

Identifying the Topology of a Coupled FitzHugh–Nagumo Neurobiological Network via a Pinning Mechanism

Jin Zhou, Wenwu Yu, Xiumin Li, Michael Small, and Jun-an Lu

Abstract—Topology identification of a network has received great interest for the reason that the study on many key properties of a network assumes a special known topology. Different from recent similar works in which the evolution of all the nodes in a complex network need to be received, this brief presents a novel criterion to identify the topology of a coupled FitzHugh–Nagumo (FHN) neurobiological network by receiving the membrane potentials of only a fraction of the neurons. Meanwhile, although incomplete information is received, the evolution of all the neurons including membrane potentials and recovery variables are traced. Based on Schur complement and Lyapunov stability theory, the exact weight configuration matrix can be estimated by a simple adaptive feedback control. The effectiveness of the proposed approach is successfully verified by neural networks with fixed and switching topologies.

Index Terms—Complex network, neural network, pinning, topology identification, weight couplings.

I. INTRODUCTION

Dynamical neural networks, consisting of a large number of neurons, have been a fascinating and important subject of research [1], [2]. These neurons are connected to each other by synapses, which are the specialized junctions where a neuron communicates with a target cell [3]. The interactions among neurons, namely, the couplings, have a great influence on the dynamical characteristics of neurobiological network [3].

The properties of a neural network with a certain coupling configuration have been extensively investigated [1]–[6]. Network topology is critical for the understanding of geometry characteristics, synchronization, and application of a network [7]–[14]. Therefore, as an inverse problem in complex network and neurobiology, topology identification of a neural network is very important.

In the human brain, there is a large number of neurons which interact mutually to represent and process information. When measuring brain activity by electroencephalography (EEG) [15], magnetoencephalography (MEG) [16], functional magnetic resonance imaging (fMRI) [17], or positron emitted tomography (PET) [18], the sensor information reflects the dynamics of neurons mediated as a local field potential (LFP). By receiving this information, it is possible to estimate the topology of the network. From signal processing point of view, there

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are many algorithms such as cross correlation and partial correlation to identify the interactions among neurons in a network [19]–[21]. In addition, by exploiting information theory algorithms such as transfer entropy [22] and mutual information [23], reconstructing the functional connectivity among neurons is possible. While in the area of mathematics and engineering, works on the rigorous theoretical derivation for these techniques have been rare.

Very recently, topology identification of complex networks has been intensively studied. First, Yu *et al.* estimated the adjacency matrix of a linearly coupled complex network in 2006 [24]; then, in 2007, Tang *et al.* modified Yu's method and applied it into a neural network in which the dynamics of each neuron is a Hindmarsh–Rose model [25]; in the same year, Zhou and Lu recognized the topology of a general weighted complex network even with different coupling nodes [26]; later, in 2008, Wu estimated the topology of a network with time-varying coupling delay [27]. In the above methods, the states of all the nodes in the network were monitored to achieve topology identification.

However, in many cases, only some of the couplings in several sub-regions are unknown or uncertain, and the remainder is known [28]. Therefore, only some of the couplings need to be identified. The pinning control mechanism, which was first applied to complex networks by Wang *et al.* [30] and Li *et al.* [31], is a more economical and practical technique. Although the pinning mechanism requires more information of the network to decide which nodes should be controlled, this mechanism can reduce the number of controllers. Provided with some known couplings, pinning mechanism is a possible way to estimate the value of those which are uncertain.

Consider the original neural network as a drive network, and design a response network which receives only the membrane potential evolution of some of the neurons. Based on Schur complement [32], [33] and Lyapunov stability theory [34], a novel criterion is presented to estimate the weight configuration matrix for a coupled FitzHugh–Nagumo (FHN) neural network. In this paper, some simple adaptive feedback controllers are used to identify the topology of this network by a pinning mechanism.

The remainder of this brief is organized as follows. In Section II, some preliminaries are briefly outlined. The mechanism of controlling the membrane potentials of a fraction of neurons in the response network to reach topology estimation is discussed in Section III. In Section IV, examples are simulated to illustrate the effectiveness of the proposed approach. The main ideas and conclusions are summarized in Section V.

II. PRELIMINARIES

A. FitzHugh–Nagumo Model

Since 1951, the quantitative study of electrically active cells has received its principal impetus from the remarkable work by Hodgkin and Huxley [35] on nerve conduction in the squid giant axon. The subject of Hodgkin and Huxley's work is the process by which the impulse travels along the axon in the giant axon of the squid using a 4-D expression [35]. Since the equations were too complicated to analyze completely, simpler systems were indeed necessary to aid in understanding the properties of the Hodgkin–Huxley equations. Thus, by taking into account the physiological background, FitzHugh (1961) and Nagumo (1962), independently derived a 2-D system that provides a convenient simplification of the 4-D Hodgkin–Huxley equations [35]–[38].

