Thermodynamic stability of small-world oscillator networks: 
A case study of proteins

Jie Ren† and Baowen Li‡

NUS Graduate School for Integrative Sciences and Engineering, Singapore 117597, Republic of Singapore and
Department of Physics and Centre for Computational Science and Engineering,
National University of Singapore, Singapore 117542

(Dated: May 7, 2009)

We study vibrational thermodynamic stability of small-world oscillator networks, by relating the average mean-square displacement $S$ of oscillators to the eigenvalue spectrum of the Laplacian matrix of networks. We show that the cross-links suppress $S$ effectively and there exist two phases on the small-world networks: 1) an unstable phase: when $p \ll 1/N$, $S \sim N$; 2) a stable phase: when $p \gg 1/N$, $S \sim p^{-1}$, i.e., $S/N \sim E_{cr}^{-1}$. Here, $p$ is the parameter of small-world, $N$ is the number of oscillators, and $E_{cr} = pN$ is the number of cross-links. The results are exemplified by various real protein structures that follow the same scaling behavior $S/N \sim E_{cr}^{-1}$ of the stable phase. We also show that it is the “small-world” property that plays the key role in the thermodynamic stability and is responsible for the universal scaling $S/N \sim E_{cr}^{-1}$, regardless of the model details.

PACS numbers: 87.14.E-, 05.40.-a, 89.75.-k

Vibrational dynamics has been widely used to study thermodynamic properties of various structures in solid state physics and/or other disciplines [1]. Since the structure is considered as a primary factor responsible for physical properties, to keep the underlying structure thermally stable is of primary importance for systems to function properly. For example, proteins, comprising an extremely heterogeneous class of biological macromolecules, must be stable enough against thermal fluctuations and/or external perturbations so as to maintain their native structures and to function correctly [2, 3].

Therefore, a natural and important question is often asked: what is the structure effect on thermodynamic stability? In this paper, we study the stability of small-world structures [4], which is then exemplified by proteins.

The dynamics of $N$ coupled oscillators on the network in contact with the external heat reservoir can be expressed as:

$$M \ddot{q} = - \sigma Lq - \Gamma \dot{q} + \xi$$  \hspace{1cm} (1)

where $q = [q_1, q_2, ..., q_N]^T$, denotes the oscillator’s displacements from the equilibrium positions. $M_{ij} = m \delta_{ij}$ is the mass matrix, where $m$ denotes the mass of the $i$th oscillator. $\sigma$ is the spring constant. $L_{ij} = \delta_{ij} \sum_m A_{im} - A_{ij}$ is the Laplacian matrix and $A_{ij}$ is the adjacency matrix of the network, where $A_{ij} = 1$ if $i$ and $j$ are connected and $A_{ij} = 0$ otherwise. $\Gamma_{ij} = \gamma_i \delta_{ij}$ is the dissipation matrix where $\gamma_i$ is the dissipation coefficient of the $i$th oscillator influenced by the heat reservoir. Vector $\xi = [\xi_1, \xi_2, ..., \xi_N]^T$ denotes the thermal fluctuation with zero mean and variance $\langle \xi_i(\tau) \xi_j(\tau') \rangle = 2k_B T \Gamma_{ij} \delta(\tau - \tau')$, which is the usual fluctuation-dissipation relation.

The harmonic potential we adopt looks very simple but can capture the main features of the system. For example, Tirion [5] demonstrates that a single-parameter harmonic potential can reproduce vibrational properties of the real macromolecular system very well. Thereafter, the Gaussian network model (GNM) [6] has been widely used in protein research and yields results in good agreement with experiments. In the GNM model, the interactions are considered as homogeneous harmonic springs, which is in analogy with the elasticity theory of random polymer networks [7, 8].

