Embarrassingly Parallel Variational Inference in Nonconjugate Models

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Abstract

We develop a parallel variational inference (VI) procedure for use in data-distributed settings, where each machine only has access to a subset of data and runs VI independently, without communicating with other machines. This type of “embarrassingly parallel” procedure has recently been developed for MCMC inference algorithms; however, in many cases it is not possible to directly extend this procedure to VI methods without requiring certain restrictive exponential family conditions on the form of the model. Furthermore, most existing (nonparallel) VI methods are restricted to use on conditionally conjugate models, which limits their applicability. To combat these issues, we make use of the recently proposed nonparametric VI to facilitate an embarrassingly parallel VI procedure that can be applied to a wider scope of models, including to nonconjugate models. We derive our embarrassingly parallel VI algorithm, analyze our method theoretically, and demonstrate our method empirically on a few nonconjugate models.

1 Introduction

Many large, modern datasets are collected and stored in a distributed fashion by multiple sensors or data-collecting agents. Examples of this include medical data recorded in hospitals throughout a country, weather data gathered by a collection of sensors, web data scraped by a network of machines, and cell phone data collected on users’ phones. Inference algorithms that can operate in these distributed settings—by processing subsets of data separately and in parallel—are particularly advantageous. This is because they mitigate the need for transferring data to a central location for analysis, reduce both the memory usage and computation time of inference [10] [12], allow for continuous data collection from independently operating agents [5], and allow for sensitive data to be processed independently in secure locations (which can yield privacy guarantees [13]).

Variational inference (VI) methods are general procedures for approximate inference in Bayesian models, and they have been applied successfully in a wide variety of domains [9] [2]. This paper is concerned with developing better VI methods for use in distributed settings. One major issue with most existing parallel methods is that they often require synchronization between machines at regular intervals [20] [11] [19]. Communication between machines due to this synchronization can greatly reduce the efficiency of these procedures, as each machine must wait for information from other machines before proceeding with computation. Furthermore, communication requirements may increase the difficulty of system implementation and maintenance [10], and necessitate the transfer of (potentially sensitive) data between machines [18].

We aim to develop a new “embarrassingly parallel” algorithm for VI in data-distributed settings, which is a type of parallel algorithm where there is no regular communication between machines. Given a dataset partitioned over a collection of machines, embarrassingly parallel VI methods carry out the following two steps:

1. Perform variational inference on the subset of data on each machine in parallel (independently, without communication between machines).

2. Combine the results from all machines to yield a variational inference result for the full-data posterior distribution.

These two steps are only performed once, and there is only communication between machines at one point in the second step, when collecting results from each of the local instances of VI.
Recently, progress has been made toward this goal for mean field variational inference methods limited to models with certain exponential family restrictions on the likelihood and prior distribution [4, 5]. These methods use a decomposition of the posterior of the form of the classic (nonparallel) Kullback-Leibler (KL) objective, which involves the product of so-called subposterior densities [6, 16]. Similar to these methods, we would like a general inference algorithm that can be applied to a wide class of Bayesian models, yet operates in this embarrassingly parallel setting. However, the variational families employed by these nonconjugate methods are not in a form that allows us to apply the above-mentioned decomposition strategy for parallelization.

Recent papers in the Markov chain Monte Carlo (MCMC) literature have introduced an alternative decomposition of the posterior for parallel inference [15, 12, 17], which involves the product of so called subposterior densities (i.e. posterior densities given a subset of data with an underweighted prior). We apply this new decomposition to a nonconjugate variational inference method called nonparametric variational inference (NVI) [6] to perform low-communication, parallel inference in a general class of models. In particular, we only require weak differentiability conditions on the joint log probability.

The main contribution of our method is that it provides a way to perform embarrassingly parallel inference in data distributed settings for a more general class of Bayesian models without requiring conditional conjugacy or exponential family assumptions on the model likelihood or prior. In the following sections, we derive the posterior decomposition used by our method, show how we can combine local nonparametric variational approximations to form a variational approximation to the full-data posterior density, and analyze the computational complexity of our algorithms. Finally, we demonstrate our method empirically on a few nonconjugate Bayesian models.

2 Preliminaries

We describe existing work on embarrassingly parallel VI with exponential family restrictions, existing work on embarrassingly parallel MCMC, and the difficulties with extending these methods to variational inference in more general, nonconjugate models.

