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Adaptive Component-Wise Multiple-Try Metropolis Sampling

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ABSTRACT

One of the most widely used samplers in practice is the component-wise Metropolis–Hastings (CMH) sampler that updates in turn the components of a vector-valued Markov chain using accept–reject moves generated from a proposal distribution. When the target distribution of a Markov chain is irregularly shaped, a "good" proposal distribution for one region of the state–space might be a "poor" one for another region. We consider a component-wise multiple-try Metropolis (CMTM) algorithm that chooses from a set of candidate moves sampled from different distributions. The computational efficiency is increased using an adaptation rule for the CMTM algorithm that dynamically builds a better set of proposal distributions as the Markov chain runs. The ergodicity of the adaptive chain is demonstrated theoretically. The performance is studied via simulations and real data examples. Supplementary material for this article is available online.

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1. Introduction

Markov chain Monte Carlo (MCMC) methods are widely used to analyze complex probability distributions, especially within the Bayesian inference paradigm. One of the most used MCMC algorithms is the Metropolis–Hastings (MH) sampler, first developed by Metropolis et al. (1953), and later expanded by Hastings (1970). At each iteration, the MH algorithm samples a new candidate state from a proposal distribution which is subsequently accepted or rejected. When the state–space of the chain is high dimensional or irregularly shaped, finding a good proposal distribution that can be used to update *all* the components of the chain simultaneously is very challenging, often impossible. The optimality results for the acceptance rate of the Metropolis–Hastings algorithm (Gelman, Roberts, and Gilks 1996; Roberts and Rosenthal 2001) have inspired the development of the so-called *adaptive MCMC (AMCMC)* samplers that are designed to adapt their transition kernels based on the gradual information about the target that is collected through the very samples they produce. Successful designs can be found in Haario, Saksman, and Tamminen (2001), Haario et al. (2006), Turro et al. (2007), Roberts and Rosenthal (2009), Craiu, Rosenthal, and Yang (2009), Giordani and Kohn (2010), and Vihola (2012), among others. Theoretical difficulties arise because the adaptive chains are no longer Markovian so ergodicity properties must be proven on a case-by-case basis. Attempts at streamlining the theoretical validation process for AMCMC samplers have been increasingly successful including Atchadé and Rosenthal (2005), Andrieu and Moulines (2006), Andrieu and Atchadé (2007), Roberts and Rosenthal (2007), Fort, Moulines, and Priouret (2011), and Craiu et al. (2015). For useful reviews of AMCMC, we refer to Andrieu and Thoms (2008) and Roberts and Rosenthal (2009). It is our experience that existing adaptive strategies for MH in high-dimensional spaces may take a very long time to "learn" good simulation parameters so that the samplers may not improve much before the simulation is ended.

We can increase the computational efficiency if, instead of using a full MH to update all the components at once, we choose to update the components of the chain one-at-a-time. The latter strategy, originally proposed by Metropolis et al. (1953), uses an MH transition kernel for each component of the chain separately and the acceptance or rejection is based on the target's conditional distribution of that component given all the other ones. More precisely, if we are interested in sampling from the continuous density $\pi(x) : \mathcal{X} \subset \mathbf{R}^d \to \mathbf{R}_+$; the component-wise MH (CMH) transition kernel updates the ith component of the chain, x_i, using a proposal $y_i \in \mathbf{R}$, $y_i \sim T_i(\cdot|x_i)$ and setting the next value of the chain as

$$z = \begin{cases} (x_1, \ldots, x_{i-1}, y_i, x_{i+1}, \ldots, x_d) & \text{w.p. } \alpha_i \\ x & \text{w.p. } 1 - \alpha_i, \end{cases}$$

where

$$\alpha_i = \min\left\{1, \frac{T_i(x_i|y_i)\pi(y_i|x_{[-i]})}{T_i(y_i|x_i)\pi(x_i|x_{[-i]})}\right\},$$

and $\pi(\cdot|x_{[-i]})$ is the target conditional distribution of the ith component given all the other components $x_{[-i]} = (x_1, \ldots, x_{i-1}, x_{i+1}, \ldots, x_d)$. The CMH replaces the difficult problem of finding one good proposal in d dimensions with that of finding d good one-dimensional proposals. However, this seemingly easier task can also be challenging when the conditional densities $\pi(\cdot|x_{[-i]})$ change significantly, for example, have very different variances, as $x_{[-i]}$ varies. Intuitively, let us imagine that for a region of the sample space of $x_{[-i]}$, the proposal T_i must have a higher spread for the chain to mix well and a smaller one for the remaining part

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of the support. In this case, an adaptive strategy based on a single proposal distribution cannot be efficient everywhere in the support of π. Some success has been obtained in lower dimensions or for distributions with a well-known structure using the regional adaptive MCMC strategies of Craiu, Rosenthal, and Yang (2009) or Bai, Craiu, and Di Narzo (2011), but extending those approaches can be cumbersome when d is even moderately large. Other adaptive MCMC ideas proposed for the CMH include Haario, Saksman, and Tamminen (2005) where the authors propose to use component-wise random walk Metropolis (RWM) and to use the component-specific sample variance to tune the proposal's variance, along the same lines that were used by Haario, Saksman, and Tamminen (2001) to adapt the proposal distribution for a joint RWM. Another intuitive approach is proposed in Roberts and Rosenthal (2009) who aim for a particular acceptance rate for each component update.

The strategy we propose here aims to close the gap that still exists between AMCMC and efficient CMH samplers. When contemplating the problem, one may be tempted to try to "learn" each conditional distribution $\pi(\cdot|x_{[-i]})$, but parametric models are likely not flexible enough while nonparametric models will face the curse of dimensionality even for moderate values of d. Note that here the difficult part is understanding how the conditional distribution changes as $x_{[-i]}$ varies, which is a $(d-1)$-dimensional problem.

Before getting to the technical description of the algorithm, we present here the intuitive idea behind our design. Within the CMH algorithm imagine that for each component we can propose m candidate moves, each generated from m different proposal distributions. Naturally, the latter will be selected to have a diverse range of variances so that we generate some proposals close to the current location of the chain and some that are further away. If we assume that the transition kernel for each component is such that among the proposed states it will select the one that is most likely to improve the trade-off between acceptance probability and jump distance, then one can reasonably infer that this approach will boost the mixing of the chain provided that the proposal distributions are reasonably calibrated. To mirror the discussion above, in a region where T_i should have small spread, one wants to have among the proposal distributions a few with small variances, and similarly in regions where T_i should be spread out we want to include among our proposal densities a few with larger variances. This intuition can be tested using an approach based on the multiple-try Metropolis (MTM) that originated with Liu, Liang, and Wong (2000) and was further generalized by Casarin, Craiu, and Leisen (2013).

This article is organized as follows. Section 2 introduces a component-wise multiple-try Metropolis (CMTM) algorithm. In Section 3, we add *adaption* to CMTM, creating a new Adaptive CMTM (henceforth denoted ACMTM) algorithm in which the proposal distributions get modified on the fly according to the local shape of the target distribution, and we prove (Theorem 1) convergence of this algorithm. Section 4 then applies the adaptive CMTM algorithm to numerical examples, and compares the efficiency of the adaptive CMTM algorithm to other adaptive Metropolis algorithms.

2. Component-Wise Multiple-Try Metropolis

2.1. Algorithm

Assume that a Markov chain $\{X_n\}$ is defined on $\mathcal{X} \subset \mathbf{R}^d$ with a target distribution π. The component-wise multiple-try Metropolis (CMTM) will update the chain one-component-at-a-time using m proposals. Specifically, the kth component of the chain is updated using proposals $\{y_j^{(k)} : \ 1 \le j \le m\}$ that are sampled from $\{T_j^{(k)} : \ 1 \le j \le m\}$, respectively. Let the value of the chain at iteration n be $X_n = x \in \mathbf{R}^d$. One step of the CMTM involves updating every coordinate X_k of the chain in a fixed order, for $k \in \{1, \ldots, d\}$. The following steps are performed to update the kth component:

1. Draw proposals $y_1^{(k)}, \ldots, y_m^{(k)}$ where $y_j^{(k)} \sim T_j^{(k)}(\cdot|x_k)$ for all $1 \le j \le m$.

2. Compute

$$w_j^{(k)}(y_j^{(k)}, x) \propto \pi(y_j^{(k)}|x_{[-k]}) T_j(x_k|y_j^{(k)}) \lambda_j^{(k)}(y_j^{(k)}, x_k), \qquad (1)$$

for each $1 \le j \le m$, where $x_{[-k]}$ denotes the state of the chain without the kth component and $\lambda_j^{(k)}(x_k, y_j^{(k)})$ is a nonnegative symmetric function satisfying $\lambda_j^{(k)}(x_k, y_j^{(k)}) > 0$ whenever $T_j^{(k)}(y_j^{(k)}|x_k) > 0$.

3. Select one $y = y_s^{(k)}$ out of $y_1^{(k)}, \ldots, y_m^{(k)}$ with probability proportional to $w_j(y_j^{(k)}, x)$.

4. Draw $x_1^{*(k)}, \ldots, x_{s-1}^{*(k)}, x_{s+1}^{*(k)}, \ldots, x_m^{*(k)}$ where $x_j^{*(k)} \sim T_j^{(k)}(\cdot|y)$ and set $x_s^{*(k)} = x$.

5. Compute

$$w_j^{(k)}(x_j^{*(k)}, y) \propto \pi(x_j^{*(k)}|x_{[-k]}) T_j(y|x_j^{*(k)}) \lambda_j^{(k)}(x_j^{*(k)}, y), \qquad (2)$$

for each $1 \le j \le m$.

6. Accept y with probability

$$\rho = \min\left[1, \frac{w_1(y_1^{(k)}, x) + \cdots + w_m(y_m^{(k)}, x)}{w_1(x_1^{*(k)}, y) + \cdots + w_m(x_m^{*(k)}, y)}\right].$$

We note that in step 1, the proposal distributions $T_j^{(k)}$ depend only on the kth component of the current state of the chain. Throughout the article, we use Gaussian distributions centered at x_k for the proposal distributions $T_j^{(k)}(y_j^{(k)}|x_k)$. More general formulations are possible, but make intuitive adaptive schemes more cumbersome and without clear benefits in terms of efficiency. Having dependent proposals can be beneficial when the proposal distributions are identical (Craiu and Lemieux 2007). However, in the current implementation the proposals have different scales so the advantage of using dependent proposals is less clear and will not be pursued in this article.