The correlation matrix of oscillator displacements at the steady state for Eq. (1) can be easily obtained (see Appendix A):

$$C_{ik} = \langle q_i q_k \rangle = \frac{k_B T}{\pi} \int_{-\infty}^{+\infty} d\omega (\omega G^{-1}(\omega) \Gamma G^{-1}(-\omega))_{ik},$$  \hspace{1cm} (2)

where matrix $G(\pm \omega) = (\pm \omega)^2 M + (\pm \omega) \Gamma + \sigma L$. Since $G(\omega) - G(-\omega) = 2i\omega \Gamma$ and $G(0) = \sigma L$, one can eliminate $\Gamma$ in the above integral and obtain:

$$C = -\frac{k_B T}{\pi} \int_{-\infty}^{+\infty} \frac{d\omega}{\omega} G^{-1}(\omega) = \frac{k_B T}{\sigma} L^\dagger,$$  \hspace{1cm} (3)

where $L^\dagger$ denotes the pseudo-inverse of $L$. It excludes zero mode which corresponds to the translational invariance of the system, and is the inverse of $L$ in the subspace orthogonal to the zero mode:

$$L^\dagger_{ij} = \sum_{\alpha=1}^{N-1} \frac{1}{\lambda_\alpha} \psi_{\alpha i} \psi_{\alpha j},$$  \hspace{1cm} (4)

where $\lambda_\alpha$ are the non-zero eigenvalues, and $\psi_{\alpha i}$ denote the corresponding normalized eigenvectors of $L$. Therefore, we can obtain the average mean-square displacement straightforwardly:

$$S = \frac{1}{N} \sum_i^{N} \langle q_i^2 \rangle = \frac{1}{N} \text{tr } C = \frac{k_B T}{N\sigma} \sum_{\alpha=1}^{N-1} \frac{1}{\lambda_\alpha}.$$  \hspace{1cm} (5)
This formula relates the dynamic vibration property $S$ to the static structure property — the eigenvalue spectrum of Laplacian matrix $L$. When the average mean-square displacement $S$ reaches the square of the typical spacing between oscillators, the structure encounters large vibrations and becomes unstable. Thus, small value of $S$ means stable, while large value means unstable. It is clear that lower temperature or larger spring constant indicates more thermal stability. Therefore, to study the structure effect on thermodynamic stability . Therefore, to study the structure effect on thermodynamic stability of the system. A specific case is when adding cross-links always decrease $S$ so as to increase the thermal stability of the system. A specific case is when adding cross-links always decrease $S$. Therefore, the new average mean-square displacement is

$$S' = \frac{1}{N} \text{tr} C' = S - \frac{1}{N(1 + R_{ij})} \sum_{k=1}^{N} (\psi_{ik} - \psi_{kj})^2 \lambda_i.$$  

(9)

The second term in Eq. (9) is positive so that the value of new $S'$ is always smaller than $S$. In other words, the cross-links always decrease $S$ so as to increase the thermodynamic stability of the system. A specific case is studied and illustrated in Fig. 1.

In the following study, we choose a typical model to construct the small-world structure [10]. We first consider $N$ oscillators (which might be an atom, a molecule,
or other module structure, depending on the system studied) on a one-dimensional (1D) ring chain, i.e., with periodic boundary conditions. Each oscillator is connected to its nearest-neighbors. Then, we add a cross-link to each oscillator with probability \( p \), which connects to another non-neighboring oscillator randomly. Thus, \( E_{cr} = pN \) is the number of cross-links. When \( p = 0 \), the structure reduces to the 1D ring chain. In all cases studied below, each data point is obtained by averaging over 50 different network configurations for a given \( p \) and \( N \).

Figure 2(a) illustrates \( S \) versus the system size \( N \) for different values of \( p \) in double logarithmic scale. The \( p = 0 \) case, corresponding to the 1D ring structure, shows the power-law divergence, \( S \sim N \). It indicates that no thermodynamically stable solid exists at finite temperature in 1D. Indeed, when the average mean-square displacement \( S \) exceeds the square of the typical spacing between oscillators, the structure behaves like a liquid rather than a solid, and the crystalline order makes no sense anymore. This behavior is also reported in Refs. 11, 12. For the case of \( p \neq 0 \), even of small value, as \( N \) increases, \( S \) is saturated to a finite value rapidly. Moreover, from Fig. 2(b), we can see that the larger \( p \), the smaller \( S \) and in the large \( N \) limit, a scaling \( S \sim p^{-1} \) emerges. All the above results indicate that the cross-links suppress the average mean-square displacement \( S \) effectively and make it convergent in the thermodynamic limit.

To eliminate the finite size effect, all the data from Fig. 2 are re-scaled and the results are illustrated in Fig. 3. It is found that all data points collapse into one single line very well and two distinct phases emerge. For \( p < 1/N \), there is a horizontal regime, \( S/N \sim \) const. It indicates an unstable phase: when the number of cross-links is smaller than one, \( S \) diverges with \( N \). For \( p \gg 1/N \), there is a regime with slope \( -1 \), \( S/N \sim E_{cr}^{-1} = (pN)^{-1} \), which indicates a convergent stable phase. In other words, when the number of cross-links is much larger than one, \( S \) approaches a finite value at large \( N \) and scales as \( p^{-1} \).

