Chapter 7

Summary and Outlook

So, is the evolution strategy the long-sought-after *universal* method of optimization? Unfortunately, things are not so simple and this question cannot be answered with a clear "yes." In two situations, in particular, the evolution strategies proved to be inferior to other methods: for linear and quadratic programming problems. These cases demonstrate the full effectiveness of methods that are specially designed for them, and that cannot be surpassed by strategies that operate without an adequate internal model. Thus if one knows the topology of the problem to be solved and it falls into one of these categories, one should always make use of such *special methods*. For this reason there will always rightly exist a number of different optimization methods.

In other cases one would naturally not search for a minimum or maximum iteratively if an analytic approach presented itself, i.e., if the necessary existence conditions lead to an easily and uniquely soluble system of equations. Nearest to this kind of indirect optimization come the hill climbing strategies, which operate with a global internal model. They approximate the relation between independent and dependent variables by a function (e.g., a polynomial of high order) and then follow the analytic route, but within the model rather than reality. Since the approximation will inevitably not be exact, the process of analysis and synthesis must be repeated iteratively in order to locate an extremum exactly. The first part, identification of the parameters or construction of the model, costs a lot in trial steps. The cost increases with n, the number of variables, and p, the order of the fitting polynomial, as $O(n^p)$. For this reason hill climbing methods usually keep to a linear model (first order strategies, gradient methods) or a quadratic model (second order strategies, Newton methods). All the more highly developed methods also try as infrequently as possible to adjust the model to the local topology (e.g., the method of steepest descents) or to advance towards the optimum during the model construction stage (e.g., the quasi-Newton and conjugate gradient strategies). Whether this succeeds, and the information gathered is sufficient, depends entirely on the optimization problem in question. A quadratic model seems obviously more suited to a non-linear problem than a linear model, but both have only a limited, local character. Thus in order to prove that the sequence of iterations converges and to make general statements about the speed of convergence and the Q-properties, very strict conditions must be satisfied by the objec-

tive function and, if they exist, also by the constraints, such as unimodality, convexity, continuity, and differentiability. Linear or quadratic convergence properties require not only conditions on the structure of the problem, which frequently cannot be satisfied, but also presuppose that the mathematical operations are in principle carried out with infinite accuracy . Many an attractive strategy thus fails not only because a problem is "pathological," having non-optimal stationary points, an indefinite Hessian matrix, or discontinuous partial derivatives, but simply because of inevitable rounding errors in the calculation, which works with a finite number of significant figures. Theoretical predictions are often irrelevant to practical problems and the strength of a strategy certainly lies in its capability of dealing with situations that it recognizes as precarious: for example, by cyclically erasing the information that has been gathered or by introducing random steps. As the test results confirm, the second order methods are particularly susceptible. A questionable feature of their algorithms is, for example, the line search for relative optima in prescribed directions. Contributions to all conferences in the late 1970s clearly showed a leaning towards strategies that do not employ line searches, thereby requiring more iterations but offering greater stability. The simpler its internal model, the less complete the required information, the more robust an optimization strategy can be. The more rigid the representation of the model is, the more effect perturbations of the objective function have, even those that merely result from the implementation on digital, analogue, or hybrid computers. Strategies that accept no worsening of the objective function are very easily led astray.

Every attempt to accelerate the convergence is paid for by loss in reliability. The ideal of guaranteed absolute reliability, from which springs the stochastic approximation (in which the measured objective function values are assumed to be samples of a stochastic, e.g., Gaussian distribution), leads directly to a large reduction in the rates of convergence. The starkest contradiction, however, between the requirements for speed and reliability can be seen in the problem of discovering a global optimum among several local optima. Imagine the situation of a blind person who arrives at New York and wishes, without assistance or local knowledge, to reach the summit of Mt. Whitney. For how long might he seek? The task becomes far more formidable if there are more than two variables (here longitude and latitude) to determine. The most reliable global search method is the volume-oriented grid method, which at the same time is the costliest. In the multidimensional case its information requirement is too huge to be satisfied. There is, therefore, often no alternative but to strike a compromise between reliability and speed.

Here we might adopt the sequential random search with normally distributed steps and fixed variances. It has the property of always maintaining a chance of global convergence, and is just as reliable (although slower) in the presence of stochastic perturbations. It also has a path-oriented character: According to the sizes of the selected standard deviations of the random components, it follows more or less exactly the gradient path and thus avoids testing systematically the whole parameter space. A further advantage is that its storage requirement increases only linearly with the number of variables. This can sometimes be a decisive factor in favor of its implementation. Most of the deterministic hill climbing methods require storage space of order $O(n^2)$. The simple operations of the algorithm guarantee the least effect of rounding errors and are safe from forbidden

numerical operations (division by zero, square root of a negative number, etc.). No conditions of continuity or differentiability are imposed on the objective function. These advantages accrue from doing without an internal model, not insisting on an improvement at each step, and having an almost unlimited set of search directions and step lengths. It is surely not by chance that this method of zero order corresponds to the simplest rules of organic evolution, which can also cope, and has coped, with difficult situations. Two objections are nevertheless sometimes raised against the analogy of mutations to random steps.

