bagnato & Punzo, 2013) is used to obtain the initial values required by the EM algorithm. The identifiability of the FM-BS model is discussed following the model proposed by Chandra (1977). An important aspect to be addressed is whether a two-component model fits the data significantly better than a one-component model. This question is answered by using the parametric bootstrap log-likelihood ratio statistic proposed by Turner (2000).

The remainder of the paper is organized as follows. In Section 2, we briefly report basic results for the BS distribution and present the finite mixture BS (FM-BS) distribution along with its properties. In Section 3, we deal with the parameter estimation of the FM-BS distribution through an EM algorithm, as well as the starting values and stopping rule used in the algorithm. Moreover, an approximation of the observed information matrix for obtaining the standard error of the ML estimates is presented. In Section 4 and 5, numerical samples using both simulated and real datasets are given to illustrate the performance of the proposed model. Finally, Section 6 contains our concluding remarks.
2 Finite mixture BS model

First, we recall that from (1.1), a positive random variable $T$ is distributed as a BS distribution if its probability density function (pdf) is

$$f_T(t; \alpha, \beta) = \phi\left(a_t(\alpha, \beta)\right)A_t(\alpha, \beta), \quad t > 0, \quad (2.2)$$

where $a_t(\alpha, \beta) = (\sqrt{t/\beta} - \sqrt{\beta/t})/\alpha$, and $A_t(\alpha, \beta) = t^{-3/2}(t + \beta)/(2\alpha \beta^{1/2})$ is the derivative of $a_t$ with respect to $t$. This distribution is denoted by $T \sim \text{BS}(\alpha, \beta)$, where $\alpha$ and $\beta$ are the shape and scale parameters, respectively. The BS distribution is related to the normal distribution by means of the representation of $T$ give by $T = \beta \left(1 + 2X^2 + 2X\sqrt{1+X^2}\right)$, where $X \sim \mathcal{N}(0, \alpha^2/4)$. The mean and variance are given respectively by $E(T) = \beta (1 + \alpha^2/2)$ and $\text{Var}(T) = (\alpha \beta)^2 (1 + 5\alpha^2/4)$. Note from (1.1), it is easy to see that $\beta$ is the median of the distribution of $T$. Moreover, the mode (denoted by $m$) is obtained as the solution of the nonlinear equation

$$(\beta - m)(m + \beta) = \alpha^2 \beta m(m + 3\beta), \quad (2.3)$$

where $m < \beta$. Then, from the above equation, $\alpha$ can be expressed in terms of $m$ and $\beta$, and consequently the pdf of the BS distribution can be re-parameterized in terms of parameters $m$ and $\beta$ as follows

$$f_T(t; m, \beta) = \frac{1}{\sqrt{2\pi}} \exp\left[ -\frac{1}{2} \frac{\beta m(m + 3\beta)}{(\beta - m)} \left(\frac{a_t(1, \beta)}{m + \beta}\right)^2 \right] \frac{t^{-3/2}(t + \beta)}{2(m + \beta)^2} \sqrt{m + 3\beta}. \quad (2.4)$$

A feature of the BS density in (2.4) is that its asymmetry changes according to the value of $m$, as can be seen in Figure [1]. As $m$ increases, the density becomes more symmetric around $\beta$.

![Figure 1: Unimodal BS densities with $\beta = 7$ and varying modes ($m$).](image)

Now, following the idea of Balakrishnan et al. [2011], we define mixtures of Birnbaum-Saunders distributions of the form:

$$f(y; p, \alpha, \beta) = \sum_{j=1}^{G} p_j f_{T_j}(y; \alpha_j, \beta_j), \quad y \in \mathbb{R}_+, \quad (2.5)$$

where $p_j$ is the mixing parameter of the $j$th sub-population which is constrained to be positive with the constraint $\sum_{j=1}^{G} p_j = 1$, and $f_{T_j}(\cdot; \alpha_j, \beta_j)$ is the pdf of sub-population $j$ of the BS($\alpha_j, \beta_j$) distribution, with $\alpha_j > 0$, $\beta_j > 0$, $j = 1, \ldots, G$. Moreover, $p = (p_1, \ldots, p_G)^\top$, $\alpha = (\alpha_1, \ldots, \alpha_G)^\top$ and $\beta = (\beta_1, \ldots, \beta_G)^\top$. One of the $p_j$ is redundant because these probabilities add up to 1. We
Theorem 1. If $Y \sim \text{FM-BS}(p, \alpha, \beta)$, then

(i) $cY \sim \text{FM-BS}(p, c\beta)$, where $c \in \mathbb{R}_+$;

(ii) $Y^{-1} \sim \text{FM-BS}(p, \alpha, \beta^{-1})$, where $\beta^{-1} = (1/\beta_1, \ldots, 1/\beta_G)^\top$;

(iii) For $\beta_1 = \beta_2 = \ldots = \beta_G = \beta$, $\beta/Y$ and $Y/\beta$ have the same distribution;

(iv) The cdf of $Y$ is $F_Y(y) = \sum_{j=1}^G p_j \Phi(a_j(\alpha_j, \beta_j))$;

(v) If $W = \log(Y)$, then the pdf of $W$ is

$$f_W(w; p, \alpha, \beta) = \sum_{j=1}^G p_j f_{w_j}(w; \alpha_j, \gamma_j), \quad w \in \mathbb{R}_+,$$

where $f_{w_j}(w; \alpha_j, \gamma_j) = (1/2)\phi(\xi_2(w; \alpha_j, \gamma_j)) \frac{\xi_1(w; \alpha_j, \gamma_j)}{\gamma_j}$, with $\xi_2(w; \alpha_j, \gamma_j) = \frac{2}{\alpha_j} \sinh\left(\frac{w-\gamma_j}{2}\right)$ and $\xi_1(w; \alpha_j, \gamma_j) = \frac{2}{\alpha_j} \cosh\left(\frac{w-\gamma_j}{2}\right)$, $\gamma_j = \log(\beta_j)$.

As mentioned, many properties of the FM-BS distribution can be obtained by using properties of the normal distribution, and from other results that come from the usual BS distribution and an associated distribution, such as the sinh-normal distribution [Rieck, 1989].

