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Estimation of Neural Network Structure by Transforming Spike Sequences to Continuous Time Series

Kaori Kuroda† and Tohru Ikeguchi†,‡

†Graduate School of Science and Engineering, Saitama University
‡Brain Science Institute, Saitama University
225 Shimo-Ohkubo, Sakura-ku, Saitama-city, Saitama 338-8570, Japan
E-mail: kuroda@nls.ics.saitama-u.ac.jp, tohru@mail.saitama-u.ac.jp

Abstract—In neural systems, many complicated behaviors are observed. To understand network dynamics, and reproduce the complicated behavior, it is important to clarify the network structures as well as their dynamics. To resolve this issue, we have already proposed a measure, partial spike time metric. Although this measure exhibits high performance to estimate the network structures, it cannot evaluate negative correlations correctly. In this paper, to resolve this problem, we transform multi-spike sequences into continuous time series to estimate the neural network structures. As a result, our proposed method is more effective for estimating neural network structures than the conventional method.

1. Introduction

Neural systems often produce complicated behaviours due to the interactions among the neurons in them. Usually, such complicated behaviours depend on how the neurons in the network are connected, that is, they depend on the network topology. Thus, to analyze, model or predict such behaviours, it is essential to understand the network structure as well as their dynamics. However, it is not so easy to analyze the anatomical structure of the neural network. On the other hand, recent developments in measurement technologies make it possible to observe multi-spike sequences. It is intuitive to expect that these observed spike sequences reflect essential information about the neural network structure. From this point of view, we have already proposed a measure based on spike time metric [1] and partialization analysis [2, 3]. Although this measure, the partial spike time metric coefficient (PSTMC), exhibits high performance to estimate the network structure [4, 5], it has a drawback: if two spike sequences have anti-phase relation, the PSTMC cannot detect the relation correctly. In this paper, to resolve this issue, we introduce a new strategy: we transform spike sequences into continuous time series to detect their relation. To transform spike sequences to continuous time series, we applied two methods. The first method is an interpolation of inter-spike intervals by sinusoidal waves. The second is a kernel density estimator which uses the Gaussian function as a kernel function. We applied the analytical results for calculating an optimal width of the kernel function [6]. Then, we applied the partial correlation analysis to the transformed continuous time series. The results show that our method exhibits higher performance than the conventional method [4, 5].

2. Transformation method

We first transform spike sequences into continuous time series. To transform the spike sequences, we applied two transformation methods.

2.1. Method 1: Interpolation of inter-spike intervals by sinusoidal waves

Let us describe the jth spike in the ith spike sequence as t_j^i. Then, the ith spike sequence is described as $s_i = \{t_1^i, t_2^i, \ldots, t_{l_i}^i\}$ where l_i is the last index of s_i. Firstly, we interpolate the jth segment (inter-spike interval, ISI) bounded by two adjacent spikes, t_j^i and t_{j+1}^i, by the following equation:

$$x_j^i(t) = \frac{1}{2} + \frac{1}{2}\cos\frac{2\pi}{T_j^i}(t - t_j^i),\ (t_j^i \le t \le t_{j+1}^i), \qquad (1)$$

where $T_j^i = t_{j+1}^i - t_j^i$. Then, $x_j^i(t)$ $(j = 1, 2, \ldots, l_{i-1})$ is concatenated to produce a transformed continuous time series from the ith spike sequence. In Fig. 1, a spike sequence and corresponding transformed continuous time series are shown.

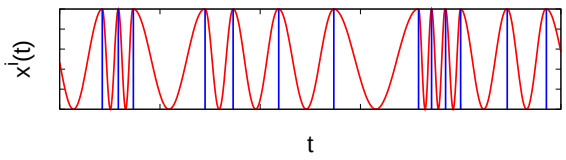

Figure 1: Example of transformation of a spike sequence into a continuous time series by the method 1. Blue lines indicate spike timings and the red curve indicates transformed continuous time series.

2.2. Method 2: The Kernel density estimator

In method 2, we transformed continuous time series from spike sequences by using the kernel density estimator. We used the Gaussian function as the kernel function. The kernel density function is described by the following equation:

$$f_K^i(t) = \frac{1}{l_i w} \sum_{j=1}^{l_i} K\left(\frac{t - t_j^i}{w}\right). \quad (2)$$

where w is the band width and $K(\cdot)$ is the kernel function. The Gaussian function with mean zero and variance unity as a kernel function is defined as:

$$K(t) = \frac{1}{\sqrt{2\pi}} e^{-\frac{1}{2}t^2}. \quad (3)$$

In Fig. 2, an observed spike sequence and corresponding transformed continuous time series are shown. Here, the bandwidth w used for the kernel estimation is optimized by the method for selecting a fixed kernel bandwidth [6].