The first is directed against randomness as such. A common point of view, which need not be explicitly countered, is to equate randomness with arbitraryness, even going so far as to suppose that "random" events are the result of a superhuman hand sharing out luck and misfortune; but it is then further asserted that mutations do after all have causes, and it is concluded that they should not be regarded as random. Against this it can be pointed out that randomness and causality are not contradictory concepts. The statistical point of view that is expressed here simply represents an avoidance of statements about individual events and their causes. This is especially useful if the causal relation is very complicated and one is really only interested in the global behavioral laws of a stochastic set of events, as they are expressed by probability density distributions. The treatment of mutations as stochastic events rather than otherwise is purely and simply a reflection of the fact that they represent undirected and on average small deviations from the initial condition. Since one has had to accept that non-linear dynamic systems rather frequently produce behaviors called deterministic chaos (which in turn is used to create pseudorandom numbers on computers), arguments against speaking of random events in nature have diminished considerably.

The second objection concerns the unbelievably small probability, as proved by calculation, that a living thing, or even a mere wristwatch, could arise from a chance step of nature. In this case, biological evolution is implicitly being equated to the simultaneous, pure random methods that resemble the grid search. In fact the achievements of nature are not explicable with this model concept. If mutations were random events evenly distributed in the whole parameter space it would follow that later events would be completely independent of the previous results; that is to say that descendants of a particular parent would bear no resemblance to it. This overlooks the sequential character of evolution, which is inherent in the consecutive generations. Only the sequential random search can be regarded as an analogue of organic evolution. The changes from one generation to the next, expressed as rates of mutation, are furthermore extremely small. The fact that this must be so for a problem with so many variables is shown by Rechenberg's theory of the two membered evolution strategy: optimal (i.e., fastest possible) progress to the optimum is achieved if, and only if, the standard deviations of the random components of the vector of changes are inversely proportional to the number of variables. The 1/5 success rule for adaptation of the step length parameters does not, incidentally, have a biological basis; rather it is suited to the requirements of numerical optimization. It allows rates of convergence to be achieved that are comparable to those of most other direct search strategies. As the comparison tests show, because of its low computational cost per iteration the evolution strategy is actually far superior to some

methods for many variables, for example those that employ costly orthogonalization processes. The external control of step lengths sometimes, however, worsens the reliability of the strategy. In "pathological" cases it leads to premature termination of the search and reduces besides the chance of global convergence.

Now instead of concluding like Bremermann that organic evolution has only reached stagnation points and not optima, for example, in ecological niches, one should rather ask whether the imitation of the natural process is sufficiently perfect. One can scarcely doubt the capability of evolution to create optimal adaptations and ever higher levels of development; the already familiar examples of the achievements of biological systems are too numerous. Failures with simulated evolution should not be imputed to nature but to the simulation model. The two membered scheme incorporates only the principles of mutation and selection and can only be regarded as a very simple basis for a true evolution strategy. On the other hand one must proceed with care in copying nature, as demonstrated by Lilienthal's abortive attempt, which is ridiculed nowadays, to build a flying machine by imitating the birds. The objective, to produce high lift with low drag, is certainly the same in both cases, but the boundary conditions (the flow regime, as expressed by the Reynolds number) are not. Bionics, the *science of evaluating nature's patents*, teaches us nowadays to beware of imitating in the sense of slavishly copying all the details but rather to pay attention to the principle. Thus Bremermann's concept of varying the variables individually instead of all together must also be regarded as an inappropriate way to go about an optimization with continuously variable quantities. In spite of the many, often very detailed investigations made into the phenomenon of evolution, biology has offered no clues as to how an improved imitation should look, perhaps because it has hitherto been a largely descriptive rather than analytic science. The difficulties of the two membered evolution with step length adaptation teach us to look here to the biological example. It also alters the standard deviations through the generations, as proved by the existence of mutator genes and repair enzymes. Whilst nature cannot influence the mutation-provoking conditions of the environment, it can reduce their effects to whatever level is suitable. The step lengths are genetically determined; they can be thought of as strategy parameters of nature that are subject to the mutation-selection process just like the object parameters.

To carry through this principle as the algorithm of an improved evolution strategy one has to go over from the two membered to a multimembered scheme. The $(\mu\,,\,\lambda)$ strategy does so by employing the population principle and allowing μ parents in each generation to produce λ descendants, of which the μ best are selected as parents of the following generation. In this way the sequential as well as the simultaneous character of organic evolution is imitated; the two membered concept only achieves this insofar as a single parent produces descendents until it is surpassed by one of them in vitality, the biological criterion of goodness. According to Rechenberg's hypothesis that the forms and intricacies of the evolutionary process that we observe today are themselves the result of development towards an optimal optimization strategy, our measures should lead to improved results. The test results show that the reliability of the $(10\,,100)$ strategy, taken as an example, is indeed better than that of the (1+1) evolution strategy. In particular, the chances of locating global optima in multimodal problems have become

considerably greater. Global convergence can even be achieved in the case of a non-convex and disconnected feasible region. In the rate of convergence test the $(10\,,100)$ strategy does a lot worse, but not by the factor 100 that might be expected. In terms of the number of required generations, rather than the computation time, the multimembered strategy is actually considerably faster. The increase in speed compared to the two membered method comes about because not only the sign of $\triangle F$, the change in the function value, but also its magnitude plays a rôle in the selection process. Nature possesses a way of exploiting this advantage that is denied to conventional, serially operating computers: It operates in parallel. All descendants of a generation are produced at the same time, and their vitality is tested simultaneously. If nature could be imitated in this way, the $(\mu\,,\lambda)$ strategy would make both a very reliable and a fast optimization method.

