Sampling from mixtures with negative weights: application to density approximation by Gaussian processes

Luca Martino*
* Università di Catania, Italy.

Abstract

Mixtures of probability densities are widely used in statistics and machine learning. While classical mixtures restrict weights to be non-negative, allowing negative weights enables more flexible density approximation. However, negative weights introduce challenges in handling and sampling such distributions. For this purpose, we propose efficient Monte Carlo (MC) methods (including MC quadratures, rejection sampling and importance sampling schemes) for computing integrals and generating samples from these mixtures. A tailored proposal density ensures accurate and efficient generation of (unweighted) samples. Applications in Gaussian process-based density estimation demonstrate the practical relevance and efficiency of proposed schemes.

Keywords: Non-convex mixtures, mixtures with negative weights, Gaussian processes, rejection sampling, importance sampling

1. Introduction

Mixtures of probability densities are fundamental tools in statistics, signal processing, and machine learning [2]. A mixture model represents a probability distribution as a convex combination of simpler component distributions, such as Gaussians, exponentials, or Gamma distributions, to name a few. Mixture models provide a powerful and flexible framework for modeling complex data [4, 15, 16].

While classical mixture models restrict weights to be non-negative, allowing negative weights opens new theoretical and practical possibilities. When weights can be negative, the resulting function may no longer be a proper

probability density. In this work, we focus on the case where the mixture remains positive and proper. Mixtures with negative components are also referred to as non-convex or pseudo-convex mixtures [1, 6, 5]. In statistics and machine learning, mixtures with negative weights can be particularly useful for density approximation [10, 12, 27]. For example, Gaussian process (GP) regressors, often used for density estimation, can lead to expansions with both positive and negative coefficients [12, 17, 18, 19]. In this context, negative weights can enable better approximation of sharp features, heavy tails, and periodic behaviorspatterns that may be difficult to capture with strictly non-negative mixtures. However, negative weights also introduce significant challenges. The resulting function may not always be a proper density, and classical sampling methods cannot be directly applied [7, 14, 21].
In this work, we describe several Monte Carlo quadrature and sampling methods for mixtures with negative coefficients. First, we focus on the efficient computation of integrals involving non-convex mixtures. Second, we propose an efficient proposal density to be used within rejection sampling (RS) and/or importance sampling with resampling (IS+R) schemes. In both cases, we obtain (unweighted) samples (exactly in RS, or asymptotically in IS+R) that are distributed according to the target mixture with negative weights. The proposal density introduced here ensures good performance in both RS and IS schemes, as it is itself a "piece" of the target density. We also describe in detail the application of these methods to GP-based density approximation. Theoretical discussions are also provided. Numerical simulations demonstrate the efficiency and accuracy of the proposed techniques.

2. Framework and main notation

Let consider a finite mixture of densities, $\phi_n(\mathbf{x})$, with potentially negative associated weights, i.e.,

$$\bar{p}(\mathbf{x}) \propto p(\mathbf{x}) = \sum_{n=1}^{N} \alpha_n \phi_n(\mathbf{x}), \tag{1}$$

$$= p_+(\mathbf{x}) + p_-(\mathbf{x}), \tag{2}$$

$$= \sum_{i=1}^{M} \alpha_i^+ \phi_i(\mathbf{x}) + \sum_{k=1}^{N-M} \alpha_k^- \phi_k(\mathbf{x}) \geq 0, \qquad \forall \mathbf{x} \in \mathcal{X} \subseteq \mathbb{R}^{d_X}, \tag{3}$$

where $\alpha_i^+ > 0$ and $\alpha_i^- < 0$. We have also set $p_+(\mathbf{x}) = \sum_{i=1}^{M} \alpha_i^+ \phi_i(\mathbf{x})$ and $p_-(\mathbf{x}) = \sum_{k=1}^{N-M} \alpha_k^- \phi_k(\mathbf{x})$. Note that, without loss of generality, we are as-

suming that the first M components are associated to positive weights, i.e., α_i^+, and the rest of $N-M$ components have assigned to the negative weights, i.e., α_i^-. Additional assumptions are:

- $\phi_n(\mathbf{x}) \geq 0$ and $\int_{\mathcal{X}} \phi_n(\mathbf{x}) d\mathbf{x} = 1$.
- We can evaluate and we can draw samples from each component $\phi_n(\mathbf{x})$.

