合肥學院
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Metaheuristic Optimization
12. Evolution Strategies

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Outline

website

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- Already discussed in the GA lecture

Truncation Selection

matePool $\longleftarrow$ truncationSelection(μ, pop)

Input: pop: the list of individuals to select from (length λ or $\mu + \lambda$)
Input: μ: the number of individuals to be placed into the mating pool matePool
Output: matePool: the survivors of the truncation which now form the mating pool

begin
    sort the pop according to fitness (best first)
    return first μ individuals from pop

Truncation Selection

Listing: The Truncation Selection Algorithm

```
public class TruncationSelection implements ISelectionAlgorithm {
  public void select(final Individual<?, ?>[] pop, final Individual<?, ?>[]
      mate, final Random r) {
    Arrays.sort(pop);
    System.arraycopy(pop, 0, mate, 0, mate.length);
  }
}
```

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- Let us assume the search space is the real numbers, i.e., $\mathbb{X} = \mathbb{G} = \mathbb{R}$.

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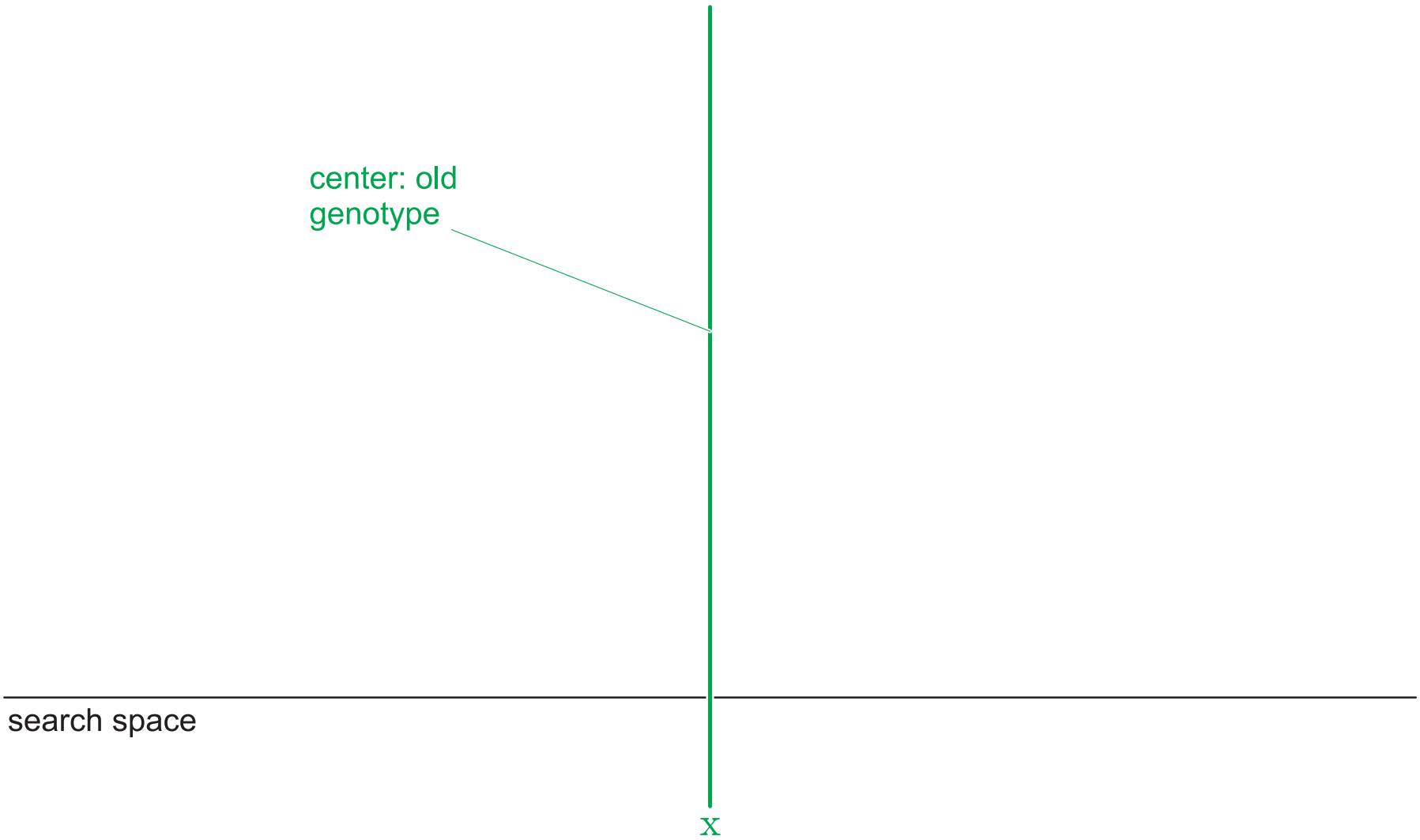

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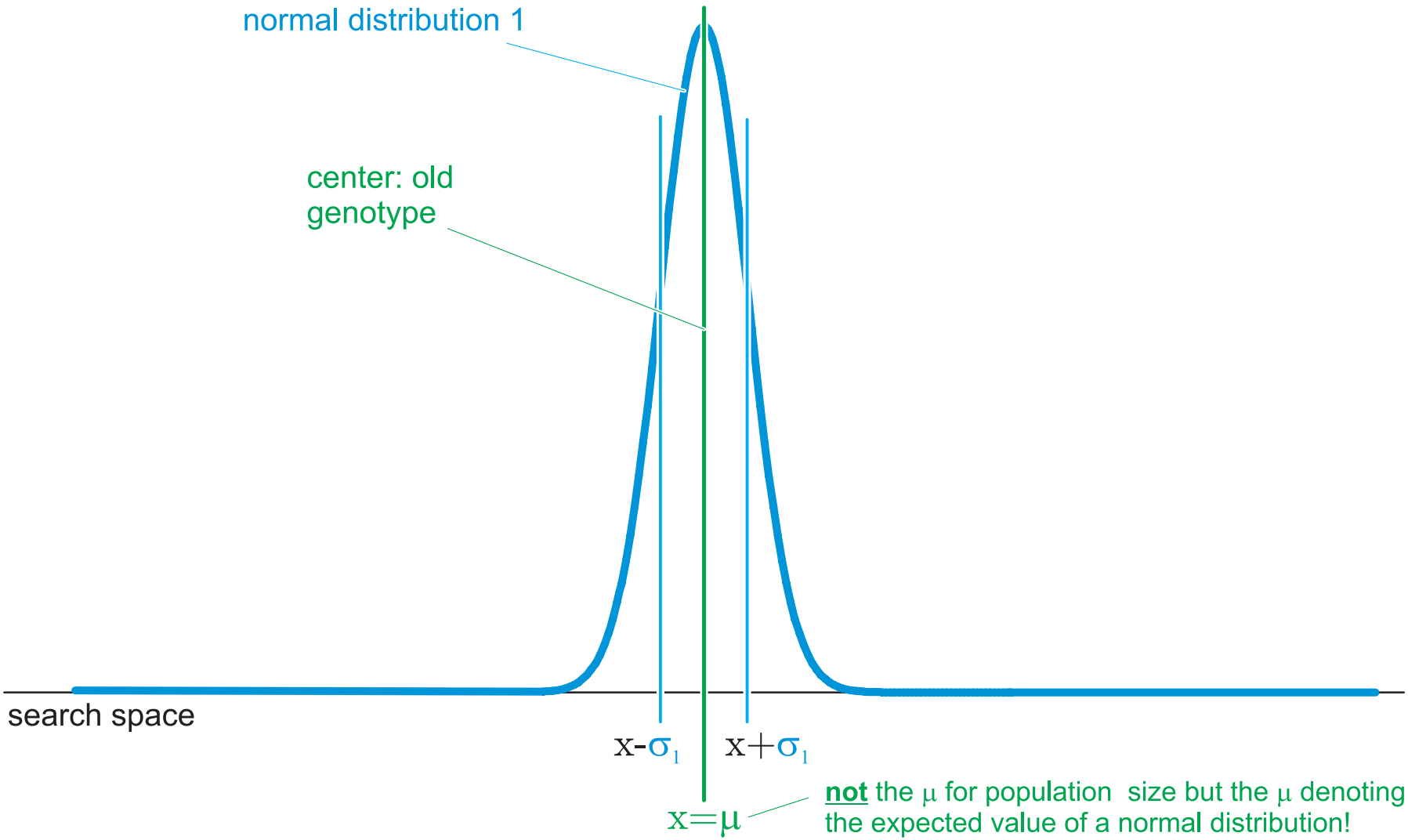
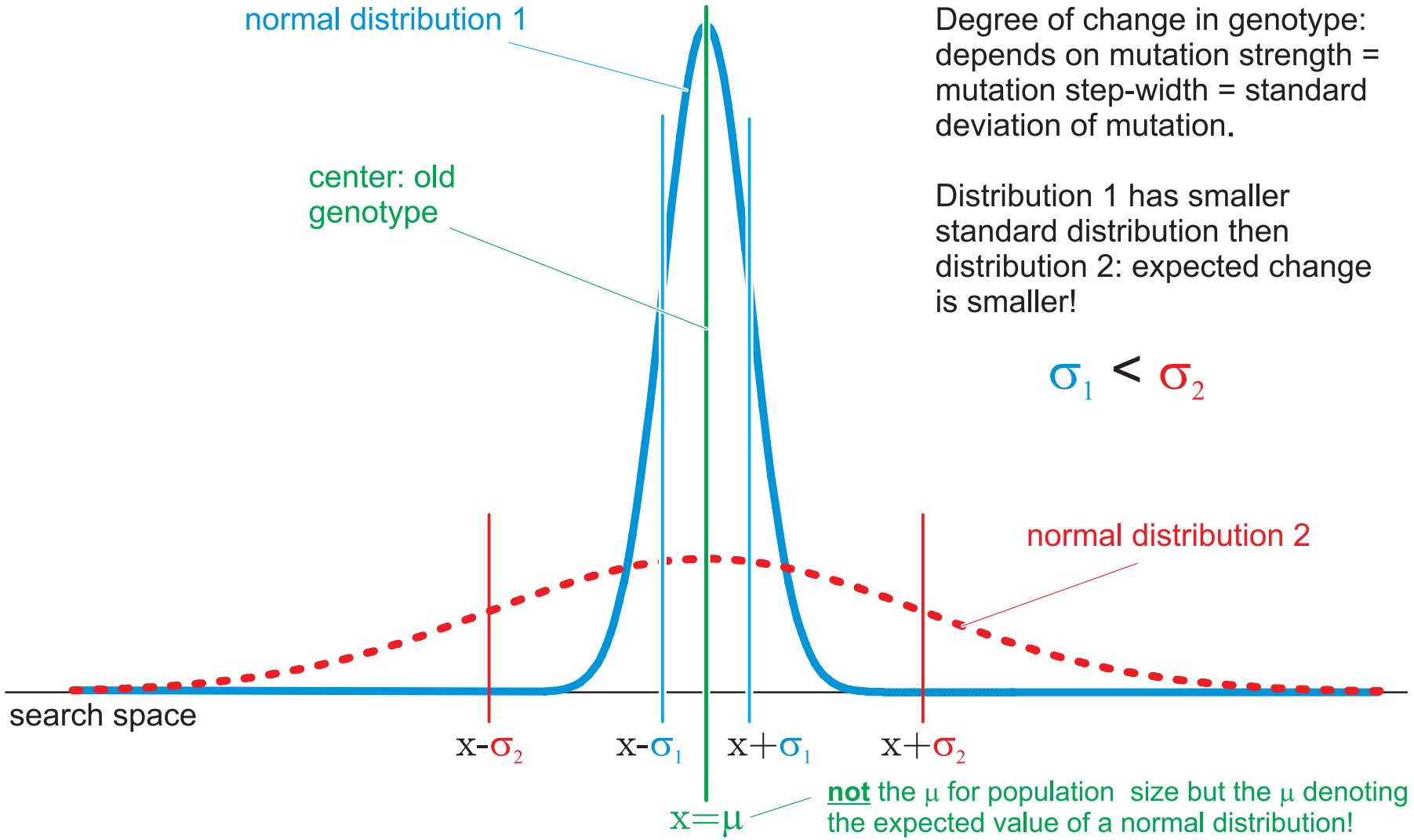

normal distribution 1
center: old genotype
search space
x-σ1
x+σ1
x=μ
not the μ for population size but the μ denoting the expected value of a normal distribution!

