

# Agent-Based Optimization of Neural Classifiers

Aleksander Byrski, Jan Dobrowolski, Krzysztof Toboła

AGH University of Science and Technology, Department of Computer Science Kraków, Poland,  
email: olekb@agh.edu.pl, {dobrowol,kreez}@student.agh.edu.pl

**Abstract.** In the paper an agent-based system of evolving neural networks dedicated to solving classification problem is presented. Next, aspects of the system concerning management of collective intelligence and evolution of parameters of neural network are discussed. Evolutionary multi-agent system (EMAS) is described with enhanced immune-inspired selection mechanism. Finally selected results of the experiments are presented.

## 1 Introduction

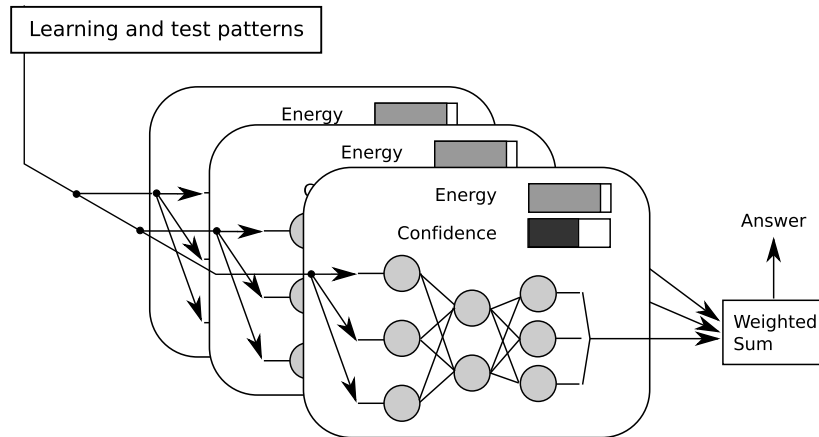
Looking for the optimal neural network is a serious problem, because this process usually involves performing multiple experiments necessary for finding optimal values of the network. Such process is a very time consuming job and can be conducted usually by an expert, who is forced to repeat all his tasks when new application of the neural network emerges.

However, evolutionary algorithms, being universal optimization technique may be employed to automatize the process of search for optimal neural network. After encoding the parameters describing neural networks (architecture, learning coefficients e.a.) in chromosomes and defining appropriate fitness function, they may be subjected to evolution process, which should yield (sub)optimal results, that may be sufficient for the given problem [10]. Evolutionary computation may be further improved by using intelligent agent-based systems. Agents managed in specific way, may become a source of *collective intelligence* [1].

Combining evolutionary computation with multi-agent systems (MAS) leads to decentralisation of the evolutionary optimisation process. Training of a neural network may be entrusted to an autonomously acting agent. Such defined *evolutionary multi-agent system* (EMAS) may help in search for the optimal configuration of a neural network for the given problem, or at least help to establish a starting point for further network structure development [7].

Computation of the value of fitness function is exceptionally difficult when dealing with evolutionary neural network optimization because of its time complexity. However the process of computation may be boosted by early removing non-promising results by additional group of agents. This immune-inspired technique leads to introducing special group of agents dedicated for manipulating of population of EMAS. Thus iEMAS *immunological evolutionary multi-agent system* is created [4].

This paper presents the concept and implementation of such a hybrid, collective intelligent system. The main task of the system is classification, and at the same time, to



**Figure 1.** MAS for classification

optimize the architecture and parameters of predicting neural networks. The experimental results let to state that introduction of immunological selection mechanism allows for increasing of computation effectivity.

## 2 MAS for classification

The problem of classification may be solved by single machine learning technique such as neural network. It should be appropriately parameterized and the problem may require multiple runs of training of such a model.

However, agent-based system may be used to concurrently train multiple models, adapt their parameters, introduce new and remove inappropriate models e.a. Particularly agent systems hybridized with evolutionary algorithms (EMAS) were already used for solving the problem of time-series prediction [5, 2]. Similar approach may be used to classification.

The classifying MAS contains the group of intelligent agents. Elements of input data are fed into the environment and passed to all agents. Agents may individually preprocess the data and produce individual answer (classification).

One may notice that a group of autonomous yet cooperating intelligent agents can exhibit a kind of *collective intelligence* [3]. While dealing with such a system an important problem arises: how to determine the answer of the whole system to given problem. For mentioned classification problem, it should be decided how to select an agent which output is the best or most representative and thus may be presented as the output of the whole system, or how to combine more than one agent's answers to produce the desired classification.

In the particular system, the way of combining multiple individuals' answers can be based on probability analysis (combined with voting-based strategy where the answer of the group of experts comes as a weighted answer of every member of the group, based on appropriately defined confidence coefficient see fig. 1) as shown in section 3.

