

CO-EVOLUTIONARY MULTI-AGENT SYSTEM WITH SPECIATION AND RESOURCE SHARING MECHANISMS

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Abstract. *Niching techniques* for evolutionary algorithms are used in order to locate basins of attraction of the local minima of multi-modal fitness functions. *Co-evolutionary techniques* are aimed at overcoming limited adaptive capabilities of evolutionary algorithms resulting from the loss of useful population diversity. In this paper the idea of *niching co-evolutionary multi-agent system (NCoEMAS)* is introduced. In such a system the species formation phenomena occurs within one of the preexisting species as a result of co-evolutionary interactions. The results of experiments with Rastrigin and Schwefel multi-modal test functions aimed at the comparison of NCoEMAS to other niching techniques are presented. Also, the influence of resource sharing mechanism's parameters on the quality of speciation processes in NCoEMAS are investigated.

Keywords: Multi-agent systems, evolutionary algorithms, co-evolution, niching, speciation, multi-modal optimization

1 INTRODUCTION

Evolutionary Algorithms (EAs) are global search and optimization techniques based on analogies to natural evolution [2]. In practice evolutionary algorithms have demonstrated efficiency and robustness as global optimization techniques. However, they often suffer from premature loss of population diversity what results in premature convergence and may lead to locating local optima instead of a global one.

Both the experiments and analysis show that for multi-modal problem landscapes a simple EA will inevitably locate a single solution [20]. If we are interested in finding multiple solutions of comparable fitness, some multi-modal function optimization techniques should be used. *Niching methods* for EAs [20] are aimed at forming and stably maintaining subpopulations (species) throughout the search process, thereby allowing to locate all or most basins of attraction of local minima.

The loss of diversity also limits the adaptive capabilities of EAs in dynamic environments. Co-evolutionary techniques are aimed at improving adaptive capabilities and introducing open-ended evolution into EAs [23].

In this paper the idea of *co-evolutionary multi-agent system (CoEMAS)* is introduced. CoEMAS systems allow modeling biological speciation mechanisms based on predator-prey and host-parasite co-evolution, sexual preferences, competition for limited resources, and geographical isolation. Also, results from runs of CoEMAS with speciation mechanism (NCoEMAS) against Rastrigin and Schwefel multi-modal test functions are presented. The goals of these experiments were to compare speciation processes taking place in NCoEMAS and classical niching techniques and the investigation of the resource sharing mechanism influence on the quality of speciation processes in NCoEMAS.

2 NICHING TECHNIQUES

In the case of multi-modal optimization problems the basin of attraction of every local minima (we assume minimization problems in the rest of this paper) can be treated as a niche. The number of individuals that live within a niche should be in direct proportion to its carrying capacity. Carrying capacity in this case means local minimum's fitness relative to other local minima present in multi-modal domain. This is called *niche proportionate population*.

During the years of research various niching techniques have been proposed. All these techniques allow niche formation via the modification of mechanism of selecting individuals for new generation (*crowding* [18]), the modification of the parent selection mechanism (*fitness sharing* [13] or *sexual selection* [26]), or restricted application of selection and/or recombination mechanisms (by *grouping* individuals into subpopulations [17] or by introducing the environment with some topography in which the individuals are located [1, 6]).

Every niching technique can also be classified as *parallel* or *sequential* [19]. Parallel niching techniques form and maintain species simultaneously within a single population (regardless of the number of processors used). Sequential niching methods locate multiple basins of attraction temporally, one after another.

2.1 Crowding Based Techniques

One of the first attempts to introduce niching into a genetic algorithm was Cavicchio's *preselection* scheme [7]. In preselection scheme offspring replaces the less fit of two parents only when it has higher fitness than the parent.

In the *crowding* technique [10] in each generation, a part of the population gg (*generation gap*) is selected (via fitness proportionate selection) for reproduction. For each offspring, a certain number – cf (*crowding factor*) – of individuals are selected at random. The most similar individual, according to a similarity metric, is then replaced by the offspring. As a similarity metric De Jong used Hamming distance in genotypic space. Crowding does not promote the formation of stable species, but rather aims at maintaining the diversity of initial population.

Harik introduced *restricted tournament selection* technique [15], in which for each child a group of ws individuals is selected at random from the population of parents and the most similar individual competes with the children for the place in new base population.

Mahfoud developed niching mechanism called *deterministic crowding* [18]. He showed that similarity metrics based upon phenotypes should be preferred to genotype based ones. It was also demonstrated that there was very high probability that the offspring most similar individual should be searched for among its parents. The new offspring is directly compared to its parents. In deterministic crowding parent is replaced only if the child has higher fitness. To determine which of the two possible parent-child pairings should be used in the process of comparing parents to their offspring the total similarities were determined for each possible combination. The pairing that had the highest total similarity (according to some similarity metric) was used.

Probabilistic crowding developed by Mengshoel and Goldberg [21] is based upon Mahfoud's deterministic crowding. The main difference from deterministic crowding is the use of a probabilistic rather than a deterministic acceptance function. This means that stronger individuals win with probability proportional to their fitness. The probability of winning the tournament by individual a_i is given by

$$p(a_i) = \frac{\varphi(a_i)}{\varphi(a_i) + \varphi(a_j)} \quad (1)$$

where $\varphi(a_i)$ is a fitness function value for individual a_i .

2.2 Sharing Based Techniques

Fitness sharing was first introduced by Holland [16] and further developed by Goldberg and Richardson [13]. This technique models the ecological phenomenon of competition for limited resources between individuals that occupy the same niche. Fitness sharing technique reduces the fitness of individuals that have highly similar members within the population. Such a mechanism rewards unique individuals and punishes redundant individuals within the population. The reduced fitness of individual a_i is given by

$$\varphi^{FS}(a_i) = \frac{\varphi(a_i)}{m_i} \quad (2)$$

where $\varphi(a_i)$ is a fitness function value for individual a_i and m_i is the niche count for individual a_i . The niche count is given by

$$m_i = \sum_{j=1}^{\mu} sh(dist(a_i, a_j)) \quad (3)$$

where μ is the size of population, $dist(a_i, a_j)$ is the distance between individual a_i and individual a_j , determined by a similarity metric. The similarity metric used can be based on either phenotype or genotype similarity. A genotype similarity metric is often domain independent (for example Hamming distance between the genotype bit strings). A phenotype similarity metric utilizes some knowledge about the domain, so it is sometimes more meaningful (or appropriate). The similarity metric should always return a distance $dist(a_i, a_j)$, which increases as similarity decreases (and vice versa). If the distance between two individuals a_i and a_j is less than some fixed radius σ_{sh} the sharing function will return a value from $[0; 1]$, which increases with greater similarity between two individuals. In fitness 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 that lives in its niche in a proportion to their similarity. The sharing function is given by

$$sh(dist(a_i, a_j)) = \begin{cases} 1 - \left(\frac{dist(a_i, a_j)}{\sigma_{sh}}\right)^{\alpha} & \text{if } dist(a_i, a_j) < \sigma_{sh}, \\ 0 & \text{otherwise} \end{cases} \quad (4)$$

where α is a constant that regulates the shape of the sharing function. It is commonly set to 1. Goldberg and Deb [11] developed formulas for determining the appropriate value for σ_{sh} given the expected number of local minima and assuming that these minima are regularly located in the search space.

