Detection of dispersed short tandem repeats using reversible jump Markov chain Monte Carlo

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ABSTRACT

Tandem repeats occur frequently in biological sequences. They are important for studying genome evolution and human disease. A number of methods have been designed to detect a single tandem repeat in a sliding window. In this article, we focus on the case that an unknown number of tandem repeat segments of the same pattern are dispersively distributed in a sequence. We construct a probabilistic generative model for the tandem repeats, where the sequence pattern is represented by a motif matrix. A Bayesian approach is adopted to compute this model. Markov chain Monte Carlo (MCMC) algorithms are used to explore the posterior distribution as an effort to infer both the motif matrix of tandem repeats and the location of repeat segments. Reversible jump Markov chain Monte Carlo (RJMCMC) algorithms are used to address the transdimensional model selection problem raised by the variable number of repeat segments. Experiments on both synthetic data and real data show that this new approach is powerful in detecting dispersed short tandem repeats. As far as we know, it is the first work to adopt RJMCMC algorithms in the detection of tandem repeats.

INTRODUCTION

A tandem repeat is a stretch of sequence composed of multiple adjacent approximate copies of a particular substring. Tandem repeats have been found abundant in both DNA (1) and protein sequences (2) of most species. They have played critical roles in genome evolution because of frequent recombination or slippage events (3). There is also an increasing amount of researches showing that tandem repeats are related to many human diseases (4), such as Huntington’s disease (5) and cancer (6). On the positive side, tandem repeats can also benefit by generating functional variability and allowing swift adaptive evolution of certain traits (7,8). As a powerful tool, tandem repeats are frequently used for genetic mapping (9), genotyping (10) and forensics studies (11).

Tandem repeats differ in the conservation of their pattern. They can be strongly conservative as in ...gt ATCC ATCC ATCC cg..., where the repeat unit ATCC occurs three times consecutively. They can also be divergent as in ...gt ATCA ATAC ATCC cg..., which allows some mismatches between the repeat units. The two versions are called exact and approximate tandem repeats, respectively. In the remainder of this article, we focus on the latter case, which is more general and harder to detect. There are mainly two ways to represent a sequence pattern (i.e. a motif): motif consensus and motif matrix (12). Using the previous approximate tandem repeat as an example, the pattern can be represented by the motif consensus as ‘ATCC’ or by the motif matrix

\[
\begin{pmatrix}
1 & 2 & 3 & 4 \\
A & 1 & 0 & 1/3 & 1/3 \\
T & 0 & 1 & 0 & 0 \\
C & 0 & 2/3 & 2/3 & 0 \\
G & 0 & 0 & 0 & 0
\end{pmatrix},
\]

where each column of the matrix denotes the relative frequencies of the four nucleotides (A, T, C, G) showing at the corresponding position.

Over the past decade, a number of softwares have been developed to detect approximate tandem repeats. Generally speaking, current repeat detection methods can be roughly classified as either a string matching approach or a signal processing approach. The string matching approach detects repeats by scoring the sequence alignment between the input sequence and a library of curated repeat consensus, k-mers (a segment composed of k nucleotides or amino acids) or itself. RepeatMasker (Smit, AFA, Hubley, R and Green, P), RepeatMasker Open-3.0, RECON (13), REPuter (14), mreprs (15), Tallymer (16) and TRF (17) are some representative softwares in this class. The signal processing approach is mainly based on periodicity in the sequence.
It uses techniques such as discrete Fourier transform, short-time periodicity transform, exact periodic subspace decomposition and autoregressive modeling to perform spectral analysis (18–21). A more comprehensive review and a performance comparison of existing softwares can be found in (22,23).

A consecutive block composed of repeat units is called a tandem repeat segment. Multiple tandem repeat segments sharing a same pattern may be dispersively distributed in a sequence. Current methods are largely based on the motif consensus representation and a sliding-window technique. Our work concentrates on the situation where multiple tandem repeat segments composed of instances of the same short motif pattern are dispersively distributed in a sequence. We name the repeats in this scenario as the DSATR.