Theorem 2. If $Y \sim \text{FM-BS}(p, \alpha, \beta)$, then

$$E(Y^s) = \sum_{j=1}^G p_j \exp(\gamma_j s) \left[ \frac{K_{(2s+1)/2}(\alpha_j^{-2}) + K_{(2s-1)/2}(\alpha_j^{-2})}{2K_{1/2}(\alpha_j^{-2})} \right],$$

where $K_v(\cdot)$ denotes the modified Bessel function of the third kind. Moreover

$$E(Y) = \sum_{j=1}^G p_j \beta_j \left(1 + \alpha_j^2/2\right) \quad \text{and} \quad E(Y^2) = \sum_{j=1}^G p_j \beta_j^2 \left(1 + 2\alpha_j^2 + 3\alpha_j^4/2\right).$$

Theorem 3. Let $Y \sim \text{FM-BS}(p, \alpha, \beta)$. Then the mode (modes) and median of the FM-BS distribution are obtained, respectively, by solving the nonlinear equations with respect to $y$

Mode: $\sum_{j=1}^G p_j \phi(a_j(\alpha_j, \beta_j)) \left[ a_y(\alpha_j, \beta_j)A_y^2(\alpha_j, \beta_j) + y^{-5/2}(y + 3\beta_j)/(4\alpha_j \beta_j^{1/2}) \right] = 0$

Median: $\sum_{j=1}^G p_j \Phi(a_y(\alpha_j, \beta_j)) = 0.5$. 

Assume that the number of components $G$ is known and fixed. A positive random variable $Y$, with density (2.5), is called a finite mixture of Birnbaum-Saunders (FM-BS) model, and will be denoted by $Y \sim \text{FM-BS}(p, \alpha, \beta)$. The pdf of the FM-BS can take different shapes as can be seen in Figure 2. Some properties of the FM-BS distribution can be derived by using the close relationship between the distribution $T_j$ and normal distribution.
Table 1 displays the mode and median of the FM-BS distribution based on different parametric choices. The values of the parameters $p_1$, $\alpha_1$, $\alpha_2$, $\beta_1$ and $\beta_2$, in Table 1 are chosen to demonstrate the unimodal and bimodal cases for the probability function of the mixture model. From Table 1 we see that the mode is slightly affected by variation in the values of the mixing proportion $p_1$, for the unimodal and bimodal case. In addition, the median decreases when $p_1$ increases for the unimodal and bimodal cases.

Table 1: The mode(s) and median of the FM-BS.

| $\theta = (p_1, \alpha_1, \alpha_2, \beta_1, \beta_2)$ | Mode(s) | Median |
|-----------------|---------|--------|
| (0.2,0.5,0.75,3,7) | 2.8649 | 5.7670 |
| (0.3,0.5,0.75,3,7) | 2.6698 | 5.1786 |
| (0.4,0.5,0.75,3,7) | 2.5521 | 4.6549 |
| (0.2,0.25,0.35,3,7) | 2.9756, 3.9871 | 6.2635 |
| (0.3,0.25,0.35,3,7) | 2.8938, 4.5233 | 5.7541 |
| (0.4,0.25,0.35,3,7) | 2.8625, 4.9819 | 5.0735 |

Figure 2: Plots of the density function for some values of $p_1$: (left panel) $(\alpha_1, \alpha_2, \beta_1, \beta_2) = (0.2,0.5,0.75,3,7)$ and (right panel) $(\alpha_1, \alpha_2, \beta_1, \beta_2) = (0.25,0.35,3,7)$.

**Theorem 4.** Let $Y \sim \text{FM-BS}(p, \alpha, \beta)$. Then,

(i) the survival function (sf) and the hazard function (hf) of $Y$ are, respectively,

$$S_Y(y) = \sum_{j=1}^{G} p_j S_{T_j}(y) \quad \text{and} \quad h_Y(y) = \sum_{j=1}^{G} p_j f_{T_j}(y; \alpha_j, \beta_j)/S_Y(y),$$

where $S_{T_j}(y) = 1 - \Phi(a_y(\alpha_j, \beta_j))$: 

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(ii) for \( G = 2 \) the hr function \( h_Y(\cdot) \) satisfies

\[
\lim_{y \to \infty} h_Y(y) = \begin{cases} 
\frac{1}{2\alpha_1^2 \beta_1}, & \text{if } \alpha_2^2 \beta_2 < \alpha_1^2 \beta_1; \\
\frac{d}{2\alpha_1^2 \beta_1} + \frac{1-d}{2\alpha_2^2 \beta_2}, & \text{if } \alpha_2^2 \beta_2 = \alpha_1^2 \beta_1; \\
\frac{1}{2\alpha_2^2 \beta_2}, & \text{if } \alpha_2^2 \beta_2 > \alpha_1^2 \beta_1,
\end{cases}
\]

where \( d = p \left( p + (1-p) \exp(1/\alpha_2^2 - 1/\alpha_1^2) \alpha_1 \beta_1^{1/2} / (\alpha_2 \beta_2^{1/2}) \right)^{-1} \).

**Proof:** Part (i) is easy to prove. For part (ii), we start by considering the hazard function, which can also be written as

\[
h_Y(y) = w(y) h_T_1(y) + \left(1 - w(y)\right) h_T_2(y),
\]

where \( w(y) = p S_{T_1}(y) / \left[p S_{T_1}(y) + (1-p) S_{T_2}(y)\right] \). Applying L’Hôpital’s rule for \( w(y) \), the derivative of \( w(y) \) can be expressed as

\[
\frac{d}{dy} w(y) = \frac{\phi(\alpha_y(\alpha_2, \beta_2)) - \phi(\alpha_y(\alpha_1, \beta_1))}{p \phi(\alpha_y(\alpha_1, \beta_1)) - \phi(\alpha_y(\alpha_2, \beta_2))}.
\]

We have that if \( y \to \infty \), then \( \alpha_y(\alpha_2, \beta_2) / \alpha_y(\alpha_1, \beta_1) \to \alpha_1 \beta_1^{1/2} / (\alpha_2 \beta_2^{1/2}) \) and

\[
\frac{\phi(\alpha_y(\alpha_2, \beta_2))}{\phi(\alpha_y(\alpha_1, \beta_1))} \to \begin{cases}
0, & \text{if } \alpha_2^2 \beta_2 < \alpha_1^2 \beta_1; \\
\exp\left(1/\alpha_1^2 - 1/\alpha_2^2\right), & \text{if } \alpha_2^2 \beta_2 = \alpha_1^2 \beta_1; \\
\infty, & \text{if } \alpha_2^2 \beta_2 > \alpha_1^2 \beta_1.
\end{cases}
\]

So, from the above results we obtain that as \( y \to \infty \),

\[
w(y) \to \begin{cases}
1, & \text{if } \alpha_2^2 \beta_2 < \alpha_1^2 \beta_1; \\
d, & \text{if } \alpha_2^2 \beta_2 = \alpha_1^2 \beta_1; \\
0, & \text{if } \alpha_2^2 \beta_2 > \alpha_1^2 \beta_1,
\end{cases}
\]

where

\[
d = p \left( p + (1-p) \exp(1/\alpha_2^2 - 1/\alpha_1^2) \alpha_1 \beta_1^{1/2} / (\alpha_2 \beta_2^{1/2}) \right)^{-1},
\]

and hence part (ii) of Theorem 4 has been proved. \( \Box \)