Suppose we have a large set of $N$ i.i.d. data points, $x^N = \{x_1, \ldots, x_N\}$, a likelihood for these data parameterized by $\theta \in \mathbb{R}^d$, written $p(x^N|\theta)$, and a prior density for $\theta$, written $p(\theta)$. We can write the posterior density given all $N$ data points (which we will also refer to as the “full-data” posterior) as

$$p(\theta|x^N) \propto p(\theta)p(x^N|\theta) = p(\theta) \prod_{i=1}^N p(x_i|\theta). \quad (1)$$

Now suppose the data $x^N$ is partitioned into $M$ subsets $\{x^{n_1}, \ldots, x^{n_M}\}$ of sizes $n_1, \ldots, n_M$, and distributed over $M$ machines. Recent works in embarrassingly parallel VI [4, 5] have proposed the following solution for inference in this setting. First, in an embarrassingly parallel fashion, compute

$$q^*_1, \ldots, q^*_M = \arg\min_{q_1, \ldots, q_M} \sum_{m=1}^M KL[q_m||p(\theta|x^{n_m})] \quad (2)$$

where $p(\theta|x^{n_m})$ is the posterior given a subset of data $x^{n_m}$. Second, form the full-data posterior variational approximation with

$$q^*(\theta) \propto \left( \prod_{m=1}^M q^*_m(\theta) \right) / p(\theta)^{M-1}. \quad (3)$$

The justification for this solution is that the full-data posterior can be decomposed as $p(\theta|x^N) \propto \left( \prod_{m=1}^M p(\theta|x^{n_m}) \right) / p(\theta)^{M-1}$, and further, it can be shown that the above objective retains an important property of the classic (nonparallel) KL objective: if the objective is zero then the full-data approximation $q^*(\theta)$ is equal to the full-data posterior $p(\theta|x^N)$. I.e., if $\sum_{m=1}^M KL[q_m||p(\theta|x^{n_m})] = 0 \implies KL[q^*(\theta)||p(\theta|x^N)] = 0 \implies q^*(\theta) = p(\theta|x^N)$.

However, this solution has a few major restrictions on the form of the variational approximation and model. Namely, to form $q^*$, these methods must tractably compute the product of the $M$ variational approximations divided by the prior density (equation (3)). These methods do this by limiting their scope to conditionally conjugate exponential family models, and then using mean field variational methods that restrict the variational approximation to the same exponential family as the prior.

To attempt to extend the scope of models to which embarrassingly parallel VI methods can be applied, we turn to a separate line of work on embarrassingly parallel MCMC methods [15, 12, 17], which use an alternative decomposition of the posterior distribution. Let the $m^{th}$ subposterior density, $p_m(\theta)$, be defined as
the posterior given the $m^\text{th}$ data subset with an unweighted prior, written $p_m(\theta) = p(\theta) \neq p(x^n | \theta)$. This is defined such that the product of the $M$ subposterior densities is proportional to the full-data posterior, i.e.

$$p_1 \cdots p_M(\theta) \propto p(\theta) \prod_{m=1}^{M} p(x^n | \theta) \propto p(\theta | x^N). \quad (4)$$

In these methods, a subposterior density estimate $\tilde{p}_m(\theta)$ is learned on each machine (via sampling), and the product of these estimates $\prod_{m=1}^{M} \tilde{p}_m(\theta)$ yields an approximation of the full-data posterior density.

However, we cannot directly apply this new decomposition to typical mean field variational inference approximations (as is done in embarrassingly parallel VI) for the following two reasons:

1. The underweighted prior $p(\theta) \neq p(x^n | \theta)$ in the subposterior may lose conjugacy necessary for the requisite exponential-family-conditionals. Hence, it may not be easy to directly apply these VI methods to approximate the subposterior.

2. Even if we are able to learn a variational approximation for each subposterior, the product of subposterior variational approximations may not have a tractable form that we can analytically compute.

Therefore, to use this alternative decomposition to apply VI to a broader scope of models, we need a family of variational approximations that can be run on general subposterior densities (including those of nonconjugate models) while maintaining a tractable density product that can be analytically computed.