The FHN model is described by

$$\begin{cases} \dot{V} = V - \frac{1}{3}V^3 - W + I_{ex} \\ \dot{W} = \epsilon(V + a - bW). \end{cases}$$

Here, V is the membrane potential, W is the recovery variable, I_{ex} is the external stimulus current, and a, b, ϵ are positive constants. Generally, $0 < \epsilon \ll 1$ makes V as a fast variable and W as a slow variable.

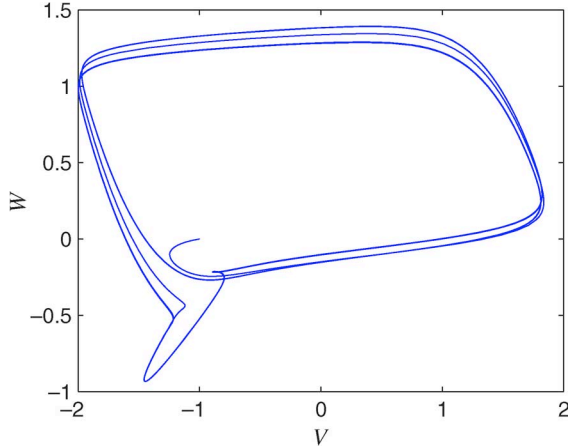


Fig. 1. Phase of W versus phase of V in FHN model with parameters $\epsilon = 0.08$, $a = 0.7$, $b = 0.8$, $I_{ex} = 0.5 \cos(t/50)$, $V(0) = -1$, and $W(0) = 0$. It is shown that the trajectories converge to a limit cycle. Thus, V and W are bounded in a certain region ultimately and the ultimate boundary of V can be chosen as 2 here.

The parameter b is one of the critical terms that can significantly influence the dynamics of the system. Choosing $\epsilon = 0.08$, $a = 0.7$, $b = 0.8$, $I_{ex} = 0.5 \cos(t/50)$, $V(0) = -1$, and $W(0) = 0$, the state variables of FHN model can be depicted by Fig. 1. Since the trajectories starting from arbitrary points will converge to a limit cycle, V and W are bounded in a certain region ultimately.

B. The Neurobiological Network Model

In general, consider a neural network with N coupled neurons which is described by FHN equations. The dynamics of the i th neuron in the network can then be formulated as

$$\begin{cases} \dot{V}_i = V_i - \frac{1}{3}V_i^3 - W_i + I_{ex} - \sum_{j=1, j \neq i}^N g_{ij}(h_i(V_i) - h_j(V_j)) \\ \triangleq f_1(V_i, W_i) + \sum_{j=1}^N g_{ij}h_j(V_j) \\ \dot{W}_i = \epsilon(V_i + a - bW_i) \triangleq f_2(V_i, W_i) \end{cases} \quad (1)$$

where $1 \leq i, j \leq N$, $f_1(V_i, W_i) = V_i - (1/3)V_i^3 - W_i + I_{ex}$, and $f_2(V_i, W_i) = \epsilon(V_i + a - bW_i)$. As for couplings, $h_j(V_j)$ is a non-linear inner-coupling function that is the output of node j , and g_{ij} is the synaptic outer-coupling strength. The network topology is determined by the weight configuration matrix $\mathbf{G} = (g_{ij})_{N \times N}$: if the j th neuron is a neighbor of the i th neuron ($j \neq i$), then the weight $g_{ij} \neq 0$; otherwise, $g_{ij} = 0$. In addition, the matrix \mathbf{G} is diffusive satisfying $g_{ii} = -\sum_{j=1, j \neq i}^N g_{ij}$.

For an FHN equation, the following facts are satisfied:

$$\begin{aligned} & (x_2 - x_1)(f_1(x_2, y_2) - f_1(x_1, y_1)) \\ &= (x_2 - x_1) \left(x_2 - x_1 - \frac{1}{3}(x_2 - x_1)(x_1^2 + x_1x_2 + x_2^2) \right) \\ & \quad - (x_2 - x_1)(y_2 - y_1) \\ &= (x_2 - x_1)^2 \left(1 - \frac{1}{3}(x_1^2 + x_1x_2 + x_2^2) \right) \\ & \quad - (x_2 - x_1)(y_2 - y_1) \\ &\leq \left(1 + \frac{M^2}{3} \right) (x_2 - x_1)^2 + |x_2 - x_1||y_2 - y_1| \end{aligned}$$

and

$$\begin{aligned} & (y_2 - y_1)(f_2(x_2, y_2) - f_2(x_1, y_1)) \\ &= \epsilon(y_2 - y_1)(x_2 - x_1) - \epsilon b(y_2 - y_1)^2 \\ &\leq \epsilon|x_2 - x_1||y_2 - y_1| - \epsilon b(y_2 - y_1)^2 \end{aligned}$$

for any two vectors $(x_1, y_1)^T$ and $(x_2, y_2)^T$, where M is a positive constant representing the ultimate boundary of the first variable. For example, when $\epsilon = 0.08$, $a = 0.7$, $b = 0.8$, $I_{ex} = 0.5 \cos(t/50)$, $V(0) = -1$, and $W(0) = 0$, M can be chosen as 2 from Fig. 1.

