



This article appeared in a journal published by Elsevier. The attached copy is furnished to the author for internal non-commercial research and education use, including for instruction at the authors institution and sharing with colleagues.

Other uses, including reproduction and distribution, or selling or licensing copies, or posting to personal, institutional or third party websites are prohibited.

In most cases authors are permitted to post their version of the article (e.g. in Word or Tex form) to their personal website or institutional repository. Authors requiring further information regarding Elsevier's archiving and manuscript policies are encouraged to visit:

<http://www.elsevier.com/copyright>



Contents lists available at SciVerse ScienceDirect

## Information Processing Letters

www.elsevier.com/locate/ipl



# Effect of increasing the energy gap between the two lowest energy states on the mixing time of the Metropolis algorithm

Apurv Nakade<sup>a</sup>, Somenath Biswas<sup>b,\*</sup>

<sup>a</sup> Chennai Mathematical Institute, H1, SIPCOT IT Park, Kelambakkam, Siruseri 603103, India

<sup>b</sup> Department of Computer Science and Engineering, IIT Kanpur, Kanpur 208016, India

## ARTICLE INFO

## Article history:

Received 5 November 2009

Received in revised form 7 August 2012

Accepted 22 August 2012

Available online 3 September 2012

Communicated by B. Doerr

## Keywords:

Metropolis algorithm

Markov chain mixing time

Protein folding

Randomized algorithms

## ABSTRACT

In order to understand what makes natural proteins fold rapidly, Šali, Shakhnovich and Karplus (1994) [6,7] had used the Metropolis algorithm to search for the minimum energy conformations of chains of beads in the lattice model of protein folding. Based on their computational experiments, they concluded that the Metropolis algorithm would find the minimum energy conformation of a chain of beads within an acceptable time scale if and only if there is a large gap between the energies of the minimum energy conformation and that of the second minimum. Clote (1999) [1] attempted to support this conclusion by a proof that the mixing time of the underlying Markov chain would decrease as the gap in energies of the minimum energy conformation and that of the second minimum increased. He was able to show that an *upper bound* on the mixing time does indeed decrease as the energy gap increases. We show in this paper that the mixing time *itself*, however, is a non-decreasing function of the value of the energy gap. Therefore, our result contradicts what Clote had attempted to prove.

© 2012 Elsevier B.V. All rights reserved.

## 1. Introduction

One of the most outstanding open issues in biology is the rapid folding of proteins: in spite of the existence of exponentially many possible configurations, a protein, after its formation as a chain of arbitrary shape, manages to fold, i.e., to reach its unique lowest free-energy state, very quickly.<sup>1</sup> In order to understand the factors responsible for the rapid folding of proteins, Šali, Shakhnovich, and Karplus [6,7] considered the *lattice model of protein folding*. In this model, one considers a chain of  $n$  beads,  $a_1, a_2, \dots, a_n$ , as an idealization of the polymeric chain of amino acids that defines the primary sequence of a protein. A *conformation* of the chain of beads is a placement of the beads in the three-dimensional lattice, a placement that is required to satisfy two constraints: that beads  $a_i$

and  $a_{i+1}$ ,  $1 \leq i < n$ , will occupy adjacent lattice positions, and that no two distinct beads will occupy the same lattice position. (In other words, the chain is folded in such a manner that each bead occupies a lattice position and this folding is, so-called, self-avoiding.) Šali et al. define the total energy  $E$  of a conformation to be  $E = \sum_{i < j} \Delta(r_i, r_j) B_{ij}$ , where  $r_i$ 's denote positions of the  $i$ th bead  $a_i$  in the lattice,  $\Delta(r_i, r_j) = 1$  if  $|i - j| > 1$  and  $r_i, r_j$  are two adjacent positions in the lattice,  $\Delta(r_i, r_j)$  is 0 otherwise. The term  $B_{ij}$  is the attractive force between the bead pair  $a_i, a_j$ , and is defined suitably to model the attractive forces between pairs of amino acids. The chain of beads is considered to be *folded* if it is in a conformation with minimum total energy.

