Coevolution in Multi-Agent System as a Niching Technique

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Abstract

Niching methods *for evolutionary algorithms are aimed at identifying all desired peaks of multimodal landscape. In this paper the idea of a* niching coevolutionary multi-agent system *(NCoEMAS) is introduced. In such a system the niche formation phenomena occurs within one of the pre-existing species as a result of coevolutionary interactions. Also, the formal model of NCoEMAS and the results from runs of NCoEMAS against commonly used test functions are presented.*

1 Introduction

Terms *Evolutionary Computation (EC)* and *Evolutionary Algorithms (EAs)* cover a wide range of global search and optimization techniques based on analogies to natural evolution. However, both experiments and analysis show that for multimodal problem landscapes a simple EA will inevitably locate a single solution [13]. If we are interested in finding multiple solutions of comparable fitness, some multimodal function optimization techniques should be used. *Niching methods* for EAs [13] are aimed at forming and stably maintaining niches (species) throughout the search process, thereby allowing to identify all desired peaks of multimodal landscape.

This paper introduces the idea of a *niching coevolutionary multi-agent system (NCoEMAS)*, which opens new possibilities of modeling biological speciation mechanisms based on coevolutionary interactions, competition for limited resources, and geographical isolation. Also the formal model of NCoEMAS and preliminary results from runs of NCoEMAS against commonly used test functions are presented.

2 Niching Techniques

Various mechanisms have been proposed to form and stably maintain species throughout the search process. Most of these techniques allow niche formation through the implementation of *crowding*, *fitness sharing* or some modifications of these mechanisms.

Every niching technique can also be classified as *parallel* or *sequential* [12]. Parallel niching methods form and maintain species simultaneously within a single population. Sequential niching methods locate multiple peaks one after another during a sequence of runs.

In the *crowding* technique [6] each generation, a proportion of the population G (*generation gap*) is selected for reproduction. For each offspring CF (*crowding factor*) individuals are selected at random. The most similar individual, according to a similarity metric, is then replaced by the offspring.

Mahfoud developed niching mechanism called *deterministic crowding* (DC) [11]. In his technique children are directly compared to their parents. Parent is replaced only if the competing child has higher fitness.

Probabilistic crowding developed by Mengshoel and Goldberg [14] is based on Mahfoud's DC algorithm. The main difference to deterministic crowding is the use of a probabilistic rather than a deterministic acceptance function in parent-offspring tournaments.

Fitness sharing was first introduced by Holland [9] and further developed by Goldberg and Richardson [7]. In sharing technique each individual is considered to be the center of a niche with radius σ_{sh}. Fitness of each individual is reduced for every other individual, which lives in its niche, in a proportion to their similarity. The reduced fitness of an individual i is given by $f_i' = \frac{f_i}{m_i}$, where f_i is its raw fitness and m_i is the niche count. The niche count is given by $m_i = \sum_{j=1}^{n} sh(d_{ij})$, where d_{ij} is the distance between individual i and individual j, determined by a similarity metric. The sharing function is given by

$$sh(d) = \begin{cases} 1 - (\frac{d}{\sigma_{sh}})^\alpha & \text{if } d < \sigma_{sh}, \\ 0 & \text{otherwise,} \end{cases} \quad (1)$$

where α is a constant that regulates the shape of the sharing function (it is commonly set to 1).

Miller and Shaw [15] developed the niching technique called *dynamic niche sharing (DNS)*. DNS technique tries to dynamically identify the q peaks of forming niches and uses these peaks to classify all individuals as either belonging to one of these dynamic niches or belonging to the "non-peak" category. An individual i is considered to be within a dynamic niche j if its distance $d_{i,j}$ from peak j in the dynamic peak set is less than σ_{sh}. The shared fitness value for an individual that belongs to one of the dynamic niches is its raw fitness value divided by the dynamic niche population size. If the individual belongs to the "non-peak" category its niche count is calculated using the standard niche count equation (1).

Coevolutionary shared niching (CSN) technique was developed by Goldberg and Wang [8]. Their technique was inspired by the economic model of *monopolistic competition*. The customer population is the usual population of candidate solutions. The businessman population evolve to obtain largest payoff (best cover the peaks in multimodal domain). Customer c is served by businessman b if b is the nearest businessman according to some similarity measure (Hamming distance of binary strings is used). The modified customer fitness is $f'(c) = \frac{f(c)}{m_{b,t}}\Big|_{c \in C_{b,t}}$, where $C_{b,t}$ is the set of customers that are served by businessman b at generation t, and $m_{b,t} = \|C_{b,t}\|$ is the number of customers that businessman b serves at generation t. The modified businessman fitness is $\phi(b) = \sum_{c \in C_{b,t}} f(c)$.

