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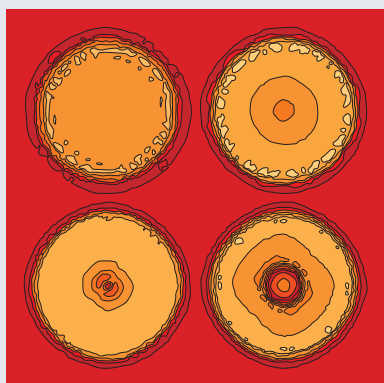
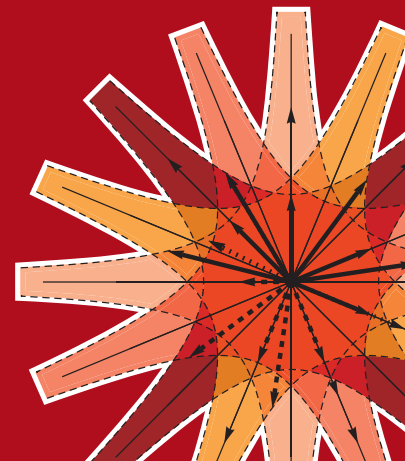


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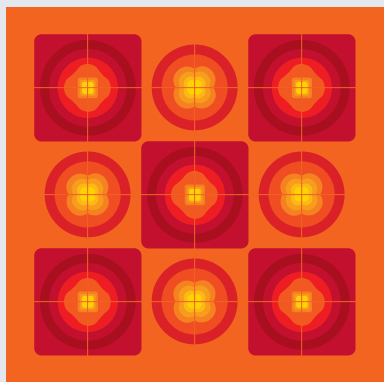
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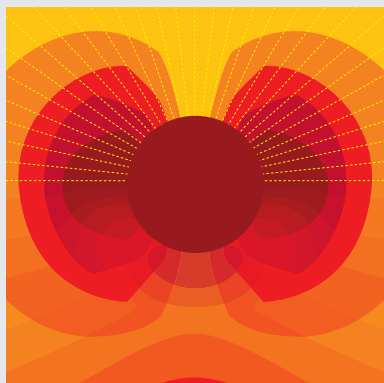
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Image: Ornamental multiplication of space-time figures of temperature transformation rules (adapted from T. S. Bíró and P. Ván 2010 *EPL* **89** 30001; artistic impression by Frédérique Swist).

Extreme variability in convergence to structural balance in frustrated dynamical systems

RAJEEV SINGH¹, SUBINAY DASGUPTA² and SITABHRA SINHA¹

¹ *The Institute of Mathematical Sciences, CIT Campus - Taramani, Chennai 600113, India*

² *Department of Physics, University of Calcutta - 92 Acharya Prafulla Chandra Road, Kolkata 700009, India*

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Abstract – In many complex systems, heterogeneous connections can subject constituent elements to conflicting influences, resulting in frustration. Here we show numerically that an initially frustrated system can achieve structural balance by a link adaptation process inspired by Hebb's principle, with interaction strengths evolving in accordance with the dynamical states of its components. In the presence of fluctuations the time required to converge to the balanced state exhibits large dispersion characterized by a bimodal distribution, pointing to an intriguing problem in the study of evolving energy landscapes.

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A variety of critical phenomena has been observed in complex systems comprising many dynamical elements and interacting via a non-trivial connection topology [1–3]. While the coevolution of network structure and nodal activity in such systems has been studied extensively [4–9], in most cases only the presence or absence of links were considered. In contrast, many naturally occurring networks have links with heterogeneously distributed properties. Connections in such systems can differ *quantitatively* by having a distribution of weights (that may for instance represent the strength of interaction) [10,11] and/or *qualitatively* through the nature of their interactions, *viz.*, positive (cooperative or activating) and negative (antagonistic or inhibitory) [12]. The presence of negative links can introduce frustration through the presence of inconsistent relations within cycles in the system [13,14]. Networks whose positive and negative links are arranged such that frustration is absent are said to be *structurally balanced* —a concept that was originally introduced in the context of social interactions [15]. A balanced network can be always represented as comprising two subnetworks, with only positive interactions within each subnetwork, while links between the two are exclusively negative [16]. Networks of dynamical elements with such structural organization are capable of exhibiting non-trivial collective phenomena, *e.g.*, “chimera” order [17]. Recently, several quantitative models have been proposed