To study the kinetics of folding, Šali, Shakhnovich and Karplus used the Metropolis algorithm to locate the minimum energy conformation, after identifying a suitable notion of neighbourhood amongst the set of conformations. A search of the space of conformations through the Metropolis algorithm is indeed an acceptable approximation for the molecular dynamics responsible for

\* Corresponding author.

E-mail addresses: apurv@cmi.ac.in (A. Nakade), sb@cse.iitk.ac.in (S. Biswas).

<sup>1</sup> This phenomenon is known as Levinthal's paradox in the literature.

folding, as explained in [8]. They considered 200 instances, each with 27 beads, with varying  $B_{i,j}$ 's. They found that the Metropolis algorithm was able to locate the global minimum within an acceptable timescale in 30 of the 200 instances. On examining the set of instances, Šali, Shakhnovich and Karplus found that what distinguished the 30 rapidly folding instances from the rest was that all those 30 instances had *pronounced global minima*, which the rest did not. A configuration is said to have pronounced global minimum if there is a large gap between the energies of the minimum energy conformation and that of the second minimum. On the basis of this finding they made the conjecture that the *necessary and sufficient* condition for a chain to fold rapidly is that it should have a pronounced global minimum.

Clote [1] attempted to provide a theoretical justification for the above conjecture by considering the effect of increasing the gap in energies of the minimum and the second minimum conformations on the mixing time of the Markov chain that the Metropolis algorithm uses. In particular, Clote considers the effect of *increasing* the energy value of the conformation with second minimum energy, leaving the energies of all other conformations as before. If the conjecture is true then it is reasonable to expect that the mixing time will decrease with increase in the gap. What Clote was able to show is that *an upper bound* on the mixing time does, indeed, decrease as the energy gap increases. However, as Clote himself had pointed out, the result does not prove anything about the mixing time *per se*.

Our work here actually *contradicts* what Clote had set out to prove. In particular, we show that the second largest eigenvalue of the underlying Markov chain, as a function of the energy gap between the minimum and the second minimum energy configurations, is non-decreasing. As the mixing time decreases with the decrease in the second largest eigenvalue, our result proves that increasing the gap in energies will not reduce the mixing time.

Our way of increasing the energy gap between the conformations with the minimum and the second minimum energy is by *reducing* the energy of the minimum energy conformation, leaving the energies of all other conformations unchanged. What we do in this respect thus is quite similar to what Clote had done.

However, our approach to the problem is different from that of Clote's for he used the notion of canonical paths [4] to argue about an upper bound on the conductance of the underlying graph of the Markov chain, whereas we directly work with the second largest eigenvalue. Further, our proof is not entirely algebraic, it also uses certain facts from analysis, e.g., that the eigenvalues of a matrix are continuous functions of its entries.

## 2. Preliminaries

To find the minimum energy conformation, the Metropolis algorithm runs a Markov chain. (We refer to the book by Levin, Peres, and Wilmer [2] as a comprehensive reference on the Markov chain theory.) The state space of the chain is the set of conformations. There is a neighbourhood structure associated with the set of conforma-

tions: one conformation  $c_1$  is a neighbour of another,  $c_2$ , if due to a local move  $c_2$  can result from  $c_1$ . We assume that the neighbourhood structure is an undirected, connected  $d$ -regular graph.<sup>2</sup> Let  $f(c)$  denote the energy of the conformation  $c$ . As per the Metropolis algorithm, if the Markov chain is in the state (i.e., the current conformation is)  $c_i$  at a certain instant of time, and  $c_j$  is a neighbour of  $c_i$ , then the chain will move to  $c_j$  with probability  $\min\{1/2d, (1/2d) \times (e^{-f(c_j)/T} / e^{-f(c_i)/T})\}$ . ( $T$  is the ambient temperature in which the modeled physical process is situated; for our purpose, it is simply a constant.) The Metropolis algorithm Markov chain is a lazy, time-reversible chain, and therefore, it has a stationary distribution. The state corresponding to the lowest energy conformation will have the largest probability mass in the stationary distribution. We recall that the mixing time of a chain is a measure of the minimum time necessary for the chain to come close to its stationary distribution. To be more specific, the mixing time,  $t_{\text{MIX}}(\epsilon)$  is defined to be

