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A1

Functional advantages of cell-type heterogeneity in neural circuits

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Neural circuits are notorious for the complexity of their organization. Part of this complexity is related to the number of different cell types that work together to encode stimuli. I will discuss theoretical results that point to functional advantages of splitting neural populations into subtypes, both in feedforward and recurrent networks. These results outline a framework for categorizing neuronal types based on their functional properties. Such classification scheme could augment classification schemes based on molecular, anatomical, and electrophysiological properties.

A2

Mesoscopic modeling of propagating waves in visual cortex

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Propagating waves are large-scale phenomena widely seen in the nervous system, in both anesthetized and awake or sleeping states. Recently, the presence of propagating waves at the scale of microns–millimeters was demonstrated in the primary visual cortex (V1) of macaque monkey. Using a combination of voltage-sensitive dye (VSD) imaging in awake monkey V1 and model-based analysis, we showed that virtually every visual input is followed by a propagating wave (Muller et al., Nat Comm 2014). The wave was confined within V1, and was consistent and repeatable for a given input. Interestingly, two propagating waves always interact in a suppressive fashion, and sum sublinearly. This is in agreement with the general suppressive effect seen in other circumstances in V1 (Bair et al., J Neurosci 2003; Reynaud et al., J Neurosci 2012).
To investigate possible mechanisms for this suppression we have designed mean-field models to directly integrate the VSD experiments. Because the VSD signal is primarily caused by the summed voltage of all membranes, it represents an ideal case for mean-field models. However, usual mean-field models are based on neuronal transfer functions such as the well-known sigmoid function, or functions estimated from very simple models. Any error in the transfer function may result in wrong predictions by the corresponding mean-field model. To palliate this caveat, we have obtained semi-analytic forms of the transfer function of more realistic neuron models. We found that the same mathematical template can capture the transfer function for models such as the integrate-and-fire (IF) model, the adaptive exponential (AdEx) model, up to Hodgkin–Huxley (HH) type models, all with conductance-based inputs.
Using these transfer functions we have built "realistic" mean-field models for networks with two populations of neurons, the regular-spiking (RS) excitatory neurons, showing spike frequency adaptation, and the fast-spiking (FS) inhibitory neurons. This mean-field model can reproduce the propagating waves in V1, due to horizontal interactions, as shown previously using IF networks. This mean-field model also reproduced the suppressive interactions between propagating waves. The mechanism of suppression was based on the preferential recruitment of inhibitory cells over excitatory cells by afferent activity, which acted through the conductance-based shunting effect of the two waves onto one another. The suppression was negligible in networks with identical models for excitatory and inhibitory cells (such as IF networks). This suggests that the suppressive effect is a general phenomenon due to the higher excitability of inhibitory neurons in cortex, in line with previous models (Ozeki et al., Neuron 2009).
Work done in collaboration with Yann Zerlaut (UNIC) for modeling, Sandrine Chemla and Frederic Chavane (CNRS, Marseille) for in vivo experiments. Supported by CNRS and the European Commission (Human Brain Project).

A3

Dynamics and biomarkers of mental disorders

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Current diagnoses of mental disorders are made in a categorical way, as exemplified by DSM-5, but many difficulties have been encountered in such categorical regimes: the high percentage of comorbidities, usage of the same drug for multiple disorders, the lack of any validated animal model, and the situation where no epoch-making drug has been developed in the past 30 years. NIMH started RDoC (research domain criterion) to overcome these problems [1], and some successful results have been obtained, including common genetic risk loci [2] and common neuroanatomical changes for multiple disorders [3] as well as psychosis biotypes [4].
In contrast to the currently dominant molecular biology approach, which basically assumes one-to-one mapping between genes and disorders, I postulate the following dynamics-based view of psychiatric disorders. Our brain is a nonlinear dynamical system that can generate spontaneous spatiotemporal activities. The dynamical system is characterized by multiple stable attractors, only one of which corresponds to a healthy or typically developed state. The others are pathological states.
The most promising research approach within the above dynamical view is to combine resting-state functional magnetic resonance imaging, machine learning, big data, and sophisticated neurofeedback.

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