Toward a Theory of Evolution Strategies: On the Benefits of Sex— the $(\mu/\mu, \lambda)$ Theory

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Abstract

The multirecombinant $(\mu/\mu, \lambda)$ evolution strategy (ES) is investigated for real-valued, N-dimensional parameter spaces. The analysis includes both intermediate recombination and dominant recombination, as well. These investigations are done for the spherical model first. The problem of the optimal population size depending on the parameter space dimension N is solved. A method extending the results obtained for the spherical model to nonspherical success domains is presented.

The power of sexuality is discussed and it is shown that this power does not stem mainly from the "combination" of "good properties" of the mates (building block hypothesis) but rather from *genetic repair* diminishing the influence of harmful mutations. The dominant recombination is analyzed by introduction of surrogate mutations leading to the concept of *species*. Conclusions for evolutionary algorithms (EAs), including genetic algorithms (GAs), are drawn.

Keywords

multimembered evolution strategies (ES), progress rate theory, multirecombination: intermediate and dominant/discrete, benefits of sexuality, genetic variety versus genetic repair, building block hypothesis, nonspherical success domains, multirecombinant GA

1. Introduction

One logical continuation of the analysis of evolution strategies (ES) presented so far (Beyer, 1993; Beyer, 1995) concerns recombination. Most of the users of EAs (evolutionary algorithms) would agree that one basic operator of an EA working with a population should be recombination. And there are people who even believe that recombination is the most important (search) operator (this holds especially for the field of genetic algorithms (GAs); see e.g., Goldberg, 1989).

In order to shed light on the effect of recombination, the so-called multirecombinant $(\mu/\mu, \lambda)$ strategies are investigated. These are special variants of the $(\mu/\rho, \lambda)$ strategies. There are two variants of recombination—the intermediate and the dominant, to be introduced in Section 2.

The intermediate $(\mu/\mu, \lambda)$ strategy is analyzed in Section 3 for the spherical fitness landscape. It can be easily tackled because intermediate recombination concentrates the parents in the "center of mass." The $(\mu/\mu, \lambda)$ strategies exhibit remarkably high progress

rates. This is due to multirecombination. The advantages of "sexuality" will be discussed and it will be shown that its power stems mainly from *genetic repair*, whereas the building block hypothesis describes, at best, a side effect.

A rather difficult problem concerns the dominant $(\mu/\mu, \lambda)$ strategy to be discussed in Section 4. This ES is very similar to GAs with uniform crossover. In the case of dominant recombination, a simple mutation-recombination model will be developed that provides an estimate for a "mutation substitute" to be used in the progress formula of the intermediate strategy. A rough approximation for the progress rate will be derived.

The analysis of the dominant recombination reveals a very interesting *synergistic effect* concerning mutation and recombination: Iterative application of these two operators produces populations reminiscent of *species* observed in biology.

Section 5 contains information on how to generalize the results that were obtained for the sphere. A differential geometry approach will be outlined that provides a local approximation of the fitness landscape by a sphere. Thus, it will be possible to extend the validity of the model to nonspherical success domains.

Section 6 resumes the discussion on the benefits of recombination. In particular, the dominant recombination will be considered. Because the concept is very general it will also be applied to the GA theory.

This article relies strongly on notations used and results presented in the author's article in *Evolutionary Computation*, *2*(4) (Beyer, 1995). Especially in Sections 3.1.1, 3.2.1, and 3.2.2 we will take advantage of methods developed for the analysis of the (μ, λ) ES. Therefore, it will be helpful to have that issue at hand.

2. The Intermediate and the Dominant $(\mu/\rho, \lambda)$- and $(\mu/\mu, \lambda)$-Algorithms

Sexuality, in the spirit of recombining hereditary factors, is a universal mechanism in biology. Therefore, it is not surprising that recombination has been regarded as an important evolution mechanism for ES, too. From Schwefel's (1974) early work onwards we can observe a continuous spreading of recombination techniques in ES algorithms.

Extending Schwefel's (μ, λ) notation, Rechenberg (1978) has introduced the $(\mu/\rho, \lambda)$ notation for (multi-)recombinant ES. Here the new strategy parameter ρ determines the number of parents that multirecombine to form a (one) new offspring. In contrast to the biological standard, $\rho = 2$ (at least for the higher creatures), it is worth using multimixing, that is, $\rho > 2$, for ES applications.

As in biology, there are two different recombination patterns—*intermediate* and *dominant* recombination. The author proposes the

$$(\mu/\rho_I, \lambda) \qquad \text{and} \qquad (\mu/\rho_D, \lambda)$$

notation for their distinction.

Intermediate recombination is some kind of averaging. In $(\mu/\rho_I, \lambda)$ strategies ρ individuals $\mathbf{y}_{m_\nu}$, $\nu = 1, \ldots, \rho$ from the parental pool $\{\mathbf{y}_1, \ldots, \mathbf{y}_\mu\}$ (consisting of μ parents) are chosen at random. The averaging is simply the determination of the "*center of mass*"

$$\text{intermediate } \mu/\rho \text{ recombination:} \qquad \langle \mathbf{y} \rangle = \frac{1}{\rho} \sum_{\nu=1}^{\rho} \mathbf{y}_{m_\nu}.$$

After recombination the mutation $\mathbf{Z}$ is additively applied. Thus, the offspring $\tilde{\mathbf{y}}_l$ can be

expressed by[1]

$$\underline{(\mu/\rho_I, \lambda)\text{-ES:}} \quad \tilde{\mathbf{y}}_l = \frac{1}{\rho}\sum_{\nu=1}^{\rho}\mathbf{y}_{m_\nu} + \mathbf{Z},$$

$$m_\nu = \text{Random}\{1 \ldots \mu\} \wedge m_{\nu_1} \neq m_{\nu_2} \quad \Leftrightarrow \quad \nu_1 \neq \nu_2.$$

The mutation vector $\mathbf{Z}$ is—as usual—generated by independent identically distributed (iid) normal random numbers with zero mean and standard deviation σ for each component. Selection acts on the $\tilde{\mathbf{y}}_l$ offspring and is equal to the (μ, λ) strategies.

Because there are μ different parents, theoretical investigation of the $(\mu/\rho_I, \lambda)$ strategies is at least as difficult as that of the (μ, λ) strategy. However, there is one exception—the $(\mu/\mu_I, \lambda)$ strategy. Because $\rho = \mu$ holds, there is no random mating. All parents are involved in the recombination

$$\underline{(\mu/\mu_I, \lambda)\text{-ES:}} \quad \tilde{\mathbf{y}}_l = \frac{1}{\mu}\sum_{m=1}^{\mu}\mathbf{y}_m + \mathbf{Z}\,. \tag{1}$$

That is, each offspring $\tilde{\mathbf{y}}_l$ is generated from the "center of mass individual" $\langle\mathbf{y}\rangle = \sum \mathbf{y}_m/\mu$ by mutation. The theoretical treatment of this strategy will be performed in the next section.

In order to describe the *dominant recombination*, the $\mathbf{y}_m$ vectors are decomposed by an orthogonal basis $\{\mathbf{e}_i\}$

$$\mathbf{y} = \sum_{i=1}^{N} y_i\,\mathbf{e}_i.$$

An offspring $\tilde{\mathbf{y}}_l$ is constituted from ρ different, randomly chosen parents $\mathbf{y}_{\pi^l}$ with index π^l_ν

$$\pi^l_\nu := \text{Random}\{1 \ldots \mu\} \wedge \pi^l_{\nu_1} \neq \pi^l_{\nu_2} \quad \Leftrightarrow \quad \nu_1 \neq \nu_2$$

by

$$\underline{(\mu/\rho_D, \lambda)\text{-ES:}} \quad \tilde{\mathbf{y}}_l = \sum_{i=1}^{N}\left(\mathbf{e}_i^T\mathbf{y}_{m_i}\right)\mathbf{e}_i + \mathbf{Z}, \qquad m_i = \text{Random}\{\pi^l_1, \pi^l_2, \ldots, \pi^l_\rho\}.$$

That is, the coordinate i of the $\tilde{\mathbf{y}}_l$ vector is given by random choice of one of the coordinate i values from the mates of the index set $\{\pi^l_1, \pi^l_2, \ldots, \pi^l_\rho\}$ and an additive mutation z_i. Here $m_i = \text{Random}\{\pi^l_1, \ldots, \pi^l_\rho\}$ indicates the random choice of an element from the set $\{\pi^l_1, \ldots, \pi^l_\rho\}$ with selection probability $1/\rho$. The constitution of the μ new parents by selection from the $\{\tilde{\mathbf{y}}_l\}$ is equal to the (μ, λ) ES.

The theoretical analysis of dominant recombination is still just beginning. Even for the $\rho = \mu$ case

$$\underline{(\mu/\mu_D, \lambda)\text{-ES:}} \quad \tilde{\mathbf{y}}_l = \sum_{i=1}^{N}\left(\mathbf{e}_i^T\mathbf{y}_{m_i}\right)\mathbf{e}_i + \mathbf{Z}, \qquad m_i = \text{Random}\{1, 2, \ldots, \mu\}, \tag{2}$$

only a rough approximation, has been developed up until now. It will be discussed in Section 4.

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1 In practice it is rather elaborate to produce ρ random indices m_ν all different from each other. A slightly different algorithm might also allow "self-fertilization" by sampling the ρ m_ν-numbers from a simple random number generator.

3. The $(\mu/\mu_I, \lambda)$-Theory

3.1 Basic Aspects of the $(\mu/\mu_I, \lambda)$-Theory

3.1.1 Definition of the Progress Rate $\varphi_{\mu/\mu,\lambda}$ Let us assume the optimum point $\hat{\mathbf{y}}$ of a spherical fitness landscape at $\hat{\mathbf{y}} = \mathbf{0}$. The parents $\mathbf{y}_m^{(g)}$ at generation (g) may form the center of mass $\langle \mathbf{y} \rangle^{(g)}$

$$\langle \mathbf{y} \rangle^{(g)} = \frac{1}{\mu} \sum_{m=1}^{\mu} \mathbf{y}_m^{(g)} =: \mathbf{R}. \tag{3}$$

Because $\hat{\mathbf{y}} = \mathbf{0}$ is assumed, $\langle \mathbf{y} \rangle^{(g)}$ is equal to the radius vector $\mathbf{R}$ measuring the distance of the center of mass to the optimum. The distance is given by $R = \|\langle \mathbf{y} \rangle^{(g)}\|$. According to Equation (1), λ offspring $\tilde{\mathbf{y}}_l$ are generated from $\langle \mathbf{y} \rangle^{(g)}$ by mutations $\mathbf{Z}$. Their distance to the optimum may be denoted by $\tilde{R}_l$. From $\hat{\mathbf{y}} = \mathbf{0}$ it follows that $\tilde{\mathbf{R}}_l = \tilde{\mathbf{y}}_l$. By fitness selection the best μ offspring $\tilde{\mathbf{y}}_l$ are chosen obeying the ordering

$$\tilde{R}_{1:\lambda} \leq \tilde{R}_{2:\lambda} \leq \cdots \leq \tilde{R}_{m:\lambda} \leq \cdots \leq \tilde{R}_{\mu:\lambda}\,. \tag{4}$$

Let us denote the mth best offspring by $\tilde{\mathbf{y}}_{m;\lambda}$. Then, the parents of the $(g+1)$ generation are given by $\mathbf{y}_m^{(g+1)} = \tilde{\mathbf{y}}_{m;\lambda}$. Hence, the new center of mass reads

$$\langle \mathbf{y} \rangle^{(g+1)} = \frac{1}{\mu} \sum_{m=1}^{\mu} \mathbf{y}_m^{(g+1)} = \frac{1}{\mu} \sum_{m=1}^{\mu} \tilde{\mathbf{y}}_{m;\lambda} \tag{5}$$

and has the distance $\|\langle \mathbf{y} \rangle^{(g+1)}\|$ to the optimum. Progress is measured as the distance change $\Delta R = R - \|\langle \mathbf{y} \rangle^{(g+1)}\|$ from (g) to $(g+1)$. Thus, the progress rate φ is the expectation of ΔR

$$\varphi_{\mu/\mu,\lambda} = E\{\Delta R\} = E\left\{R - \|\langle \mathbf{y} \rangle^{(g+1)}\|\right\}. \tag{6}$$

From Equations (1) and (3) we have for the mth best offspring

$$\tilde{\mathbf{y}}_{m;\lambda} = \mathbf{R} + \mathbf{Z}_{m;\lambda},$$

that is, the mth best offspring is generated from the "mth best mutation." The mutation $\mathbf{Z}_{m;\lambda}$ can be decomposed

$$\tilde{\mathbf{y}}_{m;\lambda} = R\mathbf{e}_R - x_{m;\lambda}\mathbf{e}_R + \mathbf{h}_{m;\lambda} \tag{7}$$

with $x_{m;\lambda}$, the component of $\mathbf{Z}_{m;\lambda}$ in $-\mathbf{R}$ direction, and the perpendicular part $\mathbf{h}_{m;\lambda}$. The center of mass at generation $(g+1)$ is obtained from Equations (5) and (7)

$$\langle \mathbf{y} \rangle^{(g+1)} = (R - \langle x \rangle)\,\mathbf{e}_R + \langle \mathbf{h} \rangle \tag{8}$$

with

$$\langle x \rangle := \frac{1}{\mu} \sum_{m=1}^{\mu} x_{m;\lambda} \qquad \text{and} \qquad \langle \mathbf{h} \rangle := \frac{1}{\mu} \sum_{m=1}^{\mu} \mathbf{h}_{m;\lambda}. \tag{9}$$

Substitution of Equation (8) into Equation (6) yields

$$\begin{aligned} \varphi_{\mu/\mu,\lambda} &= E\left\{R - \sqrt{(R - \langle x \rangle)^2 + \langle \mathbf{h} \rangle^2}\right\} \\ \varphi_{\mu/\mu,\lambda} &= E\left\{R - \sqrt{R^2 + \langle \mathbf{h} \rangle^2 - 2R\langle x \rangle + \langle x \rangle^2}\right\}. \end{aligned} \tag{10}$$

3.1.2 Stochastical Approximation for $\varphi_{\mu/\mu,\lambda}$ The progress rate expression (10) can be further simplified

$$\begin{aligned} & R - \sqrt{R^2 + \langle \mathbf{h} \rangle^2 - 2R\langle x \rangle + \langle x \rangle^2} \\ = \; & R - \sqrt{R^2 + \langle \mathbf{h} \rangle^2} \sqrt{1 - \frac{2R\langle x \rangle}{R^2 + \langle \mathbf{h} \rangle^2} + \frac{\langle x \rangle^2}{R^2 + \langle \mathbf{h} \rangle^2}} \\ \approx \; & R - \sqrt{R^2 + \langle \mathbf{h} \rangle^2} \left(1 - \frac{R\langle x \rangle}{R^2 + \langle \mathbf{h} \rangle^2} - \frac{1}{2} \left(\frac{R\langle x \rangle}{R^2 + \langle \mathbf{h} \rangle^2} \right)^2 + \cdots \right). \end{aligned} \tag{11}$$

Here we have used the assumptions

$$E\{\langle x \rangle^2\} \ll E\{\langle \mathbf{h} \rangle^2\} \qquad \text{and} \qquad E\{|\langle x \rangle|\} \ll R, \tag{12}$$

which can be easily justified by geometrical considerations and the Taylor expansion $\sqrt{1-a} = 1 - a/2 - a^2/8 + \cdots$. Neglecting the third term in the parenthesis of Equation (11) gives for Equation (10)

$$\varphi_{\mu/\mu,\lambda} = E\left\{ R\left(1 - \sqrt{1 + \frac{\langle \mathbf{h} \rangle^2}{R^2}} \right) + \frac{\langle x \rangle}{\sqrt{1 + \frac{\langle \mathbf{h} \rangle^2}{R^2}}} \right\}. \tag{13}$$

As can be seen from Equations (10) or (13), φ depends on the two variates $\langle \mathbf{h} \rangle^2$ and $\langle x \rangle$.