Since the average mean-square displacement \( S \) is related to the spectral properties of the Laplacian matrix \( L \), we can understand the scaling behavior of \( S \) in terms of its eigenvalue spectrum \( \rho(\lambda) \). For large size \( N \), Eq. (9) can be expressed as:

\[
S = \int \frac{\rho(\lambda)}{\lambda} d\lambda, \tag{10}
\]

from which we can easily see that the density of small \( \lambda \) dominates the behavior of \( S \). For the case without cross-links, the system reduces to a 1D ring chain,
where \( \rho(\lambda) \sim \lambda^{-1/2} \) and \( \lambda \sim N^{-2} \) for small \( \lambda \). Thus, \( S \sim \int \lambda^{-3/2} d\lambda \sim N \). For the case with cross-links, following the heuristic argument in [14], we can consider that the ring chain is divided into several quasi-linear segments of length \( l \), and the probability of length \( l \) is exponentially small, \( e^{-pl} \). Each segment \( l \) contributes to small eigenvalues of the order of \( l^{-2} \). Summing over lengths with the exponential weight, we obtain \( S = \int \rho(\lambda) d\lambda \sim \sum_{l=1}^{N} \frac{1}{l} e^{-pl} = \frac{1}{p} (1 - e^{-pN}) \). When \( pN \ll 1 \), \( S \sim N \); while \( pN \gg 1 \), \( S \sim 1/p \), which is exactly what our numerical results show in Fig. 2 and 3. Although the argument above is not rigorous and applies only when \( p \) is smaller than one, it gives us quite good understanding of the scaling behavior of \( S \). When \( p \) is larger than one, the model we used is more like an Erdős-Rényi model, which is also to be demonstrated to follow the same scaling of the stable regime at the end of this paper.

The small-world structure we used above is well studied [10]. Using renormalization group method, the authors in Ref. [10] showed that this model undergoes a transition between regular lattice and random one at intermediate characteristic size \( N_c \sim p^{-1} \). In other words, the phase transition has a critical point \( p_c = 0 \) in the thermodynamical limit when \( N \to \infty \). For finite size \( N \), the diameter \( l \) scales linearly with \( N \) for \( N_c \gg N \) as it is in a 1D ring chain, while \( l \sim \ln N \) for \( N \gg N_c \), where it exhibits “small-world” property. Our results about unstable and stable phases are consistent with their findings that the unstable regime corresponds to the 1D case and the stable phase corresponds to the “small-world” case.

As an illustrative example, the thermodynamic stability is further tested on real protein data. We revisit the proteins used in Ref. [2], which differ in functions and structures, with a wide size scale ranging from 100 to 3600 residues. All the structure data are downloaded from the Protein Data Bank (PDB) [15] and the number of all residue pairs is counted within a customary cut-off 7.0 Å. After eliminating the connectivity number of the primary structure of protein from the counted number, we obtain the number of cross-links, \( E_{cr} \), for each protein. The mean square displacement of \( C^\alpha \) atoms is characterized by \( B \)-factor, also called Debye-Waller or temperature factor: \( B_i = 8\pi^2(q_i^2)/3 \), where \( i \) is the index of amino acid residue. It is experimentally measured via x-ray crystallography, and also can be downloaded from the PDB. The average \( B \)-factor is calculated over all \( C^\alpha \) atoms for each protein, \( B = \sum_{i=1}^{N} B_i/N \). Notice that above theoretical analysis, \( k_BT/\sigma \) is set to be 1 for convenience, which is not always true. The value of \( k_BT/\sigma \) varies among different proteins. Thus, we use the estimated data of \( k_BT/\sigma \) [2] to obtain the normalized average \( B \)-factor, \( B' = B/(k_BT/\sigma) \). Note that \( B' \) is analogous to \( S \), defined in Eq. [10]. All the details of these proteins are listed in Table 1 in Appendix [4].