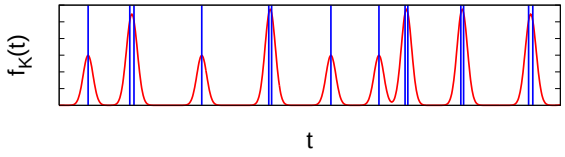

Figure 2: Example of transformation of a spike sequence into a continuous time series by the method 2. Blue lines indicate spike timings and the red curve indicates transformed continuous time series.

3. Partial correlation coefficient

We used the partial correlation coefficient [7, 8] to the transformed continuous time series to detect the relation between two neurons. The partial correlation coefficient is defined as:

$$r_{ij} = -\frac{\sigma_{ij}}{\sqrt{\sigma_{ii}\sigma_{jj}}}, \quad (4)$$

where σ_{ij} is the (i, j)th entry of the inverse of the correlation matrix of the transformed time series from the ith and jth spike sequences. The partial correlation coefficient can quantify the similarity between the two time series with removing spurious correlations between them, for example, in a case that two neurons are driven by a common input from another neuron [4, 5].

4. Simulation

To evaluate the validity of our method, we used a neural network constructed from a mathematical model of the Izhikevich simple neuron model [10] and generated multi-spike sequences. The dynamics of the ith neuron in the neural network is described by the following equations:

$$\begin{aligned} \dot{v}_i &= 0.04v_i^2 + 5v_i + 140 - u_i + I_i, \\ \dot{u}_i &= a(bv_i - u_i), \\ \text{if } v_i &\geq 30\ [\text{mV}],\ \text{then} \begin{cases} v_i \leftarrow c_i \\ u_i \leftarrow u_i + d_i \end{cases} \end{aligned}$$

where v_i is the membrane potential, u_i is the membrane recovery variable; and a, b, c_i, and d_i are dimensionless parameters. We set $a = 0.02$, $b = 0.2$, $c_i = -65 + 15 \times U^2$, $d_i = 8 - 6 \times U^2$ where U is uniform random numbers between $[0, 1]$. The variable I_i is the sum of the external and synaptic inputs from coupled neurons. The synaptic weight is set to six and the amplitude of the external inputs to five times G, where G is a Gaussian random number with a mean value and standard deviation of zero and unity, respectively. The neural network is composed of only excitatory neurons. For the sake of simplicity, we do not consider conduction delays.

We generated a complex network structure having a regular ring topology with 100 neurons by a random rewiring of the synaptic connections between neurons in the same manner as that described in Ref. [12]. We set the parameters k (the number of edges in the regular network) to four and p (rewiring probability) to 0.1.

We conducted numerical experiments according to the following procedures. First, to generate multi-spike sequences, we constructed a neural network using the Izhikevich simple neuron model and applied external inputs to the neural network. Second, we transformed the spike sequences into continuous time series. Third, we calculated the partial correlation coefficient of the transformed continuous time series. If the ith and the jth neurons are coupled, the partial correlation coefficient becomes large. On the other hand, if these neurons are not coupled, it becomes small. Finally, we classify coupled pairs and uncoupled pairs by the Otsu thresholding [11] which is based on a linear discriminant analysis.

To evaluate an overall estimation accuracy, we compared the estimated network structure with the true network structure. For this evaluation, we used the following index:

$$E = \frac{\sum_{i,j}^{N} (\alpha_{ij}\tilde{\alpha}_{ij} + (1 - \alpha_{ij})(1 - \tilde{\alpha}_{ij}))}{N(N-1)} \quad (5)$$

where α_{ij} and $\tilde{\alpha}_{i,j}$ are the directional connectivity of the true network structure and the estimated network structure, respectively. If the ith and jth elements are (estimated to be) coupled, α_{ij} and $\tilde{\alpha}_{ij}$ take a value of unity. If they are not, α_{ij} and $\tilde{\alpha}_{ij}$ take a value of zero. If E approaches unity, the estimation accuracy increases.