Following from findings presented in Beyer (1995, Eqs. [8/9]), the standard deviation of $\langle \mathbf{h} \rangle^2$ is small compared to its expectation

$$D\{\langle \mathbf{h} \rangle^2\} / E\{\langle \mathbf{h} \rangle^2\} \sim \sqrt{2/N}.$$

That is, $\mathbf{h}^2$ exhibits only small fluctuations around its mean value. Therefore, this holds for the $\langle \mathbf{h} \rangle^2$ variate, too. If one further assumes that $\langle x \rangle$ and $\langle \mathbf{h} \rangle^2$ are nearly independent of each other, then the simplest form of the stochastical approximation can be applied: The curly brace from Equation (13) as a function of $\langle \mathbf{h} \rangle^2$ and $\langle x \rangle$ is expanded in a Taylor series about $E\{\langle \mathbf{h} \rangle^2\}$ and $E\{\langle x \rangle\}$. Breaking off after the linear terms and taking the expectation yields

$$\varphi_{\mu/\mu,\lambda} = R\left(1 - \sqrt{1 + \frac{\overline{\langle \mathbf{h} \rangle^2}}{R^2}} \right) + \frac{\overline{\langle x \rangle}}{\sqrt{1 + \frac{\overline{\langle \mathbf{h} \rangle^2}}{R^2}}}, \tag{14}$$

with the abbreviations

$$\overline{\langle \mathbf{h} \rangle^2} := E\left\{ \langle \mathbf{h} \rangle^2 \right\} \qquad \text{and} \qquad \overline{\langle x \rangle} := E\left\{ \langle x \rangle \right\}. \tag{15}$$

The expression $\overline{\langle \mathbf{h} \rangle^2}$ can be further simplified. From Equations (9) and (15) we have

$$\begin{aligned} \overline{\langle \mathbf{h} \rangle^2} &= E\left\{ \left(\frac{1}{\mu} \sum_{m=1}^{\mu} \mathbf{h}_{m;\lambda} \right)^2 \right\} = \frac{1}{\mu^2} E\left\{ \sum_{m=1}^{\mu} \sum_{k=1}^{\mu} \left(\mathbf{h}_{k;\lambda}^T \mathbf{h}_{m;\lambda} \right) \right\} \\ &= \frac{1}{\mu^2} E\left\{ \sum_{m=1}^{\mu} \left(\mathbf{h}_{m;\lambda}^T \mathbf{h}_{m;\lambda} \right) \right\} + \frac{1}{\mu^2} E\left\{ \sum_{m=1}^{\mu} \sum_{k \neq m} \left(\mathbf{h}_{k;\lambda}^T \mathbf{h}_{m;\lambda} \right) \right\} \end{aligned}$$

$$= \frac{1}{\mu^2}\sum_{m=1}^{\mu} E\left\{\mathbf{h}_{m;\lambda}^2\right\} + \frac{1}{\mu^2}\sum_{m=1}^{\mu}\sum_{k\neq m} E\left\{\mathbf{h}_{k;\lambda}^T\,\mathbf{h}_{m;\lambda}\right\}$$

$$= \frac{1}{\mu^2}\sum_{m=1}^{\mu}\overline{\mathbf{h}_{m;\lambda}^2} + \frac{1}{\mu^2}\sum_{m=1}^{\mu}\sum_{k\neq m}\overline{\mathbf{h}_{k;\lambda}^T\,\mathbf{h}_{m;\lambda}}\,. \tag{16}$$

It is interesting to note that the expectation of the scalar product $\mathbf{h}_{k;\lambda}^T\,\mathbf{h}_{m;\lambda}$ vanishes

$$k \neq m \quad \Longrightarrow \quad E\left\{\mathbf{h}_{k;\lambda}^T\,\mathbf{h}_{m;\lambda}\right\} = 0. \tag{17}$$

The $\mathbf{h}_{k;\lambda}$ vectors are independent of each other. There is neutral selection normal to the $\mathbf{R}$ direction because of the symmetry of the spherical model. Each direction normal to $\mathbf{R}$ has equal likelihood. Thus, for fixed k and m

$$E\left\{\mathbf{h}_{k;\lambda}^T\,\mathbf{h}_{m;\lambda}\right\} = E\left\{\mathbf{h}_{k;\lambda}^T\right\}\,E\left\{\mathbf{h}_{m;\lambda}\right\} = 0$$

holds and from Equation (16) only the first term

$$\overline{\langle\mathbf{h}\rangle^2} = \frac{1}{\mu^2}\sum_{m=1}^{\mu}\overline{\mathbf{h}_{m;\lambda}^2} =: \frac{1}{\mu}\overline{\langle\mathbf{h}^2\rangle} \tag{18}$$

remains. Therefore one finally obtains

$$\varphi_{\mu/\mu,\lambda} = R\left(1 - \sqrt{1 + \frac{\overline{\langle\mathbf{h}^2\rangle}}{\mu R^2}}\right) + \frac{\langle\bar{x}\rangle}{\sqrt{1 + \frac{\overline{\langle\mathbf{h}^2\rangle}}{\mu R^2}}}\,. \tag{19}$$

With Equation (19) we have expressed the progress rate by the two expectancies $\overline{\langle\mathbf{h}^2\rangle}$ and $\langle\bar{x}\rangle$ to be determined in the next section.

3.2 Implementation of the Theory

3.2.1 Determination of $\langle\bar{x}\rangle$ As can be seen from Equation (9) $\langle\bar{x}\rangle$ is given by the sum of the expected values of $x_{m;\lambda}$

$$\langle\bar{x}\rangle = \frac{1}{\mu}\sum_{m=1}^{\mu}\overline{x_{m;\lambda}} = \frac{1}{\mu}\sum_{m=1}^{\mu}\int_{-\infty}^{\infty} x p_{m;\lambda}(x)\,dx. \tag{20}$$

The function $p_{m;\lambda}(x)$ is the probability density function (pdf) of x belonging to the mth best offspring. The ordering of the offspring obeys the ranking (4). The pdf $p(x)$ for a single trial x is given by

$$p(x) = \frac{1}{\sqrt{2\pi}\,\sigma} e^{-\frac{1}{2}\left(\frac{x}{\sigma}\right)^2}. \tag{21}$$

(x is a (rotated) component of the mutation vector $\mathbf{Z}$). Given a fixed x, the $\tilde{R}$ of the trial has the conditional pdf $p(r \mid x)$. Let this trial be the mth best, then there are $(m-1)$ offspring with $(\tilde{R} \leq r)$ and $(\lambda - m)$ offspring with $(\tilde{R} > r)$, and there are $\lambda!/((m-1)!\,(\lambda-m)!)$ equivalent

orderings. If integrated over the possible r values one obtains the pdf $p_{m;\lambda}(x)$

$$p_{m;\lambda}(x) = p(x)\frac{\lambda!}{(m-1)!\,(\lambda-m)!}\int_{r=0}^{\infty} p(r \mid x)[P(\tilde{R} \le r)]^{m-1}[P(\tilde{R} > r)]^{\lambda-m}\,dr. \tag{22}$$

$P(\tilde{R} \le r) = P(r)$ has already been determined (see Eq. [11] in Beyer, 1995)

$$P(r) = \frac{1}{2} + \Phi_0\left(\frac{r^2 - R^2 - \sigma^2 N}{2\sigma R\sqrt{1 + \frac{\sigma^2 N}{2R^2}}}\right), \tag{23}$$

with the Gauss-integral $\Phi_0(x) = \frac{1}{2}\,\mathrm{erf}(x/\sqrt{2})$. It remains the determination of $p(r \mid x)$, which can be derived from the conditional cumulate distribution function (cdf) $P(\tilde{R} \le r \mid x) = P(\tilde{R}^2 \le r^2 \mid x)$. From geometrical considerations provided in Beyer (1995, Eq. [7]) one has

$$\tilde{R}^2 = \mathbf{h}^2 + R^2 - 2Rx \le r^2 \tag{24}$$

and therefore $\mathbf{h}^2 \le r^2 - R^2 + 2Rx$. The $\mathbf{h}^2$ variate obeys the pdf $p_{h^2}(v_2)$, (cp. Eq. [10] in Beyer, 1995)

$$p_{h^2}(v_2) = \frac{1}{\sqrt{2\pi}\sqrt{2N\sigma^2}}\exp -\frac{1}{2}\left(\frac{v_2 - N\sigma^2}{\sqrt{2N\sigma^2}}\right)^2, \tag{25}$$

thus we find

$$P(\tilde{R} \le r \mid x) = \int_{v_2=0}^{v_2=r^2-R^2+2Rx} p_{h^2}(v_2)\,dv_2 = \frac{1}{2} + \Phi_0\left(\frac{r^2 - R^2 - N\sigma^2 + 2Rx}{\sqrt{2N\sigma^2}}\right)$$

and

$$p(r \mid x) = \frac{d}{dr}P(\tilde{R} \le r \mid x) = \frac{2r}{\sqrt{2\pi}\sqrt{2N\sigma^2}}\exp -\frac{1}{2}\left(\frac{r^2 - R^2 - N\sigma^2 + 2Rx}{\sqrt{2N\sigma^2}}\right)^2. \tag{26}$$

Continuing with Equation (20) one obtains after the exchange of the integration order

$$\langle\bar{x}\rangle = \frac{\lambda!}{\mu}\int_{r=0}^{\infty}\left(\int_{-\infty}^{\infty} xp(x)p(x \mid r)\,dx\right)\sum_{m=1}^{\mu}\frac{[P(r)]^{m-1}[1 - P(r)]^{\lambda-m}}{(m-1)!\,(\lambda-m)!}\,dr. \tag{27}$$

The expression in the parenthesis of Equation (27) can be easily calculated. After the substitution $t = x/\sigma$ the $(\cdots)$-expression reads with Equations (21) and (26)

$$(\cdots) = \frac{2r}{\sqrt{2\pi}\sqrt{2N\sigma}}\frac{1}{\sqrt{2\pi}}\int_{-\infty}^{\infty} te^{-\frac{1}{2}t^2}\exp -\frac{1}{2}\left(\frac{2R}{\sqrt{2N\sigma}}t + \frac{r^2 - R^2 - N\sigma^2}{\sqrt{2N\sigma^2}}\right)^2 dt.$$

This integral has been solved in Beyer (1994b)

$$(\cdots) = -\frac{1}{\sqrt{2\pi}}\frac{\sigma}{\sqrt{1 + \frac{N\sigma^2}{2R^2}}}\frac{2r}{2R\sigma\sqrt{1 + \frac{N\sigma^2}{2R^2}}}\frac{r^2 - R^2 - N\sigma^2}{2R\sigma\sqrt{1 + \frac{N\sigma^2}{2R^2}}}$$
$$\exp -\frac{1}{2}\left(\frac{r^2 - R^2 - N\sigma^2}{2R\sigma\sqrt{1 + \frac{N\sigma^2}{2R^2}}}\right)^2. \tag{28}$$

By performing the substitution

$$y = \left(\frac{r^2 - R^2 - N\sigma^2}{2R\sigma\sqrt{1 + \frac{N\sigma^2}{2R^2}}} \right) \tag{29}$$

in Equation (27), taking Equations (28) and (23) into account one obtains[2]

$$\langle \overline{x} \rangle = -\frac{\sigma}{\sqrt{1 + \frac{N\sigma^2}{2R^2}}} \frac{1}{\sqrt{2\pi}} \frac{\lambda!}{\mu} \int_{y=-\infty}^{y=\infty} y e^{-\frac{1}{2}y^2} \sum_{m=1}^{\mu} \frac{\left(\frac{1}{2} + \Phi_0(y)\right)^{m-1} \left(\frac{1}{2} - \Phi_0(y)\right)^{\lambda-m}}{(m-1)!\,(\lambda-m)!} dy. \tag{30}$$

If the sum in Equation (30) is expressed by an integral (this technique has been demonstrated in Beyer (1995, Section 3.1.2) we get

$$\langle \overline{x} \rangle = -\frac{\sigma}{\sqrt{1 + \frac{N\sigma^2}{2R^2}}} \frac{\lambda - \mu}{\sqrt{2\pi}} \binom{\lambda}{\mu} \int_{y=-\infty}^{y=\infty} \int_{x=0}^{\frac{1}{2} - \Phi_0(y)} y e^{-\frac{1}{2}y^2} x^{\lambda-\mu-1} (1-x)^{\mu-1} \, dx \, dy.$$

The change of the integration order and the substitution $x = \frac{1}{2} - \Phi_0(t)$ yields

$$\begin{aligned} \langle \overline{x} \rangle = & \frac{-\sigma}{\sqrt{1 + \frac{N\sigma^2}{2R^2}}} \frac{\lambda - \mu}{\sqrt{2\pi}} \binom{\lambda}{\mu} \int_{t=-\infty}^{t=\infty} \frac{e^{-\frac{1}{2}t^2}}{\sqrt{2\pi}} \left(\frac{1}{2} - \Phi_0(t)\right)^{\lambda-\mu-1} \\ & \times \left(\frac{1}{2} + \Phi_0(t)\right)^{\mu-1} \int_{y=-\infty}^{y=t} y e^{-\frac{1}{2}y^2} \, dy \, dt. \end{aligned}$$

The y-integral gives $-\exp(-t^2/2)$ and after $t \to -t$ one obtains

$$\langle \overline{x} \rangle = \frac{\sigma}{\sqrt{1 + \frac{N\sigma^2}{2R^2}}} e^{1,0}_{\mu,\lambda}, \tag{31}$$

with $e^{1,0}_{\mu,\lambda}$, a special case of the *generalized progress coefficients* introduced in Beyer (1995, Eq. [82]). The integral representation of $e^{1,0}_{\mu,\lambda}$ can be found below, Equation (40).