### 3 Neural EMAS for classification

Many techniques were invented that allow for automatic design of a neural network that fulfills the requirements of the problem. The search for the desirable neural network can be made by an evolutionary algorithm [8, 10]. Based on this approach, evolutionary agent-based system for optimization of neural network parameters is proposed.

The key idea of EMAS is the incorporation of evolutionary processes into a multi-agent system (MAS) at a population level [5, 7]. It means, that besides interaction mechanisms typical for MAS (such as communication) agents are able to reproduce (generate new agents) and may die (be eliminated from the system). A decisive factor of an agent's activity is its fitness, expressed by the amount of possessed non-renewable resource called life energy. Selection is realised in such a way that agents with high energy are more likely to reproduce, while low energy increases the possibility of death (see fig. 3).

In EMAS training of a neural network may be entrusted to an agent while the search for a suitable network architecture may be realised as the process of evolution occurring in the whole population. A genotype describing architecture and parameters of neural network, possessed by an agent, is modified by genetic operators when inherited by its offspring. Evaluation of agents is based on the quality of classification [4].

In the above-described system every agent contains a neural network, which acts as a computational model for the given (classification) problem. This is similar to the approach of modular neural networks such as the model of PREDictive MODular Neural Network. PREMONN is a group (team) of neural networks, which solve the same problem, and their responses are combined together to yield the final result [9]. Although the model was originally used for prediction, it may serve as well to compute the overall classification result.

Applying PREMONN algorithm, every classification performed by an agent may be assigned a certain probability, which can be used to determine the answer of the whole group of classifying individuals. After the epoch of neural network training, every individual based on its classification result and accuracy:

$$y_t^k = f_K(y_{t-1}, y_{t-2}, \dots, y_{t-M})$$

$$e_t^k = y_t - \hat{y}_t^k$$

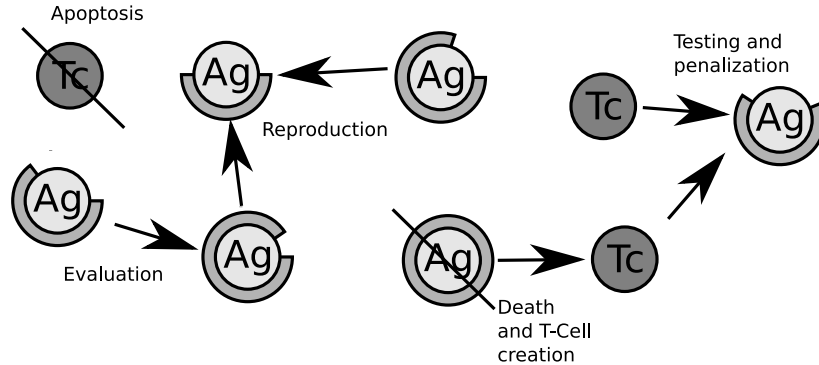
(where  $e_t^k$  is the error of classification of the k-th pattern fed into neural network during specific training epoch) computes its credit function:

$$p_t^k = \frac{p_{t-1}^k \cdot e^{-\frac{|e_t^k|^2}{2\sigma^2}}}{\sum_{n=1}^K p_{t-1}^n \cdot e^{-\frac{|e_t^n|^2}{2\sigma^2}}}$$

Based on this function the classification of the group of individuals can be a weighted combination of the answers or even can be the result of the winner-take-all combination (choosing the best individual in the meaning of credit function).

### 4 Immunological computation boosting in EMAS

Evolutionary optimization of neural network architecture is one of the problems that involves computing fitness function of very high time complexity. It is caused by the



**Figure 2.** EMAS and iEMAS structure and behavior

need for training the neural network (phenotype construction) in order to evaluate the appropriateness of the given architecture (genotype).

