A PRticle filter algorithm for nonparametric estimation of multivariate mixing distributions

Vaidehi Dixit^{*} and Ryan Martin^{*}

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Abstract

Predictive recursion (PR) is a fast, recursive algorithm that gives a smooth estimate of the mixing distribution under the general mixture model. However, the PR algorithm requires evaluation of a normalizing constant at each iteration. When the support of the mixing distribution is of relatively low dimension, this is not a problem since quadrature methods can be used and are very efficient. But when the support is of higher dimension, quadrature methods are inefficient and there is no obvious Monte Carlo-based alternative. In this paper, we propose a new strategy, which we refer to as *PRticle filter*, wherein we augment the basic PR algorithm with a filtering mechanism that adaptively reweights an initial set of particles along the updating sequence which are used to obtain Monte Carlo approximations of the normalizing constants. Convergence properties of the PRticle filter approximation are established and its empirical accuracy is demonstrated with simulation studies and a marked spatial point process data analysis.

Keywords and phrases: importance sampling; marked point process; mixture model; Monte Carlo; predictive recursion.

1 Introduction

Suppose we have independent and identically distributed (iid) data X_1, \ldots, X_n having common density m supported on \mathbb{X} . Furthermore, suppose that we believe this density has the mixture form $m = m_P$, where

$$m_P(x) = \int_{\mathbb{U}} k(x \mid u) P(du), \quad x \in \mathbb{X},$$
(1)

with $k(x \mid u)$ a known kernel density and P an unknown mixing distribution supported on U. The family in (1) indexed by P is commonly referred to as a *mixture model*. One interpretation of the mixture model is that there is a set of underlying latent variables

^{*}Department of Statistics, North Carolina State University; vdixit@ncsu.edu, rgmarti3@ncsu.edu

driving the data-generating process. That is, suppose the X_i 's are obtained through the two-step process:

$$U_1, \dots, U_n \stackrel{\text{iid}}{\sim} P$$
$$(X_i \mid U_i) \stackrel{\text{ind}}{\sim} k(x \mid U_i), \quad i = 1, \dots, n.$$

It is easy to check that X_1, \ldots, X_n from this hierarchical model formulation are iid with density m_P . This sort of hierarchical, latent variable modeling is common when heterogeneity is present in the observed data. This also covers the class of problems where Urepresents an unobservable "signal" of interest and X the corresponding noise-corrupted signal, i.e., the "signal plus noise." One also might adopt (1) simply for the flexibility the mixture model affords (e.g., DasGupta 2008, Chapter 33). In any case, the distribution of the latent variables, or signals, may be of some practical interest, in which case the goal becomes estimation of the unknown mixing distribution P based on iid data X_1, \ldots, X_n from the mixture m_P in (1). This is our focus in the present paper.

Estimation of the mixing distribution P is a notoriously difficult problem. Aside from methods tailored to specific mixture model forms, e.g., deconvolution (Fan 1991; Stefanski and Carroll 1990), there are a few general estimation methods available: the two "standard" approaches are nonparametric maximum likelihood and nonparametric Bayes. The former maximizes the likelihood based on observations X_1, \ldots, X_n from m_P , with respect to P. Given the nonparametric nature of P, the resulting estimate is almost surely discrete and the points of support are no greater than n (Lindsay 1983). The latter approach assigns a prior distribution to P, typically a Dirichlet process (Ferguson 1974; Ghosal and Van der Vaart 2017; Ghosh and Ramamoorthi 2003; Hjort et al. 2010), and evaluate the corresponding posterior mean, given (X_1, \ldots, X_n) . Even though there is no direct imposition of discreteness in the posterior, draws from the posterior distribution of P have atoms (e.g., Blackwell and MacQueen 1973) and the corresponding posterior mean is spiky, "effectively discrete." Hence, neither the likelihood nor Bayesian approaches give satisfactory solutions to the problem of estimating a mixing distribution P in (1). The point is that, in these traditional approaches, the focus is on identifying candidate P such that resulting mixture density m_P is compatible with the empirical distribution of data, not specifically estimating the mixing distribution.

A third general approach is available, which is the primary focus of this paper, called *predictive recursion* (PR). Unlike the previous two methods, which are likelihood-based, the PR estimator is based on a stochastic, recursive algorithm that aims specifically to estimating the mixing distribution P based on data from the mixture model (1). This strategy was first proposed in Newton et al. (1998) as a fast and smooth approximation to the posterior mean of P under a Dirichlet process mixture model; see Martin (2021). The idea behind PR is to start with a initial guess, P_0 , and then update that guess recursively based on each individual observation X_i for $i = 1, \ldots, n$. PR has a number of desirable computational and statistical properties. First, PR is computationally efficient—its complexity is O(n). Second, the PR estimator, P_n , is absolutely continuous with respect to P_0 , so if P_0 has a smooth density, then so does P_n . Third, the PR estimator has also been shown to consistently estimate the true mixing distribution P in a series of papers: Tokdar et al. (2009), Martin and Tokdar (2009), and Dixit and Martin (2021).

Applications of the PR algorithm have appeared in Newton (2002), Martin and Tokdar (2011), Martin and Tokdar (2012), Martin and Han (2016), Tansey et al. (2018), Woody

et al. (2022), and Dixit and Martin (2022). In each of these applications, however, the mixing distribution support \mathbb{U} is a relatively low-dimensional space, e.g., one- or two-dimensional. The reason for this constraint is that, while the algorithm itself is completely general, computation of the normalizing constant in Equation (2) below can be a challenge when \mathbb{U} is more than two- or three-dimensional. In particular, the required integration can only be done numerically, but efficient quadrature methods are available only when the domain of integration, in this case \mathbb{U} , is low-dimensional. A Monte Carlobased strategy would be less sensitive to the dimension of \mathbb{U} and, in that sense, would have an advantage. Unfortunately, no such Monte Carlo-based strategy is currently available in the literature, and this paper aims to fill this gap.

Following a brief review in Section 2 of the PR algorithm and importance sampling techniques, we propose in Section 3 below the *PRticle filter* approximation. As the name suggests, this consists of an augmentation of the original PR algorithm with a filtering step that adaptively reweights an initial set of particles along the PR updating sequence. The idea is that, at the i^{th} step, the weighted set of particles resembles a sample from the PR estimate P_{i-1} based on data X_1, \ldots, X_{i-1} . Hence, the n^{th} step gives a particle approximation of the PR estimate P_n and Theorem 1 below establishes that, for fixed data X_1, \ldots, X_n , this approximation converges almost surely in total variation distance to P_n as the number of sampled particles approaches infinity.