Given the assumptions above, and since we consider a proper/normalized mixture density, i.e., $\int_{\mathcal{X}} \bar{p}(\mathbf{x}) d\mathbf{x} = 1$, we can write

$$\bar{p}(\mathbf{x}) = \frac{p(\mathbf{x})}{\sum_{n=1}^{N} \alpha_n}, \tag{4}$$

Thus, we also have the condition $\sum_{i=1}^{M} \alpha_i^+ > \sum_{k=1}^{N-M} \alpha_k^-$, since we need $\sum_{n=1}^{N} \alpha_n > 0$. We can also define the two *partial-mixtures*,

$$\bar{p}_+(\mathbf{x}) = \frac{p_+(\mathbf{x})}{\sum_{i=1}^{M} \alpha_i^+} = \sum_{m=1}^{M} \bar{\alpha}_m^+ \phi_m(\mathbf{x}), \quad \bar{p}_-(\mathbf{x}) = \frac{p_-(\mathbf{x})}{\sum_{i=1}^{N-M} \alpha_i^-} = \sum_{m=1}^{M} \bar{\alpha}_k^- \phi_k(\mathbf{x}), \tag{5}$$

where

$$\bar{\alpha}_m^+ = \frac{\alpha_m^+}{\sum_{i=1}^{M} \alpha_i^+}, \qquad \bar{\alpha}_k^- = \frac{\alpha_k^-}{\sum_{j=1}^{N-M} \alpha_j^-}, \tag{6}$$

Note that in both cases we have proper classical mixtures with non-negative weights, i.e., $\bar{\alpha}_m^+ \geq 0$, $\bar{\alpha}_k^- \geq 0$ and $\sum_{m=1}^{M} \bar{\alpha}_m^+ = 1$, $\sum_{k=1}^{N-M} \bar{\alpha}_k^- = 1$.

3. Efficient integral approximations

The best procedure for approximating integral involving to a mixture $\bar{p}(\mathbf{x})$ of densities with negative weights is related to a quadrature trick [11, 18]. Indeed, if we are interested to approximate a generic moment or any integral involving to the distribution $\bar{p}(\mathbf{x})$, i.e.,

$$I = \int_{\mathcal{X}} f(\mathbf{x}) \bar{p}(\mathbf{x}) d\mathbf{x}, \tag{7}$$

$$= \frac{1}{\sum_{j=1}^{N} \alpha_j} \sum_{n=1}^{N} \alpha_n \int_{\mathcal{X}} f(\mathbf{x}) \phi_n(\mathbf{x}) d\mathbf{x}, \tag{8}$$

$$= \sum_{n=1}^{N} \bar{\alpha}_n J_n. \tag{9}$$

where $f(\mathbf{x})$ is a generic integrable function. Note that above we have set $J_n = \int_{\mathcal{X}} f(\mathbf{x})\phi_n(\mathbf{x})d\mathbf{x}$ and $\bar{\alpha}_n = \frac{\alpha_n}{\sum_{j=1}^N \alpha_j}$. Since we are able to draw from $\phi_n(\mathbf{x})$, we can approximate each J_n by a simple Monte Carlo procedure [14],

$$\widehat{J}_n = \frac{1}{S}\sum_{s=1}^{S} f(\mathbf{x}_n^{(s)}), \qquad \mathbf{x}_n^{(s)} \sim \phi_n(\mathbf{x}). \tag{10}$$

Therefore, replacing in the expressions above into $I = \sum_{n=1}^N \bar{\alpha}_n J_n$, we obtain the final estimator:

$$\widehat{I} = \frac{1}{S}\sum_{n=1}^{N}\sum_{s=1}^{S} \bar{\alpha}_n f(\mathbf{x}_n^{(s)}). \tag{11}$$

As $S \to \infty$, we have $\widehat{I} \to I$ [7, 14, 21].

