

**PROCEEDINGS OF THE
FOURTH INTERNATIONAL
CONFERENCE ON**

**GENETIC
ALGORITHMS**

University of California, San Diego
July 13-16, 1991

Editors/Program Co-Chairpersons:
Richard K. Belew
Lashon B. Booker

Supported By:
International Society for Genetic Algorithms
Office of Naval Research
Naval Research Laboratory

Morgan Kaufmann Publishers
San Mateo, California

Sponsoring Editor Bruce Spatz
Production Editor Yonie Overton
Cover Design Jo Jackson
Production Coordination Ocean View Technical Publications

Morgan Kaufmann Publishers, Inc.
Editorial Office:
2929 Campus Drive, Suite 260
San Mateo, CA 94403

© 1991 by Morgan Kaufmann Publishers, Inc.
All rights reserved
Printed in the United States of America

No part of this publication may be reproduced, stored in a retrieval system, or transmitted in any form or by any means—electronic, mechanical, photocopying, recording, or otherwise—without the prior written permission of the publisher.

94 93 92 91 5 4 3 2 1

Library of Congress Cataloging in Publication Data is available for this book.
ISBN 1-55860-208-9

A Naturally Occurring Niche & Species Phenomenon: The Model and First Results

Yuval Davidor

*Department of Applied Mathematics and Computer Science,
The Weizmann Institute, Rehovot 76100, Israel.
yuval@wisdom.weizmann.bitnet*

Abstract

A new concept for synthesizing the genetic operators is introduced in this paper. The novelty of the proposed model lies primarily in the way that the traditional genetic operators interact among themselves to optimize their effect. The model deals with three fundamental problems of GA applications and attempts: to offer an optimal algorithmic solution for controlled convergence, to achieve a natural emergence of a niche & species phenomenon on both the genotypical and fitness levels, and to separate the choice of representation from the applicability of controlled convergence operators. In other words, to provide a GA model which is based entirely on local, low computational cost operators which provide a more optimal information flow in a GA.

1 A Brief History Of GA Operators For The Control Of Convergence

Since the early days of the '70's, two important aspects about GAs were realized. One, that controlled convergence is an illusive goal, difficult to achieve. Two, that fine tuning of the GA operators is not a robust solution to the controlled convergence problem. In other words, it was realized that the operators themselves, through their mutual interaction, should provide an adaptive, and hopefully optimal, balance between the exploration and exploitation of the search space. Novel mechanisms to provide such a desirable controlled convergence property were suggested in recent years with varying degrees of success. The main idea is that there should be a mechanism that will control and prevent an unbalanced proliferation of genotypes. It is clear that such an operator can be imposed through an explicit testing of genotype diversity, but that such a mechanism is computationally prohibitive. The 'battle' for controlled convergence focuses on the attempt to obtain this property indirectly in order to minimize computational cost. The following is a brief history of the mechanisms that were suggested as an answer to the control of convergence issue.

Cavicchio, in his Doctoral dissertation , suggested a *preselection* mechanism as a mean of enhancing the maintenance of high genotype diversity. The preselection mechanism replaces parent members in the population with their offspring [Cavicchio, 1970].

De Jong's *crowding* scheme is an elaboration on the preselection mechanism. In the crowding scheme, an offspring replaces the most similar string in bit terms (hamming distance) from a randomly drawn subpopulation of size CF (crowding factor) from the main population. The more similar a member of the population becomes to other members in the population, it experiences a heavier selection pressure [DeJong, 1975]. The experimentally optimal size of the subpopulation was typically 3 when applied to De Jong's five-function test bed.

Booker implemented a *sharing* idea in a classifier system environment [Booker, 1982]. Booker's idea was that if related rules share payments (his classifier system used the bucket brigade mechanism), subpopulations of rules will form naturally in the system. However, it is difficult to apply this mechanism to standard GAs. Schaffer has extended the idea of subpopulations in his VEGA model in which each fitness element had its own subpopulation [Schaffer, 1984].