C. The Lemmas

In order to derive the main results, the following lemmas are needed.

Lemma 1 (Schur complement [32], [33]): See Appendix I.

Lemma 2: Assume that \mathcal{P} is a diagonal matrix whose k th ($k = 1, \dots, l$) diagonal elements are p and the others are 0, where $p > 0$ is a proper constant which is large enough. \mathcal{Q}^* is the minor matrix of a symmetric matrix \mathcal{Q} by removing all the k th ($k = 1, \dots, l$) row-column pairs of \mathcal{Q} . Then, $\mathcal{Q} - \mathcal{P} < \mathbf{0}$ is equivalent to $\mathcal{Q}^* < \mathbf{0}$.

The proof of Lemma 2 is presented in Appendix II.

III. THE CONTROLLING MECHANISM

To identify the topology of a complex network, usually the original network is served as a drive network. Design a response network through receiving the evolution of nodes; it is possible to estimate the weight configuration matrix. In previous literature, however, all the nodes in the response network should be controlled to achieve topology identification.

Inspired by pinning control and provided with some known weight couplings, it is possible to identify the topology of the neurobiological network without controlling all the neurons in the response network.

Without loss of generality, assume that in neural network (1) the couplings g_{ij} ($1 \leq i \leq l_1, 1 \leq j \leq l_2, l_1 \geq l_2$) are uncertain. To realize weight configuration matrix estimation, the following response network is designed:

$$\begin{cases} \dot{\hat{V}}_i = f_1(\hat{V}_i, \hat{W}_i) + \sum_{j=1}^N \hat{g}_{ij}h_j(\hat{V}_j) - d_i\hat{V}_i \\ \dot{\hat{W}}_i = f_2(\hat{V}_i, \hat{W}_i), \quad 1 \leq i \leq N \\ \dot{\hat{g}}_{ij} = -\delta_i\hat{V}_i h_j(\hat{V}_j), \quad 1 \leq i \leq l_1, \quad 1 \leq j \leq l_2 \end{cases} \quad (2)$$

where \hat{V}_i, \hat{W}_i are tracing state variables, $\hat{V}_i = \hat{V}_i - V_i$ is the error variable, \hat{g}_{ij} is the estimation of g_{ij} for $1 \leq i \leq l_1, 1 \leq j \leq l_2$, $\hat{g}_{ij} = g_{ij}$ for others, δ_i is positive constant, and d_i is the adaptive feedback gain satisfying

$$\begin{cases} \dot{d}_i = e_i \hat{V}_i^2, \quad 1 \leq i \leq l_1 \\ d_i = 0, \quad \text{otherwise} \end{cases} \quad (3)$$

where e_i ($1 \leq i \leq l_1$) is positive constant.

In order to propose the main results, the following hypothesis for inner-coupling function is introduced.

Hypothesis 1 (H1): Assume that $h_j(x)$ ($1 \leq j \leq l_2$) are linearly independent [39], and their differentials satisfy $m_1 \leq |h'_j(x)| \leq m_2$, where m_1 and m_2 are positive constants.

Denote $\mathbf{G}^s = (\mathbf{G}^T + \mathbf{G})/2$ as the symmetric part of the matrix \mathbf{G} . Let $\bar{\mathbf{G}}$ be a modified matrix of \mathbf{G}^s which is obtained by changing the diagonal elements g_{ii} into $(m_1/m_2)g_{ii}$ for $1 \leq i \leq N$, $\bar{\mathbf{G}}^*$ be the minor matrix of $\bar{\mathbf{G}}$ by removing the first l_1 row-column pairs, and $\lambda_{\max}(\cdot)$

be the maximum eigenvalue of a symmetric matrix. Then, for identifying topology of the coupled FHN network (1) in which the weight couplings among a section of neurons are unknown, a criterion based on pinning control is attained.

Theorem 1: Suppose that H1 holds. Then, the unknown elements g_{ij} ($1 \leq i \leq l_1, 1 \leq j \leq l_2$) of the weight configuration matrix \mathbf{G} in network (1) can be identified by the estimation \hat{g}_{ij} in the response network (2) and (3), provided that $\lambda_{\max}(\mathbf{G}^*) < -((3+M^2)/3m_2) + ((1+\epsilon)^2/4\epsilon m_2)$.

