



# Reconstructing scale-free structure of neural networks from multi spike sequences

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**Abstract**—Recent developments on measurement technologies make it possible to obtain multi spike sequences simultaneously. In this paper, to analyze the anatomical structure of the neural network, we reconstruct the neural network structures only from multi spike sequences. We used a spike time metric coefficient and a partial spike time metric coefficient which are based on a spike time metric and a partialization analysis. Using these measures, our method could reconstruct a scale-free structure in the neural network. We also show that scale-free degree distributions can be estimated.

## 1. Introduction

In neural systems, many complicated behaviors are observed. In order to analyze, model, or predict the complicated behavior, it is an important issue to understand the neural 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 of measurement technologies make it possible to access simultaneously observed multi spike sequences. The number of observed sequences is from 30 to 180 [1, 2, 3]. It is widely considered that these multi spike sequences may reflect essential information about the neural network structure. From this point of view, we have already proposed an estimation method of a neural network structure only from observed multi spike sequences [4, 7]. In this method, two measures, a spike time metric coefficient (STMC) and a partial spike time metric coefficient (PSTMC) are proposed. The STMC is based on a spike time metric [5] which quantifies a distance or the degree of dissimilarity between two spike sequences and the PSTMC is based on partialization analysis for the STMC [6].

Our method can well estimate the neural network structure corresponding to the small-world network. Although the small-world network is often observed in real world including the neural systems, the scale-free network is also an important target. Then, in this paper, we applied our method to the neural networks which have the scale-free structure, and evaluated to what extent the proposed measures (STMC and PSTMC) are applicable to such complicated situation.

## 2. Spike Time Metric

The spike time metric [5] is one of the statistics to quantify a distance or the degree of dissimilarity between two spike sequences. The statistic consists of two types of costs. The first one is a cost of deleting or inserting a spike which takes unity when a spike is deleted or inserted. The second one is a cost to move a spike and is defined as  $q\Delta t$  where  $\Delta t$  is the temporal duration and  $q$  is a parameter. The parameter  $q$  decides which factors, the deletion and insertion or the movement, are weighted. Although the value of this parameter affects the estimation performance for measuring the distance between two spike sequences, we can decide it appropriately [7]. If the spike is moved for a longer duration, this cost becomes large. If the distance takes a small value, it means that a spike sequence is similar to another spike sequence. A metric distance between two spike sequences  $Z$  and  $Z'$  is defined as follows:

$$D_q(Z, Z') = \min \sum_{k=1}^{N-1} c_q(V_k, V_{k+1}), \quad (1)$$

where  $V_1, V_2, \dots, V_N$  are elementary steps from  $Z$  to  $Z'$ . The metric distance between the two spike sequences is the minimum total cost of a set of the elementary steps to transform  $Z$  into  $Z'$ . In Fig.1, we show an example. From  $V_1 (= Z)$  to  $V_2$ , we select one spike (the third one) and delete it. From  $V_2$  to  $V_5 (= Z')$ , we move three spikes to reach  $Z'$ . Consequently, the cost between  $Z$  into  $Z'$  takes  $1 + q(\Delta t_1 + \Delta t_2 + \Delta t_3)$ .

## 3. Spike time metric coefficient and its partialization analysis

To estimate neural network structures from multi spike sequences, STMC and PSTMC have been proposed by Ashizawa et al. [4].

The STMC is defined as

$$S_q(X_i, X_j) = 1 - \frac{D_q(X_i, X_j)}{\max_{X_i, X_j} D_q(X_i, X_j)} \quad (2)$$

where  $D_q(X_i, X_j)$  is STM calculated by Eq. (1). The value of the STMC takes between 0 and 1. If two neurons are

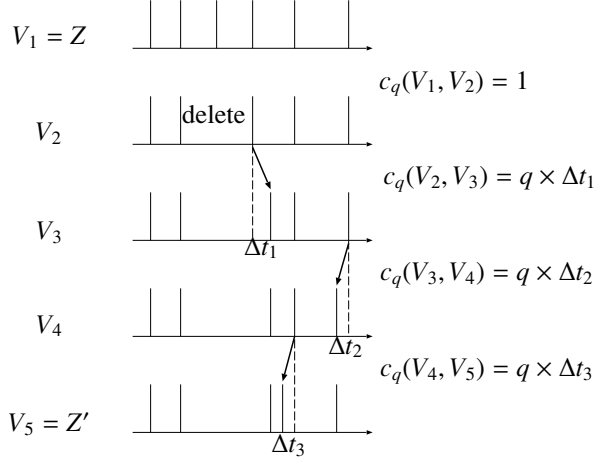


Figure 1: An example of a sequence of elementary steps to transform  $Z$  into  $Z'$ .

coupled,  $S_q(X_i, X_j)$  is expected to become larger than the case that the two neurons are uncoupled. Then, the STMC is a similar measure to the correlation coefficient. However, the STMC could be spuriously biased even if two neurons are not directly connected but they are driven by the common inputs of other neurons.