A generative model for a sequence with DSATR

A schematic view of a sequence with DSATR is shown in Figure 1. The input sequence is denoted as \( R = (r_1, r_2, \ldots, r_L) \), where the nucleotide at the l-th location, \( r_l \), takes a value from the alphabet \{A,T,C,G\}, and \( L \) denotes the length of the sequence. The input sequence consists of two parts, namely the tandem repeat region and the background region (i.e. the non-tandem repeat region). The tandem repeat region is composed of one or multiple separated repeat segments. We define a repeat segment with \( k \) repeat units as \( k \) adjacent instances of the same motif, i.e. a contiguous block with \( kw \) nucleotides in the sequence, where \( w \) denotes the width of the motif. Notice that the number of repeat segments is unknown in advance. Given the sequence \( R \), our goal is to infer the motif matrix of the tandem repeats and the locations of repeat segments. We model every nucleotide \( r_l \) in the sequence as a multinomial random variable. More specifically, for the nucleotides inside the repeat unit, we model them using a product multinomial (PM) distribution parameterized by a \( 4 \)-by-\( w \) matrix \( \Theta \) (27). We call the repeat pattern, represented by \( \Theta \), the sequence motif of the tandem repeats, where \( \Theta = \{\theta_1, \theta_2, \ldots, \theta_L\} \) and \( \theta_i = (\theta_{i,1}, \theta_{i,2}, \theta_{i,3}, \theta_{i,4})^T \) representing the proportion of the four nucleotides \{A,T,C,G\} at the i-th position of the repeat unit. These parameters satisfy that \( \sum_{j=1}^{4} \theta_{ij} = 1 \) and \( \theta_{ij} \geq 0 \) for all \( i, j \). The nucleotides in the background region are modeled as independent samples from the multinomial distribution parameterized by \( \theta_b \), where \( \theta_b = (\theta_{0,1}, \theta_{0,2}, \theta_{0,3}, \theta_{0,4})^T \) representing the proportion of the four nucleotides \{A,T,C,G\} at the positions outside the repeat region.

As shown in Figure 1, we assume that the input sequence is generated in three steps. We first use \( \theta_b \) to generate a background sequence, i.e. the non-repeat region with length \( L_b \). In the second step, we sample the number of repeat segments \( G \) from a random distribution and then construct the \( G \) repeat segments. To model the repeat segments, we introduce a vector \( K = (k_1, k_2, \ldots, k_G)^T \), where \( k_g \) is a random variable indicating the number of repeat units in the \( g \)-th segment. Each repeat unit in the repeat segments is independently sampled from the PM distribution parameterized by \( \Theta \). Finally, we randomly choose \( G \) different positions from the background sequence and insert the \( G \) repeat segments into it. We denote the final locations of the \( G \) repeat segments in the final sequence \( R \) of length \( L = L_b + \sum_g k_g w \) as \( A = (a_1, a_2, \ldots, a_G)^T \), where \( 1 \leq a_g \leq L - w + 1 \).
This generating procedure avoids the overlapping and adjacency between different repeat segments. The output of this three-step procedure is a sequence \( R \) of length \( L \), which includes \( G \) tandem repeat segments composed of instances of the same motif matrix \( \Theta \).

**Statistical inference**

For the input sequence \( R \), which is the only observed data, we are interested in estimating all parameters \( \{\theta_0, \Theta, A, K, G\} \). At this stage, we assume that the width of repeat unit \( w \) is given in advance. We use a Bayesian method to detect the tandem repeat segments modeled in the previous section. The joint posterior distribution of all parameters \( \pi(\theta_0, \Theta, A, K, G|R) \) will be used to make statistical inference.