Proof: Let $\tilde{W}_i \triangleq \hat{W}_i - W_i$ and $\tilde{g}_{ij} \triangleq \hat{g}_{ij} - g_{ij}$ for $1 \leq i, j \leq N$. In addition, denote ξ_i as a variable between V_i and \hat{V}_i satisfying $h_i(\hat{V}_i) - h_i(V_i) = h'_i(\xi_i)(\hat{V}_i - V_i)$. Then, consider a Lyapunov candidate as

$$L = \frac{1}{2} \sum_{i=1}^N (\hat{V}_i^2 + \tilde{W}_i^2) + \frac{1}{2} \sum_{i=1}^N \sum_{j=1}^N \frac{\tilde{g}_{ij}^2}{\delta_i} + \frac{1}{2} \sum_{i=1}^{l_1} \frac{(d_i - d)^2}{e_i}$$

where d is a positive constant to be determined.

Taking the derivative of L along the trajectories of (2) and (3) yields

$$\begin{aligned} \dot{L} &= \sum_{i=1}^N \left[\hat{V}_i \left(f_1(\hat{V}_i, \hat{W}_i) - f_1(V_i, W_i) \right) \right. \\ &\quad \left. + \tilde{W}_i \left(f_2(\hat{V}_i, \hat{W}_i) - f_2(V_i, W_i) \right) \right] \\ &\quad + \sum_{i=1}^N \sum_{j=1}^N \tilde{V}_i \left(\hat{g}_{ij} h_j(\hat{V}_j) - g_{ij} h_j(V_j) \right) - \sum_{i=1}^{l_1} d_i \tilde{V}_i^2 \\ &\quad - \sum_{i=1}^N \sum_{j=1}^N \tilde{g}_{ij} \tilde{V}_i h_j(\hat{V}_j) + \sum_{i=1}^{l_1} (d_i - d) \tilde{V}_i^2 \\ &\leq \sum_{i=1}^N \left[\left(1 + \frac{M^2}{3} \right) \tilde{V}_i^2 + (\epsilon + 1) |\tilde{V}_i| |\tilde{W}_i| - \epsilon b \tilde{W}_i^2 \right] \\ &\quad + \sum_{i=1}^N \sum_{j=1}^N g_{ij} \tilde{V}_i \left(h_j(\hat{V}_j) - h_j(V_j) \right) - \sum_{i=1}^{l_1} d \tilde{V}_i^2 \\ &= \sum_{i=1}^N \left[\left(1 + \frac{M^2}{3} \right) \tilde{V}_i^2 + (\epsilon + 1) |\tilde{V}_i| |\tilde{W}_i| - \epsilon b \tilde{W}_i^2 \right] \\ &\quad + \sum_{i=1}^N g_{ii} \tilde{V}_i h'_i(\xi_i) \tilde{V}_i + \sum_{i=1}^N \sum_{j \neq i, j=1}^N g_{ij} \tilde{V}_i h'_j(\xi_j) \tilde{V}_j - \sum_{i=1}^{l_1} d \tilde{V}_i^2 \\ &\leq \sum_{i=1}^N \left[\left(1 + \frac{M^2}{3} \right) \tilde{V}_i^2 + (\epsilon + 1) |\tilde{V}_i| |\tilde{W}_i| - \epsilon b \tilde{W}_i^2 \right] \\ &\quad + \sum_{i=1}^N g_{ii} m_1 \tilde{V}_i^2 + \sum_{i=1}^N \sum_{j \neq i, j=1}^N g_{ij} m_2 |\tilde{V}_i| |\tilde{V}_j| - \sum_{i=1}^{l_1} d \tilde{V}_i^2 \\ &= (\tilde{\mathbf{V}}^T, \tilde{\mathbf{W}}^T) \\ &\quad \times \begin{pmatrix} m_2 \tilde{\mathbf{G}} - \mathbf{D} + \left(1 + \frac{M^2}{3} \right) \mathbf{I}_{NN} & \frac{\epsilon + 1}{2} \mathbf{I}_{NN} \\ \frac{\epsilon + 1}{2} \mathbf{I}_{NN} & -\epsilon b \mathbf{I}_{NN} \end{pmatrix} \begin{pmatrix} \tilde{\mathbf{V}} \\ \tilde{\mathbf{W}} \end{pmatrix} \\ &\triangleq (\tilde{\mathbf{V}}^T, \tilde{\mathbf{W}}^T) \mathbf{R} \begin{pmatrix} \tilde{\mathbf{V}} \\ \tilde{\mathbf{W}} \end{pmatrix} \end{aligned}$$

where $\tilde{\mathbf{V}} = (|\tilde{V}_1|, \dots, |\tilde{V}_N|)^T$, $\tilde{\mathbf{W}} = (|\tilde{W}_1|, \dots, |\tilde{W}_N|)^T$

$$\mathbf{R} = \begin{pmatrix} \mathbf{R}_1 & \frac{\epsilon + 1}{2} \mathbf{I}_{NN} \\ \frac{\epsilon + 1}{2} \mathbf{I}_{NN} & -\epsilon b \mathbf{I}_{NN} \end{pmatrix}$$