$$t_{\text{MIX}}(\epsilon) = \min\{t \geq 0 \mid d(t) \leq \epsilon\}$$

where  $d(t)$  denotes the total variational distance between the distribution at time  $t$  (maximized over all initial states) and the stationary distribution. All the eigenvalues of the transition probability matrix of the Metropolis Markov chain are real and their values lie between 0 and 1. The largest eigenvalue is 1 and the corresponding (normalized) eigenvector is the stationary distribution of the chain. Throughout the following discussion, we use  $\lambda$  to denote the second largest eigenvalue.  $\lambda$  and the mixing time are intimately related, as given in the following [2]:

$$(t_{\text{REL}} - 1) \log(1/2\epsilon) \leq t_{\text{MIX}} \leq \log(1/\epsilon \pi_{\min}) t_{\text{REL}}$$

where  $t_{\text{REL}}$ , called the *relaxation time*, is defined as  $1/(1 - \lambda)$ , and  $\pi_{\min}$  denotes the minimum of stationary distribution probabilities. It can be seen, therefore, that  $t_{\text{MIX}}$  and  $t_{\text{REL}}$  are roughly the same. As is standard, we shall argue about the mixing time by arguing about  $\lambda$ , the second largest eigenvalue of the transition probability matrix.

Our goal in this paper is to study how the mixing time of the chain would change, as we change the  $f$  value of the minimum energy conformation, leaving the  $f$  values of the other conformations unchanged.

In order to keep the notations simple, we study the following equivalent problem. Let  $G$  be a  $d$ -regular undirected connected graph with vertex set  $\{0, 1, \dots, n-1\}$ . Associated with each vertex  $i$  is the *value* of the vertex  $V_i$ . We consider the Metropolis algorithm that aims to identify the vertex with the *highest* value. We assume without loss of generality that  $V_0 > V_1 > \dots > V_{n-1} \geq 0$ . ( $V_i$ 's are proportional to the stationary probabilities of the respective  $i$ 's, hence negative values for  $V_i$ 's are not considered.)

The Metropolis algorithm runs a Markov chain to find the vertex having the largest value; the state space of the

<sup>2</sup> The regularity condition is not necessary, but the connectedness of the neighbourhood structure is necessary for the chain to have a stationary distribution.

chain is the set of vertices of  $G$ , and its transition probability matrix  $P = \{p_{ij}\}$  is as defined below: (we recall that  $V_0 > V_1 > \dots > V_{n-1}$ ).

$$p_{ij} = \begin{cases} 0 & \text{if } i \neq j \text{ and } i \notin \text{Neighbour}(j) \\ \frac{1}{2d} \frac{V_j}{V_i} & \text{if } j \in \text{Neighbour}(i) \text{ and } j > i \\ \frac{1}{2d} & \text{if } j \in \text{Neighbour}(i) \text{ and } j < i \\ 1 - \sum_{i \neq k} p_{ik} & \text{if } i = j \end{cases}$$

Instead of working with the transition probability matrix  $P$ , it is more convenient to work with another matrix  $N$  defined as

$$N = 2d(I_{n \times n} - P)$$

$\lambda$  is an eigenvalue of  $P$  iff  $2d(1 - \lambda)$  is an eigenvalue of  $N$ . With respect to  $N$  our goal, therefore, is to show that as  $V_0$  increases, while the other  $V_i$ 's remain the same, the second smallest eigenvalue is non-increasing.

We make the substitution  $y$  for  $1/V_0$  in the matrix  $N$ ; let  $N(y)$  denote the matrix  $N$  with this substitution, and let  $\lambda(y)$  denote the second smallest eigenvalue of  $N(y)$ . Our goal is proved by showing that  $\lambda(y)$  is a non-decreasing function in  $y$ .

