Constraints on sequence processing speed in biological neuronal networks

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Introduction

Learning and processing temporal sequences is a fundamental computation performed by the neo-cortex [1].

- most cognitive tasks, such as reading, motor control, or sensory processing (visual, tactile, auditory), can be described in terms of sequence processing.
- sequence processing refers to a context dependent prediction of elements in discrete time series and the generation of a mismatch signal if the prediction doesn't match the actual input.

The **Hierarchical Temporal Memory (HTM)** model provides a mechanistic description of sequence processing by neuronal networks [2]. It accounts for

- morphology of cortical (pyramidal) neurons,
- functional role of dendritic action potentials,
- online continuous learning via local learning rules,
- context dependency (higher-order predictions), and
- multiple simultaneous predictions.

The HTM model is based on binary neurons and an abstract, discrete-time dynamics.

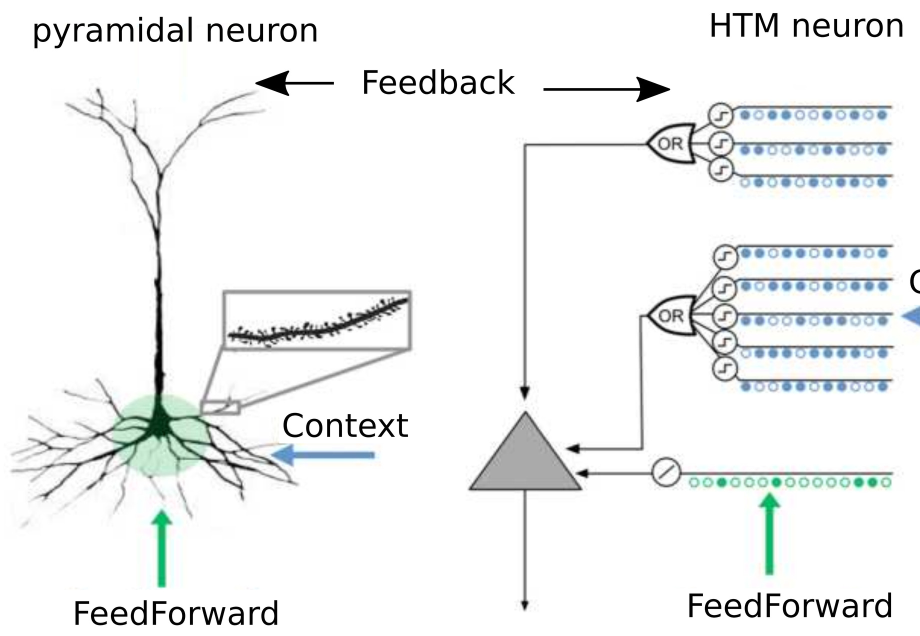
What features of biological neural networks determine sequence processing speed?

Studying sequence processing speed requires reformulating the HTM model in terms of biological ingredients, in particular

- a continuous time dynamics with spike based interaction between network elements, and
- neuronal, synaptic and plasticity dynamics with realistic time constants [3].

Hierarchical Temporal Memory (HTM)