Mutation



Degree of change in genotype: depends on mutation strength = mutation step-width = standard deviation of mutation.

Distribution 1 has smaller standard distribution then distribution 2: expected change is smaller!

$$\sigma_1 < \sigma_2$$

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- Let us assume the search space is the real numbers, i.e., $\mathbb{X} = \mathbb{G} = \mathbb{R}$.
- ESes mutate an real value $x \in \mathbb{R}$ by replacing it with a new sample from a normal distribution with $\mu = x$
- Parameter of the mutation operator: standard deviation σ of normal distribution as step length

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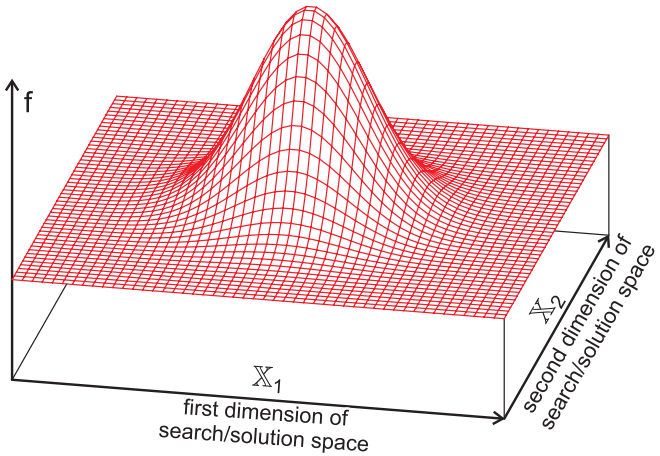

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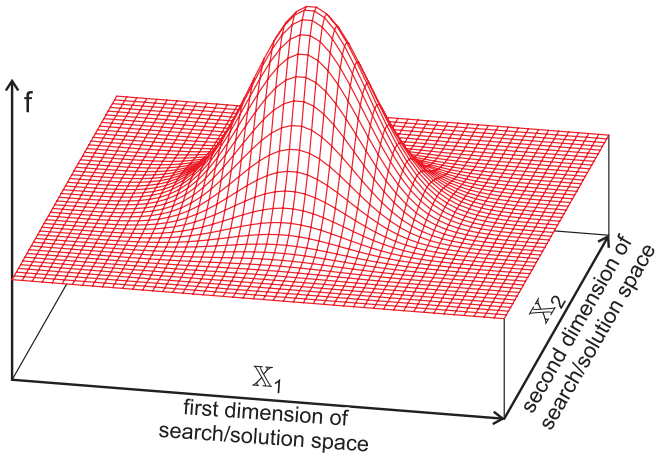

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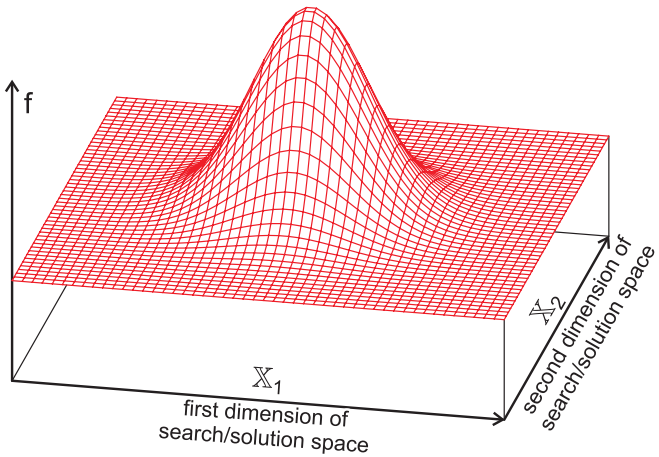

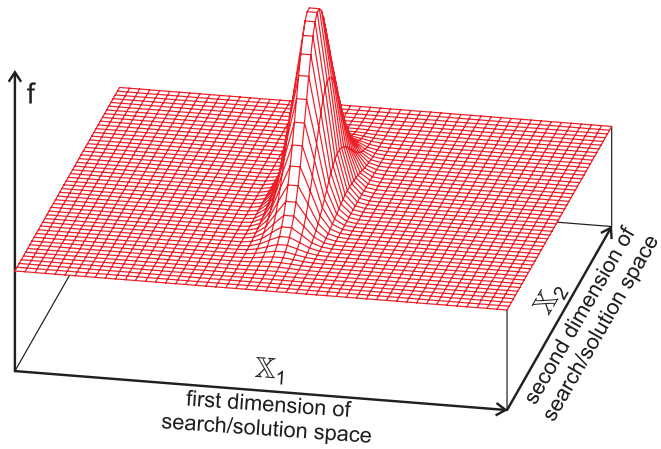

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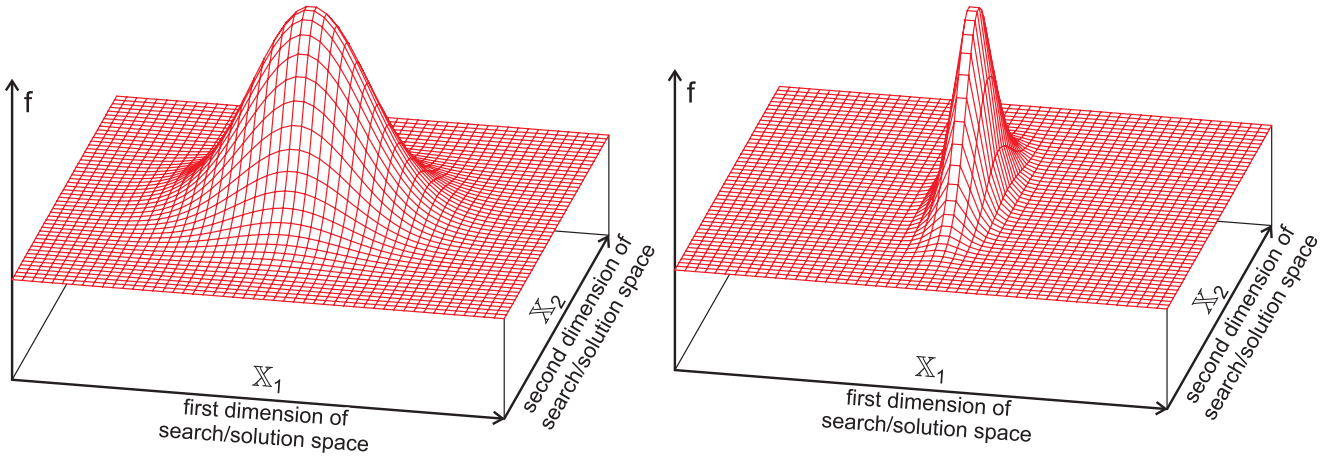

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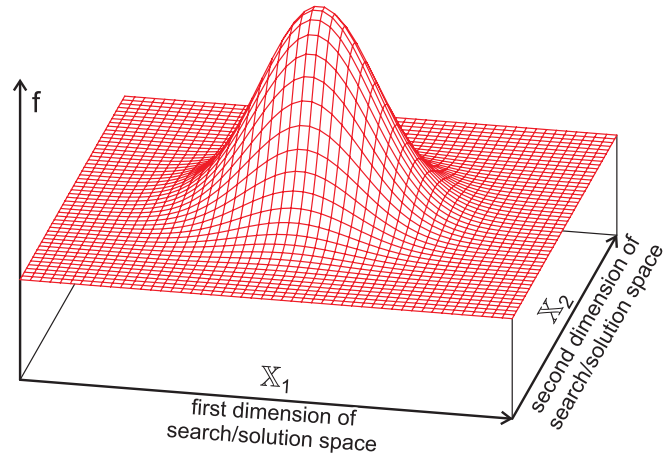

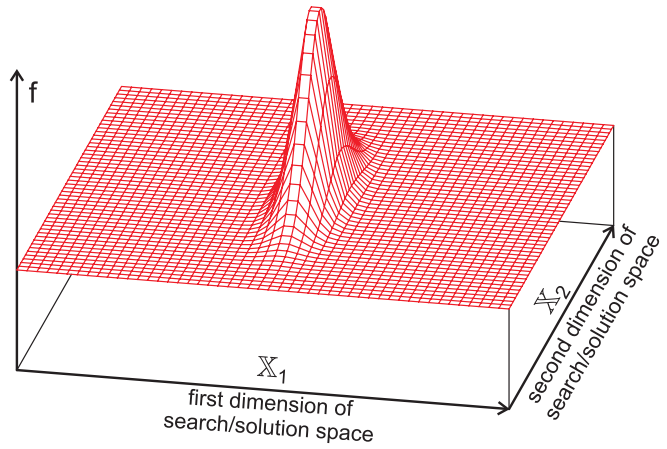

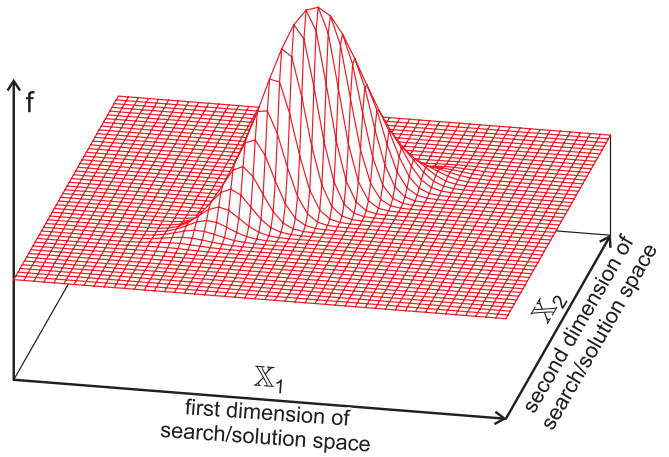

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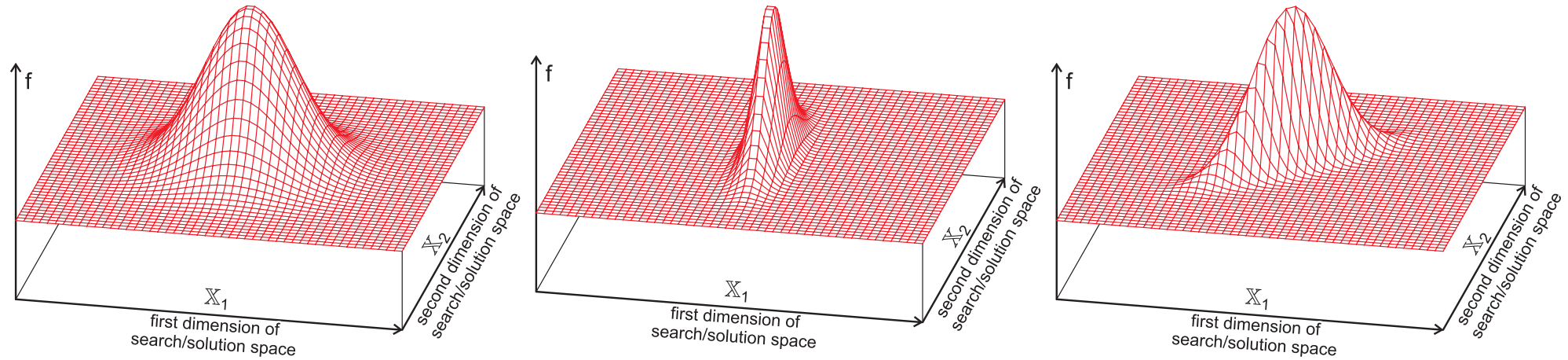