A different approach to help maintain high genotype diversity was introduced by Mauldin in his *uniqueness* operator [Mauldin, 1984]. The uniqueness operator helped to maintain diversity by incorporating a 'censorship' operator with which the insertion of an offspring into the population is possible only if the offspring is genetically different from all members of the population at a specified number of loci (hamming distance).

Recently Goldberg incorporated some of the ideas mentioned above in a mechanism he called a *sharing function* [Deb and Goldberg, 1989; Goldberg and Richardson, 1987]. This mechanism determines the reproduction probability according to the average fitness of similar strings in the population. The similarity criterion

can be either specified in terms of hamming distance in the genotype space, a metric distance in the phenotypic or fitness spaces. Experimental results from GAs running Goldberg's sharing function mechanism on function optimization problems exhibit good performance. However, sharing functions suffer from two problems. The major one being that genotypic sharing, which most effectively helps to maintain diversity, is computationally very expensive. The second drawback is the fact that the similarity criterion is not natural to the search space and therefore cannot emerge naturally from the interaction of the reproduction and selection mechanisms. The latter point becomes important when the search space is extensively multi-modal or incorporates some deception.

Although the above mechanisms partly improve the convergence, they suffer from the fact that they employ additional operators, sometimes at heavy additional computing costs, and they are not applicable to all problem domains. In other words, these models are effective for specific domains, but usually add computation complexity and, above all, do not provide a robust solution.

A novel attempt to put to use effectively some of the ideas mentioned above, in a parallel computer architecture environment led, Muhlenbein and Gorges-Schleuter to explore a particular hardware architecture called ASPARAGOS [Muhlenbein, 1989; Schleuter, 1989]. The underlying idea of ASPARAGOS is that subpopulations are held on a network of transputers, and act as interacting subpopulations. This topological arrangement of communicating subpopulations deals with an aspect of nature which is called speciation. Speciation refers to the occurrence of local optimization concurrent with global optimization. Members of a subpopulation adapt to a local optimum and then interact with other locally optimal members of other subpopulations. The main drawback of ASPARAGOS lies in its very merit – the fact that it relies on a particular (and expensive) hardware. There are other relevant works involving parallel implementations, but they are not referred to here because they recapitulate the essence of what was discussed earlier [Cohoon, et al., 1987; Jog and VanGucht, 1987; Pettey and Leuze, 1989; Tanese, 1989].

To summarize the state of the art in the field of co-evolution and controlled convergence, one has to acknowledge that there is no model which is hardware independent, capable of handling arbitrary representation formats (variable length, real value genes, etc.), and allows controlled convergence without substantially increasing computation overhead. This paper introduces a new GA model which addresses the controlled convergence problem through the introduction of a topological GA model in which speciation occurs naturally with minimal computation overhead.

2 From Population Dynamics To Controlled Convergence

There are certain assumptions regarding population genetics and population dynamics which affect the interactions between the genetic operators and the environment. Since these interactions have a major role in shaping evolution and its robust adaptive behaviour, they shall guide this work. A simplistic list of these assumptions is given below:

1. An individual's life can be characterized by three fundamental activities: foraging, mating, and winning conflicts.
2. The cost of foraging is proportional to search efforts (distance of travel, etc.).
3. Mating partners are selected from the local environment, and proportionally to fitness.
4. Offspring remain in the geographical vicinity of their parents.
5. Good habitats are more likely to be inhabited by stronger individuals.
6. The frequency of aggressive conflicts is inversely proportional to resource availability.
7. Agresive conflicts are resolved probabilistically depending on the relative strengths of the opponents.

It is clear from the above list that the behaviour of the individual is a result of mechanisms which rely only on local information. Mechanisms which at best have complete information about the individual's local environment, but in many cases only have partial view even of their immediate surroundings.

