

Multi-Parent's Niche: n-ary Crossovers on NK-Landscapes

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Abstract. Using the multi-parent diagonal and scanning crossover in GAs reproduction operators obtain an adjustable arity. Hereby sexuality becomes a graded feature instead of a Boolean one. Our main objective is to relate the performance of GAs to the extent of sexuality used for reproduction on less arbitrary functions than those reported in the current literature. We investigate GA behaviour on Kauffman's NK-landscapes that allow for systematic characterization and user control of ruggedness of the fitness landscape. We test GAs with a varying extent of sexuality, ranging from asexual to 'very sexual'. Our tests were performed on two types of NK-landscapes: landscapes with random and landscapes with nearest neighbour epistasis. For both landscape types we selected landscapes from a range of ruggednesses. The results confirm the superiority of (very) sexual recombination on mildly epistatic problems.

1 Introduction

In previous papers the multi-parent scanning crossover and diagonal crossover were tested on numerical optimization problems, [3, 4, 5]. These tests were performed on a test suite of common EA test functions, still they were chosen somewhat arbitrarily, moreover the types of fitness landscapes they span are difficult to characterize. It was therefore not possible to look for 'multi-parent's niche', [6], in a systematic way. For a better analysis of the behaviour of GAs with multi-parent recombination a systematic way of defining different fitness landscapes was necessary. We found such a way in using NK-landscapes that allow characterization and user control of ruggedness of the fitness landscape, [10]. We define what NK-landscapes are in Section 2. We give a brief overview of multi-parent operators in EA in Section 3. Thereafter in Section 4 we describe the experimental setup, and in Section 5 we summarize the test results. Finally, we draw conclusions and sketch further research in Section 6.

2 NK-landscapes

The family of NK-landscapes was introduced by Kauffman as a class of problems where the fitness landscape can be gradually tuned from smooth to chaotic, [10]. The parameters N , respectively K specify the total number of bits (which will equal the chromosome length in the GA searching this landscape) and the

number of bits that influence a particular bit. The same K is used for each bit $x_i (i = 1, \dots, N)$, although the bits that influence x_i differ for every i . Actually, K determines the degree of epistatic interactions between bits. For a certain N , K can be gradually increased from 0 to $N - 1$ leading to more and more epistasis, thereby decreasing the fitness correlation between neighboring points. Thus, for higher K 's the landscape becomes more rugged.

Formally, using the NK-model each bit x_i of a bitstring \bar{x} of length N is given a user defined fitness f_i and the fitness of \bar{x} (to be maximized) is defined as the average of the fitness of its bits, i.e.,

$$f(\bar{x}) = 1/N \cdot \sum_{i=1}^N f_i$$

The fitness f_i of x_i depends on K other bits x_{i_1}, \dots, x_{i_K} , that is f_i is context dependent, where a context is a certain configuration of the values x_{i_1}, \dots, x_{i_K} . Therefore, a lookup table of 2^{K+1} rows (2^K different contexts and 2 values for x_i) is needed to specify f_i . This lookup table is created by assigning each entry a random number between 0 and 1 drawn from a uniform distribution. If the bits that determine the fitness of x_i are chosen randomly, we have random neighbor interaction (RNI). If the interacting bits are the ones closest to x_i (assuming x_1 and x_N are neighbors) then we have nearest neighbor interaction (NNI).

NK-landscapes were used to investigate the relationship between characteristics of the fitness landscape and the performance of genetic operators, [11]. In [9] the usefulness of recombination is assessed comparing different (2 parent) crossovers and hill climbing on NK-landscapes with various ruggedness. Here we conduct an 'introspective' study, concentrating on crossover itself. In particular, we compare reproduction mechanisms where the extent of sexuality varies.