One of the examples of sequential niching methods is *sequential niche technique (SN)* developed by Beasley, Bull and Martin [1]. Their technique works by running multiple times a simple GA and maintaining the best solution of each run. Whenever SN locates peak it depresses the fitness landscape within some radius (which plays a role similar to that of σ_{sh} in sharing) of founded solution in order to avoid locating the same niche multiple times.

Parallel EAs (PEAs) represent quite different approach to species formation, which is based on *allopatric speciation* (speciation resulting from geographical isolation of subpopulations) [2].

3 Niching Coevolutionary Multi-Agent Systems

The main idea of *evolutionary multi-agent system (EMAS)* is the modeling of evolution process in multi-agent system (MAS) [4]. *Coevolutionary multi-agent system (Co-EMAS)* allows coevolution of several species. *Niching coevolutionary multi-agent system (NCoEMAS)* is CoEMAS applied to multimodal function optimization. In such a system the niche formation phenomena occurs within one of the preexisting species as a result of coevolutionary interactions.
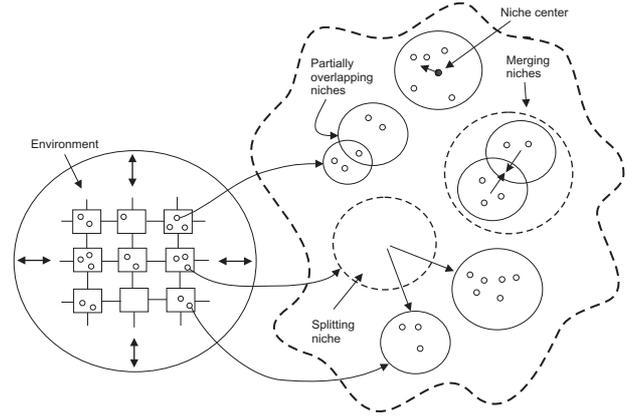

Figure 1. Sample niching coevolutionary multi-agent system

In NCoEMAS several (usually two) different species coevolve. One of them represents solutions. The goal of the second species is to cooperate (or compete) with the first one in order to force the population of solutions to proportionally populate and stably maintain niches in multimodal domain i.e. to initialize and maintain the process of speciation within the population of solutions.

In figure 1 sample system with two coevolving species: niches and solutions is presented. In such NCoEMAS we can model niches as individuals that are characterized by parameters like location, radius, etc. and evolve to best cover real niches in multimodal domain. Two additional operators can be introduced for niches: splitting and merging. Each niche can make decision on splitting into two niches based on the current distribution of its subpopulation. Also, the decision of merging can be made by two niches that are close enough and that are located on the same peak in the multimodal domain. In order to proportionally populate niches the mechanism of *explicit* resource sharing can be introduced. Agents' *life energy* can be treated as a resource for which individuals compete. This mechanism can be called *energy sharing*.

It seems that NCoEMAS is especially suited for modeling sympatric speciation (niche separation due to resource competition, predator-prey and host-parasite coevolution, sexual preferences). Also, allopatric speciation can be modeled based on environmental structure of NCoEMAS.

4 The Model of CoEMAS

In this section the formal model of CoEMAS is presented. The model is based on the idea of M-Agent [3, 5] and on the model of EMAS [10].

4.1 CoEMAS

The CoEMAS may be described as 3-tuple

$$CoEMAS = \langle ENV, \mathcal{S}, \mathcal{R} \rangle, \qquad (2)$$

where:

ENV is an environment of the $CoEMAS$;

$\mathcal{S}$ is a set of species that coevolve in $CoEMAS$ ($S \in \mathcal{S}$);

$\mathcal{R}$ is a set of relations between species.

$$\mathcal{R} = R^+ \cup R^-, \qquad (3)$$

where:

$$R^+ = \left\{ \xrightarrow{r_i+} : r_i \in RES \right\}, \qquad (4)$$

$$R^- = \left\{ \xrightarrow{r_i-} : r_i \in RES \right\} \qquad (5)$$

RES is a set of resources that exist in $CoEMAS$, $RES = \langle r_1, r_2, \ldots, r_n \rangle$.