3.2.2 Determination of $\langle \overline{\mathbf{h}^2} \rangle$

$\langle \overline{\mathbf{h}^2} \rangle$ is defined by Equation (18)

$$\langle \overline{\mathbf{h}^2} \rangle = \frac{1}{\mu} \sum_{m=1}^{\mu} \overline{\mathbf{h}^2_{m;\lambda}} = \frac{1}{\mu} \sum_{m=1}^{\mu} \int_{v_2=0}^{\infty} v_2 p_{m;\lambda}(v_2) \, dv_2. \tag{32}$$

with $v_2 := \mathbf{h}^2$ and $p_{m;\lambda}(v_2)$, the pdf of $\mathbf{h}^2$ for the mth best trial. The pdf of $\mathbf{h}^2$ from a single trial is given by Equation (25) $p(v_2) = p_{h^2}(v_2)$. By the same arguments used to derive Equation (22) we obtain

$$p_{m;\lambda}(v_2) = p_{h^2}(v_2) \frac{\lambda!}{(m-1)!\,(\lambda-m)!} \int_{r=0}^{\infty} p(r \mid v_2) [P(r)]^{m-1} [1 - P(r)]^{\lambda-m} \, dr. \tag{33}$$

2 The lower limit $y =: y_{l_0}$ in Equation (30) has been shifted to $y = -\infty$, because the upper bound $\hat{y}_{l_0}$ of y_{l_0} is $\hat{y}_{l_0} = \mathrm{Max}\{y_l\} = -\sqrt{N/2}$ and the integrand is concentrated about $y = 0$.

The pdf $p(r \mid v_2) = p(r \mid \mathbf{h}^2) = \frac{d}{dr}P(\tilde{R} \leq r \mid \mathbf{h}^2)$ can be derived from the conditional cdf $P(\tilde{R}^2 \leq r^2 \mid \mathbf{h}^2)$. From Equation (24) we find $x \geq (\mathbf{h}^2 + R^2 - r^2)/2R$. The pdf of x is given by Equation (21). Thus it is

$$P(\tilde{R} \leq r \mid \mathbf{h}^2) = P(\tilde{R}^2 \leq r^2 \mid \mathbf{h}^2) = \frac{1}{\sqrt{2\pi}\,\sigma} \int_{x=\frac{\mathbf{h}^2+R^2-r^2}{2R}}^{\infty} e^{-\frac{1}{2}\frac{x^2}{\sigma^2}} dx = \frac{1}{2} - \Phi_0\left(\frac{\mathbf{h}^2 + R^2 - r^2}{2R\sigma}\right)$$

and

$$p(r \mid v_2) = \frac{r}{\sqrt{2\pi}R\sigma} \exp -\frac{1}{2}\left(\frac{v_2 + R^2 - r^2}{2R\sigma}\right). \tag{34}$$

With Equations (33), (34), and (25) one obtains for Equation (32) analogously to Equation (27)

$$\langle\overline{\mathbf{h}^2}\rangle = \frac{\lambda!}{\mu} \int_{r=0}^{\infty} \left(\int_{v_2=0}^{\infty} v_2 p_{b^2}(v_2) p(r \mid v_2)\, dv_2 \right) \sum_{m=1}^{\mu} \frac{[P(r)]^{m-1}[1 - P(r)]^{\lambda-m}}{(m-1)!\,(\lambda - m)!}\, dr, \tag{35}$$

and the expression in the parenthesis reads

$$\begin{aligned}(\cdots) &= \frac{r}{\sqrt{2\pi}R\sigma} \frac{1}{\sqrt{2\pi}\sqrt{2N\sigma^2}} \int_{v_2=0}^{\infty} v_2 \exp -\frac{1}{2}\left(\frac{v_2 - \sigma^2 N}{\sqrt{2N\sigma^2}}\right)^2 \\ &\quad \exp -\frac{1}{2}\left(\frac{v_2 + R^2 - r^2}{2R\sigma}\right)^2 dv_2.\end{aligned}$$

From a straightforward calculation (Beyer, 1994b) there results

$$\begin{aligned}(\cdots) &= -\frac{\sigma^2 N}{\sqrt{2\pi}} \frac{r}{\sigma R\sqrt{1 + \frac{N\sigma^2}{2R^2}}} \left(1 - \frac{\sigma}{R\sqrt{1 + \frac{N\sigma^2}{2R^2}}} \frac{R^2 + \sigma^2 N - r^2}{2R\sigma\sqrt{1 + \frac{N\sigma^2}{2R^2}}}\right) \\ &\quad \exp -\frac{1}{2}\left(\frac{R^2 + \sigma^2 N - r^2}{2R\sigma\sqrt{1 + \frac{N\sigma^2}{2R^2}}}\right)^2.\end{aligned}$$

If inserted into Equation (35) taking Equation (23) into account one obtains by the substitution of Equation (29)

$$\begin{aligned}\langle\overline{\mathbf{h}^2}\rangle &= \frac{\sigma^2 N}{\sqrt{2\pi}} \frac{\lambda!}{\mu} \int_{y=-\infty}^{\infty} \left(1 + \frac{\sigma}{R\sqrt{1 + \frac{N\sigma^2}{2R^2}}} y\right) e^{-\frac{1}{2}y^2} \\ &\quad \times \sum_{m=1}^{\mu} \frac{\left(\frac{1}{2} + \Phi_0(y)\right)^{m-1} \left(\frac{1}{2} - \Phi_0(y)\right)^{\lambda-m}}{(m-1)!\,(\lambda - m)!}\, dy.\end{aligned}$$

The integration of the first part (i.e., the integrand belonging to the 1 in the parentheses) gives $\sigma^2 N$. The second part is similar to Equation (30). Hence, we find

$$\langle\overline{\mathbf{h}^2}\rangle = \sigma^2 N \left[1 - \frac{\sigma}{R\sqrt{1 + \frac{N\sigma^2}{2R^2}}} e^{1,0}_{\mu,\lambda}\right]. \tag{36}$$

3.2.3 Assembly of the Progress Rate Formula As usual, we introduce normalized quantities $\varphi^\star := \varphi N/R$ and $\sigma^\star := \sigma N/R$. The square root expression in Equation (19) can

be written with Equation (36) as

$$\begin{aligned}\sqrt{1+\frac{\langle\overline{\mathbf{h}^2}\rangle}{\mu R^2}} &= \sqrt{1+\frac{(\sigma^\star)^2}{\mu N}-\frac{(\sigma^\star)^2}{\mu N}\frac{\sigma^\star}{N\sqrt{1+\frac{(\sigma^\star)^2}{2N}}}e^{1,0}_{\mu,\lambda}} \\ &= \sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}\sqrt{1-\frac{(\sigma^\star)^2}{\mu N\left(1+\frac{(\sigma^\star)^2}{\mu N}\right)}\frac{\sigma^\star}{N\sqrt{1+\frac{(\sigma^\star)^2}{2N}}}e^{1,0}_{\mu,\lambda}} \\ &\approx \sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}-\frac{1}{2}\frac{(\sigma^\star)^3\,e^{1,0}_{\mu,\lambda}}{\mu N^2\sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}\sqrt{1+\frac{(\sigma^\star)^2}{2N}}}.\end{aligned}$$

The last line has been obtained by Taylor expansion $\sqrt{1-a}\approx 1-a/2$. With the same order of approximation $1/\sqrt{1-a}\approx 1+a/2$ one gets

$$\left(\sqrt{1+\frac{\langle\overline{\mathbf{h}^2}\rangle}{\mu R^2}}\right)^{-1} \approx \left(\sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}\right)^{-1}+\frac{1}{2}\frac{(\sigma^\star)^3\,e^{1,0}_{\mu,\lambda}}{\mu N^2\sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}\sqrt{1+\frac{(\sigma^\star)^2}{2N}}}$$

and with Equations (19/31) the normalized progress rate $\varphi^\star$ reads

$$\begin{aligned}\varphi^\star_{\mu/\mu,\lambda} &= N\left(1-\sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}\right)+\frac{\sigma^\star\,e^{1,0}_{\mu,\lambda}}{\sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}\sqrt{1+\frac{(\sigma^\star)^2}{2N}}} \\ &\quad+\frac{\sigma^\star\,e^{1,0}_{\mu,\lambda}}{\sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}\sqrt{1+\frac{(\sigma^\star)^2}{2N}}}\frac{(\sigma^\star)^2}{2\mu N}\left(1+\frac{1}{N}\frac{\sigma^\star\,e^{1,0}_{\mu,\lambda}}{\sqrt{1+\frac{(\sigma^\star)^2}{2N}}}\right). \qquad (37)\end{aligned}$$

If one neglects the last term in Equation (37), then we finally arrive at the *progress rate formula for the* $(\mu/\mu_I,\lambda)$*-ES*

$$\varphi^\star_{\mu/\mu,\lambda}(\sigma^\star) = N\left(1-\sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}\right)+\sigma^\star\,c_{\mu/\mu,\lambda}\frac{1+\frac{(\sigma^\star)^2}{2\mu N}}{\sqrt{1+\frac{(\sigma^\star)^2}{2N}}\sqrt{1+\frac{(\sigma^\star)^2}{\mu N}}}. \qquad (38)$$

We have introduced the progress coefficient $c_{\mu/\mu,\lambda}$

$$c_{\mu/\mu,\lambda} := e^{1,0}_{\mu,\lambda} \qquad (39)$$

in order to have a "notational continuity."[3] The notation $c_{\mu/\mu,\lambda}$ can be easily computed by numerical integration of Equation (40), below. Table 1 gives a collection of some $c_{\mu/\mu,\lambda}$ values. In the next section we will derive asymptotic formulas for the $c_{\mu/\mu,\lambda}$ coefficients.

3.2.4 Asymptotics of the $c_{\mu/\mu,\lambda}$ Coefficients For large λ values and moderate $\kappa := \mu/\lambda$ truncation ratios it is possible to derive asymptotic formulas for $c_{\mu/\mu,\lambda}$. The progress

3 The $c_{\mu/\mu,\lambda}$ notation was originally coined by Rechenberg (1993).

Table 1. Selected $c_{\mu/\mu,\lambda}$ coefficients.

$\mu \setminus \lambda$	10	20	30	40	50	100	150	200	300
1	1.539	1.867	2.043	2.161	2.249	2.508	2.649	2.746	2.878
2	1.270	1.638	1.829	1.957	2.052	2.328	2.478	2.580	2.718
3	1.065	1.469	1.674	1.810	1.911	2.201	2.357	2.463	2.607
4	0.893	1.332	1.550	1.694	1.799	2.101	2.263	2.372	2.520
5	0.739	1.214	1.446	1.596	1.705	2.018	2.185	2.297	2.449
10	0.000	0.768	1.061	1.242	1.372	1.730	1.916	2.040	2.206
20	—	0.000	0.530	0.782	0.950	1.386	1.601	1.742	1.928
30	—	—	0.000	0.414	0.634	1.149	1.390	1.545	1.746
40	—	—	—	0.000	0.343	0.958	1.225	1.393	1.608
50	—	—	—	—	0.000	0.792	1.085	1.265	1.494
100	—	—	—	—	—	0.000	0.542	0.795	1.088

coefficient integral for $c_{\mu/\mu,\lambda}$ is given by

$$c_{\mu/\mu,\lambda} = e^{1,0}_{\mu,\lambda} = \frac{\lambda-\mu}{2\pi}\binom{\lambda}{\mu}\int_{-\infty}^{\infty} e^{-t^2}\left(\frac{1}{2}+\Phi_0(t)\right)^{\lambda-\mu-1}\left(\frac{1}{2}-\Phi_0(t)\right)^{\mu-1} dt. \tag{40}$$

(N.B., the generalized progress coefficients $e^{\alpha,\beta}_{\mu,\lambda}$ have been defined in Beyer 1995.)

