Reconstruction and simulation of claustral microcircuitry based on optogenetic mapping

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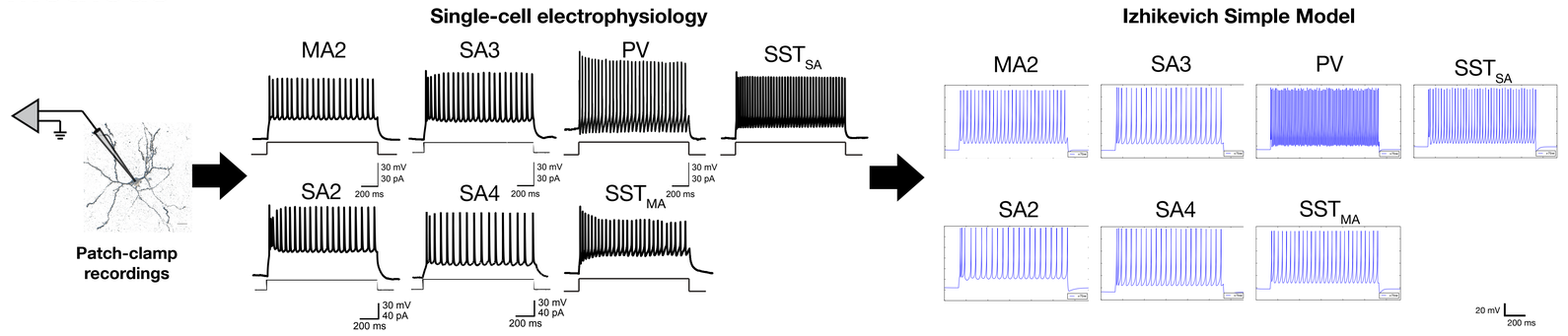
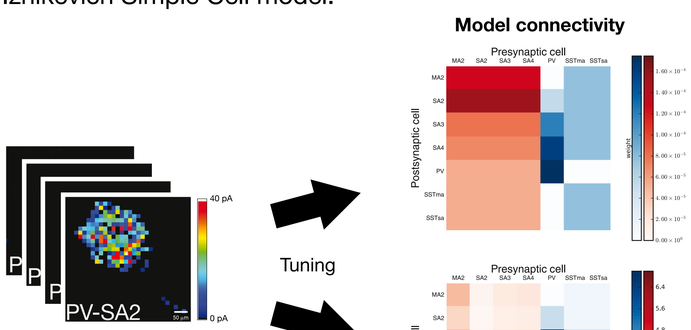
Introduction

The claustrum is a subcortical structure composed of a thin and irregular sheet of neurons. Because of its reciprocal connections with almost all of the cortical areas, the claustrum is proposed to underlie important functions, of which the "seat of consciousness" has been the most influential. However, experimentation is difficult in the absence of a claustrum-specific marker and its mechanism of action remains hard to elucidate. Here, we are developing an *in silico* network model of the claustrum. Recent simulation results suggest that the SA4 cell type may have a role as the driver of the claustral network.

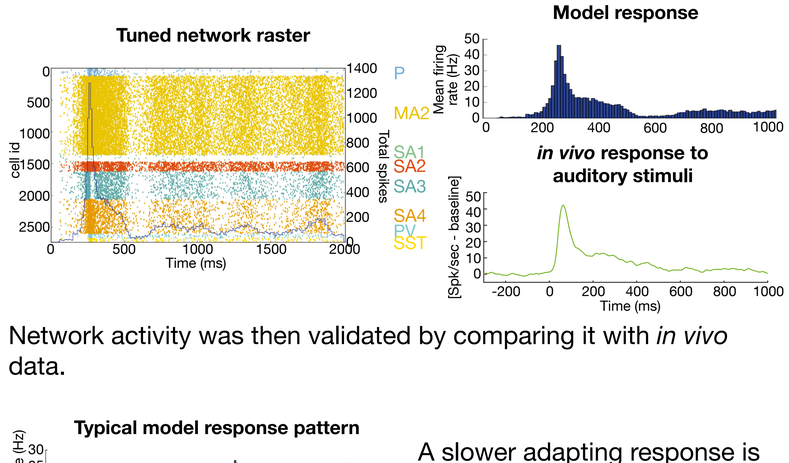
Methods



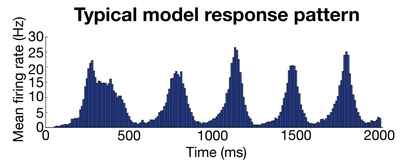
Taking overall and adaptation frequency into account, we replicated characteristic single-cell spiking patterns of 7 claustral cell types using the Izhikevich Simple Cell model.



Connectivity of the network was based on cell-type specific optogenetic maps, which is then tuned to give rise to physiological levels of network activity. The network is developed using NetPyNE and simulated on NEURON.



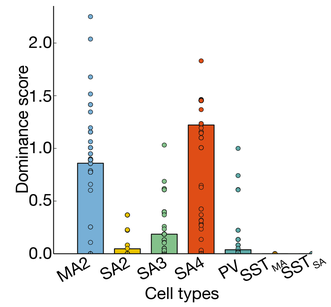
Network activity was then validated by comparing it with *in vivo* data.



A slower adapting response is commonly seen after the first peak in response to various types of stimuli.

Predictions

SA4 drives the claustral network



Future work

- Degree of decrement and rate of adaptation after the first peak
- Firing properties of individual cell types in the network
- Overall frequencies of individual cell types

Conclusions

- The model captures both single-cell and network behaviour.
- A decrementing, slower response after the first peak seems to be a feature of the network.
- The model predicts that SA4 might play a driving role to the network.

References

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Acknowledgements

We thank Yanxia Tang, Martin Graf and Zach Chia for experimental data and helpful discussions. This work is supported by A*STAR Graduate Academy and the Institute of Molecular and Cell Biology, A*STAR.

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