To remove such spurious connection, partialization analysis is applied to the STMC. Then, the PSTMC is now defined as follows:

$$P_q(X_i, X_j) = \left| \frac{p(i, j)}{p(i, i)p(j, j)} \right| \quad (3)$$

where  $p(i, j)$  is the  $(i, j)$ th element in an inverse matrix of  $S_q(X_i, X_j)$ . The PSTMC can measure the degree of association between the two spike sequences, with removing spurious correlations. Using these two measures, we can find hidden relations between the neurons and estimate the network structure [4, 7].

## 4. Simulations

### 4.1. Neural network model

To evaluate validity of our method, we use a mathematical model of Izhikevich's simple neuron model [8]. The model is described by the following equations:

$$\frac{dv_i}{dt} = 0.04v_i^2 + 5v_i + 140 - u_i + I_i \quad (4)$$

$$\frac{du_i}{dt} = a_i(bv_i - u_i), \quad (5)$$

$$\text{if } v_i \geq 30 \text{ [mV]}, \text{ then } \begin{cases} v_i \leftarrow c_i \\ u_i \leftarrow u_i + d_i \end{cases} \quad (6)$$

where  $v_i$  is the membrane potential of the  $i$ th neuron,  $u_i$  is a membrane recovery variable,  $a_i$ ,  $b_i$ ,  $c_i$  and  $d_i$  are dimensionless parameters. The variable  $I_i$  is the sum of external and synaptic inputs from coupled neurons.

The neural network is composed of only excitatory neurons. We set  $a_i = 0.02$ ,  $b_i = 0.2$ ,  $c_i = -65 + 15 \times U$ ,  $d_i = 8 - 6 \times U$ , and the amplitude of the external inputs is  $5 \times G$ , where  $U$  is uniform random numbers and  $G$  is Gaussian random numbers.

### 4.2. Network structures

In Ref.[7], the Watts and Strogatz (WS) model is used as a small-world network [9]. In this paper, we used the Barabási and Albert (BA) model as a scale-free network [10]. In this paper, the parameters  $m_0$  (the number of nodes in an initial network) and  $m$  (the number of edges that is attached to the network) in the BA model are set to 4 and 2, respectively.

### 4.3. Numerical simulation

We conducted numerical experiments according to the following procedures.

1. To generate multi spike sequences, we constructed a neural network whose element is Izhikevich's simple neuron model. The network structure is decided by the BA model. The coupling strength is constant and is fixed to 8.
2. We simulated the neural network with external inputs and obtained multi spike sequences.
3. We decided an appropriate parameter  $q$  in the spike time metric [7].
4. We applied the STMC and PSTMC to the observed multi spike sequences. If two neurons are coupled,  $S_q$  and  $P_q$  might be large while they might be small if two neurons are uncoupled.
5. We calculated a threshold that classifies the coupled and the uncoupled pairs. The threshold was decided by the Otsu thresholding [11] which is based on a linear discriminant analysis.
6. We constructed an estimated network structure whether the values of  $S_q$  and  $P_q$  take over the threshold or not.
7. To evaluate estimation accuracy, we compared the structure of the estimated network with that of the original network.

### 4.4. Estimation accuracy

To evaluate the estimation accuracy, we compared the structure of estimated network with that of the original network. To quantify the estimation accuracy in the network, we use the following two characteristics defined as:

$$C-\tilde{C} = \frac{\sum_{i,j}(\alpha_{ij}\tilde{\alpha}_{ij})}{\sum_{i,j}\alpha_{ij}}, \quad (7)$$

$$U-\tilde{U} = \frac{\sum_{i,j}((1-\alpha_{ij})(1-\tilde{\alpha}_{ij}))}{\sum_{i,j}(1-\alpha_{ij})}, \quad (8)$$

where  $\alpha_{ij}$  ( $\tilde{\alpha}_{ij}$ ) is the  $(i, j)$ th element of the adjacency matrix of the original (estimated) network structure. If the  $i$ th

and  $j$ th neurons are coupled,  $\alpha_{ij}$  and  $\tilde{\alpha}_{ij}$  take unity. If they are not coupled,  $\alpha_{ij}$  and  $\tilde{\alpha}_{ij}$  take zero. If  $C-\tilde{C}$  and  $U-\tilde{U}$  are close to unity, the network structure is estimated with high accuracy.

