Niche Formation Techniques Based on Coevolutionary Interactions in Multi-Agent System

Rafał DREŻEWSKI *

Department of Computer Science
University of Mining and Metallurgy, Kraków, Poland
drezew@agh.edu.pl

Abstract

Niching techniques for evolutionary algorithms are aimed at forming and maintaining stable subpopulations (*species*) in multimodal domain. This paper reviews some of the existing niching techniques and presents the idea of *niching coevolutionary multi-agent system* (*NCoEMAS*). In such a system the niche formation phenomena occurs within one of the preexisting species as a result of coevolutionary interactions. Also the results from runs of NCoEMAS against four 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 [7, 14]. This tendency is caused by the *genetic drift* [5]. If we are interested in finding multiple solutions of comparable fitness, some multimodal function optimization technique should be used. Such techniques are called *niching methods* [14]. Niching mechanisms create and maintain different subpopulations (*species*) in a multimodal domain.

In nature, there exist different subspaces within the environment (*niches*), which support different types of life (*species*). The number of organisms contained within each niche depends on niche fertility (its *carrying capacity*) and the efficiency of exploiting the niche resources.

Traditionally, there exist two basic approaches in evolutionary biology to understanding *speciation process* [6]. The first one called *allopatric speciation* occurs when subpopulations of a given species become geographically isolated. After isolation they follow different evolutionary paths and — eventually — become different species. Resulting species are reproductively isolated even after secondary contact [6].

The second kind of speciation is called *sympatric speciation*. Such speciation results from niche separation due to resource competition, predator-prey coevolution, sexual preferences, etc. [6, 11]. Speciation process takes place within single population and geographical separation of subpopulations is not needed.

This paper starts with the overview of the existing niching techniques for classical EAs. Then the idea of a *niching coevolutionary multi-agent system* (NCoEMAS) is introduced, which opens new possibilities of modeling biological speciation mechanisms based on coevolutionary interactions, competition for limited resources, and geographical isolation.

In the system presented in this paper, the niche (species) formation phenomena occurs as a result of coevolution of two different species: solutions and niches. Coevolution forces the process of speciation within the former one. The system is applied to multimodal function optimization and the results obtained from runs of NCoEMAS against four commonly used test functions are presented.

2 Overview of Niching Techniques

In case of a multimodal landscapes every peak (everywhere in this paper we assume maximization problems) can be treated as a niche which support different kind of life (species). The number of individuals that live within a niche should be in direct proportion to its carrying capacity, which in this case means peak's fitness relative to other peaks present in multimodal domain. This is called *niche proportionate population*.

Various mechanisms have been proposed to form and stably maintain species throughout the search process, thereby allowing to identify all desired peaks of multimodal landscape. Most of these techniques allow niche formation through the implementation of *crowding*, *fitness sharing* or some modifications of these mechanisms. Crowding and sharing based techniques are inspired by speciation resulting from niche separation due to resource competition.

Every niching technique can also be classified as *parallel* or *sequential* [13]. Parallel niching methods form and maintain species simultaneously within a single population (the notion *parallel* here has different meaning than in the case of parallel EAs). Sequential niching methods locate multiple peaks one after another during a sequence of runs.

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

In the following sections we will review some of the existing niching techniques.

2.1 Crowding Based Techniques

The *crowding* technique was introduced by De Jong [5]. In this technique, each generation, a proportion of the population G (*generation gap*) is selected for reproduction (fitness proportionate selection is used). 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. As a similarity metric, Hamming distance in genotypic space was used. Crowding does not promote the formation of stable species, but rather aims at maintaining the genetic diversity of initial population.

Mahfoud developed niching mechanism called *deterministic crowding* [12]. In his technique children are directly compared to their parents. Parent is replaced only if the competing child has higher fitness. To determine which of the two possible parent-child pairings should be used in tournament, total similarities were determined for each possible combination. The pairing with the greatest sum of phenotypic similarity was used.

Probabilistic crowding developed by Mengshoel and Goldberg [15] is based on Mahfoud's deterministic crowding algorithm. The main difference to deterministic crowding is the use of a probabilistic rather than a deterministic acceptance function in parent-offspring tournaments. This means that individuals win proportionally to their fitness relative to competitors.

2.2 Sharing Based Techniques

Fitness sharing was first introduced by Holland [10] and further developed by Goldberg and Richardson [8]. 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

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

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

Miller and Shaw [16] developed the niching technique called *dynamic niche sharing (DNS)*. They make two general assumptions: first that the number of niche peaks, q can be estimated, and second that the peaks are all a minimum distance $2\sigma_{sh}$ from each other. 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 [9]. 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 $f'(c) = \frac{f(c)}{m_{b,t}}\Big|_{c \in C_b}$, 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 $\phi(b) = \sum_{c \in C_{b,t}} f(c)$.