$\xrightarrow{r-}$ and $\xrightarrow{r+}$ are relations between species:

$$\xrightarrow{r-} = \big\{ \langle S_i, S_j \rangle \in \mathcal{S} \times \mathcal{S} : \text{individuals from species } S_i$$
$$\text{decrease fitness of individuals from species } S_j$$
$$\text{via the influence on the amount of resource } r \big\}$$
$$(6)$$

$$\xrightarrow{r+} = \big\{ \langle S_i, S_j \rangle \in \mathcal{S} \times \mathcal{S} : \text{individuals from species } S_i$$
$$\text{increase fitness of individuals from species } S_j$$
$$\text{via the influence on the amount of resource } r \big\}$$
$$(7)$$

Having such relations defined we can easily define different coevolutionary interactions between species that are modeled in CoEMAS.

Definition 1. *Mutualism between two species, A and B occurs if and only if $A \xrightarrow{r_i+} B$ and $B \xrightarrow{r_j+} A$, $r_i, r_j \in RES$.*

Definition 2. *Commensalism between two species, A and B occurs if and only if $A \xrightarrow{r+} B$ and $\neg(B \xrightarrow{r+} A \vee B \xrightarrow{r-} A)$, $r \in RES$.*

Definition 3. *Predator-prey interactions between two species, Predators and Preys occurs if and only if $Predators \xrightarrow{r-} Preys$ and $Preys \xrightarrow{r+} Predators$, $r \in RES$.*

Definition 4. *Competition for limited resources between two species, A and B occurs if and only if $A \xrightarrow{r-} B$ and $B \xrightarrow{r-} A$, $r \in RES$.*

4.2 Environment

The environment of CoEMAS may be described as 3-tuple

$$ENV = \langle T_{ENV}, RES, INF \rangle \qquad (8)$$

where:

T_{ENV} is the topography of environment ENV;

RES is a set of resources that exist in $CoEMAS$, $RES = \langle r_1, r_2, \ldots, r_n \rangle$;

INF is a set of informations that exist in $CoEMAS$, $INF = \langle i_1, i_2, \ldots, i_m \rangle$;

Topography of the environment ENV

$$T_{ENV} = \langle G, L \rangle \qquad (9)$$

where G is a graph

$$G = \langle V, E \rangle \qquad (10)$$

V — set of nodes,

E — set of edges.

L is a location function such that

$$L : Ag \to V \qquad (11)$$

$$L(ag) = v, \ ag \in AG, \ v \in V \qquad (12)$$

where

ag is an agent that live in CoEMAS;

AG is the set of all agents that live in $CoEMAS$ ($ag \in AG$).

The distance between two nodes is defined as follows

$$dist_G(v_i, v_j) = \min \big\{ |E(P)| : \text{P is the path connecting}$$
$$v_i \text{ and } v_j \big\}$$
$$(13)$$

The node v can be described as 3-tuple

$$v = \langle RES^v, INF^v, AG^v \rangle \qquad (14)$$

where

$$RES^v \subseteq RES, \ RES^v = \langle r_1, r_2, \ldots, r_k \rangle \qquad (15)$$

$$INF^v \subseteq INF, \ INF^v = \langle i_1, i_2, \ldots, i_l \rangle \qquad (16)$$

$$AG^v \subseteq AG, AG^v = \{ag : ag \in AG \wedge L(ag) = v\} \qquad (17)$$

4.3 Species

S is a species that exist in $CoEMAS$ ($S \in \mathcal{S}$).
Species can be defined as

$$S = \langle AG^S, INT^S \rangle \qquad (18)$$

where AG^S is a set of agents that belong to species S and INT^S is a set of interactions with another species.

$$AG^S = \big\{ ag : ag \in AG \wedge ag \text{ is an individual that} \\ \text{belongs to species } S \big\} \qquad (19)$$

$$AG = \bigcup_{S \in \mathcal{S}} AG^S \qquad (20)$$

ag^S is an agent that belongs to species S ($ag^S \in AG^S$).

$$INT^S = \langle int_1, int_2, \ldots, int_n \rangle \qquad (21)$$

where

$$int_i = \langle S, S_j \rangle, \quad \text{such that } S \xrightarrow{r-} S_j \vee S \xrightarrow{r+} S_j, \\ S, S_j \in \mathcal{S} \qquad (22)$$