The following two paragraphs, though completely out of date, have been left in place mainly to demonstrate the considerable shift in the development of computers during the last 20 years (compare with Schwefel, 1975a). Meanwhile parallel computers are beginning to conquer desk tops.

> Long and complicated iterative processes, such as occur in many other branches of numerical mathematics, led engineers and scientists of the University of Illinois, U.S.A., to consider new ways of reducing the computation times of programs. They built their own computer, Illiac IV, which has especially short data retrieval and transfer times (Barnes et al., 1968). They were unable to approach the 10^{20} bits/sec given by Bledsoe (1961) as an upper limit for serial computers, but there will inevitably always be technological barriers to achieving this physical maximum.
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> A novel organizational principle of Illiac IV is much more significant in this connection. A bank of satellite computers are attached to a central unit, each with its own processor and access to a common memory. The idea is for the sub-units to execute simultaneously various parts of the same program and by this true parallel operation to yield higher effective computation speeds. In fact not every algorithm can take advantage of this capability, for it is impossible to execute two iterations simultaneously if the result of one influences the next. It may sometimes be necessary to reconsider and make appropriate modifications to conventional methods, e.g., of linear algebra, before the advantages of the next generation of computers can be exploited. The potential and the problems of implementing parallel computers are already receiving close attention: Shedler (1967), Karp and Miranker (1968), Miranker (1969, 1971), Chazan and Miranker (1970), Abe and Kimura (1970), Sameh (1971), Patrick (1972), Gilbert and Chandler (1972), Hansen (1972), Eisenberg and McGuire (1972), Casti, Richardson, and Larson (1973), Larson and Tse (1973), Miller (1973), Stone (1973a,b). A version of FORTRAN for parallel computers has already been devised (Millstein, 1973).

Another significant advantage of the multimembered as against the two membered scheme that also holds for serial calculations is that the self-adjustment of step lengths can be made individually for each component. An automatic scaling of the variables results from

this, which in certain cases yields a considerable improvement in the rate of progress. It can be achieved either by separate variation of the standard deviations σ_i for $i = 1(1)n$, by recombination alone, or, even better, by both measures together. Whereas in the two membered scheme, in which (unless the $\sigma_i^{(0)}$ are initially given different values) the contour lines of equiprobable steps are circles, or hyperspherical surfaces, they are now ellipses or hyperellipsoids that can extend or contract along the coordinate directions following the n-dimensional normal distribution of the set of n random components z_i for $i = 1(1)n$:

$$w(z) = \frac{1}{(2\pi)^{\frac{n}{2}} \prod_{i=1}^{n} \sigma_i} \exp\left(-\frac{1}{2}\sum_{i=1}^{n}\left(\frac{z_i}{\sigma_i}\right)^2\right)$$

This is not yet, however, the most general form of a normal distribution, which is rather:

$$w(z) = \frac{\sqrt{\mathrm{Det}\, A}}{(2\pi)^{\frac{n}{2}}} \exp\left(-\frac{1}{2}(z-\xi)^T A (z-\xi)\right)$$

The expectation value vector ξ can be regarded as a deterministic part of the random step z. However, the comparison made by Schrack and Borowski (1972) between the random strategies of Schumer-Steiglitz and Matyas shows that even an ingenious learning scheme for adapting ξ to the local conditions only improves the convergence in special cases. A much more important feature seems to be the step length adaptation. It is now possible for the elements of the matrix A to be chosen so as to give the ellipsoid of variation any desired orientation in the space. Its axes, the regression directions of the random vector, only coincide with the coordinate axes if A is a diagonal matrix. In that case the old scheme is recovered whereby the variances σ_{ii} or the σ_i^2 reappear as diagonal elements of the inverse matrix A^{-1}. If, however, the other elements, the covariances $\sigma_{ij} = \sigma_{ji}$ are non-zero, the ellipsoids are rotated in the space. The random components z_i become mutually dependent, or correlated. The simplest kind of correlation is linear, which is the only case to yield hyperellipsoids as surfaces of constant step probability. Instead of just n strategy parameters σ_i one would now have to vary $\frac{n}{2}(n+1)$ different quantities σ_{ij}. Although in principle the multimembered evolution strategy allows an arbitrary number of strategy variables to be included in the mutation-selection process, in practice the adaptation of so many parameters could take too long and cancel out the advantage of more degrees of freedom. Furthermore, the σ_{ij} must satisfy certain compatibility conditions (Sylvester's criteria, see Faddejew and Faddejewa, 1973) to ensure an orthogonal coordinate system or a positive definite matrix A. In the simplest case, $n = 2$, with

