

# カーネル法による時系列データの解析

## Analyses of time point sequences using kernel methods

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A time sequences is a sequence of data points, consisting of consecutive measurements taken at a time interval. The analysis of time sequences is a valuable way to extract meaningful information and characteristics of the data and predict future values in forecasting. Therefore, analysis of time sequences is very important as a fundamental problem, such as neural activity analysis.

One important example of time sequences that have become important in recent years is the spike train. A spike train is a sequence of spikes or action potentials fired by a neuron as time sequences. We have great interest in how these neurons transmit information rapidly and what relationships they have between each node (neural) in a cortical network. We not only want to know information contents of neural signal systems, but also want to find the structure of neural networks. It is therefore important to estimate the strength of connectivity between nodes in such a network. Such a method can also be used for other networks where events occur at each node, dependent on events occurring at other nodes. Some of the examples include events on a social network, spreading of an epidemic, and physiological pathways.

In order to approach this problem, this paper focuses on the spike timing information and then use the spike sequences alone to estimate the synaptic weights of the network. Specifically, we suggest kernel methods for multichannel spike trains that can provide an opportunity to measure spike trains. First we use the coupled escape rate model (CERM) to simulate multichannel spike trains data and propose a distance to prove the effectivity of the result. Then we extend the CERM to a network and predict the strength of connectivity of the network using kernel ridge regression.

The results indicated that it could be effectively used for estimating the connectivity strength. In future work, we plan to use it to analyze the balance of excitatory and inhibitory synapses in a large network. We also plan to use other simulation models as well.

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