3 Multi-parent recombination

Genetic operators in EAs traditionally mimic natural reproduction mechanisms. Unary operators, such as mutation, correspond to asexual, while binary operators, such as crossover, correspond to sexual reproduction. Mutation is always used in an EA, recombination can be either used or not. In this sense sexuality is a Boolean feature: on or off. By the generalization of the binary n-point and uniform crossovers to diagonal, resp. scanning crossover (see below) recombination operators obtain an adjustable arity. Thus, sexuality loses its Boolean character and becomes a graded feature. So, the old question whether 'sexual reproduction is good or not' can be refined to 'how much sex is good'.

The first multi-parent mechanism was global recombination in ES, [1, 14] that produces one new individual that may inherit genes from more than two parents. Nevertheless, the number of parents is not determined, thus global recombination does not make sexuality a graded feature. The same holds for the recently introduced multi-parent Gene Pool Recombination [12, 17] and the Gene Linkage method [15] in GAs. A new extension of ES, the $(\mu/\rho, \lambda)$ multirecombinant strategy [2], does apply an adjustable operator arity ρ .

The first general multi-parent operators with adjustable arity in GAs are scanning crossover and diagonal crossover, introduced in [3] and further studied in [4, 5]. Scanning crossover generalizes uniform crossover, although creating only one child, by choosing one of the i -th genes of the n parents to be the i -th gene of the child. The choice can be random, based on a uniform distribution (uniform scanning), or biased by the fitness of the parents (fitness based scanning). It can also be deterministic, based on the number of occurrences of the genes (occurrence based scanning). Diagonal crossover generalizes n -point crossover by selecting $(n - 1)$ crossover points in the n parents and composing n children by taking the resulting n chromosome segments from the parents 'along the diagonals'. Figure 1 illustrates this idea.

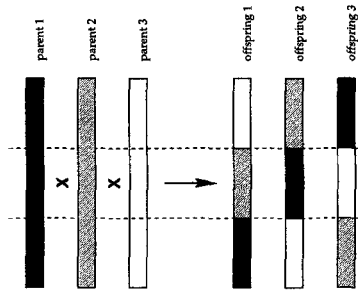


Fig. 1. Diagonal crossover with three parents

4 Experiment setup

In our experiments $N = 100$. We use two test suites, one with NNI and one with RNI. In both test suites we have landscapes for $K = 0, 1, 2, 3, 4, 5, 25$. For higher values, like $K = 50, 99$ it was shown in [9] that GAs cannot treat them well, therefore they are not tested here. Let the number of parents be denoted by P , the type of crossover operator by C and the type of epistatic interaction by I . For every combination of $\langle I, K \rangle$ 10 landscapes are generated and each test, i.e. each combination $\langle C, P \rangle$, is ran 10 times on each landscape. This results in 100 tests for each 4-tuple $\langle I, K, C, P \rangle$. We test 2, 4, 6, 8, 10, 12, 14 and 16 parents for both operators. (The NK-landscape generator can be ftp-ed from [ftp.santafe.edu](ftp:santafe.edu), [/pub/terry/nk/nklandscapes.tar.gz](ftp://pub/terry/nk/nklandscapes.tar.gz).)

The performance of the GA is measured by the mean distance percentage from the global optimum of the best individual at the end of the evolution. Since the global optimum of an NK-landscape is hard to find we assume the global optima to be the highest fitness found in all runs for a certain pair $\langle N, K \rangle$. When K increases, the validity of this assumption decreases. We performe maximization on the generated landscapes, hence the distance percentage is computed by

$$\Delta = \frac{f_{optimal} - f_{obtained}}{f_{optimal}} \times 100$$

chrom. length	100
GA type	steady state
crossover operator	diagonal crossover, uniform scanning
crossover rate	0.7
mutation rate	0.01 ($1/\text{chrom.length}$)
selection mechanism	linear rank biased (bias = 1.2)
pool size	200
stop condition	70.000 function evaluations

Table 1. GA setup

and for every combination $\langle I, K, C, P \rangle$ the Δ value presented in this article is the average over 100 tests.