**Likelihood and prior distributions**

For each tandem repeat segment, the starting position and the number of repeat units are used to characterize it. We denote the \( g \)-th segment as \( S(a_g, k_g) \), where \( S(a_g, k_g) = \{a_g+j : 0 \leq j \leq k_gw-1\} \). Let \( R_{TR0} \) denote the set of the \( i \)-th nucleotides of all repeat units and \( R_{\overline{TR}} \) denote the set of nucleotides in the non-repeat region. For convenience, we define the following indicator function \( I : I(r, \ast) = 1 \) if \( r \) is equal to \( \ast \); otherwise, \( I(r, \ast) = 0 \). Here \( \ast \) takes a value from \( \{A, T, C, G\} \). We introduce a counting function \( H \) such that \( H(F) = (h_{A,F}, h_{T,F}, h_{C,F}, h_{G,F})^T \), where \( F \) is any set of nucleotides and \( h_{k,F} = \sum_{r \in F} I(r, \ast) \). For any vectors \( \mu = (\mu_1, \ldots, \mu_d)^T \) and \( v = (v_1, \ldots, v_d)^T \), we define that \( \mu + v = (\mu_1 + v_1, \ldots, \mu_d + v_d)^T \), \( \mu^v = (\mu_1^v, \ldots, \mu_d^v)^T \), and \( |\mu|^v = \prod_{i=1}^{d} |\mu_i|^v \). With these notations, the complete likelihood can be factorized into a product of probabilities for the repeat region and the non-repeat region as follows:

\[
\pi(R|\theta_0, \Theta, A, K, G) = |\theta_0|^{H(R_{TR0})} \prod_{i=1}^{w} |\theta_i|^{H(R_{TRi})}.
\]

Let \( p(\cdot) \) denote the prior distribution of a parameter. We specify the prior for \( \Theta \) and \( \theta_0 \) independent of other parameters. Thus, we can decompose the prior for \( \{\theta_0, \Theta, A, K, G\} \) as

\[
p(\theta_0, \Theta, A, K, G) = p(\theta_0)p(\Theta)p(G)p(K)p(G)\prod_{i=1}^{G} p(A|K, G).
\]

For computational convenience, we use conjugate priors for \( \theta_i \), i.e. a Dirichlet (Dir) distribution with parameter \( \beta_i \). We denote \( B = [\beta_1, \beta_2, \ldots, \beta_G] \), where each \( \beta_i \) is associated with an 4-by-1 vector \( \beta_i \). The parameter \( \Theta \) therefore follows a product Dirichlet (PD) distribution parameterized by the matrix \( B \), i.e. \( \Theta \sim \text{PD}(B) \).

Similarly we assume \( \theta_0 \sim \text{Dir}(\beta_0) \). We further assume \( G \) takes integer values from \( G_{\min} \) to \( G_{\max} \) with equal probability. That is, \( G \) follows a discrete uniform (DU) distribution, which is denoted as \( G \sim \text{DU} \) \( [G_{\min}, G_{\max}] \).

To avoid the overlap and adjacency between the different tandem repeat segments and guarantee the identifiability, we require that \( \max(1, a_g+1+k_{g-1}w+1) \leq a_g \leq \min\{a_g+w-1, L-k_gw+1\} \). In practice, there is little prior knowledge about \( A \). Given \( K \) and \( G \), we assume that \( A \) is evenly distributed on all possible choices. Thus we have \( p(A|K, G) = \left( \frac{L-\sum_{g=1}^{G} k_gw+1}{G-1} \right) \).

Given \( G \), we assume that the elements of \( K \) are mutually independent, i.e. \( p(K|G) = \prod_{g=1}^{G} p(k_g) \), where \( p(k_g) = 1/(k_{g\max} - k_{g\min} + 1) \). Thus, we get the prior for all interested parameters as

\[
p(\theta_0, \Theta, A, K, G) = p(\theta_0)p(\Theta)p(G)p(K)p(K)\prod_{i=1}^{G} p(A|K, G).
\]

