Learning Central Pattern Generator models for rhythmic activation patterns

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A typical objective in large-scale electrophysiology is being able to **reconstruct the underlying neural architecture** from sparse and noisy measurements. The problem is ill-posed since there are infinite combinations of neural models, network architectures and parameters that can generate the measured activation patterns. In this work, we provide a method for the automatic identification of the **simplest neural architecture** that is able to reproduce a target activation pattern. According to the parsimony principle, such network is the most likely to be implemented in the brain.

As first step, we decided to restrict our analysis on **rhythmic activation patterns** (e.g. lower limb EMG activity during locomotion) and on oscillatory neural models. Among the many oscillatory models, we choose the simple two-state Matsuoka oscillator [1]. Such firing neurons are able to generate oscillations through a mechanism of adaptation and mutual inhibition and have already been used to control the locomotion of biped robots, but never to reconstruct electrophysiological signals.

Given a set of target activation patterns $\boldsymbol{y^*}$, our algorithm looks for the simplest (i.e. the smallest) recurrent neural network composed of Matsuoka neurons that is able to reproduce $\boldsymbol{y^*}$. In particular, the algorithm starts off from the smallest architecture (i.e. $\boldsymbol{N}$=2), and keeps on "adding" neurons until a given stopping condition is met (e.g. reconstruction error lower than a given threshold). In order to fit each proposal network, which constitutes a non-linear dynamical system where both the initial states and the parameters are unknown, we developed an efficient algorithm based on the **Unscented Kalman Smoother (UKS)** [2], where the state vector was *augmented* with one additional state for each parameter to be estimated. Since we found that the UKS was highly sensitive to the initial estimates of the (extended) states, we integrated it in a genetic algorithm framework, thus making the optimization algorithm global. Lastly, once the best chromosome is selected, to fine tune the parameters and impose L2 regularization, we perform least squares minimization. This final step further decreases the reconstruction error.

The algorithm was tested on the 10 Matsuoka networks described in [1]. In particular, for each network, we used as target activation pattern the outputs of 2 of the neurons, corrupted with Gaussian noise. Using the algorithm here described, we were always able to retrieve the correct architecture in each of the 10 cases. Future work will involve the use of real electrophysiological data as target signals, and will study the biological plausibility of the identified networks.

References

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