Notice that using diagonal crossover the number of children equals the number of parents, hence M parent individuals are consulted for M fitness evaluations. Scanning creates one child of n parents, thus $n \cdot M$ parent individuals are consulted for M fitness evaluations. This could give scanning an 'unfair' advantage. On the other hand, the generation gap in the steady state GA we use is 1 for scanning and equals n for diagonal crossover. In a homogeneous population this results in *one* new (mutated) individual for scanning and n new individuals for diagonal crossover. This can be advantageous for diagonal crossover. To eliminate this effect we also tested a modified version of diagonal crossover that creates only one child, the one along the main diagonal.

5 Experimental results

In figures 2 to 7 the performance results are given in a graphical form. The Δ values (vertical axis) are plotted against the number of parents used for crossover (horizontal axis). The results for $K = 0$ are not displayed, because every run terminated with the optimum. The figures show that the best performance was always achieved by a crossover using more than two parents.

We also tested asexual evolution, i.e. using only mutation. In Table 2 and Table 3 we present a comparison of asexual, (mutation only), sexual (2 parents) and 'very sexual' (16 parents) evolutions. For the sake of clarity, let's remark that in the latter two cases we used crossover **and** mutation and that we did not fine tune operator probabilities because of the extreme computational overhead.

To see regularities in the outcomes better we calculated the *gain in performance* when changing operator arities. $\Gamma_{1vs.2}^{\Delta} = ((\Delta^{mut} - \Delta_2)/\Delta^{mut}) \times 100$ is the gain in performance in terms of effectivity (Δ 's) when shifting from asexual to 2-parent sexual reproduction. Similarly, $\Gamma_{2vs.16}^{\Delta} = ((\Delta_2 - \Delta_{16})/\Delta_2) \times 100$. We also observed that not only the mean distance percentage from the optimum is improving when using more parents, but also the standard deviation w.r.t. this mean. Tables 4 and 5 also show the gain of performance in terms of standard deviation results (σ 's). As reference point we added the absolute σ values for mutation.

The results show that more parents do not only cause more effective search,

K	$\Delta^{mutation}$	$\Delta_2^{diagonal}$	$\Delta_{16}^{diagonal}$	$\Delta_2^{scanning}$	$\Delta_{16}^{scanning}$
1	0.407	0.126	0.004	0.119	0.110
2	1.765	0.843	0.344	1.020	0.837
3	2.824	1.547	0.710	2.193	1.872
4	4.069	2.630	1.340	3.478	3.260
5	5.098	3.377	2.317	4.624	4.681

Table 2. Mean distance percentage (Δ) from the global optimum of the best individual for asexual (mutation only), sexual (2 parents) and 'very sexual' (16 parents) reproduction on NNI

K	$\Delta^{mutation}$	$\Delta_2^{diagonal}$	$\Delta_{16}^{diagonal}$	$\Delta_2^{scanning}$	$\Delta_{16}^{scanning}$
1	0.310	0.277	0.171	0.167	0.153
2	1.817	1.173	0.852	0.857	0.907
3	3.208	3.059	2.083	2.395	2.144
4	4.328	4.328	3.139	3.742	3.375
5	4.808	4.856	4.837	4.400	4.271

Table 3. Mean distance percentage (Δ) from the global optimum of the best individual for asexual (mutation only), sexual (2 parents) and 'very sexual' (16 parents) reproduction on RNI

i.e. better approximation of the optimum (lower Δ 's), but also a more robust search, i.e. lower σ 's. However, there was a difference between the two test suites and the two crossovers. The highest gain in performance of using more parents is achieved on NNI (by diagonal crossover), the gains on RNI are smaller. Conform to our expectations diagonal crossover was better than scanning on NNI, while for RNI scanning proved to be better, at least for low K 's (Fig. 5, 6).

Looking at the operators, we see that the performance of diagonal crossover is (quasi) monotonously increasing with the number of parents for NNI and, although less consistently, also for RNI with lower K 's (Figures 2-7). We might get the impression that the curves of diagonal crossover are flattening as K grows. This is however caused by the different scales of the figures. Table 2-5 make clear that the absolute gain in performance increases while the relative gain decreases when K goes from 1 to 4. For uniform scanning the gains in performance are smaller and cannot be so simply related to the number of parents. This suggest that just a slight and inconsistent gain in effectivity can be expected from increasing the number of parents within the scanning scheme. Since uniform scanning is very similar to discrete global recombination in ES, this observation seems to confirm the experiences of Schwefel, [14] p. 146.