Simple CSN uses GA with selection and recombination operator for the customer population and GA with selection and mutation for the businessman population. In the time t each customer is assigned to the closest businessman. Then a new customer generation is computed with the use of proportionate selection and genetic operators. For each businessman single mutation site is selected randomly. The resulting individual replaces its parent if it is at least d_{min} from other businessmen and it is better fit than its parent. Otherwise another mutation site is selected (max. n_{limit} times).

2.3 Sequential Niching

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 of founded solution in order to avoid locating the same niche multiple times. The *niche radius* used in SN plays a role similar to that of σ_{sh} in sharing.

According to the authors, there are three potential advantages of sequential niching: simplicity, ability to work with smaller populations, and speed (partially a byproduct of smaller populations). However, Mahfoud [13] showed that two latter potential advantages in fact can never materialize. He also pointed out that there are some unavoidable disadvantages connected with the use of SN. These include [13]: loss, through deration, of optimal solutions and their building blocks, repeated search of depressed regions of the search space, repeated location of the same peaks, and slower runtime.

2.4 Parallel Evolutionary Algorithms

Parallel EAs represent quite different approach to species formation, which is based on *allopatric speciation* [2].

In the *island model* PEA [2] the population is divided into several subpopulations. Each subpopulation is assigned to a different processor (*island*). Subpopulations are relatively isolated from each other. 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 a multimodal domain.

Also *fine-grained* PEA [2] 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*. Different shapes of neighborhood can be used. Neighborhoods can also overlap, what allows the propagation of best individuals through the whole population.

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

3 Niching Coevolutionary Multi-Agent Systems

Most of niching techniques presented in the above sections *indirectly* model resource sharing within the niches (through crowding or fitness sharing techniques). On the other hand, PEAs model speciation caused by geographical isolation. However in nature there exist much more speciation mechanisms such as predator-prey coevolution, sexual preferences, etc. [6, 11].

In this section the idea of *niching coevolutionary multi-agent system (NCoEMAS)* is presented. NCoEMAS opens new possibilities of modeling species (niche) formation mechanisms. These include explicit modeling of niches and resource sharing mechanism (*energy sharing*), predator-prey interactions, and sexual preferences.

3.1 Evolutionary Multi-Agent Systems

The main idea of *evolutionary multi-agent system (EMAS)* is the modeling of evolution process in multi-agent system (MAS) [4].

In opposition to classical EAs, in EMAS there is no centralized algorithm which manipulates the whole population. All individuals (*agents*) are independent and make their own decisions concerning reproduction, changing location etc. Agents live in an environment with defined structure and topology. They can move within environment, changing their location. Every
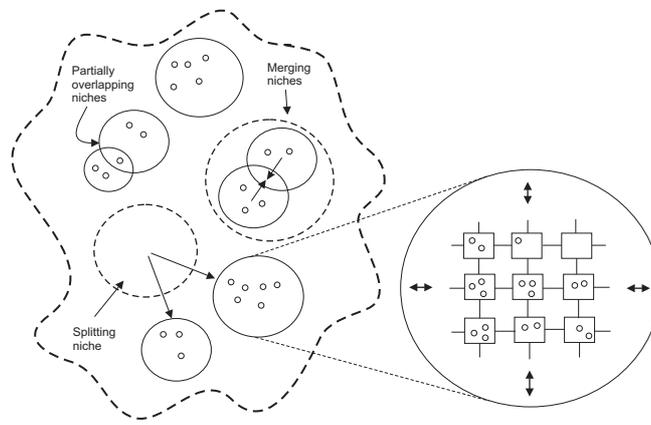
Figure 1: Sample niching coevolutionary multi-agent system

agent has some amount of resource called *life energy*. Every activity costs some energy (activities include: reproduction, migration, etc.) Energy can be gained only from the environment, and the rule is that better fit agents are given more energy than less fit ones.

It is very natural to implement the model of *allopatric speciation* in such a system because there can be many environments coexisting in parallel, each of them with different conditions. Agents can migrate between these environments, so the genetic material (information) is exchanged [3]. This model is, to some extent, similar to *island model* PEA [2] with all its advantages and disadvantages.

The idea of *niching coevolutionary multi-agent system (NCoEMAS)* presented in the following section offers us new possibilities of modeling niching-like behavior, that are not based on allopatric speciation.

3.2   The Idea of Niching Coevolutionary Multi-Agent System

The key idea that differentiates *coevolutionary multi-agent system (CoEMAS)* from EMAS is the coevolution of several species. CoEMAS can be applied, for example, to multiobjective optimization and multimodal function optimization (NCoEMAS).