In Section 4, we evaluate performance of the proposed PRticle filter approximation on both real and simulated data sets. For the simulated data sets, the evaluation is split into two types. First, to judge the accuracy of the proposed PRticle filter approximation, we compare it to the original PR estimator in cases where a quadrature scheme is feasible. In our comparisons, the PRticle filter accurately approximates the PR estimate for simulations from mixtures corresponding to univariate and bivariate mixing distributions. Second, when the dimension of the mixing distribution support is too large for a quadrature scheme to be practical, we compare our PRticle filter approximation to a Dirichlet process mixture model-based estimator. The PRticle filter approximation is faster to compute and of comparable quality compared to the nonparametric Bayes estimator, which is one of the best known solutions.

For a real data illustration, we consider an application where data consists of a marked spatial point process. That is, the observed data consists of spatial locations at which specific events take place, along with some other relevant feature of the events, called marks. As is common in spatial point process models, the relevant quantity is the intensity function. Here we follow Taddy and Kottas (2012) and model this intensity function as a mixture, with a multivariate mixing distribution support, and apply the PRticle filter approximation to estimate the mixing distribution and, in turn, the intensity function. This naturally leads to estimates of other relevant features, including conditional distribution of the marks given the spatial locations. We argue that the results obtained through our use of the PRticle approximation are consistent with patterns seen in the data and with those presented elsewhere in the literature. This application simply would have been impossible using the basic PR algorithm. Some concluding remarks are given in Section 5 and the proof of Theorem 1 is presented in Appendix A.

2 Background

2.1 Predictive recursion

Suppose we have data X_1, \ldots, X_n from m_P in (1), where the goal is estimation of the mixing distribution P. With a user-defined initial guess P_0 and weight sequence $\{w_i : i \geq 1\} \subset (0, 1)$, the i^{th} step in the PR algorithm is given by,

$$P_{i}(du) = (1 - w_{i}) P_{i-1}(du) + w_{i} \frac{k(X_{i} \mid u) P_{i-1}(du)}{\int k(X_{i} \mid u) P_{i-1}(du)}, \quad i = 1, \dots, n$$
(2)

For theoretical reasons, the weights must satisfy $\sum_{i=1}^{\infty} w_i = \infty$ and $\sum_{i=1}^{\infty} w_i^2 < \infty$; this can be achieved by taking, e.g., $w_i = (i+1)^{-\gamma}$ for some $\gamma \in (0.5, 1]$. The algorithm processes the *n* data points sequentially and returns the final update P_n as the PR estimator of the mixing distribution. The corresponding PR mixture density estimate is $m_n = m_{P_n}$, where the mapping $P \mapsto m_P$ is given in (1). It is clear that the PR estimator P_n depends on the ordering of the observations X_1, \ldots, X_n . If this dependence is undesirable, then it can be removed—or at least mitigated—by calculating P_n over multiple permutations of the data and averaging over the estimates (Newton 2002; Tokdar et al. 2009). With the superior computational efficiency of PR, this permutation-averaging can still be carried in a fraction of the run-time of its competitors.

Key features of the PR algorithm/estimator include its ability to estimate a mixing density and its computational efficiency. By the former, we mean that if the user-defined initial guess P_0 has a smooth density with respect to a particular dominating measure, then the final PR estimator P_n will too. Compare this to the maximum likelihood and Bayes estimators, which are necessarily (or "effectively") discrete. By the latter computational efficiency claim, we mean that each PR step requires a fixed number of computations, so the overall computational complexity of PR algorithm is O(n).

As mentioned in Section 1, the key step in each iteration of the PR algorithm is calculation of the normalizing constant $\int k(x_i \mid u) P_{i-1}(du)$. Since P_{i-1} is data-driven and fully nonparametric, we cannot expect there to be a closed-form expression for the normalizing constant. Often it can be approximated numerically using a quadrature scheme; this is especially easy to do so when the mixing distribution support \mathbb{U} is univariate. However, for as the dimension of \mathbb{U} increases, computation of the normalizing constant becomes more and more challenging. For example, the number of grid points required for accurate quadrature grows exponentially in the dimension of \mathbb{U} and becomes infeasible or at least inefficient even for moderate dim(\mathbb{U}). This creates a computational bottleneck.

In previous work, this challenge was side-stepped by treating some of the latent variables as mixing variables and the others as non-mixing/structural parameters. For example, instead of mixing the kernel $k(x \mid u_1, u_2)$ over both the location u_1 and scale u_2 , the proposal in Martin and Tokdar (2011) was to treat, say, the scale parameter u_2 as a fixed unknown, so that mixing is required only over the univariate u_1 -space. Then they developed a PR-based marginal likelihood for u_2 that could be used for simultaneous estimation of the scale u_2 and the corresponding mixing distribution over u_1 . This effectively reduces the dimension of the mixing distribution support, thus making it easy to side-step the challenges in computing the normalizing constant. For various reasons, however, it would be preferable to deal with the computational challenges directly, as opposed to using a "hack" to reduce the dimension artificially. This requires new ideas for evaluating the normalizing constant in (2) and, for this, here we develop a novel strategy based on the same ideas behind sequential importance sampling.

2.2 Importance sampling and filtering

The approximation we propose in Section 3 uses the principles behind importance sampling and particle filters in general. Before stating our algorithm, we first review these basic principles. Consider the general problem of integrating a function h with respect to a probability density p, where $U \in \mathbb{U} \subset \mathbb{R}^d$, for $d \ge 1$. In cases where numerical integration is infeasible, e.g., if d is too large or if either h or p is too rough, it is common to use a Monte Carlo approximation by averaging over a random set of observations from probability density p. However, a problem arises if p cannot be efficiently sampled from. In such cases, an *importance sampling* approach can be employed. This amounts to generating samples from a different distribution, say with density q, and then reweighting those samples so that they resemble samples from p. In particular, the expected value of h with respect to p can be written as

$$\int_{\mathbb{U}} h(u) p(u) \, du = \int_{\mathbb{U}} h(u) \, \frac{p(u)}{q(u)} \, q(u) \, du,$$

and this immediately suggests the Monte Carlo approximation

$$\frac{1}{T}\sum_{t=1}^{T}\alpha_t h(U_t),$$

where $\{U_t : t = 1, ..., T\}$ are iid samples from q and $\alpha_t = p(U_t)/q(U_t)$ are the weight adjustment factors. If the normalizing constant for p is unknown, then the T^{-1} factor can be replaced by $(\sum_{t=1}^T \alpha_t)^{-1}$.