3 The Basic Idea Of The ECO Genetic Algorithm

Rather than being held as an indistinguishable (apart from fitness) collection of strings in the traditional GA models, the population of strings is held on a 2-D grid having its opposite edges connected together so that each grid element has 8 adjacent elements (Figure 1). At initialization, strings are placed on the grid at random, but no more than one string per grid element.

This GA model is a steady-state GA [Syswerda, 1989; Syswerda, 1990; Whitley, 1989], and its reproduction part is slightly different than what commonly used. Nevertheless, and as will be shown latter, the ECO GA reproduction follows the schema theorem ideology. A grid element is selected at random, and defines a 9-element sub-population around it (Figure 2). For this sub-population, the reproduction cycle proceeds as in a simple GA having the population size set to 9. Two strings are selected probabilistically from this sub-population

according to their relative fitness. Mutations, if turned on, occur at the duplication phase with probability P_m per locus. The offspring are put back into the 9-element sub-population, so that they are more likely to stay in the vicinity of their parents. Placing an offspring on a grid element which is already occupied by an 'adult' string initiates a conflict between that string and the offspring. Once initiated, conflicts are resolved probabilistically according to relative fitness of the opponents so that the probability of string i to survive a conflict with string j is proportional to its relative strength.

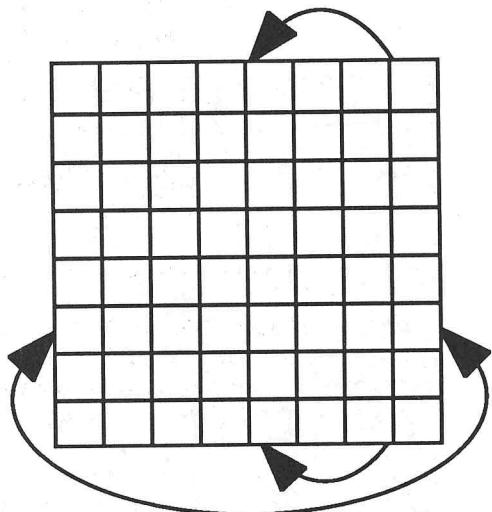


Figure 1 – The 2-D grid on which the population is stored. The opposite edges are connected and form a torus.

The schema theorem for this model becomes,

$$m(H,t+1) \geq m(H,t) + \quad (1a)$$

$$+ m(H,t) \frac{f(H)}{\bar{f}} - \quad (\text{due to replication}) \quad (1b)$$

$$- m(H,t) \frac{f(H)}{\bar{f}} P_m o(H) - \quad (\text{due to mutations}) \quad (1c)$$

$$- m(H,t) \frac{f(H)}{\bar{f}} P_c P_d P_h - \quad (\text{due to crossover}) \quad (1d)$$

$$- m(H,t) \frac{f(H)}{\bar{f}} [P_m o(H) + P_c P_d P_h] [1 - P_h] \frac{\bar{f}}{f(H) + \bar{f}} \quad (\text{due to conflicts}) \quad (1e)$$

where all arguments follow the conventional notation apart from the generation time, the probability P_h , and the average fitness \bar{f} .

The first term (Eq. 1a) involves the future frequency of schema H and its present frequency. The notation here for generation time is based on a steady-state GA model

which designates an update of the adult population reproduction probability profile [Davidor, in preparation]. The second term (Eq. 1b) designates the growth due to replication. Since the reproduction potency $R_{i,j}$ of a string $S_{i,j}$ is based only on the string's fitness $f_{i,j}$ in its local sub-population grid environment so that,

$$R_{i,j} = \frac{f_{i,j}}{\sum_{k=i-1}^{i+1} \sum_{m=j-1}^{j+1} f_{k,m}},$$

the average fitness of strings in the vicinity of strings containing schema H is,