If the substitution $z = \frac{1}{2} - \Phi_0(t)$ is applied, then one obtains

$$c_{\mu/\mu,\lambda} = \frac{\lambda}{\mu}\frac{1}{\sqrt{2\pi}}\frac{1}{B(\lambda-\mu,\mu)}\int_0^1 \exp -\frac{1}{2}\left[\Phi_0^{-1}\left(\frac{1}{2}-z\right)\right]^2 z^{\mu-1}(1-z)^{\lambda-\mu-1}\,dz. \tag{41}$$

The quotient $(\lambda-1)!/((\lambda-\mu-1)!\,(\mu-1)!)$ has been expressed by the (complete) *beta function* $B(\lambda-\mu,\mu)$, which has the integral representation (Abramowitz & Stegun, 1984, p. 79)

$$B(\lambda-\mu,\mu) = \frac{(\lambda-\mu-1)!\,(\mu-1)!}{(\lambda-1)!} = \frac{\Gamma(\lambda-\mu)\Gamma(\mu)}{\Gamma(\lambda)} = \int_0^1 z^{\mu-1}(1-z)^{\lambda-\mu-1}\,dz. \tag{42}$$

For large values of μ and $\lambda-\mu$ the function $z^{\mu-1}(1-z)^{\lambda-\mu-1}$ forms a sharp peak. Its maximum may be at $z = \hat{z}$

$$\text{Max}\left\{z^{\mu-1}(1-z)^{\lambda-\mu-1}\right\} \quad\Leftrightarrow\quad z=\hat{z} \quad\Leftrightarrow\quad \hat{z} = \frac{\mu-1}{\lambda-2}. \tag{43}$$

Expanding

$$f(z) := \exp -\frac{1}{2}\left[\Phi_0^{-1}\left(\frac{1}{2}-z\right)\right]^2$$

at $z = \hat{z}$ in a Taylor series and substitution into Equation (41) yields

$$c_{\mu/\mu,\lambda} = \frac{1}{\kappa}\frac{1}{\sqrt{2\pi}}\sum_{m=0}^{\infty}\frac{1}{m!}\left.\frac{d^m f(z)}{dz^m}\right|_{z=\hat{z}}\frac{1}{B(\lambda-\mu,\mu)}\int_0^1 (z-\hat{z})^m z^{\mu-1}(1-z)^{\lambda-\mu-1}\,dz. \tag{44}$$

The part after the derivative in Equation (44) is an integral representation of the *hypergeometric function* $F(a,b;c;z)$ (Abramowitz & Stegun, 1984, p. 215). Therefore, Equation (44)

can be written as

$$c_{\mu/\mu,\lambda} = \frac{1}{\kappa}\frac{1}{\sqrt{2\pi}}\sum_{m=0}^{\infty}\frac{(-\hat{z})^m}{m!}\left.\frac{d^m f(z)}{dz^m}\right|_{z=\hat{z}} F\left(-m,\mu;\lambda;\frac{1}{\hat{z}}\right), \qquad \kappa = \frac{\mu}{\lambda}. \tag{45}$$

Below, we derive only the first two terms of the expansion (45). For $m = 0$ one finds with Equations (42/44) $F(0,\mu;\lambda;\frac{1}{\hat{z}}) = 1$. The case where $m = 1$ needs further considerations. First, $\frac{df(z)}{dz}$ is determined. The derivative of $\Phi_0^{-1}(y)$ can be obtained by differentiation of the identity $\Phi_0^{-1}(y(t)) = t$, $y(t) = \Phi_0(t)$. One finds $\frac{df}{dz} = \sqrt{2\pi}\,\Phi_0^{-1}\left(\frac{1}{2} - z\right)$ and therefore

$$\left.\frac{df}{dz}\right|_{z=\hat{z}} = \sqrt{2\pi}\Phi_0^{-1}\left(\frac{1}{2} - \frac{\mu-1}{\lambda-2}\right). \tag{46}$$

The integral part of Equation (44) can be tackled by usage of Equation (42)

$$-\hat{z}F\left(-1,\mu;\lambda;\frac{1}{\hat{z}}\right) = \frac{1}{B(\lambda-\mu,\mu)}\int_0^1 (z-\hat{z})\,z^{\mu-1}(1-z)^{\lambda-\mu-1}\,dz = \frac{\mu}{\lambda} - \hat{z}. \tag{47}$$

Collecting the parts (43/45/46/47) gives

$$\begin{aligned} c_{\mu/\mu,\lambda} \;=\; & \frac{1}{\kappa}\frac{1}{\sqrt{2\pi}}\left\{\exp -\frac{1}{2}\left[\Phi_0^{-1}\left(\frac{1}{2} - \kappa\left(\frac{1-1/\mu}{1-2/\lambda}\right)\right)\right]^2\right. \\ & \left. + \frac{\sqrt{2\pi}}{\lambda}\left(\frac{1-2\kappa}{1-2/\lambda}\right)\Phi_0^{-1}\left(\frac{1}{2} - \kappa\left(\frac{1-1/\mu}{1-2/\lambda}\right)\right) + \cdots\right\}. \end{aligned} \tag{48}$$

For large λ values ($\lambda \gtrapprox 200$), and moderate $\kappa = \mu/\lambda$ ($0.03 \lessapprox \kappa \lessapprox 0.97$) formula (48) may be approximately used instead of Equation (40).[4] If the limit $\lambda \to \infty$ is taken in formula (48) one obtains the asymptotically exact formula

$$c_{\mu/\mu,\lambda} = \frac{\lambda}{\mu}\frac{1}{\sqrt{2\pi}}\exp -\frac{1}{2}\left[\Phi_0^{-1}\left(\frac{1}{2} - \frac{\mu}{\lambda}\right)\right]^2, \qquad 0 < \frac{\mu}{\lambda} < 1.$$

This approximation yields satisfactory results for $\lambda \gtrapprox 1000$.

3.3 Results and Conclusions from the $(\mu/\mu_I, \lambda)$-Theory

3.3.1 Comparison with Experiments The progress rate formula has been tested for different λ, μ, N-combinations. As an example, results from the $(8/8_I, 30)$-ES for $N = 30$ and $N = 200$ are shown. The experimental technique used is similar to the $(1,\lambda)$-experiments described in Beyer (1995, Section 2.3). G "one-generation" experiments are performed from a fixed parent $\mathbf{y}$ (with distance R to the optimum) with fixed σ-mutation strength. "One-generation"—according to Section 2, Equation (1)—comprises the generation of λ offspring $\tilde{\mathbf{y}}_l$ by mutation from $\mathbf{y}$, selection of the best μ offspring $\tilde{\mathbf{y}}_{m;\lambda}$, and averaging these offspring to obtain $\|\langle\tilde{\mathbf{y}}\rangle\|$. The rest is analogous to the $(1,\lambda)$-experiments (Beyer 1995, Section 2.3).

Figure 1 depicts the results gathered from $G = 10,000$ "one-generation" experiments per $\sigma^\star$ value, represented by dots. The curves are graphs from Equation (38) with $c_{8/8,30} = 1.196$.

4 Instead of $\Phi_0^{-1}(y)$ the inverse error function erf^{-1} may be used: $\Phi_0^{-1}(y) = \sqrt{2}\,\mathrm{erf}^{-1}(2y)$.

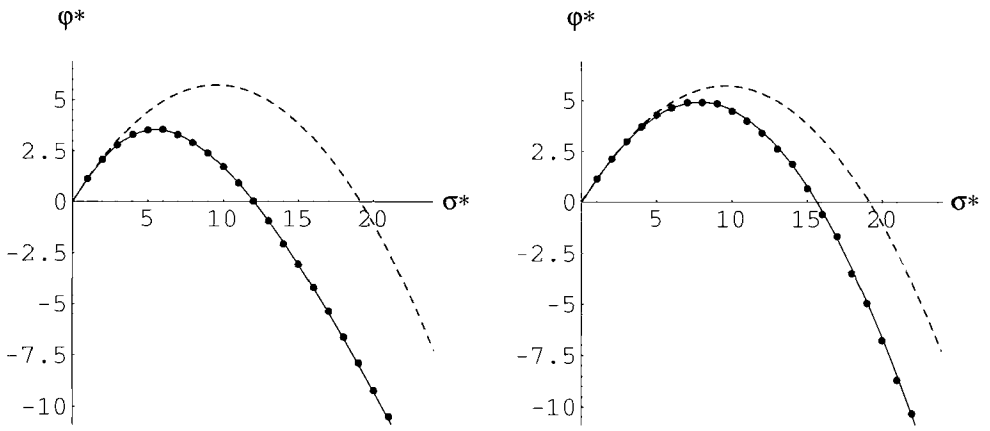

Figure 1. Comparison of theory and experiment for the $(8/8_I, 30)$ intermediate ES. The dashed curves are due to Rechenberg's formula. In the left graph, the case $N = 30$ is displayed and in the right, $N = 200$.

The dashed curves are due to Rechenberg's "universal law" (Rechenberg, 1993)

$$\varphi^{\star}_{\mu/\mu,\lambda} = \sigma^{\star} c_{\mu/\mu,\lambda} - \frac{(\sigma^{\star})^2}{2\mu} .$$

One can see that this formula holds mainly for small $\sigma^{\star}$ values: As in the case of the $(1, \lambda)$ theory, the Rechenberg formula can be recovered by expanding the roots in Equation (38) for small $(\sigma^{\star})^2/N$ values.[5]

3.3.2 On the Benefits of Sexuality The advantages of $(\mu/\mu, \lambda)$ strategies is their—at the first glance—surprisingly high progress rate in comparison with the simple (μ, λ) ES. Suppose the strategies are tuned for maximum performance, for instance, by a σ-self-adaptation mechanism developed by Schwefel (1995). If we assume that such a mechanism provides (at least) locally the maximum progress rate $\hat{\varphi}^{\star}$ for fixed strategy parameters μ, λ, and N

$$\hat{\varphi}^{\star}(\mu, \lambda, N) = \mathrm{Max}_{[\sigma^{\star}]} \{\varphi^{\star}(\sigma^{\star}, \mu, \lambda, N)\}, \tag{49}$$

then we can compare the (μ, λ) and the $(\mu/\mu, \lambda)$ ES. As an example, the $\lambda = 50$ strategies for $N = 100$ are depicted in Figure 2. The lower curve was obtained from Equation (49) by maximization of the progress rate formula for $\varphi^{\star}_{\mu,\lambda}$ derived in Beyer (1995, Eq. [98]) treating μ as a real parameter. The upper curve was computed by the same procedure applied to Equation (38). As can be seen, the $(\mu/\mu, \lambda)$ strategies are superior to the (μ, λ) strategies. What is the reason for this behavior?

5 In his new book Rechenberg (1994, pp. 22, 23) emphasizes that his theory is an asymptotic one that holds for large N and small σ-values.

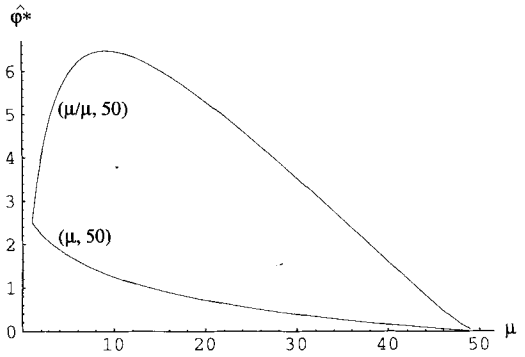

Figure 2. The maximum progress rate $\hat{\varphi}^*$ versus the number of parents μ producing $\lambda = 50$ offspring. The parameter space dimension is $N = 100$. Note, the $(\mu/\rho_I, 50)$ strategies are expected to lie between these two extremal curves.

In order to see the main difference between $\varphi^*_{\mu,\lambda}$ and $\varphi^*_{\mu/\mu,\lambda}$ we compare the simplified $\varphi^*_{\mu,\lambda}$ formula (cp. Beyer, 1995, Eq. [101])

$$\varphi^*_{\mu,\lambda}(\sigma^*) = N\left(1 - \sqrt{1 + \frac{(\sigma^*)^2}{N}}\right) + c_{\mu,\lambda}\,\sigma^*\sqrt{\frac{1 + \frac{(\sigma^*)^2}{2N}}{1 + \frac{(\sigma^*)^2}{N}}} \tag{50}$$

with Equation (38). It is eye catching that the $(\sigma^*)^2/N$ of the first term in Equation (50) is replaced by $(\sigma^*)^2/\mu N$ in Equation (38). If traced back to Equations (18/19) one recognizes that the $1/\mu$ factor is due to the averaging of the **h** vectors of the best μ mutations. Note, we had decomposed the mutations **Z** (according to Eq. [7]) in a component x in optimum direction and in a perpendicular **h**. By the intermediate recombination, that is, the averaging of these **h** vectors, the length of the resulting $\langle \mathbf{h} \rangle$ is by an approximate factor of $1/\sqrt{\mu}$ smaller than the expected length of a single **h**. This statement that holds exactly for the square of **h** was obtained from Equations (16/17). Because the **h** vectors are not correlated (random mutations, and neutral selection normal to **R**) the cross-correlation part in Equation (16) vanishes. If one interprets the **h** components as the "harmful part" of the mutation **Z** (because they increase the distance to the optimum), then a recombination producing $\langle \mathbf{h} \rangle$ decreases this part. The author will call this mechanism *genetic repair*.

As far as intermediate recombination is concerned, the statement often invoked by EA-users explaining the benefit of sexuality that recombination "combines good properties" of the mates to form better offspring is wrong: In our model the "good properties" are simply the $x_{m;\lambda}$. They are averaged according to Equation (9). It is quite obvious that $\langle x \rangle$ cannot be larger than the x value of the best offspring. The performance gain of the $(\mu/\mu, \lambda)$-ES has another reason: If one investigates the $\hat{\sigma}^*$ values that maximize φ^* (cp. e.g., Figure 1), then it becomes clear that $(\mu/\mu, \lambda)$ strategies exhibit optimal performance for larger mutation strengths than (μ, λ) strategies. Larger mutations produce larger $x_{m;\lambda}$ components and **h** vectors as well. However, due to the genetic repair, the "harmful" influence of the **h** vectors is diminished. This reminds the author of a saying by Schwefel (1987, p. 1032):

> Even if all of them were wrong they might as well be worthwhile to be recombined with each other.

From Equations (9/16) it becomes clear that the genetic repair exhibits the best performance, if all μ parents contribute to the recombination, that is, $\rho = \mu$. The averaging of ρ parents with $\rho < \mu$ yields worse results. The case $\rho = 1$ is equivalent to the (μ, λ) ES. Hence, the performance of all the other $(\mu/\rho_I, \lambda)$ strategies should lie between the two extremes (μ, λ) and $(\mu/\mu_I, \lambda)$.

Note, genetic repair relies on differing recombination mates, otherwise Equation (17) does not hold. It is worth mentioning that in zoology a phenomenon is observed that may be called "incest taboo." In the higher animals, the begetting of offspring by close relatives is relatively seldom observed. And inbreeding often produces hereditary defects.