It is clear from the results that the GA performance becomes worse on more rugged landscapes. In this sense the multi-parent operators show similar behavior to the standard crossovers, [9].

	K	$\Gamma_{1vs.2}^{\Delta}$	$\Gamma_{2vs.16}^{\Delta}$	σ_{mut}	$\Gamma_{1vs.2}^{\sigma}$	$\Gamma_{2vs.16}^{\sigma}$
diag	1	69%	97%	0.381	39%	100%
	2	52%	59%	0.953	29%	41%
	3	45%	54%	1.147	35%	30%
	4	35%	49%	1.473	24%	32%
	5	34%	31%	1.536	14%	10%
scan	1	71%	8%	0.381	44%	13%
	2	42%	18%	0.953	26%	4%
	3	22%	15%	1.147	6%	19%
	4	14%	6%	1.473	6%	8%
	5	9%	-1%	1.536	-7%	7%

Table 4. NNI: gain in performance when switching from 1 to 2, resp. from 2 to 16 parents, w.r.t. the Δ values and the standard deviation of the Δ values (σ 's)

	K	$\Gamma_{1vs.2}^{\Delta}$	$\Gamma_{2vs.16}^{\Delta}$	σ_{mut}	$\Gamma_{1vs.2}^{\sigma}$	$\Gamma_{2vs.16}^{\sigma}$
diag	1	11%	38%	0.308	-1%	29%
	2	35%	27%	1.188	24%	26%
	3	5%	32%	1.671	8%	30%
	4	0%	27%	1.567	-22%	17%
	5	-1%	0%	1.647	-16%	5%
scan	1	46%	8%	0.308	21%	26%
	2	53%	-6%	1.188	42%	2%
	3	25%	10%	1.671	27%	7%
	4	14%	10%	1.567	-9%	16%
	5	8%	3%	1.647	-19%	14%

Table 5. RNI: gain in performance when switching from 1 to 2, resp. from 2 to 16 parents, w.r.t. the Δ values and the standard deviation of the Δ values (σ 's)

6 Conclusions and future work

Using diagonal and scanning crossover reproduction operators obtain an arity that can be set by the user, thus sexuality becomes a graded feature in EAs. Our main objective in this investigation was to relate the performance of EAs to the extent of sexuality used for reproduction on less arbitrary functions than those reported in the current literature. We performed experiments in a strict GA setting using 'pure' bit-problems with tunable ruggedness. The results showed that sexual reproduction (in combination with mutation) is better than asexual reproduction (mutation only). Besides, we found that operators with a higher arity lead to better performance. Roughly speaking we observed that sex is good and more sex is even better.

Nevertheless, there are differences between the two operators we tested. Even though scanning achieves the best performance with more than two parents it shows no consistent improvement when the number of parents is increased. The lack of correlation between the number of parents and performance occurred for

both types of epistatic interactions and for every level of ruggedness. However, using other choice mechanisms within the scanning scheme (e.g. occurrence based or fitness based) may lead to different results. For diagonal crossover we could establish the advantages of more parents. Additionally, based on these experiments we can draw conclusions on the most promising area of application. On mildly epistatic problems it is worth to generalize the standard 2-parent crossover and to use diagonal crossover with higher n 's instead. If moreover the interacting genes are close to one another, the gains of diagonal crossover are higher and come more consistently with increasing the number of parents than for a random spreading of interacting genes. The one-child version of diagonal crossover showed no significant difference in performance. This rejects the hypothesis that the source of diagonal crossover's success is the bigger generational gap.