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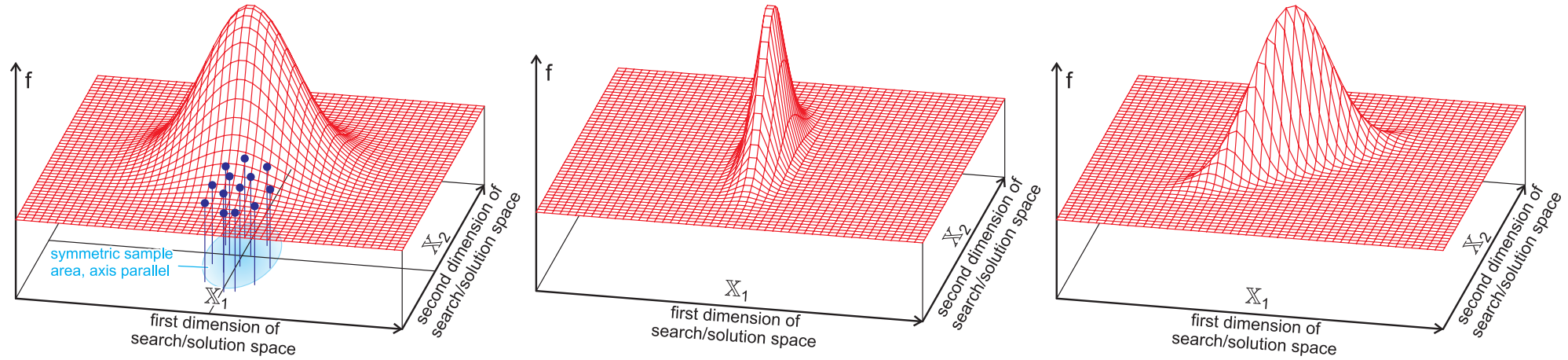

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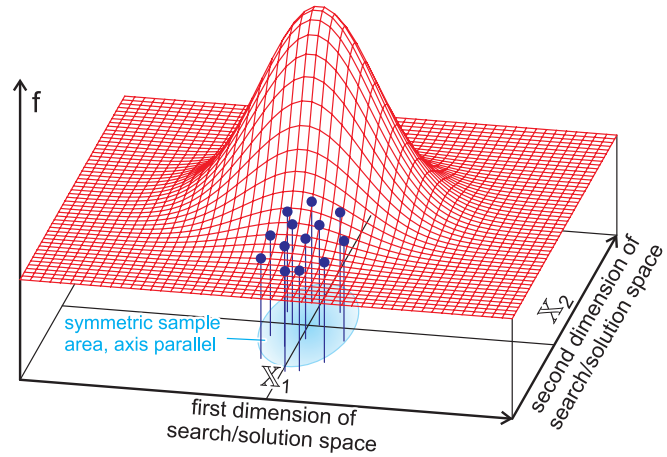

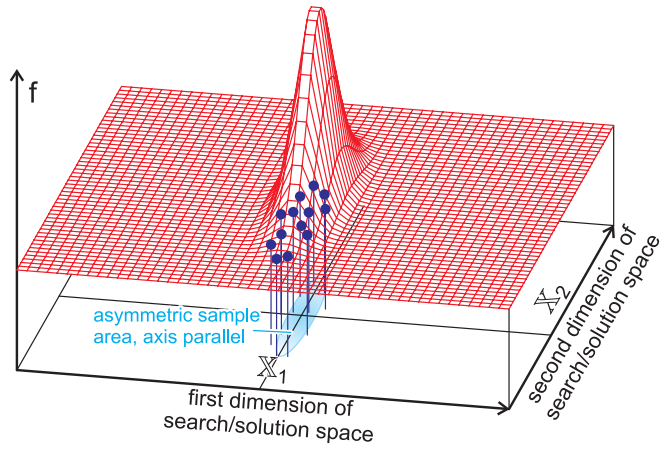

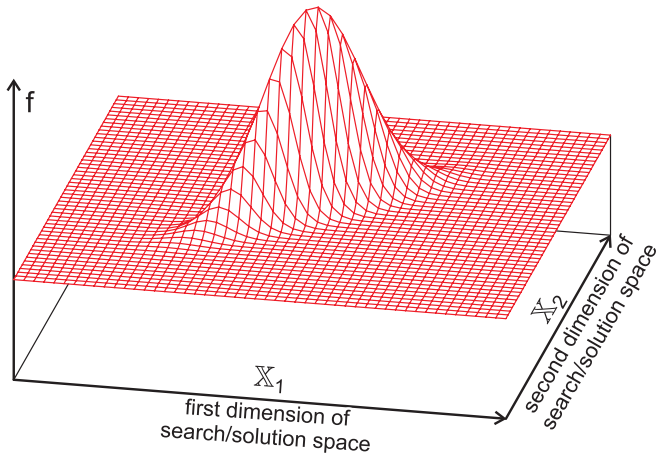

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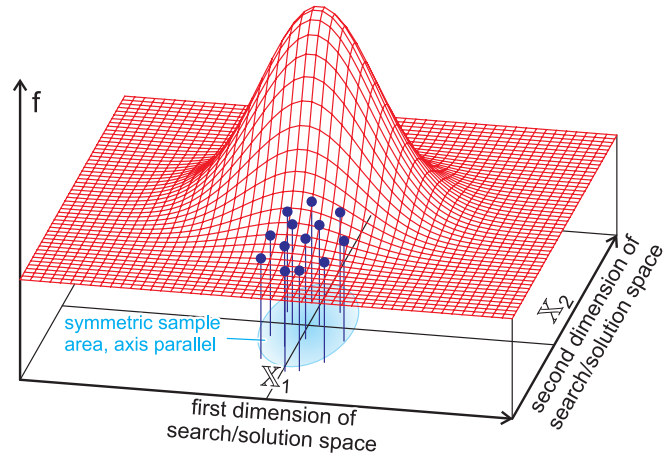

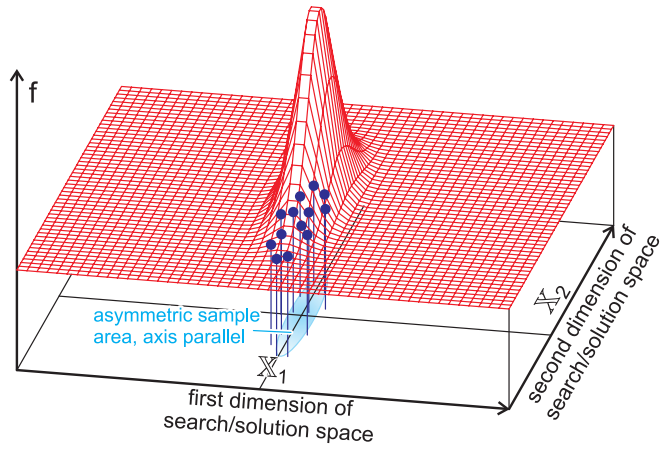

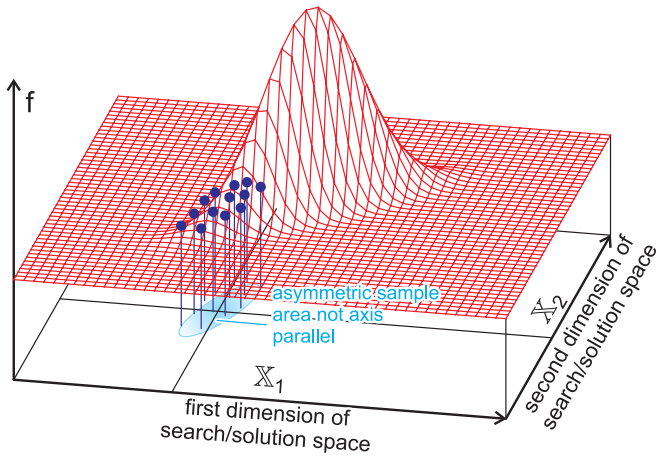

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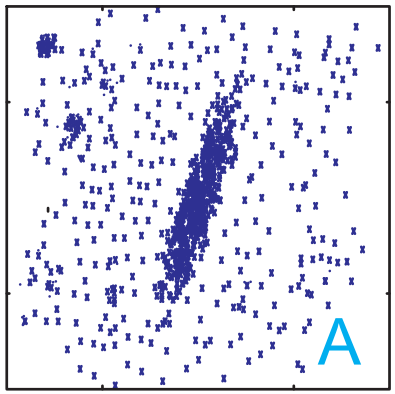

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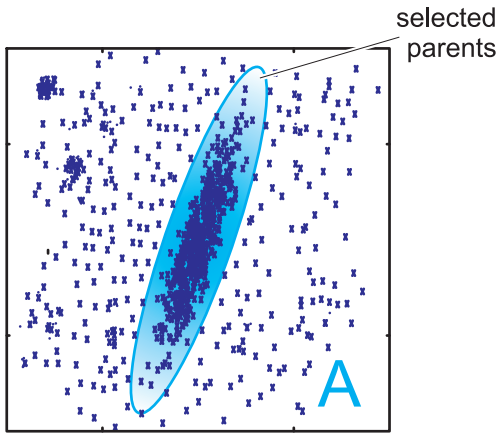
- Assume that the individuals in the blue sphere are selected, as they are the best ones for some reason



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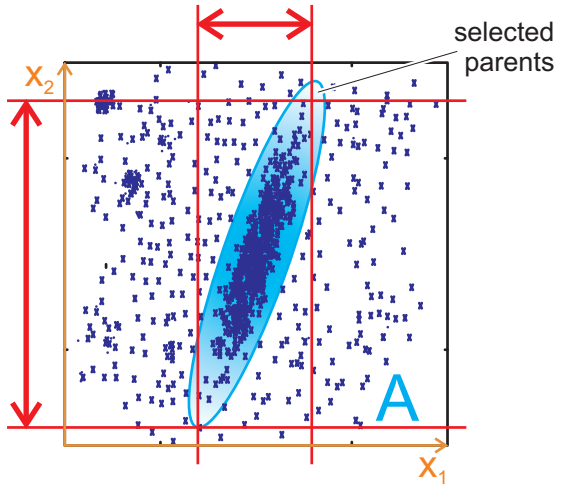

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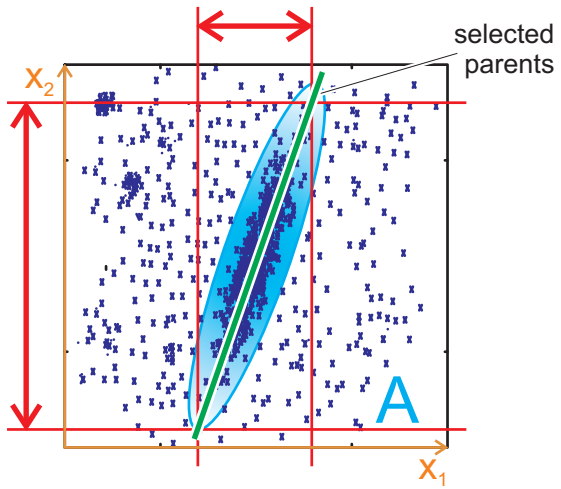
- Also, there is a correlation between the two dimensions: selected solutions with larger x_1 values also tend to have larger x_2 values and vice versa