$\mathbf{R}_1 = m_2 \tilde{\mathbf{G}} - \mathbf{D} + (1 + (M^2/3)) \mathbf{I}_{NN}$, \mathbf{I}_{NN} is the $N \times N$ identity matrix, and \mathbf{D} is the diagonal matrix whose i th ($1 \leq i \leq l_1$) elements are d and others are 0. Due to that $\lambda_{\max}(\mathbf{G}^*) < -((3+M^2)/3m_2) + ((1+\epsilon)^2/4\epsilon m_2)$, one can choose an appropriate constant $d > 0$ such that $\lambda_{\max}(\mathbf{R}_1) < -((1+\epsilon)^2/4\epsilon b)$ according to Lemma 2. It grows $\mathbf{R}_1 - (((1+\epsilon)/2) \cdot (1/ -\epsilon b) \cdot ((1+\epsilon)/2)) \mathbf{I}_{NN} < \mathbf{0}$. As a result, since $-\epsilon b \mathbf{I}_{NN} < \mathbf{0}$, \mathbf{R} is negative definite according to Lemma 1.

The largest invariant set of $\{\dot{L} = 0\}$ is $\Omega = \{\hat{V}_i = 0 \text{ and } \tilde{W}_i = 0, 1 \leq i \leq N\}$. According to LaSalle's invariance principle [34], all the trajectories of systems (1)–(3) will converge to Ω asymptotically for any initial values. In this set, it is obvious that $\hat{V}_i = 0$, and further, $\sum_{j=1}^{l_2} \tilde{g}_{ij} h_j(\hat{V}_j) = 0$. Since H1 holds, there do not exist nonzero constants η_j ($1 \leq j \leq l_2$), such that $\sum_{j=1}^{l_2} \eta_j h_j(\hat{V}_j) = 0$. Thus, we have $\tilde{g}_{ij} = 0$ for $1 \leq i \leq l_1, 1 \leq j \leq l_2$ in the set Ω . Therefore, we get $\lim_{t \rightarrow +\infty} \tilde{g}_{ij} = 0$ for $1 \leq i \leq l_1, 1 \leq j \leq l_2$, and $\lim_{t \rightarrow +\infty} \tilde{V}_i = 0$, $\lim_{t \rightarrow +\infty} \tilde{W}_i = 0$ for $1 \leq i \leq N$. As a conclusion, the unknown coupling strength in neural network (1) can be identified using the response network (2) and (3). Thus, the proof is completed.

From this theorem, it is shown that using the pinning adaptive feedback control approach, the exact topology of model (1) can be estimated. At the same time, it is obvious that although just the membrane potentials of some of the neurons are received, all the evolution of the neurons including membrane potentials and recovery variables are traced. As there are many circumstances in which the connections among some of nodes in a complex network are unknown, this mechanism is of great practical significance.

Remark 1: As a special case, if the couplings of the entire network (1) are unknown, the proposed mechanism (2) and (3) guarantees topology identification provided only with H1 holding.

Remark 2: For neurobiological networks whose weight configuration matrix is switching, our method works well too as shown in Section IV.

Remark 3: The proposed mechanism can also be applied to the neural network in which dynamics of each neuron is something other than FHN equations, and even to neural networks with different types of neurons (dynamics of each neuron need not to be identical). Similar mathematical or engineering conclusions can be derived.

IV. NUMERICAL SIMULATIONS

Here, 100 neurons are considered to form a Barabási–Albert scale-free (see Appendix III) neurobiological network ($m_0 = m = 5$) in which the dynamics of each neuron is an FHN equation with parameters $\epsilon = 0.08$, $a = 0.7$, $b = 0.8$, and $I_{ex} = 0.5 \cos(t/50)$. Assume that the adjacent matrix of this network is \mathbf{A} , the common weight is $\omega = 12$. Suppose that the weight coupling matrix is $\mathbf{G} = \omega \mathbf{A}$, where $g_{11} = -480$, $g_{21} = 72$, $g_{31} = 72$, $g_{41} = 0$, $g_{12} = 72$, $g_{22} = -420$, $g_{32} = 72$, and $g_{42} = 0$ are unknown. In addition, $h_j(x) = x + 5 \sin j$ ($1 \leq j \leq 100$) are assumed to be inner-coupling function. It is obvious that $m_1 = m_2 = 1$. Then, we have $\tilde{\mathbf{G}} = \mathbf{G}^s$.