Miller and Shaw [22] developed the niching technique called *dynamic niche sharing*. Their approach utilizes two assumptions. The first assumption is that the number of local minima ($q = |D^{\min}|$, where D^{\min} is the set of local minima) can be estimated. The second assumption is that the local minima are all at a minimum distance of $2\sigma_{sh}$ from each other. Dynamic niche sharing technique attempts to identify the q centers of forming niches and uses these dynamically identified centers to classify all individuals as either belonging to one of these dynamic niches or belonging to the “non-niche” category. The shared fitness value for an individual a_i that belongs to j^{th} dynamic niche is its raw fitness value divided by the dynamic niche population size ($m_{DNS,i} = |A^j|$). If the individual does not belong to a dynamic niche it belongs to the “non-niche” category and its niche count is calculated using the standard niche count equation (4). The shared fitness value for dynamic niche sharing is given by

$$\varphi^{DNS}(a_i) = \frac{\varphi(a_i)}{m_{DNS,i}}. \quad (5)$$

The dynamic niche count is given by

$$m_{DNS,i} = \begin{cases} |A^j| & \text{if ind. is within } j^{\text{th}} \text{ dyn. niche,} \\ m_i & \text{otherwise (non-niche individual).} \end{cases} \quad (6)$$

An individual a_i is considered to be within a j^{th} dynamic niche if its distance from the individual $a^{o,j}$ that represents the center of j^{th} dynamic niche ($\text{dist}(a_i, a^{o,j})$) is less than σ_{sh} . A greedy approach is used to identify the dynamic niches for each generation. The population is sorted in decreasing raw fitness order. First the population member with the highest fitness is inserted into *dynamic niche set*. Then for every individual in population array (in decreasing fitness value order) its distance from every niche center in dynamic niche set is calculated. If all these distances are greater than σ_{sh} the individual is inserted into dynamic niche set. The whole process is continued until there are q niche centers in dynamic niche set.

Co-evolutionary sharing technique (CSN) was developed by Goldberg and Wang [14]. Their technique is loosely inspired by the economic model of *monopolistic competition*. In CSN technique two populations (species) exist: customers (s_1) and businessmen (s_2). The customer population is the usual population of candidate solutions. The businessmen will locate themselves in solution space in order to obtain the largest payoff. The binary strings were used as genotypes in both populations. The distance between a customer $a_i^{s_1}$ and a businessman $a_j^{s_2}$ is the Hamming distance of their genotypes ($\text{dist}^G(\text{gen}(a_i^{s_1}), \text{gen}(a_j^{s_2}))$, where $\text{gen} : I \rightarrow G$ is the function whose value is the genotype of individual a , I is the space of individuals and G is the space of genotypes). Customer $a_i^{s_1}$ belongs to businessman $a_j^{s_2}$ if this is the nearest businessman, that is:

$$\text{dist}^G(\text{gen}(a_i^{s_1}), \text{gen}(a_j^{s_2})) = \min \left\{ \text{dist}^G(\text{gen}(a_i^{s_1}), \text{gen}(a_k^{s_2})) : \right. \\ \left. \text{for } k = 1, \dots, |A^{s_2}| \right\} \quad (7)$$

where $|A^{s_2}|$ is the businessmen population size.

The modified customer fitness is given by

$$\varphi^{s_1}(a_i^{s_1}) = \frac{\varphi(a_i^{s_1})}{|A^{a_j, s_2}|}, \quad a_i^{s_1} \in A^{a_j, s_2} \quad (8)$$

where A^{a_j, s_2} is the set of customers that belong to businessman $a_j^{s_2}$. The modified businessman fitness is given by

$$\varphi^{s_2}(a_j^{s_2}) = \sum_{i=1}^{|A^{a_j, s_2}|} \varphi(a_i^{s_1}) \quad (9)$$

where $|A^{a_j, s_2}|$ is the size of clients subpopulation that belongs to businessman $a_j^{s_2}$.

Simple CSN uses genetic algorithm with selection and recombination for the customer population and genetic algorithm with selection and mutation for the businessmen population. Each customer is assigned to the closest businessman. Proportionate selection and genetic operators are used to compute a new customer generation. Each businessman is chosen in turn and a single mutation site is selected randomly (from l bits of binary string). The resulting individual replaces its parent if it is at least $dist_{min}$ from other businessmen and it is an improvement over its parent; otherwise another mutation site is selected (max. $n_{limit} \leq l$ times). In the case of a massively multi-modal function it was necessary to apply *imprint* mechanism. In CSN with imprint a candidate businessman is chosen from among the best individuals of the customer population.

One of the examples of sequential niching methods is *sequential niche technique* (SN) developed by Beasley, Bull and Martin [4]. Their technique works by running multiple times a simple GA. The best solution of each run is maintained off-line. To avoid converging to the same niche, whenever a local minimum is located SN depresses the fitness landscape within some radius of that solution. The *niche radius* used in SN plays a role similar to that of σ_{sh} in sharing. In fact the authors suggest that SN is a sequentialization of fitness sharing.

The authors claim that there are three potential advantages of sequential niching: simplicity, ability to work with smaller populations, and speed (partially a byproduct of smaller populations). Mahfoud [19] showed that two latter potential advantages never materialize and additionally there are many disadvantages:

- Loss, through deration, of optimal solutions and their building blocks;
- Repeated search of depressed regions of the search space;
- Repeated convergence to the same solutions;
- Loss of cooperative population properties, including cooperative problem solving, and niche maintenance;
- Slower runtime, even on serial machines.

2.3 Techniques with Sexual Selection Mechanism

Sánchez-Velazco and Bullinaria [27] proposed *gendered selection strategies for genetic algorithms*. They introduced sexual selection mechanism, where males are selected on the basis of their fitness value and females on the basis of the so called *indirect fitness*. Female's indirect fitness is the weighted average of her fitness value, age, and the potential to produce fit offspring (when compared to her partner). For each gender different mutation rates were used. The authors applied their algorithm to Traveling Salesman Problem and function optimization.

Sexual selection as a mechanism for multi-modal function optimization was studied by Ratford, Tuson and Thompson [26]. In their technique sexual selection is based on the so called *seduction function*. This function gives a low measure when two individuals are very similar or dissimilar and high measure for individuals fairly

similar. The Hamming distance in genotype space was used as a distance metric for two individuals. The authors applied their mechanism alone and in combination with crowding and spatial population model. Although in most cases their technique was successful in locating multiple local optima of multi-modal function, the strong tendency to lose all optima except one after several hundreds simulation steps was observed.

2.4 Techniques with Restricted Application of Selection and/or Recombination Mechanisms

Parallel EAs (PEAs) represent quite different approach to species formation, which is based on *allopatric speciation* [6].

In the *island model* PEA [6] the population is divided into several subpopulations. Each subpopulation is assigned to a different processor (*island*). Individuals in each subpopulation are relatively isolated from individuals in another subpopulations. To exchange genetic material between islands, individuals with high fitness migrate occasionally from one subpopulation to another. All these techniques help maintaining genetic diversity and allow each subpopulation to search different part of multi-modal domain.

Also *fine-grained* PEA [6] can be treated as a technique that makes possible the process of species formation. In this technique usually one individual is assigned to each processor. The individuals are allowed to mate only within a neighborhood, called a *deme*. Since neighborhoods overlap, the best individuals will propagate through the whole population.

There are two basic problems with the application of PEA to multi-modal optimization. First, the number of niches (local minima of a multi-modal function) is not known *a priori*, so there exists uncertainty about how many subpopulations should exist. Second, there is no guarantee that different subpopulations will explore different areas of a search space.

3 PREVIOUS RESEARCH IN CO-EVOLUTIONARY ALGORITHMS

In classical EAs each individual in the population is considered to be a potential solution of the problem being solved. The fitness of each individual depends only on how well it solves the problem. Selection pressure causes that better fit individuals have the greater chance to survive and/or reproduce and the less fit ones have the smaller chance.

In *co-evolutionary algorithms* the fitness of each individual depends not only on the quality of solution to the given problem but also (or solely) on other individuals' fitness. This makes such techniques applicable in the cases where the fitness function formulation is difficult (or even impossible). As the result of ongoing research quite many co-evolutionary techniques have been proposed. Generally, each of these techniques belongs to one of two classes: competitive ([24]) or cooperative ([25]).