$$\bar{f} = \frac{1}{m(H,t)} \sum_{S_{i,j} \in H} R_{i,j},$$

which is similar to the conventional average fitness \bar{f} used in the schema theorem, but converges more quickly (to either 1 or 0) as the search progresses. This aspect – quick, but local convergence – is the central theme of this work. It is based on the rational (and on widely documented experiments [Goldberg, 1989; Schaffer, et al., 1989]) that a simple GA operating on a finite population converges in finite time due to irreversible loss of diversity. As convergence time in a simple GA is proportional primarily to the population size, one can view the ECO GA as a model which uses a very small population size, and hence, converges quickly (see the discussion on optimal population sizes in [Goldberg, 1989]). Nevertheless, the ECO GA is not just a multi subpopulation GA. It has an implicit parallel overlapping subpopulations which evolve locally, but allow information to flow in the form of migration to adjacent grid elements.

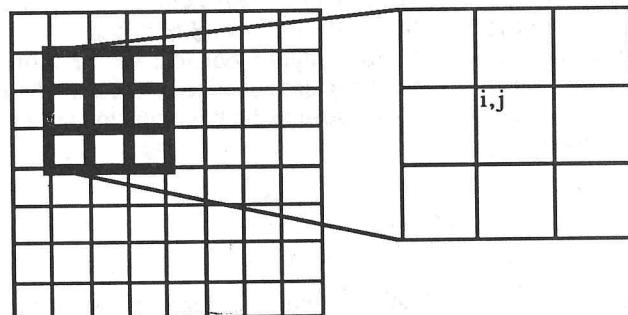


Figure 2 – The local environment of the grid element (i,j) which determines its replication potency, natural selection as a result of conflicts, and the gene pool for mating.

The third term on the right (Eq. 1c) designates the loss of schema instances due to mutations, and is the same as given in the basic schema theorem.

The fourth term on the right (1d) is the loss of schema instances due to recombination. This amounts to the number of offspring containing the given schema, times the probability a crossover was used (P_c), times the probability to disrupt the schema due to the type of crossover mechanism used (P_d), times the probability that the schema is mated with a string which does not contain the schema (P_h) [Spears and DeJong, in press]. Both P_c and P_d are as used in the schema theorem (for example, for a single-point uniform distributed crossover $P_d = \frac{8H}{l-1}$. See also [Bridges and Goldberg, 1987]).

The new probability element, P_h , designates the probability that the string which is selected as a mating partner contains a different schema than that under consideration. Though missing in Holland's original formulation, this probability is important for generating a more accurate prediction on schemata sampling, and in particular for this model. The probability of mating with a specific schema was already partly addressed in the context of a simple GA [Bridges and Goldberg, 1987]. Estimating P_h for this model has an added importance since it explains the emergence of niches, and other properties mentioned earlier.

P_h is dependent on the distribution of the $m(H,t)$ in the grid. The P_h probability of any schema at any time interval, $p_h(H,t)$, is bounded by the two extreme arrangements possible for its $m(H,t)$ members. One which packs the schema members together resulting in a minimal interaction with other schemata, and one which spreads the schema members as far apart as possible, an arrangement which maximizes the interaction with other schemata. These two extreme arrangements correspond to minimal and maximal $p_h(H,t)$ values. A conservative value of $p_h(H,t)$ is obtained when all $m(H,t)$ members have no other $m(H,t)$ member adjacent to them, an arrangement which results in $p_h(H,t) \leq 1$. This however is a rather strict upper bound and the more realistic value is the average case obtained from a random distribution of $m(H,t)$ members which is equal to the case of simple GA, hence

$$p_h(H,t) \leq 1 - \frac{m(H,t) f(H)}{n} .$$

On the other hand, at the minimal interaction when the $m(H,t)$ members are tightly packed together, only members on the perimeter of the homogeneous pack (the interface ring of grid elements) can interact with a different schemata. Hence, the lower bound of $p_h(H,t)$ is,

$$\left(4(\sqrt{m(H,t)} - 2)\frac{3}{8} + 4\frac{5}{8}\right) \leq p_h(H,t) , m(H,t) < (\sqrt{n} - 2)$$

which is a good approximation for the lower bound (derived from the number of $m(H,t)$ members on the perimeter of a $\sqrt{m(H,t)} \times \sqrt{m(H,t)}$ cube and the number of different schemata they can interact with).