Up until now, reasons for sexual recombination are subject to controversial discussions in biology. Some scientists emphasize recombination as a source of genetic variation (for a discussion of the current hypotheses, cp. Michod & Levin, 1988), and we will see in Section 4 that there is a certain counterpart in dominant $(\mu/\rho_D, \lambda)$ strategies. But this is only half the story. Genetic repair as pointed out by Bernstein, Hopf, and Michod (1987), for example, should also play an important role in the understanding of the universality of recombination. From the investigation of the $(\mu/\rho, \lambda)$ strategies the author makes a speculation somewhat different from the established ones (Michod & Levin, 1988).

In the author's opinion the benefit of sex mainly stems from the higher "evolution speed" made possible by higher mutation rates in conjunction with genetic repair diminishing the influence of the "harmful" part of the mutations. This does not necessarily imply that the physical mutation rate of a chromosome, genome, or species is always at a constant, high level (it may change depending on the environmental conditions). However, the results of dominant recombination may be interpreted as large mutations generated from an average individual—the *wild-type*. Thus, it will be possible to transform a relatively small physical mutation rate into a larger mutation rate on the level of genetic information (to be discussed in Section 4).

3.3.3 The Optimum μ-Choice Unlike parents in real life asking how many children they can afford, we have to determine the number of parents μ given a fixed number of offspring. This is because of the fact that producing offspring and calculating their fitness requires computer power that is restricted by the number of processors available. Usually the number of offspring is a multiple of the number of processors. Therefore, λ is more or less fixed and the question how to choose the number of parents μ is quite natural.

From the viewpoint of genetic repair the number of parents should be large, for instance, $\mu = \rho = \lambda$, yielding the minimum length $\langle \mathbf{h} \rangle$ vector. However, this would produce small or vanishing $\langle x \rangle$-values ($\langle x \rangle = 0 \Leftrightarrow \mu = \lambda$). Therefore, there is bound to be a trade-off between $\langle x \rangle$ (should be large) and $\langle \mathbf{h} \rangle$ (should be small). There will be an optimum μ-choice guaranteeing a maximum progress rate. This is what Figure 2 showed for the $(\mu/\mu_I, 50)$-ES.

Given fixed parameter space dimension N and λ, Equations (38/40) can be used to determine the optimum $\hat{\varphi}^\star$, $\hat{\sigma}^\star$, and $\hat{\mu}$ values. This has been done numerically by maximization of $\varphi^\star = \varphi^\star(\sigma^\star, \mu, \lambda, N)$ with respect to $\sigma^\star$ and μ

$$\hat{\varphi}^\star(\lambda, N) = \mathrm{Max}_{[\sigma^\star, \mu]} \{\varphi^\star(\sigma^\star, \mu, \lambda, N)\} \quad \Leftrightarrow \quad \sigma^\star = \hat{\sigma}^\star, \quad \mu = \hat{\mu}. \tag{51}$$

The results are depicted in Figure 3 and Figure 4.

Figure 3 shows the optimal number of parents $\hat{\mu}$ as a function of λ in the range $\lambda = 5 \ldots 1000$. It is important to note that there is a relatively strong dependence on N. The curves for $N < \infty$ are sublinear, whereas the limit case $N \to \infty$ provides a linear one with inclination ≈ 0.27. That is, for $N \to \infty$ the optimal number of parents should be $\hat{\mu} = 0.27\,\lambda$.

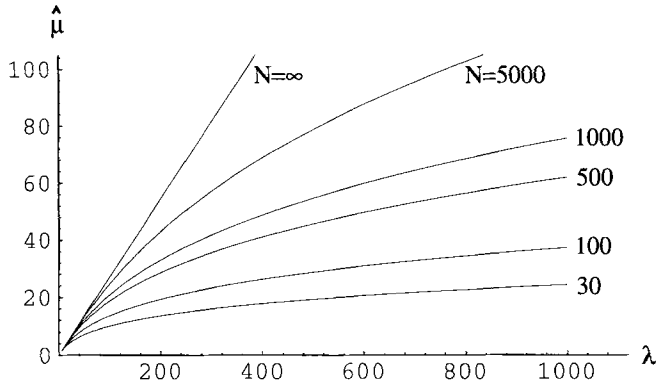

Figure 3. The optimum μ-choice versus the offspring number λ for different parameter space dimensions.

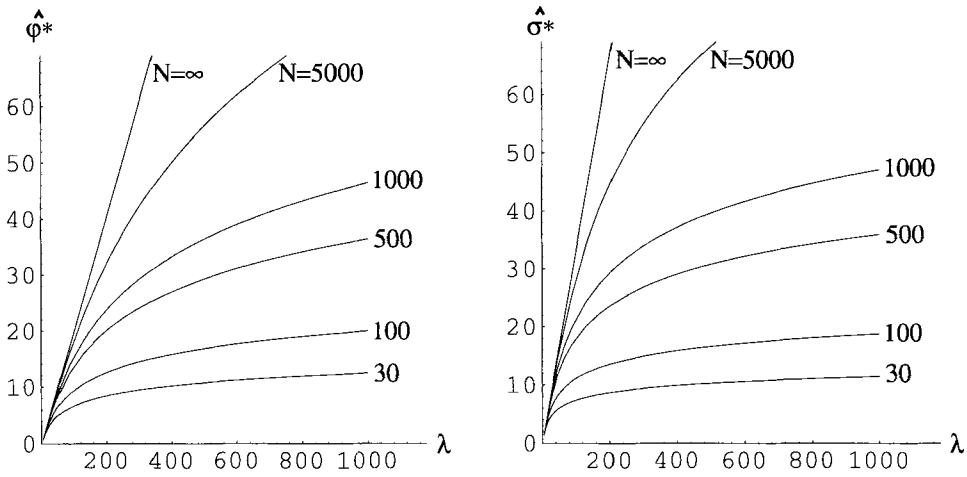

Figure 4. *Left*: The maximum progress rate $\hat{\varphi}^\star$ reachable by a strategy with optimally chosen $\mu = \hat{\mu}$ and optimally adapted mutation strength $\sigma = \hat{\sigma}$ (displayed in the right graph). *Right*: The optimum (normalized) standard deviation $\sigma^\star$ of the mutations versus the number of offspring for optimally chosen number of parents.

For $N < \infty$ the inequality $\hat{\mu} < 0.27\,\lambda$ holds. For practical applications Table 2 gives a collection of optimal parent numbers.

Figure 4 displays the $\varphi^\star$ and $\sigma^\star$ values belonging to the optimum μ choice. It is striking that for $N \to \infty$ the optimum $(\mu/\mu_I, \lambda)$ strategies exhibit an almost *linear speed-up* of the progress rate as to the number of offspring.[6] However, for "normally sized" problems the speed-up scales sublinearly sooner or later, but still will be on a remarkable level. Therefore, *as far as "fast hill climbing" is desired, the* $(\hat{\mu}/\hat{\mu}_I, \lambda)$ *ES will be the fastest one.*

6 Actually, a slightly *super-linear speed-up* for $N \to \infty$ is forecasted (cp. Table 2).

Table 2. The optimal μ choice in $(\mu/\mu_I, \lambda)$-recombinant evolution strategies. $\hat{\varphi}^*$ is the theoretically achievable progress rate, if the strategy works at the optimum mutation strength $\hat{\sigma}^*$. The optimum $\hat{\mu}$ depends on the parameter space dimension N. The cases N = 30, 100, 1000, and ∞ are displayed.

	$\hat{\mu}$				$\hat{\sigma}^*$				$\hat{\varphi}^*$			
$\lambda \setminus N$	30	100	1000	∞	30	100	1000	∞	30	100	1000	∞
10	3	3	3	3	2.788	3.035	3.177	3.196	1.529	1.638	1.695	1.703
20	4	5	5	6	4.016	5.172	5.936	6.663	2.805	3.261	3.629	3.699
30	5	7	8	8	4.826	6.763	9.055	9.568	3.692	4.545	5.503	5.721
40	6	8	10	11	5.451	7.697	11.38	13.05	4.370	5.597	7.246	7.746
50	7	9	12	14	5.966	8.468	13.49	16.54	4.916	6.469	8.865	9.766
60	8	10	14	16	6.407	9.131	15.41	19.42	5.369	7.214	10.37	11.79
70	8	11	16	19	6.562	9.717	17.16	22.91	5.754	7.864	11.76	13.81
80	9	12	18	22	6.928	10.24	18.77	26.40	6.095	8.440	13.06	15.84
90	10	13	19	25	7.258	10.72	19.86	29.88	6.394	8.955	14.26	17.86
100	10	14	21	27	7.359	11.17	21.26	32.77	6.665	9.420	15.39	19.89
150	12	17	28	41	8.126	12.57	26.09	49.60	7.706	11.25	20.10	30.01
200	14	19	33	54	8.731	13.46	29.29	65.83	8.444	12.58	23.75	40.13
250	15	21	38	68	9.084	14.21	31.96	82.67	9.016	13.61	26.71	50.25
300	16	23	42	81	9.391	14.86	34.01	98.90	9.481	14.46	29.19	60.37
350	17	25	45	95	9.666	15.45	35.59	115.7	9.872	15.17	31.33	70.50
400	18	26	49	108	9.917	15.81	37.25	132.0	10.21	15.79	33.21	80.62
450	19	27	52	122	10.15	16.15	38.55	148.8	10.51	16.33	34.88	90.74
500	19	29	55	135	10.23	16.62	39.75	165.0	10.77	16.82	36.39	100.9
600	21	31	60	162	10.63	17.18	41.71	198.1	11.22	17.66	39.01	121.1
700	22	33	64	189	10.88	17.69	43.26	231.2	11.61	18.37	41.24	141.4
800	23	34	68	216	11.10	18.01	44.68	264.2	11.93	18.98	43.18	161.6
900	23	36	72	243	11.18	18.44	45.98	297.3	12.22	19.52	44.90	181.8
1000	24	37	76	270	11.37	18.71	47.19	330.3	12.48	19.99	46.43	202.1
1500	28	43	90	406	12.10	19.99	51.35	496.3	13.45	21.81	52.33	303.3
2000	30	47	101	541	12.50	20.81	54.26	661.6	14.13	23.09	56.50	404.5

4. A Rough Estimate for the Dominant $(\mu/\mu_D, \lambda)$-ES

4.1 A Simple Model for the $(\mu/\mu_D, \lambda)$-Theory

The dominant recombinant $(\mu/\mu_D, \lambda)$ strategy cannot be analyzed as easily as the intermediate one. This is because the mutations $\mathbf{Z}$ do not act on a single intermediate parent $\langle \mathbf{y} \rangle$ but on a parent distribution (cp. Eq. [2]) just like the (μ, λ)-ES. Hence, one has to determine parental distributions by the self-consistent method. Full analysis remains as a task for the future. However, by a simple model presented below, it will be possible to give a first estimate for the progress rate φ. Similar results—without derivation—can be found in Rechenberg (1994).

The definition of the progress rate can be taken from the intermediate theory (3–6). The progress rate φ measures the expected distance change of the parental center of mass from generation (g) to $(g+1)$

$$\varphi_{\mu/\mu_D,\lambda} := E\left\{R - \tilde{R}\right\} = E\left\{\langle \mathbf{y}\rangle^{(g)} - \langle \mathbf{y}\rangle^{(g+1)}\right\}, \qquad \langle \mathbf{y}\rangle = \frac{1}{\mu}\sum_{m=1}^{\mu} \tilde{\mathbf{y}}_{m;\lambda}.$$

Given the parental distribution at (g) the recombination-mutation-selection process generates the new parental distribution at $(g+1)$. From the mathematical point of view, there is no reason to separate the recombination/mutation processes. They are both random processes without bias or correlation. Indeed, one may interpret the resulting distribution as if it were generated by a special kind of mutation starting from the parental average state $\langle \mathbf{y}\rangle^{(g)}$.[7] We may call this newly defined random (mutation) vector starting from $\langle \mathbf{y}\rangle^{(g)}$ the *surrogate mutation* $\mathbf{S}$ of the recombination-mutation process. If $p^{(g)}(\mathbf{S})$, that is, the N-dimensional pdf of $\mathbf{S}$, were known, then one could proceed as in the case of the intermediate theory: $\mathbf{S}_{m;\lambda}$ can be decomposed according to Equation (7) and the progress rate expression (10) exactly holds. Even the next steps from Section 3.1.2 are applicable and the formula (19) is valid.

All the difficulties in the $(\mu/\mu_D, \lambda)$ theory are concentrated in the self-consistent estimation of $p^{(g)}(\mathbf{S})$. A first—very rough—approximation to $p^{(g)}(\mathbf{S})$ may be obtained by neglecting the influence of selection on $p^{(g)}(\mathbf{S})$. A system evolving by a mutation-recombination process, that is, driven by symmetrical mutations normally distributed and dominant random recombination, generates an *isotropic* normally distributed $p^{(g)}(\mathbf{S})$ with iid components

$$p(s_i) = \frac{1}{\sqrt{2\pi}\,\sigma_s} e^{-\frac{1}{2}\left(\frac{s_i}{\sigma_s}\right)^2} \tag{52}$$

measured from the center of mass $\langle \mathbf{y}\rangle^{(g)}$. The only unknown in this process is the mutation strength σ_s of the *isotropic surrogate mutations* $\mathbf{S}$. We will tackle this problem in the next section. If σ_s is known, one can apply the $(\mu/\mu_I, \lambda)$-standard theory to obtain the progress rate formula: One only has to exchange the mutation strength σ producing $\langle \overline{\mathbf{h}^2}\rangle$ and $\langle \bar{x}\rangle$ in Equation (19) by $\sigma_s = \sigma_s(\mu, \sigma)$.