Figure 3 displays two different hr functions (unimodal and bimodal), considering three mixing proportions and fixed parameters \( \alpha_1, \alpha_2, \beta_1, \beta_2 \). Note that Figure 3 (left panel) considers small \( \alpha_1 \) and \( \alpha_2 \) and Figure 3 (right panel) considers large \( \alpha_1 \) and small \( \alpha_2 \). Figure 3 shows the convergence of the hr function (unimodal and bimodal) for the FM-BS model considering two conditions (the first and the last of Theorem 4) for different parameter combinations. Note that the left plot in Figure 4 satisfies the \( \alpha_2^2 \beta_2 < \alpha_1^2 \beta_1 \) condition and the right plot in Figure 4 satisfies the \( \alpha_2^2 \beta_2 > \alpha_1^2 \beta_1 \) condition.

Inspired by AL-Hussaini et al. (1997), we estimate the stress-strength reliability \( R = P(Y < X) \), when the random variables \( X \) and \( Y \) are independent and each has a FM-BS distribution. Specifically, suppose that \( X \sim \text{FM-BS}(p, \alpha, \beta) \) and \( Y \sim \text{FM-BS}(q, \gamma, \theta) \) are independent such that their pdfs are given by

\[
h_X(x) = \sum_{j=1}^{G_1} p_j f_{T_j}(x; \alpha_j, \beta_j) \quad \text{and} \quad h_Y(y) = \sum_{l=1}^{G_2} q_l g_{T_l}(y; \gamma_l, \theta_l),
\]
respectively. Then, the stress-strength reliability $R$ can be expressed as

$$ R = \int_0^\infty \int_0^x h_Y(y) h_X(x) dy dx = \sum_{j=1}^{G_1} \sum_{l=1}^{G_2} p_j q_l R_{jl}, \quad (2.6) $$

where

$$ R_{jl} = \int_0^\infty \int_0^x g_{T_l}(y; \gamma_l, \theta_l) f_{T_j}(x; \alpha_j, \beta_j) dy dx = \int_0^\infty \phi(c_x(\alpha_j, \beta_j)) \Phi(c_x(\gamma_l, \theta_l)) C_x(\alpha_j, \beta_j) dx, $$

for $j = 1, \ldots, G_1$, $l = 1, \ldots, G_2$. The expressions for $R_{jl}$, in (2.6), can be obtained using numerical methods (e.g., using the `integrate()` function in the R software).
2.1 Identifiability

A very important concept associated with mixture models is identifiability, which is the foundation for estimation problems. It’s important as testing hypotheses and classification of random variables can only be discussed if the class of all finite mixtures is identifiable. This identifiability issue has been discussed by several authors, among them, Teicher (1967), Yakowitz & Spragins (1968) and Chandra (1977). In this section, we use the results from Chandra (1977) to show that the class of all finite mixing distributions relative to the BS(α, β) distribution is identifiable, which we present briefly: Let ψ be a transform associated with each $F_j$ ∈ Ψ, where Ψ is the class of distribution functions, having the domain of definition $D_{\Psi}$, such that:

\[ \lim_{s \to \alpha} \psi_j(s) = 0 \]

\[ \lim_{s \to \beta} \psi_j(s) = \infty \]

\[ \psi_j(s) = E(T_j^s) = \beta_j^s \left[ 1 + \frac{\alpha_j s^2}{2} + \frac{\alpha_j (s^4 - s^2)}{8} + \frac{\alpha_j (s^9 - 5s^4 + 4s^2)}{48} \right], \quad j = 1, 2. \] (2.7)

From (2.7) we can see $D_{\psi_1} = D_{\psi_2} = (-\infty, \infty)$. Now we satisfy the two conditions of the previous theorem as follows:

**Condition 1:** Ordering the family $\Psi$ of all cdf’s lexicographically by $F_1 \leq F_2$ if $\alpha_1 > \alpha_2$ or $\alpha_1 = \alpha_2$ implies that $\beta_1 > \beta_2$. So, we can simply prove that $D_{\psi_1} \subseteq D_{\psi_2}$.

**Condition 2:** If we take $s_1 = +\infty$ and consider $\alpha_1 > \alpha_2$ and $\beta_1 > \beta_2$, we have

\[ \lim_{s \to +\infty} \frac{\psi_2(s)}{\psi_1(s)} = \lim_{s \to +\infty} \frac{\beta_2^s}{\beta_1^s} \left[ 1 + \frac{\alpha_2 s^2}{2} + \frac{\alpha_2 (s^4 - s^2)}{8} + \frac{\alpha_2 (s^9 - 5s^4 + 4s^2)}{48} \right] \]

\[ = \lim_{s \to +\infty} \left\{ \exp \left[ \log \left( \frac{\beta_2}{\beta_1} \right) \right] \right\}^s \]

\[ = 0, \]

and hence the identifiability of the finite mixture BS(α, β) has been proved.

\[ \square \]

3 Maximum likelihood estimation

In this section, we deal with the estimation problem for the model by using the EM (expectation maximization) algorithm that finds the maximum likelihood (ML) in the presence of missing
data, which was introduced by Dempster et al. [1977] to obtain the ML estimates of the unknown parameter \( \theta \). Moreover, we discuss starting values and the stopping rule of the EM algorithm, and how the standard errors were obtained.

### 3.1 Parameter estimation via the EM algorithm

Here, we describe how to implement the expectation conditional maximization (ECM) algorithm [Meng & Rubin, 1993] for the ML estimation of the parameters of the FM-BS model. The basic idea of the ECM is that the maximization (M) step of EM is replaced by several computationally simple conditional maximization (CM) steps. For notational convenience, let \( y = (y_1, \ldots, y_n) \) be the observations vector and \( Z = (Z_1, \ldots, Z_n) \) the set of latent component-indicators \( Z_j = (Z_{1j}, \ldots, Z_{Gj}), j = 1, \ldots, n, \) whose values are a set of binary variables with

\[
Z_{ij} = \begin{cases} 
1 & \text{if } Y_j \text{ belongs to group } j, \\
0 & \text{otherwise},
\end{cases}
\]

in which \( \sum_{j=1}^{G} Z_{ij} = 1 \). Given the mixing probabilities \( p_1, \ldots, p_G \), the component indicators \( Z_1, \ldots, Z_n \) are independent, with multinomial densities \( f(z_i) = p_1^{z_{1i}} p_2^{z_{2i}} \cdots (1 - p_1 - \cdots - p_{G-1})^{z_{Gi}}, \) which are denoted by \( Z_i \sim \text{Multinomial}(1; p_1, \ldots, p_G). \) Note that \( P(Z_{ij} = 1) = 1 - P(Z_{ij} = 0) = p_j \).