The thermodynamic stability is crucial to keep the native structure of protein for right function. Moreover the structure of protein is also found to have “small-world” property [17], i.e., \( l \sim \ln N \). It is intuitive for us to expect that nature selection forces proteins evolving into the stable phase in Fig. 3 which implies \( B'/N \sim E_{cr}^{-a} \). Figure 4(a) verifies our expectation drawn from the argument of stability analysis. In fact, we obtain a clear power-law scaling:

\[
B'/N \sim E_{cr}^{-a}, \quad a = 0.92 \pm 0.01,
\]

which is quite close to 1. This scaling reveals the universal behavior shared by various different proteins, regardless of their sources or functions. It implies an underlying general mechanism that nature selects proteins with thermodynamic stability constraints.

Although protein has more complex structures with high modularity(domains), “small-world” property captures its main feature. Thus, “small-world” might play a key role in the thermodynamic stability of structures and be responsible for the scaling in the stable regime. To validate our conjecture, we further study the thermodynamic stability in Erdős-Rényi(ER) random network model in the following.

ER model [18] has \( N \) nodes and every pair of nodes is connected with probability \( p_r \). The average degree \( \langle k \rangle = p_r(N-1) \). There are several phases in this model depending on different threshold \( p_r \): when \( \langle k \rangle = p_r(N-1) > 3.5 \) [18], the diameter of the graph equals the diameter of the giant cluster, and is proportional to \( \ln N \), i.e., “small-world” property. Thus, it is straightforward to expect that ER model might share the same behavior \( S/N \sim E_{cr}^{-1} \). The numerical result is illustrated in Fig. 4(b). As we point out above, ER model has “small-world” property [19] when \( p_r(N-1)/2-1 > 0.75 \), \( S \sim N/E_{cr} = \)
pressed as the mean of inverse eigenvalues of its Laplacian and is responsible for the universal scaling $S/N \sim E^{-1}$ in the stable regime, regardless of the model details. Note that for proteins, $S = B'(8\pi^2)$, where the factor 3 is removed since $B$-factor is measured in 3-dimension.

For convenience of comparison, we plot the data of three cases together in Fig. 5. It clearly shows the universal scaling $S/N \sim E^{-1}$ in the regime where the three structures all have “small-world” property, $l \sim \ln N$. Moreover, we have tested other network models showing the property $l \sim \ln N$. The results indicate that the “small-world” property plays a key role in the stable regime and is responsible for the universal scaling, regardless of the model details, which can be explained in the framework of a mean-field approach.

In summary, we have studied the vibrational thermodynamic stability of small-world structures. The average mean-square displacement $S$ of the structure has been expressed as the mean of inverse eigenvalues of its Laplacian matrix $L$. Therefore, the dynamic vibration property is closely related to the static structure information. It is found that the cross-links suppress $S$ effectively and on the small-world network model, there exist two phases: an unstable phase where $p \ll 1/N$, $S \sim N$ and a stable phase where $p \gg 1/N$, $S \sim p^{-1}$, i.e., $S/N \sim E^{-1}$. Further, we have tested various data from the PDB and find that native proteins belong to the stable phase and share the same scaling behavior $S/N \sim E^{-1}$. It is believed that nature selects proteins under the constraint of thermodynamic stability so that proteins can keep their specific native fold structure stable for proper function. Finally, we have studied $S$ in ER random network model and have validated our conjecture that it is the “small-world” property that plays a key role in the thermodynamic stability of structures and is responsible for the universal scaling, $S/N \sim E^{-1}$, in the stable regime. It is also interesting to examine more complex structure effects on the thermodynamic stability problem, such as scale-free networks, hierarchical structures, networks with community structure, etc. More realistic considerations such as the effect of random coupling constants, anharmonic potentials, or even quantum version of vibration dynamics are worth further studying.

The work is supported by the NUS Faculty Research Grant No. R-144-000-165-112/101.