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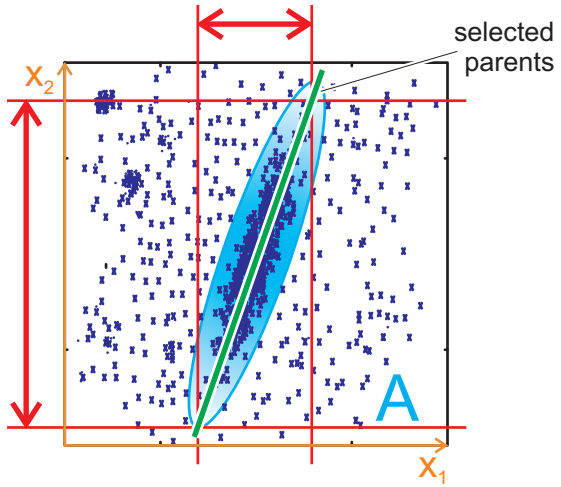

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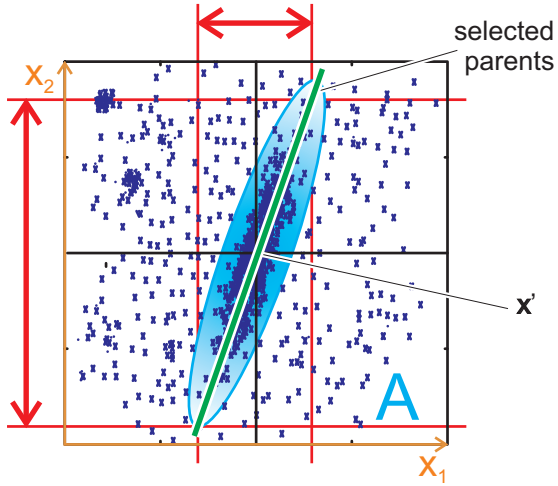

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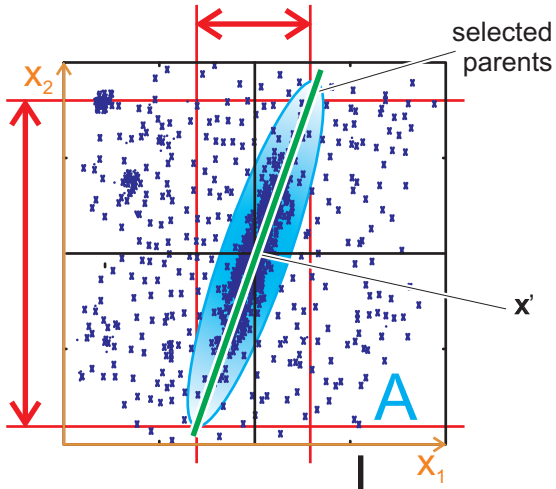

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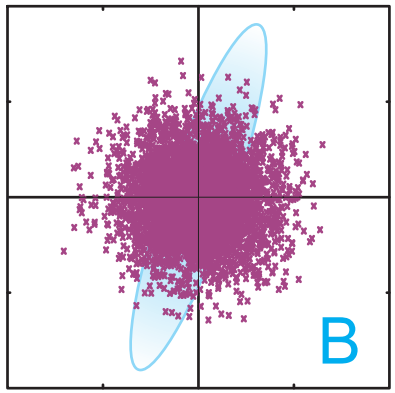

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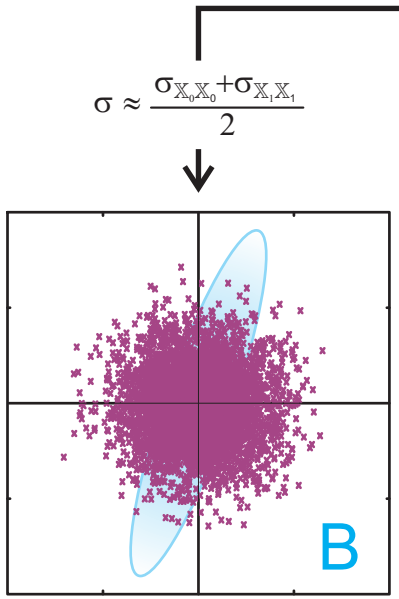

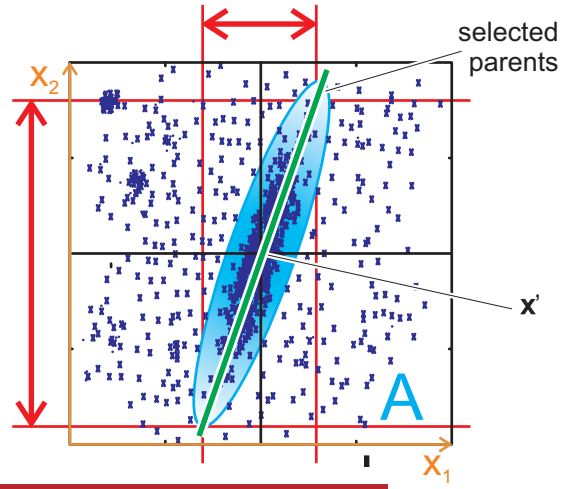

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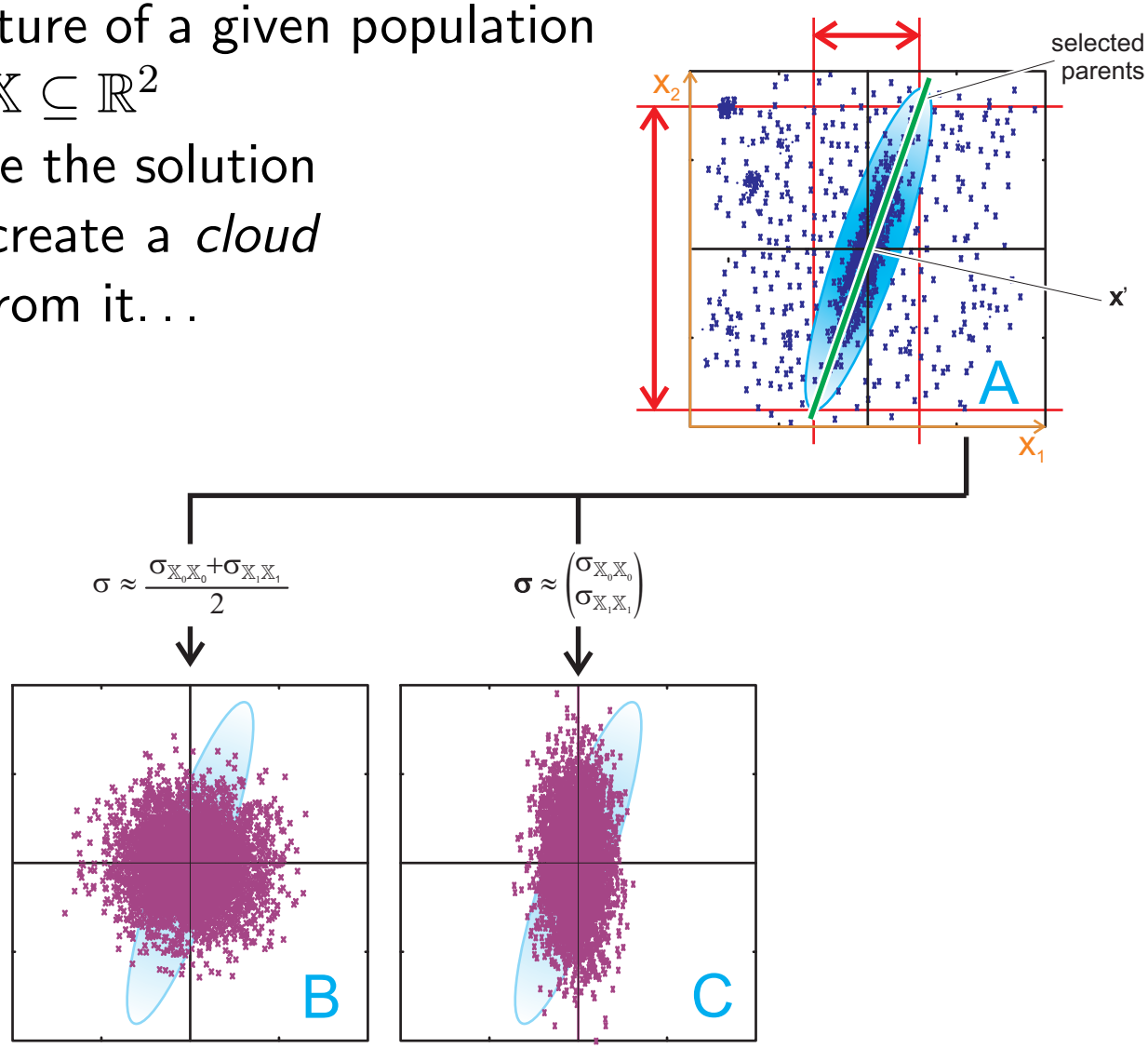

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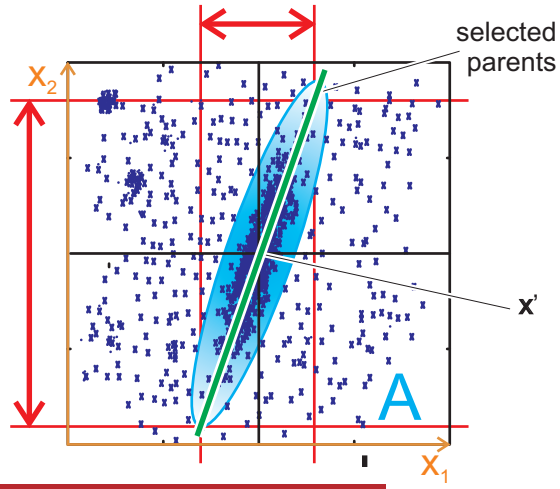

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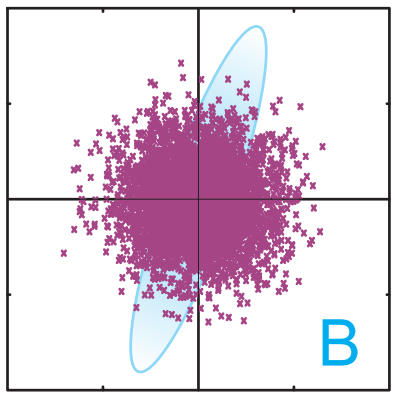

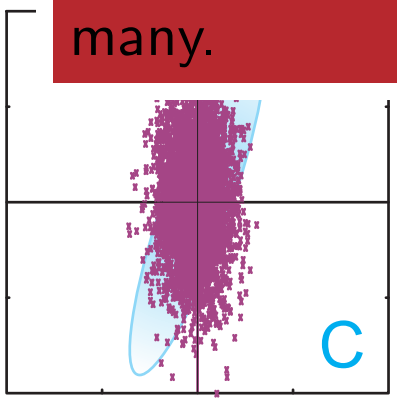

Fewer solutions generated outside the interesting range, but still many.