In competitive co-evolution based systems two (or more) individuals compete in a game and their “Competitive Fitness Functions” are calculated based on their relative performance in that game [9]. Each time step given individual competes with different opponents, so its fitness value varies. Because in such systems an individual’s fitness depends on other individuals’ fitness, they are co-evolutionary in nature.

The second group consists of systems that use cooperative co-evolution mechanism. In such systems a problem is decomposed into sub-problems and each of them is then solved by different EA [25]. Each individual is evaluated within a group of randomly chosen individuals coming from different sub-populations. Its fitness value depends on how well the group solved the problem and on how well the individual assisted in the solution.

All the niching techniques presented in the previous sections have some limitations:

- all of them work correctly only when applied to some particular class of problems,
- some of them require knowledge about the problem to set values of parameters (especially fitness sharing based ones),
- fitness sharing based techniques are very sensitive to values of fitness function – in fact they can be applied only when the fitness values of “bad” individuals (individuals which should die off) are near 0, which is rather hard to assure in the case of problems for which values of fitness function in the areas that are outside of the local minima basins of attraction differ much from each other [29],
- some of them do not stably maintain formed species (subpopulations) located within local minima basins of attraction,
- none of the presented techniques provide mechanisms for auto-adaptation of the number of individuals in population to the difficultness of problem being solved (number of local minima).

All these facts imply that there is still need for research in the area of niching and speciation mechanisms.

On the other hand, co-evolutionary techniques are not very often applied in the field of multi-modal optimization, although they are aimed at overcoming limited adaptive capabilities of evolutionary algorithms resulting from the loss of useful diversity of population. In fact, to our best knowledge, only one niching technique based on co-evolution was developed (co-evolutionary sharing [14]). Co-evolutionary multi-agent systems, which are presented in the next section, allow modeling different co-evolutionary interactions between species and sexes and, on their basis, modeling speciation processes.

4 A CO-EVOLUTIONARY MULTI-AGENT SYSTEM WITH SPECIATION MECHANISM

The main idea of *evolutionary multi-agent system (EMAS)* is the modeling of evolution process in *multi-agent system (MAS)* [8]. The basic EMAS model allows the evolution of only one species and does not have any co-evolutionary and niching mechanisms, what limits the application of such systems to hard multi-modal and multi-objective problems. Classical co-evolutionary and niching techniques can not be realized in EMAS model because of its decentralized nature.

The main goals of the research on *co-evolutionary multi-agent systems (Co-EMAS)* [12] are:

- to introduce co-evolutionary mechanisms into EMAS model and to use them as a basis for niching techniques adequate for systems based on such decentralized model of evolution,
- to research speciation processes based on co-evolutionary interactions between species and sexes.

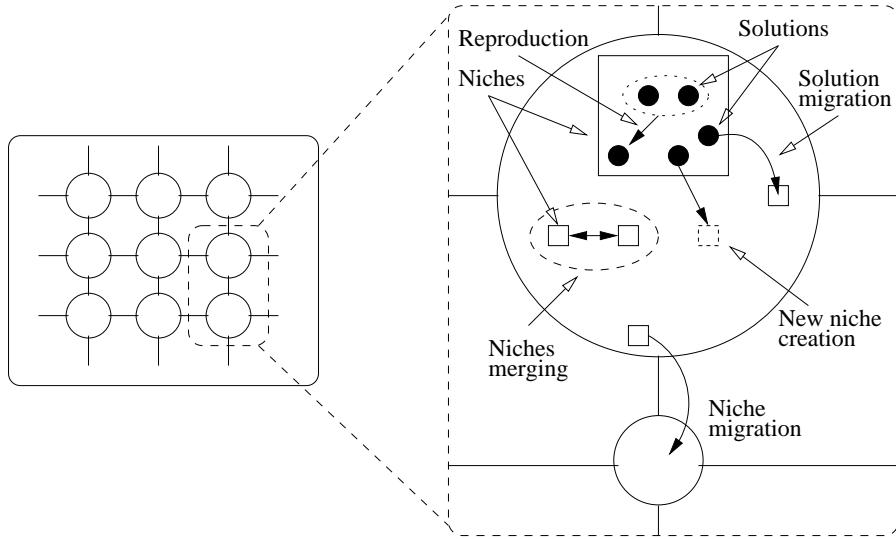
Niching techniques realized in CoEMAS model have many interesting features, which include:

- explicit resource sharing mechanism;
- possibilities of modeling sympatric speciation on the basis of co-evolutionary interactions;
- possibilities of modeling allopatric speciation on the basis of system's spacial structure;
- mechanism of auto-adaptation of the number of individuals to the difficultness of problem being solved.

Moreover, niching techniques based on co-evolutionary interactions are decentralized and can be easily introduced in decentralized systems based on EMAS model.

In Figure 1 co-evolutionary multi-agent system for multi-modal function optimization (*NCoEMAS*) is presented. The topography of environment, in which agents live, is graph with every node (place) connected with its four neighbors. Within the environment two co-evolving species (niches and solutions) live. Agents-solutions live within agents-niches (the model of co-operative co-evolution). There exists a resource within the environment. There is closed circulation of the resource within the system. The resource can be possessed by environment or agents. Environment gives the resource to agents and every agent's action (such as migration or reproduction) costs some resource, so the resource is returned to the environment.

The competition for limited resources mechanism (*resource sharing*) works as follows. First the resource is given by environment to all agents-niches, proportionally to their fitness values (the value of niche's fitness depends on the fitness values

Fig. 1. *NCoEMAS* system

of agents-solutions that currently belongs to it). In spite of the proportional amount of resource, all niches are also given some minimal amount of resource (r_{eq}) in order to keep alive less fitted species of solutions. Then each agent-niche distributes its resources among its agents-solutions (proportionally to their fitness values).

Agents-niches can migrate within the environment and all agents-solutions live within agents-niches and migrate with them within the environment. Each time step every agent-solution searches for agent-niche that is located within the basin of attraction of the same local minimum. Modified version of hill-valley function ([28]) is used in order to check if two agents are located within the basin of attraction of the same local minimum. If there are no agents-niches located within the same basin of attraction, agent-solution creates new agent-niche, whose genotype is the copy of its own genotype (agent-niche is splitted – see Figure 1).

Then each agent-solution searches its niche for the reproduction partner. Reproduction takes place only when agents have sufficient amount of resource. The genotypes of all agents are real-valued vectors. Intermediate recombination [5] and mutation with self-adaptation [3] are used for agents-solutions and special mutation for agents-niches. Each time step the agent-niche's genotype is mutated in such a way that the resulting genotype is the center of gravity of agents-solutions that belong to that agent-niche (fitness value of each agent-solution serves here as a weight value). Agents-niches can merge if they are located at the same place of environment and if they are located within the basin of attraction of the same local minimum.

4.1 NCoEMAS

The *NCoEMAS* is described as 4-tuple:

$$NCoEMAS = \langle E, S, \Gamma, \Omega = \{\omega_1, \omega_2, \omega_3, \omega_4\} \rangle \quad (10)$$

where E is the environment of the *NCoEMAS*, S is the set of species ($s \in S$) that co-evolve in *NCoEMAS*, Γ is the set of resource types that exist in the system, the amount of type γ resource will be denoted by r^γ , Ω is the set of information types that exist in the system, the information of type ω will be denoted by i^ω .

There are four information types ($\Omega = \{\omega_1, \omega_2, \omega_3, \omega_4\}$) and one resource type ($\Gamma = \{\gamma\}$) in *NCoEMAS*. Information of type ω_1 contain nodes to which agent-niche can migrate, when it is located in particular node of the graph. Information of type ω_2 contain agents-niches which are located in the particular node in time t . Information of type ω_3 describe which agents belong to the given species of solutions in the time t . Information of type ω_4 contain the time of creation of the given agent.

