The use of temporal data mining to model the *C. elegans* neuronal network

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Bioinformatics methods have become immensely popular in the past decade to study properties of molecular networks underlying protein-protein interactions, transcriptional regulation, and phenotype profiles (e.g., see [1]). With the availability of the synaptic connectivity of the *C. elegans* nematode, and large-scale datasets such as from multi-electrode arrays (MEAs), similar ‘network biology’ approaches to computational neuroscience are gaining interest. For instance, Reigl, Alon, and Chklovskii [2] have demonstrated the existence of 2-, 3-, and 4-neuron motifs that might form building blocks of larger computational modules. Recently, motifs in the *C. elegans* network have also been used as starting points to understand the neuronal basis of higher-level behaviors such as spatial orientation [3]. Here, we present the use of temporal data mining methods to gain insight into the neuronal network of *C. elegans*. Using an event sequence model formulated over the *C. elegans* neuronal system, we show how temporal patterns of firings can be captured using the notion of ‘frequent episodes’ [4] popular in the data mining literature. We identify many motifs embedded in the neuronal network that exhibit both structural and temporal (dynamic) properties and which can serve to summarize the state of the network as a whole. We define measures of network reconstruction that help characterize the sensitivity and specificity of our approach and show how the data mining algorithm can be steered to guarantee given constraints on reconstruction effectiveness.

References