The ratio $\alpha_t = p(U_t)/q(U_t)$ helps to effectively filter out points in low *p*-density regions while increasing the weight put on particles in high *p*-density regions. Agapiou et al. (2017) unify the existing literature on importance sampling with a special focus on determining the size of *T* such that error in approximation is minimized. The choice of *T*, the Monte Carlo sample size, is important, both in terms of accuracy and efficiency. A practical measure of efficiency used for importance sampling is the *effective sample size* (ESS), i.e., the effective number of particles. Following Kong (1992), a commonly used expression for ESS is

$$ESS = \frac{\left(\sum_{t=1}^{T} \alpha_t\right)^2}{\sum_{t=1}^{T} \alpha_t^2},\tag{3}$$

where $\alpha_t = p(U_t)/q(U_t)$ as before. By Cauchy–Schwartz, ESS is bounded above by T, and the closer it is to T the more efficient the importance sampler. So the goal is to choose the proposal density q such that ESS is as close to T as possible.

These basics behind importance sampling can be connected to more sophisticated Monte Carlo methods with the following interpretation. The procedure above essentially starts with a collection of tentative sample points from p, which are commonly referred to as *particles*. Particles which have small importance ratios, p/q, are given small weight, and effectively *filtered out*. In this sense, importance sampling is a (basic) form of *particle* filtering. This idea can then be extended in different directions. In particular, it would be possible for the target distribution, p, to be changing over some "time" index. In hidden Markov models, for example, the dimension of the target distribution's support is increasing with time; also, in Bayesian inference, the target p is the posterior distribution which is evolving with the sample size n. Sequential Monte Carlo methods have proved useful in these problems (e.g., Del Moral et al. 2006; Doucet et al. 2001; Doucet and Johansen 2011). Sequential importance sampling, in particular, is a powerful tool for particle filtering (Agapiou et al. 2017; Tokdar and Kass 2010). In the context of mixture models, sequential importance sampling (eg. MacEachern et al. 1999) and particle learning algorithms (eg. Carvalho et al. 2010b) have been suggested for analyzing mixture models in the Bayesian setting. In our present case, sequential updating is required because we need particles that represent the PR estimate P_i as i = 1, 2, ..., n. This problem is due to the unique recursive structure inherent in the PR sequence of target distributions and, therefore, calls for different or at least more specialized techniques compared to what is currently available in the sequential Monte Carlo literature.

3 PRticle filter approximation

3.1 Algorithm

In this section we propose a particle filter algorithm designed specifically to approximation the PR estimator. For simplicity, and without any real loss of generality, assume that P_0 has a density with respect to Lebesgue measure on $\mathbb{U} \subset \mathbb{R}^d$, denote by p_0 . Then all the subsequent PR updates P_i have such a density, denoted by p_i . At each iteration of PR, one needs to calculate a normalizing constant

$$m_{i-1}(X_i) = \int_{\mathbb{U}} k(X_i \mid u) p_{i-1}(u) \, du, \quad i = 1, \dots, n.$$

The analytical form of p_{i-1} is unknown so clearly we cannot evaluate this in closed form. Likewise, we cannot directly generate observations from it to get a Monte Carlo approximation. However, we know that it is a function of the previous updates p_0, \ldots, p_{i-2} , so the idea is to leverage the PR algorithm's recursive formulation and those core importance sampling principles to design an efficient Monte Carlo/particle filter approximation.

Recall that p_0 is a user-specified density on \mathbb{U} and we will assume that sampling from p_0 is feasible. Generate an iid sample U_1, \ldots, U_T of size $T \gg 1$ from p_0 . Then, a simple Monte Carlo average gives us an approximation of the first normalizing constant,

$$\hat{m}_0(X_1) = \frac{1}{T} \sum_{t=1}^T k(X_1 \mid U_t)$$

where each point U_t is equally weighted by T^{-1} . Next, we do not know the form of p_1 but we know that it can be expressed in terms of p_0 and the data point X_1 as

$$p_1(u) = (1 - w_1)p_0(u) + w_1 \frac{k(X_1 \mid u)p_0(u)}{m_0(X_1)}$$
$$= \left\{ 1 + w_1 \left(\frac{k(X_1 \mid u)}{m_0(X_1)} - 1 \right) \right\} p_0(u).$$

This implies the ratio of consecutive PR density estimates is

$$\frac{p_1(u)}{p_0(u)} = \delta_0(u) := \left\{ 1 + w_1 \left(\frac{k(X_1 \mid u)}{m_0(X_1)} - 1 \right) \right\}.$$

Now, since

$$m_1(X_2) = \int k(X_2 \mid u) \, p_1(u) \, du = \int k(X_2 \mid u) \, \delta_0(u) \, p_0(u) \, du,$$

we have a very natural Monte Carlo approximation of $m_1(X_2)$, namely,

$$\hat{m}_1(X_2) = \frac{1}{T} \sum_{t=1}^T k(X_2 \mid U_t) \,\hat{\delta}_0(U_t),$$

where $\hat{\delta}_0(u)$ is based on plugging in $\hat{m}_0(X_1)$ for $m_0(X_1)$ in the definition of δ_0 above. Here $\hat{\delta}_0(\cdot)$ acts as a mesh that effectively filters out those particles that are not compatible with the updated distribution p_1 . Continuing with the same logic, for the i^{th} iteration, we get

$$\hat{m}_{i-1}(X_i) = \frac{1}{T} \sum_{t=1}^T k(X_i \mid U_t) \hat{\Delta}_i(U_t), \quad i \ge 1,$$

where $\hat{\Delta}_1(u) \equiv 1$ and

$$\hat{\Delta}_{i}(u) = \hat{\Delta}_{i-1}(u)\,\hat{\delta}_{i-2}(u)$$

$$= \prod_{j=2}^{i} \left\{ 1 + w_{j-1} \left(\frac{k(X_{j-1} \mid u)}{\hat{m}_{j-2}(X_{j-1})} - 1 \right) \right\}, \quad i \ge 2.$$

The above steps make up the PRticle filter approximation and these are summarized in Algorithm 1. In the end, the algorithm returns the pairs $\{(U_t, \hat{\Delta}_n(U_t)) : t = 1, \ldots, T\}$ that collectively represent an approximate sample from the PR estimator P_n . From this sample, any features of P_n can be approximated as usual. If an estimate of the density p_n were required, then the weighted collection of particles can be smoothed using, e.g., a kernel density estimator. Just like the PR estimator, the PRticle filter approximation depends on the ordering of observations, and same permutation-averaging can be used here to mitigate the order-dependence, if desired.

