

New measures for estimating neural network structures only from multi-spike sequences

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Abstract—In neural systems, a fundamental element of the systems, a neuron, interacts with other neurons, then they often produce very complicated behavior. To model, analyze, and predict such complicated behavior, it is important to understand interactions between neurons, namely, a neural network structure. In the present paper, to estimate such a neural network structure by using only observed multi-spike sequences, we propose two new measures, which are based on spike time metric and partialization analysis. To evaluate the validity of our proposed measures, we apply the proposed measures to multi-spike sequences which are produced by an electrotonic coupling of μ -models. As a result, the proposed measures can identify regular and random neural network structures in high performance.

1. Introduction

Neural systems often show very complex behavior due to interaction among many neurons depending on a neural network topology. Such a neural network topology, or a neural network structure, is described by synapses or gap junctions between neurons. To model, analyze, and predict the behavior of neural systems, it is important to consider not only the dynamics of each neuron, but also the neural network structure. However, it is not so easy to investigate the neural network structure, which produces multi-spike sequences, by dissecting a brain cyclopaedically.

Meanwhile, it is possible to observe these multi-spike sequences simultaneously due to recent improvement of measurement technologies. It is very natural to expect that these observed spike sequences reflect essential information about the neural network structure. Thus, it is an important issue to extract such a neural network structure to study a neural system, not only from an anatomical point of view, but also a functional point of view. If we can estimate a functional connectivity between neurons, we might understand how the information is coded and processed in our brain[1].

In the present paper, to estimate the neural network structure only by these observed spike sequences, we proposed two new measures: a spike time metric coefficient and a partial spike time metric coefficient. The spike time metric coefficient uses a concept of spike time metric[2]. The spike time metric is based on spike timings and measure a distance or a similarity between two spike sequences. The partial spike time metric coefficient is based on partialization analysis[3] applied to the spike time metric coefficient. The spike time metric coefficient evaluates a static correlation between two spike sequences, while the partial spike time metric coefficient can reveal unbiased correlation between these spike sequences by removing any spurious correlations. Using two measures, we can find hidden relations between neurons and reveal the neural network structure.

Although our final target is to analyze real neural systems, before applying the proposed measures to real multispike sequences, first we examined the validity of the proposed measures with a mathematical model. Our fundamental opinion is that even if we have a good measure, the measure would be a castle in the air without evaluating its potential ability under a situation that simulates real experimental data. Then, in this paper, we assumed that we can only observe multi-spike sequences but the true network structure is unknown.

In the present paper, we used an electrotonic coupling of μ -models[4] to produce internal states of neurons. For the μ -models, we used a ring topology and a random topology. In addition, we produced multi-spike sequences from the internal states. Then, we estimated the neural network structure of the electrotonic coupling of μ -models by using the proposed measures. As a result, if we use both measures simultaneously, we can estimate the neural network with high efficiency.

2. Spike time metric

To estimate the neural network structures, we introduced a spike time metric[2] which are based on spike timings. The spike time metric quantifies a distance which means a similarity between two spike sequences. In the spike time metric, the first rule is that a cost of deleting or inserting a spike becomes 1. The second rule is that a cost of moving a single spike in time is proportional to the amount of time by which the single spike is moved. For example, if two spike sequences Z and Z' are identical except for a single spike that fires at t_z in Z and $t_{z'}$ in Z', the cost c(Z, Z')equals to $q|t_z - t_{z'}|$ in the second rule, where q is a cost per unit time. The parameter q is important parameter that determines deleting and inserting, or moving a single spike.

In these rules, a metric distance between two spike sequences Z and Z' is defined as

$$D^{\text{spike}}[q](Z, Z') = \min\left\{\sum_{k=0}^{N-1} c(V_k, V_{k+1})\right\},\$$

where $\{V_0, V_1, \ldots, V_N\}$ is an elementary step from Z to Z'[2]. Thus, the distance between the two spike sequences is the minimum total cost of a set of elementary steps that transforms one spike sequence into another sequence.

3. Two proposed measures

In the present paper, we proposed two new measures for estimating the neural network structures. The first measure is based on the spike time metric. We call it a spike time metric coefficient (STMC). The STMC between two spike sequences X_i and X_j is defined as

$$S_T[q](X_i, X_j) = 1 - \frac{D^{\text{spike}}[q](X_i, X_j)}{\max_{i, j} \{D^{\text{spike}}[q](X_i, X_j)\}}.$$

Then, we define $S_T[q]$ as a matrix consisting of $S_T[q](X_i, X_j)$. If two neurons, which produce the two spike sequences X_i and X_j , are coupled, $S_T[q](X_i, X_j)$ might become larger than the case of the two neurons are uncoupled. The reason is that $D^{\text{spike}}[q](X_i, X_j)$ becomes smaller than the uncoupled case, if the two neurons interact with each other through the coupling.