## 3 Embarrassingly Parallel Variational Inference in Nonconjugate Models

Embarrassingly parallel variational inference (EPVI) in nonconjugate models is a parallel approximate Bayesian inference method for continuous posterior distributions. It is generally applicable, requiring only that the first two derivatives of the log-joint probability density are computable. For a dataset partitioned over $M$ machines, VI is run in parallel on each machine to approximate the $M$ subposterior densities; afterwards, the local subposterior approximations are combined by computing their product, which approximates the full-data posterior density. Each machine performs variational inference without sharing information, in an embarrassingly parallel manner. We summarize this procedure in Algorithm 1

**Algorithm 1: Embarrassingly Parallel Variational Inference in Nonconjugate Models**

**Input:** Partitioned dataset $\{x^n, \ldots, x^{nM}\}$.

**Output:** Variational approximation $q^*(\theta)$ for the full-data posterior density $p(\theta | x^N)$.

1. for $m = 1, \ldots, M$ do in parallel
2. Learn a variational approximation $q^*_m(\theta)$ for the $m^\text{th}$ subposterior $p_m(\theta)$, given data $x^n_m$.
3. Compute product $\prod_{m=1}^{M} q^*_m(\theta)$ of subposterior approximations to yield the full-data variational approximation $q^*(\theta)$.

### 3.1 EPVI with Nonparametric Variational Inference

In a recently proposed method known as nonparametric variational inference (NVI) [6], a posterior approximation is selected from a variational family of densities of the form $q(\theta) = \frac{1}{K} \sum_{k=1}^{K} q_k(\theta | \mu_k, \sigma_k^2 I_d)$. Some advantages of this method are that it can capture multimodal posterior distributions, can be applied to many nonconjugate models (in fact, the only requirement is that the first two derivatives of the log joint probability are computable), and has an efficient algorithm to optimize the variational objective. In our case, NVI allows us to perform variational inference on subposterior densities without worrying if they retain the conjugacy necessary to easily apply typical mean-field approximations, and also allows us to develop a method to combine the subposterior variational approximations (i.e. allows us to derive an analytic form for the product of these approximations) to produce a full-data posterior variational approximation. After running this procedure on a subset of data $x^n_m$ on a machine $m$, we can write the inferred variational approximation for the subposterior distribution as

$$q^*_m(\theta) = \frac{1}{K} \sum_{k=1}^{K} N_d(\theta | \mu_k^{(m)}, \sigma_k^{2(m)} I_d). \quad (5)$$

Due to this choice of $q^*_m$, we have an analytic form for the product of these densities, $\prod_{m=1}^{M} q^*_m(\theta)$, which gives us a variational approximation for the subposterior density product (and hence for the full-data posterior). In particular, the product of these $M$ mixture-of-Gaussians variational densities gives a (non-uniformly weighted) mixture-of-Gaussians density with $K^M$ components. We can write this product mixture as

$$q^*(\theta) \propto \prod_{m=1}^{M} q^*_m(\theta) = \frac{1}{K^M} \prod_{m=1}^{M} \sum_{k_m=1}^{K} N_d(\theta | \mu_k^{(m)}, \sigma_k^{2(m)} I_d)$$

$$= \sum_{k_1=1}^{K} \cdots \sum_{k_M=1}^{K} w_k \cdot \prod_{m=1}^{M} N_d(\theta | \mu_k, \sigma_k^2 I_d) \quad (6)$$
where we use $k = (k_1, \ldots, k_M)$ to denote the vector of M subposterior-component-indices (one from each subposterior variational approximation mixture) associated with a given component in this product mixture, and where

$$\sigma^2_{k_i} = \left( \sum_{m=1}^{M} (\sigma^2_{k_i}^{(m)})^{-1} \right)^{-1} \quad (7)$$

$$\mu_{k_i} = \sigma^2_{k_i} I_d \left( \sum_{m=1}^{M} \left( (\sigma^2_{k_i}^{(m)})^{-1} I_d \right) \mu_{k_i}^{(m)} \right) \quad (8)$$

$$w_{k_i} = \frac{\prod_{m=1}^{M} N_d(\mu_{k_i}^{(m)} | \mu_{k_i}, \sigma^2_{k_i}^{(m)} I_d)}{N_d(\mu_{k_i} | \mu_{k_i}, \sigma^2_{k_i}^{(m)})} \quad (9)$$

3.2 Computing the Variational Density Product Mixture

After learning the optimal local parameters $\{\mu_{k_i}^{(m)}, \sigma_{k_i}^{2(m)}\}_{k_i=1}^{K}$ for each of the $m \in \{1, \ldots, M\}$ subpostersiors, we wish to form a variational approximation to the full-data posterior density by taking the product of the M mixtures. However, computing the parameters and weights for all $K^M$ components in the product mixture becomes infeasible as $M$ grows.