4.4 Agent

An agent ag^S ($ag^S \in AG^S$) can be defined as 4-tuple

$$ag^S = \langle GEN, RES^S, PRF, ACT \rangle \qquad (23)$$

GEN is a genotype of a given agent, for example $GEN = (gen_1, gen_2, \ldots, gen_k)$, $gen_i \in \mathbb{R}$, $GEN \in \mathbb{R}^k$. RES^S is a set of resources of agent ag^S that belongs to species S ($RES^S \subseteq RES$). PRF is a set of agent's profiles with the order relation $\succ$ defined.

$$PRF = \langle prf_1, prf_2, \ldots, prf_n \rangle \\ prf_1 \succ prf_2 \succ \cdots \succ prf_n \qquad (24)$$

Here, profile prf_1 is the most basic profile which means that goals within this profile have precedence of another profiles' goals.

ACT is a set of actions that an agent can perform

$$ACT = \langle act_1, act_2, \ldots, act_m \rangle \qquad (25)$$

Profile k may be the resource profile

$$prf^k = \big\{ RES^{S,k}, ST^k, RST^k, GL^k \big\} \qquad (26)$$

or the information profile

$$prf^k = \big\{ MDL, ST^k, RST^k, GL^k \big\} \qquad (27)$$

where

$RES^{S,k}$ is a set of resources that are used in a profile k, $RES^{S,k} \subseteq RES^S$;

MDL is a set of informations that represents agent's knowledge about the environment and other agents.

ST^k is a set of strategies that an agent may apply in a given profile, $ST^k = \langle st_1, st_2, \ldots st_l \rangle$;

RST^k is a set of strategies that are realized within profile k, $RST^k \subseteq ST^k$;

GL^k is a set of goals that an agent should realize within given profile, $GL^k = \{gl_1, gl_2, \ldots gl_p\}$.

Single strategy consists of actions

$$st = \langle act_1, act_2, \ldots, act_k \rangle, \quad act_i \in ACT \qquad (28)$$

where act_i is an action taken by an agent in order to realize a goal.

If agent should apply strategy that is not realized within active profile then the appropriate profile is activated.

In the case of $CoEMAS$ the set of profiles should at least include

$$PRF = \langle prf^{res}, prf^{rep}, prf^{int}, prf^{mig}, \ldots \rangle \qquad (29)$$

4.4.1 Resource Profile

Resource profile may be described as follows

$$prf^{res} = \langle RES^S, \ ST = \langle \langle die \rangle, \langle get \rangle, \langle int \rangle, \langle mig \rangle, \\ \langle clone, mut, rec, \ldots \rangle \rangle, RST = \langle \langle die \rangle, \langle get \rangle \rangle, \\ GL = \big\{ r_i > r_i^{min} : r_i \in RES^S \big\} \rangle \qquad (30)$$

The die action is realized when $r^{die} < r^{die}_{min}$, where $r^{die} = f(r_1, \ldots, r_n, \ldots)$, $r_i \in RES^S$. This action removes the agent from the environment and frees all its resources.

The get action is realized when $\exists r_i$ such that $r_i < r_i^{min}$. This action tries to get some resource r_i from the environment, $get : r_i \to r_i + r_i^{env}$.

4.4.2 Reproductive Profile

Reproductive profile realizes all strategies connected with reproduction process.

$$prf^{rep} = \langle RES^{rep} = \langle r_1, r_2, \ldots, r_k \rangle, \\ ST = \langle \langle clone, mut, rec, \ldots \rangle, \langle mig \rangle \rangle, \\ RST = \langle \langle clone, mut, rec, \ldots \rangle \rangle, \\ GL = \big\{ r^{rep} < r^{rep}_{max} \big\} \rangle \qquad (31)$$

where $RES^{rep} \subseteq RES^{S}$, $r^{rep} = g(r_1, r_2, \ldots, r_k)$, $er_i \in RES^{rep}$.

In CoEMAS there exist many different species so it must be defined when two individuals are reproductively isolated (can not recombine their genetic material).