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.

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

One of the possibilities is the coevolution of the population of individuals representing niches themselves and the population of individuals representing solutions (see fig. 1). In 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 mech-
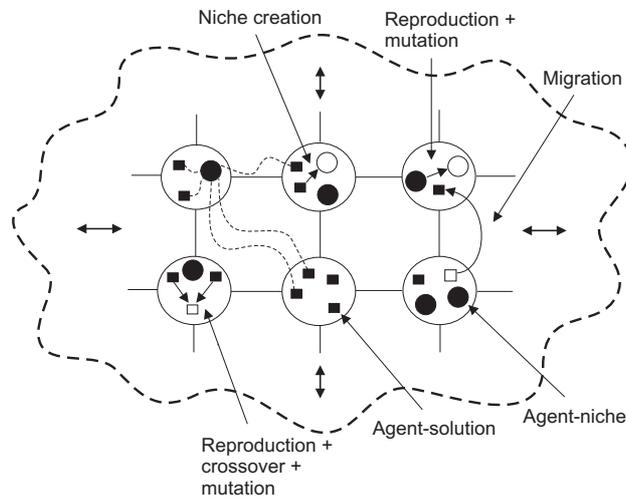
Figure 2: NCoEMAS used in experiments

anism 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*. Also, within each niche we can model the process of allopatric speciation. Each niche can have its inner spatial structure in which agents live (see fig. 1). This will help in maintaining genetic diversity within each subpopulation.

3.3   NCoEMAS — First Attempt

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.

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 [9]. 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 function). 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.

4   Simulation 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 test functions used and the results of experiments are presented.

4.1   Test Functions

There were four test functions used in experiments: F_1, F_2, F_3, F_4 [8, 14]. 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

$$F_1(x) = \sin^6(5\pi x) \quad \text{for } x \in [0, 1] \tag{2}$$

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

$$F_2(x) = \exp(-2 \ln 2((x - 0.1)/0.8)^2) \sin^6(5\pi x) \quad \text{for } x \in [0, 1]] \tag{3}$$

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

$$F_3(x) = \sin^6(5\pi(x^{0.75} - 0.05)) \quad \text{for } x \in [0, 1] \tag{4}$$

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

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

4.2   Results

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

Figure 3 shows the average numbers of agents representing solutions within each niche from ten runs of NCoEMAS against F_1 and F_2 functions. 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.

In case of F_3 and F_4 functions (see fig. 4) NCoEMAS also properly detected and stably maintained all peaks in multimodal domain. However in case of F_3 function peaks are not
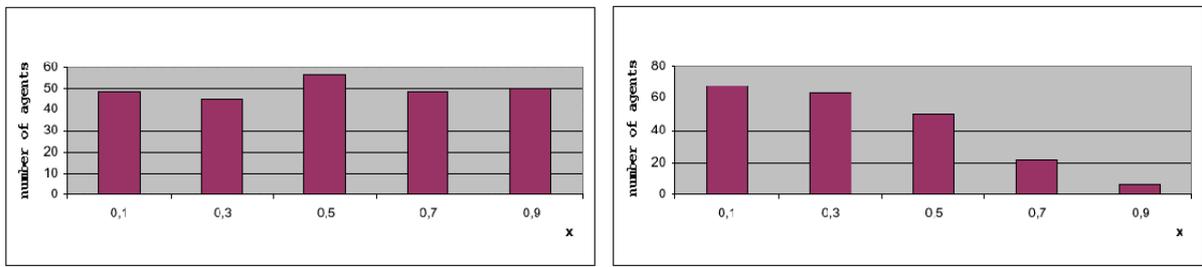
Figure 3: The average number of agents-solutions within each niche from ten runs of NCoEMAS against F_1 function (left) and F_2 function (right)
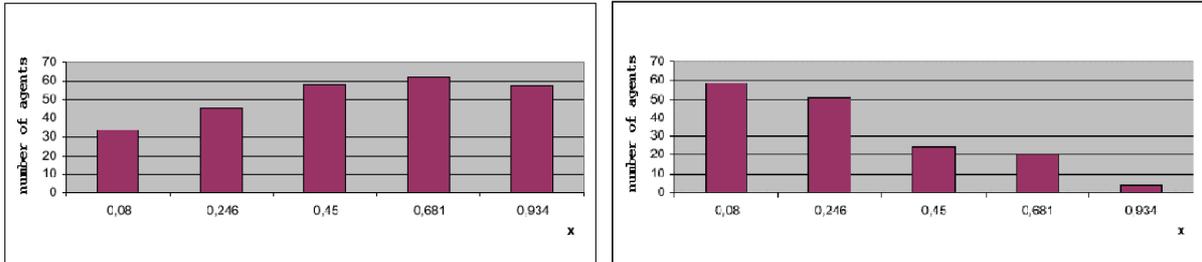

Figure 4: The average number of agents-solutions within each niche from ten runs of NCoEMAS against F_3 function (left) and F_4 function (right)

populated as we could wish. All niches should be equally populated but it seems that agents preferred wider peaks. Niches of F_4 function were populated almost proportionally to their relative fitness. The problems mentioned above are connected with energy sharing mechanism and are the subject of ongoing research.