Mutation Operations B-C

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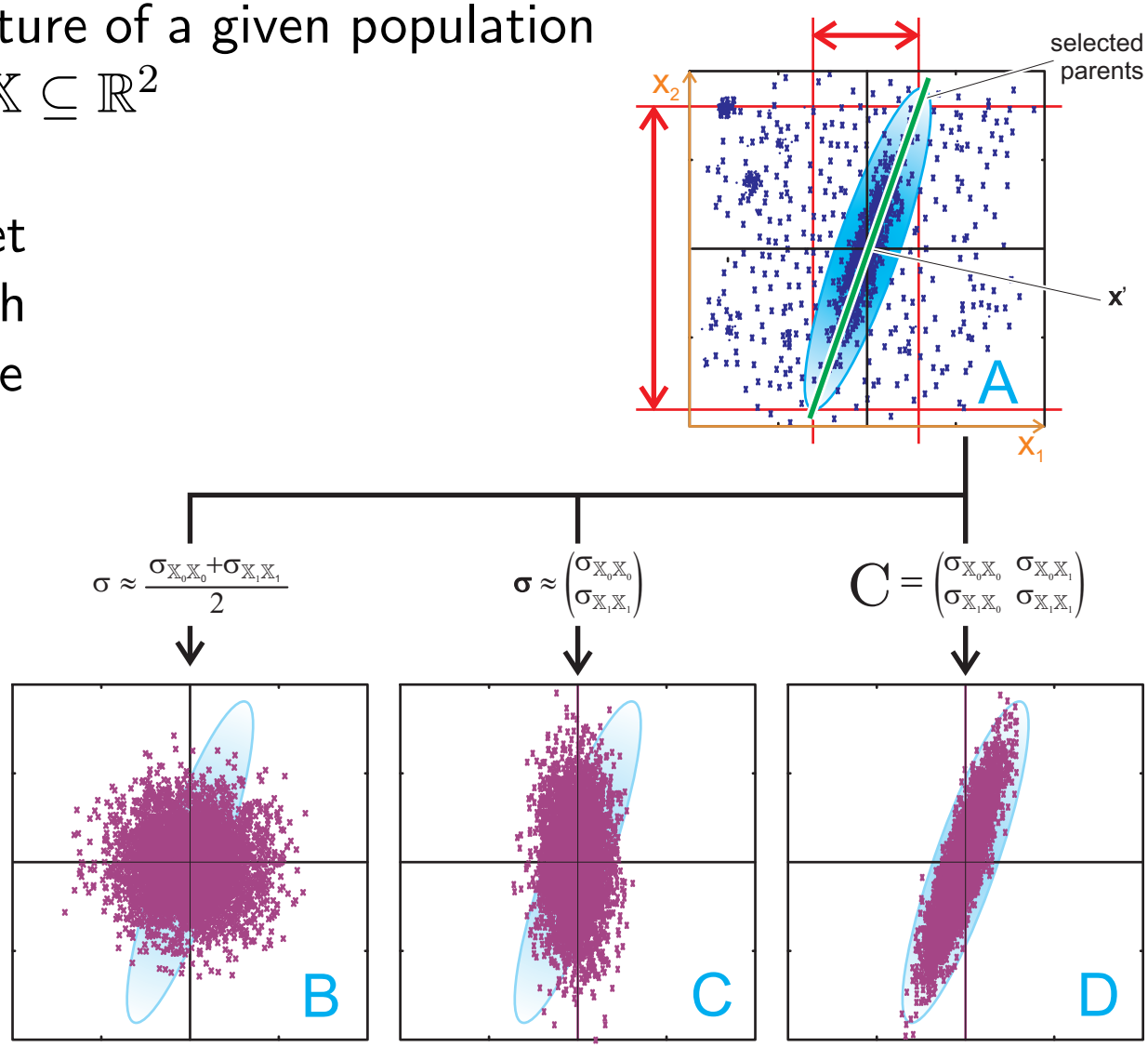

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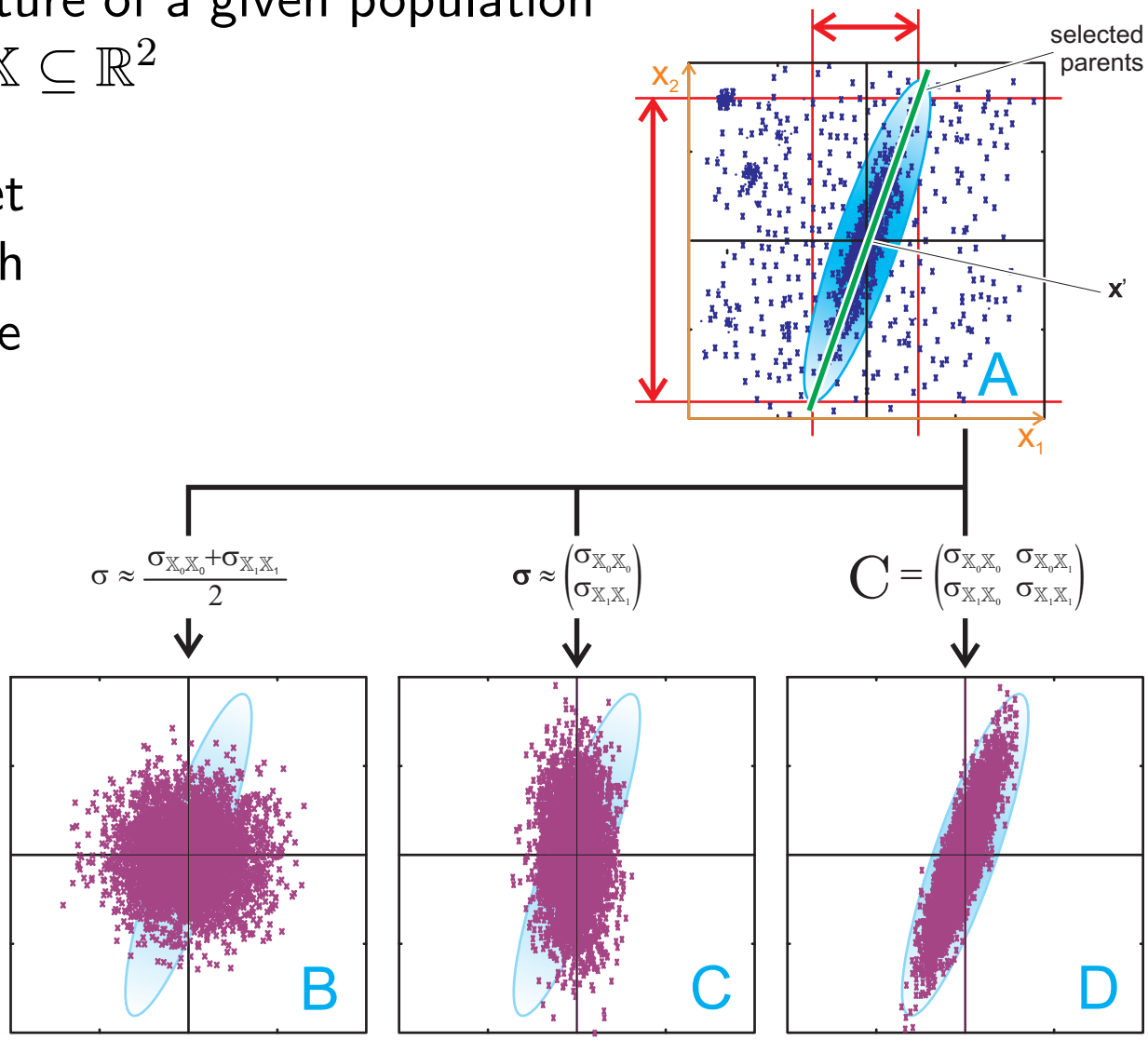
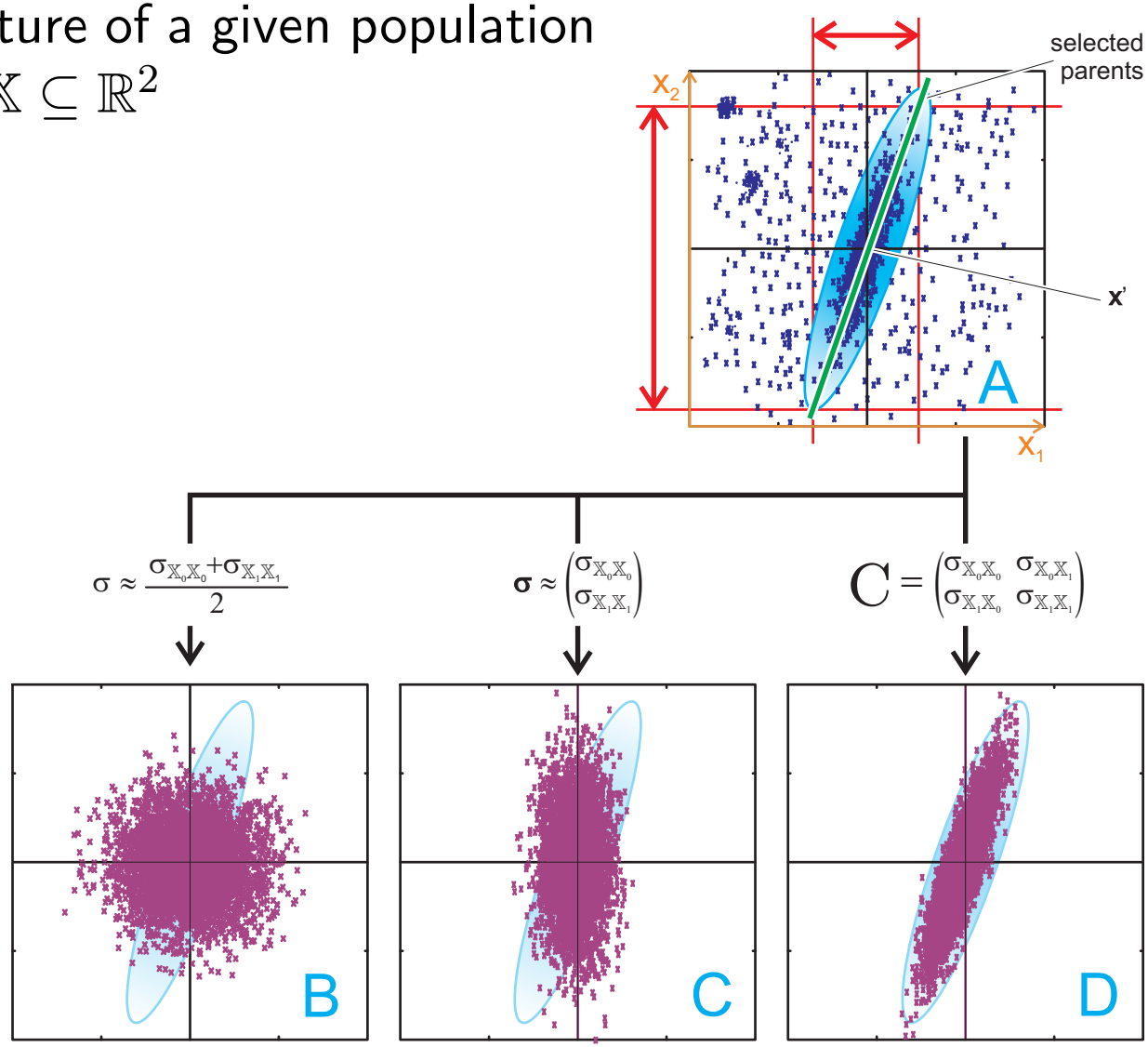
- Of course, **D** is more complicated to implement than **C**, which is more complicated to implement than **B**



Mutation Operations B-C

- Let's look at the structure of a given population in a 2D-search space $\mathbb{X} \subseteq \mathbb{R}^2$
- Of course, **D** is more complicated to implement than **C**, which is more complicated to implement than **B**
- Also: for **C** (and even more so for **D**), we need more data (σ, $\mathbf{C}$), and slower calculations



Mutation Operation B

- Single-valued standard deviation as step-width for mutation $p.w = \sigma$

$\vec{x} \longleftarrow \text{mutationES}_{w=\sigma}(\sigma, \vec{x}')$

Input: $\vec{x}' \in \mathbb{R}^n$: the input vector
Input: $\sigma \in \mathbb{R}$: the standard deviation of the mutation
Data: i: a counter variable
Output: $\vec{x} \in \mathbb{R}^n$: the mutated version of x'

begin
  for $i \longleftarrow 0$ **up to** $n-1$ **do**
    $vecx_i \longleftarrow \vec{x}'_i + \sigma\{\text{Gaussian random number}\}$
  return $\vec{x}$