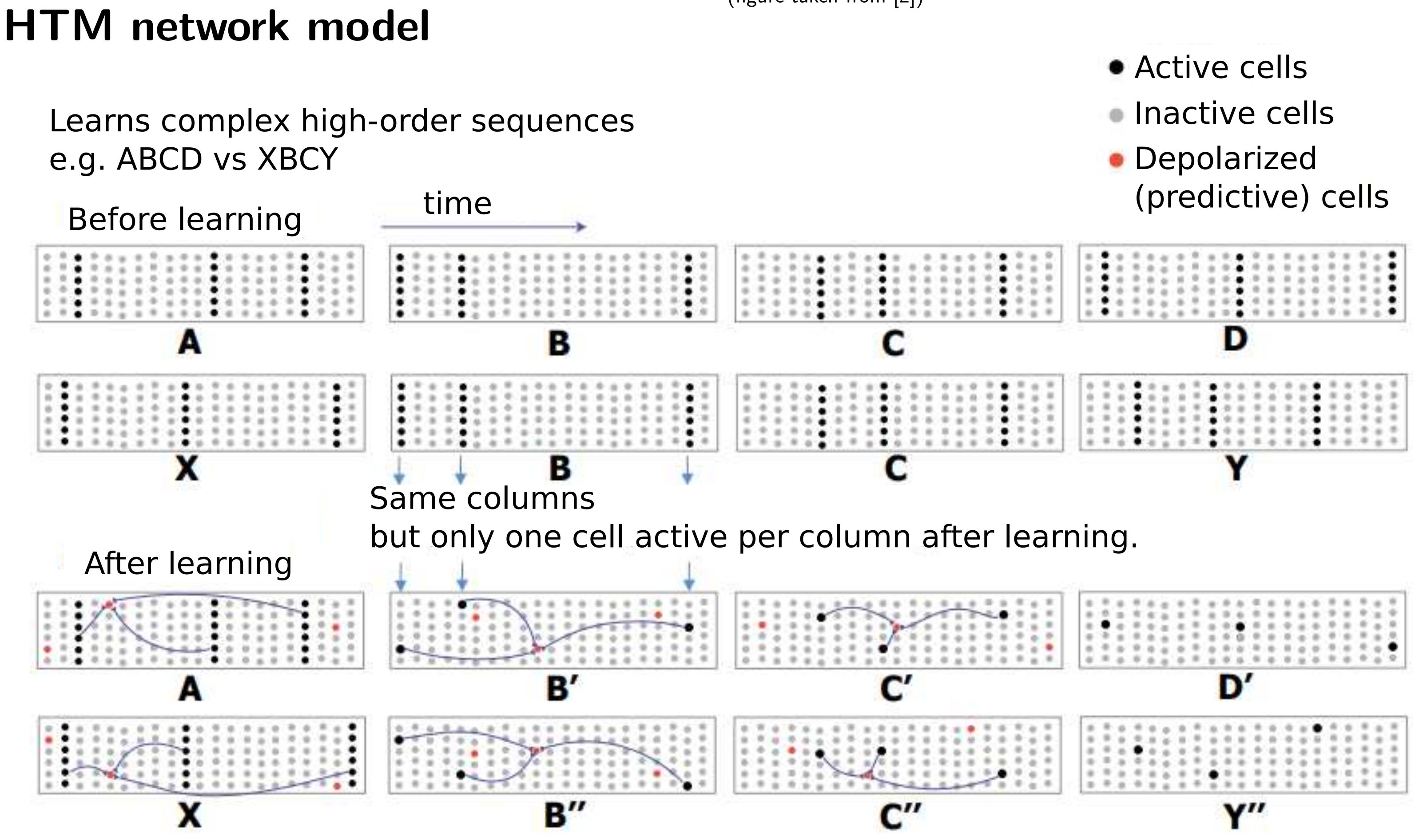
HTM neuron model



- dendritic branches serve as pattern detectors
- pattern detection leads to dendritic spike and strong depolarization of the soma ("prediction")

(figure taken from [2])

HTM network model

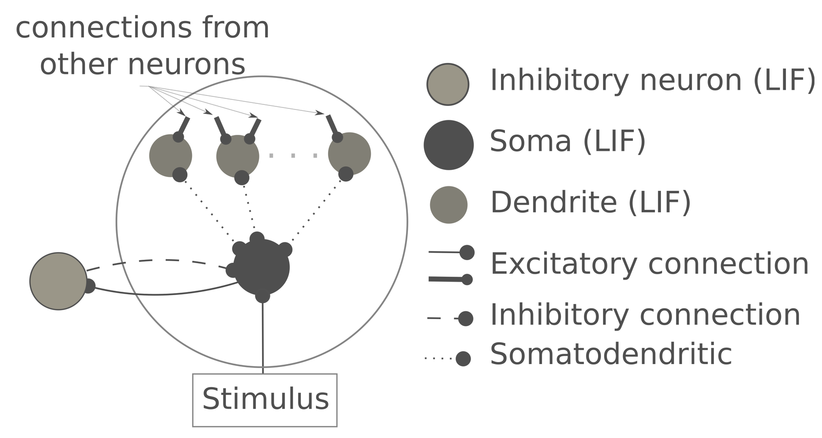


(figure taken from [2])

- external input (sequence elements) activates specific subset of minicolumns
- unpredicted stimulus causes firing of all neurons in this set of minicolumns ("mismatch signal")
- predicted stimulus leads to sparse activity