Alternative point of view. Note that the complete mixture can be expressed as a mixtures of the two partial-mixtures in Eqs. (5)-(6), the first one formed by all positive weights and the second one formed by all negative weights, i.e.,

$$\bar{p}(\mathbf{x}) = \frac{\sum_{i=1}^{M}\alpha_i^+}{\sum_{n=1}^{N}\alpha_n}\bar{p}_+(\mathbf{x}) - \frac{\sum_{k=1}^{N-M}\alpha_k^-}{\sum_{n=1}^{N}\alpha_n}\bar{p}_-(\mathbf{x}), \tag{12}$$

$$= \beta^+\bar{p}_+(\mathbf{x}) - (1-\beta^+)\bar{p}_-(\mathbf{x}), \tag{13}$$

where we have set $\beta^+ = \frac{\sum_{i=1}^{M}\alpha_i^+}{\sum_{n=1}^{N}\alpha_n}$. Recall that both $\bar{p}_+(\mathbf{x})$, $\bar{p}_-(\mathbf{x})$, are proper standard mixtures with non-negative normalized weights, with $\bar{\alpha}_m^+ \geq 0$, $\bar{\alpha}_k^- \geq 0$ and $\sum_{m=1}^M \bar{\alpha}_m^+ = 1$, $\sum_{k=1}^{N-M}\bar{\alpha}_k^- = 1$. Thus, an alternative estimator can be implemented as follows:

1. For $s = 1, ..., S$:
   (a) With probability β^+, draw $\mathbf{z}^{(s)} \sim \bar{p}_+(\mathbf{x})$ and set $\gamma_s = 1$. Otherwise, with probability $1-\beta^+$, draw $\mathbf{z}^{(s)} \sim \bar{p}_-(\mathbf{x})$ and set $\gamma_s = -1$.
2. The final estimator is:

$$\widehat{I} = \frac{1}{S}\sum_{s=1}^{S}\gamma_s f(\mathbf{z}^{(s)}). \tag{14}$$

The above procedure admits a physical analogy, wherein $\mathbf{z}^{(s)}$ with $\gamma_s = 1$ correspond to "matter" samples, and those with $\gamma_s = -1$ to "anti-matter"

samples, or any other similar physical analogy involving negative-signed particles [22, 23]. Hence this procedure is theoretically interesting, but the resulting estimator presents a greater variance of the previous quadrature scheme, due to the random choice between negative and positive parts and, then, the choice of the specific component within the chosen mixture (i.e., we have two additional sources of variability).

4. Efficient sampling schemes

In this section, we discuss two schemes: a rejection sampling method and an importance sampling technique. Note that we are able to generate samples from

$$\bar{p}_+(\mathbf{x}) = \frac{p_+(\mathbf{x})}{\sum_{i=1}^{M} \alpha_i^+} = \sum_{m=1}^{M} \bar{\alpha}_m^+ \phi_m(\mathbf{x}), \qquad \bar{\alpha}_m^+ = \frac{\alpha_m^+}{\sum_{i=1}^{M} \alpha_i^+}, \tag{15}$$

in a classical way, since $0 \leq \bar{\alpha}_m^+ \leq 1$ and $\sum_{m=1}^{M} \bar{\alpha}_m^+ = 1$. Moreover, by construction,

$$p_+(\mathbf{x}) \geq p(\mathbf{x}), \tag{16}$$

that is the inequality required for applying the RS technique [14, Chapter 3]. Furthermore, $\bar{p}_+(\mathbf{x})$ represents a part (a "piece") of the target density $p(\mathbf{x})$. Hence, $\bar{p}_+(\mathbf{x})$ constitutes an appropriate choice of proposal density in Monte Carlo methods, specially in a RS technique. Below we outline the proposed RS scheme:

Rejection sampling:

1. Set $s = 1$.
2. Draw a candidate $\mathbf{z}' \sim \bar{p}_+(\mathbf{x})$,
3. With probability

$$p_A(\mathbf{z}') = \frac{p(\mathbf{z}')}{p_+(\mathbf{z}')}, \tag{17}$$

   set $\mathbf{x}^{(s)} = \mathbf{z}'$ and increase $s \leftarrow s + 1$. Otherwise, with prob. $1 - p_A(\mathbf{z}')$ discard $\mathbf{z}'$.
4. if $s \leq S$, repeat from step 2.