Mutation Operation C

- Vector of standard deviations as step-width for mutation $p.w = \vec{\sigma}$

$\vec{x} \longleftarrow \text{mutationES}_{w=\vec{\sigma}}(\vec{\sigma}, \vec{x}')$

Input: $\vec{x}' \in \mathbb{R}^n$: the input vector
Input: $\vec{\sigma} \in \mathbb{R}^n$: the standard deviation vector of the mutation
Data: i: a counter variable
Output: $\vec{x} \in \mathbb{R}^n$: the mutated version of $\vec{x}'$

begin
  for $i \longleftarrow 0$ **up to** $n-1$ **do**
    $\vec{x}_i \longleftarrow \vec{x}'_i + \vec{\sigma}_i\{\text{Gaussian random number}\}$
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Mutation Operator B + C

Listing: Mutation Operator B + C

```
public class RnESUnaryNormal extends Rn implements IUnarySearchOperation<double[]> {
  public double[] mutate(final double[] genotype, final double[] sigma, final Random r) {
    double d;

    double[] g = genotype.clone(); // copy the original vector

    for (int i = g.length; (--i) >= 0;) {
      do { // create a value close to that gene by using the step length parameter
        d = (g[i] + (r.nextGaussian() * sigma[i % sigma.length]));
      } while ((d < this.min) || (d > this.max)); // make sure that value is OK

      g[i] = d; // store value into copied genotype
    }

    return g; // return the modified copy of the original genotype
  }
}
```

Mutation Operation D

- Rotation matrix $p.w = \mathbf{M}$

$\vec{x} \longleftarrow \text{mutationES}_{w=\mathbf{M}}(\mathbf{M}, \vec{x}')$

Input: $\vec{x}' \in \mathbb{R}^n$: the input vector
Input: $\mathbf{M} \in \mathbb{R}^{n \times n}$: an (orthogonal) rotation matrix
Data: i, j: a counter variable
Data: $\vec{t}$: a temporary vector
Output: $\vec{x} \in \mathbb{R}^n$: the mutated version of $\vec{x}'$

begin
- **for** $i \longleftarrow 0$ **up to** $n-1$ **do**
  - $\vec{t}_i \longleftarrow$ {Gaussian random number}
- $\vec{x} \longleftarrow \vec{x}'$
- // $\vec{x} \longleftarrow \vec{x} + \mathbf{M}\vec{t}$
- **for** $i \longleftarrow 0$ **up to** $n-1$ **do**
  - **for** $j \longleftarrow 0$ **up to** $n-1$ **do**
    - $\vec{x}_i \longleftarrow \vec{x}_i + \mathbf{M}_{i,j} * \vec{t}_j$
- **return** $\vec{x}$

- $\mathbf{M}$ does not directly represent a standard deviation, but can be computed from the covariance matrix[1] of an n-dimensional normal distribution

[1] $\mathbf{M}$ if measured, $\mathbf{M}$ if theoretical

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- More information on sampling multi-dimensional normal distributions based on covariance/Eigen-Vector matrices: [12, 13]

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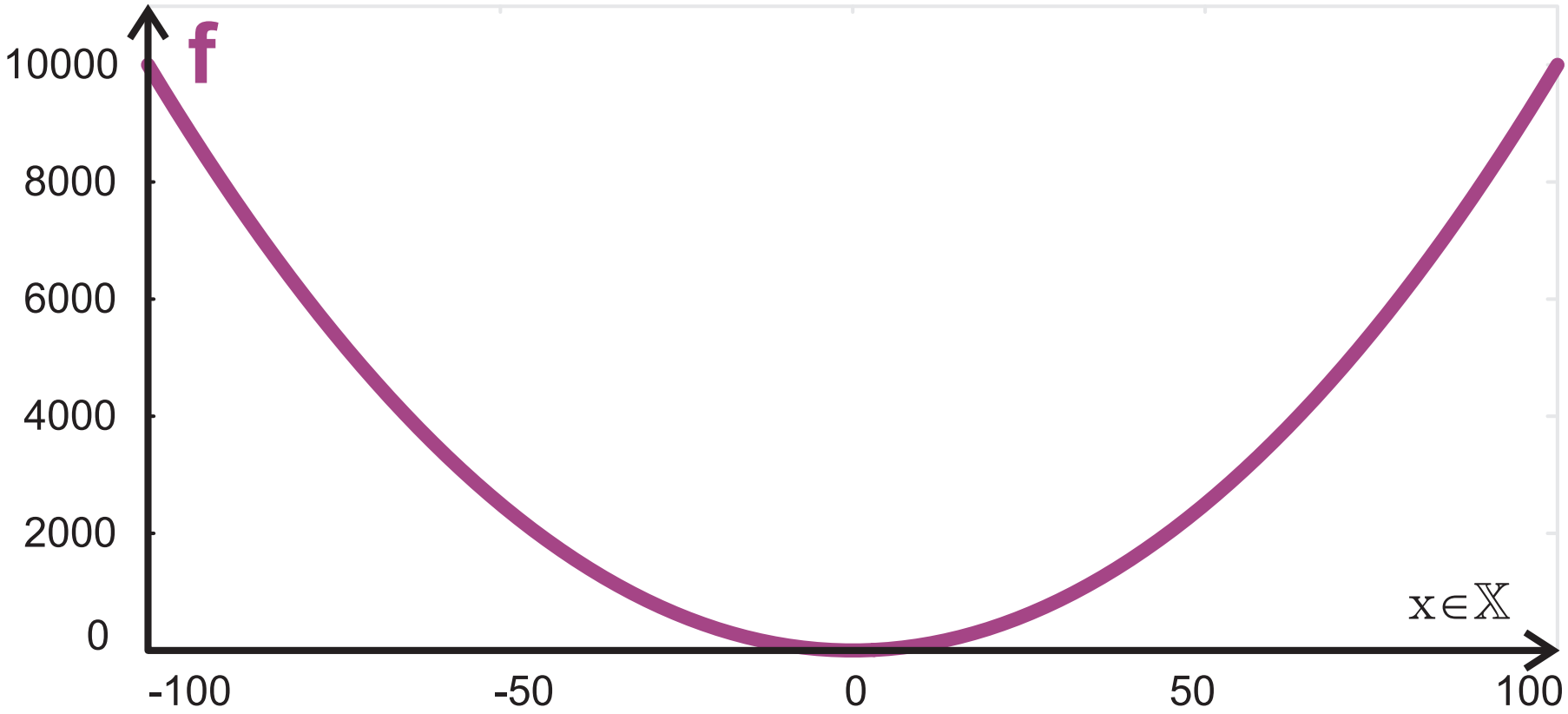
- Example: Sphere function

$$f(\vec{x}) = \sum_{i=1}^{n} \vec{x}_i^2 \text{ with } \mathbb{G} = \mathbb{X} \subseteq \mathbb{R}^n \tag{1}$$

Self-Adaptation on Sphere Function



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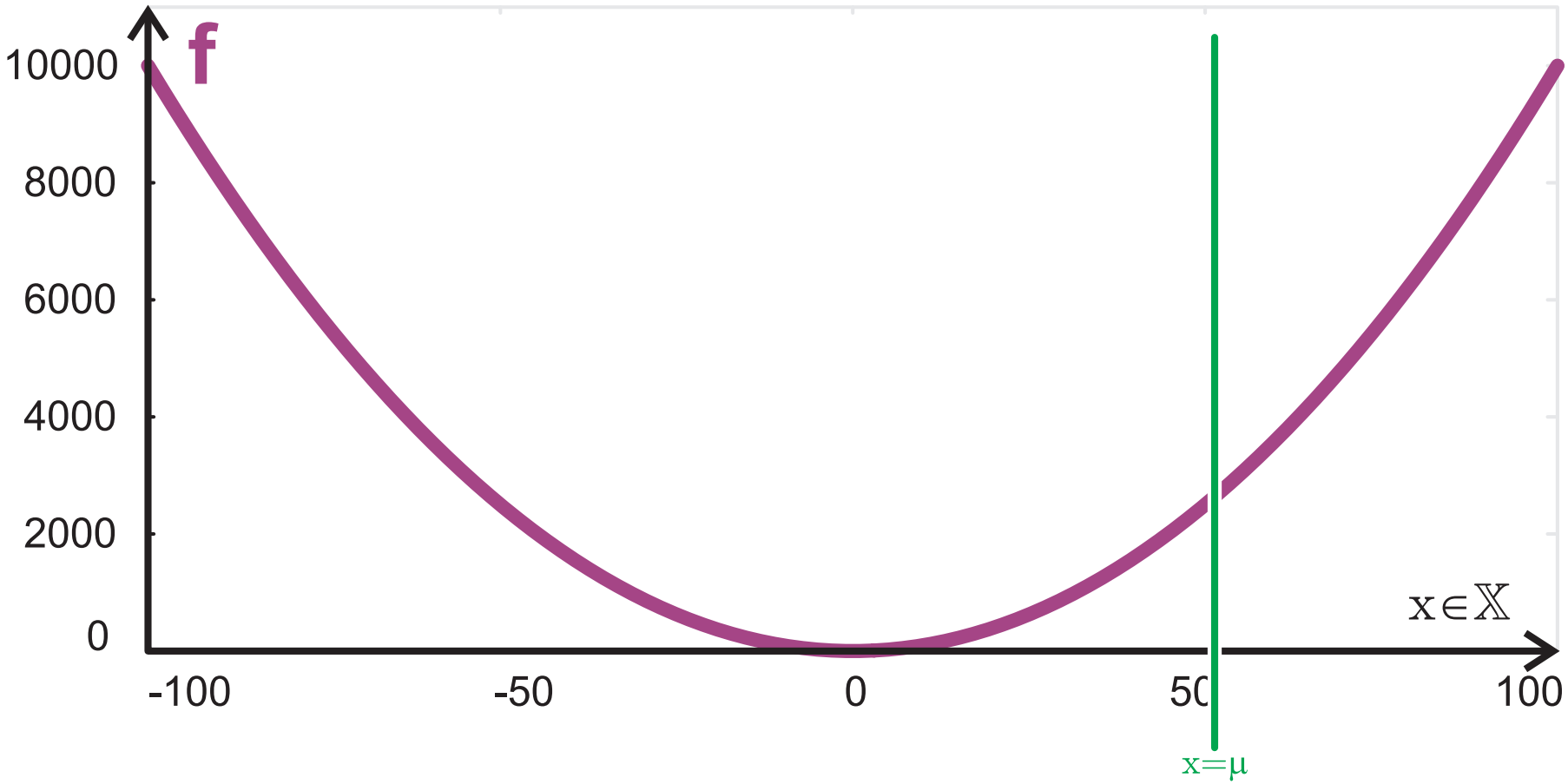