3.2 Convergence

A relevant question would be of the convergence of the PRticle filter approximation $\hat{p}_n = \hat{p}_{n,T}$ to the corresponding PR estimate p_n , as the Monte Carlo sample size T goes to ∞ . If we had just one data point X_1 , then $\hat{p}_{1,T} \to p_1$ simply by the law of large numbers as this only involves the simple Monte Carlo approximation of $m_0(X_1)$. However, as we include more observations, the i^{th} approximation of p_i consists of the previous i-1 approximations and the law of large numbers argument is not immediately clear. But it turns out that the law of large numbers can be applied to show that PRticle filter approximation, $\hat{p}_{n,T}$, converges to its target p_n in a very strong sense as $T \to \infty$.

Algorithm 1: PRticle filter approximation

Initialize: Data X_1, \ldots, X_n , initial guess p_0 , random sample U_1, \ldots, U_T from p_0 , and weight sequence $\{w_i : i \ge 1\} \subset (0, 1)$; Set $\hat{\Delta}_t = 1$ for $t = 1, \ldots, T$; for $i = 1, \ldots, n$ do $\begin{vmatrix} \text{set } N_{t,i} = k(X_i \mid U_t) p_{i-1}(U_t) \text{ for each } t, \text{ and } D_i = T^{-1} \sum_{t=1}^T k(X_i \mid U_t) \hat{\Delta}_t; \\ \text{update } p_i(U_t) = (1 - w_i) p_{i-1}(U_t) + w_i N_{t,i}/D_i \text{ for each } t; \\ \text{evaluate } \hat{\Delta}_t = \hat{\Delta}_t [1 + w_i \{k(X_i \mid U_t)/D_i - 1\}] \text{ for each } t; \\ \text{end} \\ \text{return } U_t \text{ and weights } \hat{\Delta}_t, \text{ for } t = 1, \ldots, T. \end{aligned}$

Theorem 1. For a fixed data set X_1, \ldots, X_n , let p_n and $\hat{p}_{n,T}$ denote the PR estimator and its PRticle filter approximation, respectively, both based on the same initial guess with distribution P_0 . If the kernel is such that

$$\int_{\mathbb{U}} \left\{ \prod_{i \in \mathcal{S}} k(X_i \mid u) \right\} P_0(du) < \infty, \quad \text{for all } \mathcal{S} \subseteq \{1, \dots, n\},$$
(4)

then

$$\int_{\mathbb{U}} |\hat{p}_{n,T}(u) - p_n(u)| \, du \to 0, \quad \text{with } P_0 \text{-probability 1 as } T \to \infty.$$

Proof. See Appendix A.

Theorem 1 establishes that, with a sufficiently large Monte Carlo sample size T, the PR ticle filter approximation, $\hat{p}_{n,T}$, of the PR mixing density estimator p_n will be quite accurate. Note that L_1 /total variation convergence implies weak convergence, so virtually any relevant functional of p_n can be accurately approximated by the corresponding functional of $\hat{p}_{n,T}$. The condition (4) on the kernel is rather mild, e.g., it is satisfied if $u \mapsto k(x \mid u)$ is bounded for almost all x. Beyond the fixed-data approximation, the result in Theorem 1, together with the general results in Martin and Tokdar (2009) and Dixit and Martin (2021) on the consistency properties of p_n as $n \to \infty$, suggests that $\hat{p}_{n,T}$ would also be a good estimator of p when both n and T are large.

3.3 Adaptation to handle attrition

The final estimate p_n will depend on the initial p_0 , not just through the default PR mechanism but also through the dependence on the choice of particles U_1, \ldots, U_T from p_0 . To ensure that p_n captures the true mixing density p, it is generally recommended to choose a relatively diffuse p_0 in the PR algorithm. However, the true p is likely to be more concentrated in certain regions of \mathbb{U} than in others. So those chosen particles U_1, \ldots, U_T from p_0 that happen to fall in those p-low-density regions of \mathbb{U} should be assigned relatively low weights. The concern is that too many of the particles end up in these low-density regions, hence affecting the effective number of particles. Recall that, an efficiency measure of the particle filter is given by the effective sample size (ESS) in (3). For our case this can be calculated as,

$$\text{ESS} = \frac{\left\{\sum_{t=1}^{T} \Delta_n(U_t)\right\}^2}{\sum_{t=1}^{T} \Delta_n(U_t)^2}.$$

If too many particles end up with negligible weights, i.e., if $\Delta_n(U_t) \approx 0$ for t', then ESS becomes significantly smaller than T. This loss-of-information, called *attrition*, is a common problem in importance sampling or particle filtering (eg. Doucet and Johansen 2011); and it cannot be ignored because the effective sample size is what controls the accuracy of the Monte Carlo approximations. To account for this, the general strategy is to resample points from the region of importance such that ESS does not reduce tragically (e.g., Carvalho et al. 2010b; Doucet et al. 2001). The strategy we propose here is in the same spirit as adaptive importance sampling (eg. Bugallo et al. 2017). Below we describe our approach that accounts for attrition, specific to the PRticle filter. We start by summarizing the characteristics of the final PR estimate p_n to improve upon the initial filter U_t . This summary can then be used to construct a new informed p_0 so that an updated filter has more points in the more dense regions of p.

Given points U_1, \ldots, U_T and the final weights $\Delta_n(U_t)$ representing the PR estimate p_n we can easily obtain Monte Carlo approximations of

$$\mu_n = \int u p_n(u) du$$
 and $\Sigma_n = \int (u - \mu_n)(u - \mu_n)^\top p_n(u) du$

the mean vector and covariance matrix associated with p_n , respectively, given by

$$\hat{\mu}_n = \frac{1}{T} \sum_{t=1}^T U_t \,\Delta_n(U_t) \quad \text{and} \quad \widehat{\Sigma}_n = \frac{1}{T} \sum_{t=1}^T (U_t - \hat{\mu}_n) (U_t - \hat{\mu}_n)^\top \Delta_n(U_t).$$

This helps us to identify a region where p_n —and likely p as well—has high concentration. This information can then be incorporated in a new updated p_0 . A reasonable strategy, therefore, is to redefine the initial estimate p_0 to be, e.g., a multivariate Student-t distribution with location $\hat{\mu}_n$ and scale matrix $\hat{\Sigma}_n$. An iid sample is then generated from this new p_0 and the PRticle procedure is carried out as before.

