

# A model of epigenome evolution

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## Abstract

Epigenetic marks along the mammalian genome are organized into alternating genomic domains bearing and lacking the mark. The location and size of domains enriched for an epigenetic mark are indicative of the presence, function and activity of regulatory elements and the chromatin states. Comparative epigenomic studies aim to resolve the evolutionary history of regulatory elements by comparing epigenomic profiles in multiple species. However, computational methods for comparing epigenetic marks at high resolution, inferring evolution rates along different phylogenetic lineages and reconstructing the evolutionary history are still limited. In this study, we aim to establish a simulation, sampling and inference framework for studying the evolution of the genomic distribution of an epigenetic from the profiles of multiple extant species. We model the profile of an epigenetic mark in a species with a two-state Markov chain, and model the evolution of an epigenomic sequence with a continuous-time Markov chain, where instantaneous transition rates at a site is dependent on the contemporary states of its neighboring sites. We use a MCMC sampling method for estimating the context-dependent transition rates and inferring the evolutionary history that lead to diverse profiles in extant species from a common ancestral epigenome. We show with applications to DNA methylation and histone modification profiles that our methods can reveal both genome-wide evolutionary features through estimates of the model parameters and high-resolution evolutionary patterns in local regions through posterior sampling of the evolutionary history.

## 1 Introduction

The epigenome of a mammalian cell reflects much of the complexity we associate with cell phenotype and behaviors (). Individual epigenomic marks, for example a histone modification, may be viewed from a simpler perspective as contiguous genomic intervals where the presence or absence of that mark is associated with genomic function. Intervals of the genome that have a high density of H3K9me3 are often associated with condensed chromatin state and silencing of genes within those intervals (Nakayama et al., 2001). Genomic intervals with high density of H3K4me3, on the other hand, are associated with accessibility by transcription factors and are associated with gene promoters (Santos-Rosa et al., 2002). So despite the complexity often ascribed to the mammalian epigenome (Bernstein et al., 2007), studies focusing on individual epigenomic modifications have been highly successful in elucidating transcriptional regulation in a variety of systems (Martin & Zhang, 2005).

One challenge in modeling epigenome evolution is that desirable models should account for the inherent auto-correlation of epigenomic state along the genome. The most well known models of molecular evolution, applied to amino acids or nucleotides, treat each site as evolving independently – a simplifying

assumption that has proven very useful. When models allow for dependencies between sites, we additionally hope that those dependencies can be interpreted.

Pedersen et al. (1998) examined the problem of modeling evolution at the codon level and designed an approach capable of describing CpG depression across codon boundaries, a form of interdependence between adjacent codons. With similar motivation, Jensen & Pedersen (2000) examined the properties of evolutionary models for which the stationary distribution on sequences naturally exhibits particular frequencies of dinucleotides. The result was an approach to model the evolution of an individual nucleotide as a function of that nucleotide’s neighbors in a way that induces a Markov process on the stationary distribution.

Our goal of modeling the evolution of an epigenome can be viewed in analogy with phylogenetic hidden Markov models (). The phastCons algorithm () is the best known variant of phylogenetic HMM, and has dramatically impacting the field of comparative genomics by providing a general approach to model “conserved” genomic intervals for a set of species. The states of a simple phylogenetic HMM correspond to alternating conserved and non-conserved intervals of aligned genomes. The generalization associates a binary state label with each nucleotide in each species and presents algorithmic challenges when viewed generally as a chain graph (Koller & Friedman, 2009).

The remainder of this paper is organized as follows. We first describe our model for epigenome evolution as an adaptation of the principles introduced by Jensen & Pedersen (2000) and use simulation to explore model parameterization. Then we explain how inferences are made in the context of this model, using simulation to demonstrate the accuracy of our procedures. Finally, we apply this model on an existing data set.