We typically perform Bayesian inference in order to compute expectations with respect to, and explore, the posterior distribution. In practice, one common way to achieve this is to sample from the posterior, and then compute a sample expectation: this is done in both MCMC methods and in VI methods (in the latter case, to compute expectations with respect to a variational approximation after VI has finished running [6, 3, 14]). Hence, instead of computing the product mixture (and afterwards, sampling from it to compute expectations), our solution is to bypass this step and directly generate samples from the product mixture.

We give a procedure that allows us to compute expectations with respect to the variational approximation in this common sampling manner without requiring us to actually compute the variational approximation.

We give our method for sampling from the full-data variational approximation in Algorithm 2 and then prove that this yields correct samples. The intuitive idea behind our algorithm is the following. To sample from a mixture, one can first sample a component index (proportional to the component weights) and then sample from the chosen mixture component. We therefore need a way to sample product mixture components (proportional to their weights) without first computing all of the $K^M$ component weights. Our solution is to form a Markov chain over the product mixture component indices, and prove that its stationary distribution is a categorical distribution with probability mass values proportional to the product mixture component weights. Hence, at each step in this Markov chain, we can produce a sample from the full variational approximation while only needing to compute a single new product mixture component.

Algorithm 2: Markov chain for sampling variational density product mixture components

Input: Number of samples $R$, number of burn-in steps $b$, learned subposterior variational approximations $\{q_i(\theta)\}_{i=1}^{M}$.

Output: Parameters $\{\mu_r, \sigma^2_r\}_{r=1}^{R}$ for the $R$ sampled product mixture components.

1. Draw $k \sim (k_1, \ldots, k_M)^{iid} \text{Unif}(\{1, \ldots, K\})$; /* Initialize Markov chain */
2. for $s = 1, \ldots, b + R$
3. Draw $m \sim \text{Unif}(\{1, \ldots, M\})$
4. Set $c = (c_1, \ldots, c_M) \leftarrow k$.
5. Draw $c_m \sim \text{Unif}(\{1, \ldots, K\})$
6. Draw $u \sim \text{Unif}(\{0, 1\})$;
7. if $u < w_{c_i} / w_k$ then
8. \quad Set $k \leftarrow c$.
9. if $s > b$ then
10. \quad Set $\mu_{k-b} \leftarrow \mu_k$; /* Compute mean of sampled mixture component */
11. \quad Set $\sigma^2_{k-b} \leftarrow \sigma^2_k$; /* Compute var of sampled mixture component */
Note that in Algorithm 2, at each step in the Markov chain, we perform two simple steps to sample the next product mixture component: we select a subposterior uniformly at random (line 3), and then re-draw one of its \(K\) components uniformly at random (line 5); this specifies a new product mixture component. We then compute the ratio of the weight of this new product mixture component with the previous component’s weight (line 7) and accept or reject this proposal (line 8). We then compute the parameters of the sampled component (lines 10-11).

**Correctness of Algorithm 2** We prove that Algorithm 2 defines a Markov chain whose stationary distribution is the distribution over the \(K^M\) components in the product mixture density.

**Theorem 3.1.** The procedure given by Algorithm 2 defines a Markov chain whose stationary distribution is the categorical distribution (over \(K^M\) categories) with category-probability parameter equal to the vector of product mixture component weights.