for understanding the processes that lead to structural balance. Evolving networks in which the sign of links are flipped to reduce frustration have been shown to reach balance; however, the introduction of constraints can sometimes result in jammed states that prevent convergence to the balanced state [18,19]. Another approach, using coupled differential equations for describing link adaptation [20], has been analytically demonstrated to result in balance [21,22].

While most studies on structural balance have been carried out in the context of social networks, an important question is whether other kinds of networks, in particular those that occur in biology, exhibit balance. The recent observation that the resting human brain is organized into two dynamically anti-correlated subnetworks [23] points to the intriguing possibility that the underlying network is balanced. As connections in the brain evolve according to long-term potentiation which embodies Hebb's principle [24,25], *i.e.*, the link weights change in proportion to the correlation of the activity in the connected elements, it suggests a novel process for achieving structural balance. Thus, networks can remove frustration by adjusting the weights associated with the links in accordance with the dynamical states of their nodes. Such a local adaptation process has an intuitive interpretation in social systems, *viz.*, agents that act alike have their ties strengthened, while those behaving differently gradually

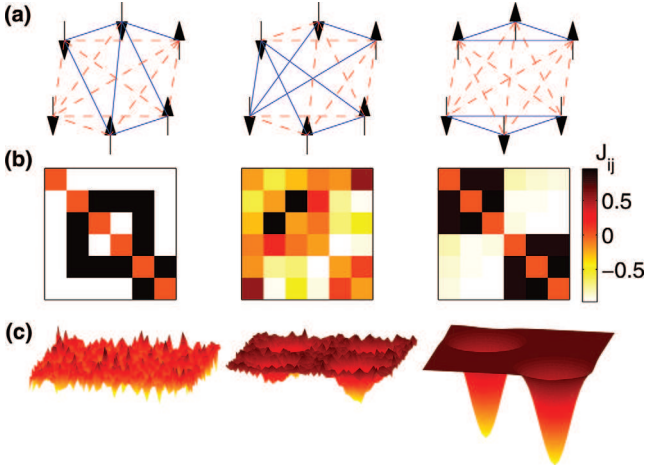


Fig. 1: (Colour on-line) Coevolution of coupling strength with the dynamics on the node starting from a disordered state of spin orientations and interaction strengths randomly selected to be ± 1 . (a) The spin configurations in the initial (left), intermediate (center) and final, *i.e.*, after convergence to structural balance (right), states. Solid (broken) lines represent positive (negative) interactions between spins. The corresponding coupling matrices J are shown in (b) while the schematic energy landscapes are represented in (c). The two minima in the balanced state correspond to the pair of degenerate ground states related by the reversal of each spin.

develop antagonistic relations. In fact, Hebb's rule may apply more broadly to a large class of systems, *e.g.*, in gene regulation networks where the co-expression of genes has been suggested to result in their co-regulation over evolutionary time-scales [26,27].

In this paper, we show that such a link-weight adaptation dynamics can in fact lead to structural balance (shown schematically in fig. 1), using only information about the pairwise correlations between the dynamical states of connected nodes. More importantly, the time required by the adaptation process to attain balance in the presence of stochastic fluctuations exhibits a surprisingly high degree of variability characterized by a bimodal distribution. We investigate this phenomenon from the perspective of an evolving energy landscape, that changes from having an initial rugged nature to a smooth structure corresponding to the balanced state. The transition occurs when the system is trapped for a sufficient duration in any of the numerous energy minima in the rugged landscape, which is then converted into a global minimum by the adaptive dynamics. The observed bimodality implies that if the system escapes being trapped at the initial stage, then it will take an extremely long time to get trapped in another minimum. Our results suggest that environmental fluctuations can prevent a system from attaining a balanced state even in the presence of appropriate adaptive dynamics, which may have important implications for biological networks.