$$A^{-1} = \begin{bmatrix} \sigma_{11} & \sigma_{12} \\ \sigma_{21} & \sigma_{22} \end{bmatrix}$$

there is only one condition:

$$\sigma_{12}^2 = \sigma_{21}^2 < \sigma_{11}\,\sigma_{22} = \sigma_1^2\,\sigma_2^2$$

and the quantity defined by

$$\rho_{12} = \frac{\sigma_{12}}{\sqrt{(\sigma_1\,\sigma_2)}}, \quad -1 < \rho_{12} < 1$$

is called the correlation coefficient. If the covariances were generated independently by a mutation process in the multimembered evolution scheme, with subsequent application of the rules of Scheuer and Stoller (1962) or Barr and Slezak (1972), there would be no guarantee that the surfaces of equal probability density would actually be hyperellipsoids. It follows that such a linear correlation of the random changes can be constructed more easily by first generating as before $(0, \sigma_i^2)$ normally distributed, independent random components and then making a coordinate rotation through prescribed angles. These angles, rather than the covariances σ_{ij}, represent the additional strategy variables. In the most general case there are a total of $n_p = \frac{n}{2}(n-1)$ such angles, which can take all values between 0^0 and 360^0 (or $-\pi$ and π). Including the $n_s = n$ "step lengths" σ_i, the total number of strategy parameters to be specified in the population by mutation and selection is $\frac{n}{2}(n+1)$. It is convenient to generate the angles α_j by an additive mutation process (cf. Equations (5.36) and (5.37))

$$\alpha_{N,j}^{(g)} = \alpha_{E,j}^{(g)} + \hat{Z}_j^{(g)}, \qquad \text{for } j = 1(1)n_p$$

where the $\hat{Z}_j^{(g)}$ can again be normally distributed, for example, with a standard deviation $\triangle\alpha$ which is the same for all angles. Let $\triangle x_i'$ represent the mutations as produced by the old scheme and $\triangle x_i$ the correlated changes in the object variables produced by the rotation; for the two dimensional case ($n = n_s = 2$, $n_p = 1$) the coordinate transformation for the rotation can simply be read off from Figure 7.1

$$\triangle x_1 = \triangle x_1' \cos\alpha - \triangle x_2' \sin\alpha$$

$$\triangle x_2 = \triangle x_1' \sin\alpha + \triangle x_2' \cos\alpha$$

For $n = n_s = 3$ three consecutive rotations would need to be made:

- In the $(\triangle x_1, \triangle x_2)$ plane through an angle α_1
- In the $(\triangle x_1', \triangle x_2')$ plane through an angle α_2
- In the $(\triangle x_2'', \triangle x_3'')$ plane through an angle α_3

Starting from the uncorrelated random changes $\triangle x_1''', \triangle x_2''', \triangle x_3'''$ these rotations would have to be made in the reverse order. Thus also, in the general case with $\frac{n}{2}(n-1)$ rotations, each one only involves two coordinates so that the computational cost increases as $O(n_p)$. The validity of this algorithm has been proved by Rudolph (1992a).

An immediate simplification can be made if not all the n_s step lengths are different, i.e., if the hyperellipsoid of equal probability of a mutation has rotational symmetry about one or more axes. In the extreme case $n_s = 2$ there are $n - n_s$ such axes and only $n_p = n - 1$ relevant angles of rotation. Except for one distinct principle axis, the ellipsoid resembles a sphere. If in the course of the optimization the minimum search leads through a narrow valley (e.g., in Problem 2.37 or 3.8 of the catalogue of test problems), it will often be quite adequate to work with such a greatly reduced variability of the mutation ellipsoid.