Definition 5. $ag_i, ag_j \in AG$. $GEN_i = (gen_1^i, gen_2^i, \ldots, gen_n^i)$, $gen_k^i \in \mathbb{R}$, $GEN_i \in \mathbb{R}^n$. $GEN_j = (gen_1^j, gen_2^j, \ldots, gen_m^j)$, $gen_k^j \in \mathbb{R}$, $GEN_j \in \mathbb{R}^m$. *In CoEMAS two individuals ag_i, ag_j are reproductively isolated (what means that $ag_i \in AG^{S1}$ and $ag_j \in AG^{S2}$) if and only if $m \neq n$ or $d^{gen}(GEN_i, GEN_j) > ri$, where d^{gen} is the distance between two genotypes in $\mathbb{R}^n$ according to some metric, $ri \in \mathbb{R}$.*

The *clone* action is realized when $r^{rep} > r_{max}^{rep}$. This action clones the agent and reduces its resources by some amount.

$$clone : \forall r_i \in RES^{rep} \quad r_i \rightarrow r_i - r_i^{clone} \quad (32)$$

These resources are given to agent's clone.

The *mut* action mutates the clone's chromosome.

$$mut : GEN \rightarrow GEN' \quad (33)$$

The *rec* action recombinates chromosomes of two parents. For example, when $GEN \in \mathbb{R}^k$

$$rec : \mathbb{R}^k \times \mathbb{R}^k \rightarrow \mathbb{R}^k$$
$$rec(GEN_i, GEN_j) = GEN_k \quad (34)$$

where GEN_i, GEN_j, GEN_k are genotypes of individuals that are not reproductively isolated according to definition 5.

4.4.3 Interaction Profile

Interaction profile is responsible for interactions with other individuals.

$$prf^{int} = \langle RES^{int} = \langle r_1, r_2, \ldots, r_l \rangle,$$
$$ST = \langle \langle intr \rangle, \langle mig \rangle \rangle,$$
$$RST = \langle \langle intr \rangle \rangle, \quad (35)$$
$$GL = \{ r_i > r_i^{min} : r_i \in RES^{int} \} \rangle$$

where $RES^{int} \subseteq RES^{S}$.

The *intr* is the interaction of agent $ag_i \in AG^{S_i}$ with individual that belongs to different species $ag_j \in AG^{S_j}$.

$$intr(ag_i, ag_j) : r^{ag_i} \rightarrow r^{ag_i} + r^{ch},$$
$$r^{ag_j} \rightarrow r^{ag_j} - r^{ch} \quad (36)$$

where $r^{ch} > 0$, $ag_j \in AG^{intr-}$, AG^{intr-} is the set of individuals that agent ag_i can interact with in order to increase the amount of resource r.

$$AG^{intr-} = \big\{ ag \in AG^v : \exists int = \langle S_i, S \rangle,$$
$$\text{such that } S_i \xrightarrow{r-} S, \quad (37)$$
$$int \in INT^{S_i}, \quad ag \in AG^S \big\}$$

where $v = L(ag_i)$.

AG^{intr+} is the set of agents that can decrease fitness of given agent via the influence on the amount of some of its resources.

If $AG^{intr+} \neq \emptyset$ then ag_i tries to escape via the activation of strategy $\langle mig \rangle$, which is realized by the profile prf^{mig}.

$$AG^{intr+} = \big\{ ag \in AG^v : \exists int = \langle S_i, S \rangle,$$
$$\text{such that } S_i \xrightarrow{r+} S, \quad (38)$$
$$int \in INT^{S_i}, \quad ag \in AG^S \big\}$$

4.4.4 Migration Profile

The migration profile is responsible for migration of given agent within the environment of CoEMAS

$$prf^{mig} = \langle V^{ag}, \ ST = \langle \langle mig \rangle \rangle, RST = \langle \langle mig \rangle \rangle,$$
$$GL = GL^{res} \cup GL^{rep} \cup GL^{int} \rangle \quad (39)$$

$$V^{ag} = \{ v \in V : dist_G(v, L(ag)) < d_{max}^{ag} \} \quad (40)$$

The *mig* action changes the location of agent ag

$$mig : v_i = L(ag) \rightarrow v_j \in V^{ag}$$
$$V^{ag} \rightarrow V^{ag'} \quad (41)$$

5 Preliminary Experiments

First simulation experiments were aimed at testing if NCoEMAS is a valuable niching technique i.e. if it is able to detect and stably maintain all peaks in multimodal domain throughout the search process. Also, it should populate peaks proportionally to their fitness. In the following sections the system, test functions and the results of experiments are presented.