Let  $D$  be the diagonal matrix  $\text{diag}(V_0^{1/2}, V_1^{1/2}, \dots, V_{n-1}^{1/2})$ . Let the matrix  $M$  be defined as  $M = DND^{-1}$ .  $M$  is similar to  $N$ , and therefore, it has the same set of eigenvalues as  $N$  does.  $M$  is also a symmetric matrix and therefore has eigenvectors which are pairwise orthogonal.

**Notations.** We use the following notations in the rest of the paper:

$N(y), M(y)$ : the matrices  $N$  and  $M$  with  $V_0$  substituted as  $1/y$ ,

$\lambda(y)$ : the second smallest eigenvalue of  $N(y)$ , therefore, of  $M(y)$ ,

$M_{ij}(y)$ : the  $i, j$ th entry of the matrix  $M(y)$ .

### 3. Results

First, we show that there is an interval starting at 0 where  $\lambda(y) > \lambda(0)$ . Using this, we prove later that  $\lambda(y)$  is a non-decreasing function in  $y$ .

**Lemma 1.** *There is a  $\delta, \delta > 0$  such that for all  $y, 0 < y \leq \delta$ ,  $\lambda(0) < \lambda(y)$ .*

**Proof.** We consider two cases:

**Case 1:**  $\lambda(0) = 0$ .

Consider  $y > 0$ , and suppose that  $\lambda(y) = 0$ . In this case, 0 is the value of the two smallest eigenvalues of  $N(y)$ , therefore, of  $M(y)$ . As  $M(y)$  is symmetric, there will exist two orthogonal eigenvectors for these two minimum eigenvalues, which in turn means that corresponding to these two 0 eigenvalues,  $N(y)$  will have two distinct eigenvectors. This will imply that  $P(y)$  will have two distinct stationary distributions, which is not possible as  $P(y)$  is ergodic for every  $y > 0$ . Therefore,  $\lambda(y) > 0$  for  $y > 0$ , which proves the lemma for the present case.

**Case 2:**  $\lambda(0) > 0$ .

First we prove the following:

**Proposition 1.** *Let  $z = (z_0, z_1, \dots, z_{n-1})$ , with  $\sum z_i^2 = 1$ , be the eigenvector corresponding to the second smallest eigenvalue,  $\lambda(y)$ , of  $M(y)$ , with the assumption that  $y > 0$ . Let  $z' = (0, z_1, z_2, \dots, z_{n-1})$ . Then if  $M_{00}(y) < \lambda(y)$  then  $\frac{z' \cdot M(0) \cdot z'^T}{z' \cdot z'^T} < \lambda(y)$ .*

**Proof.**

$$\begin{aligned} z' \cdot M(0) \cdot z'^T &= \sum_{i=0}^{n-1} \sum_{j=0}^{n-1} z'_i M_{ij}(0) z'_j \\ &= \sum_{i=1}^{n-1} \sum_{j=1}^{n-1} z'_i M_{ij}(0) z'_j \\ &\quad \text{as } M_{ij}(0) = 0 \text{ for } i = 0 \text{ or } j = 0 \\ &= \sum_{i=1}^{n-1} \sum_{j=1}^{n-1} z'_i M_{ij}(y) z'_j \\ &\quad \text{as } M_{ij}(0) = M_{ij}(y) \text{ when} \\ &\quad \text{neither } i \text{ nor } j = 0 \\ &= \sum_{i=1}^{n-1} \sum_{j=1}^{n-1} z_i M_{ij}(y) z_j \\ &\quad \text{as } z_k = z'_k \text{ when } k \neq 0 \\ &= \sum_{i=1}^{n-1} z_i \sum_{j=1}^{n-1} M_{ij}(y) z_j \\ &= \sum_{i=1}^{n-1} z_i \left( \sum_{j=0}^{n-1} M_{ij}(y) z_j - M_{i0}(y) z_0 \right) \\ &= \sum_{i=1}^{n-1} z_i (\lambda(y) z_i - M_{i0}(y) z_0) \\ &= \lambda(y) \sum_{i=1}^{n-1} z_i^2 - z_0 \sum_{i=1}^{n-1} z_i M_{i0}(y) \\ &= \lambda(y) (1 - z_0^2) \\ &\quad - z_0 \left( \sum_{i=0}^{n-1} z_i M_{i0}(y) - z_0 M_{00}(y) \right) \\ &= \lambda(y) (1 - z_0^2) \\ &\quad - z_0 \left( \sum_{i=0}^{n-1} z_i M_{0i}(y) - z_0 M_{00}(y) \right) \\ &\quad \text{as } M \text{ is symmetric} \\ &= \lambda(y) (1 - z_0^2) - z_0 (\lambda(y) z_0 - z_0 M_{00}(y)) \end{aligned}$$