In view of g_{ij} ($1 \leq i \leq 4, 1 \leq j \leq 2$) to be identified, consider the minor matrix $\tilde{\mathbf{G}}^*$ which is obtained by removing the first four row–column pairs of $\tilde{\mathbf{G}}$. The maximum eigenvalue of $\tilde{\mathbf{G}}^*$ satisfies $\lambda_{\max}(\tilde{\mathbf{G}}^*) = -12.3041 < -6.8896 = -(1 + (2^2/3) + ((1 + 0.08)^2/(4 \times 0.08 \times 0.8)))$.

Choose the initial values as $e_i = 1$, $\delta_i = 10^3$, $d_i(0) = 0$, $V_i(0) = -0.5 + 0.1i$, $\hat{V}_i(0) = 9.5 + 0.1i$, $W_i(0) = 0 + 0.1i$, $\hat{W}_i(0) = 10 + 0.1i$ for $1 \leq i \leq 100$, and $\hat{g}_{ij}(0) = 0$ with $1 \leq i \leq 4, 1 \leq j \leq 2$ in the numerical simulation. Fig. 2(a) shows the evolution of inner-coupling functions $h_1(\hat{V}_1)$ and $h_2(\hat{V}_2)$. From Fig. 2(a), it is easy to see that $h_1(\hat{V}_1)$ and $h_2(\hat{V}_2)$ are linearly independent, for example, choosing

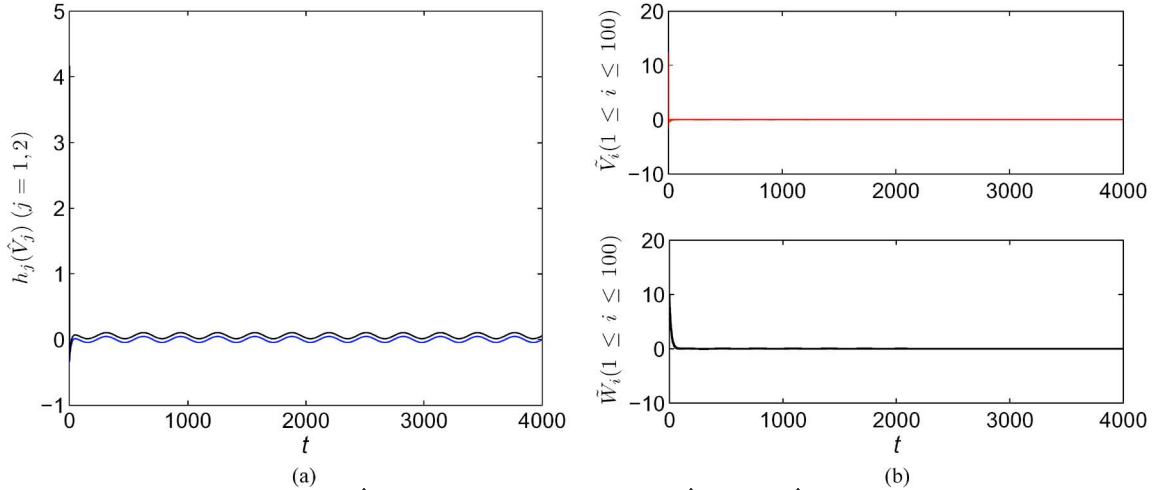


Fig. 2. (a) Evolution of inner-coupling functions $h_j(\hat{V}_j)$ ($j = 1, 2$). It is obvious that $h_1(\hat{V}_1)$ and $h_2(\hat{V}_2)$ are linearly independent. (b) Tracing errors \tilde{V}_i and \tilde{W}_i ($1 \leq i \leq 100$) versus time t . It is seen that all the state variables can be traced.