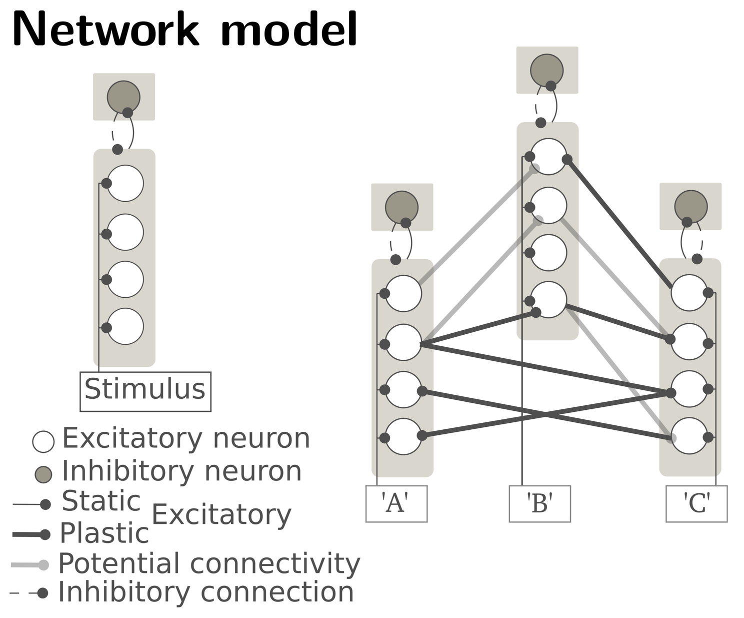
Spiking HTM Model

Neuron model



- excitatory neurons composed of a soma and a number of dendritic compartments
- each compartment modeled as a leaky integrate-and-fire (LIF) unit
- bidirectional coupling between dendritic compartments and soma (backpropagation)
- inhibitory neurons (LIF) coupled to the soma

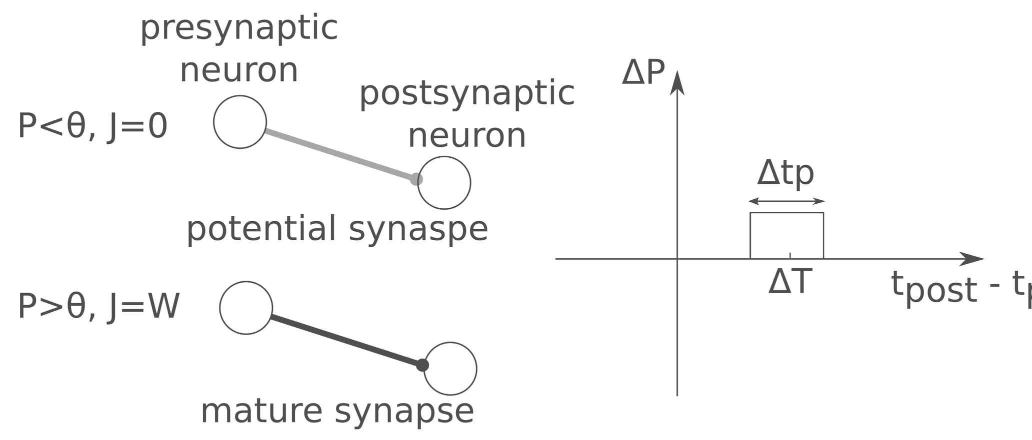
Network model



- network composed of a number of minicolumns (M), each representing an element in a sequence
- each minicolumn composed of a number of excitatory neurons (n_E), recurrently connected to an inhibitory neuron, and driven by a feed-forward input (stimulus)
- sparse random connectivity between mini-columns, subject to spike-timing-dependent structural plasticity [4]

Plasticity model

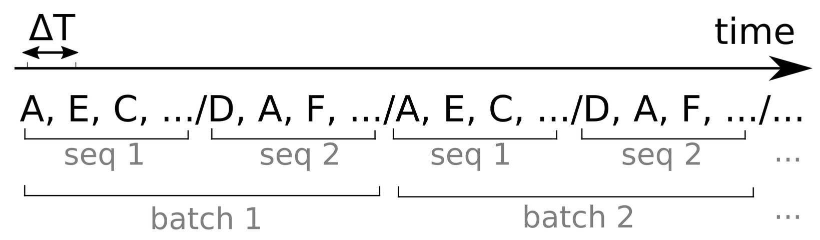
- spike-timing-dependent structural plasticity [4]
- each synapse characterized by permanence (P) and weight (J)