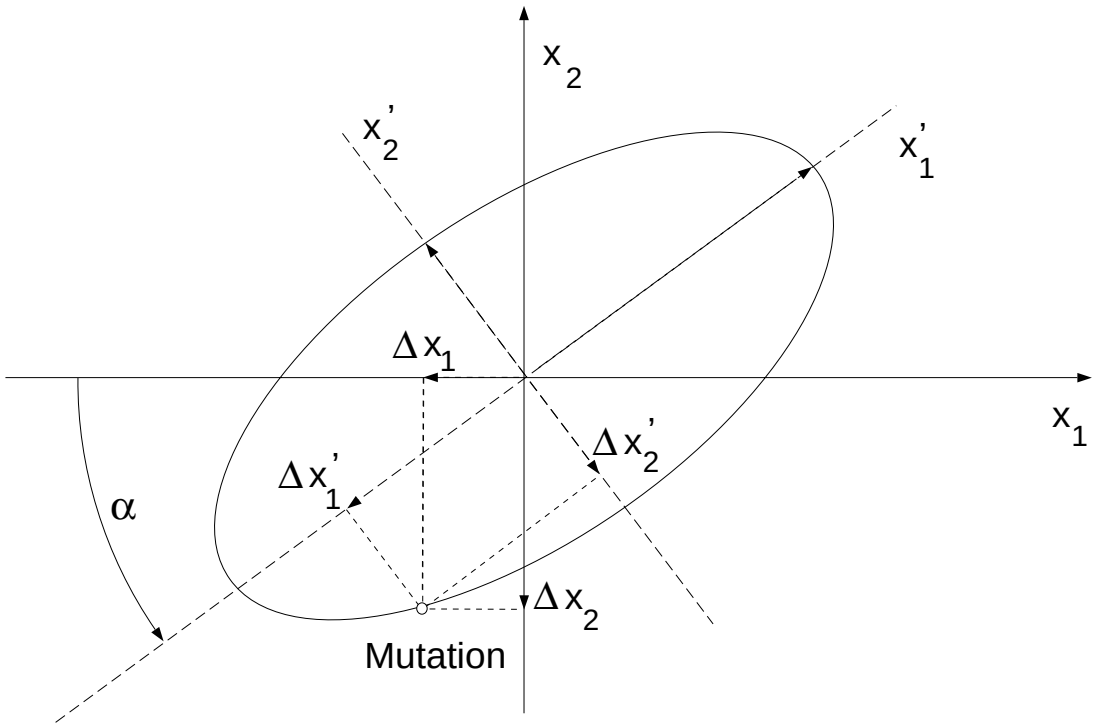

Figure 7.1: Generation of correlated mutations

Between the two extreme cases $n_s = n$ and $n_s = 2$ ($n_s = 1$ would be the uncorrelated case with hyperspheres as mutation ellipsoids) any choice of variability is possible. In general we have

$$2 \leq n_s \leq n$$

$$n_p = \left(n - \frac{n_s}{2}\right)(n_s - 1)$$

For a given problem the most suitable choice of n_s, the number of different step lengths, would have to be obtained by numerical experiment.

For this purpose the subroutine KORR and its associated subroutines listed in Appendix B, Section B.3 is flexibly coded to give the user considerable freedom in the choice of quantities that determine the strategy parameters. This variant of the evolution strategy (Schwefel, 1974) could not be fully included in the strategy test (performed in 1973); however, initial results confirmed that, as expected, it is able to construct a kind of variable metric for the changes in the object variables by adapting the angles to the local topology of the objective function.

The slow convergence of the two membered evolution strategy can often be traced to the fact that the problem has long elliptical (or nearly elliptical) contours of constant objective function value. If the function is quadratic, their extension (or eccentricity) can be expressed by the condition number of the matrix of second order coefficients. In the worst case, in which the search is started at the point of greatest curvature of the contour surface $F(x) = const.$, the rate of progress seems to be inversely proportional

to the product of the number of variables and the square root of the condition number. This dependence on the metric would be eliminated if the directions of the axes of the variance ellipsoid corresponded to those of the contour ellipsoid, which is exactly what the introduction of correlated random numbers should achieve. Extended valleys in other than coordinate directions then no longer hinder the search because, after a transition phase, an initially elliptical problem is reduced to a spherical one. In this way the evolution strategy acquires properties similar to those of the variable metric method of Davidon-Fletcher-Powell (DFP). In the test, for just the reason discussed above, the latter proved to be superior to all other methods for quadratic objective functions. For such problems one should not expect it to be surpassed by the evolution strategy, since compared to the Q n property of the DFP method the evolution strategy has only a Q $O(n)$ property; i.e., it does not find the optimum after exactly n iterations but rather it reaches a given approximation to the objective after $O(n)$ generations. This disadvantage, only slight in practice, is outweighed by the following advantages:

- Greater flexibility, hence reliability, in other than quadratic cases
- Simpler computational operations
- Storage required increases only as $O(n)$ (unless one chooses $n_s = n$)

While one has great hopes for this extension of the multimembered evolution strategy, one should not be blinded by enthusiasm to limitations in its capability. It would yield computation times no better than $O(n^3)$ if it turns out that a population of $O(n)$ parents is needed for adjusting the strategy parameters and if pure serial rather than parallel computation is necessary.

Does the new scheme still correspond to the biological paradigm? It has been discovered that one gene often influences several phenotypic characteristics of an individual (pleiotropy) and conversely that many characteristics depend on the cooperative effect of several genes (polygeny). These interactions just mean that the characteristics are correlated. A linear correlation as in Figure 7.1 represents only one of the many conceivable types in which (x_1', x_2') is the plane of the primary, independent genetic changes and (x_1, x_2) that of the secondary, mutually correlated changes in the characteristics. Particular kinds of such dependence, for example, allometric growth, have been intensively studied (e.g., Grassé, 1973). There is little doubt that the relationships have also adapted, during the history of development, to the topological requirements of the objective function. The observable differences between life forms are at least suggestive of this. Even non-linear correlations may occur. Evolution has indeed to cope with far greater difficulties, for it has no ordered number system at its disposal. In the first place it had to create a scale of measure–with the genetic code, for example, which has been learned during the early stages of life on earth.