Note that $p_A \in [0,1]$. The algorithm provides exact samples from $\bar{p}(\mathbf{x})$ and its validity is ensured by the inequality (16) [14, Chapter 3]. The acceptance rate A_r is:

$$A_r = \int_{\mathcal{X}} \frac{p(\mathbf{x})}{p_+(\mathbf{x})} \bar{p}_+(\mathbf{x}) d\mathbf{x}, \tag{18}$$

$$= \frac{1}{\sum_{i=1}^{M} \alpha_i^+} \int_{\mathcal{X}} p(\mathbf{x}) d\mathbf{x}, \tag{19}$$

$$= \frac{\sum_{n=1}^{N} \alpha_n}{\sum_{i=1}^{M} \alpha_i^+}, \tag{20}$$

$$= 1 - \frac{\sum_{k=1}^{N-M} \alpha_k^-}{\sum_{i=1}^{M} \alpha_i^+} = 1 - \rho, \tag{21}$$

where we set $\rho = \frac{\sum_{k=1}^{N-M} \alpha_k^-}{\sum_{i=1}^{M} \alpha_i^+}$. If $\rho \to 0$ then $A_r \to 1$ and we have a perfect sampler [14, 21]. Hence, the acceptance rate A_r is close to 1 is the sum of negative weights is close to zero, or the sum of positive weights is much larger than the sum of negative weights. This is particularly interesting for the Gaussian process application: in a GP approximation of a density, the number of negative weights should tend to disappear as the number of points in the regression grows, and the hyper-parameters are updated and optimized. The corresponding importance sampling (IS) 'plus' resampling scheme is described below:

Importance sampling 'plus' resampling (IS+R):

1. Draw $\mathbf{z}_1, ..., \mathbf{z}_S \sim \bar{p}_+(\mathbf{x})$,
2. Assign the weight

$$w_s = \frac{p(\mathbf{z}_s)}{\bar{p}_+(\mathbf{z}_s)} = \left[\sum_{i=1}^{M} \alpha_i^+ \right] p_A(\mathbf{z}_s), \quad s = 1, ..., S, \tag{22}$$

   and define the normalized weights

$$\bar{w}_s = \frac{w_s}{\sum_{i=1}^{S} w_i}, \tag{23}$$

3. Resample S times within the set $\{\mathbf{z}_1, ..., \mathbf{z}_S\}$ according to the probability mass function defined by the normalized weights $\bar{w}_s$, with $s = 1, ..., S$, obtaining a new set of unweighted samples $\{\mathbf{x}^{(1)}, ..., \mathbf{x}^{(S)}\}$.

Unlike RS, the IS+R does not return exact samples, but provides samples $\{\mathbf{x}^{(1)}, ..., \mathbf{x}^{(S)}\}$ that are approximately and asymptotically distributed as $\bar{p}(\mathbf{x})$. However, the quality of this approximation improves as S grows [7, 8, 21]. Furthermore, no samples are rejected/discarded as in the RS scheme. It is also important to remark that the weights w_s present good theoretically properties due to the choice of the proposal density. For instance, since $w_s \propto p_A(\mathbf{z}_s)$, the IS weights are bounded

$$w_s \in \left[0, \sum_{i=1}^{M} \alpha_i^+\right], \tag{24}$$

hence their distribution has not heavy tails, and the variance of the weights is always bounded [3, 10, 24, 26]. Standard IS can produce highly variable estimates, especially when weights have heavy right tails [25]. Namely, extreme values of the weights lead to unstable estimates [24, 25] or yield estimators with infinite variance (see numerical experiments in [9]). However, these undesirable scenarios cannot occur in the proposed IS scheme, due to the property in Eq. (24).

Recall that the proposal density, designed in this work, provides good performance within RS and IS schemes since it is itself a piece of the target density [8]. The IS+R technique is also useful for creating proper histogram approximation of the density $\bar{p}(\mathbf{x})$.