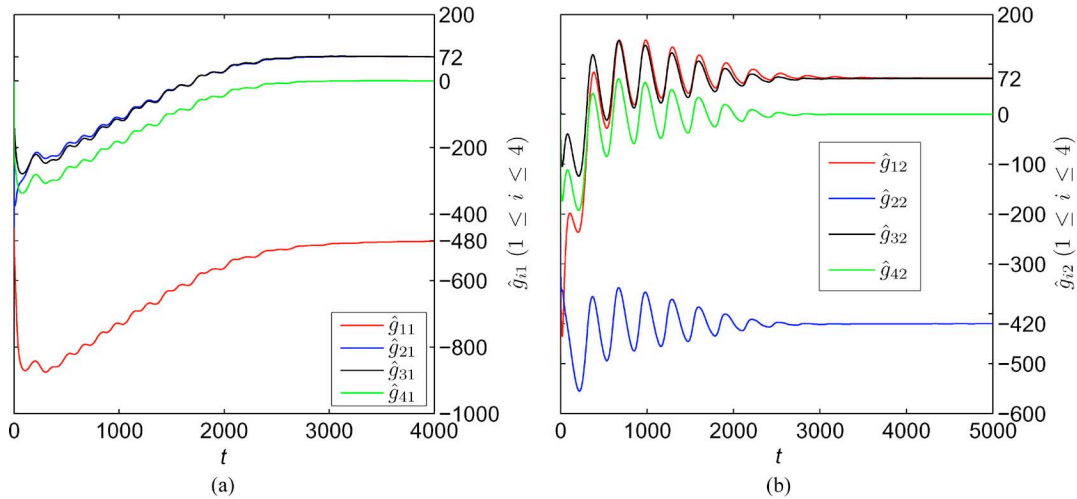


Fig. 3. (a) Estimations of the unknown coupling set $\{g_{11}, g_{21}, g_{31}, g_{41}\}$ versus time t . (b) Estimations of the unknown coupling set $\{g_{12}, g_{22}, g_{32}, g_{42}\}$ versus time t . It is shown that the estimations approach to the corresponding weight values perfectly.

two different times $t_1 > T$ and $t_2 > T$, where T is a large constant, it is seen that

$$\begin{vmatrix} h_1(\hat{V}_1(t_1)) & h_1(\hat{V}_1(t_2)) \\ h_2(\hat{V}_2(t_1)) & h_2(\hat{V}_2(t_2)) \end{vmatrix} \neq 0.$$

The synchronous errors \tilde{V}_i and \tilde{W}_i ($1 \leq i \leq 100$) are plotted in Fig. 2(b), which shows that all the state variables have been traced.

The topology estimations are illustrated in Fig. 3. It is found that the weights have been estimated precisely.

If at time $t_s = 5000$ the unknown coupling set $\{g_{11}, g_{21}, g_{31}, g_{41}, g_{12}, g_{22}, g_{32}, g_{42}\}$ switches from $\{-480, 72, 72, 0, 72, -420, 72, 0\}$ to $\{-420, 12, 12, 0, 12, -360, 12, 0\}$, the proposed topology identification approach also performs well, which is exhibited in Figs. 4 and 5. Besides the successful topology identification, all the state variables have been traced.

V. CONCLUSION

In this brief, a criterion has been presented for identifying the uncertain topology of a neurobiological network by using an adaptive feedback controlling method. Unlike similar approaches which monitor all

the states of all the nodes to reconstruct network topology, we have presented a different mechanism. By receiving the membrane potentials of only a fraction of the neurons, an estimated model is designed to identify the unknown weight couplings in the original neural network. Simulated examples are shown to illustrate the effectiveness of the proposed approach. In addition to the application in neurobiology, this technology is expected to be implemented on many other fields in which the dynamics of each agents can be monitored and received, such as remote control and diagnostics, disease transmission, management, and administration of Internet cafe, and so on.

APPENDIX I

Lemma 1 (Schur complement [32], [33]): The following linear matrix inequality (LMI):

$$\begin{pmatrix} \mathcal{A}(x) & \mathcal{B}(x) \\ \mathcal{B}(x)^T & \mathcal{C}(x) \end{pmatrix} > 0$$

where $\mathcal{A}(x)^T = \mathcal{A}(x)$ and $\mathcal{C}(x)^T = \mathcal{C}(x)$, is equivalent to one of the following conditions:

- $\mathcal{A}(x) > 0$ and $\mathcal{C}(x) - \mathcal{B}(x)^T \mathcal{A}(x)^{-1} \mathcal{B}(x) > 0$;
- $\mathcal{C}(x) > 0$ and $\mathcal{A}(x) - \mathcal{B}(x) \mathcal{C}(x)^{-1} \mathcal{B}(x)^T > 0$.