Now,

$$z' \cdot z'^T = \sum_{i=1}^{n-1} z'_i z'_i$$

$$\begin{aligned} &= \sum_{i=1}^{n-1} z_i^2 \\ &= 1 - z_0^2 \end{aligned}$$

Therefore,

$$\begin{aligned} \frac{z'.M(0).z'^T}{z'.z'^T} &= \frac{\lambda(y)(1 - z_0^2) - z_0(\lambda(y)z_0 - z_0M_{00}(y))}{1 - z_0^2} \\ &= \lambda(y) + \frac{z_0^2}{1 - z_0^2}(M_{00}(y) - \lambda(y)) \end{aligned}$$

Whenever  $y > 0$ , we have  $z_0^2 < 1$ , otherwise,  $z$  becomes  $(1, 0, \dots, 0)$ . However, such a  $z$  cannot be an eigenvector of  $M(y)$ . Reason: let  $k$  be a vertex adjacent to vertex 0. Such a  $k$  must exist as the underlying Markov chain is irreducible. As  $y > 0$ ,  $M_{k0}(y) \neq 0$ . So, denoting  $M_k(y)$  as the  $k$ th row of  $M(y)$ ,  $M_k(y)(1, 0, \dots, 0)^T \neq 0$ . Therefore,  $(1, 0, \dots, 0)$  is not an eigenvector of  $M(y)$ .

As we have  $z_0^2 < 1$ , the proposition follows from the last equality.  $\square$

**Proposition 2.** *There is a  $\delta, \delta > 0$  such that for all  $y, 0 \leq y \leq \delta$ ,  $M_{00}(y) < \lambda(y)$ .*

**Proof.** By definition,  $M_{00}(y) = y(\sum_{i \in S} V_i)$ , where  $S$  is the set of neighbouring vertices of the vertex 0. Hence,  $\lim_{y \rightarrow 0} M_{00}(y) = 0$ , but  $\lim_{y \rightarrow 0} \lambda(y) = \lambda(0)$  which is greater than 0 by assumption in the case under consideration. Hence, the proposition follows.  $\square$

Using Propositions 1 and 2, we now can complete the proof for Case 2 of Lemma 1.

We consider the interval  $(0, \delta)$ ,  $\delta$  as in Proposition 2 and any  $y$  in this interval.  $(1, 0, \dots, 0)$  is an eigenvector of  $M(0)$  corresponding to its smallest eigenvalue 0. As  $M(0)$  is a symmetric matrix, we can use the variational characterization for  $\lambda(0)$ , its second smallest eigenvalue, to get

$$\begin{aligned} \lambda(0) &= \min_{t \perp (1, 0, \dots, 0)} \frac{t.M(0).t^T}{t.t^T} \\ &\leq \frac{z'.M(0).z'^T}{z'.z'^T} \quad (\text{here } z' \text{ is as in Proposition 1}) \\ &< \lambda(y) \end{aligned}$$

for all  $y, 0 < y \leq \delta$ , where  $\delta$  is as in Proposition 2.

The first inequality is because  $z'$  is orthogonal to  $(1, 0, \dots, 0)$  and the next inequality follows then from Proposition 1.

This completes the proof of Case 2, and hence that of Lemma 1.  $\square$

We are now in a position to prove our main result which is about the behaviour of  $\lambda(y)$  as  $y$  increases from 0 onwards. (Recall that  $y$  is the inverse of  $V_0$ , and is greater than 0.)