Whether it is ultimately worth proceeding so far or further to mimic evolution is still an open question, but it is surely a path worth exploring; perhaps not for continuous, but for discrete or mixed parameter optimization. Here, in place of the normal distribution of random changes, a discrete distribution must be applied, e.g., a binomial or better still a distribution with maximum entropy (see Rudolph, 1994b), so that for small "total

step lengths" the probability really is small that two or more variables are altered simultaneously. Occasional stagnation of the search will only be avoided, in this case, if the population allows worsening within a generation. Worsening is not allowed by the two membered strategy, but it is by the multimembered (μ , λ) strategy , in which the parents, after producing descendants, no longer enter the selection process. Perhaps this shows that the limited life span of individuals is no imperfection of nature, no consequence of an inevitable weakness of the system, but rather an intelligent, indeed essential means of survival of the species. This conjecture is again supported by the genetically determined, in effect preprogrammed, ending of the process of cell division during the life of an individual. Sequential improvement and consequent rapid optimization is only made possible by the following of one generation after another. However, one should be extremely wary of applying such concepts directly to mankind. Human evolution long ago left the purely biological domain and is more active nowadays in the social one. One properly refers now to a cultural evolution. There is far too little genetic information to specify human behavior completely.

Little is known of which factors are genetically inherited and which socially acquired, as shown by the continuing discussions over the results of behavioral research and the diametrically opposite points of view of individual scientists in the field. The two most important evolutionary principles, mutation and selection, also belong to social development (Alland, 1970). Actually, even more complicated mechanisms are at work here. Oversimplifications can have quite terrifying consequences, as shown by the example of social Darwinism, to which Koch (1973) attributes responsibility for racist and imperialist thinking and hence for the two World Wars. No such further speculation with the evolution strategy will therefore be embarked upon here. The fact remains that the recognition of evolution as representing a sequential optimization process is too valuable to be dismissed to oblivion as *evolutionism* (Goll, 1972). Rather one should consider what further factors are known in organic evolution that might be worth imitating, in order to make of the evolution strategy an even more general optimization method; for up to now several developments have confirmed Rechenberg's hypothesis that the strategy can be improved by taking into account further factors, at least when this is done adequately and the biological and mathematical boundary conditions are compatible with each other. Furthermore, by no means all evolutionary principles have yet been adopted for optimizing technical systems.

The search for global optima remains a particularly difficult problem. In such cases nature seems to hunt for all, or at least a large number of maxima or minima at the same time by the splitting of a population (the isolation principle). After a transition phase the individuals of both or all the subpopulations can no longer intermix. Thereafter each group only seeks its own specific local optimum, which might perhaps be the global one. This principle could easily be incorporated into the multimembered scheme if a criterion could be defined for performing the splitting process.

Many evolution principles that appeared later on the scene can be explained as affording the greater chance of survival to a population having the better mechanism of inheritance (for these are also variable) compared to an other forming a worse "strategy of life." In this way the evolution method could itself be optimized by organizing a compe-

tition between several populations that alter the concept of the optimum seeking strategy itself. The simplest possibility, for example, would be to vary the number of parents μ and of descendants λ; two or more groups would be set up each with its own values of these parameters, each group would be given a fixed time to seek the optimum; then the group that has advanced the most would be allowed to "survive." In this way these strategy variables would be determined to best suit the particular problem and computer, with the objective of minimizing the required computation time. One might call such an approach meta- or hierarchical evolution strategy (see Bäck, 1994a,b).

The solution of problems with multiple objectives could also be approached with the multimembered evolution strategy. This is really the most common type of problem in nature. The selection step, the reduction to the best of the descendants, could be subdivided into several partial steps, in each of which only one of the criteria for selection is applied. In this way no weighting of the partial objectives would be required. First attempts with only two variables and two partial objectives showed that a point on the Pareto line is always approached as the optimum. By unequal distribution of the partial selections the solution point could be displaced towards one of the partial objectives. At this stage subjective information would have to be applied because all the *Pareto-optimal* solutions are initially equally good (see Kursawe, 1991, 1992).

Contrary to many statements or conjectures that organic evolution is a particularly wasteful optimization process, it proves again and again to be precisely suited to advancing with maximum speed without losing reliability of convergence, even to better and better local optima. This is just what is required in numerical optimization. In both cases the available resources limit what can be achieved. In one case these are the limitations of food and the finite area of the earth for accommodating life, in the other they are the finite number of satellite processors of a parallel-organized mainframe computer and its limited (core) storage space. If the evolution strategy can be considered as the sought-after universal optimization method, then this is not in the sense that it solves a particular problem (e.g., a linear or quadratic function) exactly, with the least iterations or generations, but rather refers to its being the most readily extended concept, able to solve very difficult problems, problems with particularly many variables, under unfavorable conditions such as stochastic perturbations, discrete variables, time-varying optima, and multimodal objective functions (see Hammel and Bäck, 1994). Accordingly, the results and assessments introduced in the present work can at best be considered as a first step in the development towards a universal evolution strategy.