**Proof.** Note that each of the \(K^M\) product mixture components is associated with an \(M\)-dimensional vector \(k = (k_1, \ldots, k_M) \in \{1, \ldots, K\}^M\) (where \(k_m\) denotes the index of the \(m\)th subposterior’s component that contributed a factor to this product mixture component). Hence, instead of sampling an index from a categorical distribution, we can equivalently view our task as sampling an \(M\)-dimensional vector from a joint distribution over the space \(\{1, \ldots, K\}^M\), where each element in this space has a probability mass proportional to its associated product mixture component weight. We can therefore perform Gibbs sampling over this space, where we sample from the conditional distribution over a subposterior component index \(k_m\) given all other component indices. To compute and then sample from this conditional distribution, we could iterate over the \(K\) possible values of \(k_m\) (and compute the component weight of each); however, this could potentially be expensive for large \(K\). Instead, we sample one of the \(K\) values for \(k_m\) uniformly at random (line 5), and our algorithm becomes a Metropolis-within-Gibbs algorithm \[7\] where we’ve used an independent Metropolis proposal \[8\] \[11\] (which we achieve by accepting or rejecting, in lines 6-8, the independent Metropolis proposal made in line 5). Note that the dimension \(m\) along which we take a Gibbs sampling step is chosen in line 3. Since this Metropolis-within-Gibbs algorithm has been shown to have the correct stationary distribution \[7\], our proof is complete. \(\square\)

We describe the complexity of Algorithm 2 in Section 3.3. In Section 3.4, we verify that this algorithm achieves the same results as taking expectations after computing the mixture product exactly, while drastically speeding-up performance.

**Sequential subposterior subset products.** In some cases, it may be simpler to sample from the product mixture in a sequential fashion by sampling from the product of only a few subposteriors multiple times: we first sample \(R\) components from the product of groups of \(M < M\) approximations, and then repeat this process on the resulting (uniform) mixtures formed by the sampled components. This continues until samples from only one mixture remain. For example, one could begin by sampling components from the product of all \(\frac{M}{2}\) pairs (leaving one subposterior approximation alone if \(M\) is odd), thereby forming \(\frac{M}{2}\) uniformly weighted mixtures comprised of the sampled components. This process is then repeated—forming pairs and sampling from the pair product mixture—until there are only samples from one product mixture remaining (which are approximate samples from the full-data posterior). This method is potentially advantageous because each intermediate round of product mixture sampling could be done in parallel. However, more samples are potentially required from each intermediate round to generate valid samples from the full variational approximation at the final product. We compare the effectiveness of this method in Section 3.4.

**3.3 Method Complexity**

Consider a dataset with \(N\) observations, partitioned over \(M\) machines. Assume we have approximated each subposterior using NVI with \(K\) components, where each component is defined by a \(d\)-dimensional parameter. Computing all components of the product mixture exactly requires \(O(dMK^M)\) operations. Computing \(R\) samples from the product mixture approximation via Algorithm 2 requires \(O(dRM)\) operations (assuming a constant number \(b\) of burn-in steps). Computing sequential subposterior subset product samples with \(R\) samples at each intermediate product requires \(O(dRM^2)\) operations overall, but this could be reduced to \(O(dR\log M)\) operations on a single machine if each of the \(O(\log M)\) rounds of sampling are done in parallel.

Each machine learns and then communicates the optimal variational parameters, which consist of \(K\) mean parameter vectors (each in \(d\) dimensions), \(K\) variance parameter scalars, and \(K\) weight parameter scalars. In total, \(MK(d + 2)\) scalars are communicated throughout the entire procedure.

**3.4 Method Scope**

The algorithms described in this paper hold for posteriors distributions with twice-differentiable densities in finite-dimensional real spaces. This method may be applied to nonconjugate Bayesian models, and models with multimodal posteriors, with little further restriction on the form of the model and prior distribution.
3. Expectations computed via our product mixture sampling method (Algorithm 2) achieve similar performance as those computed via exact computation of the product mixture.

To demonstrate these, we conduct experimental comparisons with the following strategies:

• **Full-data nonparametric variational inference** (NVI)—A (nonparallel) variational inference method designed for use in nonconjugate models, which we run on the full dataset. This method takes as a parameter the number of mixture components $K$.

• **Subposterior inference on data subsets** (Subposterior)—The subposterior variational approximations, run on subsets of data. This method takes as a parameter the number of mixture components $K$, and each run returns $M$ of these approximations.

• **Embarrassingly parallel variational inference (exact product)** (EPVI_exact)—The method introduced in this paper, which combines the $M$ subposteriors by computing all components of the product mixture density.