However, the STMC is spuriously biased if the two neurons are driven by a common input from other neurons. Then, we proposed the second measure which is based on partialization analysis[3] applied to the STMC. We call it a partial spike time metric coefficient (PSTMC). The PSTMC between X_i and X_j is defined as

$$P_T[q](X_i, X_j) = \left| \frac{\alpha(i, j)}{\alpha(i, i)\alpha(j, j)} \right|,$$

where $\alpha(i, j)$ is the (i, j)-th element of inverse matrix of $S_T[q]$. The PSTMC estimates a partial correlation between the two spike sequences, X_i and X_j , or a correlation by removing spurious correlations.

4. Experiments

We cannot evaluate the validity of the proposed measures only by using real spike sequences, because we do not have any information of the true neural network structure producing the spike sequences. Then, we used a neural network model to check the validity of the proposed measures because we can have the information of the true neural network structure.

4.1. Neural network model

To evaluate the validity of our proposed measures, we used an electrotonic coupling of μ -models[4] to produce internal states of neurons:

$$\begin{cases} \frac{dx_i}{dt} = -y_i - \mu x_i^2 (x_i - \frac{3}{2}) + I + J_i \\ \frac{dy_i}{dt} = -y_i + \mu x_i^2 \\ J_i = g \sum_{j=1}^{n} (x_j - x_i), \end{cases}$$

where x_i and y_i are the internal states of the *i*-th neuron, μ is a parameter, *I* is an injected background current, J_i is a total current induced by electrotonic couplings to the *i*-th neuron, *g* is a coupling strength, and *n* is the number of couplings to the *i*-th neuron. In the present paper, we set $\mu = 1.65$, I = 0.005, g = 0.05, and dt = 0.02[ms]. We used two types of network structure as a neural network: the first one has a regular ring topology with 30 neurons, and the second has a random topology produced from the 30 ring topology (Fig.1). In Fig.2, we show the typical outputs of internal states time series of μ -models, and its spike sequences in the case of the regular topology.



Figure 1: The network structures which are used to produce the internal states of neurons. (a) Regular ring topology which consists of 30 neurons, and (b) random topology produced from the 30 ring topology. To obtain the random topology, we rewired all the connections with rewiring probability 1.

4.2. Estimation method

We observed the internal states of all neurons in the electrotonic coupling of μ -models. Then, we produced multispike sequences from the internal states with thresholding, and calculated the STMC and the PSTMC between two spike sequences, X_i and X_j (i, j = 1, 2, ..., 30).

For our measures, it is important to decide q appropriately, because it determines a relative sensitivity of deleting and inserting, and moving a single spike. Then, we first checked $S_T[q](X_i, X_j)$ and $P_T[q](X_i, X_j)$ in the case of the regular topology by changing q as shown in Fig.3. From these results, we set q = 500 because the disparity between



Figure 2: (a) Time series of internal states, and (b) a raster plot of output spikes from the electrotonic couplings of μ -models in the case of the regular topology. To obtain the output sequences, we used thresholding at the value of 0.65[mV].

coupled and uncoupled neurons is relatively larger than the other q cases. The random topology has the same tendency as the regular topology.



Figure 3: Relation between q and (a) $S_T[q]$, and (b) $P_T[q]$ in the case of the regular topology. Green lines show $S_T[q]$ and $P_T[q]$ between coupled neurons. Red lines show $S_T[q]$ and $P_T[q]$ between uncoupled neurons. Error bars with 30 trials are the range of $S_T[q]$ and $P_T[q]$, respectively.

If the corresponding two neurons are coupled, the two spike sequences must interact with each other. In such a case, $S_T[q](X_i, X_j)$ and $P_T[q](X_i, X_j)$ might become large. On the other hand, if these neurons are not coupled, $S_T[q](X_i, X_j)$ and $P_T[q](X_i, X_j)$ might become small. Thus, to find coupled neurons pairs, we have extracted large $S_T[q](X_i, X_j)$ and $P_T[q](X_i, X_j)$. Then, we calculated a threshold which divides the coupled or the uncoupled pairs. The threshold was decided by the Otsu thresholding[5] which is based on a linear discriminant analysis.