**Theorem 1.** *With  $y \geq 0$ ,  $\lambda(y)$ , the second smallest eigenvalue of  $N(y)$ , hence that of  $M(y)$ , is a non-decreasing function in  $y$ .*

**Proof.** We consider the characteristic polynomial  $p(x, y)$  of  $N(y)$ . The polynomial  $p(x, y)$ , being  $\det(N(y) - xI_{n \times n})$ , is a degree  $n$  polynomial in  $x$ , and is linear in  $y$ . It can be easily seen that for each  $y$ ,

$$\lim_{x \rightarrow -\infty} p(x, y) = \infty$$

We recall that all the roots of  $p(x, y)$  are non-negative. Therefore, if  $x < 0$  then  $p(x, y) > 0$  and if  $0 < x < \lambda(y)$  then  $p(x, y) < 0$ .

Suppose the theorem is false, let

$$(\exists y_a, y_b) \quad [0 < y_a < y_b \text{ and } \lambda(y_a) > \lambda(y_b)]$$

(As a witness of the contradiction, the assumption that  $y_a > 0$  is justified because if  $\lambda(0) > r$ , for some  $r$ , then for a  $z$  within a small neighbourhood of 0,  $\lambda(z) > r$ , as the function  $\lambda(y)$  is continuous in  $y$ .) Further, we assume that the  $\delta$  in Lemma 1 is such that

$$0 < \delta < y_a < y_b \quad (1)$$

This condition can be made true by making  $\delta$  take a value smaller than  $y_a$ , if so needed.

Consider  $x = \lambda(0)$ . From Lemma 1, we have that  $p(\lambda(0), 0) > p(\lambda(0), \delta)$ . Now, the fact that  $p(x, y)$  is linear in  $y$  gives us

$$p(\lambda(0), 0) > p(\lambda(0), \delta) > p(\lambda(0), y_a) > p(\lambda(0), y_b) \quad (2)$$

However, as  $\lambda(y_b) < \lambda(y_a)$ , the two curves  $p(x, y_a)$  and  $p(x, y_b)$  will intersect at some value of  $x$ , say  $x^*$ , i.e.,  $p(x^*, y_a) = p(x^*, y_b) = b$  (say). Clearly, we have that  $x^* < \lambda(y_b)$ . Again, the fact that  $p(x, y)$  is linear in  $y$  implies that for every value, say  $y_1$ , that  $y$  takes, the resultant curve  $p(x, y_1)$  will also pass through that point of intersection. In particular,  $p(x^*, 0)$  will also be  $b$ . We consider two cases (i)  $\lambda(0) < x^*$  and (ii)  $\lambda(0) > x^*$ .

**Case (i):**  $\lambda(0) < x^*$ .

Since  $0 < x^* < \lambda(y_b)$ ,  $p(x^*, y_b) < 0$ . Therefore, the number of intersections of  $p(x, y_b)$  between  $x = 0$  and  $x = x^*$ , both inclusive, with the  $x$ -axis is exactly 1.

But  $x^* > \lambda(0)$  and  $p(x^*, 0) = p(x^*, y_b) < 0$ , therefore, the curve  $p(x, 0)$  will intersect the  $x$ -axis at some  $x_2$ ,  $\lambda(0) < x_2 < x^*$ . This implies that there is some  $y_1$  such that  $p(x, y_1)$  is tangent to the  $x$ -axis at some point between  $\lambda(0)$  and  $x_2$ . The reason is as follows.

For the sake of convenience, let  $x_1$  denote  $\lambda(0)$ . We recall that the function  $p(x, y)$  is of the form  $r(x) + ys(x)$ . We show that there exist  $x_m, x_1 < x_m < x_2$ , and some  $y_1$  such that  $r(x_m) + y_1s(x_m) = 0$  as well as  $r'(x_m) + y_1s'(x_m) = 0$ . ( $r'(x)$  and  $s'(x)$  denote the derivatives of  $r(x)$  and  $s(x)$ .) For this to happen,

$$\frac{r(x_m)}{s(x_m)} = \frac{r'(x_m)}{s'(x_m)} = -y_1$$

will hold.