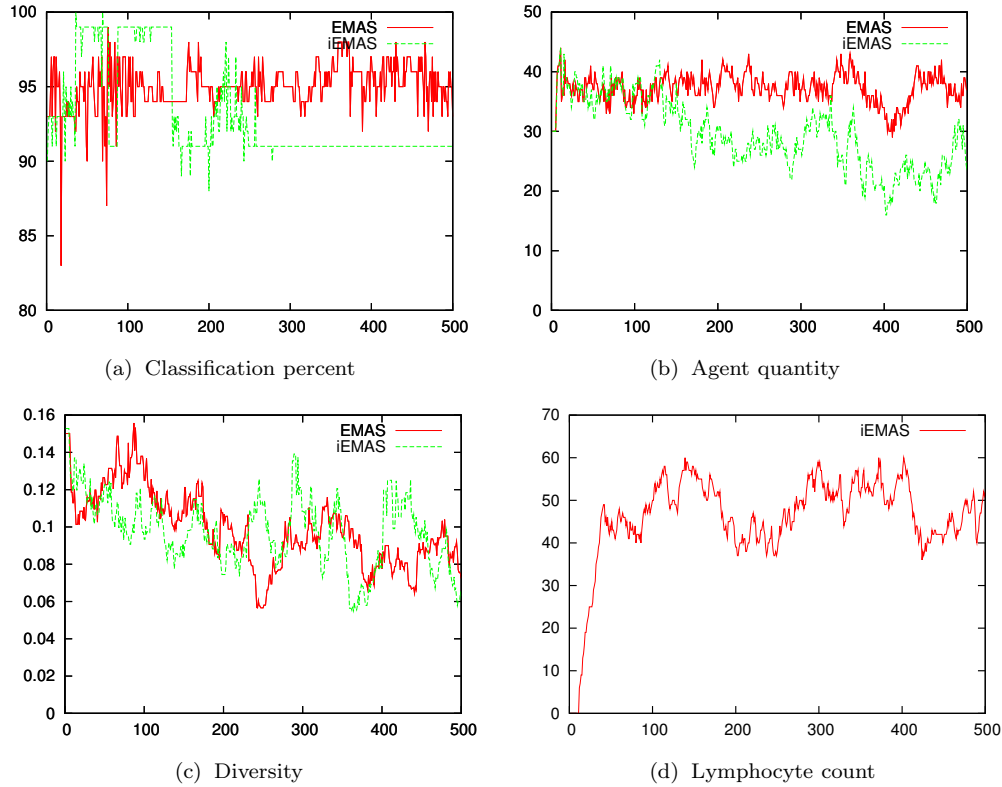
The efficiency of the computation may be increased by early removing of certain individuals, instead of training them. However, the cause of this removal must be appropriately defined. This cause may be based on the observation, that "bad" phenotypes come from the "bad" genotypes. Thus, a new group of agents (acting as lymphocyte T-cells) may be introduced [4]. They are responsible for recognizing and removing agents with genotypes similar to the genotype pattern possessed by these lymphocytes. Other approach may introduce specific penalty applied by T-cells for recognized agents (certain amount of agent's energy is removed) instead of removing them from the system. Of course there must exist some predefined affinity function, which may be based on the percentage difference between corresponding genes (see fig. 3).

In order to avoid rapid changes in the population and removal of possibly "good" agents, new lymphocytes must undergo the process of negative selection. In a specific period of time, the affinity of immature lymphocytes patterns to "good" agents (possessing relative high amount of energy) is tested. If it is high (lymphocytes recognize "good" agents as "non-self") they are removed from the system. If the affinity is low, it is assumed that they will be able to recognize "non-self" individuals ("bad" agents) leaving agents with high energy intact [4].

## 5 Experimental results

In this section selected results generated by a system implemented based on presented EMAS and iEMAS idea are presented. The system was developed with use of AgE platform (<http://age.iisg.agh.edu.pl>). As the classification models multi-layered perceptrons trained by backpropagation algorithm were used. The architecture of the network was indirectly encoded into a genotype (containing number of neurons in every layer and learning parameters) which was subjected to the evolution process performed in EMAS and iEMAS.

The performed experiments were aimed at proving that the EMAS is appropriate to optimize architecture of classifying neural network (multi-layered perceptrons). Moreover, efficiency of iEMAS was compared to EMAS in order to examine the possibilities



**Figure 3.** Classification percent, agent quantity, diversity and lymphocyte count for EMAS and iEMAS, thyroid problem

of computation boosting by early removing weak solutions.

The benchmark datasets were taken from well known UCI Machine Learning Repository, being one of the most widely benchmark for machine learning problems:

- Iris – 4 dimensions, 3 classes, 150 instances, one class is linearly separable from the others 2, remaining two classes are not linearly separable from each other,
- Wine – 13 dimensions, 3 classes, 178 instances, classes are linearly separable,
- Breast cancer – 9 dimensions, 2 classes, approximately 700 instances, determining wheter given sample is benign or malignant.
- Thyroid – 21 dimensions, 3 classes, 1000 instances (chosen from over 7000), determining wheter given sample refers to normal functioning, hyperfunctioning or subfunctioning of thyroid.

One of the most important features of the introduced immunological inspired mechanism is early removing of certain (weak) individuals. It may be seen in the graph 3(b), that there is noticeably fewer agents in the population of iEMAS than in EMAS, so the introduced mechanism really works.