To evaluate the estimation accuracy for each neuron, we defined the following quantifies:

$$C_i-\tilde{C}_i = \frac{\sum_j(\alpha_{ij}\tilde{\alpha}_{ij})}{\sum_j\alpha_{ij}}, \quad (9)$$

$$U_i-\tilde{U}_i = \frac{\sum_j((1-\alpha_{ij})(1-\tilde{\alpha}_{ij}))}{\sum_j(1-\alpha_{ij})}. \quad (10)$$

#### 4.5. Strength distribution

To evaluate the performance of the PSTMC, we also investigated a strength distribution. If two neurons are connected, the value of the PSTMC is close to one. If two neurons are not connected, the value of the PSTMC is close to zero. Thus, we considered the PSTMC as the weight and defined the strength as

$$s_i = \sum_j (P_q(i, j))^x \quad (11)$$

where  $x$  is a parameter and is set to 6. The reason why we introduced the  $x$ th power in Eq. 11, is that although the value of PSTMC between a coupled pair of two neurons is larger than that of uncoupled pairs, the absolute difference is relatively small. Then, the values of PSTMC of uncoupled pairs affect to the strength. Using Eq. 11, the influence on the PSTMC of the uncoupled pairs could be avoided.

## 5. Results and discussions

In Fig. 2, we show an example raster plot from the neural network. The results of estimating network structures for various network sizes are shown in Fig. 3. The PSTMC shows high estimation accuracy of  $U-\tilde{U}$  (Fig. 3(b)) for all the network sizes. However, even if the PSTMC is used, the estimation accuracy  $C-\tilde{C}$  becomes gradually worse as the network size increases.

Figure 4 shows histograms of  $S_q$  and  $P_q$ . The results for the small-world network structure are depicted in Figs. 4(a) and (b). On the other hand, Figs. 4(c) and (d) are results for the scale-free network structure. Blue lines show a threshold which divides two classes of coupled and uncoupled pairs of neurons. If  $S_q$  or  $P_q$  are less than the threshold, we regard these pairs as uncoupled ones. On the other hand, if  $S_q$  or  $P_q$  are longer than the threshold, we regard these pairs as coupled ones. In Fig. 4(b), we can see coupled and uncoupled pairs are clearly distinguished by the PSTMC in the case of the small-world network. In the case of the scale-free network, coupled and uncoupled pairs of the histogram of  $P_q$  (Fig. 4(d)) are more clearly distinguished than that of  $S_q$  (Fig. 4(c)). However, even in this case, the estimation accuracy for the scale-free network becomes lower than that for the small-world network.

We also investigated how long the temporal epoch are needed to estimate the network structure (Figs. 5(a) and (b)). The estimation accuracy of  $U-\tilde{U}$  is high when the temporal epoch of the spike sequences is longer than 30,000 [ms]. In contrast, the estimation accuracy of  $C-\tilde{C}$  is not improved (the value is less than 0.8). To keep the high estimation accuracy for  $U-\tilde{U}$ , our method needs spike sequences for 30,000 [ms] at least.

To investigate why the estimation accuracy for the scale-free network is lower than that for the small-world network, we examined the relation between estimation accuracy of the  $i$ th neuron and the average degree of its adjacent neurons (Fig. 6). Color bars indicate the average degree of adjacent neurons. The estimation accuracy tends to be low if the  $i$ th neuron has a high degree (Fig. 6(a)). Even though the  $i$ th neuron has a low degree, its estimation accuracy decreases if the average degree of its adjacent neurons is high. The reason of decreasing the estimation accuracy is the difference of the firing rates between these neurons. If the difference of the firing rate is large, the value of the STM becomes large. This intrinsic property of the STM leads to the results that even if two neurons are connected, spike sequences from these two neurons have dissimilarity due to difference of firing rates.

Figure 7 shows the strength distribution. the strength distribution obeys a power-law  $P(s) \propto s^{-3}$ . It indicates that the feature of the original networks is duplicated by the PSTMC.

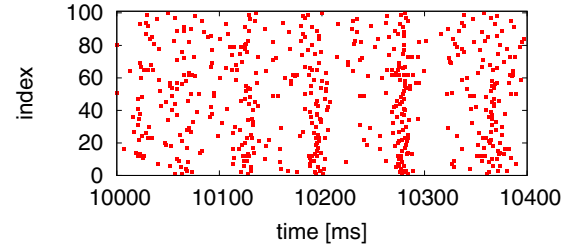


Figure 2: An example raster plot from the neural network.

