Mapping, Learning and Mining of Brain Spatiotemporal Data with 3D Evolving Spiking Neurogenetic Models

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Spatio- and spectro-temporal data are the most common data in many domain areas, including bioinformatics and neuroinformatics. Still there are no sufficient methods to model such data and to discover complex spatio-temporal patterns from it. The brain is functioning as a spatio-temporal information processing machine and brilliantly deals with spatio-temporal data, thus being a natural inspiration for the development of new methods for brain data modeling and pattern recognition. The presented research aims at the development of a 3D neurogenetic model of the human brain, called NeuCube, that can be efficiently utilized for spatio-temporal brain-gene data modeling and pattern recognition. The NeuCube is a 3D evolving probabilistic SNN (epSNN).

epSNN are built on the principles of evolving connectionist systems [1] and eSNN in particular [2,3] and on probabilistic neuronal models (e.g. [4]). The latter extent the popular leaky integrate-and-fire spiking model with the introduction of some biologically plausible probabilistic parameters. The epSNN are evolving structures that learn and adapt to new incoming data in a fast incremental way.

The overall architecture of the NeuCube is presented in [5]. It consists of a reservoir type brain structural map, an input module for converting input stimuli into spike trains, an eSNN classifier and a gene regulatory network module. The research explores different types of neuronal models and dynamic synapses, including a SPAN model [6,7] and a novel deSNN model that implements the time-to-first spike principle and Fusi's algorithm implemented on the INI Zurich (www.ini.unizh.ch) SNN chip [8].

Examples of using the NeuCube architecture for brain data modeling are given on EEG-, fMRI-, MEG- and other types of brain spatio-temporal data with applications including BCI. Neurogenetic models are promising for modeling and prognosis of neurodegenerative diseases such as Alzheimer's disease [9,10] and for personalized medicine in general [11]. Future research is expected to continue through tighter integration of knowledge and methods from information science, bioinformatics and neuroinformatics [12]. The research is relevant to the future development in the neuromorphic engineering area.

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Biodata:

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