The formula implies that the prior \( p(\theta_0, \Theta, A, K, G) \) varies with \( \theta_0, \Theta, K, G \) and \( A \), but not with the specific values in \( A \). We can now write down the full posterior probability as

\[
\pi(\theta_0, \Theta, A, K, G|R) \propto p(\theta_0, \Theta, A, K, G)p(R|\theta_0, \Theta, A, K, G)
\]

\[
\propto \prod_{g=1}^{G} \text{Dir}(\beta_0)^{G+1}(G+1)\prod_{g=1}^{G} (L-\sum_{g=1}^{G} k_gw+2-G)\prod_{i=1}^{w} |\theta_i|^{H(R_{TRi})} \left( \frac{L-\sum_{g=1}^{G} k_gw+1}{G-1} \right) \frac{1}{(k_{g\max} - k_{g\min} + 1)^G}.
\]

(1)

**Sampling from posterior distribution**

Our MCMC algorithm is composed of three steps. We first use a Gibbs sampling algorithm to explore the posterior distribution when \( G \) is given. Then, we use RJMCMC to update \( G \). Two versions of RJMCMC are designed and compared. Finally, we will discuss extra moves to further improve the efficiency of the sampling algorithm.

**Gibbs sampling when \( G \) is given.** The joint posterior distribution of \( \theta_0, \Theta, A \) and \( K \), while \( R \) and \( G \) are given, can be explored by a Gibbs sampling algorithm. We iteratively sample all our interested parameters except \( G \) via corresponding conditional posterior probability as follows.
We can obtain the conditional posterior distribution of $\Theta$ from the full posterior probability as follows

$$
\pi(\Theta|R, \theta_0, K, A, G) \propto \prod_{j=1}^{w} \left[ p_{j}^{HR_{TR_{j}}(0)+b_{i}} \right].
$$

(2)

Here a conjugate prior $\Theta \sim \text{PD}(B)$ leads to the conditional posterior distribution $\Theta|R, \theta_0, K, A, G \sim \text{PD}(Q+B)$, where $Q = [H(R_{TR_{1}}), H(R_{TR_{2}}), \ldots, H(R_{TR_{w}})]$. Similarly, we derive the conditional posterior distribution of $\theta_0$

$$
\pi(\theta_0|R, \Theta, A, K, G) \propto |\theta_0|^{H_{TB}+b_i}. 
$$

(3)

Let $A[-g]$ and $K[-g]$ denote all elements of $A$ excluding $a_g$ and all elements of $K$ excluding $k_g$, respectively. As pointed out previously, the prior $\pi(\theta_0, \Theta, A, K, G)$ keeps invariant as we update $A$. Thus, we obtain the following conditional posterior distribution for $a_g$

$$
\pi(a_g|R, \theta_0, \Theta, K, A[-g], G) = \frac{\pi(R(\theta_0, \Theta, A[-g], a_g, K, G)}{\sum_{b=\max[1,a_g+1-k_g-w+1]}^{\min[a_g+1-k_g-w-1,L-a_g+1]} \pi(R(\theta_0, \Theta, A[-g], b, K, G))},
$$

(4)

where $\max[1,a_g+1-k_g-w+1] \leq a_g \leq \min[a_g+1-k_g-w-1,L-a_g+1]$. It is important to note that the conditional prior $p(A|K, G)$ may change as we update $k_g$. Thus we obtain the conditional posterior distribution for $k_g$

$$
\pi(k_g|R, \theta_0, \Theta, K[-g], A, G) \propto \pi(R(\theta_0, \Theta, K[-g], k_g, A, G)p(A|K, G),
$$

(5)

where $k_g$ takes value from $[k_{\text{min}}, k_{\text{max}}]$. 