5.1 The System

The system presented in this paper is the first one, which construction is based on the idea of NCoEMAS (see fig. 2). There exist two different species: niches and solutions. All agents live in 2D space, which has the structure of discrete torus. Every node of this graph-like structure has connections with its four neighbors.
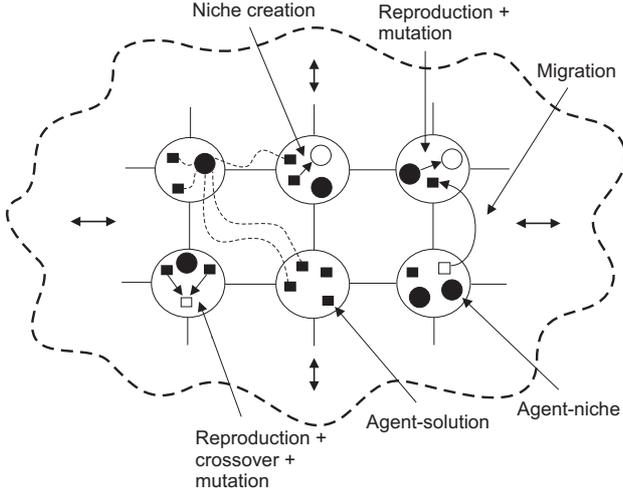
Figure 2. NCoEMAS used in experiments

All agents representing niches are located in nodes and can not change their location. Agents representing solutions are also located in nodes but they can change their location in environment migrating from node to node. Every agent-solution has some amount of resource called *life energy*. There is closed circulation of energy in the system, which means that the total energy possessed by agents and the environment is constant during the whole simulation. Agents need energy for almost every activity: migration, reproduction etc. An individual dies when its energy is equal to 0. An agent can migrate from one node to another guided by the total energy of agents living in that node. The reproduction process can take place when agent's energy is above the given level. Agent starts reproduction, searches in its neighborhood for partner and then new agent is created. Mutation and crossover (one point crossover is used) are applied with the given probability in order to produce child's chromosome. An agent created in reproduction process obtains energy from the environment.

The EA for niche population is very similar to that used for businessman population in CSN [8]. Each time step a single mutation site is selected randomly. The resulting individual replaces its parent if it is at least d_{min} from other niche and it is better fit than its parent. Otherwise another mutation site is selected (max. n_{limit} times).

In the time t every agent-solution searches for the closest niche (the weighted sum of Hamming distance in genotype space and Euclidean distance in environment is used). If there is no niche, such that its distance from the agent is less than given value, then the new niche is created with the copy of agent's chromosome (imprint mechanism).

In each time step less fit agents must give some amount of their energy to better fit agents (according to fitness func-

tion). Agents are compared within niches and also outside niches in the environment space. The latter comparisons are realized within nodes. Given agent is compared with agents that stay in its node and also with agents from the neighboring nodes.

5.2 Test Functions

There were four test functions used in experiments: F_1, F_2, F_3, F_4 [7, 13]. These functions are commonly used as baseline tests in studies of niching methods. They are a starting place for testing new niching techniques and comparing them to earlier works. Although these are very simple functions many potential nichers have in the past had problems with detecting and maintaining all of their peaks.

Function F_1 has five maxima located at the x values of $0.1, 0.3, 0.5, 0.7, 0.9$. All maxima are of height 1.0. F_1 is given by

$$F_1(x) = \sin^6(5\pi x) \quad \text{for } x \in [0, 1] \tag{42}$$

Maxima of function F_2 are located at the same x values as F_1. Maxima are of rounded height $1.000, 0.917, 0.707, 0.459, 0.250$. F_2 is given by

$$F_2(x) = \exp(-2\ln 2((x - 0.1)/0.8)^2)\sin^6(5\pi x)$$
$$\text{for } x \in [0, 1]] \tag{43}$$

Maxima of F_3 are at x values of approximately $0.080, 0.246, 0.450, 0.681, 0.934$, all with height of 1.0. F_3 is defined as follows

$$F_3(x) = \sin^6(5\pi(x^{0.75} - 0.05)) \quad \text{for } x \in [0, 1] \tag{44}$$

Maxima of F_4, with the same height as F_2, are located at the same x values as F_3. F_4 is defined as follows

$$F_4(x) = \exp(-2\ln 2((x - 0.08)/0.854)^2)$$
$$\sin^6(5\pi(x^{0.75} - 0.05))$$
$$\text{for } x \in [0, 1] \tag{45}$$

5.3 Results

In this section the results from runs of NCoEMAS against test functions are presented.