There is one resource type ($\Gamma = \{\gamma\}$) in *NCoEMAS*, and there is closed circulation of resource within the system.

4.2 Environment

The environment of *NCoEMAS* may be described as 3-tuple:

$$E = \langle T^E, \Gamma^E = \Gamma, \Omega^E = \{\omega_1, \omega_2\} \rangle \quad (11)$$

where T^E is the topography of environment E , Γ^E is the set of resource types that exist in the environment, Ω^E is the set of information types that exist in the environment. The topography of the environment is given by

$$T^E = \langle H, l \rangle \quad (12)$$

where H is directed graph with the cost function c defined: $H = \langle V, B, c \rangle$, V is the set of vertices, B is the set of arches. The distance between two nodes is defined as the length of the shortest path between them in graph H .

The l function makes it possible to locate particular agent in the environment space:

$$l : A \rightarrow V \quad (13)$$

where A is the set of agents that exist in *NCoEMAS*.

Vertice v is given by

$$v = \langle A^v, \Gamma^v = \Gamma^E, \Omega^v = \Omega^E, \varphi \rangle \quad (14)$$

where A^v is the set of agents that are located in the vertice v . Agents can collect two types of informations from the vertice. The first one includes all vertices that

are connected with the vertice v and the second one includes all agents of species nch that are located in the vertice v :

$$i^{\omega_1, v} = \{u : u \in V \wedge \langle v, u \rangle \in B\} \quad (15)$$

$$i^{\omega_2, v} = \{a^{nch} : a^{nch} \in A^v\}. \quad (16)$$

4.3 Species

The set of species in the time t is given by

$$S(t) = \{nch(t), sol_1(t), \dots, sol_{nn}(t)\} \quad (17)$$

where $nn(t) = |A^{nch}(t)|$, and $A^{nch}(t)$ is the set of species nch agents in the time t . The changes in the number of species result from the mutual location of agents in the fitness landscape.

4.3.1 Niches Species

The niches species (nch) is defined as follows:

$$nch = \langle A^{nch}, SX^{nch} = \{sx\}, Z^{nch}, C^{nch} \rangle \quad (18)$$

where SX^{nch} is the set of sexes which exist within the nch species, Z^{nch} is the set of actions that agents of species nch can perform, and C^{nch} is the set of relations of species nch with other species that exist in the *NCoEMAS*.

There is only one sex sx ($sx \equiv sx^{nch}$) within the nch species, which is defined as follows:

$$sx = \langle A^{sx} = A^{nch}, Z^{sx} = Z^{nch}, C^{sx} = \emptyset \rangle. \quad (19)$$

The set of actions Z^{nch} is defined as follows:

$$Z^{nch} = \{die, give, get, adapt, seek, merge, migr\} \quad (20)$$

where *die* is the action of death (agent a^{nch} dies when there is no agents-solutions living within it), *give* action distributes the resources of agent a_i^{nch} among the agents from species sol_i that live within the agent a_i^{nch} , *get* action gains resources from the environment, *adapt* action is the special mutation operator which moves the center of the agent-niche a_i^{nch} (coded in its genotype) to the center of gravity of the population of agents-solutions that live within the agent a_i^{nch} , *seek* action seeks for agents-niches that are located within the basin of attraction of the same local minimum, *merge* action merges two agents-niches when they are located within the basin of attraction of the same local minimum, and *migr* is the action of migration between nodes within the environment.

The set of relations of *nch* species with other species that exist within the system are defined as follows:

$$C^{nch} = \left\{ \xrightarrow{nch.get-}, \xrightarrow{nch.merge-}, \xrightarrow{nch.give+} \right\}. \quad (21)$$

The individual relations are defined as follows:

$$\xrightarrow{nch.get-} = \{\langle nch, nch \rangle\}. \quad (22)$$

$$\xrightarrow{nch.merge-} = \{\langle nch, nch \rangle\} \quad (23)$$

$$\xrightarrow{nch.give+} = \{\langle nch, ind_i \rangle : nch, ind_i \in S \text{ for } i = 1, \dots, |A^{nch}| \}. \quad (24)$$

First two of them model intra species competition for limited resources. The last one models symbiotic relation between *nch* and *ind_i* species. The *give* action allows a_i^{nch} agent to give some resource to agent of species *ind_i* (which live within the agent a_i^{nch}).

4.3.2 Solutions Species

Each of the species $sol_i(t)$, for $i = 1, \dots, |A^{nch}(t)|$ in the time t live within one of the agents of species *nch(t)*. Species *sol* ($sol \equiv sol_i(t)$) is defined as follows:

$$sol = \langle A^{sol}, SX^{sol} = \{sx\}, Z^{sol}, C^{sol} \rangle. \quad (25)$$

Within the species *sol* there exists sex *sx* ($sx \equiv sx^{sol}$), which is defined as follows:

$$sx = \langle A^{sx} = A^{sol}, Z^{sx} = Z^{sol}, C^{sx} = \emptyset \rangle. \quad (26)$$

The set of actions Z^{sol} is defined as follows:

$$Z^{sol} = \{die, get, accept, seekind, clone, rec, mut, seeknch, create, migr\} \quad (27)$$

where *die* is the action of death (agent-solution dies when it is out of resources), *get* action gets some resource from a^{nch} agent (within each the given agent-solution lives in the time t), *accept* action accepts partner for reproduction, *seekind* seeks for partner for reproduction, *clone* is the action of cloning individual (new agent with the same genotype as parent's one is created), *rec* is the recombination operator (intermediate recombination is used [5]), *mut* is the mutation operator (mutation with self-adaptation is used [3]), *seeknch* action seeks for agent-niche located within the basin of attraction of the same local minimum as agent a^{sol} is located, *create* action creates new agent from *nch* species, which is located within the basin of attraction of the same local minimum, *migr* action allows agent to migrate between agents from *nch* species.

The set of relations C^{sol} is defined as follows:

$$C^{sol} = \left\{ \xrightarrow{sol, get-}, \xrightarrow{sol, migr+} \right\}. \quad (28)$$

The first relation models inner species competition for limited resources:

$$\xrightarrow{sol, get-} = \{\langle sol, sol \rangle\}. \quad (29)$$

The second one is defined as follows:

$$\xrightarrow{sol, migr+} = \{\langle sol, nch \rangle\}. \quad (30)$$

It models the symbiotic relationship between species sol and nch .

4.4 Agent of nch Species

Agent a of species nch ($a \equiv a^{nch}$) is defined as follows:

$$a = \langle gn^a, Z^a, \Gamma^a = \Gamma, \Omega^a = \{\omega_1, \omega_2, \omega_3\}, PR^a \rangle. \quad (31)$$

Genotype of agent a is composed of one real-coded vector of floating point values:

$$gn^a = \langle \vec{x} = (x_1, \dots, x_{ng}) \rangle \quad (32)$$

where $x_i \in \mathbb{R}$.

$Z^a = Z^{nch}$ (see (20)) is the set of actions that agent a is able to perform. Information of type ω_3 is the set of agents of species sol , which live within the agent a :

$$i^{\omega_3} = A^{sol}. \quad (33)$$

The set of profiles includes resource profile (pr_1), adaptation profile (pr_2), interaction profile (pr_3), and migration profile (pr_4):

$$PR^a = \{pr_1, pr_2, pr_3, pr_4\} \quad (34a)$$

$$pr_1 \trianglelefteq pr_2 \trianglelefteq pr_3 \trianglelefteq pr_4. \quad (34b)$$

Each time step agent tries to realize goals of the profiles (taking into account the priorities of the profiles – here pr_1 has the highest priority). In order to realize goals of the given profile agent uses strategies which can be realized within this profile.