We consider a system of N globally coupled Ising spins $\sigma_i = \pm 1$ ($i = 1, \dots, N$), the energy for a given

configuration of spins being

$$\mathcal{E} = - \sum_{i \neq j} J_{ij} \sigma_i \sigma_j, \quad (1)$$

where $J_{ij} (= J_{ji})$ represents the interaction strength between the spin pair (i, j) (see footnote ¹). The balanced state corresponds to the situation where the interactions are consistent with the states of the corresponding spin pairs, *i.e.*, J_{ij} and $\sigma_i \sigma_j$ have the same sign. Starting from a disordered spin configuration and random distribution of interactions, the states of the spins are updated stochastically at discrete time-steps using the Metropolis Monte Carlo (MC) algorithm with temperature T [29]. The interaction strengths also evolve after every MC step according to the deterministic adaptation dynamics,

$$J_{ij}(t+1) = (1 - \epsilon)J_{ij}(t) + \epsilon \sigma_i(t)\sigma_j(t), \quad (2)$$

where the adaptation rate, ϵ , governs the rate of change of the interaction relative to the spin dynamics. The J_{ij} dynamics alters the energy landscape on which the state of the spin system evolves. The *relaxation time* τ is defined as the characteristic time for reaching the balanced state. Note that the form of eq. (2) ensures that the relaxation time $\sim 1/\epsilon$ in the absence of any thermal fluctuation (*i.e.*, at $T = 0$). Also, it restricts the asymptotic distribution of J_{ij} to the range $[-1, 1]$, independent of whether the system converges to a balanced state or not.

In our simulations, the initial state of the system for each realization is constructed by choosing the spins σ_i to be ± 1 with equal probability. For most results shown here, each initial J_{ij} is chosen independently from a distribution with two equally weighted δ function peaks at ± 1 , *i.e.*,

$$P(z; \mu) = \frac{1 + \mu}{2} \delta(z - 1) + \frac{1 - \mu}{2} \delta(z + 1), \quad (3)$$

where the mean $\mu = 0$. We have verified that the results do not change qualitatively if the initial distribution has a bias, *i.e.*, non-zero mean, or has a different functional form (*e.g.*, a uniform distribution in $[-1, 1]$), provided that the system is initially far from balance. For each set of parameters (T, ϵ) , 10^4 different realizations have been used to statistically quantify the relaxation behavior of the system, which is identified using the energy per bond $E = \mathcal{E}/\binom{N}{2}$, as the order parameter. We have carried out simulations with systems of sizes ranging from $N = 64$ to $N = 512$ to ensure that the results reported here are not dependent on the system size.

In the absence of thermal fluctuations (*i.e.*, at $T = 0$), the dynamics of the system can be understood intuitively. Starting from a random initial state, the spin dynamics stop when the system gets trapped in a local energy minimum within a few MC steps. The subsequent evolution of the interaction strengths makes this configuration

¹Structural balance in real social networks have been recently investigated using a similar energy function [28].