## 2 The model

### 2.1 Biological assumptions and assumed representation for the epigenome

We assume that the epigenome is a sequence of binary states super-imposed on the genome. This assumption is restrictive, but it allows us to consider the epigenome from either the perspective of an individual epigenomic modification, or as reflecting a particular type of functional interval. One example of former is a sequence of binary variables corresponding to the presence or absence of a H3K27me3. Another example is a binary variable to indicate accessibility, as determined by a particular assay. An example of a functionally-defined binary variable may be “accessible” or “enhancer,” both of which can be associated with different epigenomic modifications, but are known to be organized as contiguous intervals. Epigenomic state is correlated along the genome as a reflection of the organization of the epigenome into contiguous intervals.

Most types of data that inform us about the epigenome are based on sequencing, and usually based on density of mapped reads (e.g. from ChIP-seq or ATAC-seq). Often these data are summarized in non-overlapping “bins” through the genome. When we refer to a position in the epigenome, we assume that such position corresponds in a meaningful way to either individual nucleotide positions in the genome, or appropriate bins. We only require that the neighboring relations are preserved.

Let epigenome  $s$  be the sequence  $s = s_1 s_2 \cdots s_N$  with  $s_i$  denoting the state at position  $i$ . As a graphical model, neighboring sites are connected with undirected edges. An epigenome  $s$  evolves over time, but we assume the stationary distribution for the epigenome has a Gibbs distribution that factorize over pairs of

neighboring sites:

$$\Pr(s) = \frac{1}{Z} \exp \left\{ \phi(s_1) + \sum_{n=1}^{N-1} \phi(s_n, s_{n+1}) + \phi(s_N) \right\} \quad (1)$$

As the epigenome evolves the state at each position may change. Although we have operationally defined the epigenome by associating a state with each position along the genome, the types of changes we hope to model are more naturally interpreted in terms of sets of contiguous intervals. We use the term epigenomic “feature” to refer to a consecutive interval having the “1” state. The main types of changes we are interested in are the following:

- *Birth and death:* During evolution, some new epigenomic feature may appear, or a feature that existed in an ancestor may disappear.
- *Expansion and contraction:* As the epigenome evolves, epigenomic segments can become wider or more narrow, and this may happen in either direction.
- *Merging and separating:* Two epigenomic features that are nearby in the ancestral genome may merge into a single interval. Conversely, a single epigenomic feature in the ancestral epigenome may separate into two intervals.

We will describe a model that treats the expansion and contraction of features symmetrically in both directions along the genome. This choice in modeling is often reasonable, but not always. For example, certain epigenomic modifications are frequently associated with parts of genes, which have directionality.

For a site  $n$  and an evolutionary time interval  $[0, \tau)$ , the initial state and all the time points of state transitions within this time interval constitute a complete evolutionary history for this site. This is because we have assumed binary states, and an evolutionary path is consecutive time intervals with alternating states. In other words, an observation of the evolutionary path at site  $n$  can be summarized as

$$L_n = \{s_n(0), J_n = \{t_1, \dots, t_{m_n}\}, \tau\},$$

where  $s_n(t) \in \{0, 1\}$  is the state of site  $n$  at time  $t$ ,  $\tau$  is the total length of the time interval, and  $J_n$  is an ordered sequence of  $m_n$  jumping times at site  $n$  within this time interval, *i.e.*  $0 < t_1 < \dots < t_{m_n} < \tau$ .

The evolution of states at a given site depends on the states of its neighboring sites during evolution. Consider site  $n$  and its two immediate neighbors  $n - 1$  and  $n + 1$ , and let the contemporaneous states at these sites be  $s_{n-1}(t) = i$ ,  $s_n(t) = j$  and  $s_{n+1}(t) = k$ . The instantaneous rate for a transition from state  $j$  to its alternative state  $\bar{j}$  at site  $n$  is  $\gamma(i, j, k)$ . In other words, the instantaneous rates  $\gamma(i, j, k)$  is a function of the states at the site of interest and its two immediate neighbors. In addition, since we assume the evolutionary process is symmetric with respect to the two directions along the genome, we require  $\gamma(i, j, k) = \gamma(k, j, i)$ . When the states at all positions except for site  $n$  stay constant for a time interval  $[0, \tau)$ , the state at site  $n$ ,  $s_n$ , follows a two-state continuous-time Markov process within this time interval.