• **Embarrassingly parallel variational inference (mixture product sampling)** (EPVI_sample)—The method introduced in this paper (Algorithm 2), which samples from the product of the $M$ subposterior approximations.

• **Embarrassingly parallel variational inference (sequential subset products)** (EPVI_subset)—The method introduced in this paper, which samples from products of pairs of subposteriors sequentially.

Experiments were conducted with a standard cluster system. We obtained subposterior variational approximations by submitting batch jobs to each worker, since these jobs are all independent. We then saved the results to the disk of each worker and transferred them to the same machine, which performed the product mixture sampling algorithms. In each of the following experiments involving timing, we first ran the variational inference optimization procedures until convergence (to provide a time for the Subposteriors and NVI strategies). Afterwards, we added the (maximum) time required for learning the subposterior approximations, the time needed to transfer the learned parameters to a master machine, and the time required to run the product mixture sampling algorithms (to provide a time for the EPVI methods).

4.1 Bayesian Generalized Linear Models

Generalized linear models are widely used for a variety of regression and classification problems. We use a hierarchical Bayesian logistic regression model as a test case in the following experiments. This model places a Gaussian prior on a set of coefficients $\mathbf{w} \in \mathbb{R}^V$ and draws class labels $\mathbf{y} \in \mathbb{R}^N$, conditioned on the prod-
Figure 3: Experimental results for hierarchical Bayesian logistic regression under varying numbers of (a) data-splits $M$ and (b) NVI mixture components $K$. In (c) we show that the EPVI\textsubscript{sample} method maintains a consistent classification accuracy over a wide range of $M$.

![Graphs](image1)

Figure 4: Comparison of the two product mixture sampling methods with the exact product mixture computation under (a)-(b) varying $M$ and (c)-(d) varying $K$.

![Graphs](image2)

put of an observation matrix $X \in \mathbb{R}^{N \times V}$ and the coefficients, passed through a logistic transform; further, Gamma priors are placed on the variance parameter for each coefficient. Notably, this model lacks conditional conjugacy. We write the generative model as

1. Draw global hyperparameter $\alpha \sim$ Gamma $(a, b)$
2. For $v = 1, \ldots, V$, draw coefficient $w_v \sim \mathcal{N}(0, \alpha^{-1})$
3. For $n = 1, \ldots, N$, draw observation $y_n \sim$ Bernoulli $(\text{logit}^{-1}(-w^\top x_n))$

where $x_n$ denotes the $n^{th}$ row of $X$. We partition the data by splitting $X$ and $y$ into $M$ disjoint subsets each of size $\frac{N}{M}$, and inferring a variational approximation on each subset. This is illustrated in Figure 2(a).

Data. We demonstrate our methods on the SUSY particles dataset\textsuperscript{4} in which the task is to classify whether or not a given signal (measured by particle detectors in an accelerator) will produce a supersymmetric particle. This dataset has $N = 5,000,000$ observations, of which we hold out 10\% for evaluating the test log-likelihood.

Performance under varying $M$. We vary the number of data-splits $M$ from 2 to 20, and record the held-out negative log-likelihood and time taken to converge for each method. For the Subposteriors result, we report the maximum time taken to converge and the average negative log-likelihood (over the set of $M$ sub-posteriors). We also record the time taken to converge and the negative log-likelihood for the NVI ($M = 1$) standard VI result. The number of mixture components for the NVI part of all methods is fixed at $K = 4$. We plot these results in Figure 3(a), and see that EPVI\textsubscript{sample} reduces the time to convergence by over an order of magnitude while maintaining nearly the same test negative log-likelihood as NVI. In Figure 3(c) we show that performance of the EPVI\textsubscript{sample} method does not suffer as we increase the number of machines over a greater range, from $M = 10$ to $M = 200$. In this table, to give a more interpretable view of performance, we show classification accuracy (on the held out data) for each $M$. We see that classification accuracy stays nearly constant at approximately 0.7865 as we increase $M$ throughout this range.

Performance under varying $K$. Next, we vary the number of NVI mixture components $K$ from 2 to 8, and record the held-out negative log-likelihood and time taken to converge for each method. For parallel methods, we fix $M = 10$. We plot these results in Figure 3(b), and see that for all values of $K$, EPVI\textsubscript{sample} decreases the time to convergence by nearly tenfold, while maintaining virtually identical test negative log-likelihood values.