Within pr_1 profile all strategies connected with type γ resource are realized ($\langle die \rangle$, $\langle get \rangle$). This profile uses information of type ω_3 . Within pr_2 profile strategy of adaptation ($\langle adapt \rangle$) is realized (information of type ω_3 are used). Within pr_3 profile the interactions with other agents are realized (strategies $\langle give \rangle$ and $\langle seek, merge \rangle$, and information of type ω_2 are used). Within pr_4 profile the migration strategy ($\langle migr \rangle$), which uses information i^{ω_1} , is realized.

4.5 Agent of *sol* species

Agent a of species *sol* ($a \equiv a^{sol}$) is defined as follows:

$$a = \langle gn^a, Z^a, \Gamma^a = \Gamma, \Omega^a = \{\omega_2, \omega_4\}, PR^a \rangle. \quad (35)$$

Genotype of agent a consists of two vectors (chromosomes): \vec{x} of real-coded decision parameters' values and $\vec{\sigma}$ of standard deviations' values, which are used during mutation:

$$gn^a = \langle \vec{x} = (x_1, \dots, x_{ng}), \vec{\sigma} = (\sigma_1, \dots, \sigma_{ng}) \rangle \quad (36)$$

where $x_i, \sigma_i \in \mathbb{R}$.

$Z^a = Z^{sol}$ (see (27)) is the set of actions which agent a can perform.

Information of type ω_2 is defined by (16). Information of type ω_4 contains the time of agent a creation:

$$i^{\omega_4} = \{t_{create}\}. \quad (37)$$

The set of profiles includes resource profile (pr_1), reproduction profile (pr_2) and interaction profile (pr_3):

$$PR^a = \{pr_1, pr_2, pr_3\} \quad (38a)$$

$$pr_1 \trianglelefteq pr_2 \trianglelefteq pr_3. \quad (38b)$$

Within pr_1 profile all strategies connected with type γ resource are realized ($\langle die \rangle, \langle get \rangle$). This profile uses information of type ω_4 . Within pr_2 profile all strategies connected with the reproduction ($\langle accept \rangle, \langle seekind, clone, rec, mut \rangle$) are realized, and information of type ω_3 are used. Within pr_3 profile the interactions with other agents from species *nch* are realized (strategy $\langle seeknch, create, migr \rangle$ and information of type ω_2 are used).

5 SIMULATION EXPERIMENTS

Simulation experiments were aimed at testing if NCoEMAS described in previous section is able to form and stably maintain species located within the basins of attraction of local minima throughout the evolution process. Also, the experiments comparing NCoEMAS to other niching techniques (deterministic crowding and fitness sharing), and EMAS were carried out and the influence of resource sharing mechanism was investigated. All simulations were run for 5000 time steps (the event driven simulation mechanism was used in all systems) because the main goal of the experiments was to investigate whether the compared systems are able to stably maintain subpopulations (they do not disappear during the simulation).

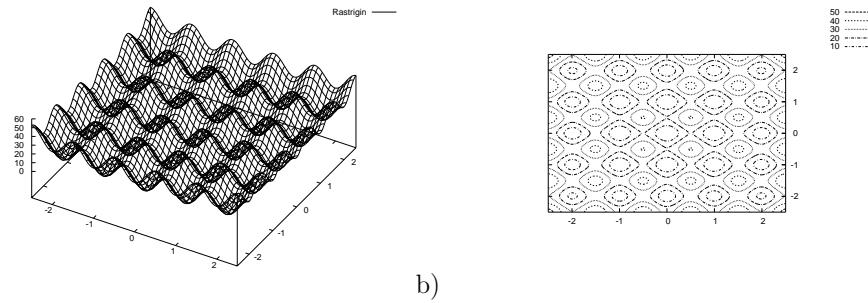


Fig. 2. a) Rastrigin's function and b) its contour plot

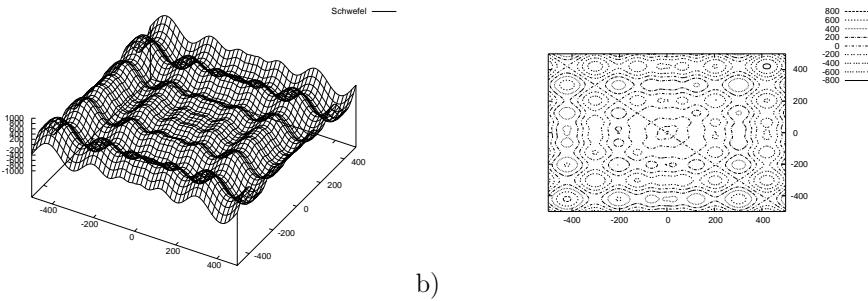


Fig. 3. a) Schwefel's function and b) its contour plot

5.1 Test Functions

In all experiments Rastrigin and Schwefel functions were used (see Figures 2 and 3). These are multi-modal functions commonly used in studies of niching methods.

Rastrigin function used in the experiments is given by

$$f_1(\vec{x}) = 10 * n + \sum_{i=1}^n (x_i^2 - 10 * \cos(2 * \pi * x_i)) \quad (39)$$

$$x_i \in [-2.5; 2.5] \text{ for } i = 1, \dots, n$$

where n is the number of dimensions ($n = 2$ in all experiments). The function has 25 local minima for $x_1, x_2 \in [-2.5; 2.5]$.

Schwefel function is given by

$$f_2(\vec{x}) = \sum_{i=1}^n \left(-x_i * \sin \left(\sqrt{|x_i|} \right) \right) \quad (40)$$

$$x_i \in [-500.0; 500.0] \text{ for } i = 1, \dots, n.$$

This is deceptive function with unevenly distributed 62 local minima.

5.2 Representation, Operators and Parameters

In all compared systems real-coded vectors, intermediate recombination [5] and mutation with self-adaptation [3] are used.

The parameters' values (see Table 1) were set on the basis of results from the number of initial experiments in order to get correct results and to assure the stable work of each system (because in all systems, except DC algorithm, the variable population size mechanism was used). The initial population size ($|A(0)|$) was also set on the basis of initial experiments in order to minimize this value and assure the stable work of each system. All the parameters are described in Table 2.

Parameter	<i>NCoEMAS</i>	<i>EMAS</i>	<i>DC</i>	<i>FS</i>
$r_{min}^{\gamma,nch}$	0.0	—	—	—
$r_{max}^{\gamma,nch}$	25 000.0	—	—	—
$r_{min}^{\gamma,sol}$	0.0	0.0	0.0	0.0
$r_{max}^{\gamma,sol}$	100.0	100.0	100.0	100.0
r_{rep}^{γ}	$0.6r_{max}^{\gamma,sol}$	$0.6r_{max}^{\gamma,sol}$	—	$0.6r_{max}^{\gamma,sol}$
r_{clone}^{γ}	$0.25r^{\gamma,sol}$	$0.25r^{\gamma,sol}$	—	$0.25r^{\gamma,sol}$
r_{rec}^{γ}	$0.25r^{\gamma,sol}$	$0.25r^{\gamma,sol}$	—	$0.25r^{\gamma,sol}$
r_{create}^{γ}	$0.3r^{\gamma,sol}$	—	—	—
t_{maxage}	100	100	—	100
$r_{eq}^{\gamma,v}$	$5r_{max}^{\gamma,sol}$	—	—	—
$c(\langle u, v \rangle)$	$0.01r_{max}^{\gamma,nch}$	$0.05r_{max}^{\gamma,sol}$	—	—
$prec$	0.8	0.8	0.8	0.8
$pmut$	0.1	0.1	0.1	0.1
α	—	—	—	0.5
σ_{sh} for func.				
f_1	—	—	—	0.5
f_2	—	—	—	100
$ A(0) $ for func.				
f_1	10	10	1 500	25
f_2	20	50	2 000	30
$ V $ for func.				
f_1	4	4	1	1
f_2	4	4	1	1

Table 1. Parameters' values for systems used in the experiments

5.3 Experimental Results

5.3.1 The Comparison of *NCoEMAS* and Classical Niching Techniques

The results presented in Figures 4–7 show the location of individuals within the search space during the typical experiments with compared systems.