5   Conclusions and Future Work

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

However, something more is needed if we want to model other biological speciation mechanisms. The idea is to allow the coevolution of several different species in EMAS. The resulting *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 coevolution, sexual preferences, etc. At the same time *allopatric 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. Also the mechanism of *energy sharing* was used. 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 improvements in niche modeling (variable niche radius, mechanisms of splitting and merging niches) and parallelization of NCoEMAS. Experiments with more complex test functions should be carried out. It also seems that predator-prey coevolution and sexual preferences are very promising mechanisms of speciation in NCoEMAS.

References

[1] D. Beasley, D. R. Bull, and R. R. Martin. A sequential niche technique for multimodal function optimization. *Evolutionary Computation*, 1(2), 1993.

[2] E. Cantú-Paz. A survey of parallel genetic algorithms. Technical Report IlliGAL 97003, Illinois Genetic Algorithms Laboratory, University of Illinois at Urbana-Champaign, Urbana, IL, USA, 1997.

[3] K. Cetnarowicz and R. Dreżewski. The mechanism of supervising the evolution process realized in multi-agent world. In *Proc. of the 2nd Int. Conf. on Formal Methods and Intelligent Techniques in Control, Decision Making, Multimedia and Robotics*, Warszawa, 2000. Polish-Japanese Institute of Information Technology.

[4] K. Cetnarowicz, M. Kisiel-Dorohinicki, and E. Nawarecki. The application of evolution process in multi-agent world to the prediction system. In *Proc. of the 2nd Int. Conf. on Multi-Agent Systems — ICMAS'96*, Osaka, Japan, 1996. AAAI Press.

[5] K. A. De Jong. *An analysis of the behavior of a class of genetic adaptive systems*. PhD thesis, University of Michigan, Ann Arbor, Michigan, USA, 1975.

[6] M. Doebeli and U. Dieckmann. Evolutionary branching and sympatric speciation caused by different types of ecological interactions. Technical Report IR-00-040, International Institute for Applied Systems Analysis, July 2000.

[7] D. Goldberg. *Genetic Algorithms in Search, Optimization, and Machine Learning*. Addison-Wesley, 1989.

[8] D. E. Goldberg and J. Richardson. Genetic algorithms with sharing for multimodal function optimization. In J. J. Grefenstette, editor, *Proc. of the 2nd Int. Conf. on Genetic Algorithms*, Hillsdale, NJ, 1987. Lawrence Erlbaum Associates.

[9] D. E. Goldberg and L. Wang. Adaptive niching via coevolutionary sharing. Technical Report IlliGAL 97007, Illinois Genetic Algorithms Laboratory, University of Illinois at Urbana-Champaign, Urbana, IL, USA, 1997.

[10] J. H. Holland. *Adaptation in natural and artificial systems*. The University of Michigan Press, Ann Arbor, Michigan, USA, 1975.

[11] H. Krzanowska, A. Łomnicki, J. Rafiński, H. Szarski, and J. Szymura. *Zarys mechanizmów ewolucji*. PWN, Warszawa, 1997. In polish.

[12] S. W. Mahfoud. Crowding and preselection revisited. In R. Manner and B. Manderick, editors, *Parallel Problem Solving From Nature, 2*, Amsterdam, 1992. Elsevier Science Publishers (North Holland).

[13] S. W. Mahfoud. A comparison of parallel and sequential niching methods. In *Proc. of the 6th Int. Conf. on Genetic Algorithms*, 1995.

[14] S. W. Mahfoud. *Niching methods for genetic algorithms*. PhD thesis, University of Illinois at Urbana-Champaign, Urbana, IL, USA, 1995.

[15] O. J. Mengshoel and D. E. Goldberg. Probabilistic crowding: Deterministic crowding with probabilistic replacement. Technical Report IlliGAL 99004, Illinois Genetic Algorithms Laboratory, University of Illinois at Urbana-Champaign, Urbana, IL, USA, 1999.

[16] B. L. Miller and M. J. Shaw. Genetic algorithms with dynamic niche sharing for multimodal function optimization. Technical Report IlliGAL 95010, Illinois Genetic Algorithms Laboratory, University of Illinois at Urbana-Champaign, Urbana, IL, USA, 1995.