5. Results and discussions

To compare the proposed methods which transform spike sequences to continuous time series and the con-

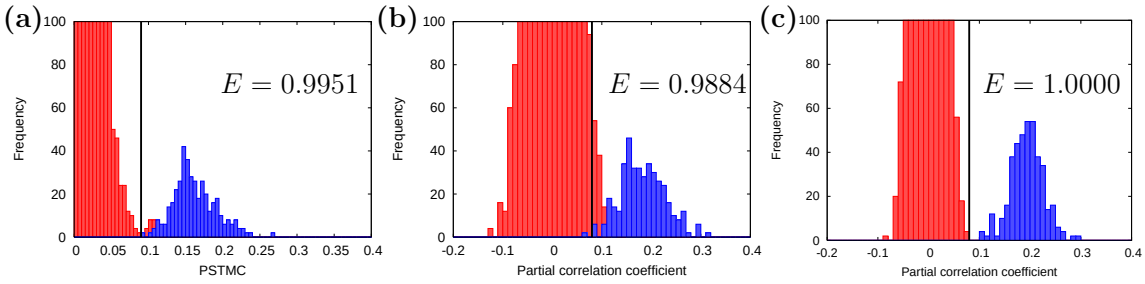

Figure 3: Histograms of (a) PSTMC in the conventional method [4, 5], partial correlation coefficients by (b) the method 1 and (c) the method 2. The number of neurons is 100. The temporal epoch of spike sequences used for estimation is 50 [s]. Histograms of all of the PSTMC and the partial correlation coefficients are indicated in red, and those of the coupled elements are superimposed by blue. The black vertical lines show thresholds decided by the Otsu thresholding. If the PSTMC and the partial correlation coefficients are less than the threshold, corresponding neurons are classified into the uncoupled class.

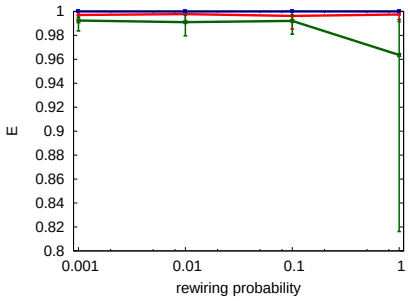

Figure 4: Estimation accuracy E of the network structure for rewiring probabilities p. The number of neurons, the temporal epoch and the coupling strength are 100, 50 [s] and 6. The red line indicates the conventional method, the green line indicates the method 1 and the blue line indicates the method 2. Error bars with 20 trials are also provided.

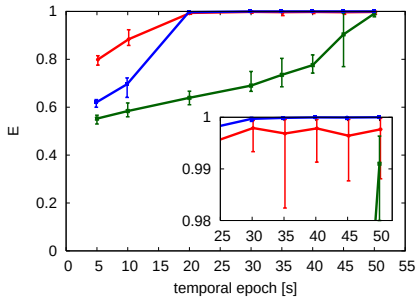

Figure 5: Estimation accuracy E of the network structure for several temporal epochs. The number of neurons and the coupling strength are 100 and 6. Red line indicates the conventional method, green line indicates the method 1 and blue line indicates the method 2. Error bars with 20 trials are also provided. The inset shows an enlargement.

ventional method which uses PSTMC, we also apply the PSTMC [4, 5] to the same network structure.

Figure 3 shows histograms of PSTMC and partial correlation coefficients. Although the conventional method and the method 1 can separate coupled and uncoupled pairs of neurons, a few uncoupled pairs are estimated as coupled pairs. However, coupled and uncoupled pairs of neurons are more clearly distinguished by the method 2.

In Fig. 4, we show the results when the rewiring probability is changed. In the method 1, the estimation accuracy for the random network ($p = 1.0$) is low. However, the conventional method and the method 2 show high estimation accuracy for all rewiring probabilities.

We examined how the estimation accuracy depends on the temporal epoch for observing spikes (Fig. 5). The conventional method exhibits higher accuracy than other methods when the temporal epoch of the spike sequences is shorter than 20 [s]. However, in method 2, the estimation accuracy is higher than the other methods when the temporal epoch of the spike sequences is longer than 20 [s].

In Fig. 6, we show the results when the coupling strength is changed. If the coupling strength becomes larger than four, the estimation accuracy of the conventional method is high. If the coupling strength becomes larger than five, the estimation accuracy becomes higher in the method 2. If the coupling strength becomes larger than six, the estimation accuracy of the method 1 is the highest.

In addition, we show the results for different network sizes (Fig. 7). In the method 1, the estimation accuracy worsens as the network size increases. However, the estimation accuracy in the method 2 and the conventional method are still high even if the network size is large.