Results

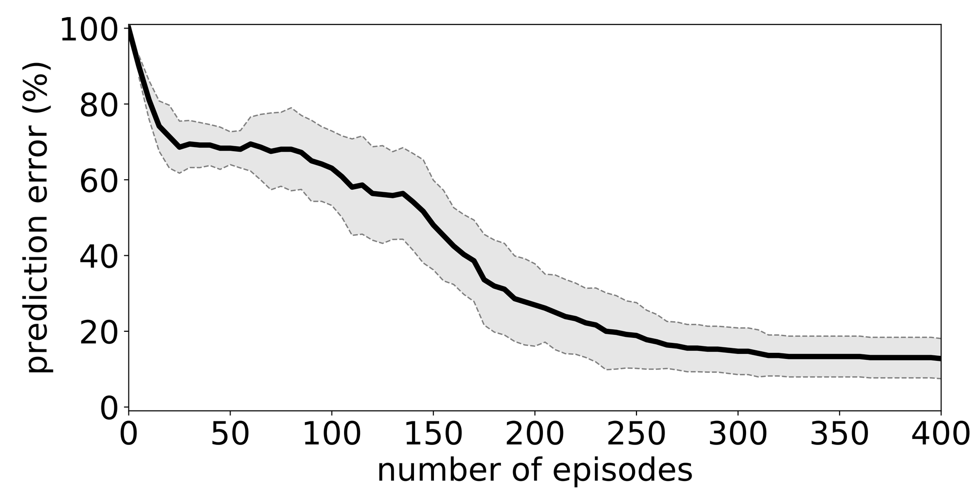
Task

- prediction of characters in a set of sequences
- each sequence is composed of C characters



Prediction performance

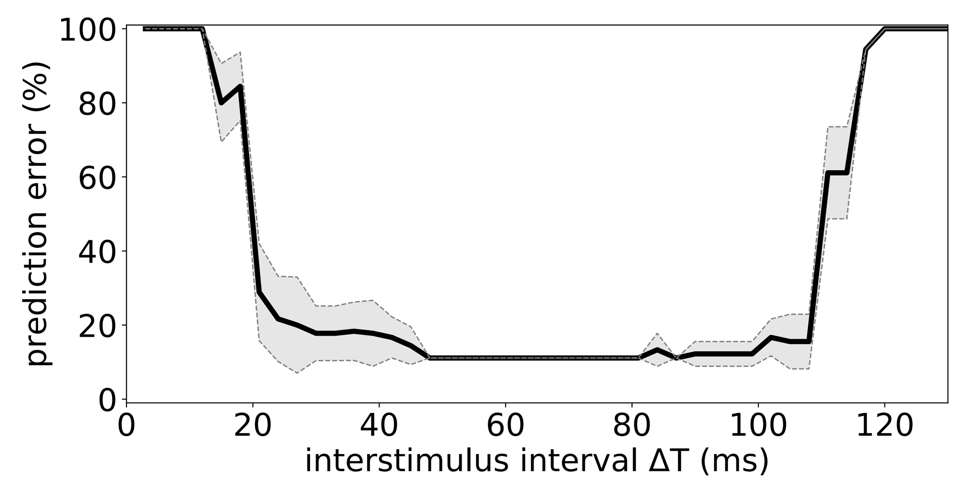
- monotonous decrease of prediction error with number of training episodes
- saturation of prediction error due to residual task ambiguity



n_E=30, M=10, C=10

Processing speed

- model predicts optimal range of interstimulus intervals
- lower and upper bound of interstimulus interval determined by neuronal time constants and postsynaptic potential amplitudes



Conclusion

- revised HTM model supports successful sequence processing
- prediction of optimal range of processing speeds (inter-stimulus intervals) with lower and upper bounds constrained by neuronal and synaptic parameters (e.g. time constants, coupling strengths)

Outlook

- upscaling of task complexity
- comparison to results of psychophysical experiments

References

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