## 2.2 Stationary Gibbs measure as Markov chain

The stationary distribution in (1) is equivalent to the distribution of a Markov chain. Therefore, when the epigenome is modeled with a Gibbs measure, we can sample an instance of the sequence epigenomic states or evaluate its probability with the equivalent Markov chain. We can derive the relationship between

the factors in (1) and the transition probabilities of a Markov chain. The pair-wise potentials are  $Q_{ij} = \exp(\phi(i, j))$ , where  $i, j \in \{0, 1\}$  are binary states. The largest eigenvalue of  $Q$  is

$$q = \frac{1}{2} \left( Q_{00} + Q_{11} + \sqrt{\Delta} \right), \text{ where } \Delta = (Q_{00} - Q_{11})^2 + 4Q_{01}Q_{10}.$$

Let  $h$  be a right eigenvector of  $Q$  corresponding to  $q$ , then we have

$$\frac{h_0}{h_1} = \frac{Q_{01}}{q - Q_{00}} = \frac{q - Q_{11}}{Q_{10}}$$

Then we have the Markov chain transition matrix:

$$T(i, j) = \frac{Q_{ij}h_j}{qh_i}, \text{ where } i, j \in \{0, 1\}.$$

More specifically,

$$\begin{aligned} T(1, 1) &= \frac{2Q_{11}}{Q_{00} + Q_{11} + \sqrt{\Delta}}, & T(0, 0) &= \frac{2Q_{00}}{Q_{00} + Q_{11} + \sqrt{\Delta}}, \\ T(0, 1) &= \frac{4Q_{01}Q_{10}}{(Q_{00} + \sqrt{\Delta})^2 - Q_{11}^2}, & T(1, 0) &= \frac{4Q_{01}Q_{10}}{(Q_{11} + \sqrt{\Delta})^2 - Q_{00}^2}. \end{aligned} \tag{2}$$

The expected fraction of an epigenome residing within functional domains is thus:

$$1 - \frac{2Q_{01}Q_{10}}{(Q_{00} - Q_{11})^2 + 4Q_{01}Q_{10} + (Q_{11} - Q_{00})\sqrt{\Delta}}.$$

### 2.3 Relating the substitution model and the stationary distribution

Jensen & Pedersen (2000) gave a sufficient condition for the continuous time evolutionary model  $\gamma$  to have a stationary distribution determined by  $\phi$ . In particular, if

$$\frac{\gamma(i, j, k)}{\gamma(i, \bar{j}, k)} = \frac{\exp(\phi(i, \bar{j}) + \phi(\bar{j}, k))}{\exp(\phi(i, j) + \phi(j, k))}, \tag{3}$$

then (1) is the stationary distribution for the Markov process with intensities  $\gamma(i, j, k)$ .

Proposition 2 of Jensen & Pedersen (2000) provides a way of specifying  $\gamma$  from  $\phi$ : substitution rates  $\gamma$  satisfy the relation (4) if and only if they can be written in the form

$$\log(\gamma(i, j, k)) = -\psi(i, j, k) + \ell(i, k). \tag{4}$$

This criteria was introduced in the context of an arbitrary number of states, and the  $\ell$  function can be understood as  $\ell(j, j'; i, k)$ , for any two different states  $j$  and  $j'$ , which is symmetric in  $(j, j')$ . In our setting of modeling epigenomic features, the states are binary and  $\ell$  is only a function of the two neighboring states  $(i, k)$ . Moreover, we can directly verify that if we define substitution rates as

$$\log(\gamma(i, j, k)) = \ell(i, k) + (\phi(i, \bar{j}) + \phi(\bar{j}, k)), \tag{5}$$

then they satisfy the condition of (4).