From these results, the estimation accuracy in the method 2 is better than the other methods. In this neural network model, we used different dynamics of neurons; regular spiking, intrinsically bursting, and chattering neurons. If two neurons of different dynamics are coupled, the correlation between the two transformed continuous time series decreases in the conventional method [4, 5] and the

method 1. However, in the method 2, true relation can be identified if observed spike sequences of two neurons are transformed with an optimal bandwidth, even though the dynamics of the two neurons differs.

The proposed methods are similar to the method of Sameshima and Baccala [14] in the point of transforming spike sequences to continuous time series and using partialization analysis. However, in the method of Sameshima and Baccala [14], parameters are not optimized when spike sequences are transformed. Moreover, the proposed methods can estimate whole network structure, while the method of Sameshima and Baccala estimate interaction between two neurons.

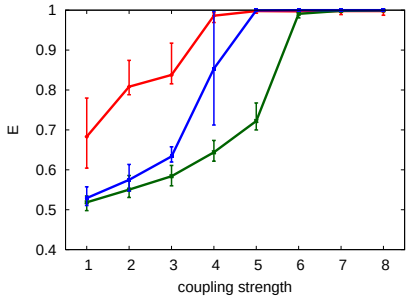

Figure 6: Estimation accuracy E of the network structure for several coupling strength. The number of neurons and the temporal epoch are 100 and 50 [s]. Red line indicates the conventional method, green line indicates the method 1 and blue line indicates the method 2. Error bars with 20 trials are also provided.

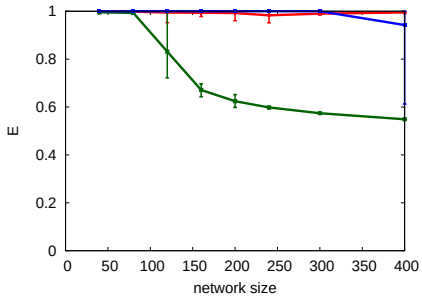

Figure 7: Estimation accuracy E of the network structure for several network sizes. The temporal epoch and the coupling strength are 50 [s] and 6. The red line indicates the conventional method, the green line indicates the method 1 and the blue line indicates the method 2. Error bars with 20 trials are also provided.

6. conclusions

In this paper, we proposed new methods for estimating network structures only from the information of observed multi-spike sequences. We transformed spike sequences to continuous time series by two methods and applied the partial correlation analysis to them. As a result, method 2 (which used the kernel density estimator) exhibits higher performance than the conventional method [4, 5] and method 1.

In this paper, although we only consider the case in which neurons are compiled without delay, real spike sequences can be produced from a network in which the neurons interact through coupling delays. Thus, in future works, it is important to treat delays by modifying the estimation method of optimized bandwidth. In addition, we apply the partialization analysis to a different measure, for example, mutual information [15].

Acknowledgments

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References

[1] J. D. Victor and K. P. Purpura, *Network: Comp. Neur. Sys*, **8**:127, 1997.

[2] K. Kuroda and T. Ikeguchi, *Tech. Rep. of IEICE (NLP2009-102)*, **109**(269):115, 2009.

[3] K. Kuroda et al., *Tech. Rep. of IEICE (NLP2009-140)*, **109**(366):1, 2010.

[4] T. Ashizawa et al., *Proc. of NOLTA'07*, 417, 2007.

[5] K. Kuroda and T. Ikeguchi, *Proc. of NOLTA'09*, 54, 2009.

[6] H. Shimazaki and S. Shinomoto, *J. Comput. Neurosci*, doi:10.1007/s10827-009-0180-4, 2009.

[7] H.A. Simon, *J. Am. Stat. Assoc*, **49**(267):467, 1954.

[8] R. Dahlhaus, *Metrika*, **51**:157, 2000.

[9] J. J. Collins et al., *PRE*, **52**(4):R3321, 1995.

[10] E. M. Izhikevich, *IEEE Trans. NN*, **14**(6):1569, 2003.

[11] N. Otsu, *IEEE Trans. on Syst., MC*, **SMC-9**(1):62, 1979.

[12] D. J. Watts and S. H. Strogatz, *Nature*, **393**:440, 1998.

[13] A. L. Barabasi and R. Albert, *Science*, **286**:509, 1999.

[14] K. Sameshima and L.A. Baccalá, *J. Neurosci. Meth*, **94**:93, 1999.

[15] S. Frenzel et al, *PRL*, **99**(204101):1, 2007.