This idea of updating the PRticle filter can be extended in various ways. One way is to repeat the aforementioned process more than once. However, in our experience, this can lead to shrinkage of the region of interest beyond of what is needed resulting into points from only a highly dense region and no points elsewhere. Alternatively, one could identify several particles having relatively large weight following the initial pass of PRticle filter; use these as locations around which a multivariate Gaussian or Student-t distribution could be centered; and then take the updated p_0 to be a mixture of these few distributions and sample particles from there. Yet another strategy is to resample particles from p_0 after one run of PR and rerun the algorithm by replacing the low-weight particles by the new particles. This allows for identifying new regions of interest while removing any low-probability regions. This is a classical strategy of resampling used in particle filters for Bayesian problems (Carvalho et al. 2010a). Any of the approaches suggested above would be useful in reducing attrition of particles, but more deliberation is needed to conclude which of these strategies would be most efficient. For our purposes here, we use the strategy mentioned before and our simulation results in Section 4 show that this is effective in reducing attrition.

T	ESS	$K(m_n, \hat{m}_n)$	T	ESS	$K(m_n, \hat{m}_n)$
100	33.6	0.0063	100	10.5	0.0600
300	105.3	0.0001	300	44.8	0.0326
500	162.9	0.0003	500	81.7	0.0260
1000	330.7	0.0002	1000	140.7	0.0200

Table 1: Numerical results for Example 1: comparisons between m_n and \hat{m}_n with d = 1 (left) and d = 2 (right). Comparisons are made in terms of effective sample size (ESS) and Kullback–Leibler divergence $K(m_n, \hat{m}_n)$.

4 Numerical results

4.1 Density estimation

Here we show three density estimation examples. Examples 1–2, involving Euclidean data and data on a sphere, respectively, compare the PRticle filter approximation to the original PR estimator in low-dimensional cases where the latter can be computed efficiently. Example 3 considers cases where the mixing distribution support is too high-dimensional to compute the original PR estimator, so we compare the PRticle filter approximation results to those of the Dirichlet process mixture model fit.

Example 1. For d-dimensional data X, consider a normal mixture model of the form (1)with $k(x \mid u) = \mathsf{N}_d(x \mid u, \sigma^2 I_d)$ the multivariate normal density with mean vector u, where I_d is the *d*-dimensional identity matrix. Throughout, $\sigma^2 = 0.5$ will be taken as fixed. So that we can compare the PRticle filter approximation directly to the original PR estimator, we consider only the cases d = 1 and d = 2 here. For the d = 1 case, we take the true mixing distribution to be $P = \mathsf{Beta}_{[0,10]}(10,5)$, a beta distribution scaled to $\mathbb{U} = [0,10]$; for the d = 2 case, we take $P = \mathsf{Beta}_{[0,10]}(10,5) \times \mathsf{Beta}_{[0,10]}(5,10)$, a joint distribution supported on $\mathbb{U} = [0, 10]^2$ corresponding to independent scaled beta marginals. In both cases, samples of size n = 500 are generated and we compare the PRticle filter approximation to the original PR estimator in terms of the Kullback-Leibler divergence $K(m_n, \hat{m}_n)$, where m_n is the PR estimator of the mixture density and \hat{m}_n is the corresponding PR ticle filter approximation. Both are based on weight sequence $w_i = (i+1)^{-1}$ and initial guess $P_0 = \mathsf{Unif}(\mathbb{U})$. The PRticle filter approximation relies on samples U_1, \ldots, U_T taken from P_0 and here we consider four samples sizes, $T \in \{100, 300, 500, 1000\}$. Table 1 summarizes both the Kullback-Leibler divergence and the ESS for both the d = 1 and d = 2cases. As expected, the ESS tends to be smaller for d = 2 than for d = 1, with the former retaining about 15% of the original sample while the latter retains about 33%. However, the Kullback–Leibler divergence tends to be small across the board and does not vary much as a function of T for both cases.

Example 2. Next, following Dixit and Martin (2022), we compare the PRticle filter approximation to the original PR estimate for mixture models on the unit sphere $\mathbb{S} \subset \mathbb{R}^3$ commonly used for directional data. The particular mixture model we consider is one

with a so-called angular Gaussian distribution (Tyler 1987) kernel

$$k(x \mid \mu, \beta) \propto |\Sigma_{\mu,\beta}|^{-1/2} (x^{\top} \Sigma_{\mu,\beta}^{-1} x)^{-3/2}, \quad x \in \mathbb{S}, \quad (\mu,\beta) \in \mathbb{S} \times (0,\infty),$$

where $\Sigma_{\mu,\beta} = Q_{\mu}^{\top} D_{\beta} Q_{\mu}$, with $D_{\beta} = \text{diag}(1, 1, \beta^{-2})$ and Q_u is the rotation matrix mapping $(0, 0, 1)^{\top}$ onto the unit vector $\mu \in \mathbb{S}$, given by

$$Q_{\mu} = \begin{pmatrix} \cos \theta_{\mu} \cos \phi_{\mu} & -\sin \phi_{\mu} & \sin \theta_{\mu} \cos \phi_{\mu} \\ \cos \theta_{\mu} \sin \phi_{\mu} & \cos \phi_{\mu} & \sin \theta_{\mu} \sin \phi_{\mu} \\ -\sin \theta_{\mu} & 0 & \cos \theta_{\mu} \end{pmatrix}$$

and $(\theta_{\mu}, \phi_{\mu})$ is the spherical coordinate representation of μ . For the original PR estimator, Dixit and Martin (2022) treated β as a fixed unknown structural parameter, not a latent variable being mixed over. That is, they treated the kernel as $k_{\beta}(x \mid u)$, depending on the unknown β , where $u = \mu$ is the only latent variable mixed over. Then they employed the PR marginal likelihood strategy to estimate the fixed unknown β . Here, using the added flexibility of the PRticle filter approximation, we fit the model that mixes over latent variable $u = (\mu, \beta)$, so that there are no unknown structural parameters to be estimated separately. Here we generate n = 2000 samples from the above mixture model where the true mixing distribution P has a smooth bimodal density in μ and a point mass at $\beta = 0.1$ —this means that PR's mixture model, that takes β fixed and unknown, is correctly specified while the PRticle filter's mixture model is misspecified. For the PR estimator, we take $w_i = (i+1)^{-1}$ and P_0 to be uniform on S. For the PR ticle filter approximation, which mixes over both μ and β , the initial guess P_0 is a product of uniform distributions on S and a uniform distribution on (0, 0.5]. Plots of the PR estimate m_n and PRticle approximation \hat{m}_n , based on T = 1000 initial particles, are provided in Figure 1. The approximation based on PRticle filter clearly captures all the relevant features of the PR estimate, and in much less time thanks to not needing to employ the marginal likelihood strategy to estimate a fixed β .

