

Discovering Rules of Adaptation and Interaction: From Molecules and Gene Interaction to Brain Functions

Nikola Kasabov

Knowledge Engineering and Discovery Research Institute, KEDRI
Auckland University of Technology, Auckland, New Zealand
nkasabov@aut.ac.nz, www.kedri.info

Abstract: Many systems in Biology and Nature are characterized by a continuous adaptation and by a complex interaction of many variables over time. Such systems can be observed at different levels of the functioning of a living organism, e.g.: molecular, genetic, cellular, multi-cellular, neuronal, brain function, evolution. One of the challenges for information science is to be able to represent the dynamic processes, to model them, and to reveal “the rules” that govern the adaptation and the variable interaction over time.

The paper presents one approach to address the above issues through adaptive, knowledge-based connectionist systems. These systems evolve their structure and functionality through learning from data in both on-line and off-line incremental mode, in both supervised and unsupervised modes, and facilitate data and knowledge integration, rule extraction and rule manipulation. Evolving Connectionist Systems (ECOS) are presented as an example of such systems. The evolving process of an ECOS is defined by parameters, “genes” [1]. ECOS extend further the classical knowledge-based neural networks [2].

Adaptive, knowledge-based connectionist systems, and ECOS in particular, are applied on data and problems from Bioinformatics and Neuroinformatics to discover rules of adaptation and interaction. Such problems are: microarray gene expression analysis and profiling; gene regulatory network modeling (GRN); medical prognostic systems; modeling visual and auditory perception states of the human brain, etc [1]. Recently new, biologically plausible ECOS have been developed, called computational neurogenetic models [3,4]. In these models the neuronal parameters correspond to real genes expressed in the brain and related to learning processes and brain diseases [3,4]. A dynamic model of a GRN within each neuron is evolved during the modeling process that governs the neuronal processes. All neurons have a spiking behavior to form spiking neural networks, characterized by a spectral profile [3,4]. The computational neurogenetic modeling paradigm is illustrated on a case study of modeling epileptic/normal state transitions and the discovery of the gene interaction networks that are likely to cause this phenomenon. Further directions include: the development of dynamic evolving neurogenetic models; modeling complex brain processes and diseases; cancer prognosis; hardware implementation.

References

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