**RJMCMC for updating $G$**

In contrast to other parameters, the updating procedure for $G$ will give rise to the change of the dimensions of $A$ and $K$, which leads to a Bayesian model selection problem. Let $M_G = \{A, K\}$ indicate that both $A$ and $K$ contain $G$ elements. We present a RJMCMC algorithm which aims to sample $G$ and $M_G$ from the conditional posterior distribution $\pi(G, M_G|\theta_0, \Theta, R)$. To impose the dimension matching, auxiliary random variables are introduced to propose new repeat segments in the jumping process. The main difficulty in RJMCMC algorithm is how to effectively propose the new segments, i.e. auxiliary variables. Two different versions, namely vanilla and piloted, of the proposal distribution for auxiliary variables are proposed in Section 1 of Supplementary Materials. Since the vanilla RJMCMC has the drawback of slow convergence, we introduce a so-called piloted RJMCMC by constructing the transdimensional move based on one-step-ahead prediction. More specifically, the piloted version takes advantage of the relationship between the input sequence and the current motif model $\Theta$ to propose auxiliary variables. We conclude theoretically that the acceptance rate (i.e. the expected acceptance probability) of the piloted version is larger than that of the vanilla version. Since the major hindrance of RJMCMC from wide applications is its rather slow move around the state space, the increased acceptance rate will then generally improve the convergence rate of the RJMCMC chain. An experimental verification of this point will be given later. The details of RJMCMC are given in Section 1 of Supplementary Materials.

The Gibbs sampling procedure for updating $(\theta_0, \Theta, A, K)$ and the RJMCMC step for updating $G$ compose the basic MCMC algorithm for computing our DSATR model. Many factors can affect the efficiency of a MCMC algorithm, such as the high correlation between parameters. We design three extra MCMC moves, namely a local group move, a global group move and a phase-shift move, to improve the mixing of the Markov chain. The details of these moves are given in Section 2 of the Supplementary Materials. A summary of the complete algorithm is provided in Section 3 of the Supplementary Materials. It clearly listed all inputs, outputs, tuning parameters and the detailed procedure of the algorithm.

**RESULTS**

We have implemented two versions of our complete algorithm in Matlab. The only difference between these two versions is the RJMCMC step, namely the vanilla and piloted versions. To evaluate the model and the algorithm, we apply the proposed algorithm to both synthetic and real data. We will discuss our experiment results and evaluate the performance of our algorithm in terms of convergence and accuracy.

**Evaluation and comparison of the two RJMCMC versions using synthetic data**

The synthetic sequence with DSATR, which is generated according to the generative model introduced in previous section, is used to compare the performance of two versions in Section 4 of Supplementary Materials. In summary, the piloted version outperforms the vanilla version in terms of convergence speed, the acceptance rate for the RJMCMC moves and the effective sample size within the same number of iterations. But for the accuracy of the statistical inference, they show a similar performance after a sufficient number of iterations.

**Comparison with existing methods using synthetic data**

Some existing methods can be used to detect DSATR although not specifically designed for this purpose. For a comparison with our algorithm, we tested three widely used methods using synthetic data, including TRF, GMS and RepeatMasker. As non-probabilistic algorithms, both TRF and RepeatMasker construct an explicit alignment score to evaluate a sequence segment and use the score to decide whether to report it as a repeat segment. We explain their scoring functions in Section 4.2.1 of Supplementary Materials.

**Synthetic data from the generative model**

We begin by defining the signal strength of repeat segments. Here, the signal strength is measured by the degree of conservation of the motif matrix $\Theta$. According
Table 1. Performance comparison on synthetic data sets from the generative model