Finally, some early applications of the evolution strategy will be cited. Experimental tasks were the starting point for the realization of the first ideas for an optimization strategy based on the example of biological evolution. It was also first applied here to the solution of practical problems (see Schwefel, 1968; Klockgether and Schwefel, 1970; Rechenberg, 1973). Meanwhile it is being applied just as widely to optimization problems that can be expressed in computational or algorithmic form, e.g., in the form of simulation models. The following is a list of some of the successful applications, with references to the relevant publications.

1. Optimal dimensioning of the core of a fast sodium-type breeder reactor (Heusener, 1970)

2. Optimal allocation of investments to various health-service programs in Columbia (Schwefel, 1972)
3. Solving curve-fitting problems by combining a least-squares method with the evolution strategy (Plaschko and Wagner, 1973)
4. Minimum-weight designing of truss constructions partly in combination with linear programming (Leyßner, 1974; and Höfler, 1976)
5. Optimal shaping of vaulted reinforced concrete shells (Hartmann, 1974)
6. Optimal dimensioning of quadruple-joint drives (Anders, 1977)
7. Approximating the solution of a set of non-linear differential equations (Rodloff, 1976)
8. Optimal design of arm prostheses (Brudermann, 1977)
9. Optimization of urban and regional water supply systems (Cembrowicz and Krauter, 1977)
10. Combining the evolution strategy with factorial design techniques (Kobelt and Schneider, 1977)
11. Optimization within a dynamic simulation model of a socioeconomic system (Krallmann, 1978)
12. Optimization of a thermal water jet propulsion system (Markwich, 1978)
13. Optimization of a regional system for the removal of refuse (von Falkenhausen, 1980)
14. Estimation of parameters within a model of floods (North, 1980)
15. Interactive superimposing of different direct search techniques onto dynamic simulation models, especially models of the energy system of the Federal Republic of Germany (Heckler, 1979; Drepper, Heckler, and Schwefel, 1979).

Much longer lists of references concerning applications as well as theoretical work in the field of evolutionary computation have been compiled meanwhile by Alander (1992, 1994) and Bäck, Hoffmeister, and Schwefel (1993).

Among the many different fields of applications only one will be addressed here, i.e., non-linear regression and correlation analysis. In general this leads to a multimodal optimization problem when the parameters searched for enter the hypotheses non-linearly, e.g., as exponents. Very helpful under such circumstances is a tool with which one can switch from one to the other minimization method. Beginning with a multimembered evolution strategy and refining the intermediate results by means of a variable metric method has often led to practically useful results (e.g., Frankhauser and Schwefel, 1992).

In some cases of practical applications of evolution strategies it turns out that the number of variables describing the objective function has to vary itself. An example was

the experimental optimization of the shape of a supersonic one-component two-phase flow nozzle (Schwefel, 1968). Conically bored rings with fixed lengths could be put side by side, thus forming potentially millions of different inner nozzle contours. But the total length of the nozzle had to be varied itself. So the number of rings and thus the number of variables (inner diameters of the rings) had to be mutated during the search for an optimum shape as well. By imitating *gene duplication* and *gene deletion* at randomly chosen positions, a rather simple technique was found to solve the variable number of variables problem. Such a procedure might be helpful for many *structural optimization* problems (e.g., Rozvany, 1994) as well.

If the decision variables are to be taken from a discrete set only (the distinct values may be equidistant or not; integer and binary values just form special subclasses), ESs may be used sometimes without any change. Within the objective function the real values must simply undergo a suitable rounding-off process as shown at the end of Appendix B, Section B.3. Since all ESs handle unchanged objective function values as improvements, the self-adaptation of the standard deviations on a plateau will always lead to their enlargement, until the plateaus $F(x) = const.$ built by rounding off can be left. On a plateau, the ES performs a random walk with ever increasing step sizes.

Towards the end of the search, however, more and more of the individual step sizes have to become very small, whereas others–singly or in some combination–should be increased to allow hopping from one to the next n-cube in the decision-variable space. The chances for that kind of adaptation are good enough as long as sequential improvements are possible; the last few of them will not happen that way, however. A method of escaping from that awkward situation has been shown (Schwefel, 1975b), imitating *multicellular individuals* and introducing so-called *somatic mutations*. Even in the case of binary variables an ES thus can reach the optimum. Since no real application has been done this way until now, no further details will be given here.

An interesting question is whether there are intermediate cases between a plus and a comma version of the multimembered ES. The answer must be, "Yes, there are." Instead of neglecting the parents during the selection step (within comma-ESs), or allowing them to live forever in principle (within plus-ESs; only until offspring surpass them, of course), one might implant a generation counter into each individual. As soon as a prefixed limit is reached, they leave the scene automatically. Such a more general ES version could be termed a $(\mu\,,\,\kappa\,,\,\lambda)$ *strategy*, where κ denotes the maximal number of generations (iterations), an individual is allowed to "survive" in the population. For $\kappa = 1$ we then get the old comma-version, whereas the old plus-version is reached if κ goes to infinity. There are some preliminary results now, but as yet they are too unsystematic to be presented here.