Histograms. Histograms can be constructed in the usual way using the unweighted samples, that are generated by the RS or IS+R schemes. Alternatively, one can directly use the weighted samples $\{\mathbf{z}_s, w_s\}_{s=1}^{S}$ obtained by the IS procedure. Indeed, in each bin of the histogram, instead of considering the number of samples inside the bin, we can sum the corresponding weights. Namely, let consider the bin $\mathcal{B} \subset \mathcal{X}$. The value of the histogram in the bin must be $\sum_{\mathbf{z}_j \in \mathcal{B}} w_j$, where we sum each w_j with j such that $\mathbf{z}_j \in \mathcal{B}$ (for the underlying theory see [13]). The histogram can be normalized dividing all the values by the complete sum of the weights, i.e., $\sum_{s=1}^{S} w_s$.

5. Applications to GP approximation of a density

In many applications, a good approximation of a distribution is needed. For instance some Monte Carlo adaptive scheme, the key idea is the construction (via regression) of a non-parametric density (a.k.a., emulator/surrogate model), which mimics a posterior distribution [10, 12]. More precisely, let us

consider a target-posterior distribution $\bar{\pi}(\mathbf{x}) \propto \pi(\mathbf{x})$. Related to this target density, we have a (possibly noisy) set of points $\{\mathbf{x}_n, t_n\}$ with $n = 1, ..., N$, where $t_n = \pi(\mathbf{x}_n)$ or $t_n = \pi(\mathbf{x}_n) + \epsilon_n$ (where ϵ_n is a noise perturbation) but always we have $t_n \geq 0$ [10, 12].
Let us assume to apply a GP regression method [20]. We consider a (proper) kernel function $k(\mathbf{x}, \mathbf{z}) : \mathcal{X} \times \mathcal{X} \to \mathbb{R}$, then we can define a $N \times N$ kernel matrix $\mathbf{K}$ where each entry is $[\mathbf{K}]_{ij} := k(\mathbf{x}_i, \mathbf{x}_j)$, and a $N \times 1$ kernel vector $\mathbf{k}(\mathbf{x}) = [k(\mathbf{x}, \mathbf{x}_1), ..., k(\mathbf{x}, \mathbf{x}_N)]^\top$. For simplicity, we assume Gaussian kernels,

$$k(\mathbf{x}, \mathbf{z}) = \left(\frac{1}{2\pi\lambda^2}\right)^{\frac{d_X}{2}} \exp\left(-\frac{||\mathbf{x} - \mathbf{z}||^2}{2\lambda^2}\right), \quad \lambda > 0. \tag{25}$$

Defining also the vector $\mathbf{t} = [t_1, ..., t_J]^\top$, the density approximation is given by the formulas:

$$\bar{p}(\mathbf{x}) \propto p(\mathbf{x}) = \mathbf{k}(\mathbf{x})^\top (\mathbf{K} + \eta \mathbf{I}_J)^{-1} \mathbf{t}, \tag{26}$$

$$= \mathbf{k}(\mathbf{x})^\top \boldsymbol{\alpha}, \tag{27}$$

$$= \sum_{n=1}^{N} \alpha_n k(\mathbf{x}, \mathbf{x}_n), \qquad \eta \geq 0, \tag{28}$$

where $\boldsymbol{\alpha} = [\alpha_1, ..., \alpha_N]^\top$ is defined as

$$\boldsymbol{\alpha} = (\mathbf{K} + \eta \mathbf{I}_J)^{-1} \mathbf{t}. \tag{29}$$

Note that $p(\mathbf{x})$ is a mixture of Gaussian kernels ($k(\mathbf{x}, \mathbf{x}_n)$ plays the role of $\phi_n(\mathbf{x})$) and, generally, the coefficients α_n's can be positive or negative.
We can assume of choosing a vector of hyper-parameters $[\lambda, \eta]$ such that $p(\mathbf{x}) \geq 0$, for all $\mathbf{x} \in \mathcal{X}$. It is always possible to find such hyper-parameters. For instance, decreasing the value of λ helps to obtain $p(\mathbf{x}) \geq 0$ for all $\mathbf{x}$. This assumption can be avoided just defining $\widetilde{p}(\mathbf{x}) = \max[p(\mathbf{x}), 0]$. However, this issue tends to disappear as N grows and the hyper-parameters are optimized. if a suitable optimization criterion is employed for updating the hyper - parameters $[\lambda, \eta]$ (as the classical marginal likelihood optimization [9, 20]), the number of negative values of α_n's should decrease as the number N of acquired data, $\{\mathbf{x}_n, t_n\}_{n=1}^N$, grows. However, for a finite N, we can have negative values of α_n. Since the emulator $\bar{p}(\mathbf{x}) \propto p(\mathbf{x})$ is often used as proposal density in a sophisticated sampling schemes, we need to be able to draw from it. The RS and IS+R schemes proposed here can be employed for this purpose.