Example 3. For the third part of the simulation study, we mix a bivariate normal kernel over all mean (μ_1, μ_2) and covariance $(\sigma_1^2, \sigma_2^2, \rho)$ parameters. This means that the mixing distribution P is defined over five variables. Using PR with numerical integration is not possible in this situation as a quadrature scheme is infeasible. The PRticle filter approximation can instead be used to fit this mixture density. For comparison, we consider a Dirichlet process mixture model fit, where the prior for the mixing distribution is $P \sim \mathsf{DP}(\alpha, P_0)$, a Dirichlet process with precision parameter $\alpha > 0$ and base measure P_0 , which we take to be the same as PR's initialization (see below). The Dirichlet process mixture model estimate of the mixture density is the corresponding posterior mean, which is calculated using the DirichletProcessMvnormal function in the R package dirichletprocess (Ross and Markwick 2019) with 1000 iterations. To compare the two approaches we take $U = (\mu_1, \mu_2, \sigma_1^2, \sigma_2^2, \rho)$ with the true mixing distribution P corresponding to independent $\mu_1 \sim N(5, 3^2), \mu_2 \sim N(10, 3^2), \sigma_1^2 \sim \text{Gamma}(1, 1),$ $\sigma_2 \sim \mathsf{Gamma}(5,1)$, and $\rho \sim \mathsf{Beta}(10,5)$. In this, we generate n = 500 observations from the true mixture density and fit a multivariate normal mixture density using the PRticle filter approximation and the Dirichlet process mixture model machinery. As before we



Figure 1: Estimated mixture density on the sphere based on the PR algorithm and the PR ticle filter approximation for bimodal continuous mixing distribution, views from north and south poles.

initialize the PRticle filter with a uniform distribution P_0 over all parameters and a weight sequence $w_i = (i + 1)^{-1}$. However, to avoid possible attrition we improve the filter by using the strategy proposed in Section 3.3 and rerun the algorithm with an updated P_0 . Contour plots of the estimated mixture densities are given in Figure 2. The PRticle filter approximation plots are able to capture the structure of the true mixture density, m, just like the Dirichlet process mixture model fit. For a numerical comparison we calculate the Monte Carlo approximation of the Kullback–Leibler divergence between the true mixture density and the estimated density. This is 0.024 for a comparison between m and \hat{m}_{PR} while it is 0.006 for a comparison between m and \hat{m}_{DP} . The Dirichlet process estimate performs slightly better than PR for mixture density estimation, but it is important to note that PR is solving the harder problem of estimating a multivariate mixing density, which the Dirichlet process mixture formulation struggles with because the resulting estimator is effectively discrete. To illustrate this, we draw independent samples of U from the true mixing distribution P and both the PRticle filter and Bayes estimates of P, and display quantile–quantile plots for comparison in Figure 3. The PR quantiles match



(c) PRticle estimate with updated p_0

Figure 2: Mixture density estimates for a multivariate normal mixture with the observed data overlaid.

the true distribution quantiles much more closely compared to the Dirichlet process-based Bayes estimator quantiles. Computationally, fitting of the Dirichlet process mixture takes almost four minutes on our machine, while the PRticle filter approximation is calculated in about one minute.

4.2 Marked point process modeling

Here we showcase an interesting application of multivariate mixture modeling using PR, which is made possible by the PRticle filter approximation. Suppose our data consists of spatial locations s of an interesting occurrence possibly accompanied by some attributes x at those locations. Typically, when only location observations s_1, \ldots, s_n are available, there is interest in the intensity of the incident occurrence. These are typically modeled as realizations from a non-homogeneous Poisson process with intensity function $\lambda(s)$, $s \in \mathbb{S} \subseteq \mathbb{R}^d$ (e.g. Liang et al. 2008). For example, in an epidemiological study, s_i might be the geographic location of the i^{th} individual showing symptoms of a particular disease and hence there is interest in modeling the intensity of the disease occurrences. For such



Figure 3: Quantile–quantile plots for each component of $U = (\mu_1, \mu_2, \sigma_1^2, \sigma_2^2, \rho)$ of the mixing distribution corresponding to the multivariate normal mixture. Black line corresponds to quantiles from the PRticle filter estimate, while the red line corresponds to quantiles from the Dirichlet process-based Bayes estimate.

a non-homogeneous Poisson process, a likelihood function can be written as,

$$L(\lambda \mid s_1, \dots, s_n) = \Lambda^n \exp\{-\Lambda\} \prod_{i=1}^n m(s_i)$$

where *m* is the normalized intensity function, i.e., $m(s) = \lambda(s)/\Lambda$, and $\Lambda = \int \lambda(t) dt$. Given the separable nature of the likelihood above, Λ and *m* can be estimated separately. A regression approach is to model λ by a log Gaussian Cox process (e.g. Liang et al. 2008). However given the nonparametric nature of the problem it is desirable to use a robust model for λ to capture all the shape/scale features of the function. Mixture models offer this flexibility and an approach to modeling λ or *m* by a Dirichlet process mixture was proposed in Kottas and Sansó (2007).

Additionally, there could be other attributes X_1, \ldots, X_n present with the location data, for example, indicator variable for type of disease, when there is interest in the association between disease locations. Then to account for this association and its effect on the model, a joint intensity function $\psi(s, x)$ can be defined. The resulting process is known as the marked point process, where the attributes are called *marks*. The nonparametric mixture density in (1) offers the required flexibility to model a fully nonparametric function $\psi(s, x)$. Taddy and Kottas (2012) propose mixture models for such marked point processes using conditionally conjugate Dirichlet process mixture models. The idea is to model the joint intensity $\psi(s, x)$ of the locations s and marks x as,

$$\psi(s,x) = \lambda(s) g(x \mid s) = \Lambda m(s) g(x \mid s) = \Lambda m(s,x),$$
(5)

where $g(x \mid s)$ represents the conditional density of mark X, given location s. Features

of this joint intensity can be identified by modeling m(s, x) with a mixture model. The flexibility and computational efficiency offered by PR means that it is tailor-made to fit such a mixture model. However, given the multivariate nature of the problem we need the PR filter approximation to actually implement PR.