In the graph 5 classification percent for EMAS and iEMAS is presented. One can see, that the classification level of iEMAS is similar to EMAS, both being above 90%. This

**Table 1.** Averaged values from 400 last iterations for Wine, Iris, Thyroid and Breast cancer problems

Parameter	Wine		Iris	
	EMAS	iEMAS	EMAS	iEMAS
<i>Classification percent</i>	98.89 ± 0.81	97.38 ± 1.60	92.57 ± 2.36	93.61 ± 2.36
<i>Agent quantity</i>	36.92 ± 0.64	29.55 ± 1.28	37.02 ± 0.65	29.80 ± 1.46
<i>Lymphocytes quantity</i>	0 ± 0	54.83 ± 2.54	0 ± 0	56.14 ± 2.63
<i>Diversity</i>	0.086 ± 0.003	0.097 ± 0.009	0.088 ± 0.005	0.108 ± 0.009
<i>Overall time</i>	479	414	373	290
Parameter	Thyroid		Breast cancer	
	EMAS	iEMAS	EMAS	iEMAS
<i>Classification percent</i>	96.03 ± 0.90	95.04 ± 0.93	97.34 ± 0.74	96.55 ± 0.83
<i>Agent quantity</i>	37.24 ± 0.65	30.08 ± 1.21	36.59 ± 0.60	30.34 ± 1.39
<i>Lymphocytes quantity</i>	0 ± 0	53.90 ± 2.54	0 ± 0	55.67 ± 2.62
<i>Diversity</i>	0.091 ± 0.005	0.099 ± 0.010	0.094 ± 0.004	0.111 ± 0.009
<i>Overall time</i>	3106	2416	1440	1261

proves that removing of certain individuals does not affect significantly the classification process. Moreover, because of this activity, iEMAS tends to be significantly more effective in the meaning of time used for computation than EMAS (see table 1).

Early removing of certain individuals may lead to reduction of genotype diversity which means that possible search space of solution may be distorted. In the graph 3(c) the diversity of the both systems is presented. One may see, that diversity of iEMAS is similar to EMAS, proving that introducing immunological selection did not work as a handicap for the possibilities of search space exploration.

In the figure 3(d) the number of lymphocytes in iEMAS is presented, in order to compare them to the number of computation agents, it may be seen that they are in the same range. The population of lymphocytes is stable, so the system is not flooded with them and at the same time their number is high enough to significantly affect the population of computation agents.

## 6 Conclusions

In the paper the idea of EMAS applied for optimization of classifying neural network architecture was presented. Because of high time complexity of the fitness function, specific selection mechanism enhancement based on the introduction of immune cells was described. Whole population of agents was managed with use of PREMONN approach adapted to classification purposes.

The proposed ideas were successfully implemented and the benchmark tests let to state that introduction of immune-based selection increased the effectivity of EMAS by approximately 20% for most of the examined problems.

In the future the formalization of the presented ideas will be performed. Authors plan to explore further the possibility of introduction various types of immune-based selection. More problems of various complexity will be solved and the results will be compared with other heuristics.

## Bibliography

- [1] E. Alpaydin. Techniques for combining multiple learners. In *Proc. of the International ICSC Symposium on Engineering of Intelligent Systems (EIS'98)*. ICSC Academic Press, 1998.
- [2] A. Byrski and M. Kisiel-Dorohinicki. Evolving rbf networks in a multi-agent system. *Neural Network World*, 5(12):433–440, 2002.
- [3] A. Byrski and M. Kisiel-Dorohinicki. Collective intelligence from a population of evolving neural networks. In M. A. Kłopotek, S. T. Wierzchoń, and K. Trojanowski, editors, *Intelligent Information Processing and Web Mining, Proc. of the Int. IIS:IIPWM'03 Conference*. Springer Verlag, 2003.
- [4] A. Byrski and M. Kisiel-Dorohinicki. Agent-based evolutionary and immunological optimization. In Yong Shi, G. Dick van Albada, Jack Dongarra, and Peter M. A. Sloot, editors, *International Conference on Computational Science (2)*, volume 4488 of *Lecture Notes in Computer Science*, pages 928–935. Springer, 2007.
- [5] A. Byrski, M. Kisiel-Dorohinicki, and E. Nawarecki. Agent-based evolution of neural network architecture. In M. Hamza, editor, *Proc. of the IASTED Int. Symp.: Applied Informatics*. IASTED/ACTA Press, 2002.
- [6] S. Haykin. *Neural networks: a comprehensive foundation*. Prentice Hall, 1999.
- [7] M. Kisiel-Dorohinicki. Agent-oriented model of simulated evolution. In William I. Grosky and Frantisek Plasil, editors, *SofSem 2002: Theory and Practice of Informatics*, volume 2540 of *LNCIS*. Springer-Verlag, 2002.
- [8] M. Mitchell. *An Introduction to Genetic Algorithms*. MIT Press, 1998.
- [9] V. Petridis and A. Kehagias. *Predictive Modular Neural Networks – Application to Time Series*. Kluwer Academic Publishers, 1998.
- [10] X. Yao. Evolving artificial neural networks. *Proceedings of the IEEE*, 87(9):1423–1447, 1999.