| w | Conservation | GMS (Std.) | RepeatMasker<sup>a</sup> (Std.) | TRF (Std.) | Vanilla (Std.) | Piloted (Std.) |
|---|---|---|---|---|---|---|
| Sensitivity | 3 | High | 0.258(0.379) | 0.966(0.041) | 0.967(0.061) | 0.976(0.028) | 0.980(0.028) |
| Specificity | 3 | High | 0.597(0.048)<sup>f</sup> | 0.931(0.046) | 0.896(0.080) | 0.967(0.025) | 0.969(0.022) |
| Sensitivity | 3 | Median | 0.000(0.000) | 0.724(0.145) | 0.662(0.175) | 0.918(0.059) | 0.920(0.062) |
| Specificity | 3 | Median | 0.936(0.047) | 0.932(0.058) | 0.937(0.040) | 0.944(0.033) |
| Sensitivity | 3 | Low | 0.000(0.000) | 0.232(0.179) | 0.241(0.173) | 0.771(0.122) | 0.782(0.125) |
| Specificity | 3 | Low | 0.952(0.064)<sup>h</sup> | 0.908(0.141)<sup>h</sup> | 0.907(0.061) | 0.905(0.061) |
| Sensitivity | 6 | High | 0.922(0.026) | 0.993(0.010) | 0.993(0.009) | 0.995(0.073) | 0.991(0.010) |
| Specificity | 6 | High | 0.848(0.037) | 0.960(0.024) | 0.837(0.104) | 0.982(0.014) | 0.984(0.014) |
| Sensitivity | 6 | Median | 0.634(0.049) | 0.942(0.051) | 0.871(0.100) | 0.959(0.046) | 0.976(0.020) |
| Specificity | 6 | Median | 0.790(0.050) | 0.965(0.025) | 0.906(0.074) | 0.976(0.019) | 0.977(0.019) |
| Sensitivity | 6 | Low | 0.192(0.106) | 0.310(0.176) | 0.216(0.125) | 0.901(0.063) | 0.909(0.054) |
| Specificity | 6 | Low | 0.603(0.114)<sup>f</sup> | 0.977(0.034)<sup>f</sup> | 0.900(0.121)<sup>f</sup> | 0.948(0.033) | 0.952(0.033) |
| Sensitivity | 9 | High | 0.989(0.010) | 0.976(0.015) | 0.998(0.002) | 0.953(0.069) | 0.988(0.011) |
| Specificity | 9 | High | 0.959(0.024) | 0.983(0.012) | 0.763(0.126) | 0.988(0.010) | 0.989(0.010) |
| Sensitivity | 9 | Median | 0.804(0.039) | 0.954(0.026) | 0.937(0.080) | 0.944(0.079) | 0.981(0.023) |
| Specificity | 9 | Median | 0.883(0.047) | 0.981(0.017) | 0.882(0.078) | 0.984(0.016) | 0.984(0.017) |
| Sensitivity | 9 | Low | 0.399(0.049) | 0.456(0.151) | 0.302(0.164) | 0.944(0.045) | 0.944(0.037) |
| Specificity | 9 | Low | 0.738(0.077) | 0.954(0.021) | 0.961(0.057)<sup>b</sup> | 0.963(0.022) | 0.965(0.024) |

Note: Each cell of the table shows the corresponding mean and standard deviation (in the bracket) of the sensitivity or specificity calculated from the 100 different synthetic sequences.

<sup>a</sup>The true consensus is given as the sole repeat pattern in RepeatMasker library, so this comparison favors RepeatMasker.

<sup>b</sup>68 trails did not report any repeat element.

<sup>c</sup>All trails did not report any repeat element.

<sup>d</sup>4 trails did not report any repeat element.

<sup>e</sup>17 trails did not report any repeat element.

<sup>f</sup>5 trails did not report any repeat element.

<sup>g</sup>4 trails did not report any repeat element.

<sup>h</sup>1 trails did not report any repeat element.

To the probability of the dominant nucleotide (39), we define the degree of conservation as high, median or low. Nine data sets of inputs data are generated according to different width (3, 6, 9) and different signal strength (High, Median and Low) to compare these methods more comprehensively. Here, each data set contains 100 independent synthetic sequences with 5000 nucleotides.