These results are used to build the ECM algorithm, since the FM-BS model can be represented hierarchically as

\[
\begin{align*}
Y_i | Z_{ij} &= 1 \quad \text{ind} \quad \text{BS}(\alpha_j, \beta_j), \quad (3.8) \\
Z_i & \quad \text{ind} \quad \text{Multinomial}(1, p_1, \ldots, p_G) \quad (i = 1, \ldots, n). \quad (3.9)
\end{align*}
\]

According to (3.8) and (3.9), the complete data log-likelihood function of \( \theta = (p_1, \ldots, p_{G-1}, \alpha_1, \ldots, \alpha_G, \beta_1, \ldots, \beta_G) \) given \((y, Z)\), aside from additive constants, is

\[
\ell_c(\theta | y, Z) = \sum_{i=1}^{n} \log p_j - \log(\alpha_j) - \frac{1}{2} \log(\beta_j) + \log(y_i + \beta_j) - \frac{1}{2} \alpha_j^2. 
\]

Hence, the expected value of the complete data log-likelihood \( \ell_c(\theta | y, Z) \), evaluated with \( \theta = \theta^{(k)} \), is the \( Q \)-function given by \( Q(\theta | \theta^{(k)}) = E(\ell_c(\theta | y, Z) | y, \theta^{(k)}) \). To evaluate the \( Q \)-function, the necessary conditional expectations include \( \hat{z}_{ij}^{(k)} = E(Z_{ij} | y_i, \theta^{(k)}) \). By using known properties of conditional expectation, we obtain

\[
\hat{z}_{ij}^{(k)} = \hat{p}_j^{(k)} f_{r_j}(y_i; \hat{\alpha}_j^{(k)}, \hat{\beta}_j^{(k)}) / \sum_{j=1}^{G} \hat{p}_j^{(k)} f_{r_j}(y_i; \hat{\alpha}_j^{(k)}, \hat{\beta}_j^{(k)}).
\]

Therefore, the \( Q \)-function can be written as

\[
Q(\theta | \hat{\theta}^{(k)}) = \sum_{i=1}^{n} \sum_{j=1}^{G} \left[ \log p_j - \log \alpha_j - \frac{1}{2} \log \beta_j + \frac{1}{2} \log(y_i + \beta_j) - \frac{1}{2} \alpha_j^2 \right]. 
\]

In summary, the implementation of the ECM algorithm for ML estimation of the parameters of the FM-BS model proceeds as follows:
E-step: Given $\theta = \hat{\theta}^{(k)}$, compute $z_{ij}^{(k)}$ for $i = 1, \ldots, n$ and $j = 1, \ldots, G$.

CM-step 1: Fix $\beta_j^{(k)}$ and update $\alpha_j^{(k)}$ and $p_j^{(k)}$ as

$$
\hat{\alpha}_j^{(k)} = \frac{\sum_{i=1}^n z_{ij}^{(k)} a_{ij}(1, \hat{\beta}_j^{(k)})}{\sum_{i=1}^n z_{ij}^{(k)}} \quad \text{and} \quad \hat{p}_j^{(k)} = \frac{\sum_{i=1}^n z_{ij}^{(k)}}{n};
$$

CM-step 2: Fix $\hat{p}^{(k+1)}$, $\hat{\alpha}^{(k+1)}$ and update $\hat{\beta}^{(k+1)}$ using

$$
\hat{\beta}^{(k+1)} = \arg \max_{\beta} Q(\hat{p}^{(k+1)}, \hat{\alpha}^{(k+1)}, \beta, |\hat{\theta}^{(k)}|).
$$

### 3.2 Starting values of the EM algorithm

It is well known that mixture models can provide a multimodal log-likelihood function. In this sense, the method of maximum likelihood estimation through the EM algorithm may not give maximum global solutions if the starting values are far from the real parameter values. Thus, the choice of starting values for the EM algorithm in the mixture context plays a key role in parameter estimation, since good initial values for the optimization process hasten or enable the convergence.

The adopted starting values are summarized as follows:

- Initialize the zero-one membership indicator $\hat{Z}_j^{(0)} = \{\hat{z}_{ij}^{(0)}\}_{i=1}^G$ according to a partitional clustering method.

- The initial values for mixing probabilities, component locations and scale can be specified as

$$
\hat{p}_j^{(0)} = \frac{\sum_{i=1}^n \hat{z}_{ij}^{(0)}}{n}, \quad \hat{\alpha}_j^{(0)} = \frac{\sum_{i=1}^n \hat{z}_{ij}^{(0)} a_{ij}(1, \hat{\beta}_j^{(0)})}{\sum_{i=1}^n \hat{z}_{ij}^{(0)}}, \quad \hat{\beta}^{(0)} = \arg \max_{\beta} Q(\hat{p}^{(0)}, \hat{\alpha}^{(0)}, \beta, |\hat{\theta}^{(0)}|).
$$

It is well known that the success of EM-type algorithms largely depends on the initialization values, so they have some limitations. For instance, label switching can get trapped at a local maximum or converge to the boundary of the parameter space. Unfortunately, when the partitions provided by partitional clustering methods, for example $k$-means [Basso et al., 2010] and $k$-medoids (Kaufman & Rousseeuw, 1990) algorithms, are used to initialize the EM-algorithm, the final estimates may change every time the algorithm is executed. As the EM-algorithm inherits the random initialization of the partitional clustering algorithm, we recommend using an algorithm that always gives the same initial values. Following Bagnato & Punzo (2013), we used the $k$-bumps algorithm; an algorithm that always provides the same final partition.

**Remark 1.**

(a) The $k$-bumps algorithm can be summarized via the following steps:

- detect $k$ bumps $B_j$ of the observed data $y$;
- find the maximum point $m_j^{(0)}$ for each $B_j$, where $m_j$ is the mode, for $j = 1, \ldots, G$;
- assign each observation to the cluster with the closest maximum point.
After obtaining \( m_j^{(0)} \) and \( \beta_j^{(0)} \) can be calculated. Using equation (2.3), the initial value of the parameter \( \alpha_j^{(0)} \) (the shape parameter) can be estimated. More details about the k-bumps algorithm are available in Bagnato & Punzo (2013).