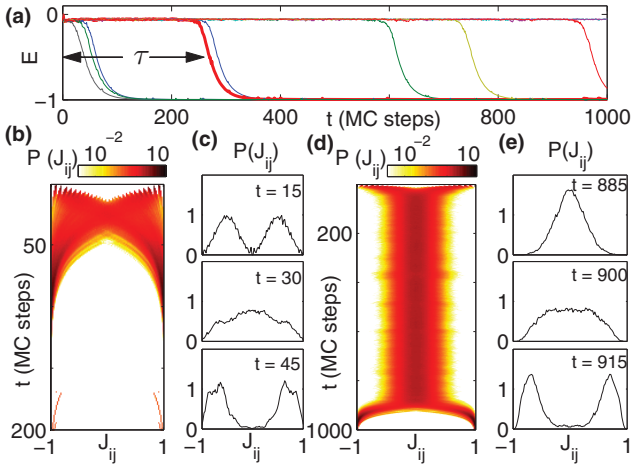


Fig. 2: (Color on-line) (a) Typical time-evolution of the energy per bond E for a system of N spins starting from different initial conditions. The relaxation time τ indicated in the figure is the duration after which E decreases below -0.5 . (b)–(e): time-evolution of the distributions for the interaction strength J_{ij} shown for two cases: when the system relaxes rapidly ((b), (c)) and when convergence takes much longer ((d), (e)). Snapshots of the J_{ij} distribution at specific times immediately before, during and immediately after the convergence are shown for the two cases in (c), (e), respectively. For all figures $N = 256$ with $T = 51$, $\epsilon = 0.05$.

a global minimum. However, at finite temperature, the stochastic fluctuations of the spins may prevent the system from remaining in a metastable state for sufficiently long. This does not allow the J_{ij} dynamics to alter the energy landscape sufficiently to make the configuration the global minimum. Thus, an extremely long time may be required to reach structural balance, and the relaxation time diverges due to the stronger fluctuations on increasing temperature.

Figure 2(a) shows the time-evolution of the order parameter E for several typical runs with different initial conditions and noise realizations of a system at finite T and ϵ . The order parameter of the system initially has a value corresponding to a maximally disordered state ($E \approx 0$) but eventually relaxes to a balanced state ($E = -1$). The time required for reaching balance, τ , is estimated by measuring the duration (starting from the initial state) after which E reaches $-1/2$ (fig. 2(a)). For a large range of parameters, we observe two very distinct types of behavior: in one, the system relaxes rapidly, while in the other this takes a longer time. Characteristic time-evolution corresponding to these two types of behavior are shown in fig. 2(b)–(e). When the system relaxes rapidly, we observe that at first smaller peaks emerge from the two peaks of the initial J_{ij} distribution (located at ± 1). These eventually cross each other to reach the opposite ends asymptotically, converging to a two-peaked distribution again (fig. 2(b), (c)), indicating that all interactions are now balanced. However, in the case where convergence takes significantly longer (fig. 2(d), (e)), the initial

distribution is first completely altered to a form resembling a Gaussian distribution with zero mean. After a long time, the system abruptly converges towards a balanced state with a corresponding transformation of the J_{ij} distribution to one having peaks at ± 1 . Note that even with the same initial spin configuration and realization of J_{ij} distribution, different MC runs generate distinct trajectories similar to those shown in fig. 2(a). This implies that knowledge of the initial conditions is not sufficient to decide whether the system will relax rapidly or not.

To quantitatively characterize the distinction between the two types of relaxation behavior, we focus on the statistics of τ . Figure 3(a) shows the distribution of the relaxation time for a given set of (T, ϵ) where cases of both fast and slow convergences are seen. The bimodal nature can be clearly observed, with the peak at lower τ (~ 100 MC steps) corresponding to fast convergence to balanced state while that occurring at a higher value ($\sim 10^7$ MC steps) arises from the instances of slow relaxation. The distribution decays exponentially at very high values of τ . Figure 3(b) shows the temperature dependence of the distribution of relaxation time for two different values of the adaptation rate. For the smaller ϵ ($= 0.03$), the second peak is well separated from the first when bimodality appears, while for the larger ϵ ($= 0.05$) the second peak appears close to the first one. To estimate the temperature at which the second peak appears, we plot the standard deviation of $\log_{10}(\tau)$ as a function of T (inset), as bimodality is characterized by an increase in the dispersion of relaxation times. In fig. 3(c), we show how varying both T and ϵ can affect the probability that the relaxation takes a long time (*viz.*, $\geq 10^5$ MC steps). We observe a monotonic increase in the probability $P(\tau > 10^5)$ from 0 to 1 as the temperature is increased for a given value of ϵ . Indeed, this is expected, as the system relaxes rapidly when the temperature is low and this probability is negligible, while, at larger temperatures the relaxation takes increasingly longer and the probability approaches 1. We can define a transition temperature $T_{1/2}(\epsilon)$ as the value of T at which this probability is equal to $1/2$. We observe that $T_{1/2}(\epsilon)$ increases with ϵ , which implies that the relaxation to the balanced state requires a longer duration as the interaction dynamics becomes slower. For a given adaptation rate, the variation of the probability $P(\tau > 10^5)$ with T for different system sizes allows us to do finite-size scaling, with data collapse occurring for a scaling exponent α (Fig. 3(d)) that varies with ϵ (inset). The variation of α with ϵ (inset) appears to reflect the transition from one type of bimodality, *i.e.*, where the second peak is clearly separated from the first, to another type where they are close (fig. 3(b)).