\footnote{https://archive.ics.uci.edu/ml/datasets/SUSY}
Product mixture sampling methods. We also conduct experiments to judge the quality of our two product mixture sampling procedures. We aim to show that our methods yield similar test log-likelihoods as computing expectations via the exact product mixture while greatly decreasing the computation time. We demonstrate this empirically over a range of $M$ and $K$ values. Note that, since we need to compare with the exact product, we restrict this range to values in which we can compute all of the (exponentially-many) product mixture components. For both sampling methods, we fix $R = 500$. Note that we perform the $O((\log(M))$ rounds of EPVI$_\text{subset}$ sequentially on the machine on which all samples are collected (not in parallel). We plot our results in Figure 3 and see that our sampling methods yield very similar held-out negative log-likelihoods as the exact product over all $M$ (Figure 3(a)) and $K$ (Figure 3(c)) values. We also see that for roughly $M > 6$ (Figure 3(b)) and $K > 4$ (Figure 3(d)), the time needed to compute the exact product increases substantially. Additionally, EPVI$_\text{sample}$ appears to fare slightly better than EPVI$_\text{subset}$ in terms of both the test log-likelihood and computation time.

4.2 Nonlinear Matrix Factorization

We next apply our algorithm to a nonlinear matrix factorization model known as topographic latent source analysis (TLSA) [6]. This model can be viewed as representing an observed matrix as a covariate-dependent superposition of $L$ latent sources. In particular, an observed matrix $U \in \mathbb{R}^{N \times V}$ is assumed to be drawn conditioned on an observed matrix of covariates $X \in \mathbb{R}^{N \times C}$, an inferred weight matrix $W \in \mathbb{R}^{C \times L}$, and a basis matrix $G \in \mathbb{R}^{C \times V}$ constructed by evaluating a parameterized spatial basis function with parameters $\{\bar{r}_l, \lambda_l\}$, written $g_{vl} = \exp\{\lambda_l^{-1}(||\bar{r}_l - \bar{r}_l||^2)\}$. Similar to the previous model, this model lacks conditional conjugacy. We can write the full generative process as

1. For latent source $l = 1, \ldots, L$,
   (a) For $d = 1, \ldots, M$, draw $\bar{r}_{ld} \sim \text{Beta}(1, 1)$
   (b) For $c = 1, \ldots, C$, draw $w_{cl} \sim \mathcal{N}(0, \sigma_w^2)$
   (c) For $v = 1, \ldots, V$, draw observation $u_{nv} \sim \mathcal{N}\left(\sum_{c=1}^{C} \sum_{v=1}^{V} w_{cl} g_{vl}, \tau^{-1}\right)$

We partition the data by splitting observed matrices $U$ and $X$ into $M$ disjoint subsets each of size $N/M$, and inferring a variational approximation on each subset. This is illustrated in Figure 2(b).

Data. In the following experiments, we generate $N = 1,000$ observations in $V = 50$ dimensions by choosing hyperparameters $\{\tau = 1, \sigma_w^2 = 5, \rho = 1\}$, and drawing from the above generative process. We hold out 10% of the data for evaluating the test log-likelihood.

Performance under varying $M$, $K$, and $L$. Similar to the previous model, we first conduct experiments showing held-out negative log-likelihood versus time under varying values for the number of data-splits $M$ and NVI mixture components $K$. These results are shown in Figure 5(a)-(b). We see that EPVI$_\text{sample}$ reduces the time to convergence (particularly as the number of subposteriors $M$ increases) while maintaining a similar test negative log-likelihood as NVI. We also evaluate the performance of our method under different numbers of latent sources $L$. We vary $L$ from 2 to 8, and record the held-out negative log-likelihood and time taken to converge, and again see positive results (Figure 5(c)).

5 Conclusion

In this paper, we developed an embarrassingly parallel VI algorithm for Bayesian inference in a distributed setting, that does not require models with conditional conjugacy and exponential family assumptions. Unlike existing methods, our strategy uses a decomposition of the full-data posterior involving a product of subposterior densities, which was recently developed in the parallel MCMC literature. We have shown promising empirical results on nonconjugate models, which illustrate the ability of our method to perform VI in a distributed setting, and provide large speed-ups, while maintaining an accurate posterior approximation.
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