(b) Only for the k-means and k-medoids algorithm, for each group \( j \), we utilize the modified moment estimates proposed by Ng et al. (2003), which is implemented in the function \texttt{mmmeth()} in the R package \texttt{bssn} (Maehara & Benites, 2015) to obtain the initial values for \( \alpha \) and \( \beta \).

### 3.3 Stopping rule

To assess the convergence of the EM algorithm, the two most useful ways of confirming convergence are: (i) the difference between two successive log-likelihood values is less than a user-specified error tolerance; or (ii) all parameter estimates are changing by a very small degree. As suggested by Andrews & McNicholas (2011), we adopt the Aitken acceleration-based stopping criterion (McLachlan & Krishnan, 2008, Chap. 4.9):

\[
|\ell^{(k+1)} - \ell^{(k)}| < \varepsilon,
\]

deciding when to terminate computations where \( \ell^{(k+1)} \) is the observed log-likelihood evaluated at \( \theta^{(k+1)} \), \( \varepsilon \) is the desired tolerance (\( \varepsilon = 10^{-6} \) will be used to decide when to terminate computations), and the asymptotic estimate of the log-likelihood at iteration is (see, Böhning et al., 1994)

\[
\ell^{(k+1)} = \ell^{(k)} + \left( \ell^{(k+1)} - \ell^{(k)} \right) / (1 - c^{(k)}),
\]

with \( c^{(k)} \) denoting the Aitken’s acceleration at the \( k \)th iteration, given by \( c^{(k)} = \ell^{(k+1)} - \ell^{(k)} \ell^{(k-1)} \). Assuming convergence to the ML estimator \( \hat{\theta} \), also \( \ell^{(k+1)}_{\infty} \) is the asymptotic estimate of the log-likelihood at iteration \( k + 1 \). Note that the above procedure is also applicable to the simple case \( (G = 1) \) by treating \( Z_{ij} = 1 \).

### 3.4 Standard error approximation

This section presents an outline of the standard errors of the ML estimates from the FM-BS model, which are obtained in a simple way by differentiating the log-likelihood function twice and obtaining the inverse. However, this is somewhat complex to carry out. By assuming the usual regularity conditions, these guarantee that the ML estimates solve the gradient equation and that the Fisher information exists according to Louis (1982). So, the variance estimates are obtained from the diagonal of the inverse of the empirical information matrix, defined as:

\[
I_o = \sum_{i=1}^{n} s(y_i|\theta) s^\top (y_i|\theta) - n^{-1} S(y|\theta) S^\top (y|\theta),
\]

where \( S(y|\theta) = \sum_{i=1}^{n} s(y_i|\theta) \), with \( s(y_i|\theta) = \partial \log f(y_i|\theta) / \partial \theta \) being the empirical score function for the \( i \)th individual. Substituting the ML estimates \( \hat{\theta} \) by \( \theta \) in (3.11), \( I_o \) reduces to

\[
I_o = \sum_{i=1}^{n} \hat{s}_i \hat{s}_i^\top,
\]
where \( \hat{s}_i \) is an individual score vector given by
\[
\hat{s}_i = (\hat{s}_{i_1}, \ldots, \hat{s}_{i_{G-1}}, \hat{s}_{i_G}, \hat{s}_{i_1}, \ldots, \hat{s}_{i_G}, \hat{s}_{i_1}, \ldots, \hat{s}_{i_G})^\top.
\]
Explicit expressions for the elements of \( \hat{s}_i \) are given by
\[
\begin{align*}
\hat{s}_{i,p} &= \frac{f_{T_j}(y_i; \alpha_j, \beta_j) - f_{T_G}(y_i; \alpha_G, \beta_G)}{f(y_i; \mathbf{p}, \alpha, \beta)}, \\
\hat{s}_{i,\alpha_j} &= \frac{p_j D_{\alpha_j}(f_{T_j}(y_i; \alpha_j, \beta_j))}{f(y_i; \mathbf{p}, \alpha, \beta)}, \\
\hat{s}_{i,\beta_j} &= \frac{p_j D_{\beta_j}(f_{T_j}(y_i; \alpha_j, \beta_j))}{f(y_i; \mathbf{p}, \alpha, \beta)},
\end{align*}
\]
where \( D_{\alpha_j}(f_{T_j}(y_i; \alpha_j, \beta_j)) = \partial f_{T_j}(y_i; \alpha_j, \beta_j) / \partial \alpha_j \) and \( D_{\beta_j}(f_{T_j}(y_i; \alpha_j, \beta_j)) = \partial f_{T_j}(y_i; \alpha_j, \beta_j) / \partial \beta_j \).

For simplicity of notation, we omit the index \( i \) in the expressions without causing any confusion:
\[
D_{\delta_j}(f_{T_j}(y; \alpha_j, \beta_j)) = \phi(a_y(\alpha_j, \beta_j)) \left[ \frac{\partial A_y(\alpha_j, \beta_j)}{\partial \delta_j} - \frac{\partial a_y(\alpha_j, \beta_j)}{\partial \delta_j} a_y(\alpha_j, \beta_j) A_y(\alpha_j, \beta_j) \right],
\]
where \( \delta_j = \alpha_j, \beta_j \) and
\[
\begin{align*}
\frac{\partial a_y(\alpha_j, \beta_j)}{\partial \alpha_j} &= -\frac{1}{\alpha_j} a_y(\alpha_j, \beta_j), & \frac{\partial A_y(\alpha_j, \beta_j)}{\partial \alpha_j} &= -\frac{1}{\alpha_j} A_y(\alpha_j, \beta_j), \\
\frac{\partial a_y(\alpha_j, \beta_j)}{\partial \beta_j} &= -\frac{1}{\alpha_j \beta_j} \left( \sqrt{\frac{\alpha}{\beta_j}} + \sqrt{\frac{\beta_j}{\alpha}} \right), & \frac{\partial A_y(\alpha_j, \beta_j)}{\partial \beta_j} &= \frac{y^{-3/2} (\beta_j - \alpha)}{4 \alpha \beta_j^{1/2}}.
\end{align*}
\]

Standard errors of \( \hat{\theta} \) are extracted from the square root of the diagonal elements of the inverse of equation (3.12). The information based approximation in that equation is asymptotically applicable.

Figure 5: Target mixture densities from which the data were simulated: For (left panel) \( \theta = (0.6, 0.25, 0.5, 0.5, 1.5) \) and for (right panel) \( \theta = (0.8, 0.25, 0.25, 1.0, 5.0) \).