The last term (Eq. 1d) is the schema loss due to conflicts. This loss is the compound effect of the total number of offspring produced at the current time step, times the probability that an offspring contains a different schema, times the probability it is conflicting with a string containing schema H , times the probability it wins the conflict.

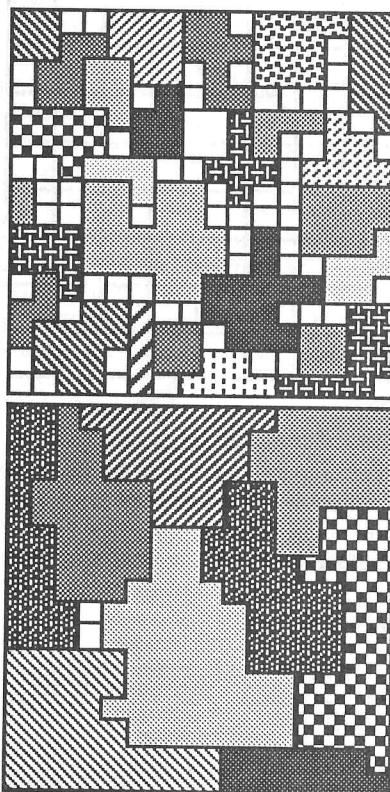


Figure 3 – The emergence of genotypically similar islands in the grid system. Above, at an early stage of the simulation, while on the bottom can be seen an advanced stage of island growth.

4 Niche & species emerge naturally in the ECO GA

At initial stages of the search, schemata sampling rate in the ECO GA is very similar to that in a SGA. However, islands of growing genotypic and fitness homogeneity emerge relatively quickly in comparison to the convergence in a SGA of the same population size. These islands represent near local optimum. As the search advances, These islands of near optimum strings mature

and approach local optimality. Certain islands of highly fit strings (schemas) take-over lower fitness islands which are in their vicinity (Figure 3). Thus, an hierarchical growth and convergence is maintained until the entire grid is occupied by one schema.

It is important to notice the effect of the different operators while local genotypically/fitness islands emerge. One, proliferation of the dominating string/schemata within an island is reduced since its potency factor $R_{i,j} \rightarrow 1$. This leads to a global control over highly fit schemata. Two, the disruption due to recombination is reduced substantially within islands since $p_h \rightarrow 0$, and so does the probability of schema elimination due to conflicts. At this stage, a balance between schema growth and elimination within the islands is reached, and mutations introduce low probability perturbations for greedy optimization.

This process enables the concurrent assessment of highly fit schemata, without having to pay the price of global operators or unnecessarily risking premature convergence. Furthermore, it provides a natural balance between the effect of mutations recombination, and selection.

5 Initial trials

Initial experiments with the ECO GA model are presented in this section primarily to demonstrate the quality of naturally emerging niches. The model is applied to a demonstrative multi-modal function optimization problem with a standard binary representation. The function, $f(x) = e^{-\left(\frac{x-0.1}{0.8}\right)^2} \sin^6(5\pi x)$, is similar to the type of functions used to analyze and demonstrate the effect of controlled convergence operators [Goldberg and Richardson, 1987].

The ECO GA model used here was not tailored to achieve high performance. The main purpose is to demonstrate the workings of the new model, and primarily the emergence of niche & species phenomenon. To this end, the results presented here intend only to show the basic behaviour of the ECO GA.

When the distribution of strings in the grid is chaotic and rugged, islands of similar genotypes/phenotypes/fitness are expected to be present. Such a distribution is expected to be present during initial stages of ECO GA run. Figure 4 presents a contour map of the phenotype distribution in the grid after 500 evaluations. This map shows the beginning of island formation, though in general the distribution of phenotypic values is still quite chaotic.

On the other hand, after 5000 evaluations were performed, the grid contains phenotypically flat regions (phenotypic value plateaus). This is demonstrated in Figure 5.