Whether a proposal distribution is "good" or not will depend on the current state of the Markov chain, especially if the target distribution π have conditional densities with varying properties, for example, different variances, across the target's support. In addition to choosing the m proposals, an added flexibility of the CMTM algorithm is that we have freedom in choosing the nonnegative symmetric maps $\lambda_j^{(k)}$ as long as they satisfy $\lambda_j^{(k)}(x_k, y_j^{(k)}) > 0$ whenever $T_j^{(k)}(y_j^{(k)}|x_k) > 0$. In subsequent

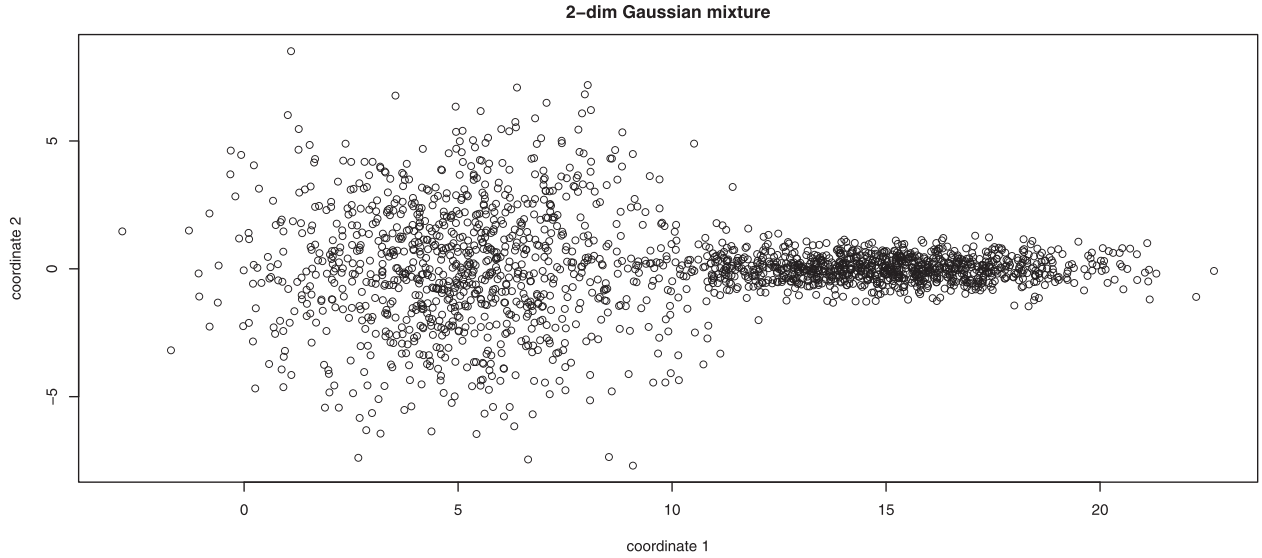

Figure 1. Target density plot. Two-dimensional mixture of two normals.

sections, we show that the CMTM algorithm with Gaussian proposals can benefit from choosing a particular form of the function $\lambda_j^{(k)}(x_k, y_j^{(k)})$.

Our choice of $\lambda_j^{(k)}$ is guided by a simple and intuitive principle. Between two candidate moves $y_1^{(k)}$ and $y_2^{(k)}$ that are equally far from the current state we favor $y_1^{(k)}$ over $y_2^{(k)}$ if $\pi(y_1^{(k)}|x_{[-k]})$ is greater than $\pi(y_2^{(k)}|x_{[-k]})$, but if $\pi(y_1^{(k)}|x_{[-k]})$ is similar to $\pi(y_2^{(k)}|x_{[-k]})$, we would like CMTM to favor whatever candidate is further away from the current state. These simple rules lead us to consider

$$\lambda_j^{(k)}(x, y) = T_j^{(k)}(y_j^{(k)}|x_k)^{-1}\|(y_j^{(k)} - x_k)\|^\alpha, \tag{3}$$

where $\|\cdot\|$ is the Euclidean norm. Note that this choice of $\lambda_j^{(k)}$ is possible because $T_j^{(k)}(y_j^{(k)}|x_k)$ is a symmetric function in x_k and $y_j^{(k)}$ as it involves only one draw from a normal distribution with mean x_k.

Replacing (3) in the weights Equation (1) results in

$$\begin{aligned} w_j^{(k)}(y_j^{(k)}, x) &= \pi(y_j^{(k)}|x_{[-k]})T_j^{(k)}(x_k|y_j^{(k)})\lambda_j^{(k)}(y_j^{(k)}, x_k) \\ &= \pi(y_j^{(k)}|x_{[-k]})\|(y_j^{(k)} - x_k)\|^\alpha. \end{aligned} \tag{4}$$

With this choice of λ, the selection probabilities are only dependent on the value of the target density at the candidate point $y_j^{(k)}$ and the size of the potential jump of the chain, where this candidate accepted. From (3), we can see that the size of α will negotiate the balance between the jump distance from the current state and the weight of the new state under π. However, while we understand the trade-off imposed by the choice of α for selecting a candidate move, it is less clear how it will impact the overall performance of the CMTM, for example, acceptance rate or average (over coordinates and iterations) jump distance.

Therefore, it is paramount to gauge what are good choices for the parameter α for the mixing of the CMTM chain. In the next section, we approach this task via the average squared jumping distance (ASJ) and the autocorrelation time (ACT). To obtain the average squared jumping distance, we calculate the squared jumping distance for each iteration, $(X_{n+1} - X_n)^2 = \sum_{kj=1}^{d}(X_{n+1,k} - X_{n,k})^2$ and average them over the whole Markov chain run. Note that if a new proposal is rejected for the jth coordinate, then $(X_{n+1,k} - X_{n,k})^2$ is equal to zero, so we still add zero to total sum of the squared jumping distances and divide the sum by the total number of iterations. The ACT can be calculated component-wise for the kth coordinate using

$$\tau_k = 1 + 2\sum_{j=1}^{\infty}\rho_{kj},$$

where for the kth coordinate $\rho_{kj} = \text{cov}(X_{0,k}, X_{j,k})/\text{var}(X_{0,k})$ is the autocorrelation at lag j, $1 \le k \le d$. Higher ACT for a Markov chain implies successive samples are highly correlated, which reduces the effective information contained in any given number of samples produced by the chain.

While ACT has long been known to relate directly with the variance of the Monte Carlo estimators (Geyer 1992), the ASJ incorporates both the jump distance and the acceptance rate, a combination that has turned out to be useful in other adaptive MCMC designs (e.g., Craiu, Rosenthal, and Yang 2009). Estimates of ACT and ASJ are obtained by averaging over the coordinates and the realized path of the chain.

2.2. Choice of α

To study the influence of the parameter α on the CMTM efficiency, we have conducted a number of simulation studies, some of which are described here.

We considered first a two-dimensional mixture of two normal distributions

$$0.5N(\mu_1, \Sigma_1) + 0.5N(\mu_2, \Sigma_2), \tag{5}$$

where

$$\begin{aligned} \mu_1 &= (5, 0)^T \\ \mu_2 &= (15, 0)^T \\ \Sigma_1 &= \text{diag}(6.25, 6.25) \\ \Sigma_2 &= \text{diag}(6.25, 0.25). \end{aligned}$$

An iid sample of size 2000 from (5) is plotted in Figure 1. We run the CMTM algorithm repeatedly with $\lambda_j(x, y_j)$ functions

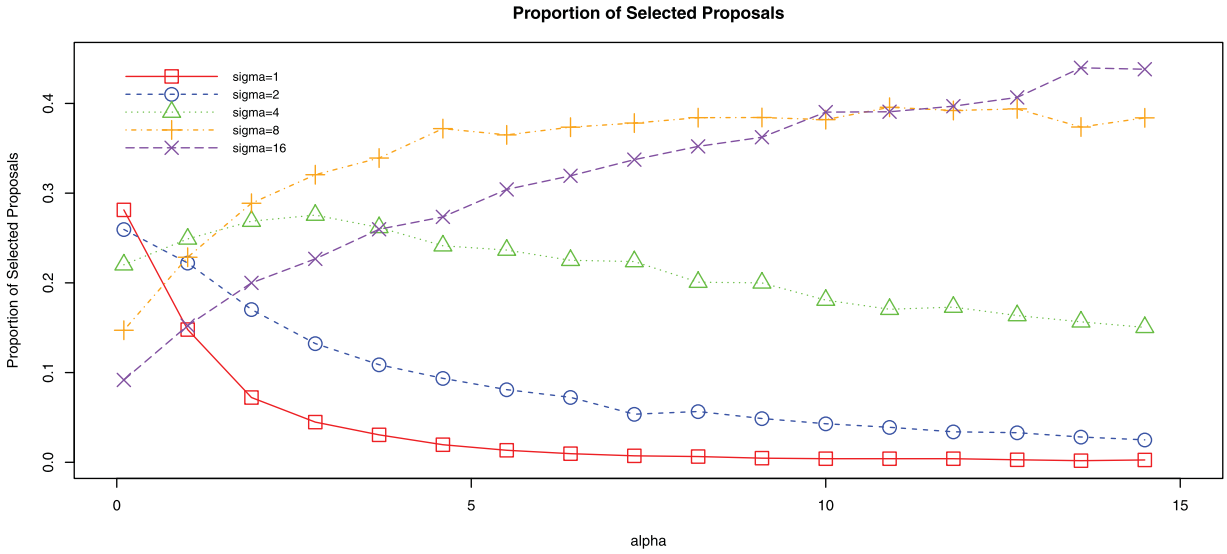

Figure 2. Proportion of proposal distribution selected. Coordinate 1: Red, blue, green, orange, and purple lines show behavior when $\sigma_{k,j} = 1, 2, 4, 8, 16$, respectively.

in (3) while changing the value of α from 0.1 to 15. We choose $m = 5$ as the number of proposals for each component, while the proposal standard deviations $\sigma_{k,j}$'s are for each component 1, 2, 4, 8, and 16. As we see in Figure 2, the proportion of each proposal distribution selected increases/decreases as α changes. As expected, when α increases we see the selection percentages of the proposal distributions with smaller $\sigma_{k,j}$'s drop and those with larger $\sigma_{k,j}$'s increase. Figure 2 shows, with larger α's, our algorithm favors proposal distributions with larger scales, which makes sense based on Equation (4).