Parameter	Description
$r_{min}^{\gamma,nch}$	Minimal value of γ resource for agents of species nch
$r_{max}^{\gamma,nch}$	Maximal value of γ resource for agents of species nch
$r_{min}^{\gamma,sol}$	Minimal value of γ resource for agents of species sol
$r_{max}^{\gamma,sol}$	Maximal value of γ resource for agents of species sol
r_{rep}^{γ}	Minimal amount of γ resource needed for reproduction
r_{clone}^{γ}	The amount of resource given to child by parent
r_{rec}^{γ}	The amount of resource given to child by second parent during recombination
r_{create}^{γ}	The amount of resource given to created agent-niche by agent-solution
t_{maxage}	Maximal age that agent-solution can live within the system
$r_{eq}^{\gamma,v}$	The equal amount of resource γ given to every agent-niche by node v
$c(\langle u, v \rangle)$	The cost of migration from node u to node v
$prec$	The probability of recombination
p_{mut}	The probability of mutation
α	The parameter of sharing function in FS algorithm
σ_{sh}	The parameter of FS algorithm
$ A(0) $	The initial number of agents in the system
$ V $	The number of nodes of graph H

Table 2. Parameters' descriptions

In the case of *EMAS* system subpopulations (species) located within the basins of attraction of “worse” local minima disappear quite quickly and almost the whole population is located within the basin of attraction of global minimum (see Figure 4). However, the existence of system’s environment causes that individuals are distributed over the whole basin of attraction (and to some extent even outside it) and population diversity is maintained.

In the case of *DC* system species are quickly formed within the basins of attraction of local minima; however, the species located within the basins of “worse” local minima disappear during the remaining part of experiment, and finally there exists only one species located within the basin of attraction of global minimum (see Figure 5).

Fitness sharing technique forms and maintains species; however, the population diversity within the species is very high. The individuals are not located within the closest neighborhoods of local minima but they are distributed over the whole basins of attraction of local minima and even outside them (see Figure 6).

Figure 7 shows the location of *NCoEMAS* individuals within the search space during the typical experiment. At the beginning there are only 5 agents-niches (represented with squares) and 5 agents-solutions (represented with diamonds) with identical genotypes as in the case of agents-niches to which they belong. It can be seen that as the experiment goes on the agents reproduce and locate themselves

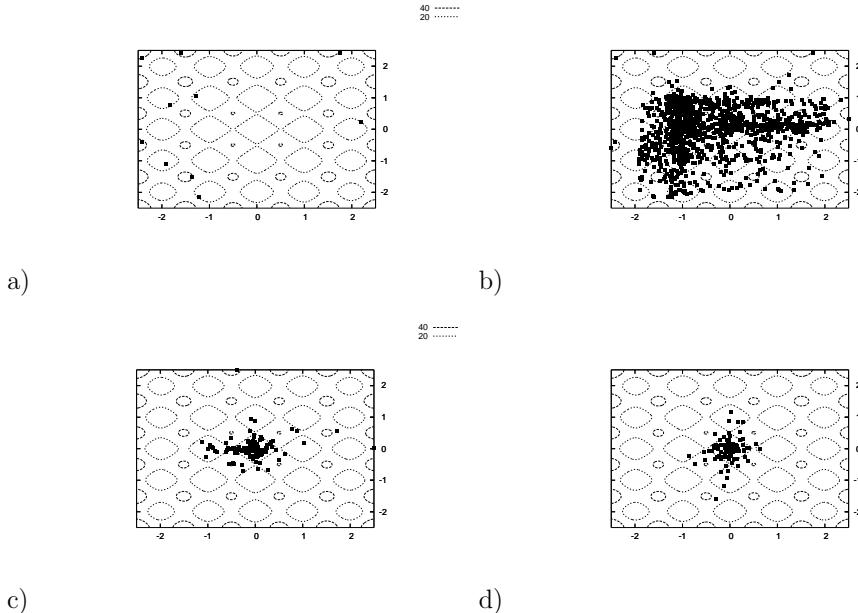


Fig. 4. The location of individuals in *EMAS* during a) the 0th, b) 50th, c) 500th and d) 5000th simulation step

within the closest neighborhoods of the local minima of Rastrigin's function. Moreover, the species are stable, and do not disappear during the experiment.

Figures 8 and 9 show the average number of local minima neighborhoods located and the value of proportional species' sizes indicator for compared systems during experiments with Rastrigin's and Schwefel's functions. The experiments were carried out for four techniques: *NCoEMAS*, *EMAS*, deterministic crowding (*DC* [18]) and fitness sharing (*FS* [13]).

Figures 8 a) and 9 a) show the average number of local minima neighborhoods located. The local minima neighborhood was classified as "located" when there was at least $n_{i_{min}} = 3$ individuals closer than 0.05 (in the case of Rastrigin's function) and 10.0 (in the case of Schwefel's function) to that local minima.

NCoEMAS stood relatively well when compared to other techniques. On the average, it stably maintained about 22 local minima neighborhoods of Rastrigin's function and 40 local minima neighborhoods of Schwefel's function. *DC* quickly located about 13–14 local minima neighborhoods of Rastrigin's function and 35 local minima neighborhoods of Schwefel's function but there was quite strong tendency to lose almost all of them during the remaining part of experiments. *FS* technique detected and stably maintained about 12–13 local minima neighborhoods of Rast- rigin's function and about 20 local minima neighborhoods of Schwefel's function on the average. *EMAS* without any niching mechanism was not able to stably popu-

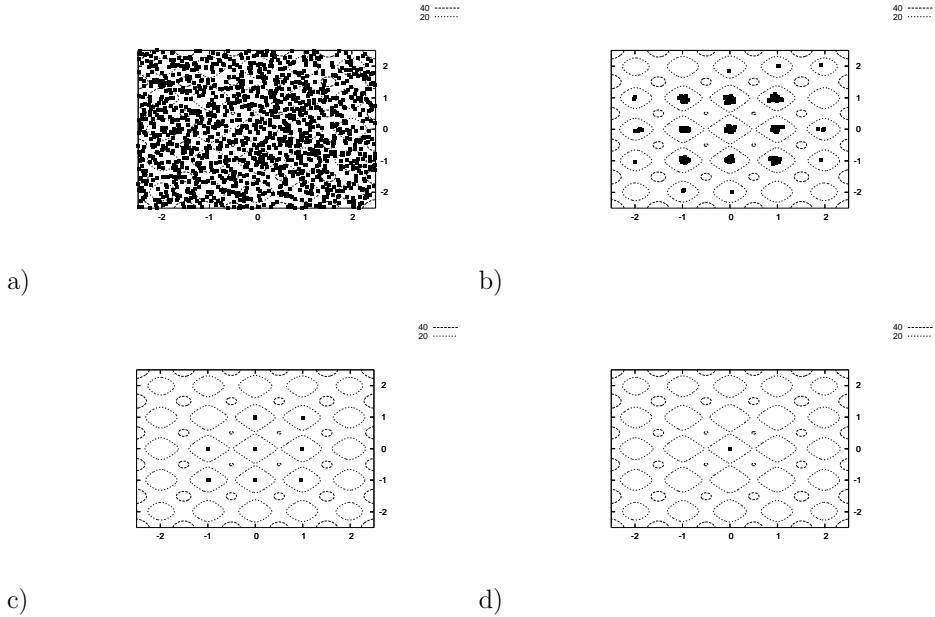


Fig. 5. The location of individuals in DC system during the a) 0th, b) 50th, c) 500th and d) 5000th simulation step

late more than one local minima neighborhood. It turned out that in the case of multi-modal optimization problems it works just like simple EA.

