Adaptive Neural Networks, Gene Networks, and Evolutionary Systems – Real and Artificial Evolving Intelligence

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Abstract

The paper presents an integrated approach to building evolving artificial intelligent systems in terms of evolving connectionist systems (ECOS) that capture principles from neural networks, gene interaction networks and evolutionary systems. The ECOS can be used to solve complex problems from computational biology that is illustrated on a simplified gene regulatory network modeling problem. The paper first presents some principles of real neural networks, gene regulatory networks and evolutionary systems before it presents ECOS and their applications.

Keywords: adaptive systems, neural networks, evolving systems, gene regulatory networks.

1. Introduction

In living systems dynamic, adaptive, evolving processes are observed at different levels (Tabl.1). At a molecular level and a cell level the DNA, the RNA and the protein molecules evolve and interact in a continuous way. The genes form dynamic *gene regulatory networks* that define the complexity of the living organism. It is not just the number of the genes in a genome, but the interaction between the genes that makes one organism more complex than another (e.g. humans versus mice).

Many functions are associated with a neuronal cell and a neural network level. An ensemble of cells (neurons) operates in a concert defining the function of the network, e.g. perception of a sound.

At the level of the human brain, a complex dynamic interaction is observed and certain cognitive functions are performed, e.g. speech and language learning, visual pattern recognition.

Many processes of perception and cognition are multi-modal, involving auditory-, visual-, tactile-, and other type of information processing. All these processes are extremely difficult to model without having a flexible, multi-modular evolving system in place. Some of these modalities are smoothly added at a later stage of the development of a system without the need to "reset" the whole system.

Table 1. Four levels of evolving processes in living organisms[1]

4. Evolutionary level (e.g. the evolution of a genome)
3. Brain level *(cognition, speech and language, decision making)*
2. Neuronal and neural network level *(e.g. neuronal information processing, auditory or visual perception*)
1. Molecular and cell level *(e.g. DNA, RNA, genes, proteins)*

A biological system evolves its structure and functionality through both, life-long learning of an individual, and evolution of populations of many such individuals, i.e. an individual is part of a population and is a result of evolution of many generations of populations, as well as a result of its own developmental life-long learning process.

The paper first presents some principles of adaptive biological systems. Then it presents some principles of artificial evolving connectionist systems (ECOS)[1] and illustrates their applicability on a small scale gene regulatory network modeling problem. The discussion section outlines some future directions.

2. Adaptive Biological Gene Networks, Neural Networks, and Evolutionary Systems

2.1. Gene Regulatory Networks

In a single cell, the DNA, the RNA and the protein molecules interact in a continuous way during the process of the RNA transcription from DNA

(genotype), and the subsequent RNA to protein (phenotype) translation[2,3]. A single gene interacts with many other genes in this process, inhibiting, directly or indirectly, the expression of some of them, and promoting others at the same time. This interaction can be represented as a gene regulatory network (GRN). GRN dynamically evolve and change their structure based on DNA and environmental information. Modelling GRN is an extremely difficult task that requires a large amount of data and sophisticated information methods. A large amount of data on gene interactions for specific genomes, as well as on partial models, is available from public domain databases such as NCBI (http://www.ncbi.nlm.nih.gov/), KEGG (http://www.genome.ad.jp/kegg/), Stanford Microarray Database, and many more[4] . Collecting both static and time course gene expression data from up to 30,000 genes is now a common practice in many biological, medical and pharmaceutical laboratories in the world through the introduction of microarray technologies (see for example (www.ebi.ac.uk/microarray).

2.2. Adaptive Neural Networks: Gene Networks within Neural Networks

The brain consists of many interrelated neural networks (NN). Each of them is a tremendously complex adaptive information system characterised by learning, generalisation, and development. Every neuron contains the whole genome of the organism and therefore its functions are defined by both the environment it learns from and by the GRN that is activated in this neuron. Adaptation of the GRN now take place along with the adaptation process of the NN that makes the modelling of real NN a complex task.

2.3. Adaptive Evolutionary Systems: Gene Networks, within Neural Networks, within Evolutionary Population Systems, within …

Evolutionary processes take place over generations of populations of individual systems; each individual system represented as adaptive neural networks. The evolutionary process affects the DNA and the genes that result in a modified GRN, thus affecting the learning processes of t6he neural networks. This is a very complex interaction that can't be modelled in its entirety, but a part of it, e.g. modelling of GRN can be attempted with the use of methods based principles of adaptive neural learning, gene interaction and gene evolution. Such methods are the evolving connectionist systems (ECOS) methods[1] as discussed below.

