Pseudo random sequences from neural circuits

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Abstract

We have developed a time-shift map in brain showing signals in brain are transferred from/to where. The map changes time to time. We are analyzing its principle how the signals are composed and how it is sent/delivered to due destination. We are assuming that signals are encoded with pseudo random sequence. In circuit theory it is well known that loop circuit with a feedback link generates a pseudo-random sequence including an M-sequence with maximum period length. On the other hand, it remains unclear how memory is stored in neural circuits of the human brain. We propose that M-sequence and its family sequences compose temporal independent basis functions in brain neural network for communication and memory storage. We have already shown its feasibility by computer simulations that show a loop circuit can be copied to another area by back-propagation leaning algorithm; this is a key function of brain intelligence, which includes functions such as memory, association, reasoning, and abstraction. We found M-sequence family responses in the instantaneous firing rates as well as direct spike trains from cultured neural networks of published data and our own data.

Key Words: neural networks, communication in brain, M-sequence, neural spike train

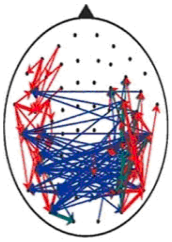

Fig.1. Time-shift diagram of 10.2Hz MEG, for a number counting task. Red: lag time < 5ms within each hemisphere, Blue: >10ms across the callosum. Green: 5-10 ms.

Introduction

Fig. 1 shows a time-shift diagram of 10.2 Hz MEG data that we obtained [1, 2], which represents a snap shot of communication occurring in the human brain. We note that each part of the brain can communicate with another part similar to that seen in a human society that utilizes multi-access communication tools. The most representative and effective pseudo-random sequence in synchronous mode under common clock signal is the M-sequence, that is used, for example, to measure the distance in GPS.

In circuit theory it is well known that loop circuit with a feedback link generates a pseudo-random sequence including an M-sequence with maximum period length. On the other hand, it remains unclear how memory is stored in neural circuits of the human brain. We are proposing that M-sequence composes temporal independent basis functions in brain neural network for communication and memory storage.

Spatial and temporal independent components

It has been shown that directional receptive fields as seen in mammal simple-cells emerge by minimum information criterion and independent component analysis (ICA) for natural and facial images. That is, spatially independent basis functions are derived by self-organization. In the receptive fields of visual system, independent components are obtained by self-organization in the neural circuit with well known mutual inhibition [3]. We therefore expect to find the existence of temporal independent basis functions, which cooperatively work with the spatial independent basis functions.

Poststimulus time histogram

We used PSTH (poststimulus time histogram, or equivalently IFR(instantaneous firing rate) after stimulus) data of hippocampal neurons isolated from a Wister rat (embryonic day 18) and cultured for 37 days (first data) and 22 days (second data) on a multi-electrode arrays dish. We found a series of M-sequences with different lengths as sequence and time as shown in Fig.2. Since this is PSTH sequence, we should interpret as shown in Fig.3.

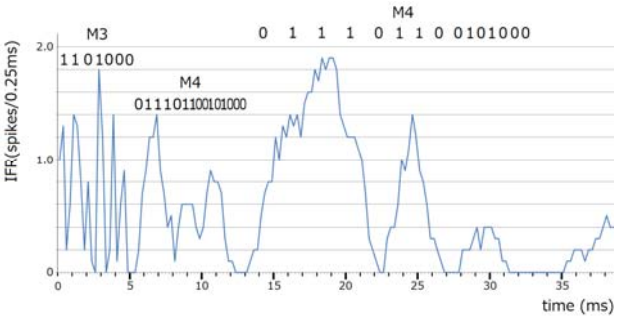

Fig.2. Detected M-sequences in the IFR of our first data. Top sequences M3 and M4 represent the expected response as reversed M sequence of 3 and 4 elements, respectively. In case of M3, it is interpreted as "0's" correspond valley of the curve.

Automatic detection of fragmental M-sequence

Above data are by manual inspection and lack objectivity. To confirm the presence of M-sequences, its family, or fragments, we performed their automatic detection from PSTH patterns. Example of number of detected fragmental 0-1 reversal M-sequences "1101" is shown in Fig.4. Also the results of six randomly shuffled sequences are shown and we can estimate the sequence "1101" is significantly more generated than by chance with p=0.035 for detection time margin margin=0.01 and p=0.076 for margin=0.1. Fig.5 shows detection rate of M-sequence family "1011" in 10 raw spike trains comparing with shuffled and randomly generated sequences.

Conclusion

We could confirm the neural spike coding includes M-sequence family.

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[1] Y. Mizuno-Matsumoto, et al., *IEEE Trans. Biomed. Eng.* **46**, pp.271-279, 1999.
[2] Y. Mizuno-Matsumoto, et al., *Brain Topography* **13**, pp.269-274, 2001.
[3] S. Tamura,et al., *IHMSP2009* A10-07(No.546) Sep. 12-14, 2009.

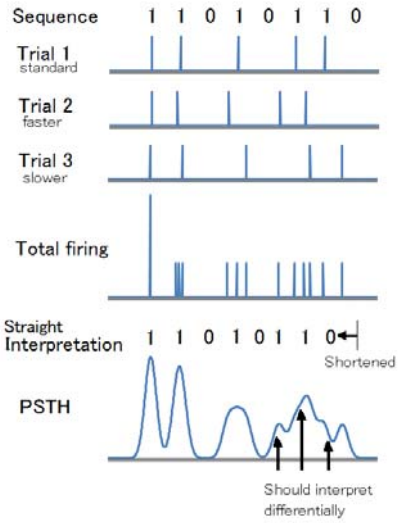

Fig.3 Interpretation of PSTH. Since the spike position varies trial to trial, PHTS should be interpreted differentially in the time elapsed area, which causes shortening of sequence tail..

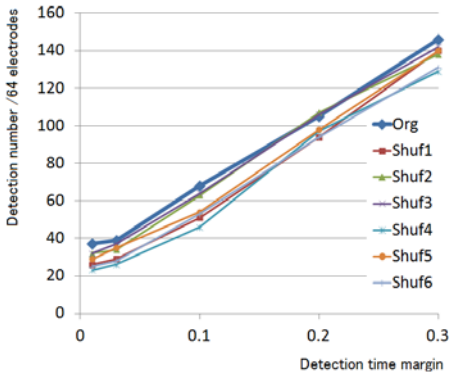

Fig.4 Number of fragmental reversal M-sequence "1101" detected in PSTH from 64 electrodes for 20ms after electrical stimulation

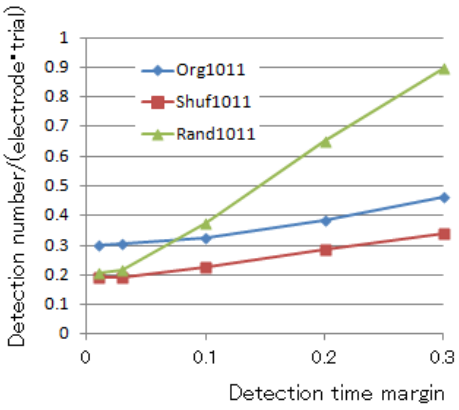

Fig.5 Detection rate of M-sequence family "1011" in 10 raw spike trains comparing with shuffled and randomly generated sequences.