Figure 3 shows how the ASJ and ACT change as the value of α changes. We can infer that the highest efficiency is achieved for $\alpha \in (2, 4)$.

We also examined a four-dimensional mixture of two normal distributions as our target density:

$$0.5N(\mu_1, \Sigma_1) + 0.5N(\mu_2, \Sigma_2),$$

where

$$\mu_1 = (5, 5, 0, 0)^T$$
$$\mu_2 = (15, 15, 0, 0)^T$$
$$\Sigma_1 = \text{diag}(6.25, 6.25, 6.25, 0.01)$$
$$\Sigma_2 = \text{diag}(6.25, 6.25, 0.25, 0.01).$$

The number of proposals, $m = 5$ and $\sigma_{k,j}$'s of the set of proposal distributions for each coordinate are 0.5, 1, 2, 4, and 8. Figure 4 shows the results. We notice that the ACT measurements are more noisy, while the ASJ ones yield a more precise message that is in line with the previous example. Once again we can see from Figure 4 that the average squared jumping distances are largest for $\alpha \in (2, 4)$.

Other numerical experiments not reported here agree with the two examples presented and suggest that optimal values of α are between 2 and 4. In the absence of theoretical results, we cannot claim a universal constant α that would be optimal in every

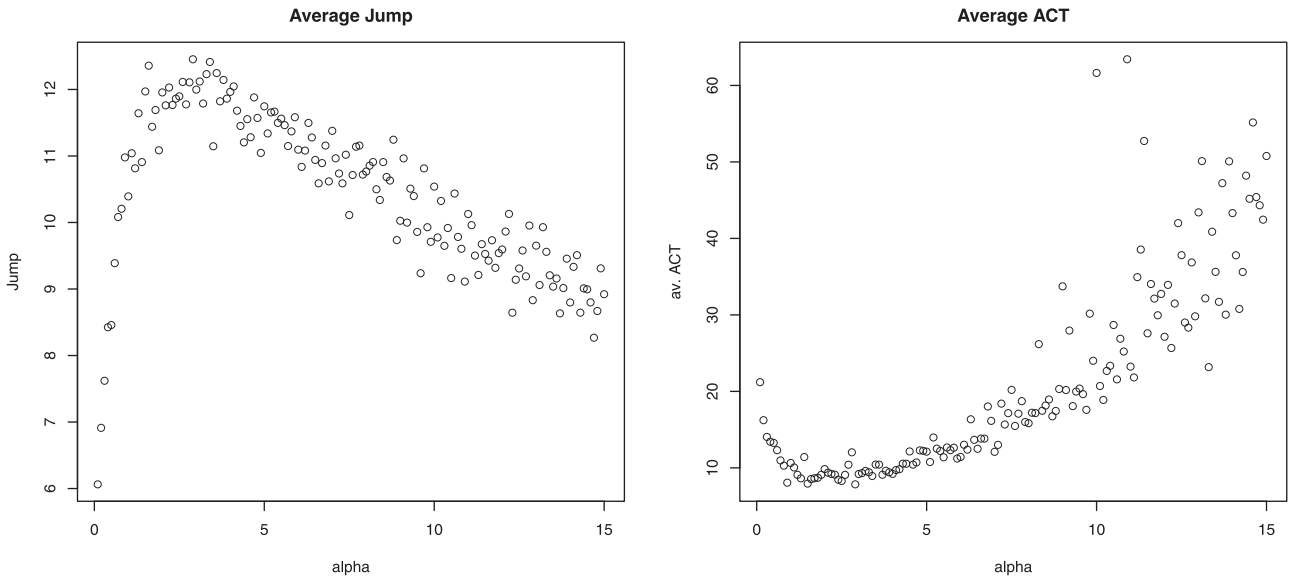

Figure 3. Two-dimensional mixture of two Gaussians: ASJ (left panel) and ACT (right panel) for different values of α. For each α, the estimates are obtained from a single run with 100,000 iterations.

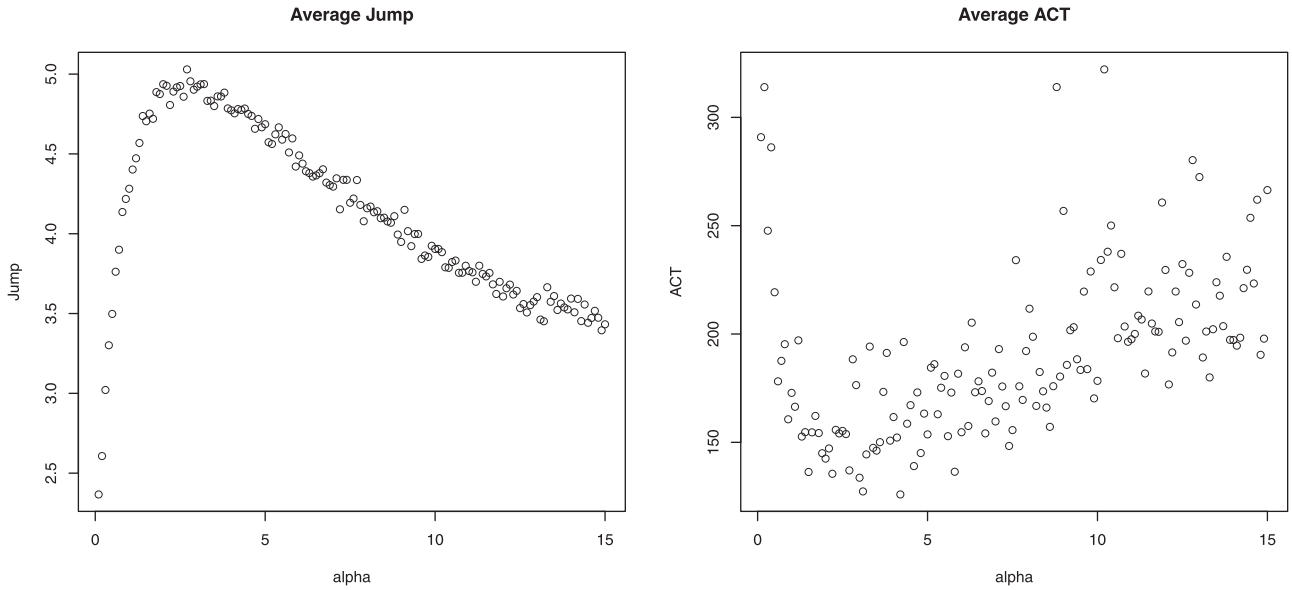

Figure 4. Four-dimensional mixture of two Gaussians: ASJ (left panel) and ACT (right panel) for different values of α. For each α, the estimates are obtained from a single run with 100,000 iterations.

example. However, based on the available evidence, we believe that a value of α in the $(2, 4)$ range will increase the efficiency of the chain. Henceforth, we fix $\alpha = 2.9$ in all simulations involving CMTM.

3. Adaptive Component-Wise Multiple-Try Metropolis

3.1. CMTM Favors Component-Wise "Better" Proposal Distributions

The intuition behind our construction as described in the introduction, relies on the idea that CMTM will automatically tend to choose the "right" proposal among the m possible ones. In this section, we verify empirically that this is indeed the case.

We consider the same four-dimensional mixture of normal distributions from Section 2.2 as our target distribution and run the CMTM algorithm. The target parameters are set to reflect the numerical experiments reported in Section 4, that is, $m = 20$ and $\sigma_{k,j} = 2^j$ with $j \in \{-10, -9, \ldots, 9\}$. Table 1 reports the selection probabilities computed from 10,000 samples for each proposal and each coordinate.

Tables 2(a) and 2(b) present the proportion of candidate selection and acceptance rates for each proposal. We compare the proportion of proposals selected in the regions $A_1 = \{X \in \mathbf{R}^4 : X_2 < 8\}$ and $A_2 = \{X \in \mathbf{R}^4 : X_2 \geq 8\}$. While these regions are defined based on knowing the target exactly, they do not enter in any way in the design of the CMTM and are used here only to verify that the sampler indeed automatically adapts to local characteristics of the target. We can see that the CMTM favors proposal distributions with smaller $\sigma_{k,j}$'s when updating the third coordinate in the region A_2. This is appropriate given that in that region larger moves for the third coordinate will tend to be rejected. This pattern does not hold for the first two coordinates for which larger moves are appropriate throughout the sample space. This is in line with what is expected since the target variances $(= 6.25)$ are the same in both directions in that region and confirms that the CMTM algorithm tends to choose the "better" proposal distribution out of the available choices provided at each iteration.

3.2. Comparison with a Mixture Transition Kernel

An astute reader may wonder about a different strategy for using the different proposals that one may have at one's disposal. Maybe the most natural alternative is a random mixture of the component-wise Metropolis–Hastings (CMH) algorithms. The set of proposal distributions used in both algorithms is the same and we assign equal weights for the proposal distributions in the mixture. The mixture CMH kernel selects each proposal at random with equal probability, but since a single proposal is produced each time a coordinate is updated, it is different than a CMTM algorithm with equal weights w_j.

Table 1. CMTM: Frequency of selection for each proposal and each coordinate.

	Coordinate			
$\sigma_{k,j}$	coord1	coord2	coord3	coord4
2^{-10}	0.00	0.00	0.00	0.00
2^{-9}	0.00	0.00	0.00	0.00
2^{-8}	0.00	0.00	0.00	0.00
2^{-7}	0.00	0.00	0.00	0.00
2^{-6}	0.00	0.00	0.00	0.00
2^{-5}	0.00	0.00	0.00	0.03
2^{-4}	0.00	0.00	0.00	0.11
2^{-3}	0.00	0.00	0.01	0.25
2^{-2}	0.00	0.00	0.03	0.27
2^{-1}	0.01	0.01	0.11	0.17
2^{0}	0.05	0.05	0.15	0.08
2^{1}	0.15	0.14	0.19	0.04
2^{2}	0.26	0.26	0.20	0.02
2^{3}	0.24	0.25	0.15	0.01
2^{4}	0.14	0.14	0.08	0.01
2^{5}	0.08	0.07	0.04	0.00
2^{6}	0.04	0.04	0.02	0.00
2^{7}	0.02	0.02	0.01	0.00
2^{8}	0.01	0.01	0.01	0.00
2^{9}	0.00	0.00	0.00	0.00

Table 2. Selection frequencies for each proposal and each coordinate calculated on two regions of the support, $A_1 = \{X \in \mathbf{R}^4 : X_2 < 8\}$ (left table) and $A_2 = \{X \in \mathbf{R}^4 : X_2 \geq 8\}$ (right table). The entries in boldface show the difference in selection frequencies for some of the proposals in the two regions of the support considered.