## 2.4 Parameterization and interpretation

We can organize the neighbor-dependent transition rates of defined above according to an  $8 \times 8$  matrix:

$$\Gamma = \begin{matrix} & \begin{matrix} 000 & 010 & 001 & 011 & 100 & 110 & 101 & 111 \end{matrix} \\ \begin{matrix} 000 \\ 010 \\ 001 \\ 011 \\ 100 \\ 110 \\ 101 \\ 111 \end{matrix} & \left( \begin{array}{cccccccc} \cdot & \mathcal{B} & 0 & 0 & 0 & 0 & 0 & 0 \\ \mathcal{D} & \cdot & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \cdot & \mathcal{E} & 0 & 0 & 0 & 0 \\ 0 & 0 & \mathcal{C} & \cdot & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \cdot & \mathcal{E} & 0 & 0 \\ 0 & 0 & 0 & 0 & \mathcal{C} & \cdot & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \cdot & \mathcal{M} \\ 0 & 0 & 0 & 0 & 0 & 0 & \mathcal{S} & \cdot \end{array} \right) \end{matrix} \quad (6)$$

We may interpret the non-zero entries in  $\Gamma$  as corresponding to biological events outlined in Section 2.1. The values  $\mathcal{B}$  and  $\mathcal{D}$  are the rates of “birth” and “death,” respectively, for epigenomic features. The value  $\mathcal{M}$  corresponds to the merging of two features into a single contiguous interval ( $101 \rightarrow 111$ ). Conversely, the value  $\mathcal{S}$  corresponds to epigenomic features “splitting” and becoming two separate intervals ( $111 \rightarrow 101$ ). The remaining non-zero values,  $\mathcal{E}$  and  $\mathcal{C}$ , correspond to the expansion (widening) and contraction (narrowing), of epigenomic features. Both of these parameters appear twice in  $\Gamma$ , reflecting our assumption that the rates governing any widening or narrowing of intervals do not depend on direction, as explained in Section 2.1.

If an epigenome evolves according to substitution rates  $\Gamma$  with stationary distribution (1), then the condition in (4) holds, and we have the following constraints for the rates in the above matrix:

$$\mathcal{B}\mathcal{C}^2\mathcal{M} = \mathcal{D}\mathcal{E}^2\mathcal{S}. \quad (7)$$

So given substitution rates  $\mathcal{B}, \mathcal{D}, \mathcal{E}, \mathcal{C}$ , we have the following relationships between horizontal potentials:

$$\phi(0,0) = \phi(0,1) + \frac{1}{2} \log \left( \frac{\mathcal{D}}{\mathcal{B}} \right), \text{ and } \phi(1,1) = \phi(0,1) + \frac{1}{2} \log \left( \frac{\mathcal{D}\mathcal{E}^2}{\mathcal{B}\mathcal{C}^2} \right). \quad (8)$$

In summary, the transition rate matrix  $\Gamma$  has 5 free parameters. If we add an additional constraint on the expected number of changes per unit time, then the model will have only 4 free parameters. The two ratios  $\mathcal{D}/\mathcal{B}$  and  $\mathcal{D}\mathcal{E}^2/(\mathcal{B}\mathcal{C}^2)$  then uniquely determine the stationary distribution (1) through equation (8).

## 3 Simulate epigenomic changes during evolution

We model the evolution of the entire epigenome (as a sequence of states) using a continuous time Markov process that only allows instantaneous transitions from one sequence to another if the two differ at a single position. The jumping rate at each position in the epigenome is dependent on the state at that position and on the states of the left and right neighboring positions. We assume for convenience that the states of the first and last sites are fixed throughout evolution.

Consider the  $2^N \times 2^N$  transition rate matrix  $M$  for any pair of epigenomes  $x$  and  $y$  that differ at exactly one position. The state at that position is  $j$  in epigenome  $x$  and  $\bar{j}$  in epigenome  $y$ . Neighboring positions in both  $x$  and  $y$  have states  $i$  and  $k$ . The instantaneous rate of a jump between  $x$  and  $y$  is

$$\lambda_{ijk} = \gamma(i, j, k) = \Gamma(ijk, i\bar{j}k).$$

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**Algorithm 1** Simulating epigenome evolution