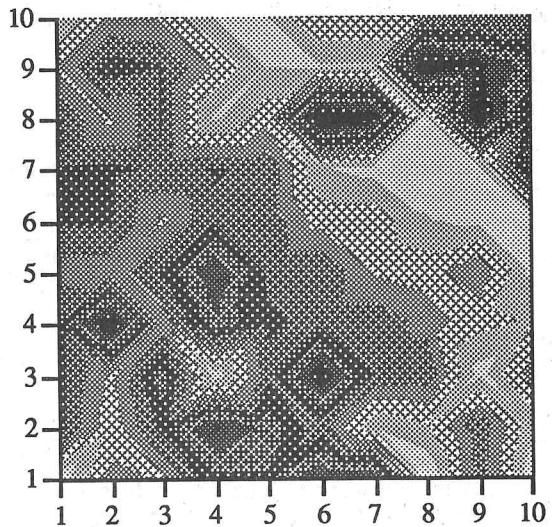


Figure 4 – A contour map of the phenotypic values in the 2D grid system after 500 evaluations (the light colours indicate low values and solid black indicates values between 0.9 and 1.0. The surface is quite rugged indicating that island of similar strings have not been formed yet, or that they are relatively small.

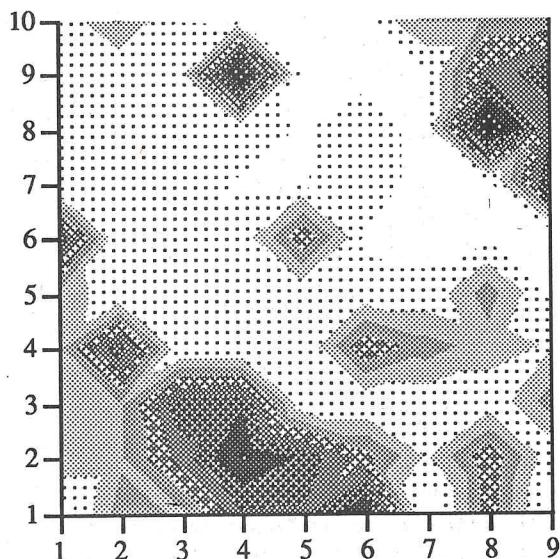


Figure 5 – After 5,000 evaluations one can easily observe large regions of phenotypically similar strings indicating that islands of similar strings have been formed. Also, the dominating phenotypic values concentrate at low values which corresponds to the global optimum of the fitness function.

6 Summary

The ECO GA model discussed in this paper presents a new synthesis of the conventional genetic operators. In this model all operators are based on local interaction among strings in a 2D grid system. The decision on a 2D topology rather than an n-dimensional grid system is not arbitrary. The number of dimensions in the topology determines the size of the sub-population (3 for 1D, 9 for 2D, 27 for 3D, and so forth). The 2D configuration was chosen to achieve a balance between the overall number of sub-populations and their size. This new population interaction arrangement results in a GA model which allows a rapid local convergence. The local convergence produces a niche & species like behaviour. Concurrent to the local convergence within niches, global optimum is obtained through the interaction among the locally optimized strings.

This work did not include a performance comparison study between conventional GA and the ECO GA. Though more experimental work is necessary before a conclusive assessment of the ECO GA model is possible, initial results indicate that this model improves on the problems associated with controlling the convergence. Furthermore, this model can be immediately applied to most parallel architectures.

The ECO GA model as presented, does not claim to maintain niche & species *ad infinitum*. Rather, it allows niches to emerge in order to enhance the efficiency and robustness of a GA search. To achieve a complete niche & species equilibrium, additional operators are needed. Another aspect of the model is the implicit small population size used for local convergence. Since all of the genetic operators are local, the effective population size to be considered for convergence is much smaller than the actual grid capacity. The small population size aspect conforms to recent experimental and theoretical results which suggest that multiple small population runs are more effective than a few larger population runs [Goldberg, 1989].