Figures 8 b) and 9 b) show the average values of proportional species' sizes indicator $npd(t)$. The $npd(t)$ indicator is defined as follows:

$$npd(t) = \sum_{i=1}^{|D^{min}|} g(|A^i(t)|) \quad (41a)$$

$$g(|A^j(t)|) = \begin{cases} 1 - \frac{|A^j(t)| - ni_{opt}^j}{ni_{opt}^j} & \text{if } |A^j(t)| \leq ni_{opt}^j \\ 1 - \frac{|A^j(t)| - ni_{opt}^j}{|A(t)|} & \text{if } |A^j(t)| > ni_{opt}^j \end{cases} \quad (41b)$$

$$ni_{opt}^j = \frac{f'(\vec{x}_j^+)}{\sum_{k=1}^{|D^{min}|} f'(\vec{x}_k^+)} |A(t)| \quad (41c)$$

where:

$D^{min} \subseteq D$ is the set of local minima of the goal function f ,

$A(t)$ is the set of agents that exist in the system in time t ,

\vec{x}_j^+ is j^{th} local minima,

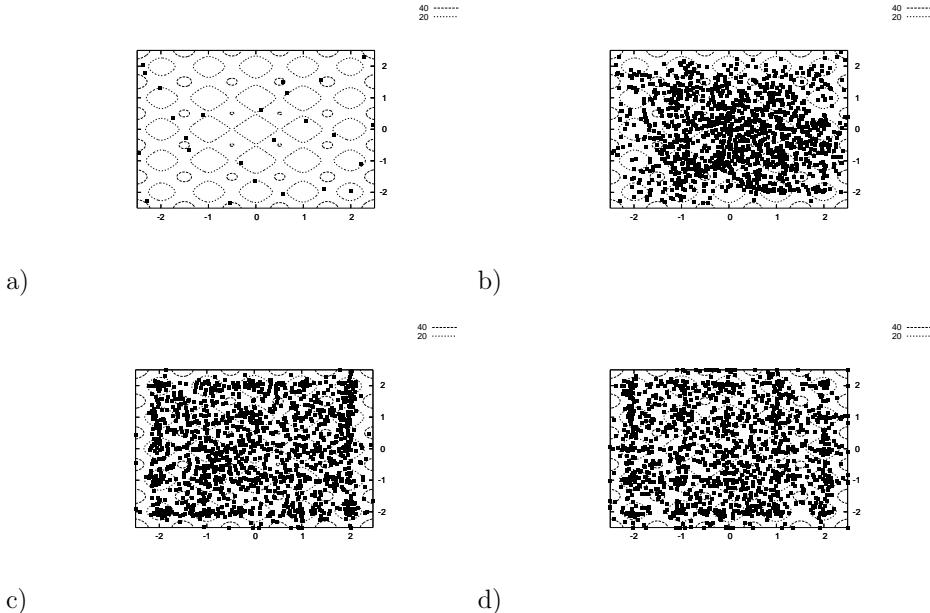


Fig. 6. The location of individuals in *FS* system during the a) 0th, b) 50th, c) 500th and d) 5000th simulation step

$A^j(t)$ is the set of agents that are closer than $dist_{max}$ to j -th local minima in the time t ,

$f' = \delta \circ f$ is the modified goal function,

$\delta : \mathbb{R} \rightarrow \mathbb{R}$ is scaling function which assures that the values of f' function are greater than 0 and that local maxima of this function are located in the same places as local minima of function f .

In the case when all subpopulations (species) located within the neighborhoods of local minima are of optimal sizes then $npd(t)$ indicator has the maximal value (equal to the number of local minima). In the case when some subpopulations' sizes are not optimal then the value of this indicator falls down.

In the case of $npd(t)$ indicator, the best results were obtained with the use of *NCoEMAS* system (see Figures 8 b) and 9 b)). Relatively poor performance of *FS* technique results from the tendency to distribute individuals over the whole basins of attraction of local minima (what was also observed earlier in this section). The results of *DC* and *EMAS* indicate that in these systems all species except one disappear during the simulation.

To sum up, simple EMAS cannot be applied to multi-modal function optimization without introducing special mechanisms such as co-evolution. *FS* and *DC* have some limitations as niching techniques. *DC* has the strong tendency to lose located

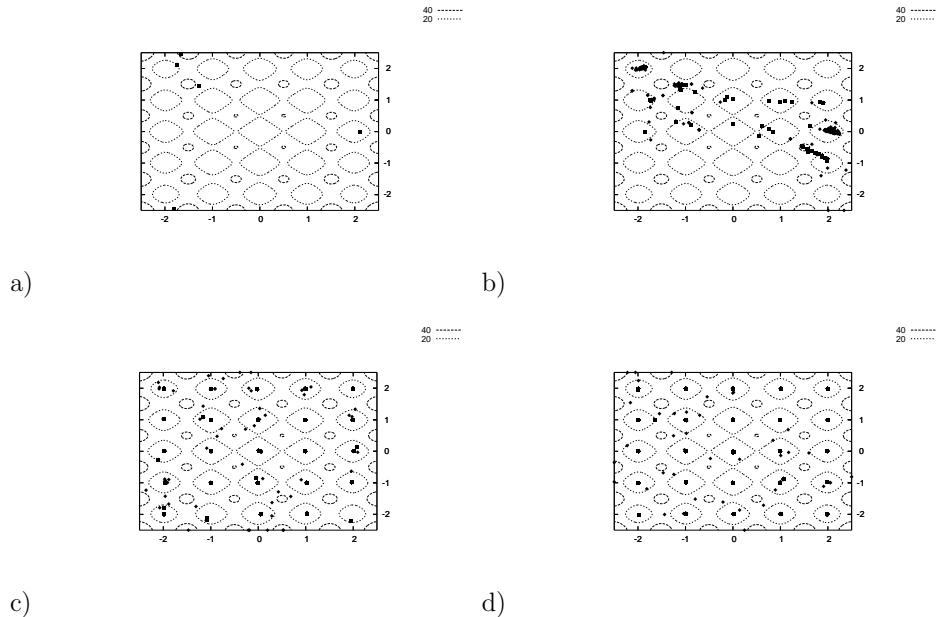


Fig. 7. The location of individuals in *NCoEMAS* during the a) 0th, b) 50th, c) 500th and d) 5000th simulation step

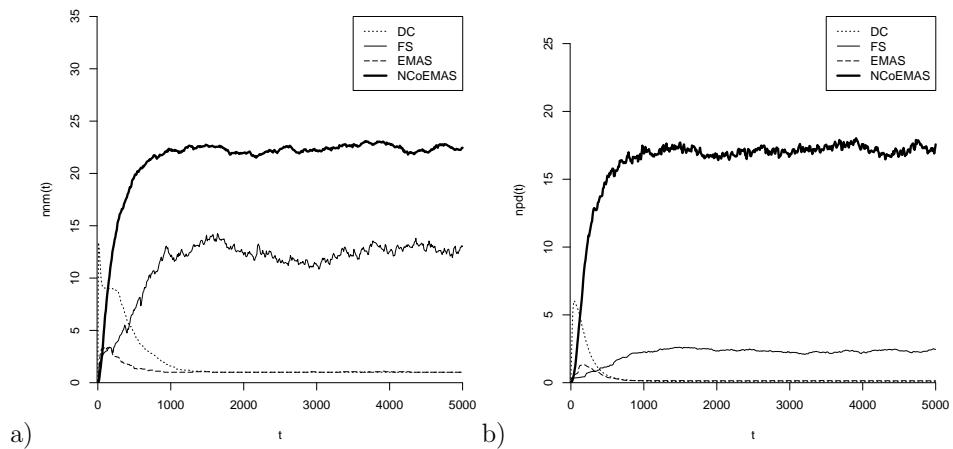


Fig. 8. a) The number of Rastrigin's function local minima neighborhoods located (the average values from 20 experiments, $ni_{min} = 3$) and b) the value of proportional species' sizes indicator (the average values from 20 experiments). The comparison of different systems' results