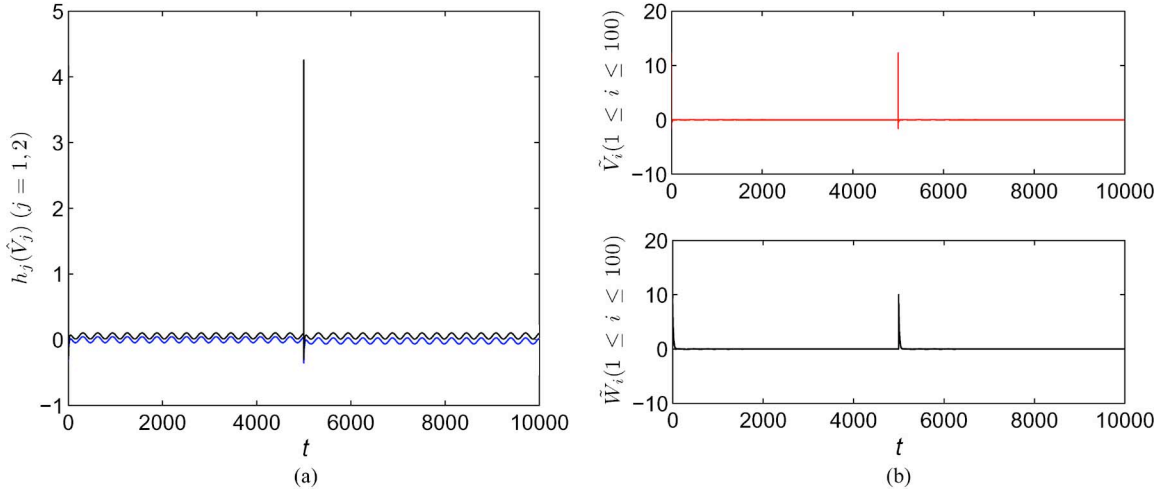


Fig. 4. Evolution of inner-coupling functions and variable tracing of the neural network whose topology switches at $t_s = 5000$. (a) Evolution of inner-coupling functions $h_j(\hat{V}_j)$ ($j = 1, 2$). (b) Tracing errors \tilde{V}_i and \tilde{W}_i ($1 \leq i \leq 100$) versus time t . It is seen that all the state variables can be traced.

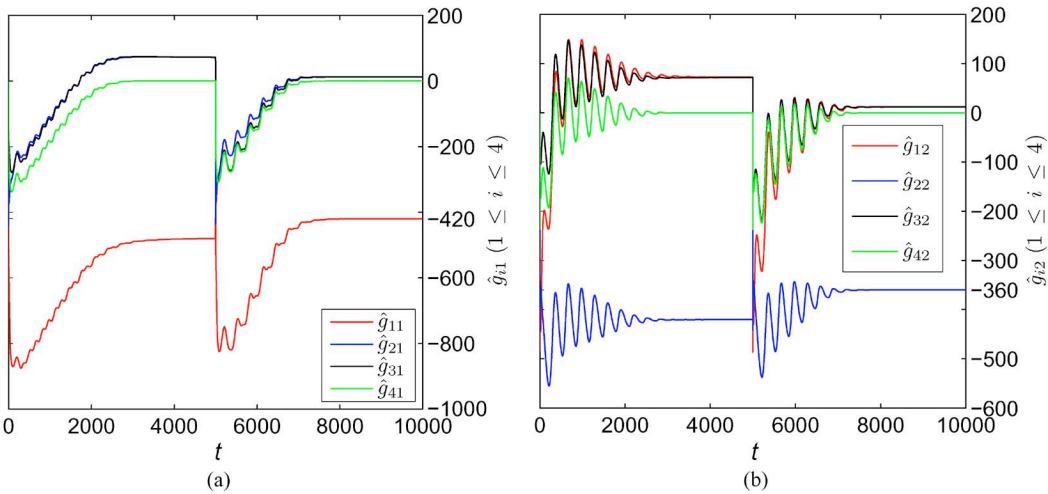


Fig. 5. Topology identification for the neural network whose topology switches at $t_s = 5000$. (a) The estimations of the unknown coupling set $\{g_{11}, g_{21}, g_{31}, g_{41}\}$ vs. time t . (b) The estimations of the unknown coupling set $\{g_{12}, g_{22}, g_{32}, g_{42}\}$ vs. time t . It is shown that the estimations approach to the corresponding weight values perfectly.

APPENDIX II

The Proof of Lemma 2: On the one hand, if $Q - P < 0$, one has $Q^* < 0$ clearly.

On the other hand, we will prove that if $Q^* < 0$, then $Q - P < 0$. It is obvious that

$$Q - P = \begin{pmatrix} Q - p\mathbf{I}_l & Q_1 \\ Q_1^T & Q^* \end{pmatrix}$$

where \mathbf{I}_l represents the $l \times l$ identity matrix, and Q_1 is the corresponding matrix with compatible dimension. Since $Q - p\mathbf{I}_l - Q_1 Q^{*-1} Q_1^T < \mathbf{0}$ when $p > 0$ is a sufficiently large constant, we have

$$\begin{pmatrix} Q - p\mathbf{I}_l & Q_1 \\ Q_1^T & Q^* \end{pmatrix} < \mathbf{0}$$

if $Q^* < \mathbf{0}$ according to Lemma 1. That is, $Q^* < \mathbf{0}$ leads to $Q - P < \mathbf{0}$. Thus, the proof is completed.

APPENDIX III

The Barabási–Albert model (widely known as the BA model) [40] introduced in 1998 explains the power-law degree distribution of networks by considering two main ingredients: growth and preferential attachment. The algorithm used in the BA model is as follows.

- Growth: Starting with m_0 fully connected nodes, at every time step, a new node is introduced and connected to m ($m \leq m_0$) existing nodes in the network.
- Preferential attachment: Assume that the probability P that a new node is connected to node i depends on the degree k_i of node i , such that $P \sim (k_i / \sum_i k_i)$.

Numerical simulations and analytic results indicate that this algorithm evolves a scale-free network.

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