Figures 3 and 4 shows the average numbers of agents representing solutions within each niche from ten runs of NCoEMAS against F_1 and F_2 functions respectively. It can be seen that NCoEMAS properly detected and stably maintained peaks of these two test functions. What is more, peaks were populated proportionally to their relative fitness.
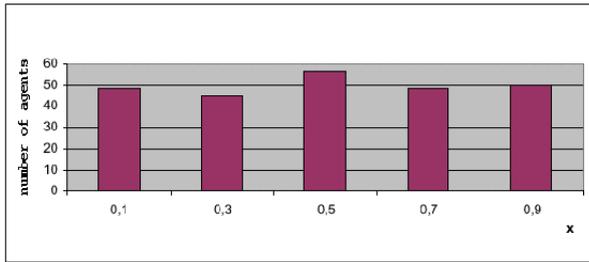
Figure 3. The average number of agents-solutions within each niche from ten runs of NCoEMAS against F_1 function
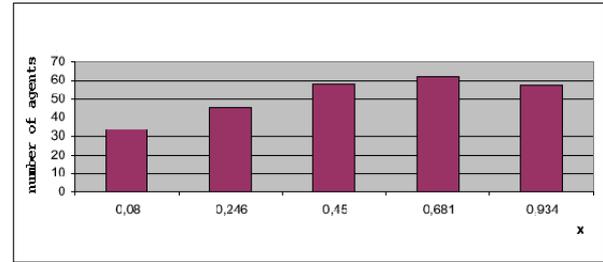

Figure 5. The average number of agents-solutions within each niche from ten runs of NCoEMAS against F_3 function
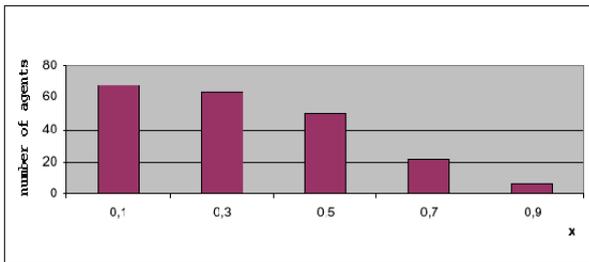

Figure 4. The average number of agents-solutions within each niche from ten runs of NCoEMAS against F_2 function
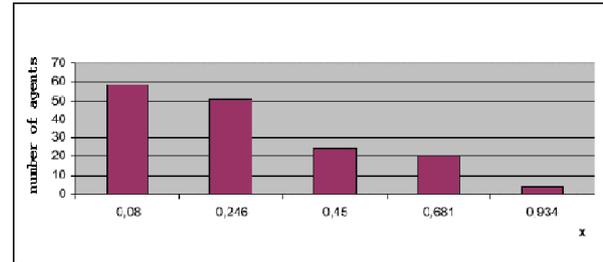

Figure 6. The average number of agents-solutions within each niche from ten runs of NCoEMAS against F_4 function

In case of F_3 (see fig. 5) NCoEMAS also properly detected and stably maintained all peaks in multimodal domain. However peaks were not populated as we could wish. All niches should be equally populated but it seems that agents preferred wider peaks. Niches of F_4 function (fig. 6) were also properly located and populated almost proportionally to their relative fitness. The problems mentioned above are connected with energy sharing mechanism and are the subject of ongoing research.

6 Concluding Remarks

Most of classical niching techniques *indirectly* model resource sharing within the niches. On the other hand, PEAs model speciation caused by geographical isolation of sub-populations. Also in EMAS only *allopatric speciation* can be modeled.

The idea of *niching coevolutionary multi-agent system (NCoEMAS)* allows us to model the process of *sympatric speciation* based on niche separation due to resource competition (*energy sharing*), predator-prey and host-parasite coevolution, sexual preferences, etc. At the same time *al-*

lopatric speciation can be modeled based on environmental structure of NCoEMAS.

The NCoEMAS presented in this paper was based on coevolution of two species: niches and solutions. System properly detected and maintained all peaks of test functions and, as presented preliminary results show, has proved to be the valid and promising niching technique.

Future research should include:

- experiments with more complex test functions,

- the application of NCoEMAS to engineering shape design problems,

- NCoEMAS based on the mechanisms of predator-prey and host-parasite coevolution, sexual preferences,

- parallel NCoEMAS.

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