4.2 Isotropic Surrogate Mutations, Progress Rate, and Is There Genetic Repair in Dominant Recombinant Strategies?

4.2.1 Isotropic Surrogate Mutations Because dominant recombination acts on the level of independent coordinates, the consideration for one component $s = s_i$ suffices. For the sake of simplicity we will describe the recombination-mutation process starting from a fixed point

$$\langle s\rangle^{(0)} = s_1^{(0)} = s_2^{(0)} = \cdots = s_m^{(0)} = \cdots = s_\mu^{(0)} = 0.$$

The superscript index counts the generations whereas the subscript index labels the parents. Recombination and mutation are independent processes. Therefore the effect of recombination can be described by a single pdf. Because the (physical) mutations are $N(0, \sigma)$ normally distributed and recombination is simply a sampling from certain normal variates generated by these mutations, the resulting offspring are normally distributed, too. Let $\sigma_s^{(g+1)}$ be the standard deviation of a single component of the surrogate mutations $\mathbf{S}^{(g+1)}$ that produce the

7 This is exactly what has been done for one dimension—the r-direction—in the case of the (μ, λ) ES (cp. Beyer, 1995, Section 3.1.3).

$(g+1)$ generation from the center of mass $\langle \mathbf{S} \rangle^{(g)}$, which reads for a single component

$$\langle s \rangle^{(g)} = \frac{1}{\mu} \sum_{m=1}^{\mu} s_m^{(g)}. \tag{53}$$

The value $\sigma_s^{(g+1)}$ is computed from the recombinative $\sigma_R^{(g)}$ and the (physical) mutational part σ (independent of each other)

$$\sigma_s^{(g+1)} = \sqrt{\left(\sigma_R^{(g)}\right)^2 + \sigma^2}. \tag{54}$$

The recombinative part $\sigma_R^{(g)}$ is an estimate of the sampling from the distribution of the $s_m^{(g)}$ characterized by the standard deviation of the surrogate mutations $\sigma_s^{(g)}$. Thus we have for $\sigma_R^{(g)}$

$$\sigma_R^{(g)} = \sqrt{E\left\{\left(s^{(g)} - \langle s \rangle^{(g)}\right)^2\right\}}. \tag{55}$$

Note, $\langle s \rangle^{(g)}$ as defined by Equation (53) is a random variate itself. The $s_m^{(g)}$ variates generated by mutation and recombination have the expectation

$$E\left\{s_m^{(g)}\right\} = 0$$

and are not correlated

$$E\left\{s_k^{(g)} s_l^{(g)}\right\} = \begin{cases} 0, & k \neq l \\ \left(\sigma_s^{(g)}\right)^2, & k = l \end{cases}.$$

For a fixed parent m one obtains from Equation (55)

$$\begin{aligned}
E\left\{\left(s_m^{(g)} - \langle s \rangle^{(g)}\right)^2\right\} &= E\left\{\left(s_m^{(g)} - \frac{1}{\mu}\sum_{k=1}^{\mu} s_k^{(g)}\right)^2\right\} \\
&= E\left\{\left(\left(1 - \frac{1}{\mu}\right) s_m^{(g)} - \frac{1}{\mu}\sum_{k \neq m} s_k^{(g)}\right)^2\right\} \\
&= E\left\{\left(1 - \frac{1}{\mu}\right)^2 \left(s_m^{(g)}\right)^2 - 2\left(1 - \frac{1}{\mu}\right)\frac{1}{\mu}\sum_{k \neq m} s_m^{(g)} s_k^{(g)} \right. \\
&\qquad \left. + \frac{1}{\mu^2}\sum_{k \neq m}\sum_{l \neq m} s_k^{(g)} s_l^{(g)}\right\} \\
&= \left(1 - \frac{1}{\mu}\right)^2 E\left\{s_m^{(g)} s_m^{(g)}\right\} + \frac{1}{\mu^2}\sum_{k \neq m}\sum_{l \neq m} E\left\{s_k^{(g)} s_l^{(g)}\right\} \\
&= \left(1 - \frac{1}{\mu}\right)^2 E\left\{\left(s_m^{(g)}\right)^2\right\} + \frac{\mu - 1}{\mu^2} E\left\{\left(s_m^{(g)}\right)^2\right\} \\
&= \frac{\mu - 1}{\mu} E\left\{\left(s_m^{(g)}\right)^2\right\} = \frac{\mu - 1}{\mu}\left(\sigma_s^{(g)}\right)^2.
\end{aligned}$$

This gives for Equation (54) the iterative scheme

$$\sigma_s^{(g+1)} = \sqrt{\frac{\mu-1}{\mu}\left(\sigma_s^{(g)}\right)^2 + \sigma^2}\,. \tag{56}$$

Because $\sigma_s^{(0)} = 0$ holds (cp. Eq. [52]) one finds by recurrence

$$\sigma_s^{(g+1)} = \sigma\sqrt{1 + \frac{\mu-1}{\mu} + \cdots + \left(\frac{\mu-1}{\mu}\right)^{g-1} + \left(\frac{\mu-1}{\mu}\right)^{g}}\,.$$

Within the square root there is a sum of geometric progression

$$\sigma_s^{(g+1)} = \sigma\sqrt{\left[1 - \left(\frac{\mu-1}{\mu}\right)^{g+1}\right] \Big/ \left[1 - \left(\frac{\mu-1}{\mu}\right)\right]} \tag{57}$$

and the steady-state case $g \to \infty$ yields[8]

$$\sigma_s = \lim_{g\to\infty} \sigma_s^{(g)} = \sigma\sqrt{\mu}. \tag{58}$$

This result is very remarkable. By the dominant recombination, physical mutations with standard deviation σ are transformed into larger surrogate mutations. However, although there is no selective pressure in this model the resulting mutation strength (Equation (58)) is restricted. The population is concentrated around the center of mass (the "wild-type") forming what a biologist would call a *species*. Note, the derivation given does not rely on a special kind of distribution (e.g., normal distribution), but on the statistical independence of mutation and recombination only. Therefore, the result is very general and should hold, for instance, for GAs too. The author will come back to this point in the conclusion of this article.

4.2.2 The Progress Rate Formula Now we can finish with the $\varphi_{\mu/\mu_D,\lambda}$ formula. As pointed out at the end of Section 4.1, Equation (19) holds for the dominant case, too. The unknown values are $\langle\overline{\mathbf{h}^2}\rangle$ and $\langle\bar{x}\rangle$, now produced by the surrogate mutations with standard deviation $\sigma_s = \sqrt{\mu}\,\sigma$. Because the actual influence of the selection process is not known the simplest approximation for $\langle\overline{\mathbf{h}^2}\rangle$ is to assume no selection. That is, each component of the $\mathbf{h}$ vectors is $N(0, \sigma_s)$ normally distributed. Therefore, the expectation for $\langle\overline{\mathbf{h}^2}\rangle$ becomes (cp. Beyer, 1995, Eq. [8])

$$\langle\overline{\mathbf{h}^2}\rangle \approx N(\sigma_s)^2 = \mu N\sigma^2. \tag{59}$$

For $\langle\bar{x}\rangle$ we assume a simple selection process taking the best μ offspring of a sample from the $N(0, \sigma_s)$-distribution comprising λ offspring. Formula (20) holds with $p_{m:\lambda}(x) = p_{m:\lambda}(x)$, that is, these are the simple order statistics of the normal variate x: $p(x) = \exp(-\frac{1}{2}x^2/\sigma_s^2)/\sqrt{2\pi}\sigma_s$. The result is similar to Equation (31)

$$\langle\bar{x}\rangle = \sigma_s\, e^{1,0}_{\mu,\lambda} = \sigma_s\, c_{\mu/\mu,\lambda} = \sqrt{\mu}\,\sigma\, c_{\mu/\mu,\lambda}. \tag{60}$$

8 This formula might also be obtained by the self-consistent method solving Equation (56) for $\sigma_s^{(g+1)} = \sigma_s^{(g)} = \sigma_s$.

If Equations (59/60) are inserted into Equation (19), one finally obtains

$$\varphi^{\star}_{\mu/\mu_D,\lambda} = N\left(1 - \sqrt{1 + \frac{(\sigma^{\star})^2}{N}}\right) + \frac{\sqrt{\mu}\, c_{\mu/\mu,\lambda}\, \sigma^{\star}}{\sqrt{1 + \frac{(\sigma^{\star})^2}{N}}}. \tag{61}$$

It turns out that the progress rates reachable by dominant recombinant strategies are comparable with those from the intermediate one (cf. Section 4.3, below).

4.2.3 Is There Genetic Repair in Dominant Recombinant Strategies? The mechanism responsible for high progress rates in intermediate strategies is quite clear—the genetic repair (i.e., building the center of mass), *explicitly performed by the algorithm* (cp. Eq. [1]). However, in dominant strategies there is not such an algorithmic averaging of the genes. What is the reason for their benefits then? It is indeed genetic repair, too, but *implicitly performed.* This—at first glance—astonishing answer becomes clear if one interprets the dominant recombination as a sampling process estimating the distribution of the parents. Thus, the information from the best μ offspring forms an "internal model" of the fitness landscape as already conjectured by Schwefel (1987). But, up until now, it was not quite clear what the notion "internal model" really means and how an algorithm—as simple as the dominant ES—can take advantage of it. As was shown in the case of the (μ, λ) ES (Beyer, 1995, Section 3.1.3), estimating a distribution is equivalent to determining its moments. In other words, estimating the internal model by dominant recombination includes the implicit estimation of the first moment of the parental distribution. However, the first moment of the parental distribution is nothing else but the center of mass. Now, the wheel turns full circle—dominant recombination estimates the center of mass, thus it performs (estimated or approximative) *implicit genetic repair.*

Returning to the debate regarding the alternative "genetic variety *or* genetic repair" we thus come to a remarkable conclusion. Actually there is no alternative. The dominant recombinant ES produces genetic variety *and* performs (implicit) genetic repair. Both mechanisms work together in a synergistic fashion.

4.3 Comparison with Experiments

In order to produce the dotted graphs in Figure 5 the author has used a simulation technique that reconstructs the actual progress rate $\varphi^{\star}$ and $\sigma^{\star}$ from ES runs by classification. That is, the mutation strength σ is held constant during the evolution run and the observed $\varphi^{\star}$- and $\sigma^{\star}$-values are collected in $\sigma^{\star}$-classes. The class averages are computed and displayed. The left graph is a reconstruction from 100 ES runs and the right one from 200 ES runs. The graphs of Equation (61) (solid curves) deviate considerably from the experiments as expected; however, the order of magnitude is correct. The same holds for the Rechenberg formula (dashed curves)

$$\varphi^{\star}_{\mu/\mu_D,\lambda} = \sqrt{\mu}\, c_{\mu/\mu,\lambda}\sigma^{\star} - \frac{(\sigma^{\star})^2}{2},$$

which can be obtained from Equation (61) by Taylor expansion.

The large deviations in the interesting $\sigma^{\star}$-range ($\varphi^{\star} > 0$) are due to the simple isotropic surrogate mutation model used. The real $p(\mathbf{Z})$ distribution is not isotropic, but compressed in the **R**-direction. A refined surrogate mutation model should take into account different distributions for x and $\mathbf{h}$ in Equations (10/19). This is a task for the future.

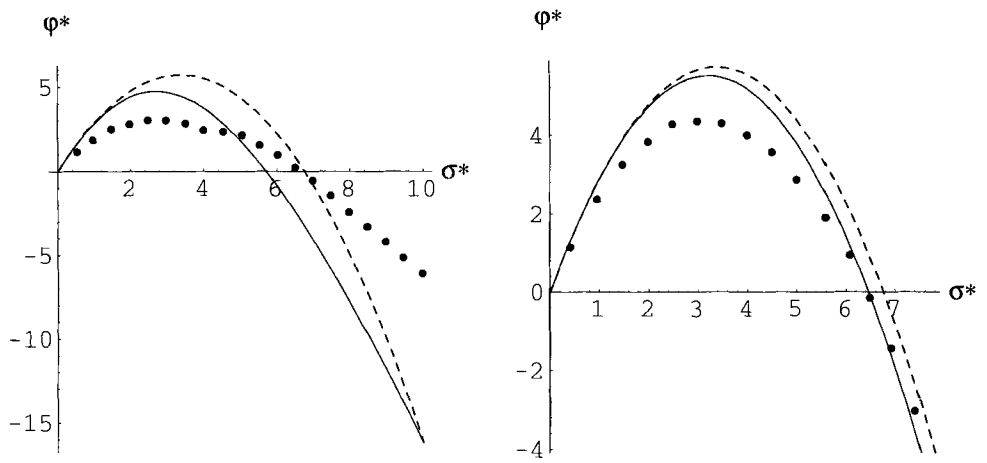

Figure 5. *Left*: $(8/8_D, 30)$ ES with $N = 30$. *Right*: $(8/8_D, 30)$ ES with $N = 200$.

5. Non-Spherical Fitness Landscapes

The effort necessary for the determination of progress rates on spherical models is great; however, the results would be of relatively little value if they were restricted to the fitness function $F(\mathbf{y}) = \mathbf{y}^2$ only. This brings up the question about the extendibility of the spherical model to nonspherical success domains. And indeed, under certain conditions such an extension can be obtained straightforwardly by Riemannian geometry.

The basic idea is to approximate the fitness landscape locally by a hypersphere surface. That way, the problem reduces to the task of determining the (local) *mean radius* $R_{\overline{\kappa}}$ of the success domain at the parental point. This is a differential geometry problem to be solved in Section 5.2.

Note, in this section the author uses Einstein's summation convention for Greek dummy indices running from 1 to $N - 1$, for instance,

$$a_\alpha b^\alpha := \sum_{\alpha=1}^{N-1} a_\alpha b^\alpha.$$

It is assumed that the reader is familiar with the tensor calculus and some basics from Riemannian geometry (cp., for example, Kreyszig, 1968).