## 4 Simulation study

In this section, we run a simulation study to evaluate the performance of the ML estimators with different partitional clustering methods for initialization of the EM algorithm proposed in Section 4. To perform these numerical experiments, we used the statistical computing environment R (R Core Team, 2016). Specifically, the goals are to evaluate the accuracy of the estimates based on the EM algorithm for the FM-BS models and evaluate the consistency of the standard errors of the
Table 2: Comparison of average CPU time (in seconds) for FM-BS model under various sample sizes. The log-likelihood values are in parentheses.

| n     | k-means | k-medoids | k-bumps | k-means | k-medoids | k-bumps |
|-------|---------|-----------|---------|---------|-----------|---------|
| 75    | 0.0819  | 0.0606    | 0.9300  | 0.0173  | 0.0209    | 0.8203  |
|       | (-52.269) | (-51.8858) | (-39.9022) | (-94.3336) | (-94.0662) | (-61.3887) |
| 100   | 0.0860  | 0.0700    | 1.0397  | 0.0159  | 0.0261    | 0.8106  |
|       | (-72.299) | (-71.5438) | (-53.9624) | (-125.8039) | (-130.7341) | (-81.1129) |
| 500   | 0.2652  | 0.2229    | 2.1783  | 0.0470  | 0.1017    | 1.4188  |
|       | (-366.1519) | (-358.7772) | (-274.4587) | (-623.2053) | (-645.317) | (-420.7042) |
| 1000  | 0.493   | 0.5403    | 3.4901  | 0.0891  | 0.2829    | 2.1967  |
|       | (-740.8493) | (-698.7736) | (-555.5299) | (-1252.646) | (-1263.654) | (-840.9494) |
| 5000  | 2.7449  | 5.3584    | 15.3325 | 0.3996  | 4.1035    | 8.7529  |
|       | (-3673.296) | (-3531.957) | (-2777.863) | (-6317.537) | (-6327.193) | (-4228.801) |

estimates (Study 1). Another goal is to show that our proposed EM algorithm estimates provide good asymptotic properties (Study 2). In all cases, the simulation data were artificially generated from the following models with two components ($G = 2$):

$$f(y; \mathbf{p}, \alpha, \beta) = p_1 f_1(y; \alpha_1, \beta_1) + (1 - p_1) f_2(y; \alpha_2, \beta_2).$$ (4.13)

One thousand random samples of sample size $n = 75, 100, 500, 1000$ and 5000 were generated for the FM-BS model under scenarios of poorly separated (PS) components and well separated (WS) components

Scenario 1: $p_1 = 0.6, \alpha_1 = 0.25, \alpha_2 = 0.50, \beta_1 = 0.5, \beta_2 = 1.5$ (PS components);

Scenario 2: $p_1 = 0.8, \alpha_1 = 0.25, \alpha_2 = 0.25, \beta_1 = 1.00, \beta_2 = 5$ (WS components).

Our analyses were performed with a 3.40GHz Intel Core i7 processor with 31.9GB of RAM. The R code for the $k$-bumps algorithm is available in [Bagnato & Punzo 2013], but we adapted it to our context, while for the $k$-medoids algorithm we used the R package ClusterR. Figure 5 (left panel and right panel) shows the mixture densities generated using Scenarios 1 and 2, respectively. This is the first step to ensure that the estimation procedure works satisfactorily. Table 2 shows a comparison of the average CPU times for the FM-BS model under different sample sizes and considering $k$-means, $k$-medoids and $k$-bumps algorithms in order to obtain the initial values.

**4.1 Study 1: Parameter recovery and consistency of the standard errors of the estimates**

In this section the goal is to show the ML estimation of $\theta = (p_1, \alpha_1, \alpha_2, \beta_1, \beta_2)^T$ through the EM algorithm considering the stopping criterion given in (3.10). The mean values of the estimates across the 1000 Monte Carlo samples are computed, and the results are presented in Tables 3 and 4, where the ML estimates of the parameters are close to the true values and become closer as the sample size increases. These tables show the information matrix standard error (IM SE), the Monte Carlo standard deviation (MC Sd) and the coverage probability, reported to examine the consistency of the approximation method given in Subsection 3.4 for the standard errors (SE) of the ML estimates of parameters $\theta$. From these tables, we note that the standard errors provide relatively close results (MC Sd and IM SE), which indicates that the proposed asymptotic approximation for the variances of the ML estimates is reliable. Moreover, the tables report the coverage probability.
(COV) and the percentage of coverage of the resulting 95% confidence intervals (CI) assuming asymptotic normality. The COV is defined as \( COV(\hat{\theta}) = (1/m) \sum_{j=1}^{m} I(\hat{\theta} \in [\hat{\theta}_L, \hat{\theta}_U]) \), where \( I \) is the indicator function such that \( \hat{\theta} \) lies in the interval \([\hat{\theta}_L, \hat{\theta}_U] \), with \( \hat{\theta}_L \) and \( \hat{\theta}_U \) being the estimated lower and upper bounds of the 95% CI, respectively. The COV for the parameters is quite stable for both scenarios, which indicates that the proposed asymptotic approximation for the variance estimates of the ML estimates is reliable. This can also be seen in the COV of parameters, since in general a confidence interval above 95% coverage is maintained for each parameter.

Table 3: Study 1: Mean fit of the FM-BS model based on different initialization algorithms and samples sizes when \( \theta = (0.6, 0.25, 0.5, 1.5, 1.5) \).

| n   | Measure | \( \hat{\alpha}_1 \) | \( \hat{\alpha}_2 \) | \( \hat{\alpha}_3 \) | \( \hat{\alpha}_4 \) | \( \hat{\alpha}_5 \) | \( \hat{\beta}_1 \) | \( \hat{\beta}_2 \) | \( \hat{\beta}_3 \) | \( \hat{\beta}_4 \) | \( \hat{\beta}_5 \) |
|-----|---------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|
| 100 | Mean    | 20.1%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            |
|     | IM SE   | 19.3%            | 11.9%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            |
|     | MC Sd   | 19.2%            | 11.9%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            |
| 750 | Mean    | 20.1%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            |
|     | IM SE   | 19.3%            | 11.9%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            |
|     | MC Sd   | 19.2%            | 11.9%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            | 12.0%            |

Note that when the samples are poorly separated, the estimates using the \( k \)-bumps algorithm obtain better estimates for small sample sizes compared with the \( k \)-means and \( k \)-medoids algorithms. When the samples are well separated the estimates are good regardless of sample size.
using all algorithms. In general, the results suggest that the proposed FM-BS model produces satisfactory estimates, as expected.