Is the strict synchronization of the evolutionary process within ESs as well as GAs the best way to do the job? The answer to this even more interesting question is, "No," especially if one makes use of MIMD parallel machines or clusters of workstations. Then one should switch to imitating life more closely: Birth and death events may happen at the same time. Instead of modelling a central decision maker for the selection process (which is an oversimplification) one could use a *predator-prey model* like that of Lotka and Volterra. Adding a *neighborhood model* (see Gorges-Schleuter, 1991a,b; Sprave, 1993, 1994) for the

recombination process would free the whole strategy from all kinds of synchronization needs. Initial tests have shown that this is possible. *Niching* and *migration* as used by Rudolph (1991) will be the next features to be added to the APES (*asynchronous parallel evolution strategy*).

A couple of earlier attempts towards parallelizing ESs will be mentioned at the end of this chapter. Since all of them are somehow intermediate solutions, however, none of them will be explained in detail. The reader is referred to the literature.

A *taxonomy*, more or less complete with respect to possible ways *of parallelizing EAs*, may be found in Hoffmeister and Schwefel (1990) or Hoffmeister (1991). Rudolph (1991) has realized a *coarse-grained parallel ES* with *subpopulations* on each processor and more or less frequent *migration* events, whereas Sprave (1994) gave preference to a *fine-grained diffusion model*. Both of these more *volume-oriented* approaches delivered great advances in solving *multimodal* optimization problems as compared with the more *greedy* and *path-oriented* "canonical" (μ , λ) ES. The comma version, by the way, is necessary to follow a *nonstationary optimum* (see Schwefel and Kursawe, 1992), and only such an ES is able to solve *on-line optimization* problems.

Nevertheless, one should never forget that there are many other specialized optimum seeking methods. For a practitioner, a tool box with many different algorithms might always be the "optimum optimorum." Whether he or she chooses a special tool by hand, so to speak (see Heckler and Schwefel, 1978; Heckler, 1979; Schwefel, 1980, 1981; Hammel, 1991; Bendin, 1992; Bäck and Hammel, 1993), or relies upon some *knowledge-based selection* scheme (see Campos, 1989; Campos and Schwefel, 1989; Campos, Peters, and Schwefel, 1989; Peters, 1989, 1991; Lehner, 1991) will largely depend on his or her experience.

Chapter 8

References

Glossary of abbreviations at the end of this list

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Glossary of Abbreviations

AAAS	American Association for the Advancement of Science
ACM	Association for Computing Machinery
AEG	Allgemeine Elektricitäts-Gesellschaft
AERE	Atomic Energy Research Establishment
AFIPS	American Federation of Information Processing Societies
AGARD	Advisory Group for Aerospace Research and Development
AIAA	American Institute of Aeronautics and Astronautics
AIChE	American Institute of Chemical Engineers
AIEE	American Institute of Electrical Engineers
ANL	Argonne National Laboratory
ARC	Automation and Remote Control
	(cover-to-cover translation of Avtomatika i Telemechanika)
ASME	American Society of Mechanical Engineers
BIT	Nordisk Tidskrift for Informationsbehandling
CACM	Communications of the ACM
DFVLR	Deutsche Forschungs- und Versuchsanstalt für Luft– und Raumfahrt
DGRR	Deutsche Gesellschaft für Raketentechnik und Raumfahrt
DLR	Deutsche Luft- und Raumfahrt
FEBS	Federation of European Biochemical Societies
GI	Gesellschaft für Informatik
GMD	Gesellschaft für Mathematik und Datenverarbeitung
IBM	International Business Machines Corporation
ICI	Imperial Chemical Industries Limited
IEE	Institute of Electrical Engineers
IEEE	Institute of Electrical and Electronics Engineers
	Transactions AC on Automatic Control
	BME on Bio-Medical Engineering
	C on Computers
	MIL on Military Electronics
	MTT on Microwave Theory and Techniques
	NN on Neural Networks
	SMC on Systems, Man, and Cybernetics
	SSC on Systems Science and Cybernetics
IFAC	International Federation of Automatic Control
IIASA	International Institute for Applied Systems Analysis
IMACS	International Association for Mathematics and Computers in Simulation
IRE	Institute of Radio Engineers
	Transactions EC on Electronic Computers
	EM on Engineering Management
ISA	Instrument Society of America
JACM	Journal of the ACM

JIMA	Journal of the Institute of Mathematics and Its Applications
JOTA	Journal of Optimization Theory and Applications
KFA	Kernforschungsanlage (Nuclear Research Center) Jülich
KfK	Kernforschungszentrum (Nuclear Research Center) Karlsruhe
MIT	Massachusetts Institute of Technology
NASA	National Aeronautics and Space Administration
NBS	National Bureau of Standards
NTZ	Nachrichtentechnische Zeitschrift
PPSN	Parallel Problem Solving from Nature
SIAM	Society for Industrial and Applied Mathematics
UKAEA	United Kingdom Atomic Energy Authority
VDE	Verband Deutscher Elektrotechniker
VDI	Verein Deutscher Ingenieure
WGLR	Wissenschaftliche Gesellschaft für Luft- und Raumfahrt
ZAMM	Zeitschrift für angewandte Mathematik und Mechanik
ZAMP	Zeitschrift für angewandte Mathematik und Physik