So far, we have an explanation for some of our observations only. The advantage of more parents is most probably caused by the higher mixing of genes and the usage of a bigger sample (more parents) from the search space to base decisions upon. However, we cannot explain why using more parents consistently improves the performance of diagonal crossover and not the performance of uniform scanning. To answer this question we need additional tests. For instance looking at other performance measures, like speed or success rate, can supply additional information.

The explanation for the performance differences between the two crossovers on NNI respectively RNI is rather straightforward. On NNI landscapes diagonal crossover outperforms uniform scanning, because it is better at preserving alleles that are near each other in the representation. Uniform scanning on the other hand, is better in preserving alleles that are spread all over the chromosome, and therefore outperforms diagonal crossover on RNI landscapes. In other words: both perform better on landscapes where they are better at preserving epistatically interacting alleles.

Our results can also be related to those of Hordijk and Manderick [9], who concluded that sexual recombination is useful for low and medium epistasis (not very rugged landscapes). We found that on these very problems a generalization of 1-point 2-parent crossover (that they use) to n -parent diagonal crossover increases GA performance. Also the results of Schaffer and Eshelman, [13], come into mind looking at our observations. They conclude that crossover is useful on mildly epistatic non-deceptive problems. On such problems it is worth to use more parents (within the diagonal scheme), that is 'multi-parent's niche' is (at least) as big as usual crossover's niche, but comes with higher performance.

There is a growing number of studies on the usefulness of sexual recombination. Besides those within the GA paradigm [6, 13, 16], also comparisons of GAs and EP (where no recombination is used) have been performed. The results in [7, 8] indicate that EAs with mutation only can be better than EAs with crossover and mutation. Our observations on multi-parent crossovers and the comparisons between asexual and sexual reproduction can give new ammunition for the supporters of crossover. Further research is planned to compare asexual, sexual and 'very sexual' operators in EAs using floating point representations.

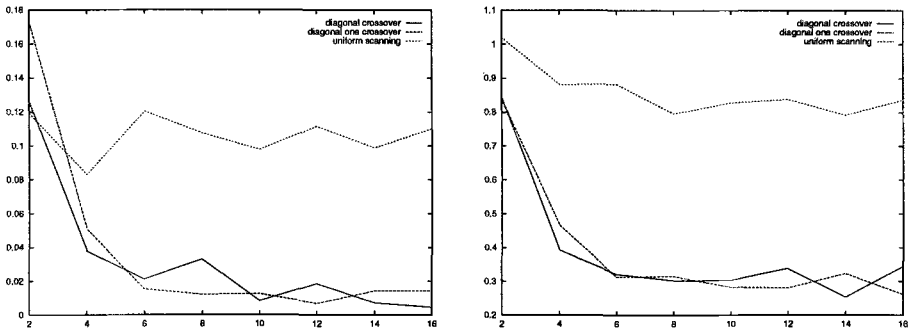


Fig. 2. NNI: mean distance percentage from global optimum (Δ_i) plotted against the number of parents (i) for $K = 1$ and $K = 2$.

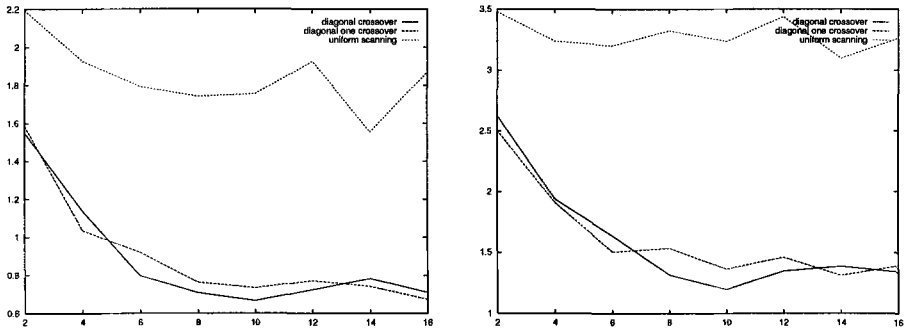


Fig. 3. NNI: mean distance percentage from global optimum (Δ_i) plotted against the number of parents (i) for $K = 3$ and $K = 4$.