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1:  $t \leftarrow 0$ 
2: Initialize paths  $L_n = \{x_n(0), k_n = 0, T_n = \emptyset, t\}$ , for  $n = 1, \dots, N$ 
3: while  $t < T$  do
4:   Generate  $y \sim \text{Exp}(-M_{x(t)x(t)})$ , where  $-M_{x(t)x(t)} = \sum_{i,j,k} c_{ijk}(x(t))\lambda_{ijk}$ .
5:   if  $t + y < T$  then
6:     Choose triple  $ijk \in \{0, 1\}^3$  with probability proportional to  $c_{ijk}(x(t))\lambda_{ijk}$ .
7:     Sample position  $n$  uniformly from the  $c_{ijk}(x(t))$  positions having pattern  $ijk$ 
8:      $x(t + y) \leftarrow x(t)[1..n - 1]\overline{x(t)_n}x(t)[n + 1..N]$ .
9:      $k_n \leftarrow k_n + 1$ 
10:     $T_n \leftarrow T_n \cup \{t + y\}$ 
11:   else
12:     $x(T) \leftarrow x(t)$ 
13:   end if
14:    $t \leftarrow t + y$ 
15: end while
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If the current epigenome is denoted  $x$  then the holding time is an exponential variable:

$$X_x \sim \text{Exp}(-M_{xx}).$$

The rate parameter  $-M_{xx}$  is the sum of instantaneous rates for jumps from  $x$  to any other epigenome that only differs from  $x$  at one position:

$$-M_{xx} = \sum_{i,j,k} c_{ijk}(x)\lambda_{ijk},$$

where  $c_{ijk}(x) = \sum_{n=1}^{N-2} I(x_n = i, x_{n+1} = j, x_{n+2} = k)$  is the total number of times the pattern  $ijk$  appears as consecutive triplets of positions in  $x$ .

Given that a jump has occurred, the probability that the jump changed  $x$  at the middle position of a triple  $ijk$  is proportional to  $c_{ijk}(x)\lambda_{ijk}$ . Further, given that a jump happend with context  $ijk$ , we assume the jump is equally likely to have changed any position in  $x$  having state  $j$  with left and right neighbors having states  $i$  and  $k$ . The expected number of changes per site, per unit time, is  $\sum_{ijk} \pi_{ijk}\lambda_{ijk}$ , where  $\pi_{ijk}$  is the stationary distribution for the pattern  $ijk$  in the epigenome. These assumptions suggest a simulation procedure for the evolutionary process followed by an epigenome of  $N$  sites over a time interval  $[0, T]$ , starting from an initial sequence  $x(0)$ .

To implement this simulation scheme requires maintaining the variables  $c_{ijk}$  at each time point, and updating them by removing

## 4 Parameter inference

If we are given the complete epigenome evolution path from time 0 to time  $t$ , can we effectively recover the initial distribution and mutation parameters and evolutionary time? We are interested in the parameters describing the evolutionary process, which are the transition rates  $\{\lambda_{ijk}\}$ . These parameters will be inferred from the state changes in the evolutionary path for the entire epigenome. Meanwhile, we do not require the

process to be stationary, so we may also be interested in the properties of the epigenome at time 0, which are characterized by the Markov chain transition probabilities  $T_0$ . These transition probabilities are easy to infer given the complete observations at the time-0 epigenome.

Let  $c_{ij} = \sum_{n=1}^{N-1} I\{s_n(0) = i, s_{n+1}(0) = j\}$ . Then

$$\hat{T}(0, 0) = \frac{c_{00}}{\sum_{n=1}^{N-1} I\{s_n(0) = 0\}}, \quad \hat{T}(1, 1) = \frac{c_{11}}{\sum_{n=1}^{N-1} I\{s_n(0) = 1\}}.$$

We first assume that the time span of this complete evolutionary history is known, *i.e.* the value of  $t$  is given.

Recall that  $L_n = \{s_n(0), K, \{t_k\}_{k=1}^K, t\}$  is a full path at position  $n$  in the epigenome. We can pool all the jumping times at all positions as an ordered sequence of timepoints  $J = \{(t_m, \text{pos}_m, \text{con}_m)\}_{m=1}^M$ , where  $\text{pos}_m$  is the position of the  $m$ -th jump in the entire evolutionary history of the epigenome,  $\text{con}_m$  is the 3-tuple context of the change that occurred at the  $m$ -th jump.