APPENDIX A: DERIVATION OF THE CORRELATION MATRIX

To make this paper self-contained and readable, we complement the detailed derivation of Eq. (2) which is expressed in terms of $G$ in Fourier transform space. We follow Ref. [21] by defining the Fourier transform as

$$Q(\omega) = \frac{1}{2\pi} \int_{-\infty}^{+\infty} q(t)e^{-i\omega t} dt; \quad (A1)$$

$$\eta(\omega) = \frac{1}{2\pi} \int_{-\infty}^{+\infty} \xi(t)e^{-i\omega t} dt. \quad (A2)$$

Applying Fourier transform to both sides of Eq. (1), one obtains

$$-\omega^2 MQ = -\sigma LQ - i\omega \Gamma Q + \eta. \quad (A3)$$

Simple algebraic operation yields,

$$Q = G^{-1}(i\omega)\eta, \quad (A4)$$

where matrix $G(i\omega) = -\omega^2 M + i\omega \Gamma + \sigma L$ as defined in text. The two point correlation function is

$$\langle q(t + \tau)q_k(t) \rangle = \int_{-\infty}^{+\infty} d\omega e^{i\omega(t+\tau)} \int_{-\infty}^{+\infty} d\omega' e^{-i\omega' t} \langle Q(\omega)Q^{*}\rangle$$

$$= \int_{-\infty}^{+\infty} d\omega e^{i\omega(t+\tau)} \int_{-\infty}^{+\infty} d\omega' e^{-i\omega' t} \times \langle \eta(\omega)\eta^{*}(\omega') \rangle [G^{-1}(i\omega)G^{-1}(-i\omega')]_{kk}. \quad (A5)$$

where $\ast$ denotes the conjugate transpose and $Q^{*}(\omega') = \eta^{*}(\omega')G^{-1}(-i\omega')$. Moreover, since

$$\langle \eta(\omega)\eta^{*}(\omega') \rangle = \frac{1}{2\pi} \int_{-\infty}^{+\infty} dt e^{-i\omega t}$$

$$\times \frac{1}{2\pi} \int_{-\infty}^{+\infty} dt' e^{i\omega' t'} \langle \xi(t)\xi^{*}(t') \rangle$$

$$= \frac{k_B T T}{\pi} \frac{1}{2\pi} \int_{-\infty}^{+\infty} e^{i(\omega'-\omega)t}$$

$$= \frac{k_B T}{\pi} \delta(\omega'-\omega), \quad (A6)$$

substitute Eq. (A6) into Eq. (A5) and we have:

$$\langle q(t + \tau)q_k(t) \rangle = \frac{k_B T}{\pi} \int_{-\infty}^{+\infty} d\omega e^{i\omega T} [G^{-1}(i\omega)G^{-1}(-i\omega)]_{kk}. \quad (A7)$$
The expression of correlation matrix Eq. (2) corresponds to the special case $\tau = 0$.

APPENDIX B: INFORMATION OF PROTEINS

| PDB code | Size $N$ | $E_{cr}$ | $B$ | $kB T/\sigma$ | $B'/N$ |
|----------|----------|---------|-----|--------------|--------|
| 9RNT  | 104 | 303 | 10.9147 | 1.537 | 0.06334 |
| 1BVC  | 153 | 469 | 8.33124 | 0.575 | 0.03086 |
| 1G12  | 167 | 584 | 14.4393 | 0.793 | 0.10903 |
| 1AMM  | 174 | 612 | 0.06793 | 0.003 | 0.13013 |
| 1KNB  | 186 | 616 | 18.7711 | 1.104 | 0.09141 |
| 1CUS  | 197 | 671 | 16.6598 | 0.914 | 0.09252 |
| 1HQQ  | 200 | 634 | 10.1640 | 0.480 | 0.05468 |
| 2AYH  | 214 | 744 | 9.9678 | 0.539 | 0.08642 |
| 1AE5  | 223 | 768 | 19.9342 | 0.952 | 0.09390 |
| 1LST  | 239 | 799 | 20.2462 | 0.654 | 0.05547 |
| 1NAR  | 289 | 925 | 13.5809 | 0.602 | 0.06355 |
| 1AS8  | 298 | 928 | 16.3599 | 0.664 | 0.08268 |
| 1A3H  | 309 | 1088 | 21.3477 | 1.068 | 0.03581 |
| 1ADS  | 315 | 993 | 10.7205 | 0.5  | 0.06807 |
| 1A40  | 321 | 1117 | 34.2736 | 1.369 | 0.07133 |
| 1A54  | 321 | 1144 | 11.6098 | 0.601 | 0.06018 |
| 1A0I  | 332 | 1175 | 27.2887 | 1.109 | 0.07412 |
| 3PTE  | 347 | 1210 | 8.13032 | 0.366 | 0.06402 |
| 1A26  | 351 | 1070 | 21.3477 | 1.068 | 0.03581 |
| 1BVW  | 360 | 1209 | 13.0188 | 0.652 | 0.05547 |
| 8JDW  | 360 | 1191 | 12.8334 | 1.293 | 0.05120 |
| 7GDC  | 387 | 1266 | 19.8278 | 0.859 | 0.05964 |
| 1OYC  | 399 | 1378 | 20.4127 | 1.056 | 0.04845 |
| 1A39  | 410 | 1474 | 21.4742 | 1.113 | 0.04706 |
| 1A54  | 321 | 1114 | 11.6098 | 0.601 | 0.06018 |
| 1A0I  | 332 | 1175 | 27.2887 | 1.109 | 0.07412 |
| 3PTE  | 347 | 1210 | 8.13032 | 0.366 | 0.06402 |
| 1A26  | 351 | 1070 | 21.3477 | 1.068 | 0.03581 |
| 1BVW  | 360 | 1209 | 13.0188 | 0.652 | 0.05547 |
| 8JDW  | 360 | 1191 | 12.8334 | 1.293 | 0.05120 |
| 7GDC  | 387 | 1266 | 19.8278 | 0.859 | 0.05964 |
| 1OYC  | 399 | 1378 | 20.4127 | 1.056 | 0.04845 |
| 1A39  | 410 | 1474 | 21.4742 | 1.113 | 0.04706 |