The author is currently involved in extending the research on ecological models of GAs in two directions. One, gathering additional experimental data comparing the ECO GA model to a SGA. Two, extending the basic model to a model which exhibits a complete niche & species behaviour, and is able to maintain niches at equilibrium.

Acknowledgements

Preparation of this article was supported in part by the Centre for Absorption in Science, The Ministry of Immigrant Absorption, The State of Israel. Y. Davidor is a recipient of a Sir Charles Clore Fellowship.

References

- Booker, L. B. (1982) Intelligent behavior as an adaption to the task environment, (Doctoral dissertation, University of Michigan) *Dissertation Abstracts International*, 43(2), 469B
- Bridges, C. L. and Goldberg, D. E. (1987) An analysis of reproduction and crossover in a binary-coded genetic algorithms, *2nd International Conference on Genetic Algorithms*, 9-13
- Cavicchio, D. J. (1970) Adaptive search using simulated evolution, (Doctoral dissertation, University of Michigan) *Unpublished doctoral dissertation*
- Cohoon, J. P., et al. (1987) Punctuated equilibria: A parallel genetic algorithm, *2nd International Conference on Genetic Algorithms*, 148-154
- Davidor, Y., and Syswerda, G., (in preparation). *Analytical and experimental comparison between generational and steady-state genetic algorithm*.
- Deb, K. and Goldberg, D. E. (1989) An investigation of niche and species formation in genetic function optimization, *3rd International Conference on Genetic Algorithms*, 42-50
- DeJong, K. (1975) An analysis of the behavior of a class of genetic adaptive systems, (Doctoral dissertation, University of Michigan) *Dissertation Abstracts International* 36(10), 5140B
- Goldberg, D. E. (1989) Sizing population for serial and parallel genetic algorithms, *3rd International Conference on Genetic Algorithms*, 70-79
- Goldberg, D. E. and Richardson, J. (1987) Genetic algorithms with sharing for multimodal function optimization, *2nd International Conference on Genetic Algorithms*, 41-49
- Jog, P. and VanGucht, D. (1987) Parallelisation of probabilistic sequential search algorithms, *2nd International Conference on Genetic Algorithms*, 170-176
- Mauldin, M. L. (1984) Maintaining diversity in genetic search, *National Conference on Artificial Intelligence*, 247-250
- Muhlenbein, H. (1989) Parallel genetic algorithms, population genetics and combinatorial optimization, *3rd International Conference on Genetic Algorithms*, 416-421

Pettey, C. C. and Leuze, M. R. (1989) A theoretical investigation of a parallel genetic algorithm, *3rd International Conference on Genetic Algorithms*, 398-405

Schaffer, J. D. (1984) Some experiments in machine learning using vector evaluated genetic algorithms, (Doctoral dissertation, Vanderbilt University)
Unpublished

Schaffer, J. D., et al. (1989) A study of control parameters affecting online performance of genetic algorithms for function optimization, *3rd International Conference on Genetic Algorithms*, 51-60

Schleuter, M. G. (1989) ASPARAGOS, An asynchronous parallel genetic optimization strategy, *3rd International Conference on Genetic Algorithms*, 422-427

Spears, W. M. and DeJong, K. A. (in press) An analysis of multi-point crossover, *International Workshop on the Foundations of Genetic Algorithms*,

Syswerda, G. (1989) Uniform crossover in genetic algorithms, *3rd International Conference on Genetic Algorithms*, 2-9

Syswerda, G. (1990) A study of reproduction in generational and steady state genetic algorithms, *International Workshop on the Foundations of Genetic Algorithms*,

Tanese, R. (1989) Distributed genetic algorithms, *3rd International Conference on Genetic Algorithms*, 434-439

Whitley, D. (1989) The GEnitor algorithm and selection pressure: Why rank-based allocation of reproductive trials is best, *3rd International Conference on Genetic Algorithms*, 116-123