Let  $\Delta_m = t_m - t_{m-1}$  be the holding time just prior to the  $m$ -th jump. Then  $\Delta_m$  is an exponential variable

$$\Delta_m \sim \text{Exp}(\lambda_m), \quad \text{with } \lambda_m = \sum_{i,j,k} c_{ijk}(t_m - \epsilon) \lambda_{ijk}.$$

The constant  $\epsilon \in (0, \min_m \Delta_m)$  is defined so that  $c_{ijk}(t_m - \epsilon)$  is the sequence context distribution between the  $(m-1)$ th jump and the  $m$ -th jump.

#### 4.1 Likelihood expressions

The likelihood function for parameters  $\{\lambda_{ijk}\}$  is thus

$$L = \prod_{m=1}^M \lambda_m \exp(-\lambda_m \Delta_m) \times \frac{\lambda_{\text{con}_m}}{\lambda_m} = \prod_{m=1}^M \lambda_{\text{con}_m} \exp(-\lambda_m \Delta_m). \quad (9)$$

And the log-likelihood function is

$$\begin{aligned} l &= \sum_{i,j,k} \left( \sum_{m=1}^M \log \lambda_{ijk} \times I_{\{\text{con}_m = ijk\}} - c_{ijk}(t_m - \epsilon) \lambda_{ijk} \Delta_m \right) \\ &= \sum_{ijk} (J_{ijk} \log \lambda_{ijk} - D_{ijk} \lambda_{ijk}) \end{aligned} \quad (10)$$

where  $J_{ijk} = \sum_{m=1}^M I_{\{\text{con}_m = ijk\}}$ , and  $D_{ijk} = \sum_{m=1}^M c_{ijk}(t_m - \epsilon) \Delta_m$ .

The constraints on the transition rates  $\lambda_{ijk}$  as indicated in the matrix (6) and equation (7) are:

$$\begin{aligned} \lambda_{001} &= \lambda_{100} \\ \lambda_{011} &= \lambda_{110} \\ \lambda_{000} \lambda_{110}^2 \lambda_{101} &= \lambda_{010} \lambda_{100}^2 \lambda_{111} \end{aligned} \quad (11)$$

So the log-likelihood function (10) becomes

$$\begin{aligned}
l = & J_{000} \log \lambda_{000} - D_{000} \lambda_{000} + \\
& J_{010} \log \lambda_{010} - D_{010} \lambda_{010} + \\
& J_{101} \log \lambda_{101} - D_{101} \lambda_{101} + \\
& (J_{100} + J_{001}) \log \lambda_{001} - (D_{100} + D_{001}) \lambda_{001} + \\
& (J_{011} + J_{110}) \log \lambda_{011} - (D_{011} + D_{110}) \lambda_{011} + \\
& J_{111} \log \left( \frac{\lambda_{000} \lambda_{011}^2 \lambda_{101}}{\lambda_{010} \lambda_{001}^2} \right) - D_{111} \frac{\lambda_{000} \lambda_{011}^2 \lambda_{101}}{\lambda_{010} \lambda_{001}^2}.
\end{aligned} \tag{12}$$

## 4.2 Estimates when evolutionary time is a parameter

When the total time span of this complete evolutionary history is unknown, the value of  $t$  is also a model parameter to be estimated. If we assume that all the jump times are expressed as a fraction of  $t$ , then the transition rates and the evolutionary time are jointly identifiable and can be estimated. We require an additional constraint: the unit branch length corresponds to 1 expected mutation per site. This is a common constraint in phylogenetic studies.

Here we explain how to formulate this constraint on the  $\lambda_{ijk}$  transition parameters. Given  $\lambda_{ijk}$  according to (8), the ratios  $\frac{\lambda_{010}}{\lambda_{000}}$  and  $\frac{\lambda_{001}}{\lambda_{011}}$  uniquely determine the stationary distribution for the epigenome described by a Gibbs measure of the form (1). The Gibbs measure for the epigenome sequence, in turn, is equivalent to the Markov chain (2). Given the Markov chain formulation, we can compute the expected frequency of triplet patterns