(a) $A_1 = \{X \in \mathbf{R}^4 : X_2 < 8\}$

	Coordinate			
$\sigma_{k,j}$	coord1	coord2	coord3	coord4
2^{-10}	0.00	0.00	0.00	0.00
2^{-9}	0.00	0.00	0.00	0.00
2^{-8}	0.00	0.00	0.00	0.00
2^{-7}	0.00	0.00	0.00	0.00
2^{-6}	0.00	0.00	0.00	0.01
2^{-5}	0.00	0.00	0.00	0.03
2^{-4}	0.00	0.00	0.00	0.10
2^{-3}	0.00	0.00	0.00	0.25
2^{-2}	0.00	0.00	**0.00**	0.27
2^{-1}	0.01	0.01	**0.01**	0.18
2^{0}	0.05	0.05	**0.04**	0.09
2^{1}	0.16	0.14	**0.17**	0.04
2^{2}	0.27	0.26	**0.28**	0.02
2^{3}	0.24	0.25	**0.23**	0.01
2^{4}	0.13	0.14	**0.13**	0.01
2^{5}	0.07	0.08	0.07	0.00
2^{6}	0.03	0.04	0.03	0.00
2^{7}	0.02	0.02	0.01	0.00
2^{8}	0.01	0.00	0.01	0.00
2^{9}	0.00	0.00	0.01	0.00

(b) $A_2 = \{X \in \mathbf{R}^4 : X_2 \geq 8\}$

	Coordinate			
$\sigma_{k,j}$	coord1	coord2	coord3	coord4
2^{-10}	0.00	0.00	0.00	0.00
2^{-9}	0.00	0.00	0.00	0.00
2^{-8}	0.00	0.00	0.00	0.00
2^{-7}	0.00	0.00	0.00	0.00
2^{-6}	0.00	0.00	0.00	0.00
2^{-5}	0.00	0.00	0.00	0.04
2^{-4}	0.00	0.00	0.00	0.12
2^{-3}	0.00	0.00	0.02	0.24
2^{-2}	0.00	0.00	**0.06**	0.26
2^{-1}	0.01	0.01	**0.20**	0.17
2^{0}	0.05	0.06	**0.24**	0.08
2^{1}	0.14	0.14	**0.20**	0.04
2^{2}	0.26	0.26	**0.13**	0.02
2^{3}	0.24	0.25	**0.08**	0.01
2^{4}	0.14	0.14	**0.03**	0.00
2^{5}	0.09	0.07	0.02	0.00
2^{6}	0.04	0.04	0.01	0.00
2^{7}	0.02	0.02	0.01	0.00
2^{8}	0.01	0.01	0.00	0.00
2^{9}	0.00	0.00	0.00	0.00

However, this comparison will help us determine whether adjusting the selection probabilities of each proposal distribution is an improvement over equal probability selection. Our target distribution is the four-dimensional mixture of two normals introduced in Section 2.2 We use $m = 20$ and the same proposal scales discussed in the previous section. In Tables 3(a) and 3(b), we present the acceptance rates for each coordinate and each proposal for the two samplers. The results in Table 3 suggest that proposal distributions with small variances have their proposals, if selected, accepted with high frequency. In the case of mixture of CMH this also means that if we were to guide our selection of proposals based on acceptance rates, we would favor small jumps. The selection step in the CMTM yields more even acceptance probabilities across proposals. This leads us to believe that the acceptance rates are not very informative about which variances are preferable in each coordinate.

To compare the efficiency of the two algorithms, we report in Table 4 the ASJ and ACT calculated from 100 replicated runs as well as the CPU time. We note that the average squared jumping distance significantly improves with the CMTM compared to the mixture CMH. We can also see that for all the chain's coordinates the ACT is an order of magnitude smaller for the CMTM

Table 3. Postselection acceptance frequencies. The NA's in the table are because some proposals are never selected for some of the coordinates.

(a) Mixture of CMH

	Coordinate			
$\sigma_{k,j}$	coord1	coord2	coord3	coord4
2^{-10}	1.00	1.00	1.00	1.00
2^{-9}	1.00	1.00	1.00	0.99
2^{-8}	1.00	1.00	1.00	0.98
2^{-7}	0.99	1.00	1.00	0.98
2^{-6}	1.00	1.00	0.99	0.93
2^{-5}	0.99	1.00	1.00	0.90
2^{-4}	0.99	0.99	0.98	0.78
2^{-3}	0.99	0.97	0.96	0.65
2^{-2}	0.97	0.95	0.97	0.39
2^{-1}	0.91	0.94	0.88	0.23
2^{0}	0.88	0.87	0.77	0.11
2^{1}	0.76	0.76	0.63	0.06
2^{2}	0.58	0.58	0.43	0.04
2^{3}	0.39	0.36	0.26	0.01
2^{4}	0.21	0.21	0.19	0.01
2^{5}	0.11	0.12	0.11	0.00
2^{6}	0.05	0.05	0.04	0.00
2^{7}	0.02	0.04	0.02	0.00
2^{8}	0.02	0.00	0.01	0.00
2^{9}	0.01	0.01	0.00	0.00

(b) CMTM

	Coordinate			
$\sigma_{k,j}$	coord1	coord2	coord3	coord4
2^{-10}	NaN	NaN	NaN	NaN
2^{-9}	NaN	NaN	NaN	NaN
2^{-8}	NaN	NaN	NaN	NaN
2^{-7}	NaN	NaN	NaN	0.17
2^{-6}	NaN	NaN	NaN	0.52
2^{-5}	NaN	NaN	1.00	0.44
2^{-4}	0.50	NaN	0.50	0.52
2^{-3}	0.00	0.00	0.42	0.50
2^{-2}	0.17	0.43	0.53	0.47
2^{-1}	0.49	0.38	0.58	0.47
2^{0}	0.54	0.45	0.49	0.44
2^{1}	0.57	0.52	0.52	0.45
2^{2}	0.51	0.49	0.49	0.37
2^{3}	0.48	0.45	0.47	0.41
2^{4}	0.46	0.45	0.48	0.33
2^{5}	0.41	0.48	0.48	0.33
2^{6}	0.40	0.35	0.50	0.43
2^{7}	0.45	0.31	0.45	0.38
2^{8}	0.47	0.24	0.35	0.00
2^{9}	0.33	0.45	0.61	NaN

Table 4. Comparison of performance indicators that were computed from 100 independently replicated runs. The tables contain statistics about the execution time for a complete run (cputime), the average squared jump distance, and the ACT. For CMTM, two cputimes are shown: fast ("vectorized") and slow (no "vectorization" for likelihood evaluations is used).

(a) Mixture of CMH				
	Min.	Median	Mean	Max.
cputime(s)	4.47	4.56	4.57	4.97
sq. jump	0.467	0.619	0.622	0.784
	coord1	coord2	coord3	coord4
ACT	464.21	460.41	28.07	26.70
(b) CMTM				
	Min.	Median	Mean	Max.
cputime(s)-fast	10.25	10.41	10.43	11.22
cputime(s)-slow	140.11	142.30	142.58	153.79
sq. jump	6.20	6.62	6.62	7.07
	coord1	coord2	coord3	coord4
ACT	41.96	41.25	1.64	1.64

than the mixture CMH. When programming the examples in this article, we were able to take advantage of the R software's efficient handling of vector operations (the programs used are included in the online supplementary materials for the article). This explain the small difference in CPU time even as CMTM requires m times more evaluations of the target than the mixture CMH.

3.3. The Adaptive CMTM Algorithm (ACMTM)

Given its propensity to choose a good candidate among those put forward by the proposal distributions, it is reasonable to infer that CMTM's performance will be roughly aligned with the most suitable proposal for the region of the state–space currently visited by the chain. The other side of the coin is that a whole set of bad proposals will compromise the efficiency of the CMTM algorithm. Therefore, we focus our efforts in developing an adaptive CMTM (ACMTM) design that aims to minimize, possibly annihilate, the chance of having at our disposal only poorly calibrated proposal distributions in any region of the space.

The adaptation strategy is centered on finding well-calibrated values for the set $S_k = \{\sigma_{k,j} : 1 \le j \le m\}$ for every coordinate $1 \le k \le d$. Note that S_k varies across coordinates.

Consider an arbitrarily fixed coordinate k and suppose we label the m proposal distributions such that $\sigma_{k,1} < \sigma_{k,2} < \cdots < \sigma_{k,m}$. Changes in the kernel occur at fixed points in the simulation process, called *adaption points*. We want our adaptive algorithm to adapt less and less as the simulation proceeds, a condition known as *diminishing adaptation (DA)* and long recognized as being useful for establishing the chain's valid asymptotic behavior (Roberts and Rosenthal 2007). However, the adaption strategy proposed above may not diminish in the long run, so we ensure the DA condition more directly by only adapting on ath iteration (for $a \ge 1$) with probability $P_a = \max(0.99^{a-1}, \frac{1}{\sqrt{a}})$. Since $P_a \to 0$, the DA condition is ensured. On the other hand, we chose P_a so that it decreases slowly and has high values at the beginning of the run when most adaptations will take place. Furthermore, the Borel–Cantelli lemma guarantees that the adaption will keep occurring for as long as we run the chain since $\sum_{a=1}^{\infty} P_a = \infty$. For instance, in 10,000 iterations we have recorded between 60 and 70 adaptation attempts, a quarter of which occurred within the first 2000 iterations. An adaption is performed only if the selection frequencies are anomalous, as detailed below.