So far we have assumed that the initial J_{ij} distribution is unbiased (*i.e.*, $\mu = 0$). However, having a higher fraction of interactions of a particular sign can have significant consequences for both the structure of the final balanced state and the time required to converge to it. To investigate the role of this initial bias among the interaction

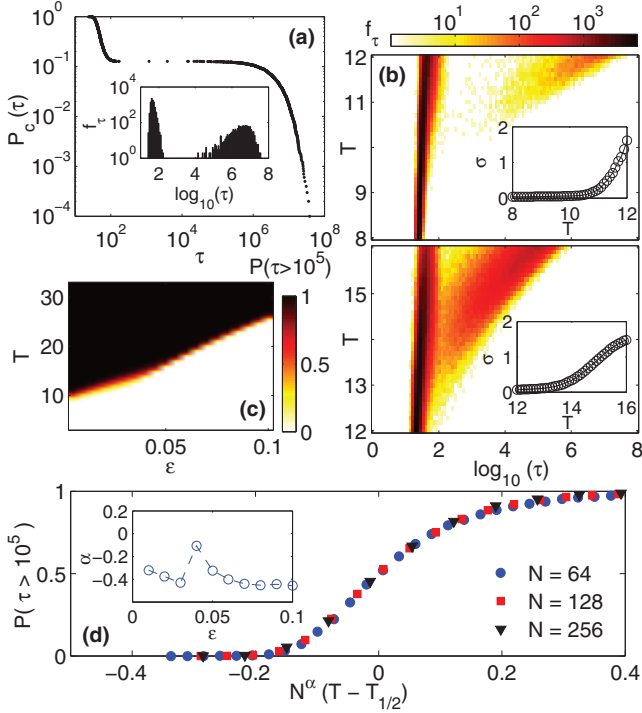


Fig. 3: (Colour on-line) (a) The cumulative distribution of relaxation time τ for a system of $N = 64$ spins with $T = 12, \epsilon = 0.03$ shows a gap, implying a bimodal nature for the distribution. The inset, showing the corresponding frequency (in log scale) histogram with logarithmic binning clearly indicates this bimodal nature. (b) Probability distributions of $\log_{10}(\tau)$, shown as a function of temperature T for $\epsilon = 0.03$ (top) and 0.05 (bottom), indicates the onset of bimodal behavior at higher values of temperature, *e.g.*, for $T \gtrsim 10$ in (top). Bimodality appears around the temperature where the standard deviation of $\log_{10}(\tau)$ starts increasing appreciably from an almost constant value (insets). (c) The probability that relaxation takes longer than 10^5 MC steps, $P(\tau > 10^5)$ shown as a function of ϵ and T . The point of transition from fast to slow convergence can be quantified by $T_{1/2}(\epsilon)$, *i.e.*, the temperature at which $P(\tau > 10^5) = 1/2$ for a given value ϵ (indicated by the boundary between the dark and light regions). (d) Finite-size scaling of the probability that relaxation takes longer than 10^5 MC steps, $P(\tau > 10^5)$, as a function of T for different system sizes N ($\epsilon = 0.05$). Reasonable data collapse is seen for the exponent $\alpha \approx -0.32$. The inset shows the scaling exponent values resulting in the best data collapse as a function of ϵ .