6. Numerical Simulations

Let us consider the multi-modal target density

$$\bar{\pi}(x) \propto \pi(x) = \sin(x)^2 \exp\left(-\frac{x^2}{30}\right),$$

that is shown in solid line in Figure 1(a). We consider two scenarios.

Scenario 1: We consider $N = 9$ points in the regression, more precisely,

$$x_i \in \{-5, -4, -1, 0, 0.5, 1, 2, 5, 10\}, \tag{30}$$

and $t_i = \pi(x_i)$. We apply the GP regressor with Gaussian kernel and hyper-parameters $\lambda = 1$, $\eta = 0$. In this case, we obtain 6 positive coefficients and 3 negative coefficients in the vector $\boldsymbol{\alpha}$. The 3 negative coefficients are associated to the kernels localized at $x_i = 0, 0.5$ and 2. Applying the proposed RS scheme, the histogram of the accepted samples is given in Figure 1(d). The acceptance rate $A_r = 1 - \rho = 0.417$. The unnormalized densities $p(x)$, $p_+(x)$ and the corresponding versions are also shown in Figure 1.

Scenario 2: Now, we consider $N = 11$ points in the regression,

$$x_i \in \{-8, -5, -4, -1.2, -0.8, 0.5, 1, 2, 5, 8, 10\}, \tag{31}$$

and again $t_i = \pi(x_i)$. We apply the GP regressor with Gaussian kernel and hyper-parameters $\lambda = 0,5$, $\eta = 0$. In this case, we have a unique negative coefficient, α_6, corresponding to $x_6 = 0.5$. The acceptance rate $A_r = 1 - \rho = 0.974$, that is sensibly greater than in scenario 1. However, in both scenarios, we obtain more than reasonable acceptance rates, due to the suitable choice of the proposal density.

7. Conclusions

In this work, we focused on mixtures with negative weights. These generalized mixture models enable more flexible and accurate density approximations, though they introduce challenges for handling and sampling such distributions. To address these challenges, we proposed efficient Monte Carlo methods (including quadrature techniques, rejection sampling, and importance sampling schemes) capable of accurately approximating integrals and