Specifically, an adaption is required for the standard deviations $\sigma_{k,j}$ only if we notice that the candidates generated by the proposal distribution $T_j^{(k)}$ with the smallest scale, $\sigma_{k,1}$, or the largest one, $\sigma_{k,m}$, are under- or over-selected. For instance, suppose that in an interadaptation time interval the candidates generated using $\sigma_{k,1}$ are selected more than $100 \times \frac{2}{m}\%$ or less than $100 \times \frac{1}{2m}\%$ of the time. If we denote q_j the frequency of selecting the candidate generated using $\sigma_{k,j}$, we have $m \max q_j \ge \sum_j q_j = 1 \ge m \min q_j$. Thus, the thresholds represent, respectively, more than double the selection percentage for the least selected proposal and less than half of the selection percentage for the most popular proposal. A high selection percentage for $\sigma_{k,1}$ suggests that the chain tends to favor, when updating the kth coordinate, proposals with smaller scale so the ACMTM design requires to: (1) halve the value of $\sigma_{k,1}$; (2) recalculate the intermediate values, $\sigma_{k,2}, \ldots, \sigma_{k,m-1}$ to be equidistant between $\sigma_{k,1}$ and $\sigma_{k,m}$ on the log-scale. A low selection percentage for $\sigma_{k,1}$ will ensure that the lowest scale is doubled up followed by step (2).

Similarly, if the largest element in S_k, $\sigma_{k,m}$, produces proposals with selection percentages above or below the thresholds mentioned above, we will double or halve $\sigma_{k,m}$, respectively. Each modification is followed by redistribution of the intermediate scales.

If neither the smallest nor the largest elements in S_k produce proposals that are outside the boundaries set by the two thresholds, we wait until the algorithm reaches the next "adaption point" and recalculate the proportion of each proposal candidate being selected during the last interadaption time interval.

Let us denote by m the number of multiple-try proposals, d the number of coordinates for the Markov chain, β the length of interadaptation period, P_a the probability to at each attempt, and M the number of MCMC iterations. With these notations we lay out the rules for the ACMTM update in Algorithm 1.

Finally, we make two minor technical modifications to our ACMTM algorithm, to ensure the Containment condition of Roberts and Rosenthal (2007), and thus allow us to prove the convergence of our algorithm in Section 3.5. Namely:

(A1)We choose a (very large) nonempty compact subset $K \subset \mathcal{X}$, and force $X_n \in K$ for all n. Specifically, we reject all proposals $Y_{n+1} \notin K$ (but if $Y_{n+1} \in K$, then we still accept/reject Y_{n+1} by the usual rule for the CMTM algorithm described in Section 2.1). Correspondingly, the initial value X_0 should be chosen in K.

(A2)We choose a (very large) constant $L > 0$ and a (very small) constant $\epsilon > 0$, and force the proposal scalings $\sigma_{k,j}$ to always be in $[\epsilon, L]$. Specifically, if $\sigma_{n,k,j}$ is the value of $\sigma_{k,j}$ used at the nth iteration in our adaptive CMTM algorithm, then if $\sigma_{n,k,j}$ would be greater than L, we instead set $\sigma_{n,k,j} = L$, while if $\sigma_{n,k,j}$ would be less than ϵ, we instead set $\sigma_{n,k,j} = \epsilon$. Correspondingly, the initial values $\sigma_{0,k,j}$ should all be chosen in $[\epsilon, L]$.

Remark 1. Our adaptive algorithm keeps the number of different proposals at each iteration fixed at some constant m. We have also experimented with allowing the value m itself to be updated adaptively. This strategy did not outperform the algorithms with fixed $m = 20$ design in any of the experiments conducted, so we

Algorithm 1 Adaption Rules for ACMTM

Given: $\{\sigma_{k,j} : 1 \le k \le d, 1 \le j \le m\}$ - initial proposal variances
Set initial values $\beta = 100$, $P_a = 1$
for $t = 1$ to M **do**
  if $t = 0 \mod \beta$ **then**
    Let $a = t/\beta$ and $u \sim u[0, 1]$
    if $u \le P_a$ **then**
      Let $\sigma_{k,j} \le \cdots \le \sigma_{k,m}$ be the scales used and $\{S_{k,j} : 1 \le k \le d, 1 \le j \le m\}$ be the selection rates computed since the previous adaptation till now. Then
      for $k = 1$ to d **do**
        if $S_{k,m} > 2/m$ **then**
          $\sigma_{k,m} = 2\sigma_{k,m}$
          Adjust $\{\sigma_{k,j}\}$ so that they are equidistant on log base 2 scale.
        else if $(S_{k,m} < 1/(2m)) \wedge (\sigma_{k,1} < \sigma_{k,m}/2)$ **then**
          $\sigma_{k,m} = \sigma_{k,m}/2$
          Adjust $\{\sigma_{k,j}\}$ so that they are equidistant on log base 2 scale.
        end if
        if $S_{k,1} > 2/m$ **then**
          $\sigma_{k,1} = \sigma_{k,1}/2$
          Adjust $\{\sigma_{k,j}\}$ so that they are equidistant on log base 2 scale.
        else if $(S_{k,1} < 1/(2m)) \wedge (2\sigma_{k,1} < \sigma_{k,m})$ **then**
          $\sigma_{k,1} = 2\sigma_{k,1}$
          Adjust $\{\sigma_{k,j}\}$ so that they are equidistant on log base 2 scale.
        end if
      end for
    end if
    $P_a = \max(0.99^{a-1}, \frac{1}{\sqrt{a}})$
  end if
  Perform CMTM update as described in Section 2
end for

do not pursue it further here. However, our theoretical justification also covers this case as long as the possible m values are bounded; see the remark following the proof of Theorem 1.

3.4. To Adapt or Not To Adapt?

We compare the ACMTM algorithm with the CMTM algorithm without adaption to see if the adaption indeed improves the efficiency of the algorithm. We use the four-dimensional mixture of two normal distributions from Section 2.2 as our target distribution. The $\sigma_{k,j}$'s for the nonadaptive algorithm are those given in Section 3.1 and they are also the starting $\sigma_{k,j}$'s for the adaptive algorithm. Evidently, the final values are the same as the initial ones for the nonadaptive version of the sampler. In Table 5, we report the final values of the $\sigma_{k,j}$'s obtained after the last adaption in one random run of ACMTM. For this particular run, the last adaption occurred right after 1800 iterations out of 10,000 iterations in total. We notice that the scales chosen vary from component to component. For instance, the fourth component of the chain has a smaller marginal variance so the adaption will favor smaller scales. Similarly, the third component requires both large and small proposal scales and we can see that reflected in the range of values for $\{\sigma_{3,j};\ 1 \le j \le m\}$ which is different than for the first two components.

Table 5. Adaptive CMTM: Final $\sigma_{k,j}$ for each coordinate and each proposal used.

	coord1	coord2	coord3	coord4
prop1	4.0000	4.0000	2.0000	0.1250
prop2	4.1486	4.1486	2.0743	0.1345
prop3	4.3028	4.3028	2.1514	0.1446
prop4	4.4626	4.4626	2.2313	0.1556
prop5	4.6284	4.6284	2.3142	0.1674
prop6	4.8004	4.8004	2.4002	0.1800
prop7	4.9788	4.9788	2.4894	0.1937
prop8	5.1638	5.1638	2.5819	0.2083
prop9	5.3556	5.3556	2.6778	0.2241
prop10	5.5546	5.5546	2.7773	0.2410
prop11	5.7610	5.7610	2.8805	0.2593
prop12	5.9750	5.9750	2.9875	0.2789
prop13	6.1970	6.1970	3.0985	0.3000
prop14	6.4273	6.4273	3.2136	0.3227
prop15	6.6661	6.6661	3.3330	0.3472
prop16	6.9138	6.9138	3.4569	0.3734
prop17	7.1707	7.1707	3.5853	0.4017
prop18	7.4371	7.4371	3.7185	0.4321
prop19	7.7134	7.7134	3.8567	0.4648
prop20	8.0000	8.0000	4.0000	0.5000

The comparison in terms of ASJ and ACT is based on 100 independent replicates. The results shown in Table 6 indeed confirm the benefits of adaptation, as both ASJ and ACT are in agreement regarding the superiority of ACMTM over CMTM.

When comparing the rate of selection for each proposal, as reported in Tables 1 and 7, we observe the almost constant selection probabilities for the ACMTM which suggests that all the proposal scales selected are important in the simulation. Finally, we also compare the acceptance frequencies for the selected proposals for CMTM and ACMTM, as shown in Tables 3(b) and 8, respectively. The adaptive version of the algorithm clearly makes better use of the generated proposals. There are no longer any NA's, that is, all proposals are occasionally accepted in each coordinate. In fact, the acceptance rates for ACMTM are quite even, again suggesting a balanced use of the proposal distributions. In almost every instance, the acceptance rates have gone up compared to the CMTM values in Table 3(b).

Table 6. Comparison of performance indicators that were computed from 100 independently replicated runs. The tables contain statistics about the execution time for a complete run (cputime), the average squared jump distance, and the ACT.

(a) Nonadaptive CMTM

	Min.	Median	Mean	Max.
cputime(s)	10.25	10.41	10.43	11.22
sq. jump	6.20	6.62	6.62	7.07
	coord1	coord2	coord3	coord4
ACT	41.96	41.25	1.64	1.64

(b) Adaptive CMTM

	Min.	Median	Mean	Max.
cputime(s)	10.42	10.57	10.65	13.14
sq. jump	8.88	10.15	10.04	10.76
	coord1	coord2	coord3	coord4
ACT	22.55	22.46	1.43	1.00

Table 7. Adaptive CMTM: Rate of selection for each proposal and each coordinate.

	coord1	coord2	coord3	coord4
prop1	0.04	0.05	0.05	0.04
prop2	0.05	0.05	0.05	0.05
prop3	0.05	0.05	0.05	0.05
prop4	0.05	0.04	0.05	0.05
prop5	0.05	0.05	0.05	0.05
prop6	0.05	0.05	0.05	0.05
prop7	0.05	0.05	0.05	0.04
prop8	0.05	0.05	0.05	0.05
prop9	0.05	0.05	0.05	0.06
prop10	0.05	0.05	0.05	0.05
prop11	0.05	0.05	0.04	0.05
prop12	0.05	0.05	0.05	0.05
prop13	0.05	0.05	0.05	0.06
prop14	0.05	0.05	0.05	0.05
prop15	0.05	0.05	0.05	0.05
prop16	0.05	0.05	0.05	0.05
prop17	0.05	0.05	0.05	0.05
prop18	0.05	0.05	0.05	0.04
prop19	0.05	0.05	0.05	0.04
prop20	0.05	0.05	0.05	0.04

3.5. Convergence of Adaptive CMTM

We prove below the convergence of the adaptive CMTM algorithm described in Section 3.3 As explained in Section 3.3, Diminishing Adaptation condition holds by the construction of the adaption mechanism.