TABLE I: Information of Proteins used in the present study. Size $N$ is the number of residues. $E_{cr}$ is the number of cross-links, counted within cutoff 7 Å. $B$ is the average $B$-factor over all Cα atoms for each protein. The estimated $kB T/\sigma$ are collected in Ref. [2]. $B'/N$ is the normalized $B$-factor over the size of protein.

[1] C. Kittel, Introduction to Solid State Physics, (John Wiley, Singapore, 1996).
[2] R. Burioni, D. Cassi, F. Cecconi, and A. Vulpiani, Proteins: Struct. Funct. Bioinf. 55, 529 (2004).
[3] S. Reuveni, R. Granek, and J. Klafter, Phys. Rev. Lett. 100, 208101 (2008).
[4] D.J. Watts and S.H. Strogatz, Nature 393, 440 (1998).
[5] M.M. Tirion, Phys. Rev. Lett. 77, 1905 (1996).
[6] T. Haliloglu, I. Bahar, and B. Erman, Phys. Rev. Lett. 79, 3090 (1997); I. Bahar, A.R. Atilgan, and B. Erman, Folding Des. 2, 173 (1997); Q. Cui and I. Bahar, Normal Mode Analysis, (Chapman&Hall/CRC, London, 2006).
[7] P.J. Flory, Proc. R. Soc. London A 351, 351 (1976).
[8] D.S. Pearson, Macromolecules 10, 696 (1977).
[9] G.D. Mahan, Many-Particle Physics, (Plenum Press, New York, 2000).
[10] M.E.J. Newman and D.J. Watts, Phys. Lett. A 263, 341 (1999).
[11] R. Peierls, Helv. Phys. Acta 7, Suppl. 2, 81 (1934).
[12] R. Burioni, D. Cassi, M.P. Fontana, and A. Vulpiani, Europhys. Lett. 58, 806 (2002).
[13] We add two more cases ($p = 5$ and $p = 10$) for all sizes. Here, $p$ is larger than one, which means adding to each oscillator $p$ cross-links on average.
[14] A.J. Bray and G.J. Rodgers, Phys. Rev. B 38, 11461 (1988); R. Monasson, Eur. Phys. J. B 12, 555 (1999).
[15] F.C. Bernstein et al., J. Mol. Biol. 112, 535 (1977).
[16] U.G. Wagner et al., J. Mol. Biol. 247, 326 (1995).
[17] M. Vendruscolo, N.V. Dokholyan, E. Paci, and M. Karplus, Phys. Rev. E 65, 061910 (2002); A.R. Atilgan, P. Akan, and C. Baysal, Biophys J. 86, 85, (2004).

[18] B. Bollobás, Random Graphs (Academic Press, New York, 1985).

[19] Note that in this paper, we only refer to the “small-world” property to short average path length, i.e., $l \sim \ln N$, although the “small-world” properties used nowadays include the additional property of high clustering, after Ref. [4].

[20] J. Ren and B. Li (in preparation).

[21] R. Kubo, M. Toda, and N. Hashitsume, Statistical Physics II, (Springer, New York, 1991).