The speed of sequence processing in biological neuronal networks

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Sequence processing has been proposed to be the universal computation performed by the neocortex. The Hierarchical Temporal Memory (HTM) model provides a mechanistic implementation of this form of processing. While the model accounts for a number of neocortical features, it is based on networks of highly abstract neuron and synapse models updated in discrete time. Here, we reformulate the model in terms of a network of spiking neurons with continuous-time dynamics to investigate how neuronal and synaptic parameters constrain the sequence-processing speed.

CCS Concepts: • **Networks** → *Network dynamics*; • **Computing methodologies** → *Massively parallel algorithms*; *Temporal reasoning*.

Additional Key Words and Phrases: sequence processing, neocortex, hierarchical temporal memory, spiking neurons, dendritic action potentials, spike timing dependent structural plasticity

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1 INTRODUCTION

Learning and processing temporal sequences have been suggested to be *the* fundamental computation performed by the neocortex [1–3]. The Hierarchical Temporal Memory (HTM) model constitutes a mechanistic description of this type of computation [4]. It accounts for the specific anatomical structure of cortical (pyramidal) neurons, explains the functional role of dendritic action potentials, and learns continuously and in unsupervised manner by means of local learning rules. The model can simultaneously learn and predict multiple sequences in streams of data and is robust with respect to failure of network elements and noise. So far, implementations of this model are based on highly abstract models of neurons and synapses with discrete-time dynamics. To foster an understanding of the sequence processing characteristics in humans and other mammals, the model needs to be reformulated in terms of biophysical principles and parameters.

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2 MODEL

In this study, we deliver a continuous-time implementation of the temporal-memory algorithm proposed by the HTM theory [5], which comprises networks of spiking point neurons with nonlinear synaptic input integration mimicking the effect of dendritic action potentials [6]. The model learns sequences by means of spike timing dependent structural plasticity [7] and generates sparse spiking activity using lateral inhibition.

3 RESULTS

In the framework of our model, we investigate to what extent the sequence processing speed is determined by low level neuronal and synaptic parameters. We test the implementation in a task where the network learns higher-order sequences of characters, and study the role of the inter-stimulus (inter-character) interval on the sequence prediction error, thereby deriving lower and upper bounds for the sequence processing speed. In the context of our study, the sequence processing speed is determined by the time interval ΔT between subsequent presentations of sequence elements that guarantee a successful prediction. Our model demonstrates that the optimal range of inter-stimulus intervals is constrained by neuronal parameters such as cell-intrinsic time constants and synaptic weights, as well as the parameters of the structural plasticity dynamics.

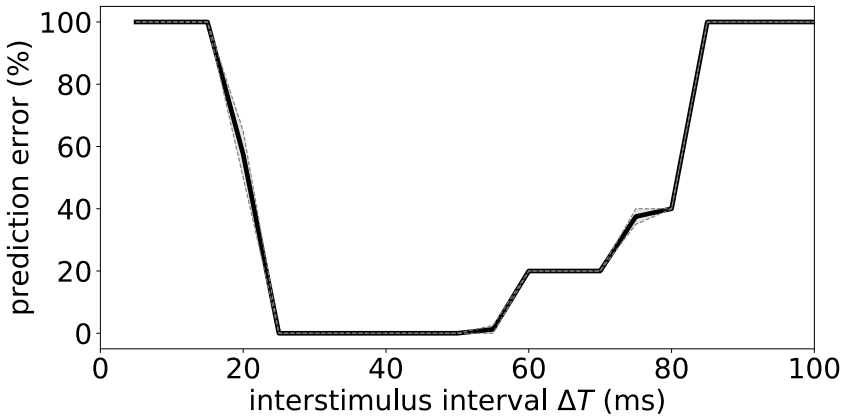

Fig. 1. Dependence of the sequence prediction error on the inter-character interval ΔT (after 400 training episodes). Here, the network learns two higher-order sequences DAEFGB and CAEFGB with a high degree of overlap. After successful learning, the network generates context specific sparse spiking activity, i.e. the response to the last five characters depends on the first character.

4 DISCUSSION

With biologically plausible parameter values, our network can learn sequences with inter-character intervals in the range $\sim$ 20–80 ms. Indeed, many sequences that can be learned by birds, humans and other mammals fall into this speed range (e.g. certain motor patterns; [8]). However, humans can clearly process slower sequences with inter-character intervals exceeding 1 second [2]. Extensions of our network model may account for this by employing a working memory mechanism.

Our model suggests a number of biological mechanisms by which the processing speed could be modulated. Candidates are variations in synaptic or membrane time constants, e.g. controlled by the level of synaptic background input, or a modulation in the effective synaptic coupling strength, e.g. through synaptic or intrinsic plasticity.

Note that an HTM implementation based on spiking neurons with continuous-time dynamics was already presented in [9]. This implementation mainly served the purpose of porting the HTM model to an analog-digital neuromorphic hardware system, and differs from our model in several respects. The study did not address the role of neuronal parameters for the sequence processing speed.

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