Theorem 1. Consider the adaptive CMTM algorithm in Section 3.3 to sample from state–space $\mathcal{X}$ that is an open subset of $\mathbf{R}^d$ for some $d \in \mathbf{N}$. Let π be a target probability distribution, which has a continuous positive density on K with respect to the Lebesgue measure. Then, the adaptive CMTM algorithm converges to stationarity as in

$$\lim_{n\to\infty} \sup_{A\in\mathcal{F}} |\mathbf{P}(X_n \in A) - \pi(A)| = 0. \tag{6}$$

Proof. By Roberts and Rosenthal (2007), the convergence of an adaptive MCMC algorithm as in (6) can be ensured by two conditions diminishing adaptation and containment. Our algorithm satisfies diminishing adaptation (DA) as explained in Section 3.3 So, it suffices to show that our algorithm satisfies the containment condition.

The containment condition of Roberts and Rosenthal (2007) (see also Craiu et al. 2015; Rosenthal and Yang 2016) states that the process's convergence times are bounded in probability, that is, that $\{M_\epsilon(X_n, \Gamma_n)\}_{n=1}^\infty$ is bounded in probability, where $M_\epsilon(x, \gamma) := \inf\{n \geq 1 : \|P_\gamma^n(x, \cdot) - \pi(\cdot)\| \leq \epsilon\}$ for all $\epsilon > 0$, and P_γ^n is a fixed n-step proposal kernel.

We proceed similarly to the proof of Proposition 23 of Craiu et al. (2015). By our assumption (A1), the process $\{X_n\}$ is bounded in probability, in fact $\|X_n\| \leq L$ for all n. To continue, we let $\mathcal{Y}$ be the collection of all $d \times m$ matrices of real numbers in $[\epsilon, L]$. Then by our assumption (A2), $\mathcal{Y}$ is compact. Here each $\gamma \in \mathcal{Y}$ corresponds to a particular choice of MTM proposals, where $\gamma_{k,j}$ equals the scaling of the jth proposal kernel for the kth coordinate. And, our adaption rule is such that choosing which $\gamma \in \mathcal{Y}$ to use for each iteration n is determined by the past and/or current information obtained from the chain.

Next, let P_γ be the Markov kernel corresponding to one full sequence of updates for all coordinates of the chain, in sequence. Then P_γ is Harris ergodic to π, since it is known that any *non*adaptive CMTM algorithm must converge to π (see Liu, Liang, and Wong 2000; Casarin, Craiu, and Leisen 2013). It follows that $\Delta(x, \gamma, n) := \|P_\gamma^n(x, \cdot) - \pi(\cdot)\| \to 0$ as $n \to \infty$ for each (x, γ), where $\|\cdots\|$ is the usual total variation distance convergence metric. Now, with our algorithm as set up in Section 3.3, $\Delta(x, \gamma, n)$ is a continuous function of (x, γ): indeed, it is a composition of single-coordinate MTM updates each of which is continuous as in the proof of Corollary 11 of Roberts and Rosenthal (2007).

To finish, we note (following Rosenthal and Yang 2016) that by Dini's theorem,

$$\lim_{n\to\infty} \sup_{x\in\mathcal{C}} \sup_{\gamma\in\mathcal{Y}} \Delta(x, \gamma, n) = 0$$

for any compact set $\mathcal{C} \subset \mathcal{X}$. Hence, for any $\epsilon > 0$, there is $D < \infty$ such that $\sup_{x\in\mathcal{C}} \sup_{\gamma\in\mathcal{Y}} \Delta(x, \gamma, D) < \epsilon$. It follows that $\sup_{x\in\mathcal{C}} \sup_{\gamma\in\mathcal{Y}} M_\epsilon(x, \gamma) \leq D < \infty$. In particular, choosing $C = K$ from our assumption (A1), we know that $P(X_n \notin K) = 0$ for all n, so if $D := \sup_{x\in K} \sup_{\gamma\in\mathcal{Y}} M_\epsilon(x, \gamma)$, then for any $\delta > 0$, $P(M_\epsilon(X_n, \Gamma_n) > D) = 0 \leq \delta$ for all n. In particular, $\{M_\epsilon(X_n, \Gamma_n)\}_{n=1}^\infty$ is bounded in probability. Therefore, the Containment condition holds, thus finishing the proof. □

Remark 2. Our theorem is still valid if the number of proposals m is allowed to change from iteration to iteration, provided m is forced to remain between 1 and some large finite upper bound M. Indeed, in that case $\mathcal{Y}$ is a discrete union of M different collections of $d \times m$ matrices, and $\Delta(x, \gamma, n)$ is continuous separately on each collection, and the rest of the proof can then proceed without further change.

Table 8. ACMTM: Postselection acceptance probabilities for each proposal.

	coord1	coord2	coord3	coord4
prop1	0.58	0.66	0.49	0.60
prop2	0.57	0.58	0.58	0.60
prop3	0.60	0.65	0.62	0.60
prop4	0.63	0.55	0.59	0.60
prop5	0.61	0.59	0.58	0.65
prop6	0.65	0.53	0.60	0.60
prop7	0.59	0.59	0.60	0.62
prop8	0.64	0.65	0.58	0.60
prop9	0.58	0.57	0.59	0.60
prop10	0.57	0.61	0.60	0.56
prop11	0.61	0.66	0.59	0.54
prop12	0.57	0.54	0.62	0.66
prop13	0.53	0.54	0.66	0.60
prop14	0.55	0.58	0.57	0.61
prop15	0.61	0.60	0.58	0.55
prop16	0.58	0.61	0.60	0.60
prop17	0.54	0.65	0.61	0.57
prop18	0.58	0.61	0.58	0.53
prop19	0.56	0.56	0.62	0.60
prop20	0.61	0.63	0.66	0.59

4. Applications

In the following examples, we compare the CMTM and ACMTM started with the same set of $\sigma_{k,j}$. We also compare their performance with CMH and adaptive CMH. The design of the latter is based on the theoretical results of Gelman, Roberts, and Gilks (1996) and Roberts and Rosenthal (2001) who found

Table 9. Dyestuff batch yield (in grams).

Batch 1	1545	1440	1440	1520	1580
Batch 2	1540	1555	1490	1560	1495
Batch 3	1595	1550	1605	1510	1560
Batch 4	1445	1440	1595	1465	1545
Batch 5	1595	1630	1515	1635	1625
Batch 6	1520	1455	1450	1480	1445

that the optimal acceptance rate for one-dimensional Metropolis algorithm is 0.44 and therefore adjusts the proposal variance to get an acceptance rate close to this value for each coordinate.

First, we compare CMTM (with different number of proposals m) with CMH, both with generic proposals. For CMTM with m proposals, we set $\sigma_{k,j} = 2^{j-1-\lfloor m/2 \rfloor}$ for each coordinate $1 \le j \le m$. The CMH's proposals are fixed at 1 for each coordinate.

In second comparisons, we compare adaptive CMTM with different number of proposals and adaptive CMH. The starting σ's are identical to the ones used in their nonadaptive counterparts.

For all the examples, we use the effective sample size (ESS) and ESS/CPUtime (CPUtime is the time needed to complete the simulation) to compare the efficiency of MCMC algorithms. The latter is particularly relevant for algorithm comparison since it is a way to quantify the resource allocation efficiency. Since $\text{ESS} = M/\tau$, where M is the number of samples obtained from a Markov chain and τ is the ACT, one can see that ESS is equivalent to ACT. One may intuitively interpret ESS the number of iid