$$p_{ijk} = \frac{1}{N} \mathbb{E}(c_{ijk}),$$

where  $c_{ijk}$  is the frequency of the triplet pattern in an epigenomic sequence of length  $N$  sampled from the Gibbs distribution. Then the expected number of changes per position per unit time is  $\sum_{ijk} p_{ijk} \lambda_{ijk}$ . When the evolutionary time is also unknown, we add the constraint:

$$\sum_{ijk} p_{ijk} \lambda_{ijk} = 1, \tag{13}$$

where  $\{p_{ijk}\}$  as explained above are functions of  $\{\lambda_{ijk}\}$ . Estimation maximizes the log-likelihood (10) over  $\{\lambda_{ijk}\} \cup \{t\}$  under the constraints (11) and (13), where the unknown parameter  $t$  is included within  $\{D_{ijk}\}$  in (10).

## 4.3 Posterior distribution of a path given two neighboring paths

Here we consider inference on the path for a single position in an epigenome that is evolving for some specified time. We assume the paths for all other positions are known for the entire evolutionary time span. In particular, we will make inferences about site  $n$  and have access to the jump times  $J = \{(t_m, \text{pos}_m, \text{con}_m)\}_{m=1}^M$  are known for all positions except position  $n$ . We also assume that the model parameters  $\{\lambda_{ijk}\}$  and total evolutionary time  $t$  are known, along with the the initial state of the epigenome. We seek inferences related to the posterior distribution of the path  $L_n$ :

$$\Pr(L_n | L_{-n}, \{\lambda_{ijk}\}) \propto \Pr(L_n \cup L_{-n}),$$



where  $L_{-n}$  denotes all paths for sites other than  $n$ . The approach we adopt is using MCMC to sample from the posterior distribution of  $L_n$ .

**Method 1:** First, sample a starting state  $s_0$  from a Bernoulli distribution with probabilities  $(\pi_0, \pi_1)$ . Then, propose a number  $K$  of jumps from a Poisson distribution with rate parameter  $\lambda = \sum \lambda_{ijk}/8$ , which is chosen to approximate average mutation rate among different contexts. Given  $K$ , sample jump times uniformly on the time interval  $(0, t)$ ; In other words, from the Dirichlet distribution with concentration parameters all equal to 1. Therefore, the probability (density) of proposing a specific path  $L' = \{s_0, K, \{t_k\}_{k=1}^K, t\}$  is

$$q(L') = \pi_{s_0} \frac{\lambda^K \exp(-\lambda)}{K!} \frac{1}{(K-1)!}.$$

This is known as an *independence sampler*. If the current path at position  $n$  is  $L_n$ , then we accept the proposed path  $L'$  with probability

$$\alpha(L') = \min \left\{ \frac{\pi(L', L_{-n})/q(L')}{\pi(L_n, L_{-n})/q(L_n)}, 1 \right\}, \quad (14)$$

where  $\pi$  is the complete data likelihood function (9).

**Method 2:** The method outlined above uses a proposal distribution that is approximately uniform. This can be highly inefficient, *i.e.* lead to a low rate of acceptance, although Jensen & Pedersen (2000) used a sampling procedure in the same spirit. If we use more information from the paths at neighboring sites, we may be able to improve sampling efficiency. The neighboring paths  $L_{n-1}$  and  $L_{n+1}$  partition the evolutionary time interval  $(0, t)$  into time segments during which the states at positions  $n-1$  and  $n+1$  do not change.

- Collect the time intervals from site  $n-1$  and site  $n+1$ , so that within each of the intervals the states of the neighboring sites are unchanged. Let the intervals be represented by a sorted array  $\{t_0, t_1, \dots, t_M\}$ .
- For  $m = 1, \dots, M$ :
  - Let  $X$  be a random variable from an exponential distribution, representing the jumping time of the middle site given that the states of its two neighbors are constant. For a time interval  $[t_{m-1}, t_m]$  during which the neighboring sites' states are unchanged, suppose  $X \sim \text{Exp}(\lambda_{ijk})$ , where  $i$  and  $k$  are the states of the two neighboring sites in this time interval, and  $j$  is the starting state of position  $n$ .
  - Let  $t = t_{m-1}$ , and a sample value of  $X = x$ .
  - While  $t + x < t_m$ :
    - (1) Add 1 to the number of jumps  $k_n \leftarrow k_n + 1$ .
    - (2) Update  $T_n \leftarrow T_n \cup \{t + x\}$ .
    - (3) Update  $t \leftarrow t + x$ ,
    - (4) Sample another value of  $X = x$  from  $\text{Exp}(\lambda_{ijk})$ .