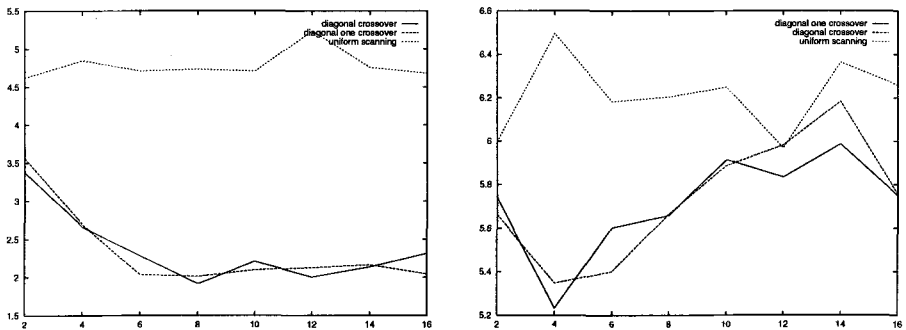


Fig. 4. NNI: mean distance percentage from global optimum (Δ_i) plotted against the number of parents (i) for $K = 5$ and $K = 25$.

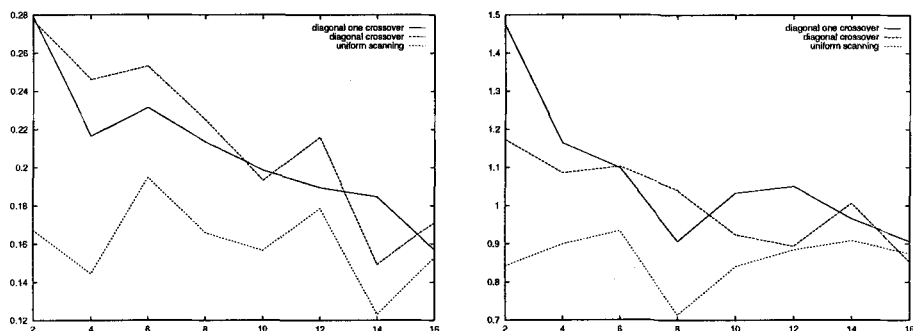


Fig. 5. RNI: mean distance percentage from global optimum (Δ_i) plotted against the number of parents (i) for $K = 1$ and $K = 2$.

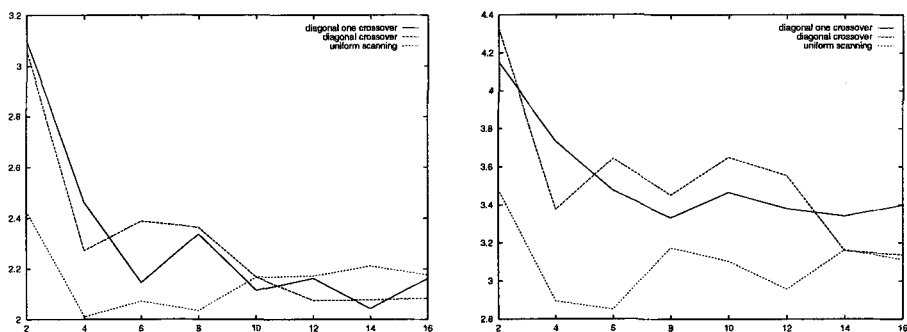


Fig. 6. RNI: mean distance percentage from global optimum (Δ_i) plotted against the number of parents (i) for $K = 3$ and $K = 4$.