4.3. Evaluation

In order to evaluate an estimation accuracy, we have to compare an estimated neural network structure with the true neural network structure. For this end, we used four evaluation measures, C- \tilde{C} , C- \tilde{U} , U- \tilde{U} and U- \tilde{C} . C- \tilde{C} , and U- \tilde{C} are a ratio of the estimated number of coupled neuron pairs to the truly coupled number of neuron pairs, and to the number of truly uncoupled neuron pairs, respectively. C- \tilde{U} , and U- \tilde{U} are a ratio of the estimated number of uncoupled neuron pairs to the truly coupled number of neuron-pairs, and to the number of truly uncoupled neuron-pairs, respectively. The more C- \tilde{C} and U- \tilde{U} approach one, or C- \tilde{U} and C- \tilde{U} approach zero, the more the estimation accuracy becomes high.

5. Results

For the case of the 30 ring topology, we show an example of frequency histograms of $S_T[q]$ and $P_T[q]$ (Fig.4). Blue lines show a threshold which divides coupled or uncoupled classes. If $S_T[q]$ and $P_T[q]$ are less than the threshold, we decided that corresponding neurons are uncoupled. On the other hand, if $S_T[q]$ and $P_T[q]$ are more than the threshold, we decided that they coupled. Table 1 shows the estimation accuracy of the neural network structure.

As shown in Fig.4(a), if we use the STMC, the frequency distribution shows that coupled or uncoupled is classified, even if the discriminant analysis does not work well. However, if we use the PSTMC, the frequency distribution is not classified (Fig.4(b)). The reason is that even if the neuron A is coupled to the neuron C as shown in Fig.5, a coupling between the neurons A and C is estimated as uncoupled, and the $P_T[q]$ between these neurons becomes low.

Figure 6 and Table 2 show the results in the case of the random topology. In Fig.6(a), if we use the STMC, the frequency distribution does not show clear classification, then the discriminant analysis does not work well. However, as shown in Fig.6(b), if we use the PSTMC, the frequency distribution shows clearer classification of the coupled and the uncoupled pairs, and the discriminant analysis works well.

The results in the case of the 30 ring topology indicate that we have to use the STMC and the PSTMC simultaneously to discriminate the coupled and the uncoupled pairs as shown in Fig.7. If we use the STMC and the PSTMC simultaneously, we can discriminate the coupled and the uncoupled pairs with much higher accuracy. In addition, we have already confirmed that the proposed measures work well for another model, such as Izhikevich's simple neuron model[6, 7]. From these results, we found that the proposed measures exhibit high performance.

Table 1: Estimation accuracy for the 30 ring topology.

| measure | C-Ĉ | U-Ũ | C-Ũ | U-Ĉ |
|----------|-------|-------|-------|-------|
| $S_T[q]$ | 1.000 | 0.920 | 0.000 | 0.080 |
| $P_T[q]$ | 0.500 | 1.000 | 0.500 | 0.000 |



Figure 4: Frequency histograms of (a) $S_T[q]$ and (b) $P_T[q]$. Histograms of all of $S_T[q]$ and $P_T[q]$ are shown in red, and histograms of $S_T[q]$ and $P_T[q]$ corresponding to the coupled neurons are shown in green. Blue lines show a threshold decided by the Otsu thresholding. The network structure is the 30 ring topology.



Figure 5: A partial diagram of the ring topology with 30 neurons.



Figure 6: The same as Fig.4, but using the random topology.

Table 2: The same as Table 1, but using the random topology.

| measure | C-Ĉ | U-Ũ | C-Ũ | U-Ĉ |
|----------|-------|-------|-------|-------|
| $S_T[q]$ | 0.783 | 0.774 | 0.217 | 0.226 |
| $P_T[q]$ | 0.833 | 0.985 | 0.167 | 0.015 |

6. Conclusions

In the present paper, we proposed two new measures in order to solve an important issue of estimating neural network structures only from the information of observed multi-spike sequences. We applied our proposed measures to two types of network structure, the 30 ring topology and the random topology. As a result, we used both mea-



Figure 7: An example of discriminating coupled and uncoupled pairs by using both measures. (a) The 30 ring topology, and (b) the random topology. Green dots show $S_T[q]$ and $P_T[q]$ between coupled neurons. Red dots show $S_T[q]$ and $P_T[q]$ between uncoupled neurons. Blue lines divide coupled and uncoupled pairs.

sures simultaneously, we could estimate the neural network structures more completely.

As future works, we apply our measures to different neuron models and different neural structures such as complex networks. In addition, we have to optimize how to decide q only from the spike sequences. Moreover, we improve the discriminant analysis to decide the threshold which divides into coupled or uncoupled. Our goal is that to evaluate the validity of our framework to simultaneously observed real multi-spike sequences, and to analysis brain systems.

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