5.1 The Basic Aspects of the Differential Geometry Approach

5.1.1 The Local Fitness Function $Q(\mathbf{x})$ Given the fitness function $F(\mathbf{y})$, the local behavior of F at the parental state $\mathbf{y} = \mathbf{y}^{(g)}$ may be approximated by a Taylor expansion

$$F(\mathbf{y} + \mathbf{x}) = F(\mathbf{y}) + \sum_{i=1}^{N} \frac{\partial F}{\partial y_i} x_i + \frac{1}{2} \sum_{i=1}^{N} \sum_{j=1}^{N} \frac{\partial^2 F}{\partial y_i \partial y_j} x_i x_j + \cdots$$

breaking off after the quadratic term. Such an approximation is permissible if F is differentiable at $\mathbf{y}$ and $\mathbf{x}$ is not too large, usually fulfilled for the mutations $\mathbf{x} = \mathbf{Z}$. Therefore, the

local behavior of F can be approximated by the bilinear form

$$Q_{\mathbf{y}}(\mathbf{x}) = F(\mathbf{y}+\mathbf{x}) - F(\mathbf{y}) = \sum_{i=1}^{N} \frac{\partial F}{\partial y_i} x_i + \frac{1}{2} \sum_{i=1}^{N} \sum_{j=1}^{N} \frac{\partial^2 F}{\partial y_i \partial y_j} x_i x_j$$

$$= \sum_{i=1}^{N} a_i x_i - \sum_{i=1}^{N} \sum_{j=1}^{N} q_{ij} x_i x_j \tag{62}$$

with

$$a_i = a_i(\mathbf{y}) = \frac{\partial F}{\partial y_i} \quad \text{and} \quad q_{ij} = q_{ij}(\mathbf{y}) = -\frac{1}{2} \frac{\partial^2 F}{\partial y_i \partial y_j}, \quad q_{ij} = q_{ji}.$$

$Q_{\mathbf{y}}(\mathbf{x}) = 0$ defines the boundary ∂Q of the *local success domain*, that is, that part of the $\mathbb{R}^N$ parameter space containing individuals (if produced) fitter than the parent $\mathbf{y} = \mathbf{y}^{(g)}$. The boundary ∂Q: $Q(\mathbf{x}) = 0$, geometrically interpreted, is a hypersurface in the $\mathbb{R}^N$. Introducing the Cartesian system $\{\mathbf{e}_i\}$, $i = 1, \ldots, N$, the hypersurface ∂Q may be described by the vector function

$$\mathbf{x}(u^1, u^2, \ldots, u^{N-1}) = \sum_{i=1}^{N} x_i(u^1, u^2, \ldots, u^{N-1})\, \mathbf{e}_i \tag{63}$$

depending on $(N-1)$ (contravariant) coordinates u^α ($\alpha = 1, \ldots, N-1$). Because the local geometry of ∂Q at the parental position $\mathbf{x} = \mathbf{0}$ is of interest, a natural coordinate system is given by

$$x_1 = u^1, \quad x_2 = u^2, \ldots, x_{N-1} = u^{N-1}, \quad x_N = f(u^1, u^2, \ldots, u^{N-1}). \tag{64}$$

Hence, x_N is obtained by solving $(Q = Q(\mathbf{x}(u^1, \ldots, u^{N-1})) = 0$ for x_N. It is obvious that x_N depends on the $(N-1)$ coordinates u^α and $u^\alpha = 0$ $(\alpha = 1, \ldots, N-1) \Rightarrow \mathbf{x} = \mathbf{0}$.

5.1.2 The Metric Tensor $g_{\alpha\beta}$ The local metric on the $(N-1)$-dimensional Riemannian manifold is given by the first fundamental form

$$(ds)^2 = g_{\alpha\beta} du^\alpha du^\beta \tag{65}$$

established by the (covariant) metric tensor $g_{\alpha\beta}$

$$g_{\alpha\beta} = \mathbf{x}_{u^\alpha}^T \mathbf{x}_{u^\beta}; \qquad \mathbf{x}_{u^\alpha} := \frac{\partial}{\partial u^\alpha} \mathbf{x}$$

constituted by the scalar products of the tangent vectors $\mathbf{x}_{u^\alpha}$, $\mathbf{x}_{u^\beta}$. For the tangent vectors $\mathbf{x}_{u^\alpha}$ one finds from Equations (63/64)

$$\mathbf{x}_{u^\alpha} = \mathbf{e}_\alpha + \mathbf{e}_N \frac{\partial f}{\partial u^\alpha}. \tag{66}$$

Thus, the metric tensor reads

$$g_{\alpha\beta} = \delta_{\alpha\beta} + \frac{\partial f}{\partial u^\alpha} \frac{\partial f}{\partial u^\beta} \tag{67}$$

with Kronecker's delta symbol $\delta_{\alpha\beta}$. For further calculations the contravariant metric tensor

will be needed. Because of

$$g_{\alpha\beta}g^{\beta\gamma} = g_{\alpha}{}^{\gamma} = \begin{cases} 1, & \alpha = \gamma \\ 0, & \alpha \neq \gamma \end{cases}, \tag{68}$$

$g^{\beta\gamma}$ is the inverse tensor to $g_{\alpha\beta}$. The tensor $(g_{\beta\gamma})^{-1}$ can be formally obtained by a matrix power series, adapted from the simple Taylor expansion

$$(1+c)^{-1} = 1 - c + c^2 - c^3 + c^4 - \cdots, \tag{69}$$

for the matrix $\mathbf{E} + \mathbf{C}$ with $\mathbf{E}$ as identity matrix

$$(\mathbf{E}+\mathbf{C})^{-1} = \mathbf{E} - \mathbf{C} + \mathbf{C}\mathbf{C} - \mathbf{C}\mathbf{C}\mathbf{C} + \mathbf{C}^4 - \cdots. \tag{70}$$

Let

$$\{\mathbf{C}\}_{\beta\gamma} := \frac{\partial f}{\partial u^\beta}\frac{\partial f}{\partial u^\gamma} \qquad \text{and} \qquad \{\mathbf{E}\}_{\beta\gamma} = \delta_{\beta\gamma}.$$

One obtains from Equation (70)

$$\begin{aligned}
(g_{\beta\gamma})^{-1} &= \left(\delta_{\beta\gamma} + \frac{\partial f}{\partial u^\beta}\frac{\partial f}{\partial u^\gamma}\right)^{-1} \\
&= \delta_{\beta\gamma} - \frac{\partial f}{\partial u^\beta}\frac{\partial f}{\partial u^\gamma} + \frac{\partial f}{\partial u^\beta}\left(\sum_\alpha \frac{\partial f}{\partial u^\alpha}\frac{\partial f}{\partial u^\alpha}\right)\frac{\partial f}{\partial u^\gamma} \\
&\quad - \frac{\partial f}{\partial u^\beta}\left(\sum_\alpha \frac{\partial f}{\partial u^\alpha}\frac{\partial f}{\partial u^\alpha}\right)\left(\sum_\alpha \frac{\partial f}{\partial u^\alpha}\frac{\partial f}{\partial u^\alpha}\right)\frac{\partial f}{\partial u^\gamma} + \cdots \\
(g_{\beta\gamma})^{-1} &= \delta_{\beta\gamma} - \frac{\partial f}{\partial u^\beta}\frac{\partial f}{\partial u^\gamma}\left[1 - \left(\sum_\alpha \frac{\partial f}{\partial u^\alpha}\frac{\partial f}{\partial u^\alpha}\right) + \left(\sum_\alpha \frac{\partial f}{\partial u^\alpha}\frac{\partial f}{\partial u^\alpha}\right)^2 - \cdots\right].
\end{aligned} \tag{71}$$

If Equation (69) is compared with the bracket in Equation (71) one reads

$$g^{\beta\gamma} = (g_{\beta\gamma})^{-1} = \delta_{\beta\gamma} - \frac{\frac{\partial f}{\partial u^\beta}\frac{\partial f}{\partial u^\gamma}}{1 + \sum_{\alpha=1}^{N-1}\frac{\partial f}{\partial u^\alpha}\frac{\partial f}{\partial u^\alpha}}. \tag{72}$$

The correctness of Equation (72) can be easily proved by contraction with Equation (67) yielding Equation (68).

5.1.3 The Second Fundamental Form Consider a curve C through the parental point $\mathbf{x} = \mathbf{0}$ on the surface ∂Q parametrized by its arc length s

$$C: \quad \mathbf{x}_C = \mathbf{x}\left(u^1(s), u^2(s), \ldots, u^{N-1}(s)\right).$$

The principal normal $\mathbf{h}$ to C is given by the second derivative of $\mathbf{x}$

$$\mathbf{h} = \frac{\mathbf{x}''}{\kappa}, \qquad \kappa = \|\mathbf{x}''\|, \qquad (\cdots)' = \frac{d}{ds}(\cdots), \tag{73}$$

with the curvature κ of $\mathcal{C}$. For the second derivative one finds

$$\mathbf{x}'' = \mathbf{x}_{u^\alpha u^\beta} u^{\alpha\prime} u^{\beta\prime} + \mathbf{x}_{u^\alpha} u^{\alpha\prime\prime}. \tag{74}$$

If the curve $\mathcal{C}$ is of such a kind that in the parental point $\mathbf{x} = \mathbf{0}$ the principal normal is parallel to the surface normal $\mathbf{n}$ of ∂Q, then one speaks of a normal section curve $\mathcal{C}_n$ with the normal curvature κ_n. The scalar product of $\mathbf{h}$ and $\mathbf{n}$ for such a curve is $\mathbf{h}^T \mathbf{n} = 1$. Hence, we obtain from Equations (73/74)

$$\mathcal{C}_n: \quad \mathbf{h}^T \mathbf{n} = 1 \quad \Longrightarrow \quad \kappa_n = \mathbf{n}^T \mathbf{x}'' = \mathbf{n}^T \mathbf{x}_{u^\alpha u^\beta} u^{\alpha\prime} u^{\beta\prime} + \mathbf{n}^T \mathbf{x}_{u^\alpha} u^{\alpha\prime\prime}. \tag{75}$$

The normal vector $\mathbf{n}$ on ∂Q is given by

$$\mathbf{n} = \frac{\nabla Q}{\|\nabla Q\|}, \qquad \nabla Q := \sum_{i=1}^{N} \mathbf{e}_i \frac{\partial}{\partial x_i}. \tag{76}$$

The differentiation of $Q\left(\mathbf{x}(u^1, u^2, \ldots, u^{N-1})\right) = 0$ yields

$$\frac{\partial Q}{\partial u^\alpha} = 0 \quad \Longrightarrow \quad 0 = \sum_{i=1}^{N} \frac{\partial Q}{\partial x_i} \frac{\partial x_i}{\partial u^\alpha} = \nabla^T Q \, \mathbf{x}_{u^\alpha},$$

and therefore $\mathbf{n}^T \mathbf{x}_{u^\alpha} = 0$ holds. Thus, one obtains from Equation (75) the second fundamental form for the normal curvature κ_n

$$\kappa_n = b_{\alpha\beta} u^{\alpha\prime} u^{\beta\prime}, \tag{77}$$

$$b_{\alpha\beta} := \mathbf{n}^T \mathbf{x}_{u^\alpha u^\beta}. \tag{78}$$

Note, the normal curvature κ_n depends on the tangent direction of the curve in the parental point. There are $N - 1$ independent directions forming the basis for the calculation of the mean curvature.

5.1.4 The Mean Curvature $\bar{\kappa}$ of ∂Q The normal curvature κ_n still depends on the tangent direction of the curve in the parental point. We are interested, however, in a curve-independent characterization of the behavior of ∂Q at the parental state $\mathbf{x} = \mathbf{0}$. This can be achieved by determination of the principal curvatures κ_p defined as the extreme values of κ_n. To proceed, we first rewrite Equation (77)

$$\kappa_n = b_{\alpha\beta} u^{\alpha\prime} u^{\beta\prime} = b_{\alpha\beta} \frac{du^\alpha}{ds} \frac{du^\beta}{ds} = \frac{b_{\alpha\beta} du^\alpha du^\beta}{(ds)^2}.$$

By application of the first fundamental form (Equation (65)) one obtains

$$\kappa_n = \frac{b_{\alpha\beta} du^\alpha du^\beta}{g_{\alpha\beta} du^\alpha du^\beta}.$$

As can be seen, κ_n depends only on the tangent direction given by du^α. Therefore, the principal curvatures κ_p are determined by the extremal condition

$$\kappa_p = \kappa_n \quad \Longleftrightarrow \quad \frac{\partial \kappa_n}{\partial l^\alpha} = 0$$

for the function

$$\kappa_n(l^1,\ldots,l^{N-1}) = \frac{b_{\alpha\beta}l^\alpha l^\beta}{g_{\alpha\beta}l^\alpha l^\beta}.$$

Performing the derivation yields $b_{\alpha\beta}l^\beta = \kappa_p g_{\alpha\beta}l^\beta$. With $l^\beta = g^{\beta\gamma}l_\gamma$ and Equation (68) we obtain

$$b_\alpha{}^\gamma l_\gamma = \kappa_p l_\alpha,$$

which is an eigenvalue problem. Because of Equation (78) $b_\alpha{}^\gamma$ is a symmetric matrix. Therefore, the eigenvalues $\kappa_1, \kappa_2, \ldots, \kappa_{N-1}$ will be real and there is an orthogonal system of eigenvectors defining the $N-1$ principal directions. Each of these tangent directions has its specific normal curvature $\kappa_n = \kappa_p$, called principal curvature. The sum of these principal curvatures defines the so-called *mean curvature* M^* (cp. Kreyszig, 1968). For our purpose the author will give a slightly different definition interpreting the mean curvature as *averaging the* $N-1$ *principal curvatures*

$$\overline{\kappa} = \frac{1}{N-1}\sum_{p=1}^{N-1}\kappa_p.$$

The sum over the eigenvalues κ_p can be easily obtained. From the eigenvalue theory it is well known that the sum of the eigenvalues is equal to the trace of the matrix

$$\sum_{p=1}^{N-1}\kappa_p = Tr\{b_\alpha{}^\gamma\} = b_\alpha{}^\alpha = b_{\alpha\beta}g^{\alpha\beta}.$$

This is a very satisfactory result because the trace of a second-order tensor as a contraction by means of $g^{\alpha\beta}$ is a scalar invariant representing a property of the "inner" geometry independent of the coordinate system used. Furthermore, the mean curvature $\overline{\kappa}$ does not depend on the curve C chosen on ∂Q. And for the hypersphere, $\overline{\kappa}$ is simply the reciprocal of its radius R. Therefore, for nonspherical success domains we may use the *mean radius* $R_{\overline{\kappa}}$

$$R_{\overline{\kappa}} = \frac{1}{\overline{\kappa}} = \frac{N-1}{b_{\alpha\beta}g^{\alpha\beta}} \tag{79}$$

as an approximation describing the local behavior of the fitness landscape by a hypersphere.