We illustrate the above on a real dataset as suggested in Example 5.3 of Taddy and Kottas (2012). The suggested dataset, longleaf is part of the R package spatstat (Baddeley and Turner 2005) and a detailed space-time survival analysis based on this was developed in Rathbun and Cressie (1994). The observations are locations of 584 pine trees in a 200×200 square and the marks are diameters of the trees at breast height (only for trees having this diameter greater than 2 cm). A scatter plot of the data is given in Figure 4. One can clearly see that the distribution of trees is not uniform, i.e., mature (larger diameter) trees are more evenly distributed than younger (smaller diameter) trees, which appear in clusters. Hence, the goal is to model the joint intensity of the locations and marks of these trees. Taddy and Kottas (2012) model m(s, x) as a mixture model with a trivariate normal kernel and a mixing distribution defined over all the parameters of this multivariate normal distribution, i.e.,

$$m(s,x) = \int \frac{\mathsf{N}_3(\operatorname{logit}(s_1/200, s_2/200), \log(x-2) \mid \mu, \Sigma)}{(x-2) \prod_{i=1}^2 (s_i/200)(1-s_i/200)} P(d\mu, d\Sigma)$$
(6)

With the model in (6), we can estimate the conditional distribution of the marks at different locations to capture the varying distribution of trees, which in essence is an indication of the survival. We propose using the PR approach to fit this joint intensity function and estimate P. Of course, that this is a mixture of a nine-dimensional latent variable space—three mean parameters and six covariance matrix parameters—makes it impossible to fit with the PR algorithm directly, so the PR ice filter approximation is necessary. Assuming a mixing distribution over all nine dimensions is possible using the PRticle filter approximation, but for model comparison we actually fit two models: the nine-dimensional model above and a reduced model that assumes the covariance terms in Σ are fixed at 0. The mixing distribution is then estimated by PR with the PR ticle filter approximation. From this fitted mixture model m(s, x) we extract the conditional density $g(x \mid s)$ at specific locations to see how the diameter distribution varies with s as displayed in Figure 5. As we can see in the scatter plot, each chosen location has unique characteristics in terms of diameter distribution. Locations s = (81, 120)and s = (100, 100) have higher concentrations of mature, large-diameter trees, which is correctly captured by both models (nine-dimensional and six-dimensional) in Figure 5. On the other hand, locations s = (105, 140) and s = (185, 87) have clusters of younger, smaller-diameter trees which, again, is correctly captured in Figure 5. Each plot in Figure 5 is overlaid with an empirical probability density of marks using the density function in R based on observations that are within a radius of 30 units from the chosen location. The fitted model retains these local features while being globally smoother than the empirical density. In terms of model comparison, both the six and nine-dimensional model reasonably capture the varying diameter distribution at all locations. A difference between the two estimates is that the full model estimate is smoother than the reduced model one. This is because the kernel density in the former inherently contains an average over the covariance parameters, while the latter fixes these at zero. The full model also appears to capture certain features better than the reduced model. For example, consider



Figure 4: Tree locations on a 200×200 grid (longleaf dataset), where the size of each point is proportional to the respective tree diameter; gray coloring is to make different points easier to distinguish. Yellow triangles indicate locations at which the conditional mark density is estimated in Figure 5.

the locations s = (105, 140) and s = (185, 87), whose conditional mark density is shown in Panels (c) and (d) of Figure 5, respectively. These two points have relatively high concentration of small-diameter trees, as seen in Figure 4; but upon closer inspection, the concentration at s = (105, 140) seems higher than at s = (185, 87), and we see that the conditional density estimates based on the full model capture these differing features better than those based on the reduced mode. Similar results were obtained in Taddy and Kottas (2012) via their proposed Dirichlet process mixture fit. An interesting difference between our results and those of Taddy and Kottas is that their plot at s = (100, 100)shows a sharp spike in the conditional density near x = 0, whereas ours does not. Since there is no evidence in the scatter plot for a high concentration of small-diameter trees, our guess is that their spike is actually a boundary effect, commonly seen in density estimation on bounded domains, and not an inherent feature in the data. That the PR estimate does not suffer from a boundary effect in this case is another benefit.

5 Conclusion

In this paper we proposed a new filtering mechanism, a PRticle filter, for fitting nonparametric mixture models using the PR algorithm in multivariate problems. This new development is an important addition because, previously, the PR algorithm could only handle mixtures over relatively low-dimensional spaces. This contribution creates new opportunities for PR-based methodology in non-trivial problems like marked spatial point process modelling in Section 4.2. Theoretically, we show that the PRticle filter approximation of the mixing distribution converges to the PR estimate in a strong sense as the number of particles T goes to infinity, when the data X_1, \ldots, X_n of size n remains fixed. This holds for the primary PR run only, an analysis of the attrition-handling embellishments in Section 3.3 would require more sophisticated techniques. Coupling this with



Figure 5: Conditional density estimates for the marks, i.e., the diameter of trees in the longleaf dataset at four specific locations, s, in the 200 × 200 grid with full ninedimensional (black), reduced six-dimensional (red) mixture model overlayed with an empirical distribution of marks in the neighborhood (dashed)

results in literature on consistency (as $n \to \infty$) of the PR estimator strengthens both the theoretical and practical aspects of PR. Our numerical results show that the PR ticle filter approximation gives as accurate results as the traditional PR approach for univariate and bivariate mixtures and is also effective in estimating a multivariate mixture density.

One might also be interested in quantifying uncertainty about the mixing distribution and its features, like in Section 4.2. Capturing the variability in the PR estimate is a difficult problem, but suggestions have been made in Fortini and Petrone (2020) and Dixit and Martin (2019). The former uses a quasi-Bayes strategy to construct credible intervals for the PR estimate, while in the latter we leverage the order dependence of the PR estimator for uncertainty quantification. This strategy, which constructs multiple PR estimates based on distinct permutation of the data sequence, would be applicable for the PR ticle filter approximation. There are some theoretical gaps that need to be filled, however, so remains an ongoing work.

One of our numerical illustrations considered nonparametric estimation of mixing distributions supported on the sphere in three-dimensions. A natural question is if this approach could be extended to other cases involving mixture defined on more general compact manifolds, e.g., higher-dimensional spheres, tori, etc. All that would be needed to extend the proposed strategy in such cases is a map from the surface of the manifold to an underlying Euclidean space where the comptutations can be carried out. In the special case of the sphere, there is a "global" Euclidean-space representation but, for more general manifolds, the corresponding Euclidean spaces would be "local," which creates some new and interesting conceptual and computational challenges.

An interesting theoretical question is if consistency of the PRticle filter approximation could be established. That is, if $\hat{P}_{n,T}$ is the PRticle filter approximation of the PR estimator P_n , then the goal would be to show that $\hat{P}_{n,T} \to P$ as both n and T go to infinity. Of course, this would require $T = T_n$ to be increasing sufficiently fast with n. Direct extension of the argument used in the proof of Theorem 1 may be possible using some naive techniques, e.g., the classical union bound, but, if successful, this would require T to be exponentially large with n. Our gut feeling is that such a large number of particles would not be necessary, so some important insights are still missing. We save this as a topic for future work.