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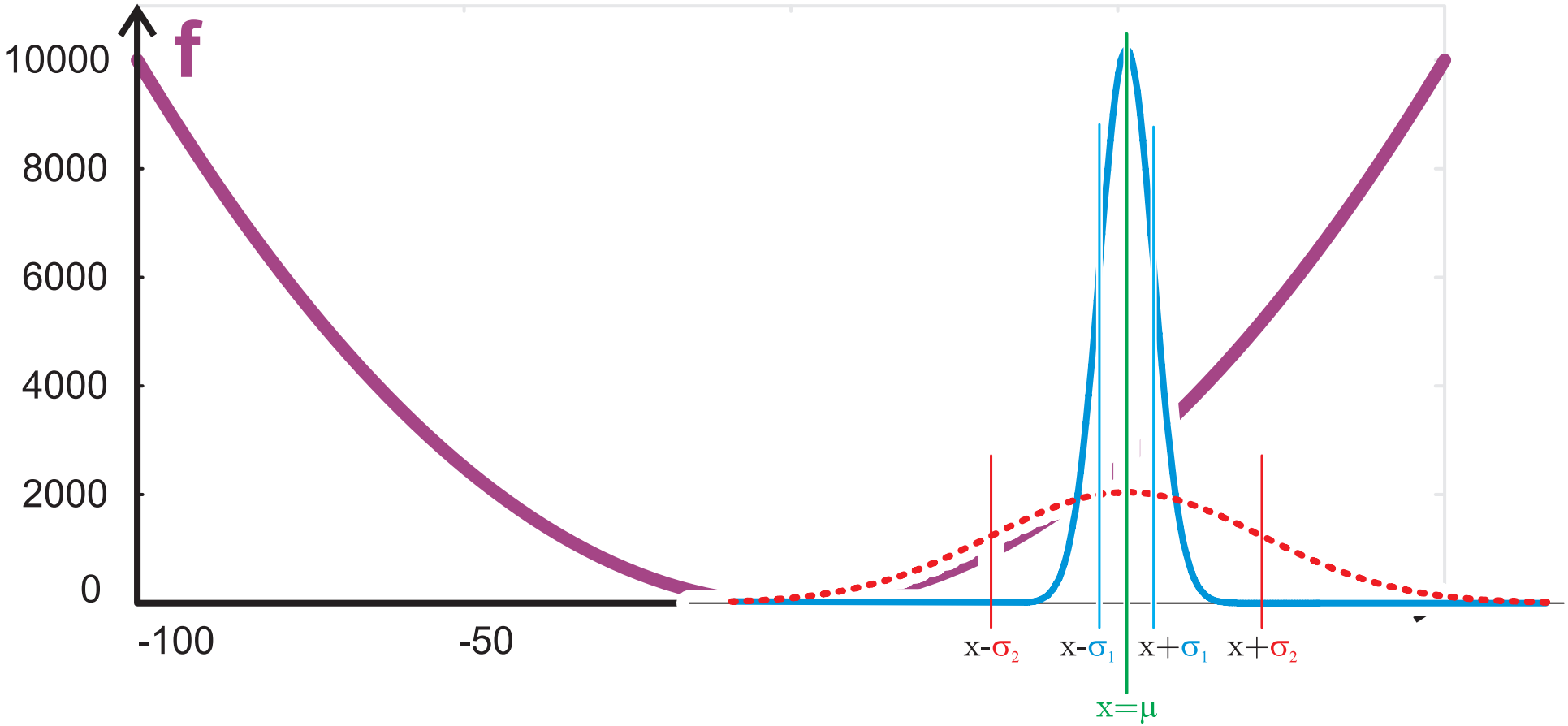

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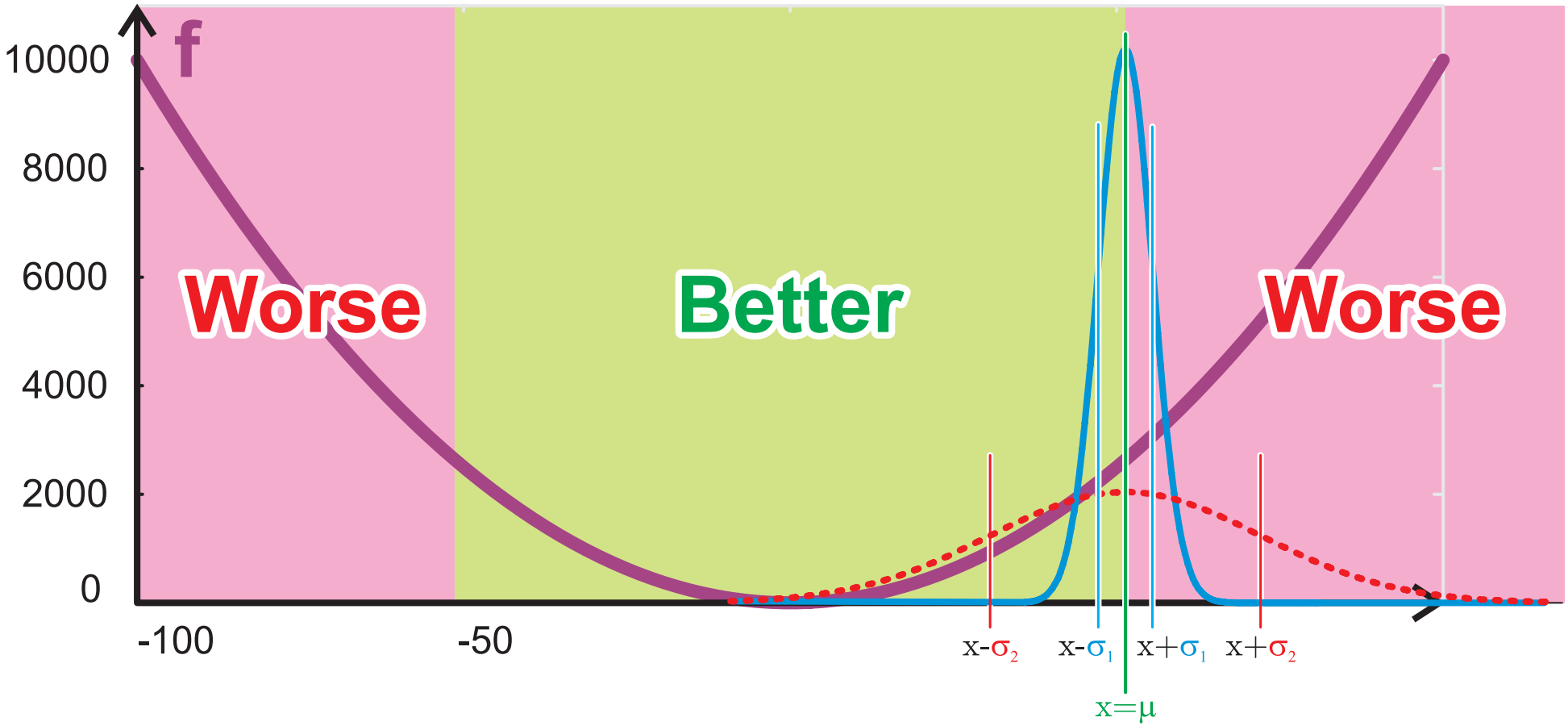

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$$\lim_{\sigma \to +\infty} P(S) = 0 \tag{4}$$

$$\lim_{\sigma \to +\infty} \varphi = 0 \tag{5}$$

- In between the two extreme cases (for $0 < \sigma < +\infty$) lies an area where $\varphi > 0$ and $0 < P(S) < 0.5$.

The $1/5$th Rule

Definition ($1/5$th Rule)

In order to obtain nearly optimal (local) performance of the $(1+1)$-ES with isotropic mutation, tune the mutation strength σ in such a way that the success rate $P(S)$ (estimated based on past operator applications) is about $1/5$ [15].

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  1. if success probability $P(S) > 0.2$, increase the mutation strength $\sigma \Rightarrow$ faster progress towards optimum

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Definition ($1/5$th Rule)

In order to obtain nearly optimal (local) performance of the $(1+1)$-ES with isotropic mutation, tune the mutation strength σ in such a way that the success rate $P(S)$ (estimated based on past operator applications) is about $1/5$ [15].

- $P(S)$ is monotonously decreasing with rising σ from $\lim_{\sigma \to 0} P(S) = 0.5$ to $\lim_{\sigma \to +\infty} P(S) = 0$
  1. if success probability $P(S) > 0.2$, increase the mutation strength $\sigma \Rightarrow$ faster progress towards optimum
  2. if the fraction of accepted mutations falls below 0.2, step size is too large and σ must be reduced

$1/5$th Rule-based $(1+1)$ Evolution Strategy

$p_{best} \longleftarrow (1+1)\ \mathrm{ES}_{\frac{1}{5}}(f, L, a, \sigma_0)$

begin
- $t \longleftarrow 1$
- $s \longleftarrow 0$
- $\sigma \longleftarrow \sigma_0$
- $p_{best}.g \longleftarrow$ create starting point
- $p_{best}.x \longleftarrow \mathrm{gpm}(p_{best}.g)$
- $p_{best}.y \longleftarrow f(p_{best}.x)$
- $p_{new} \longleftarrow p_{best}$
- **while** $\neg shouldTerminate$ **do**
  - $p_{new}.x \longleftarrow \mathrm{gpm}(p_{new}.g)$
  - $p_{new}.y \longleftarrow f(p_{new}.x)$
  - **if** $p_{new}.y < p_{best}.y$ **then**
    - $p_{best} \longleftarrow p_{new}$
    - $s \longleftarrow s + 1$
  - **if** $(t \bmod L) = 0$ **then**
    - $P(S) \longleftarrow \frac{s}{L}$
    - **if** $P(S) < 0.2$ **then** $\sigma \longleftarrow \sigma * a$
    - **else if** $P(S) > 0.2$ **then** $\sigma \longleftarrow \sigma / a$
    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber

1/5th Rule-based $(1+1)$ Evolution Strategy

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    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- Initialize iteration counter t, success counter s, and mutation strength σ

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- Create initial point in search space $p_{best}.g$, map it to candidate solution $p_{best}.x$, compute its objective value $p_{best}.y = f(p_{best}.x)$, and store it in "current" individual p_{new}

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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- **while** $\neg shouldTerminate$ **do**
  - $p_{new}.x \longleftarrow \mathrm{gpm}(p_{new}.g)$
  - $p_{new}.y \longleftarrow f(p_{new}.x)$
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    - $p_{best} \longleftarrow p_{new}$
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    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- map point in search space $p_{new}.g$ of current individual to candidate solution $p_{new}.x$ and compute its objective value $p_{new}.y = f(p_{new}.x)$

$1/5$th Rule-based $(1+1)$ Evolution Strategy

$p_{best} \longleftarrow (1+1)\ \mathrm{ES}_{\frac{1}{5}}(f, L, a, \sigma_0)$

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- **while** $\neg shouldTerminate$ **do**
  - $p_{new}.x \longleftarrow \mathrm{gpm}(p_{new}.g)$
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  - **if** $p_{new}.y < p_{best}.y$ **then**
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    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
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- $(1+1)$-ES = self-adaptive hill climber
- If current individual p_{new} is better then best known individual p_{best},

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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  - **if** $p_{new}.y < p_{best}.y$ **then**
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  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t+1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- If current individual p_{new} is better then best known individual p_{best},
- store it in p_{best} and

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  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- If current individual p_{new} is better then best known individual p_{best},
- store it in p_{best} and
- increase success counter s by one.

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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- $(1+1)$-ES = self-adaptive hill climber
- After every L iterations, it is time for self-adaptation.

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- After every L iterations, it is time for self-adaptation.
- Compute the achieved success rate $P(S)$ during the last L steps.

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- After every L iterations, it is time for self-adaptation.
- Compute the achieved success rate $P(S)$ during the last L steps.
- if less than $0.2\ldots$

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- $(1+1)$-ES = self-adaptive hill climber
- After every L iterations, it is time for self-adaptation.
- Compute the achieved success rate $P(S)$ during the last L steps.
- if less than 0.2, decrease σ by multiplying it with constant $a \in [0, 1]$.

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- After every L iterations, it is time for self-adaptation.
- Compute the achieved success rate $P(S)$ during the last L steps.
- if less than 0.2, decrease σ by multiplying it with constant $a \in [0, 1]$.
- if larger than $0.2\ldots$

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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  - $p_{new}.x \longleftarrow \mathrm{gpm}(p_{new}.g)$
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  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- After every L iterations, it is time for self-adaptation.
- Compute the achieved success rate $P(S)$ during the last L steps.
- if larger than 0.2, increase σ by dividing it by constant $a \in [0, 1]$.