We define  $g(x)$  as

$$g(x) = r(x)s'(x) - r'(x)s(x)$$

As  $p(x_1, 0) = p(x_2, 0) = 0$ , we have  $r(x_1) = r(x_2) = 0$ . Further, as  $p'(x_1, 0) > 0$  and  $p'(x_2, 0) < 0$ , we have  $r'(x_1) > 0$



and  $r'(x_2) < 0$ . Since  $p(x, y_a) < 0$  for  $x_1 \leq x \leq x_2$ , and  $y_a > 0$ , we have  $s(x_1) < 0$  and  $s(x_2) < 0$ . These facts imply that  $g(x_1) > 0$  and  $g(x_2) < 0$ . Therefore, there is an  $x_m$ ,  $x_1 < x_m < x_2$  such that  $g(x_m) = 0$ . Setting  $y_1$  as  $-\frac{r(x_m)}{s(x_m)}$ , we have that  $p(x, y_1)$  is tangent to the  $x$ -axis at  $x_m$ . Continuity of  $p(x, y)$  in  $y$  implies that there is a  $y_c$  in the neighbourhood of  $y_1$  such that  $p(x, y_c)$  either has a maximum below the  $x$ -axis, or a minimum above the  $x$ -axis. But  $p(x, y_c)$  is a degree  $n$  polynomial in  $x$ , therefore, it can have at most  $(n-1)$  maxima/minima in total. Further,  $p(x, y_c)$  has  $n$  real roots. So, between each pair of consecutive roots there will be exactly one maximum or one minimum, counting multiplicities, implying that it cannot have a maximum below the  $x$ -axis or a minimum above the  $x$ -axis. Hence, the assumption that  $\lambda(y_b) < \lambda(y_a)$ , even though  $y_b > y_a$ , is false in the present case.

**Case (ii):  $\lambda(0) > x^*$ .**

Consider an  $x_1$ ,  $x_1 > x^*$  but very close to  $x^*$ . It is clearly the case that  $p(x_1, y_b) > p(x_1, y_a)$ . From the linearity of  $p(x, y)$  in  $y$ , we get  $p(x_1, \delta) > p(x_1, 0)$  (recall that  $\delta$  is strictly greater than 0). This will imply that either  $\lambda(\delta) < \lambda(0)$  which contradicts Lemma 1, or that the curve  $p(x, \delta)$  will have a maximum below the  $x$ -axis in the range  $x_1 < x < \lambda(\delta)$ , which is again not possible, as we argued in Case (i) proof. This concludes the proof of Case (ii), as well as the proof of the theorem.  $\square$

#### 4. Discussion

We discuss in this section the relevance of our main result to the conjecture of Šali, Shakhnovich, and Karplus. First, we note that our result is about mixing times whereas the experiments on which their conjecture was based [6] measured the first passage times to the goal states, namely, configurations with the lowest free energy. This difference however does not diminish the relevance of our result for the following reasons. One may state their conjecture as: *When the Metropolis algorithm is used in the lattice model of protein folding to search for minimum energy conformations, the search will be efficient, i.e., the expected time to reach the goal state will be bounded by a fixed polynomial in the instance size, if and only if in the problem instance there is a pronounced gap in the energies between the conformation with the minimum energy and the one with the second minimum energy.* However, we know from [5] that if the expected time the Metropolis algorithm takes to find the minima in a search problem is bounded by a fixed polynomial in the instance size then, necessarily, the Markov chains that the Metropolis algorithm runs on the instances will all be rapidly mixing. In this paper we have considered the effect of increasing  $V_0$  leaving the other  $V_i$ 's unchanged. Now, if for every instance, the expected time to reach the minimum energy conformation depends solely on the energy difference between the energies of the minimum energy state and the state with the second minimum energy, it is not unreasonable to expect that the mixing time will decrease with an increase in  $V_0$  value. However, as we have seen in our Theorem 1, this does not happen.