We run our algorithm and the three other programs once on each of the 900 synthetic sequences. To favor the three other programs, we set them as follows. For RepeatMasker, since it needs a repeat library in order to detect corresponding repeats, the dominant nucleotides in each column of motif matrix are selected to build the sole consensus pattern for its repeat library. In other words, RepeatMasker is favored by knowing the true consensus pattern in the input data. This guarantees the high specificity for RepeatMasker. Meanwhile, we set the minimum report score for TRF as 20 (the default value is 50) and the cutoff of RepeatMasker as 100 (the default value is 225) to increase their sensitivities. To favor these three existing methods, we compare the results from all the methods at the nucleotide level. Each nucleotide in the given sequence is labeled as either in repeat region or in background region. The sensitivity is defined as the proportion of true repeat-region nucleotides that are correctly identified, and the specificity is defined as the proportion of the reported repeat-region nucleotides that are true repeat-region nucleotides. More details for the setting of GMS, RepeatMasker and TRF are listed in Section 4 of the Supplementary Materials. In addition, the detailed scoring functions for RepeatMasker and TRF and an experiment for a single sequence with detailed discussion on the sequences are also presented in Section 4 of the Supplementary Materials. For both versions of our RJMCMC algorithm, we run them separately for 3000 iterations with the same prior setting and tuning parameters.

The results are reported in Table 1. It summarizes the sensitivity and specificity of these algorithms on the nine different motif matrices. Each cell of the table shows the corresponding mean and standard deviation (in the bracket) of the sensitivity or specificity calculated from the 100 different synthetic sequences. In some cases, GMS, RepeatMasker and TRF did not report any repeat elements, therefore the corresponding specificities are not defined.

Table 1 shows that all our algorithms have better performance than GMS for all signal strength and motif width. Since GMS does not make use of the local enrichment of repeat units, it often misses some repeat units of a repeat segment, or even reports only one repeat unit for one repeat segment. Also, the performance of GMS is heavily dependent on the motif width and conservation level. Although our algorithms are able to offset the short width and low conservation of the motif matrix by profiting from the local clustering effect of repeat units. Although RepeatMasker and TRF are favored by knowing true repeat consensus sequences or high-sensitivity setting, our algorithms generally outperform TRF and RepeatMasker by either better sensitivity at similar specificity, or both better sensitivity and specificity. The advantage of our algorithms is more obvious for short
and divergent repeat segments. This is because both TRF and RepeatMasker, as window-based local search methods, cannot integrate the signal from multiple repeat segments. Therefore, the weak signal in individual repeat segments, when treated mutually independently, is likely to be missed by window-based methods. Another drawback of TRF is its incapability in handling the phase-shift between different repeat segments. In addition, we present a synthetic sequence experiment with detailed repeat units to illustrate that the gained efficiency of our algorithm is due to the more efficient modeling and computing, rather than due to different repeats definitions in algorithms, in Section 4.2.2 of Supplementary Materials.

Synthetic data from the coalescent model
To evaluate our algorithm on more realistic data instead of the data purely generated from our generative model, we also used a coalescent model (40–42) to produce a second version of the synthetic data for testing. The details are given in Section 5 of Supplementary Materials. The coalescent model considers the relations between different repeat segments and the mutation for short tandem repeats at both repeat unit and nucleotide levels. The results (see Table S2 in the Supplementary Materials) indicate that our algorithm still outperforms other methods on the data from the coalescent model.

Real data experiment
A real DNA sequence may contain more than one repeat pattern, which will result in multiple local modes in the posterior distribution. Thus we run multiple independent chain from random initial parameter values for real data and report the overall maximum a posteriori (MAP) estimate.

Another concern about the real data is the existence of indels, which has not been directly handled in our algorithm so far because of the lack of experimental knowledge support and technical difficulty. However, our current algorithm can accommodate indels to certain extent due to two reasons. On one hand, since the indels rate in repeat segments is much lower than the substitution rate, the main repeat region and motif matrix can be identified fairly well by our current algorithm without handling indels. On the other hand, if a repeat unit with indels exists in the middle of a repeat segment, our current algorithm can simply treat this repeat unit as background nucleotides and detect the remaining part as two repeat segments. But in case the user prefers reporting the repeat units with short indels, just like what TRF and RepeatMasker do using a special indel step, we also designed a post-processing step to glean repeat units with short indels. The details of the post-processing step are given in Section 6 of Supplementary Materials.

For comparison, a list of real genomic segments from different species are sampled from the Pre-Masked Genomes in RepeatMasker website (http://www.repeatmasker.org/cgi-bin/AnnotationRequest, 21 June 2012, date last accessed).