### 4.2 Study 2: Asymptotic properties of the EM estimates

In this section the goal is to show the asymptotic properties of the EM estimates. Our strategy is to generate artificial samples for the model in (4.13). Various settings of sample sizes were chosen ($n = 75, 100, 500, 1000$ and $5000$). The true values of the parameters in this study are as in Study 1 (Scenario 1). For each combination of parameters and sample sizes, we generated 1000 random samples from the FM-BS model. To evaluate the estimates obtained by the proposed EM algorithm, we compared the bias (Bias) and the root mean square error (RMSE) for each parameter over the 1000 replicates. They are defined as

$$
\text{Bias}(\theta_i) = \frac{1}{1000} \sum_{j=1}^{1000} (\hat{\theta}_i^{(j)} - \theta_i) \quad \text{and} \quad \text{RMSE}(\theta_i) = \sqrt{\frac{1}{1000} \sum_{j=1}^{1000} (\hat{\theta}_i^{(j)} - \theta_i)^2},
$$

where $\hat{\theta}_i^{(j)}$ is the estimates of $\theta_i$ from the $j$th sample. The results for $p_1, \alpha_1, \alpha_2, \beta_1$ and $\beta_2$ are shown in Figures 6 and 7. As a general rule, we can say that Bias and RMSE tend to approach zero when the sample size increases, which indicates that the estimates based on the proposed EM algorithm under the FM-BS model provide good asymptotic properties.
Figure 7: Study 2. (Scenario 1) Average RMSE of parameter estimates in the FM-BS model with different algorithms.

5 Real applications

In order to illustrate the proposed method, we consider two real datasets, and adopt the Bayesian information criterion (BIC, [Schwarz, 1978]) and Akaike information criterion (AIC) to select the number of components in mixture models (AIC = −2ℓ(\(\hat{\theta}\)) + 2\(\rho\) and BIC = −2ℓ(\(\hat{\theta}\)) + \(\rho\) log\(n\), where \(\rho\) is the number of the parameters in the model).

5.1 Real dataset I

We applied the proposed method to data corresponding to the enzymatic activity in the blood and representing the metabolism of carcinogenic substances among 245 unrelated individuals that were studied previously by Bechtel et al. (1993), who fitted a mixture of two skewed distributions and Balakrishnan et al. (2011), who considered three different mixture models based on the BS and length-biased models. Recently, a bimodal BS (BBS) model has been considered by Olmos et al. (2016) to fit these data. Here we perform the EM algorithm described in Section 3.1 to carry out the ML estimation for the FM-BS model. The competing models are compared using the AIC, BIC and the associated rate of convergence, \(r\), which is assessed in practice as

\[
r = \lim_{t \to \infty} \frac{\|\theta^{(t+1)} - \theta^{(t)}\|}{\|\theta^{(t)} - \theta^{(t-1)}\|}.
\]

The rate of convergence depends on the fraction of missing information, and a greater value of \(r\) implies slower convergence; see [Meng, 1994]. Models with lower convergence rates and BIC...
Figure 8: Initialization strategy for the EM algorithm used in Balakrishnan et al. (2011) vs. \( k \)-bumps strategy for 100 runs.

Table 5: Comparison of log-likelihood maximum and BIC for fitted FM-BS model using the enzyme data. The number of parameters and the rate of convergence are denoted by \( m \) and \( r \), respectively.

| \( G \) | \( m \) | log-lik | AIC | BIC | Iterations | \( r \) |
|-------|------|--------|-----|-----|------------|-----|
| BBS   | 1    | -86.2856 | 178.5713 | 189.075 | 40 | 0.2697 |
| FM-BS | 1    | -105.5071 | 215.0141 | 222.0167 | 2 | - |
| FM-BS | 2    | -54.2027 | **118.4054** | **135.9117** | 7 | 0.2236 |
| FM-BS | 3    | -51.6763 | 119.2884 | 147.3627 | 759 | 0.9958 |
| FM-BS | 4    | -39.7009 | 122.7353 | 139.9157 | 275 | 0.9888 |

are considered more preferable. Table 5 shows the ML estimates obtained by fitting the FM-BS model (\( G = 1 \) – 4 components) and BBS model. Note that the estimation procedure for fitting the FM-BS model does not converge properly for \( G \geq 3 \). Figure 9 (a) and (b) display histograms with estimated pdfs for the data superimposed with \( G = 1 \) – 4 components. In Figure 9 (c) and (d) we show the cumulative and estimated survival functions and the empirical survival function of enzyme data for four fitted FM-BS models respectively. The graphical visualization shows that the FM-BS model (\( G = 2 \), \( G = 3 \) or \( G = 4 \)) adapts to the shape of the histogram very accurately.

As reported by Turner (2000), we can use parametric or semiparametric bootstrapping to test the hypothesis concerning the number of components in the mixture. Following the method proposed by Turner (2000), we considered 1000 bootstrap statistics to test \( G = 1 \) versus \( G = 2 \). The
$p$-value is 0.031 for the parametric bootstrap.

Figure 9: (a) and (b) Histogram of the enzyme data overlaid with ML-fitted densities (c) Cumulative and (d) estimated survival functions and the empirical survival function for four fitted FM-BS models.

Accordingly, there is strong evidence that there are at least two components. For the $G = 2$ versus $G = 3$ test, the bootstrap $p$-value is 0.415, thus there is no evidence that more than two components are required. Moreover, the results based on AIC, BIC and $r$ (see equation 5.14) to test hypotheses and figures indicate that the FM-BS model with $G = 2$ provides much better fit of the data than the other models considered. Note also in Table 5 that the BIC obtained using the proposed method is lower than that reported in Table 3 of Balakrishnan et al. (2011) for the mixture distribution of two different BS (146.02). This is due to the method used to obtain the initial values for the EM algorithm used in Balakrishnan et al. (2011), which change every time the algorithm is executed, resulting in different estimates and BIC values, as can be seen in Figure 8.
Table 6: Estimated parameter values via the EM algorithm with corresponding standard errors (SE) and two-sided 95% confidence interval for the FM-BS model applied to the enzyme data.

| Parameter | Estimates | SE  | SE_b | L    | U    | L_b  | U_b  |
|-----------|-----------|-----|------|------|------|------|------|
| $\alpha_1$ | 0.5239    | 0.0231 | 0.0232 | 0.4788 | 0.5689 | 0.4187 | 0.6289 |
| $\alpha_2$  | 0.3231    | 0.0284 | 0.0539 | 0.2677 | 0.3785 | 0.2779 | 0.3683 |
| $\beta_1$  | 0.1734    | 0.0083 | 0.0070 | 0.1572 | 0.1896 | 0.1597 | 0.1870 |
| $\beta_2$  | 1.2669    | 0.0464 | 0.0445 | 1.1764 | 1.3574 | 1.1801 | 1.3537 |
| $p_1$      | 0.6259    | 0.0312 | 0.0395 | 0.5651 | 0.6867 | 0.5489 | 0.7029 |

The results clearly show that the 2-component FM-BS model has the best fit. Based on Section 3.2, the initial values are $p_1^{(0)} = 0.6408$, $\alpha_1^{(0)} = 0.5630$, $\alpha_2^{(0)} = 0.3017$, $\beta_1^{(0)} = 0.1802$ and $\beta_2^{(0)} = 1.3008$. Table 6 presents the ML estimates of $p_1$, $\alpha_1$, $\alpha_2$, $\beta_1$ and $\beta_2$ for the FM-BS model along with the corresponding standard errors (SE), obtained via the information-based procedure presented in Section 3.4, which is used to obtain the lower (L) and upper (U) confidence limits. Moreover, the bootstrap approach, developed by Efron & Tibshirani (1986), provides another way of deriving confidence intervals. This table presents the bootstrap estimated standard errors (SE_b), and the two-sided 95% confidence intervals (L_b and U_b are bootstrap confidence limits with 400 bootstrap replicates).