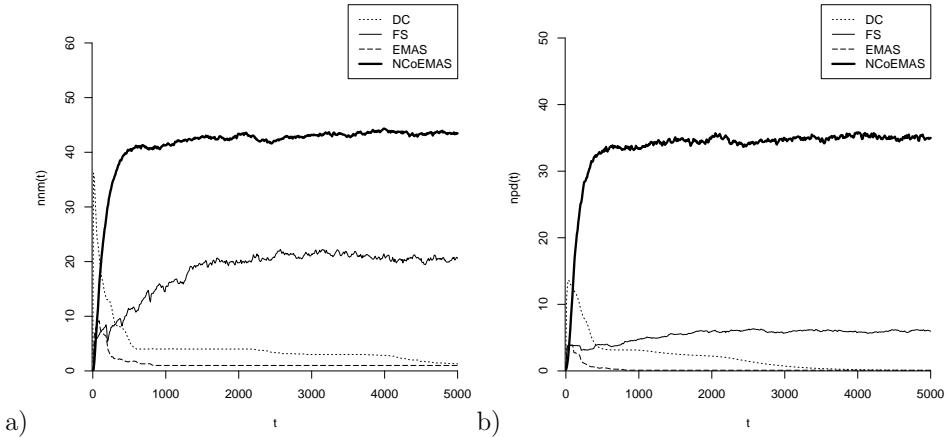


Fig. 9. a) The number of Schwefel's function local minima neighborhoods located (the average values from 20 experiments, $n_{min} = 3$) and b) the value of proportional species' sizes indicator (the average values from 20 experiments). The comparison of different systems' results

basins of attraction of local minima during the evolution process. The fact of relatively poor performance of DC was also observed in other works [30]. FS technique maintains high diversity within the species and does not locate individuals within the closest neighborhoods of local minima (it does not promote useful population diversity). NCoEMAS is valid and promising niching technique but still more research is needed.

5.4 The Influence of Resource Sharing Mechanism

In this section the results of the experiments with different values of r_{eq} parameter (the equal amount of resource which is given to all agents-niches by environment) are presented. In all these experiments Rastrigin's function was used. The value of r_{eq} parameter is crucial to the correct working of the resource sharing mechanism in *NCoEMAS* system. Table 3 shows the values of r_{eq} parameter used in different types of experiments.

Parameter	E1	E2	E3	E4	E5	E6
r_{eq}	$5r_{max}^{sol}$	0	$2.5r_{max}^{sol}$	$3.75r_{max}^{sol}$	$15r_{max}^{sol}$	$27.5r_{max}^{sol}$

Table 3. The values of r_{eq} parameter for different experiments, r_{max}^{sol} is the maximal amount of resource that can be in the possession of agent-solution

Figure 10 a) shows the number of local minima neighborhoods of Rastrigin's function located in experiments with different values of r_{eq} parameter. The results

are worst in the case of $E2$ ($r_{eq} = 0$) and $E3$ ($r_{eq} = 2.5r_{\max}^{sol}$) experiments. In the case of other experiments the results are quite comparable. This means that if there is no minimal amount of resource given to the agents-niches (experiments of type $E2$) or this amount is too small (experiments of type $E3$), the species located within the basins of attraction of “worse” (that means with greater value of fitness function) local minima have no chances to survive and to win the competition for limited resources with the species located within the basins of attraction of “better” local minima.

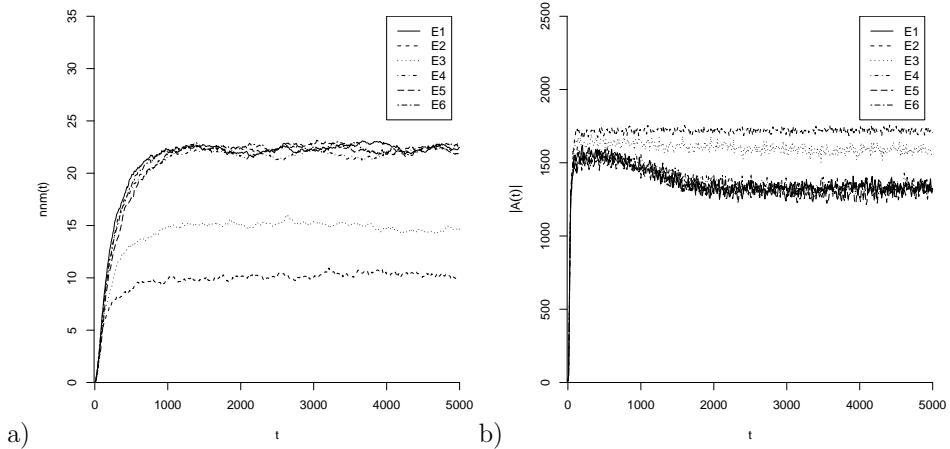


Fig. 10. a) The number of Rastrigin's function local minima neighborhoods located and b) the population sizes in experiments with different values of r_{eq} parameter of $NCoEMAS$ system (the average values from 20 experiments, $ni_{min} = 3$)

In the case of $E2$ and $E3$ experiments the population sizes are generally larger than in the case of other experiments (see Figure 10 b)). The number of agents rapidly grows at the beginning of experiment, approaches some level and then stays approximately the same during the remaining part of the experiment. There is no adaptation of the population size to the difficultness of the problem (to the number of local minima of the fitness function in the case of presented experiments). In the case of $E2$ and $E3$ experiments, species located within the basins of attraction of “worse” local minima quickly loose the competition with other species and die off. In such case the operator of merging niches does not work, simply because there are no niches to merge. The number of agents stays generally at the higher level than in the case of other experiments, because the same amount of resource is given by environment to the smaller number of agents-niches and the subpopulations of agents-solutions that belong to them are generally bigger. In the case of other types of experiments, when there is enough resource given to each agent-niche, the number of agents in the system adapts to the number of local minima of fitness function (see Figure 10 b)). In such case species of agents-solutions (which live within the agents-

niches) do not die off. All species have the chance to survive. The mechanism of merging niches located within the basins of attraction of the same local minima causes that after the rapid growth of the number of agents the population size decreases slightly and approaches the optimal level.

6 CONCLUDING REMARKS

The idea of *co-evolutionary multi-agent system (CoEMAS)* allows us to model many ecological co-evolutionary interactions between species and sexes such as resource competition, predator-prey and host-parasite co-evolution, sexual preferences, etc.

In this paper sample CoEMAS with two co-evolving species: niches and solutions was presented. This system was applied to multi-modal function optimization. The presented results show that *NCoEMAS* was able to detect and stably maintain more neighborhoods of Rastrigin and Schwefel functions' local minima than two classical niching techniques (deterministic crowding and fitness sharing) and *EMAS* system. *NCoEMAS* also formed species of sizes proportional to the "quality" of local minima.

The presented results also indicate that it is necessary to loosen the competition for limited resources between species located within the basins of attraction of different "quality" local minima. In the case of strong competition, the species located within the basins of attraction of "worse" local minima could eventually die off completely. Moreover, in such case there is no adaptation of the population size to the difficulty level of the problem being solved (to the number of local minima in the case of multi-modal function minimization problems).

Future research will include more detailed comparison to other niching techniques, and the implementation of CoEMAS based on the mechanisms of predator-prey or host-parasite co-evolution. Also the parallel implementation of CoEMAS using MPI is included in future research plans.

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