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Computational Neuroscience / Technology in Neuroscience

P-2049

Winner-take-all competition and sparsely synchronized rhythms in the hippocampal dentate gyrus

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We consider a biological network of the hippocampal dentate gyrus (DG). The DG is a preprocessor for pattern separation which facilitates pattern storage and retrieval in the CA3 area of the hippocampus. The granule cells (GCs) in the DG receive the sensory information from the entorhinal cortex (EC) and send their output to the CA3. The activation degree of GCs is so low (~ 5%). This sparsity has been thought to enhance the pattern separation. We investigate the dynamical origin for the winner-take-all competition which leads to the sparse activation of the GCs. The whole GCs are grouped into clusters. In each GC cluster, there is one inhibitory (I) basket cell (BC) along with excitatory (E) GCs. There are three kinds of external inputs into the GCs; the direct excitatory EC input, the indirect inhibitory EC input, mediated by the HIPP cells, and the excitatory input from the hilar mossy cells (MCs). The firing activities of the GCs are determined via competition between the external E and I inputs. The ratio of the external E to I conductance ($R_{E-I}^{(con)}$) may represents well the degree of external E-I input competition. GCs become active when their $R_{E-I}^{(con)}$ is larger than a threshold. In each GC cluster, the feedback inhibition of the BC may select the winner GCs. GCs with larger $R_{E-I}^{(con)}$ become winners. In this way, winner-take-all occurs via interaction of the excitation of the GCs and the feedback inhibition of the BC in each GC cluster. The hilar MCs play a role of enhancing the activity of the GC-BC loop. Moreover, the feedback inhibition from the BCs also leads to emergence of sparsely synchronized rhythms in the GC-BC loop. Successive synchronized stripes appear with the population frequency f_p (=13 Hz) in the raster plots of spikes in each population of GCs and BCs. Such population rhythm also appears in the population of MCs via interaction with the GCs. In addition to population behavior, we also study individual firing activity of GCs, BCs, and MCs.

Key Words: Hippocampal dentate gyrus, Winner-take-all competition, Sparsely synchronized rhythms

P-2050

Fast simple clearing method for efficient deep and high-resolution imaging using multiple microscopies in mouse brain tissue

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In the past few years, many optical clearing techniques have been developed and we can take improved deep tissue imaging by reducing obscuring effects of light scattering and light absorption. However, these optical clearing methods still have various issues such as a tissue volume changes, fluorescent bleaching, hard sample handling and image distortion by high viscosity of reflex index solution. Here, we suggest that a new Immersion solution for Clearing refractive index matching (ISCRIM) based on low viscosity and high refractive index (RI=1.466). ISCRM solution can rapidly clarify 1mm thick brain slice within 90 min with simultaneously optical clearing and RI matching which means directly applicates to imaging of optical microscopy. We developed ISCRIM solution to overcomes limitation of recent tissue clearing protocols and other commercial RI matching solution. The viscosity of ISCRIM solution is close to water and the tissue linear morphology change was less than 2.2% at 36h. Moreover, the fluorescence signal of GFP were highly conserved more than half even after 10 day and can keep the fluid state for 30 day in air expose condition. Although ISCRIM solution limited to clarify until 3mm thick brain regardless of the long-time immersion, it preserved fine neuronal structure such as dendritic spine in a deep brain slice. Therefore, ISCRIM solution can easily achieve high-resolution fluorescence imaging of thick tissues without another clear step and applicates to deep imaging of various biological tissue. ISCRIM solution with Electrophoretic Tissue Clearing (ETC) can apply to deep antibody staining and preserving fluorescence after 30 days stored in ISCRIM solution. Lectin histochemical analysis in brain deep tissue can easily do with only ISCRIM solution without ETC step. ISCRIM solution has potential feature to intervention in various clearing methods for immunohistology.

Key Words: Tissue clearing, Deep brain imaging

P-2051

Robustness of the compass circuit model in Drosophila

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Although spatial working memory has been studied intensively for the past several decades, the circuit-level understanding of its underlying mechanism is still incomplete. Recently, with the advent of new behavioral, physiological, anatomical techniques, Drosophila has become an important model organism for the study of the spatial working memory. In particular, the detailed neural mechanism as to how rotational and translational locomotion and associated optic flow are translated into the activity of compass (heading) cells has been discovered recently. In this study, we built a connectome-based spiking neural network model of the Drosophila compass neural network, called central complex, that captures its two main properties. First, the model maintains the heading signal in the absence of the visual cue as well as in response to an overt visual cue. Second, the model rotates its activity peak according to the rotation of the visual cue and the body. Furthermore, we have tested the robustness of these behaviors of the compass network model against changes in the synaptic weights. We found that the compass network keeps its proper heading signal for a large range of synaptic parameters, highlighting the robustness of this circuit. In the future, we plan to expand our model to incorporate the most up-to-date experimental results on this structure such as the emergence of a new heading signal in a new visual environment and the translation of allocentric spatial information to the heading signal. Together, our work will provide a novel, robust neural network model for spatial working memory that is based on the structural and functional properties of the Drosophila central complex.

Key Words: Central complex, Modeling, Spike neural network, Connectome, Plasticity

P-2052

ICT-based evaluation of cognitive improvement of sleep disorders

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The main goal of this research project is to investigate the spatiotemporal features of EEG activities reflecting an effect of treatment in patients with sleep disorders, based on machine learning approach.

The focus of this project is on patients in restless legs syndrome (RLS), which are known that cognitive deficits appear. The patients with severe restless legs syndrome (RLS) were participated in this study. RLS is a disorder characterized by an unsuppressed response to sensory urges arisen from a deficit of pathways between sensory input and motor output. The follow-up data were obtained for the RLS patients treated with pramipexole consistently. The EEGs were recorded during Sternberg's working memory task. We developed the deep learning model for classifying RLS patients after treatment against patients before treatment. we tried to identify biomarkers for treatment response based on explainable machine learning approach.

To achieve the goal, we developed the deep learning model to classify RLS patients with treatment and we investigated neuromarkers for the effects of treatment in RLS patients using layer-wise relevance propagation method. Our proposed model was successfully predicted RLS patients with treatment against RLS patients without treatment. Our findings may help to open a new prospect of evaluation for the effect of therapy.

Key Words: Cognitive/behavioral characteristics, Neural signal and neuroimage, Machine learning and pattern recognition, Restless legs syndrom (RLS)