3. ECOS

3.1. Main principles of ECOS

The main principles of *evolving connectionist systems (ECOS*) and some of their models are presented in [1,5,6]. ECOS are connectionist structures that evolve their composite nodes (neurons) and connections through both supervised and unsupervised incremental learning from data. One of the ECOS models is shown as a simple implementation in fig.1. It consists of five layers of neurons (nodes) to represent respectively: input variables; fuzzy representation interval for each input variable, such as Small, Medium and High; rule nodes, that represent cluster centers of data vectors in the problem space; output fuzzy representation nodes; outputs. The ECOS may include a feedback layer as a short-term memory that links rule nodes, highly activated at consecutive time moments.

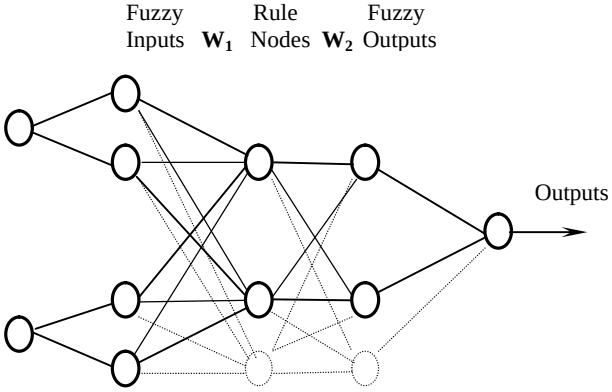


Fig.1. A simple version of an ECOS [1]

ECOS learn input streams of data starting with no rule nodes, or with a few pre-initialized nodes based on existing knowledge. ECOS grow through the creation of new rule nodes, allocated at cluster centers in the input space, and through learning a local output function for each cluster. In the first year of the project the information theoretic framework of ECOS will be developed (the general goal) that will include the methods described below.

ECOS automatically create (learn) local models from data through clustering of the data and associating a local output function to each cluster. Rule nodes evolve from the input data stream to cluster the data, so that the first layer W_1 of connection weights of these nodes represent the co-ordinates of the nodes in the input space (see fig.1). The second layer W_2 represents the local models (functions) allocated to each of the clusters.

3.2. EFuNN and DENFIS

Clusters of data are created based on similarity measured either in the input space (this is the case in some of the ECOS models, e.g. the dynamic neuro-fuzzy inference system DENFIS[6]) or in both the input space and the output space (this is the case in the evolving fuzzy neural networks EfuNN[5] – fig.1]). Samples that have a distance to an existing cluster center (rule node) N of less than a threshold R_{max} (the

EfuNN models it is also needed that the output vectors of these samples are different from the output value of this cluster center in not more than an error tolerance *E*) are allocated to the same cluster N_c. Samples that do not fit into existing clusters, form new clusters over time. Cluster centers are continuously adjusted according to new data samples, or new clusters are created incrementally.

The similarity between samples can be measured in different ways, the most popular of them being the normalized Euclidean distance. In a partial case of missing values for some variables in the input vectors, a partial normalized Euclidean distance can be used, i.e. only the existing variables in a current sample $S = (\boldsymbol{x,y})$ are used for the similarity measure between this sample and an existing rule node $N = (\boldsymbol{W}_{1N}, \boldsymbol{W}_{2N})$:

$$d(S,N)=[S_{(i=1,..,n)}(x_i - W_{1N}(i))^2]/n_e, \qquad (1)$$

for all input variables x_i having a defined value in the sample S and an already established connection $W_{1N}(i)$ to the cluster node N, n_e being the number of such variables in the sample S. In a partial Euclidean space, cluster centers can be defined based on a different number of variables.

ECOS learn from data to automatically create a local output function for each cluster, the function being represented in the $\boldsymbol{W}_2$ connection weights, thus creating local models. Each model is represented as a local rule with an antecedent – the cluster area, and a consequent – the output function applied to data in this cluster, e.g.:

IF [data is in cluster N_{cj}, defined by its cluster center N_j, the cluster radius R_j and the number of examples N_{jex} in this cluster] THEN [the output function is f_c]

In case of DENFIS, first order local fuzzy rule models are derived incrementally from data, for example: IF [the value of x_1 is in the area defined by a triangular membership function with a center at 0.7, left point of 0.4 and right point at 0.83) AND (the value of x_2 is in the area defined a triangular function (0.1,0.3,0.6) respectively] THEN [the output value y is calculated with the use of the formula $y= 3.7 + 0.5x_1 - 4.2\ x_2$]

In case of EfuNNs, local simple fuzzy rule models are derived, for example: IF [x_1 is High (0.7) and x_2 is Low (0.9)] THEN y is High (0.8) [radius of the input cluster 0.3, number of examples in the cluster 13], where: High and Low are fuzzy membership functions defined on the range of the variables. The number and the type of the membership functions can either be deduced from the data through learning algorithms, or it can be predefined based on human knowledge.