A remaining practical challenge is the handling of attrition when the dimension of the mixing distribution support is relatively high. What we proposed in Section 3.3 is able to adequately control attrition rates for mixtures over at least nine-dimensional spaces. We have not thoroughly tested the performance of the PRticle filter approximation in dimensions higher than this, but we fully expect that controlling the attrition rate will be more and more difficult as the dimension increases. This is not a limitation of the proposed method, it is a challenge that any importance sampling-based method will face in high-dimensional applications. New insights would be needed to make this leap to high-dimensional mixtures but it may be possible to take advantage of the PR-specific recursive structure that we used to develop the PRticle filter approximation here.

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A Proof of Theorem 1

Recall that,

$$\hat{m}_{i-1}(X_i) = \frac{1}{T} \sum_{t=1}^T k(X_i \mid U_t) \hat{\Delta}_i(U_t), \quad i \ge 1,$$

where $\hat{\Delta}_1(u) \equiv 1$ and

$$\hat{\Delta}_{i}(u) = \hat{\Delta}_{i-1}(u)\,\hat{\delta}_{i-2}(u)$$

$$= \prod_{j=2}^{i} \left\{ 1 + w_{j-1} \left(\frac{k(X_{j-1} \mid u)}{\hat{m}_{j-2}(X_{j-1})} - 1 \right) \right\}, \quad i \ge 2.$$

By the strong law of large numbers, we have that

$$\hat{m}_{0,T}(X_1) = \frac{1}{T} \sum_{t=1}^T k(X_1 \mid U_t) \to m_0(X_1), \quad \text{with } P_0\text{-probability 1 as } T \to \infty.$$

To prove a similar claim for all $\hat{m}_{\ell,T}(X_{\ell+1})$, we proceed by induction. That is, we start by assuming that

$$\hat{m}_{i-1,T}(X_i) \to m_{i-1}(X_i) \quad \text{with } P_0\text{-probability 1, for all } i \le \ell,$$
 (7)

and then use that assumption, along with the structure of the algorithm, to prove

$$\hat{m}_{\ell,T}(X_{\ell+1}) \to m_{\ell}(X_{\ell+1}), \text{ with } P_0\text{-probability 1, as } T \to \infty.$$

Towards this, we have

$$\hat{m}_{\ell,T}(X_{\ell+1}) = \frac{1}{T} \sum_{t=1}^{T} k(X_{\ell+1} \mid U_t) \hat{\Delta}_{\ell+1}(U_t) = \frac{1}{T} \sum_{t=1}^{T} k(X_{\ell+1} \mid U_t) \prod_{i=1}^{\ell} \Big\{ (1 - w_i) + w_i \frac{k(X_i \mid U_t)}{\hat{m}_{i-1,T}(X_i)} \Big\}.$$

The product above can be expanded as

$$\prod_{i=1}^{\ell} \left\{ (1-w_i) + w_i \frac{k(X_i \mid U_t)}{\hat{m}_{i-1,T}(X_i)} \right\} = \sum_{\mathcal{S}(\ell)} \prod_{j \in \mathcal{S}(\ell)} (1-w_j) \prod_{i \notin \mathcal{S}(\ell)} w_i \frac{k(X_i \mid U_t)}{\hat{m}_{i-1,T}(X_i)},$$

where $S(\ell)$ is a generic subset of $\{1, \ldots, \ell\}$ and the sums and products are over all 2^{ℓ} such subsets. Going back the formula for $\hat{m}_{\ell,T}(X_{\ell+1})$, we can distribute the average over t through the product, which gives

$$\hat{m}_{\ell,T}(X_{\ell+1}) = \sum_{\mathcal{S}(\ell)} \frac{\prod_{j \in \mathcal{S}(\ell)} (1 - w_j) \prod_{i \notin \mathcal{S}(\ell)} w_i}{\prod_{i \notin \mathcal{S}(\ell)} \hat{m}_{i-1,T}(X_i)} \left\{ \frac{1}{T} \sum_{t=1}^T k(X_{\ell+1} \mid U_t) \prod_{i \notin \mathcal{S}(\ell)} k(X_i \mid U_t) \right\}$$

By the induction hypothesis (7), we have that

$$\prod_{i \notin \mathcal{S}(\ell)} \hat{m}_{i-1,T}(X_i) \to \prod_{i \notin \mathcal{S}(\ell)} m_{i-1}(X_i), \quad \text{with } P_0\text{-probability 1, uniformly in } \mathcal{S}(\ell).$$

Moreover, by the assumption (4), the strong law of large numbers gives

$$\frac{1}{T}\sum_{t=1}^{T}k(X_{\ell+1} \mid U_t)\prod_{i \notin \mathcal{S}(\ell)}k(X_i \mid U_t) \to \int k(X_{\ell+1} \mid u)\prod_{i \notin \mathcal{S}(\ell)}k(X_i \mid u) P_0(du),$$

with P_0 -probability 1, as $T \to \infty$, again uniformly in $\mathcal{S}(\ell)$. The two "uniformly in $\mathcal{S}(\ell)$ " claims above follow because there are only finitely many such $\mathcal{S}(\ell)$. Putting everything together, we have that $\hat{m}_{\ell,T}(X_{\ell+1})$ converges with P_0 -probability 1, as $T \to \infty$, to

$$\sum_{\mathcal{S}(\ell)} \frac{\prod_{j \in \mathcal{S}(\ell)} (1 - w_j) \prod_{i \notin \mathcal{S}(\ell)} w_i}{\prod_{i \notin \mathcal{S}(\ell)} m_{i-1}(X_i)} \left\{ \int k(X_{\ell+1} \mid u) \prod_{i \notin \mathcal{S}(\ell)} k(X_i \mid u) P_0(du) \right\}.$$

Moving the integration over u to the outside of the sum over $\mathcal{S}(\ell)$ and undoing the product expansion above eventually leads to $\hat{m}_{\ell,T}(X_{\ell+1}) \to m_{\ell}(X_{\ell+1})$ with P_0 -probability 1.

We showed above that

 $\hat{m}_{i-1,T}(X_i) \to m_{i-1}(X_i)$ with P_0 -probability 1 as $T \to \infty$,

uniformly in i = 1, ..., n without any assumptions on the convergence of the mixing distribution approximation. Since the final mixing density estimator $\hat{p}_{n,T}$ is a continuous function of $\{\hat{m}_{i-1,T}(X_i): i = 1, ..., n\}$, it follows that

$$\hat{p}_{n,T}(u) \to p_n(u)$$
, with P_0 -probability 1, as $T \to \infty$, for all u .

Since these are density functions, it follows from Scheffé's theorem that $\hat{p}_{n,T}$ converges in $L_1(du)$ to p_n , with P_0 -probability 1, as $T \to \infty$.

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