The detailed settings of the programs are given in Section 6 of Supplementary Materials. The results are summarized in Table 2. Since no ground truth about the
repeat pattern and locations in the real data are known, the sensitivity and specificity are not well defined here. Thus this experiment can only provide pairwise coverage comparisons instead of a systematic performance comparison. Each cell in Table 2 represents the proportion of repeat segments identified by the corresponding column algorithm (Algorithm B) that are also identified by the corresponding row algorithm (Algorithm A). Thus, the paired cells (i,j) and (j,i) can demonstrate the consistency between the i-th and j-th algorithms.

The results showed that the post-processing step expanded the reported repeat regions and therefore increased the consistency between our algorithms and other methods. But generally there is a slight inconsistency among the results of different algorithms in most of examples because of the difference in the scoring functions of all three algorithms. RepeatMasker and TRF may differ significantly, e.g. for Human Chr2 201650001-201670000. Our algorithm agreed well with either RepeatMasker or TRF on all cases. The missed repeat units in the results of our algorithm as compared with other methods are mostly due to the occurrence of indels. This is an empirical proof that the lack of indel treatment in our generative model does not seriously hinder the search of the motif pattern and the main repeat segments.

Comparing with TRF and RepeatMasker, the main advantage of our algorithm is that, relying on the motif matrix, our algorithm will collect the information from the whole sequence which makes our algorithm to be sensitive to the case where multiple tandem repeat segments with the same motif pattern are dispersively distributed in a sequence. A detailed comparison of our algorithm with TRF and RepeatMasker, in terms of modeling and computing, is presented in Section 4.2.2 of Supplementary Materials.

**DISCUSSION**

Based on a matrix representation of the tandem repeat pattern, we built a probabilistic model for sequences with DSATR and introduced a de novo Bayesian approach to detect both the repeat pattern and the repeats locations. MCMC algorithms, including Gibbs sampler, M-H and RJMCMC, are used to estimate all parameters in the model. As to our knowledge, this article might be the first to use RJMCMC for repeat detection in biological sequences.

Although MCMC methods are appealing for exploring complex posterior distributions, it is always a concern that the MCMC chain will be trapped in some local modes. We used group moves for highly correlated parameters, such that the chains move more globally to avoid being trapped in local modes.

To tackle the unknown number of repeat segments in a full Bayesian way, we used RJMCMC to jump between models of different dimensions, which allowed the posterior probability to speak up and search for the number of repeat segments within one single MCMC chain. Two versions of our RJMCMC algorithms are introduced. Both theoretical analysis and computational experiments showed that the piloted version significantly increased the efficiency upon the vanilla version. Comparing with existing methods which can be used for DSATR identification, our RJMCMC algorithm outperforms GMS and TRF in terms of both sensitivity and specificity, and appears more sensitive than RepeatMasker for the synthetic sequences even if RepeatMasker is given with the true consensus pattern. Similar to GMS, we did not consider indels in our main algorithm, but a post-processing step for indels was applied as an auxiliary part to detect the possible repeat units with indels. The real data experiments suggest that our main algorithm is suitable for searching the main repeat region and the motif matrix of DSATR, and the post-processing step efficiently detects the nearly repeat units with indels.

Once we generalized the motif model to detect tandem repeats, many previous works on motif discovery can be adapted to address related problems in tandem repeat studies. For example, Gupta and Liu (43) and Jensen et al. (30) discussed how to learn the motif width from the data. One possible extension of our current DSATR detection algorithm is to relax the fixed motif width by placing a prior on $w$ and then update $w$ via one more RJMCMC step. Another natural extension of the current work would be the application of the algorithm on multiple input sequences which share the same tandem repeat pattern. Future studies may also consider indels in the generative model to improve the performance on this aspect.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online: Supplementary Tables 1–3, Supplementary Figures 1–2, Supplementary Material and Supplementary References [24,26,32,39–42,44–49].

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