3.3. ECOS optimization through evolutionary computation

The ECOS parameters, such as learning rate, cluster radius, error threshold, membership functions can be interpreted as the genes of the evolving NN. They need to be self-optimized during the incremental, continuous learning of ECOS in order for the ECOS system to be autonomous. This is achieved with the use of several methods for on-line and off-line parameter self-optimization as presented in [7,8].

4. ECOS for Adaptive Learning of Simple GRN- A Case Study

4.1. The Problem of GRN Modelling

Several generic information methods for modelling and for the discovery of variable interaction networks from time course data have been proposed and used in the domain of GRN modelling. Among them are: statistical methods[9]; neural networks[10,11]; evolutionary computation [4,12,13]; directed graphs; Petri nets; ordinary and partial differential equations[14]. Each of these methods lacks at least several of the following characteristics: (i) dealing with a large number of variables of different types and with imprecise data; (ii) adaptive incremental learning in a changing environment; (iii) dealing with missing values and adding new variables "on the fly"; (iv) continuous model parameter optimization.

4.2. ECOS for GRN Modelling

The suitability of ECOS for modeling GRNs was first demonstrated on a small data set[15] in [16]. Here the main principles of applying ECOS for the GRN modeling are presented.

An ECOS is incrementally evolved from incoming data $\mathbf{X}(t_0)$, $\mathbf{X}(t_1)$, $\mathbf{X}(t_2)$, …, representing the values of all, or some of the variables or their clusters. Consecutive vectors $\mathbf{X}(t)$ and $\mathbf{X}(t+k)$ are used as input and output vectors respectively in an ECOS model, as shown in fig.2a. After training of an ECOS, e.g. EfuNN, on data, rules are extracted through IF-THEN representation of the rule nodes, e.g.: IF x1(t) is High (0.87) and x2(t) is Low (0.9) THEN x3 (t+k) is High (0.6) and x5(t+k) is Low (see fig.1). Each rule represents a transition between a current and a next state of the variables as shown in fig.2b, where each rule is shown as an arrow.

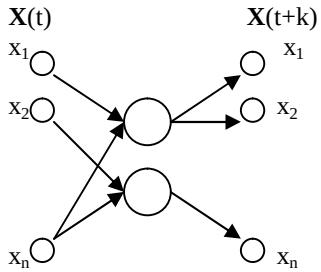
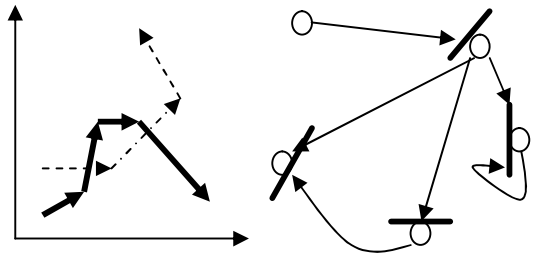


Fig.2a. A hypothetical ECOS for GRN modeling

All rules together form a representation of the GRN. Fig.2b shows two trajectories, N_1 and N_2 that represent

two VRNs, derived under different conditions, in the 2D PCA (principal component analysis) coordinate space of all *n* variables.



(b) (c)

Fig.2.b, c: (b) State transitions (rules, represented as arrows) in the two PCA dimensional space of the n variables; (c) Part of a GRN extracted from an ECOS model.

Using the DENFIS[6] ECOS model, other types of variable relationship rules can be extracted, e.g.: *IF x1(t) is (0.63 0.70 0.76) and x2(t) is (0.71 0.77 0.84) and x3(t) is (0.71 0.77 0.84) and x4(t) is (0.59 0.66 0.72) THEN x5(t+k) = 1.84 -1.26x1(t) - 1.22x2(t) + 0.58x3(t) - 0.3 x4(t),* where the cluster for which the value of x_5 is defined in the rule above, is a fuzzy cluster represented through triangular membership functions defined as triplets of values for the left-, centre-, and right points of the triangle on a normalisation range of [0,1].

5. Evolving Intelligence – Real and Artificial

The availability of DNA data, brain development data and evolutionary development data now makes it possible for the creation of artificial intelligent systems that evolve and learn in a similar way as biological systems do. Good candidates for such systems are ECOS[1] that evolve their neural network structure in an incremental way and optimize their parameters (genes) through methods of evolutionary computation.

Future research includes:

- A further development of the ECOS methods with the inclusion of statistical methods, such as Bayesian networks, Hidden Markov Models, and others;
- the application of ECOS to modeling large GRN;
- the application of ECOS to the problem of modeling brain functions and their related gene networks;
- the application of ECOS for the development of intelligent decision support systems for biological data analysis and knowledge discovery.

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