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Session PSTR377 - Network Computations: Data Analytics and Statistics

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PSTR377.03 / WW70 - Atlas of intrinsic timescales in the mouse brain

November 14, 2023, 8:00 AM - 12:00 PM | WCC Halls A-C

Presenter at Poster
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[1]Princeton Neurosci. Inst., Princeton, NJ; [2]Univ. of Tübingen, Tübingen, Germany; [3]Intl. Brain Lab., London, United Kingdom. Atlas of intrinsic timescales in the mouse brain. Program No. PSTR377.03. 2023 Neuroscience Meeting Planner. Washington, D.C.: Society for Neuroscience, 2023. Online.

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Abstract
Neural activity fluctuates over a wide range of timescales, which vary systematically across the forebrain. Differences in intrinsic timescales have been related to functional specialization and hierarchical organization of cortical areas and have been hypothesized to originate from the anatomical connectivity in the cortex. However, the distribution of timescales and their relationship to anatomical structure have not been characterized beyond the forebrain. We report a cellular-resolution brain-wide map of intrinsic timescales in the mouse brain and quantify the link between timescales, connectivity, and gene expression profiles.

We measured timescales in the spontaneous spiking activity of single neurons using a dataset of brain-wide Neuropixels recordings in mice, which consists of 504 insertions covering 245 brain regions in 326 sessions from 11 laboratories. Spatial locations of neurons recorded in individual experiments are registered into a common reference brain.

We quantified timescales by the exponential decay rate of spike-count autocorrelation in 19,289 single neurons. Most brain regions showed a broad distribution of timescales. The average timescales varied across brain regions ranging from tens of milliseconds to several seconds. The midbrain and hindbrain showed three-fold longer timescales than the cortex and thalamus. The median timescales of cortical and thalamic regions were weakly correlated with their anatomical hierarchy scores.

We then quantified timescales of communication between 10,159 pairs of simultaneously recorded regions, measured by the exponential decay rate of cross-correlation between their population spiking activity. The communication timescales among cortical and thalamic areas showed a weak correlation with the strength of mesoscale anatomical connectivity.

Finally, we tested the relationship between brain-wide heterogenous timescales and molecular signatures of cell types in gene expression profiles. We used spatial expression profiles of 4,345 genes from the Allen Gene Expression Atlas to predict the local intrinsic timescales in 200um3 voxels across the entire brain volume. The gene-expression profiles accounted for 6% of the variance in the spatial distribution of timescales, significantly more than the variance explained by the brain-region parcellation. Thus, spatial gene-expression profiles partially explain fine-scale variability of timescales within brain regions.

In summary, we provide a comprehensive brain-wide survey of intrinsic

timescales and show that gene-expression profile and anatomical connectivity contribute to the spatial distribution of timescales.