strengths, we consider a distribution with two differently weighted δ -function peaks at ± 1 (*i.e.*, $\mu \neq 0$). If all the interactions are anti-ferromagnetic ($\mu = -1$), the system is extremely frustrated and the relaxation to a balanced state may take a long time, whereas in the case where the interactions are all ferromagnetic ($\mu = 1$), the system is balanced to begin with. Thus, with increasing μ , we expect the relaxation time to decrease, which is indeed observed; in addition, the peak at higher values of τ disappears as μ approaches 1. On the other hand, when μ approaches -1 , the peak corresponding to shorter relaxation times is no longer present. The two clusters that comprise

the final balanced state can have very different size distributions depending on the bias in the initial distribution of J_{ij} . For the unbiased case, the two clusters are approximately of the same size. This property holds for the entire range of negative values for μ . As μ increases from 0, the size difference between the two clusters start increasing, eventually leading to a single cluster where all the spins interact with each other ferromagnetically ($\mu \simeq 1$). Note that if the system initially has a very low degree of frustration, the system relaxes almost immediately to a balanced state where the larger cluster comprises almost the entire system. To visualize the coevolving dynamics in the link weights and spin orientations as the system approaches balance for different values of μ , we use an additional order parameter [18,19] that measures the frustration in a signed network in terms of the fraction of triads deviating from balance (a triad being balanced if the product of its link weights approaches +1),

$$U = - \sum_{i,j,k} \frac{J_{ij} J_{jk} J_{ki}}{\binom{N}{3}}. \quad (4)$$

Figure 4(c) shows that the trajectories corresponding to different values of μ converge to a single curve after transients, eventually reaching the balanced state ($E = -1, U = -1$). For $\mu < 0$, the initial trajectory is approximately vertical indicating that it is dominated by the adaptation dynamics (eq. (2)), whereas for $\mu > 0$, it has a strong horizontal component implying that it is governed primarily by the MC update of the spin states. Realizations in which the system takes a long time to relax to the balanced state are distinguished by trajectories that appear to be trapped in a confined region in the (E, U) space for a considerable period (fig. 4(c), inset).

We can qualitatively explain the appearance of short relaxation times as follows. In the initial state, when the system has a random assignment of interaction strengths, the energy landscape is extremely rugged, resembling that of a spin glass [13,14]. The system starts out in a potential well corresponding to one of the many initially available local minima. As the state of the system evolves, the J_{ij} dynamics (eq. (2)) lowers the energy of the state by making the interactions consistent with the spin orientations of the system, while the spin dynamics can either result in a further lowering of energy as the state moves towards the bottom of the potential well, or escape from the initial local minimum due to thermal fluctuations. The probability of escaping from the well at the t -th iteration, $p(t)$, depends on the potential barrier height with neighboring wells. If the state cannot escape in the first few iterations from the local minimum in whose basin it starts, successive lowering of the energy of this well by the J_{ij} dynamics results in the deepening of the minimum, further reducing the probability of escape. Eventually, the system relaxes to the balanced state with a time-scale of $\sim 1/\epsilon$, when the well becomes the global minimum of a smooth energy landscape.