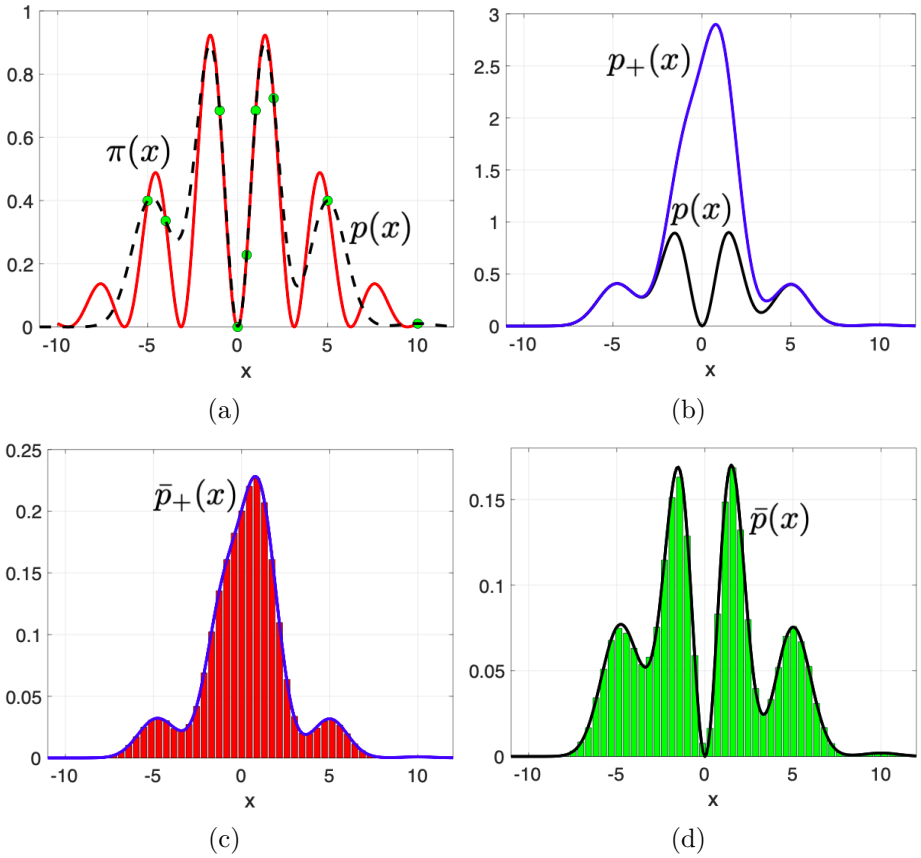
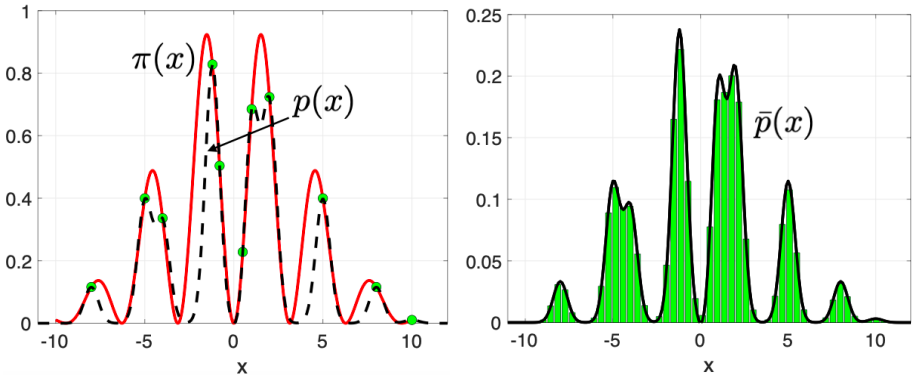


Figure 1: **Scenario 1:** $N = 9$ input points $x_i \in \{-5, -4, -1, 0, 0.5, 1, 2, 5, 10\}$ in regression; in this scenario, with $\lambda = 1$, $\eta = 0$, we have 6 positive coefficients and 3 negative coefficients in $\boldsymbol{\alpha}$. The 3 negative coefficients are associated to the kernels localized at $x_i = 0,\ 0.5$ and 2. the theoretical acceptance rate is $A_r = 1 - \rho = 0.417$, and the empirical acceptance rate is ≈ 0.416, in line with the theoretical expression. This means that drawing 20000 samples from $\bar{p}_+(x)$, in one run we obtain $S = 8326$ samples from $\bar{p}(x)$. The corresponding histogram is depicted in figure (d).

generating (unweighted) samples from these non-convex mixtures. The use of a tailored proposal density ensures both accuracy and efficiency. Applications to Gaussian processbased density estimation illustrate the practical relevance and effectiveness of the proposed methods, highlighting their potential for broader use in complex density modeling tasks.



(a) (b)

Figure 2: **Scenario 2:** we have $N = 11$ input points, $x_i \in \{-8, -5, -4, -1.2, -0.8, 0.5, 1, 2, 5, 8, 10\}$ in regression; in this scenario, with $\lambda = 0.6$, $\eta = 0$, we have only one negative coefficient in $\boldsymbol{\alpha}$. the theoretical acceptance rate $A_r = 1 - \rho = 0.974$ which is virtually identical with the empirical acceptance rate obtained, i.e., ≈ 0.974. This means that drawing 20000 samples from $\bar{p}_+(x)$, in one run we obtain $S = 19481$ samples from $\bar{p}(x)$. The corresponding histogram is depicted in figure (b).

References

[1] D. J. Bartholomew. Sufficient conditions for a mixture of exponentials to be a probability density function. *The Annals of Mathematical Statistics*, 40(6):2183–2188, 1969.

[2] C. M. Bishop. *Pattern Recognition and Machine Learning*. Springer, 2006.