Table 7: Comparison of log-likelihood, AIC and BIC for fitted FM-BS, FM-logN and FM-SN models using the BMI data.

| G | log-lik | AIC     | BIC     |
|---|---------|---------|---------|
| FM-LogN 1 | -86.2856 | 14212.65 | 14223.95 |
| FM-LogN 2 | -86.2856 | 14283.20 | 17165.83 |
| FM-LogN 3 | -86.2856 | 15134.94 | 18895.17 |
| FM-SN 1   | -7234.190 | 14474.38 | 14491.34 |
| FM-SN 2   | -6911.778 | 13837.56 | 13877.13 |
| FM-SN 3   | -6862.755 | 13804.74 | 13809.69 |
| FM-BS 1   | -7099.455 | 14202.91 | 14214.22 |
| FM-BS 2   | -6886.495 | 13782.99 | 13811.26 |
| FM-BS 3   | -6858.605 | 13733.21 | 13778.43 |

5.2 Real dataset II

As a second application, we consider the body mass index for 2107 men aged between 18 to 80 years. The dataset comes from the National Health and Nutrition Examination Survey, conducted by the National Center for Health Statistics (NCHS) of the Centers for Disease Control (CDC) in the USA. These data have been analyzed by Basso et al. (2010), who fitted them to finite mixture of skewed distributions, for example finite mixture of skew-normal (FM-SN). The estimation algorithm is implemented in the R package mixsmsn where the k-means clustering algorithm is used to obtain the initial values. We performed the EM algorithm to carry out the ML estimation for the FM-BS, finite mixture of Log-normal (FM-logN), defined by Mengersen et al. (2011), and FM-SN, for model comparison. Table 7 contains the log-likelihood together with AIC and BIC.
for several components. Figure 10 (a) and (b) displays histograms with estimated pdfs for the data superimposed with $G = 1 - 4$ components. The graphs show that the FM-BS model ($G = 3$ or $G = 4$) adapts to the shape of the histogram very accurately. The results indicate that the FM-BS model with $G = 3$ components provides a better fit than the other models considered and this is verified by hypothesis testing using parametric bootstrapping like in application 1.

![Figure 10: (a) and (b) Histogram of the BMI data with overlaid ML-fitted densities (c) Cumulative and (d) estimated survival functions and the empirical survival function for four fitted FM-BS models.](image)

The $p$-value for the $G = 2$ versus $G = 3$ test is <0.000. Thus, there is strong evidence that at least three components exist. For the $G = 3$ versus $G = 4$, test the $p$-value is 0.132, so there is no evidence that more than three components are required. In conclusion, results based on AIC, BIC,
hypothesis testing and figures indicate that the FM-BS model with \( G = 3 \) components provides the best fit. Table 8 presents the MLE of \( p_1, p_2, \alpha_1, \alpha_2, \alpha_3, \beta_1, \beta_2 \) and \( \beta_3 \) for the FM-BS model along with the corresponding standard errors (SE) and L and U confidence limits. In Figure 10 (c) and (d) we show the cumulative and estimated survival functions and the empirical survival function of BMI data for four fitted FM-BS models respectively.

Table 8: Estimated parameter values via the EM algorithm and with the corresponding standard errors (SE) for the FM-BS model applied to the BMI data.

| Parameter | Estimates | SE  | SE_b | L   | U   | L_b | U_b |
|-----------|-----------|-----|------|-----|-----|-----|-----|
| \( \alpha_1 \) | 0.1113    | 0.0050 | 0.0541 | 0.1016 | 0.1210 | 0.0058 | 0.2168 |
| \( \alpha_2 \) | 0.1829    | 0.0270 | 0.0366 | 0.1302 | 0.2356 | 0.1115 | 0.2543 |
| \( \alpha_3 \) | 0.0908    | 0.0170 | 0.0650 | 0.0577 | 0.1240 | -0.0359 | 0.2176 |
| \( \beta_1 \) | 21.7281   | 0.2025 | 1.9123 | 21.3332 | 22.1230 | 17.9991 | 25.4571 |
| \( \beta_2 \) | 35.5421   | 3.6312 | 3.0561 | 28.4613 | 42.6229 | 29.5827 | 41.5015 |
| \( \beta_3 \) | 32.6542   | 0.3640 | 1.7669 | 31.9444 | 33.3640 | 29.2087 | 36.0997 |
| \( p_1 \) | 0.4932    | 0.0330 | 0.0234 | 0.4288 | 0.5576 | 0.4476 | 0.5388 |
| \( p_2 \) | 0.2357    | 0.1570 | 0.0305 | -0.0704 | 0.5418 | 0.1581 | 0.3133 |

6 Conclusions

This work proposes finite mixture of Birnbaum-Saunders distributions, extending some results proposed by Balakrishnan et al. (2011) and providing important supplementary findings regarding mixture of BS distributions. The resulting model simultaneously accommodates multimodality and skewness, thus allowing practitioners from different areas to analyze data in an extremely flexible way.

We pointed out some important characteristics and properties of FM-BS models that allow us to obtain qualitatively better ML estimates and efficiently compute them by using the proposed EM-algorithm, which can be easily implemented and coded with existing statistical software such as the R language. The efficiency of the EM algorithm is supported by the use of the \( k \)-bumps algorithm to obtain the initial values of model parameters. We noted interesting advantages in comparison with the other algorithms (\( k \)-mean and \( k \)-medoids), because the final estimates do not change each time the algorithm is executed.

The FM-BS model can be extended to multivariate settings, following the recent proposal of Khosravi et al. (2014) for mixtures of bivariate Birnbaum-Saunders distributions. We intend to pursue this in future research. Another worthwhile task is to develop a fully Bayesian inference via the Markov chain Monte Carlo method.

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