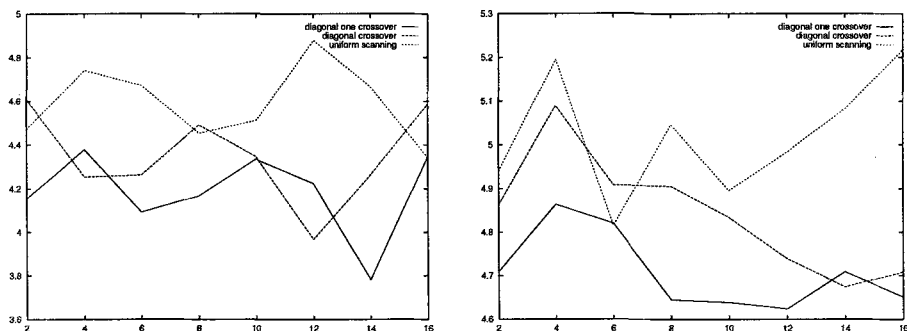


Fig. 7. RNI: mean distance percentage from global optimum (Δ_i) plotted against the number of parents (i) for $K = 5$ and $K = 25$.

References

1. T. Bäck and H.-P. Schwefel. An overview of evolutionary algorithms for parameter optimization. *Journal of Evolutionary Computation*, 1:1–23, 1993.
2. H.-G. Beyer. Toward a theory of evolution strategies: On the benefits of sex- the $(\mu/\mu, \lambda)$ theory. *Journal of Evolutionary Computation*, 3(1):81–111, 1995.
3. A.E. Eiben, P-E. Raué, and Zs. Ruttkay. Genetic algorithms with multi-parent recombination. In *Parallel Problem Solving from Nature - 3, LNCS 866*, pages 78–87. Springer-Verlag, 1994.
4. A.E. Eiben and C.H.M. van Kemenade. Performance of multi-parent crossover operators on numerical function optimization problems. Technical Report TR-95-33, also as <ftp://ftp.wi.leidenuniv.nl/pub/CS/TechnicalReports/1995/tr95-33.ps.gz>, Leiden University, 1995.
5. A.E. Eiben, C.H.M. van Kemenade, and J.N. Kok. Orgy in the computer: Multi-parent reproduction in genetic algorithms. In *Third European Conference on Artificial Life, LNAI 929*, pages 934–945. Springer-Verlag, 1995.
6. L.J. Eshelman and J.D. Schaffer. Crossover's niche. In *Fifth International Conference on Genetic Algorithms*, pages 9–14, 1993.
7. D.B. Fogel and J.W. Atmar. Comparing genetic operators with gaussian mutations in simulated evolutionary processes using linear systems. *Biological Cybernetics*, 63:111–114, 1990.
8. D.B. Fogel and L.C. Stayton. On the effectiveness of crossover in simulated evolutionary optimization. *Biosystems*, 32:3:171–182, 1994.
9. W. Hordijk and B. Manderick. The usefulness of recombination. In *Third European Conference on Artificial Life, LNAI 929*, pages 908–919. Springer-Verlag, 1995.
10. S.A. Kauffman. *Origins of Order: Self-Organization and Selection in Evolution*. Oxford University Press, 1993.
11. B. Manderick, M. de Weger, and P. Spiessens. The genetic algorithm and the structure of the fitness landscape. In *Fourth International Conference on Genetic Algorithms*, pages 143–150, 1991.
12. H. Mühlenbein and H.-M. Voigt. Gene pool recombination in genetic algorithms. In *Proc. of the Metaheuristics Conference*. Kluwer Academic Publishers, 1995.
13. J.D. Schaffer and L.J. Eshelman. On crossover as an evolutionary viable strategy. In *Fourth International Conference on Genetic Algorithms*, pages 61–68, 1991.
14. H.-P. Schwefel. *Evolution and Optimum Seeking*. Sixth-Generation Computer Technology Series. Wiley, New York, 1995.
15. J. Smith and T.C. Fogarty. Recombination strategy adaptation via evolution of gene linkage. In *Third IEEE Conference on Evolutionary Computation*, pages 826–831. IEEE Service Center, 1996.
16. W.M. Spears. Crossover or mutation? In *Foundations of Genetic Algorithms - 2*, pages 221–238, 1993.
17. H.-M. Voigt and H. Mühlenbein. Gene pool recombination and utilization of covariances for the Breeder Genetic Algorithm. In *Second IEEE Conference on Evolutionary Computation*, pages 172–177, 1995.