We note, however, that in the experiments of Šali et al., the energy of a configuration was determined by the mod-

eling of the attractive forces between pairs of beads (representing the amino acids of a polypeptide) in a certain, physically justified, manner. When we simply increase  $V_0$  as we did, keeping the rest of the  $V_i$ 's the same, it is quite possible that the resultant stationary probabilities in the new chain will not correspond to any energy distribution that would have the physical justification provided in [6]. Also, the proof of our result depends crucially on the fact that the characteristic polynomial is linear in  $y$  (i.e.,  $1/V_0$ ). Our proof technique, therefore, will fail if a change in  $V_0$  affects some other  $V_i$ 's as well. In other words, our result may be interpreted as a refutation of a very strong reading of the conjecture, namely, if the energy of the minimum energy configuration decreases then *necessarily* the mixing time will decrease also.

#### 5. Concluding remarks

We have investigated in the paper the effect of increasing the difference between the energies of the lowest and the second-lowest energy states on the mixing time of the Markov chain of a Metropolis algorithm that seeks to find the lowest energy state. We show that such an increase in the difference will not reduce the mixing time of the chain; our result thus contradicts what [1] had expected. The limitation of our result is that the difference is increased in a certain manner which has been crucially exploited in the proof of our result; our proof technique, therefore, is unlikely to extend to cases where the minimum energy state is made more pronounced in some other way. Thus, an immediate open problem is to consider different, possibly physically more justifiable, ways of increasing the gap between the energies of the minimum energy state and the state with the next minimum energy. On a more technical note, it would be nice to strengthen our result to show that the second smallest eigenvalue  $\lambda(y)$  of  $N(y)$  is an *increasing* function in  $y$ . To do so, besides what we have done here, we would also need to prove that there exist no  $y_1, y_2, 0 \leq y_1 < y_2$  with  $\lambda(y_1) = \lambda(y_2) = w$ , (say). It would follow immediately then that for every value of  $y$ ,  $w$  would be an eigenvalue of  $N(y)$ . The limited experimentation that we did suggests that such is not the case; however, we have not been able to provide a proof for it.

Besides the immediate context of the Šali, Shakhnovich and Karplus conjecture, our result may be considered of interest because ours is a statement about the performance of the Metropolis algorithm solely on one aspect of the stationary probabilities of the underlying Markov chain. The work of Sasaki [3] is also of a similar kind, as it provides a lower bound on a performance measure of the Metropolis algorithm in terms of *density* of states, the density  $D(\pi)$  being the ratio of the number of states with the stationary probability  $\pi$  and the total number of states.

#### References

- [1] Peter Clote, Protein folding, the Levinthal paradox and rapidly mixing Markov chains, in: Proceedings of 26th International Colloquium on Automata, Languages and Programming, in: LNCS, vol. 1644, 1999, pp. 240–249.

- [2] David A. Levin, Yuval Peres, Elizabeth L. Wilmer, *Markov Chains and Mixing Times*, American Mathematical Society, 2009.
- [3] Galen Sasaki, The effect of the density of states on the Metropolis algorithm, *Inform. Process. Lett.* 37 (1991) 159–163.
- [4] Alistair Sinclair, *Algorithms for Random Generation and Counting: A Markov Chain Approach*, Birkhäuser, Berlin, 1993.
- [5] Swagato Sanyal, S. Raja, Somenath Biswas, Necessary and sufficient conditions of the Metropolis algorithm for optimization, in: *Proceedings of the Tenth ACM GECCO 2010*, 2010, pp. 1417–1424.
- [6] Andrej Šali, Eugene Shakhnovich, Martin Karplus, How does a protein fold?, *Nature* 369 (1994) 249–252.
- [7] Andrej Šali, Eugene Shakhnovich, Martin Karplus, Kinetics of protein folding: A lattice model study of the requirement for folding to the native state, *J. Mol. Biol.* 235 (1994) 1614–1636.
- [8] J. Skolnick, A. Kolinski, Dynamic Monte Carlo simulation of a new lattice model of globular protein folding, structure and dynamics, *J. Mol. Biol.* 221 (1991) 499–531.