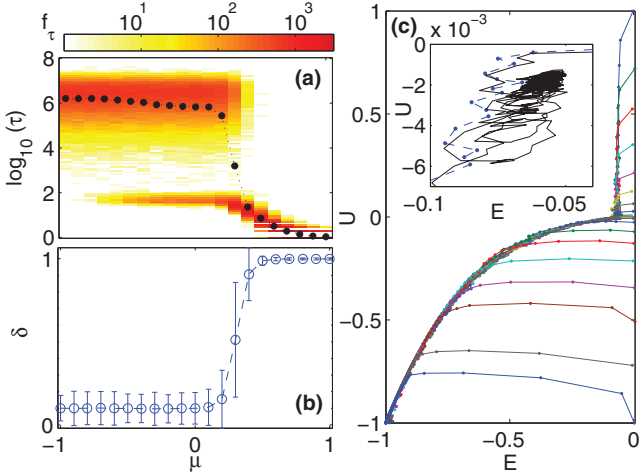


Fig. 4: (Colour on-line) (a) Probability distribution of $\log_{10}(\tau)$ shown as a function of the mean μ of the initial distribution for J_{ij} for $T = 17$, $\epsilon = 0.05$. The filled circles represent the average of $\log_{10}(\tau)$ for different values of μ . The distribution does not change much for small bias ($|\mu|$); however the lower peak disappears as μ approaches -1 while the relaxation behavior occurs faster as μ approaches $+1$. (b) Scaled size difference $\delta = (C_1 - C_2)/N$ between the two clusters of aligned spins shown as a function of μ . As μ increases from negative values to 1, δ increases from values close to 0 towards 1. (c) Trajectories representing the time-evolution of the system ($N = 256$) in the (E, U) order parameter space for different values of μ (from top to bottom, μ increases from -1 to 1 in steps of 0.1). After transients, all trajectories converge to a single curve independent of the time required to converge to the balanced state. A magnified view (inset) compares the trajectory corresponding to a long relaxation time (solid curve), which appears to be trapped in this region, with the one corresponding to a short relaxation time (broken curve) for $\mu = 0$.

If, on the other hand, the system escapes from the initial well within the first few iterations, the system jumps from well to well with ease as the barrier heights separating the local minima are all relatively low. In this case, the relaxation time will be large as balance can be attained only through a low-probability event of the system getting trapped in a local minimum for sufficiently long. This can be approximated by a stochastic process where a particle can decay with a given probability at each time-step, the survival time distribution decaying exponentially. This tail is manifested as the higher peak in the relaxation time distribution in our model.

Distributions of time-scales having high variability and characterized by the appearance of multiple modes, have been reported in many different contexts. These include physical phenomena, such as the distribution of the time between eruptions of certain geysers [30] and earthquake inter-event times [31], as well as, social systems, *e.g.*, the intervals in short-message communication between individuals [32]. Another instance in which bimodality has been reported is in the distribution of the

duration of public hearings in the U.S. Senate for confirmation of Supreme Court nominees [33]. As hearings presumably continue until the members have a clear polarization, which one can interpret as convergence to a structurally balanced state, one can see this process as a networked system of agents adapting their links. Thus, the duration of these hearings corresponds to the time required to reach balance, suggesting that our results may be relevant for explaining the bimodality. Bimodal distributions are also seen in several biological systems [34], which brings us to the intriguing question raised at the beginning of the paper, *viz.*, whether balance occurs in biological networks. While the observation of two dynamically anti-correlated functional subnetworks in the resting human brain [23] suggests one possible example of a balanced system, it would be of interest to look for signatures of this phenomenon in other biological contexts, such as, in intra-cellular signaling. Our model can provide insights in this case as the specific adaptation process we have investigated has been suggested to be also operating in the cell [26,27]. However, instead of the entire network, balance may be manifested only in specific subnetworks. This will appear as clustering of the constituent elements into two groups with strongly anti-correlated activities, and the balanced configuration should be invariant across different cell types and species. An important implication of our results is that even if networks are evolving according to the process outlined here, it is possible that the system will not be able to achieve balance due to fluctuations in the cellular environment. This can be a possible reason why balance may not be commonly observed in biological systems.

To conclude, we have shown that a link adaptation dynamics inspired by the Hebbian principle can lead to structural balance in an initially frustrated network. However, in the presence of fluctuations, we observe that the system exhibits a large dispersion in the time-scale of relaxation to the balanced state, characterized by a bimodal distribution. This extreme variability of the time required for removing frustration completely by a link adaptation is a novel phenomenon that requires further investigation. Our results suggest that even when a system has the potential of attaining structural balance, the time required for this process to converge may be so large that it will not be observed in practice. Although we have considered a globally connected network of binary state dynamical elements, it is possible to extend our analysis to sparse networks [35,36] and different nodal dynamics.

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