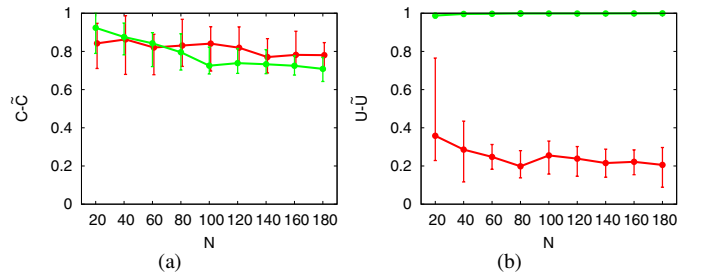


Figure 3: Estimation accuracy of the network structure in case of changing network sizes  $N$ : (a)  $C-\tilde{C}$  and (b)  $U-\tilde{U}$ . Red and green lines represent  $S_q$  and  $P_q$ , respectively.

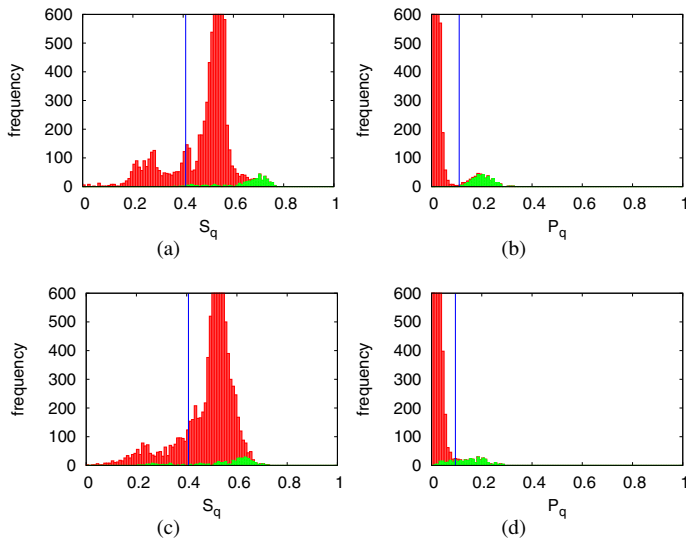


Figure 4: Histograms of (a)  $S_q$  and (b)  $P_q$  for the small world network, and (c)  $S_q$  and (d)  $P_q$  for the scale-free network. The number of neurons is 100. Histograms of all of  $S_q$  and  $P_q$  are shown by red bars, and those of the coupled elements are overwritten by green bars. Blue lines show a threshold.

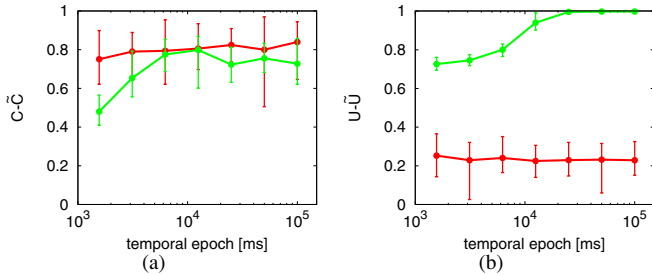


Figure 5: Estimation accuracy of the network structure for several temporal epoch of measuring spike sequences: (a)  $C-\tilde{C}$  and (b)  $U-\tilde{U}$ . The number of neurons is 100. Red and green lines represent  $S_q$  and  $P_q$ , respectively.

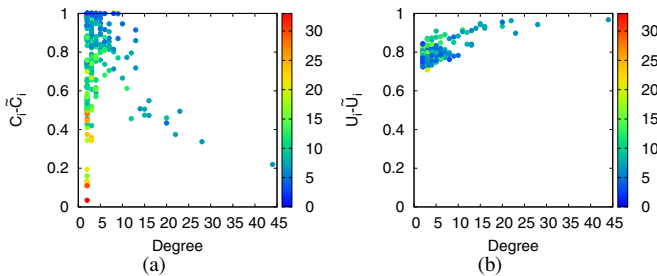


Figure 6: Estimation accuracy of connectivity of the  $i$ th neuron: (a)  $C_i-\tilde{C}_i$  and (b)  $U_i-\tilde{U}_i$ . Color bars indicate the average degree of adjacent neurons. The number of neurons is 300.

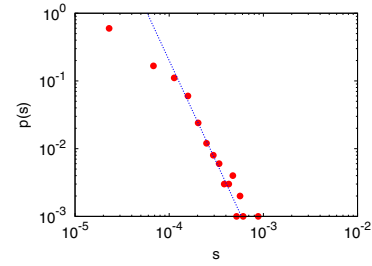


Figure 7: Estimated strength distribution from the PSTMC. Blue dotted line corresponds to a power-law distribution  $p(s) \propto s^{-3}$ .

## 6. Conclusions

In this paper, we reconstructed a network structure only from multi spike sequences. Comparing with the estimation accuracy of the small-world network, the estimation accuracy of the scale-free network decreases. Even if two neurons are actually connected, our method regards these neurons as uncoupled pairs due to the difference of the firing rate between them. As a future work, we apply the partialization analysis to a different measure, for example, mutual information [6], coincidence measure [12] and so on.

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