5.2 Determination of the Mean Radius $R_{\overline{\kappa}}$

In order to calculate $R_{\overline{\kappa}}$, $g^{\alpha\beta}$ and $b_{\alpha\beta}$ are determined for the manifold (64) at the parental state $\mathbf{x} = \mathbf{0}$, that is, for $u^1 = u^2 = \cdots = u^{N-1} = 0$.

5.2.1 The Metric Tensor The metric tensor $g^{\alpha\beta}$ is given by Equation (72). This needs the calculation of $\frac{\partial f}{\partial u^\alpha}$ at $u^\alpha = 0$. Because $f(u^1,\ldots,u^{N-1})$ is the root of x_N to the equation $Q\left(\mathbf{x}(u^1,\ldots,u^{N-1})\right) = 0$ (cp. Eq. [64]), the direct determination of $\frac{\partial f}{\partial u^\alpha}$ is rather tedious. Implicit differentiation will be used instead. If $Q(u^1,\ldots,u^{N-1}) = 0$ is differentiated taking Equation (64) into account one obtains

$$\frac{\partial Q}{\partial u^\alpha} = \frac{\partial Q}{\partial x_\alpha} + \frac{\partial Q}{\partial x_N}\frac{\partial x_N}{\partial u^\alpha} = \frac{\partial Q}{\partial x_\alpha} + \frac{\partial Q}{\partial x_N}\frac{\partial f}{\partial u^\alpha} = 0 \tag{80}$$

and therefore

$$\left.\frac{\partial f}{\partial u^\alpha}\right|_{u^{(\cdot)}=0} = -\left(\left.\frac{\partial Q}{\partial x_\alpha}\right|_{\mathbf{x}=\mathbf{0}}\right) \Big/ \left(\left.\frac{\partial Q}{\partial x_N}\right|_{\mathbf{x}=\mathbf{0}}\right).$$

For the fitness bilinear form (62) we thus obtain

$$\left.\frac{\partial f}{\partial u^\alpha}\right|_{u^{(\cdot)}=0} = -\frac{a_\alpha}{a_N}, \tag{81}$$

and the components of the contravariant metric tensor (72) read

$$g^{\alpha\beta} = \delta_{\alpha\beta} - \frac{a_\alpha a_\beta / a_N^2}{1 + \frac{1}{a_N^2}\sum_{\gamma=1}^{N-1} a_\gamma a_\gamma} = \delta_{\alpha\beta} - \frac{a_\alpha a_\beta}{\sum_{i=1}^{N} (a_i)^2}. \tag{82}$$

5.2.2 The $b_{\alpha\beta}$-Tensor The tensor $b_{\alpha\beta}$ is defined by Equation (78). First, the surface normal vector $\mathbf{n}$ at $\mathbf{x} = \mathbf{0}$ is determined. From Equation (76) with Equation (62) one finds

$$\nabla Q|_{\mathbf{x}=\mathbf{0}} = \sum_{i=1}^{N} a_i \mathbf{e}_i \quad \Longrightarrow \quad \mathbf{n} = \frac{\sum_{i=1}^{N} a_i \mathbf{e}_i}{\sqrt{\sum_{i=1}^{N} (a_i)^2}}. \tag{83}$$

The determination of $\mathbf{x}_{u^\alpha u^\beta}$ needs further considerations. Applying $\partial/\partial u^\beta$ on Equation (66) yields

$$\mathbf{x}_{u^\alpha u^\beta} = \frac{\partial}{\partial u^\beta}\mathbf{x}_{u^\alpha} = \mathbf{e}_N \frac{\partial^2 f}{\partial u^\alpha \partial u^\beta}. \tag{84}$$

The second derivatives of f are implicitly obtained. Differentiation of Equation (80) taking Equation (64) into account gives

$$\begin{aligned}\frac{\partial^2 Q}{\partial u^\beta \partial u^\alpha} = & \frac{\partial^2 Q}{\partial x_\beta \partial x_\alpha} + \frac{\partial^2 Q}{\partial x_N \partial x_\alpha}\frac{\partial f}{\partial u^\beta} + \frac{\partial^2 Q}{\partial x_\beta \partial x_N}\frac{\partial f}{\partial u^\alpha} \\ & + \frac{\partial^2 Q}{\partial x_N \partial x_N}\frac{\partial f}{\partial u^\beta}\frac{\partial f}{\partial u^\alpha} + \frac{\partial Q}{\partial x_N}\frac{\partial^2 f}{\partial u^\beta \partial u^\alpha} = 0.\end{aligned}$$

At $\mathbf{x} = \mathbf{0}$ (i.e., $u^{(\cdot)} = 0$) we have for the bilinear case (62) with Equation (81)

$$\begin{aligned}\left.\frac{\partial^2 Q}{\partial u^\beta \partial u^\alpha}\right|_{u^{(\cdot)}=0} = & -2q_{\alpha\beta} - 2q_{\alpha N}\left(-\frac{a_\beta}{a_N}\right) - 2q_{\beta N}\left(-\frac{a_\alpha}{a_N}\right) \\ & - 2q_{NN}\left(-\frac{a_\alpha a_\beta}{a_N^2}\right) + a_N \left.\frac{\partial^2 f}{\partial u^\beta \partial u^\alpha}\right|_{u^{(\cdot)}=0} = 0,\end{aligned}$$

and Equation (84) becomes

$$\mathbf{x}_{u^\alpha u^\beta} = \mathbf{e}_N \frac{2}{a_N}\left(q_{\alpha\beta} - \frac{q_{\alpha N}a_\beta + q_{\beta N}a_\alpha}{a_N} + \frac{q_{NN}}{a_N^2}a_\alpha a_\beta\right). \tag{85}$$

From Equations (78), (83), and (85) we obtain the second fundamental tensor $b_{\alpha\beta}$

$$b_{\alpha\beta} = \mathbf{n}^T \mathbf{x}_{u^\alpha u^\beta} = \frac{2}{\sqrt{\sum_{i=1}^{N} a_i^2}}\left(q_{\alpha\beta} - \frac{q_{\alpha N}a_\beta + q_{\beta N}a_\alpha}{a_N} + \frac{q_{NN}}{a_N^2}a_\alpha a_\beta\right). \tag{86}$$

5.2.3 Calculation of the Mean Radius $R_{\overline{\kappa}}$ The contraction of $b_{\alpha\beta}$ with the metric tensor (82) gives

$$b_{\alpha\beta}g^{\alpha\beta} = \frac{2}{\sqrt{\sum_{i=1}^{N} a_i^2}} \left\{ \sum_{\alpha=1}^{N-1} \left(q_{\alpha\alpha} - 2\frac{q_{\alpha N}a_\alpha}{a_N} + \frac{q_{NN}}{a_N^2} a_\alpha^2 \right) - \frac{1}{\sum_{i=1}^{N} a_i^2} \left[\sum_{\alpha=1}^{N-1}\sum_{\beta=1}^{N-1} a_\alpha q_{\alpha\beta} a_\beta - \frac{2}{a_N} \left(\sum_{\alpha=1}^{N-1} q_{\alpha N} a_\alpha \right) \left(\sum_{\beta=1}^{N-1} a_\beta^2 \right) + \frac{q_{NN}}{a_N^2} \left(\sum_{\alpha=1}^{N-1} a_\alpha^2 \right) \left(\sum_{\beta=1}^{N-1} a_\beta^2 \right) \right] \right\}.$$

By extending the sums from $N-1$ to N one obtains

$$b_{\alpha\beta}g^{\alpha\beta} = \frac{2}{\sqrt{\sum_{i=1}^{N} a_i^2}} \left[\sum_{i=1}^{N} q_{ii} - \frac{\sum_{i=1}^{N}\sum_{k=1}^{N} a_i q_{ik} a_k}{\sum_{i=1}^{N} a_i^2} \right]. \tag{87}$$

This is an astonishingly simple expression, especially if expressed with (by matrix algebra) $\{\mathbf{Q}\}_{ik} := q_{ik}$, $\{\mathbf{a}\}_i := a_i$, and $\|\mathbf{a}\| = \left(\sum_{i=1}^{N} a_i^2\right)^{1/2}$, which further simplifies Equation (87) to[9]

$$b_{\alpha\beta}g^{\alpha\beta} = \frac{2}{\|\mathbf{a}\|} \left(Tr\{\mathbf{Q}\} - \frac{\mathbf{a}^T\mathbf{Q}\,\mathbf{a}}{\|\mathbf{a}\|^2} \right). \tag{88}$$

Therefore, the mean radius (79) can be expressed by

$$R_{\overline{\kappa}} = \frac{N-1}{2} \frac{\|\mathbf{a}\|}{Tr\{\mathbf{Q}\} - \frac{\mathbf{a}^T\mathbf{Q}\,\mathbf{a}}{\|\mathbf{a}\|^2}}. \tag{89}$$

The normalized mutation strength $\sigma^\star = \sigma N/R_{\overline{\kappa}}$ and the progress rate $\varphi^\star = \varphi N/R_{\overline{\kappa}}$ becomes (assuming $N/(N-1) \to 1$ for large N)

$$\sigma^\star = \sigma \frac{2}{\|\mathbf{a}\|} \left(Tr\{\mathbf{Q}\} - \frac{\mathbf{a}^T\mathbf{Q}\,\mathbf{a}}{\|\mathbf{a}\|^2} \right), \quad \varphi^\star = \varphi \frac{2}{\|\mathbf{a}\|} \left(Tr\{\mathbf{Q}\} - \frac{\mathbf{a}^T\mathbf{Q}\,\mathbf{a}}{\|\mathbf{a}\|^2} \right). \tag{90}$$

Thus, progress rate formulas on the spherical model can be used as approximations for nonspherical success domains.

The quality of the $R_{\overline{\kappa}}$-approximation depends on the local fitness function $Q(\mathbf{x})$ to be approximated. For the discussion of experimental results the reader is referred to Beyer (1994a). The quality mainly depends on the eigenvalue spectrum of Q. If the eigenvalues are concentrated around $Tr\{\mathbf{Q}\}/(N-1)$, then the results will be excellent. In such a case, provided $\mathbf{Q}$ is definite, one can even drop the second term in Equation (88). This is due to the second term—also known as the Rayleigh quotient—that is bounded by the minimum/maximum of the $\mathbf{Q}$ spectrum.

9 $Tr\{\mathbf{Q}\}$ is the *trace* of $\mathbf{Q}$: $Tr\{\mathbf{Q}\} = \sum_i q_{ii}$.

6. Conclusions and Outlook

This article has dealt with multirecombinant evolution strategies. The theory developed applies to the spherical model, but can be extended to nonspherical fitness landscapes by introducing a mean curvature/radius depending on the local properties of the parental (or center of mass) state.

Unlike the (μ, λ) theory developed in issue 2(4) of *Evolutionary Computation*, the $(\mu/\mu_I, \lambda)$ intermediate recombinant strategy has been easily analyzed. This was due to the multirecombinant averaging concentrating the parents in the center of mass of the best μ offspring. The progress formula is similar to the $(1, \lambda)$ formula.

For $(\mu/\mu_I, \lambda)$ one observes astonishingly large progress rates. Genetic repair accounts for this phenomenon. This led the author to some speculations concerning the benefits of sexuality (in the sense of recombination). In biology, arguments against and also in favor of the genetic repair hypothesis are concentrated mainly on the advantage for the *single individual* produced by recombination/crossover. This is questionable in the author's opinion. At least for EA theory, *genetic repair is mainly a statistical phenomenon acting on the whole population/species.*

For ES practice it is important to know the optimum number of parents producing a fixed number of offspring. Because this is an N-dependent problem, a table has been presented meeting the needs for most of the applications.

A rather difficult problem concerns the $(\mu/\mu_D, \lambda)$ dominant recombinant strategies. It was the basic idea to interpret the results of the recombination as if they were produced by a mutation substitute, called the surrogate mutation, performed from the "center of mass parent." Note, from probability theory there is not a big difference between recombination and mutation. Both can be described by densities. However, the question arises on how to determine this recombination/mutation density. A very first approach, used in this article, neglects the selection. It was interesting to discover that the system mutation-recombination without selection, but iteratively performed, generates a steady-state distribution of the parents concentrated around an "average parent." (One might also expect a successive dispersal of the parental distribution!)

The isotropic surrogate mutation approach yields results lying in the order of magnitude of the experiments. Further research effort will be necessary to improve the progress rate formula. However, the principle and the reason for the benefits of dominant recombination should have become clear.

Unlike most of the EA researchers explaining the advantages of recombination (in parameter optimizing ESs and GAs, as well) by some kind of building block hypothesis (see, e.g., Goldberg, 1989), the author advocates for genetic variety and genetic repair implicitly performed by the dominant recombination process. This statement is of general validity. It should hold for GAs, too, and we may draw three conclusions for GA theory/practice (omitting a fourth one concerning selection).

First, *mutation is the motor of evolution.* It is the source for the variation of the genome. Therefore, never underestimate the power of mutation: An EA without recombination can work, whereas *an EA without mutations will get stuck* (N.B., in real GAs the population size is always limited).

Second, recombination is a process forming a "species" crowded around the "wild-type parent." This is equivalent to estimating the parent/offspring distribution, including, implicitly, the estimation of the center of mass (the wild-type). Thus, the dominant recombination implicitly performs genetic repair.

Third, dominant recombination has a triple effect: genetic repair, transformation of physical mutations into larger recombinant mutations (genetic variation), and building a *species by variational restriction*. Note, as in biology, recombination of different species (different building blocks) does not work in general, because of the violation of the species condition.[10] However, another concept may work well in GAs, too—multirecombination. That is, producing an offspring from more than two parents. Multimixing is only rarely observed in biology[11] due to the high costs of sexuality nowadays (at least for the higher creatures: the problem of gender). However, this is not a problem for GAs as far as the "group sex members" fit into the processor's local cache. It will be worth investigating such multimixing GAs.

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10 This does not exclude—under certain, but very limiting conditions—that different building blocks may recombine to fitter ones, for instance, if the fitness is an additive function of the different gene loci. However, this linear case is not very interesting for real-world optimizations.

11 It seems to be a very archaic mechanism, today mainly observed in bacteria species (Margulis & Sagan, 1988).

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