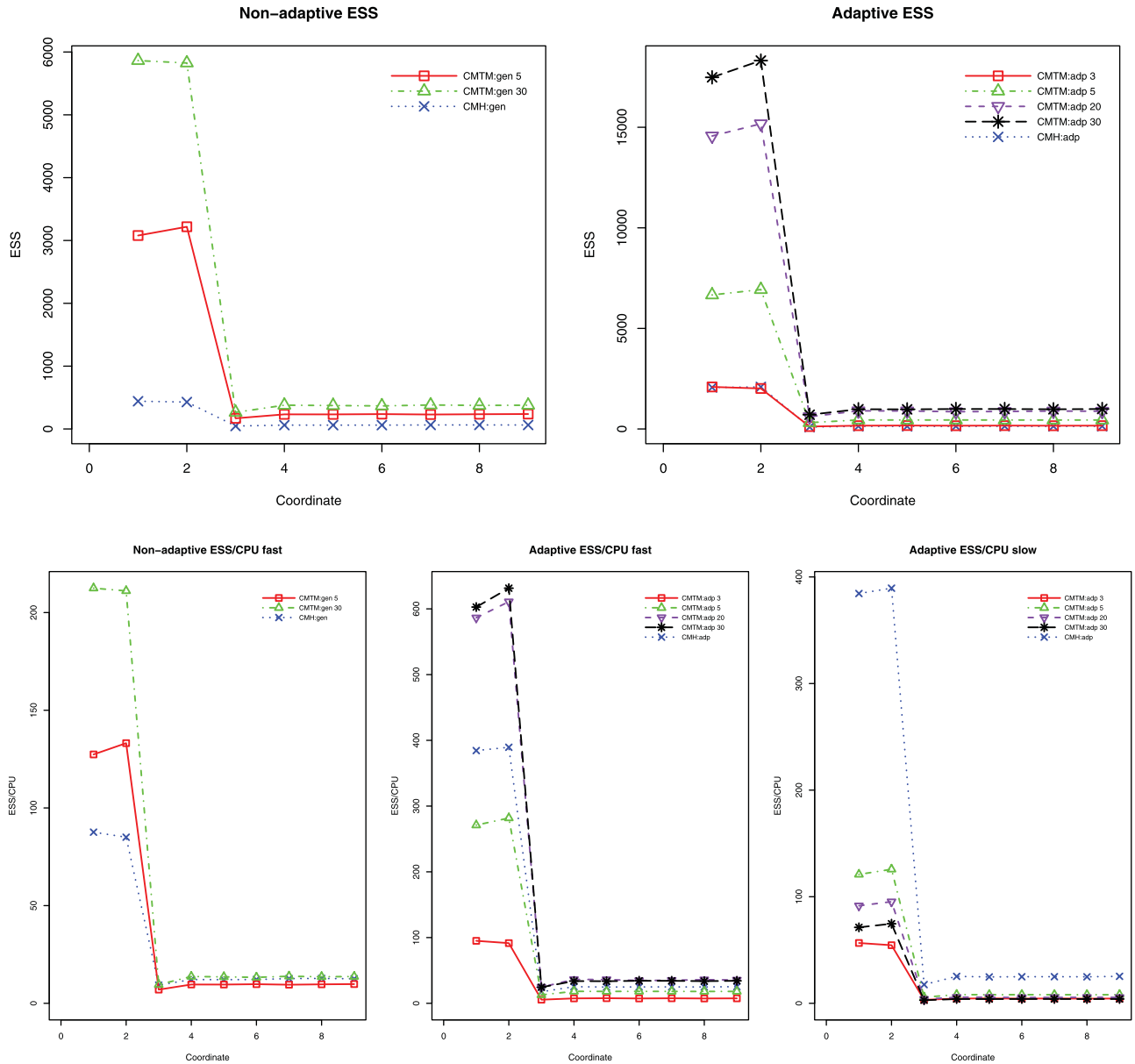

Figure 5. Variance components model. For nonadaptive samplers, we compare CMTM with 5 and 30 generic proposals and CMH represented by red, green, and blue lines, respectively. For adaptive samplers, we compare between ACMTM with 3, 5, 20, or 30 proposals and the adaptive CMH represented by red, green, purple, black, and blue lines, respectively. Top row: Comparison of ESS for nonadaptive (left panel) and adaptive (right panel) samplers. Bottom row: Comparison of ESS/CPU for nonadaptive samplers (left panel) using "vectorized operations" for likelihood evaluations in CMTM, ESS/CPU for adaptive samplers with "vectorized operations" (middle panel), and without (right panel).

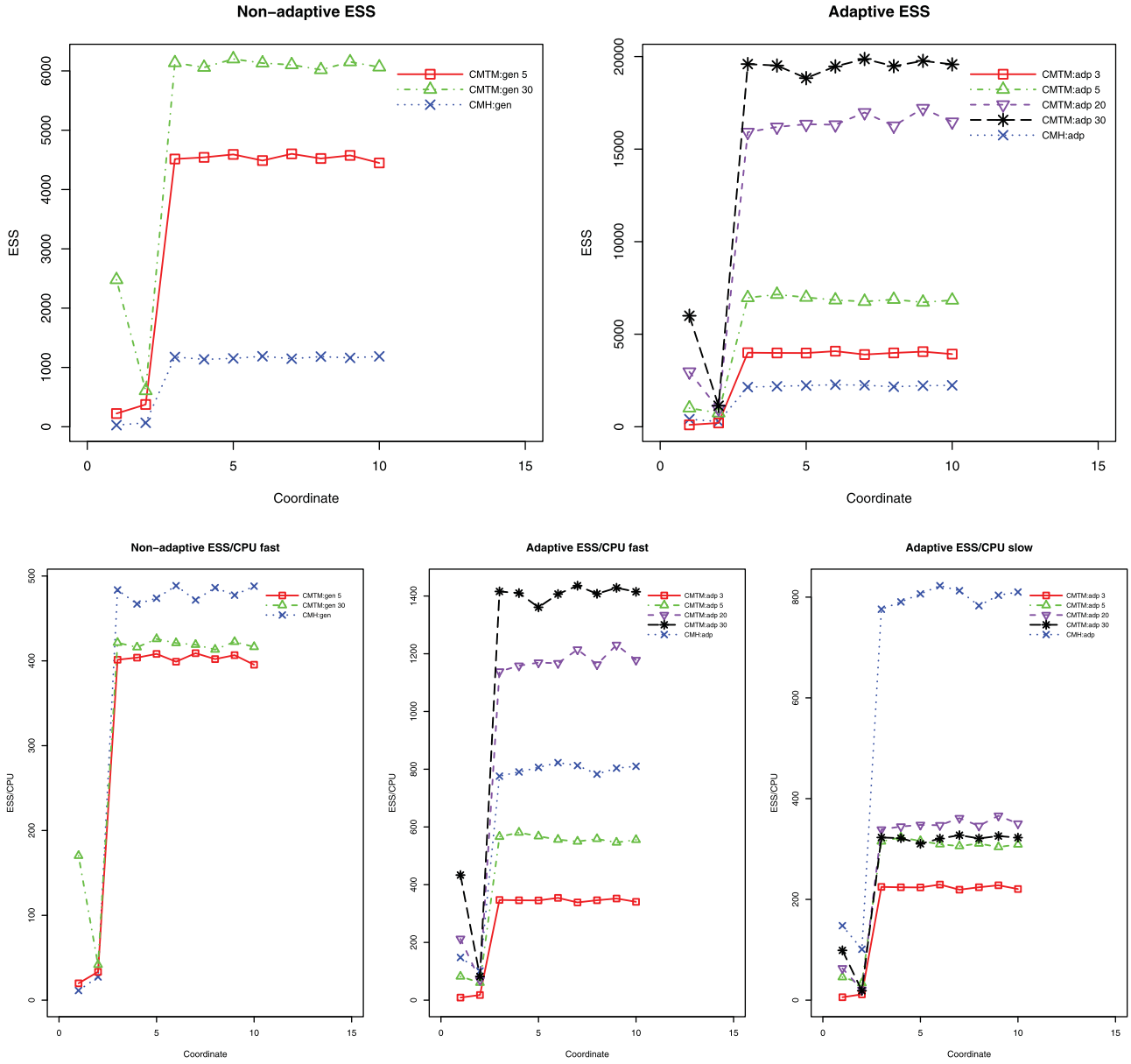

Figure 6. Banana-shaped distribution. For nonadaptive samplers, we compare CMTM with 5 and 30 generic proposals and CMH represented by red, green, and blue lines, respectively. For adaptive samplers, we compare between ACMTM with 3, 5, 20, or 30 proposals and the adaptive CMH represented by red, green, purple, black, and blue lines, respectively. Top row: Comparison of ESS for nonadaptive (left panel) and adaptive (right panel) samplers. Bottom row: Comparison of ESS/CPU for nonadaptive samplers (left panel) using "vectorized operations" for likelihood evaluations in CMTM, ESS/CPU for adaptive samplers with "vectorized operations" (middle panel), and without (right panel).

samples from the target that would contain the same amount of information about the target as the MCMC sample. The chains are run for 10,000 iterations. The first 5000 samples obtained are discarded while the remaining ones are used to calculate the ACT. The reported ESS is based on averaging the ACT over 50 independent runs. The R programs used to generate these results are included in the online supplementary material.

4.1. Variance Components Model

The Variance Components Model (VCM) is a typical hierarchical model, often used in Bayesian statistics community. Here, we use the data on batch to batch variation in dyestuff yields. The data were introduced in Davies (1967) and later analyzed by Box and Tiao (1973). The Bayesian set-up of the Variance Components Model on dyestuff yields is also well-described in Roberts and Rosenthal (2004). The data record yields on dyestuff of five samples, from each of six randomly chosen batches. The data are shown in Table 9.

Let y_{ij} be the yield on the dyestuff batch, with i indicating which batch it is from and j indexing each individual sample from the batch. The Bayesian model is then constructed as

$$y_{ij}|\theta_i, \sigma_e^2 \sim N(\theta_i, \sigma_e^2), \qquad i = 1, 2, \ldots, K, \quad j = 1, 2, \ldots, J,$$

where $\theta_i|\mu, \sigma_\theta^2 \sim N(\mu, \sigma_\theta^2)$. θ_i's are conditionally independent of each other given μ, σ_θ^2. The priors for the $\sigma_\theta^2, \sigma_e^2$, and μ are: $\sigma_\theta^2 \sim \text{IG}(a_1, b_1)$, $\sigma_e^2 \sim \text{IG}(a_2, b_2)$, and $\mu \sim N(\mu_0, \sigma_0^2)$. Letting $\vec{\theta} = \{\theta_1, \theta_2, \ldots, \theta_K\}$ and $\mathcal{D} = \{y_{ij} : i = 1, 2, \ldots, K, \ j = 1, 2, \ldots, J\}$, the posterior