[3] G. Deligiannidis, P. E. Jacob, E. M. Khribch, and G. Wang. On importance sampling and independent Metropolis-Hastings with an unbounded weight function. *arXiv:2411.09514*, pages 1–43, 2025.

[4] M. D. Escobar and M. West. Bayesian density estimation and inference using mixtures. *Journal of the American Statistical Association*, 90(430):577–588, 1995.

[5] M. Felgueiras. Mixtures with negative weights. Technical report, Center for Statistics and Applications, University of Lisbon, 2018.

[6] M. Felgueiras, J. Martins, and R. Santos. Pseudo-convex mixtures. *AIP Conference Proceedings*, 1479(1):1125–1128, 2012.

[7] J. S. Liu. *Monte Carlo Strategies in Scientific Computing*. Springer, 2004.

[8] F. Llorente and L. Martino. Optimality in importance sampling: a gentle survey. *arXiv:2502.07396*, 2025.

[9] F. Llorente, L. Martino, D. Delgado, and J. López-Santiago. Marginal likelihood computation for model selection and hypothesis testing: An extensive review. *SIAM Review*, 65(1):3–58, 2023.

[10] F. Llorente, L. Martino, D. Delgado-Gomez, and G. Camps-Valls. Deep importance sampling based on regression for model inversion and emulation. *Digital Signal Processing*, 116:103104, 2021.

[11] F. Llorente, L. Martino, V. Elvira, D. Delgado, and J. López-Santiago. Adaptive quadrature schemes for Bayesian inference via active learning. *IEEE Access*, 8:208462–208483, 2020.

[12] F. Llorente, L. Martino, J. Read, and D. Delgado-Gómez. A survey of Monte Carlo methods for noisy and costly densities with application to reinforcement learning and ABC. *International Statistical Review*, 93(1):18–61, 2025.

[13] L. Martino, V. Elvira, and G. Camps-Valls. Group importance sampling for particle filtering and MCMC. *Digital Signal Processing*, 82:133–151, 2018.

[14] L. Martino, D. Luengo, and J. Mguez. *Independent Random Sampling Methods*. Springer Publishing Company, Incorporated, 1st edition, 2018.

[15] A. Mazza and A. Punzo. Mixtures of multivariate contaminated normal regression models. *Statistical Papers*, 61(2):577–608, 2020.

[16] G. McLachlan and D. Peel. *Finite Mixture Models*. Wiley, 2000.

[17] I. Murray, D. MacKay, and R. P. Adams. The Gaussian process density sampler. In *Advances in Neural Information Processing Systems*, volume 21, 2008.

[18] C. J. Oates, J. Cockayne, F.-X. Briol, and M. Girolami. Control functionals for monte carlo integration. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 79(3):695–718, 2017.

[19] G. Rabusseau and F. Denis. Learning negative mixture models by tensor decompositions. *ArXiv:1403.4224*, 2014.

[20] C. E. Rasmussen and C. K. I. Williams. *Gaussian Processes for Machine Learning*. The MIT Press, 2006.

[21] C. P. Robert and G. Casella. *Monte Carlo Statistical Methods*. Springer, 2004.

[22] J.-M. Sellier. A signed particle formulation of non-relativistic quantum mechanics. *Journal of Computational Physics*, 297:48–74, 2015.

[23] M. Troyer and W.-J. Wiese. Computational complexity and fundamental limitations to fermionic quantum monte carlo simulations. *Physical Review Letters*, 94(17):170201, 2005.

[24] M. A. Vazquez and J. Míguez. Importance sampling with transformed weights. *Electronics Letters*, 53(12):783–785, 2017.

[25] A. Vehtari, D. Simpson, A. Gelman, Y. Yao, and J. Gabry. Pareto smoothed importance sampling. *J. Mach. Learn. Res.*, 25(1), 2024.

[26] T. Yu, L. Lu, and J. Li. A weight-bounded importance sampling method for variance reduction. *arXiv:1811.09436*, pages 1–14, 2019.

[27] B. Zhang and C. Zhang. Finite mixture models with negative components. In *Machine Learning and Data Mining in Pattern Recognition*, pages 31–41. Springer Berlin Heidelberg, 2005.