The proposal probability density  $q()$  is thus the product of the appropriate Exponential distribution probability densities for the holding times at position  $n$ . The proposal distribution is independent of any current guess of the path. Therefore, this is also an *independence sampler*. The rejection rule stays the same, as in (14).

**Note:** A jump at time  $\tau$  within the path  $L_n$  will affect the probability of all jumps that occur after time  $\tau$ , regardless of their position within the epigenome. This is because such a jump affects  $\{c_{ijk}(t)\}$  for any  $t > \tau$ . Therefore, we cannot cancel out factors in the likelihood function. However, we may try to make things easy by only considering the evolutionary paths at positions  $n - 2$ ,  $n - 1$ ,  $n + 1$ , and  $n + 2$ .

## 5 Inferences in the context of a tree structure with fixed leaf data

Now we assume the epigenome has evolved according to a tree structure, and we wish to make inferences about a bifurcating evolutionary process. The paths associated with a given site must satisfy additional constraints to be “consistent.” We first consider a tree with 3 nodes, a root  $u$  with a single child node  $v$  and two leaf nodes below  $v$ , denoted  $w_1$  and  $w_2$ . The branches of the tree are  $(u, v)$ ,  $(v, w_1)$  and  $(v, w_2)$ . We assume we are given the epigenome at each node in this tree, with the exception of the state at position  $n$  of node  $v$ . We are also given all paths for sites other than site  $n$ . We want to make inferences about the state at position  $n$  of  $v$ , and also about the paths for edges incident on  $v(n)$ . We require a method for sampling paths at site  $n$  that share a common state at their common end-point.

Hobolth & Stone (2009) reviewed and compared three approaches to sample paths of discrete-state continuous-time Markov chain conditional on end-point states, namely the rejection sampling, direct sampling and uniformization. Method 1 in the previous section is similar to uniformization, since the neighboring sites may have state changes, and the rate of jumps depends on the contemporary states of the neighboring sites. We proposed to use an averaged rate to for the Poisson distribution, and let the acceptance probability to do most of the work of correcting the proposal distribution towards the posterior distribution. Method 2 is forward sampling, which is the basis of rejection sampling.

**Rejection sampling for the proposal:** This approach first does forward sampling as described in Method 2 above for position  $n$  along the branch  $(u, v)$  and  $(v, w_1)$ , which can be viewed as a single path that proceeds along two consecutive edges. The sampled path provides a state  $x$  corresponding to node  $v$ . Next, a path is sampled for edge  $(v, w_2)$  assuming state  $x$  at node  $v$ . If this path finishes with the known state at position  $n$  in  $w_2$ , we retain the 3 paths  $L_n^{(u,v)}$ ,  $L_n^{(v,w_1)}$  and  $L_n^{(v,w_2)}$  as a proposal. The proposal is evaluated using the same acceptance rule given above in equation (14).

A couple of performance statistics should be measured for this proposed sampling method. These include (1) the success rate for generating valid paths that satisfy the end conditions; (2) the acceptance rate of proposed valid paths in MCMC sampling.

## 6 Discussion

As noted earlier, the generalizations previously described for phylo-HMMs have many similarities with the model we proposed. In particular, these generalizations associate a binary variable with each nucleotide in

each sequence, including ancestral sequences. The most notable difference is our emphasis on interpretability of the horizontal relationships, specifically that an individual epigenome (extant or ancestral) follows a Markov process. Another difference is our adoption of a homogeneous continuous time process, which is both built into the model, and exploited by our inference procedure. Phylogenetic HMMs are applied to determine states along aligned genomes where those genome sequence evolve according to a particular substitution model. Our notion of the epigenome corresponds more closely to the idea of “conserved” and “non-conserved” states, but the details of our approaches are more similar to the substitution process of nucleotides, rather than general time-dependent graphical models.

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