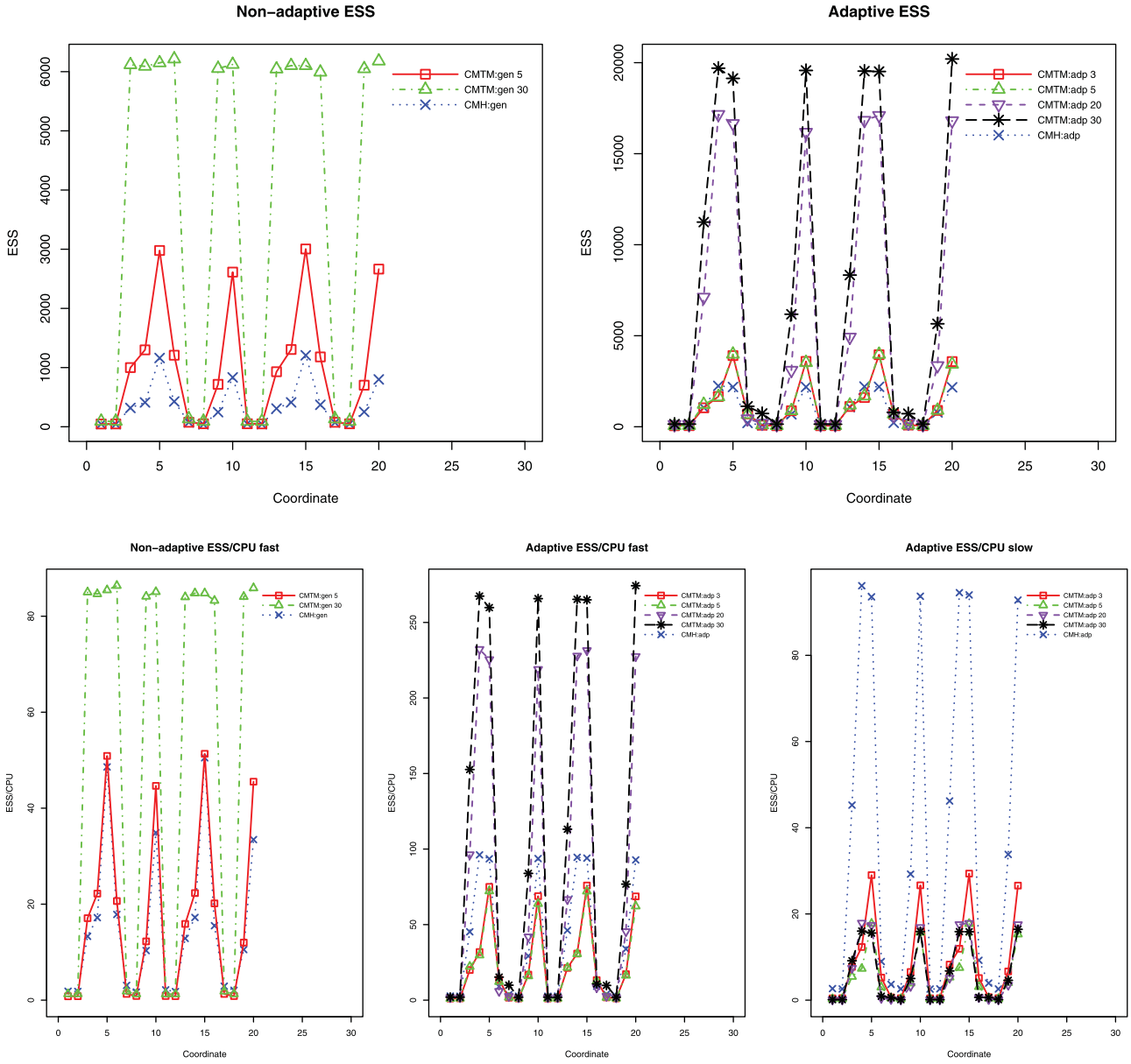

Figure 7. 20-dimensional mixture distribution. For nonadaptive samplers, we compare CMTM with 5 and 30 generic proposals and CMH represented by red, green, and blue lines, respectively. For adaptive samplers, we compare between ACMTM with 3, 5, 20, or 30 proposals and the adaptive CMH represented by red, green, purple, black, and blue lines, respectively. Top row: Comparison of ESS for nonadaptive (left panel) and adaptive (right panel) samplers. Bottom row: Comparison of ESS/CPU for nonadaptive samplers (left panel) using "vectorized operations" for likelihood evaluations in CMTM, ESS/CPU for adaptive samplers with "vectorized operations" (middle panel), and without (right panel).

density function of this VCM model is

$$f(\sigma_\theta^2, \sigma_e^2, \mu, \vec{\theta}|\mathcal{D}, a_1, a_2, b_1, b_2, \sigma_0^2, \mu_0) \propto (\sigma_\theta^2)^{-(a_1+1)} e^{-b_1/\sigma_\theta^2} (\sigma_e^2)^{-(a_2+1)} e^{-b_2/\sigma_e^2} e^{-(\mu-\mu_0)^2/2\sigma_0^2} \times \prod_{i=1}^{K} \frac{e^{(\theta_i-\mu)^2/2\sigma_\theta^2}}{\sigma_\theta} \prod_{i=1}^{K}\prod_{j=1}^{J} \frac{e^{(y_{ij}-\theta_i)^2/2\sigma_e^2}}{\sigma_e}.$$

We set the hyperparameters $a_1 = a_2 = 300$ and $b_1 = b_2 = 1000$, making inverse gamma priors very concentrated and let $\sigma_0^2 = 10^{10}$ and $\mu_0 = 0$. The variance components are updated on the log scale.

Figure 5 shows ESS and ESS/CPU (averaged over 50 runs) of the CMTM algorithms with and without adaption and of standard CMH and adaptive CMH algorithm. For both CMTM algorithms (with and without adaption), the starting proposals were generic for every coordinate as described above.

The plots for nonadaptive samplers clearly show that CMTM with 30 proposals is the most efficient in ESS and even when CPU time is taken into account it still performs better than CMH. Similar results are evident for adaptive samplers. Clearly adaptive CMTM with 20 or 30 proposals have much better ESS than adaptive CMH. When CPU time is considered than adaptive CMTM with 20 proposals is the most efficient.

4.2. "Banana-Shaped" Distribution

The "banana-shaped" distribution was originally presented in Haario, Saksman, and Tamminen (1999) as an irregularly

shaped target that may call for different proposal distributions for the different parts of the state–space.

The target density function of the "banana-shaped" distribution is constructed as $f_B = f \circ \phi_B$, where f is the density of d-dimensional multivariate normal distribution $N(\mathbf{0}, \text{diag}(100, 1, 1, \ldots, 1))$ and $\phi_B(\mathbf{x}) = (x_1, x_2 + Bx_1^2 - 100B, x_3, \ldots, x_d)$. $B > 0$ is the nonlinearity parameter and the nonlinearity or "bananacity" of the target distribution increases with B. The target density function is

$$f_B(x_1, x_2, \ldots, x_d) \propto \exp[-x_1^2/200 - \frac{1}{2}(x_2 + Bx_1^2 - 100B)^2 - \frac{1}{2}(x_3^2 + x_4^2 + \cdots + x_d^2)].$$

We set $B = 0.01$ and $d = 10$, the results are shown in Figure 6 (averaged over 50 runs starting with generic proposals).

Focusing on ESS plots, CMTM, and adaptive CMTM with 30 proposals clearly outperform standard CMH and adaptive CMH in all coordinates. When CPU time is taken into account then CMH and adaptive CMH performs a little better than CMTM algorithms on most coordinates. However on coordinate 1, CMTM methods perform much better than CMHs, actually by a factor of 2.5 or more.

4.3. Mixture of 20-Dimensional Gaussians

We are also examining the gains brought by the ACMTM in the case of bimodal distributions. We consider the mixture

$$0.5N_{20}(\mu_1, \Sigma_1) + 0.5N_{20}(\mu_2, \Sigma_2),$$

where

$$\begin{aligned}
\mu_1 &= (5, 5, 0, 0, 0, 0, 10, 15, 0, 0, 5, 5, 0, 0, 0, 0, 10, 15, 0, 0),\\
\mu_2 &= (10, 10, 0, 0, 0, 0, 7, 20, 0, 0, 10, 10, 0, 0, 0, 0, 7, 20, 0, 0),\\
\Sigma_1 &= \text{diag}\,(16.00, 16.00, 0.25, 4.00, 1.00, 0.01, 9.00, 16.00, 9.00,\\
&\qquad 0.01, 16.00, 16.00, 0.25, 4.00, 1.00, 0.01, 9.00, 16.00, 9.00, 0.01),\\
\Sigma_2 &= \text{diag}\,(16.00, 16.00, 6.25, 4.00, 1.00, 4.41, 9.00, 16.00, 0.25,\\
&\qquad 0.01, 16.00, 16.00, 6.25, 4.00, 1.00, 4.41, 9.00, 16.00, 0.25, 0.01).
\end{aligned}$$

In this example, CMTM methods with 30 proposals (in each coordinate) is the most efficient in ESS and ESS/CPU. The comparison is reported in Figure 7. We note that the adaptive and nonadaptive versions of CMTM perform much better than the CMHs counterparts.

The ESS/CPU calculations suggest that the best performance is achieved when the number of chains m is between 20 and 30. When programming the examples (the programs are available as online supplemental material), we have taken advantage of the software R's ability to handle vectorial operations much more efficiently than loops. When similar savings can be obtained, we recommend using $m = 20$ in practice. In instances where the likelihood is expensive to compute due to the large number of observations in the data, embarrassingly parallel strategies could be used efficiently in conjunction with ACMTM (Neiswanger, Wang, and Xing 2013; Scott et al. 2013; Wang and Dunson 2013; Reihaneh, Craiu, and Rosenthal 2016).

It is also important to note that in all three examples described above adaptive CMTM is always more efficient than CMTM with generic proposals. CPU time for both are about the same but ESS generally much larger for the latter. Hence, adaptive CMTM generally produces much better results and it is advisable to use it for real-world problems especially since it only requires a few lines of extra code.

5. Conclusion and Discussion

It is known that adaptive algorithms can be highly influenced by initial values given to their simulation parameters and by the quality of the chain during initialization period, that is, the period during which no modifications of the transition kernel take place. ACMTM is no exception, but some of its features can be thought of as means toward a more robust behavior. For instance, the fact that we can start with multiple proposals makes it less likely that all initial values will be poor choices for a given coordinate. The ACMTM is motivated by situations in which the sampler requires very different proposals across coordinates and across regions of the state–space. In such situations, traditional adaptive samplers are known to fail unless special modifications are implemented (Craiu, Rosenthal, and Yang 2009; Bai, Craiu, and Di Narzo 2011), but even these tend to underperform when the sample space dimension is high.

The adaption mechanism is very rapid as the scales can change in multiple of 2's and is also stable since modifications to the kernel occur only if over selection from one of the boundary scale proposals is detected. Thus, even if proposal scales are not perfect but good enough, they would not change much under this adaptive design.

The increase in CPU time is the price we pay for the added flexibility of having multiple proposals and the ability to dynamically choose the ones that fit the region of the space so that acceptance rate and mixing rates are improved. And while this tends to attenuate the ACMTM's efficiency, one cannot find among the algorithms we used for comparison in this article one that is performing better *on average* even after taking CPU time into account. However, we recommend using ACMTM in difficult sampling problems (e.g., multimodal target, variable variances for the conditional distributions across the sample space) when other approaches do not perform well.

Finally, it is the authors' belief that AMCMC samplers will be used in practice more if their motivation is intuitive and their implementation is easy enough. We believe that the ACMTM fulfills these basic criteria and further modifications can be easily implemented once new needs are identified.

Supplementary Materials

`function_description.pdf` contains a description of the R program used for the examples in the article.

`CMTM_sampling_fun.pdf` contains the R program used for the examples in the article.

`target_densities_used.R` contains the R program that implements the method for the targets used in the article.

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