$1/5$th Rule-based $(1+1)$ Evolution Strategy

$p_{best} \longleftarrow (1{+}1)\ \mathrm{ES}_{\frac{1}{5}}(f, L, a, \sigma_0)$

begin
- $t \longleftarrow 1$
- $s \longleftarrow 0$
- $\sigma \longleftarrow \sigma_0$
- $p_{best}.g \longleftarrow$ create starting point
- $p_{best}.x \longleftarrow \mathrm{gpm}(p_{best}.g)$
- $p_{best}.y \longleftarrow f(p_{best}.x)$
- $p_{new} \longleftarrow p_{best}$
- **while** $\neg shouldTerminate$ **do**
  - $p_{new}.x \longleftarrow \mathrm{gpm}(p_{new}.g)$
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  - **if** $p_{new}.y < p_{best}.y$ **then**
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    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- After every L iterations, it is time for self-adaptation.
- Compute the achieved success rate $P(S)$ during the last L steps.
- if larger than 0.2, increase σ by dividing it by constant $a \in [0, 1]$.
- Finally, reset success counter s to 0.

$1/5$th Rule-based $(1+1)$ Evolution Strategy

$p_{best} \longleftarrow (1+1)\ \mathrm{ES}_{\frac{1}{5}}(f, L, a, \sigma_0)$

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- $t \longleftarrow 1$
- $s \longleftarrow 0$
- $\sigma \longleftarrow \sigma_0$
- $p_{best}.g \longleftarrow$ create starting point
- $p_{best}.x \longleftarrow \mathrm{gpm}(p_{best}.g)$
- $p_{best}.y \longleftarrow f(p_{best}.x)$
- $p_{new} \longleftarrow p_{best}$
- **while** $\neg shouldTerminate$ **do**
  - $p_{new}.x \longleftarrow \mathrm{gpm}(p_{new}.g)$
  - $p_{new}.y \longleftarrow f(p_{new}.x)$
  - **if** $p_{new}.y < p_{best}.y$ **then**
    - $p_{best} \longleftarrow p_{new}$
    - $s \longleftarrow s+1$
  - **if** $(t \bmod L) = 0$ **then**
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    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t+1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- Perform mutation by using step-width σ

$1/5$th Rule-based $(1+1)$ Evolution Strategy

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begin
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- $\sigma \longleftarrow \sigma_0$
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    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- Increase iteration counter t

$1/5$th Rule-based $(1+1)$ Evolution Strategy

$p_{best} \longleftarrow (1{+}1)\ \mathrm{ES}_{\frac{1}{5}}(f, L, a, \sigma_0)$

begin
- $t \longleftarrow 1$
- $s \longleftarrow 0$
- $\sigma \longleftarrow \sigma_0$
- $p_{best}.g \longleftarrow$ create starting point
- $p_{best}.x \longleftarrow \mathrm{gpm}(p_{best}.g)$
- $p_{best}.y \longleftarrow f(p_{best}.x)$
- $p_{new} \longleftarrow p_{best}$
- **while** $\neg shouldTerminate$ **do**
  - $p_{new}.x \longleftarrow \mathrm{gpm}(p_{new}.g)$
  - $p_{new}.y \longleftarrow f(p_{new}.x)$
  - **if** $p_{new}.y < p_{best}.y$ **then**
    - $p_{best} \longleftarrow p_{new}$
    - $s \longleftarrow s + 1$
  - **if** $(t \bmod L) = 0$ **then**
    - $P(S) \longleftarrow \frac{s}{L}$
    - **if** $P(S) < 0.2$ **then** $\sigma \longleftarrow \sigma * a$
    - **else if** $P(S) > 0.2$ **then** $\sigma \longleftarrow \sigma / a$
    - $s \longleftarrow 0$
  - $p_{new}.g \longleftarrow \mathrm{mutationES}_{\sigma}(\sigma, p_{new})$
  - $t \longleftarrow t + 1$
- **return** p_{best}

- $(1+1)$-ES = self-adaptive hill climber
- Return best candidate solution discovered.

(1+1) ES with 1/5th rule

Listing: (1+1) ES with 1/5th rule

```java
public class ES1P1<X> extends OptimizationAlgorithm<double[], X> {
  public Individual<double[], X> solve(final IObjectiveFunction<X> f) {
    Individual<double[], X> pstar = new Individual<>(); // best individual
    Individual<double[], X> pnew  = new Individual<>(); // "new" individual
    RnESUnaryNormal esUnary       = ((RnESUnaryNormal) (this.unary));

    double[] sigma = new double[] { this.sigma0 };
    int       s    = 0;
    int       t    = 1; // init success and iteration counter

    pstar.g = this.nullary.create(this.random); // create first genotype
    pstar.x = this.gpm.gpm(pstar.g);            // get phenotype for that genotype
    pstar.v = f.compute(pstar.x);               // evaluate: how good is the phenotype?

    while (!(this.termination.shouldTerminate())) { // until we should finish...
      pnew.g = esUnary.mutate(pstar.g, sigma, this.random); // mutate using sigma
      pnew.x = this.gpm.gpm(pnew.g);                        // get phenotype for that genotype
      pnew.v = f.compute(pnew.x);                           // evaluate the new phenotype

      if (pnew.v <= pstar.v) { // if the new individual is better...
        pstar.assign(pnew);    // it becomes the new best individual
        s++;                   // count the success
      }

      if ((t % this.L) == 0) { // is it time to update sigma?
        double Ps = (((double) s) / ((double) (this.L))); // need floating point div!
        if (Ps < 0.2d) {
          sigma[0] *= this.a;   // not enough success: decrease sigma
        } else {
          if (Ps > 0.2d) {
            sigma[0] /= this.a; // too successful: increase sigma
          }
        }
        s = 0; // reset success counter
      }

      t++; // count iteration
    }
    return pstar; // return the best individual that we have discovered
  }
}
```

$1/5$th Rule: Advantages and Drawbacks

- The $1/5^{th}$ rule has **advantages**

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  - intended for $(1+1)$-ES: makes no use of population
  - Only a single parameter σ: cannot model different step widths for different dimensions or dependencies between dimensions
  - Only a single parameter σ: cannot easily be extended for population-based methods

Section Outline

Endogeneous Parameters

- Instead of having one central exogeneous[1] (set of) strategy parameter(s)...

[1] ≡ outside of the genes

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- create one set of parameters of each individual in the Evolution Strategy!
- i.e., , the individual records extended with information $p.w$ encoding the strategy parameters
- Strategy parameters are now similar to (or inside) the genotype/genes, i.e., are endogeneous
- $p.w$ could be step-width for mutation if applied to individual p
- Information $p.w$ undergoes reproduction, similar to genotypes $p.g \in \mathbb{G}$
- As it is subject to selection, good strategy parameters will be discovered in the same way in which good candidate solutions are discovered.

Endogeneous Adaptation

$p_{best} \longleftarrow \text{generalES}(f, \mu, \lambda, \rho)$

begin
- $t \longleftarrow 1$
- pop $\longleftarrow$ random initialization
- **while** $\neg shouldTerminate$ **do**
  - perform genotype-phenotype mapping
  - compute objective values (possibly update best-so-far solution p_{best})
  - **if** $t > 1$ **then**
    - **if** strategy $= (\mu/\rho, \lambda)$ **then**
      - matePool $\longleftarrow$ truncationSelection(μ, pop)
    - **else**
      - matePool $\longleftarrow$ truncationSelection$(\mu, \text{pop} \cup \text{matePool})$
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  - **for** $i \longleftarrow 1$ **up to** λ **do**
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    - $population[i] \longleftarrow p_{new}$
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- **return** best solution $\tilde{x}$ discovered

- Evolution Strategies follow same basic pattern as GAs

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- Evolution Strategies follow same basic pattern as GAs
- Start with creating a random initial population, where each individual p has a (random) point in search space $p.g$ (genotype) and (random) information $p.w$ component

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- Evolution Strategies follow same basic pattern as GAs
- Perform the genotype-phenotype mapping, i.e., translate the genotypes $p.g$ to the corresponding candidate solutions $p.x$

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- **return** best solution $\tilde{x}$ discovered

- Evolution Strategies follow same basic pattern as GAs
- Compute the objective values (update best-so-far solution p_{best} if a new, better one is discovered)

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- Evolution Strategies follow same basic pattern as GAs
- Perform survival selection

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- Perform survival selection
  - in (μ, λ)-ESs, select only from the current population

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  - in (μ, λ)-ESs, select only from the current population
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- Evolution Strategies follow same basic pattern as GAs
- Perform survival selection
  - in (μ, λ)-ESs, select only from the current population
  - in $(\mu + \lambda)$-ESs, select from the current population and the mating pool
- *Only* in first iteration: no selection.

Endogeneous Adaptation

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- Evolution Strategies follow same basic pattern as GAs
- For each offspring individual that we want to create...

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- **return** best solution $\tilde{x}$ discovered

- Evolution Strategies follow same basic pattern as GAs
- For each offspring individual that we want to create. . .
  - . . . first select ρ parents,

Endogeneous Adaptation

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            population[i] ⟵ p_new
        t ⟵ t + 1
    return best solution x̃ discovered
```

- Evolution Strategies follow same basic pattern as GAs
- For each offspring individual that we want to create. . .
  - . . . first select ρ parents,
  - (re)combine the parental genotypes,

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            population[i] ⟵ p_new
        t ⟵ t + 1
    return best solution x̃ discovered
```

- Evolution Strategies follow same basic pattern as GAs
- For each offspring individual that we want to create...
  - ...first select ρ parents,
  - (re)combine the parental genotypes,
  - and then (re)combine the endogenous information.

Endogeneous Adaptation

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- **return** best solution $\tilde{x}$ discovered

- Evolution Strategies follow same basic pattern as GAs
- For each offspring individual that we want to create...
  - One endogeneous set of parameters (for mutation operation) exists per individual

Endogeneous Adaptation

$p_{best} \longleftarrow \text{generalES}(f, \mu, \lambda, \rho)$

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- $t \longleftarrow 1$
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- **while** $\neg shouldTerminate$ **do**
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  - Parameter setting of algorithm evolves along with the solutions
  - Good settings survive along with the candidate solutions that they have created

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- Evolution Strategies follow same basic pattern as GAs
- Mutate the endogenous information (parameter settings for genotype mutation)

Endogeneous Adaptation

$p_{best} \longleftarrow \text{generalES}(f, \mu, \lambda, \rho)$

```
begin
    t ⟵ 1
    pop ⟵ random initialization
    while ¬shouldTerminate do
        perform genotype-phenotype mapping
        compute objective values (possibly update best-so-far solution p_best)
        if t > 1 then
            if strategy = (μ/ρ, λ) then
                matePool ⟵ truncationSelection(μ, pop)
            else
                matePool ⟵ truncationSelection(μ, pop ∪ matePool)
        else
            matePool ⟵ pop
        for i ⟵ 1 up to λ do
            parents ⟵ choose ρ parents from matePool
            p_new.g ⟵ recombinationES(p.g ∀p ∈ parents)
            p_new.w ⟵ infoRecombinationES(p.w ∀p ∈ parents)
            p_new.w ⟵ infoMutationES(p_new.w)
            p_new.g ⟵ mutationES(p_new.g, p_new.w)
            population[i] ⟵ p_new
        t ⟵ t + 1
    return best solution x̃ discovered
```

- Evolution Strategies follow same basic pattern as GAs
- Mutate the endogenous information (parameter settings for genotype mutation)
- Endogenous information is mutated before applying it in the mutation operation: only the values that actually influenced the fitness are in w

Endogeneous Adaptation

$p_{best} \longleftarrow \text{generalES}(f, \mu, \lambda, \rho)$

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- Evolution Strategies follow same basic pattern as GAs
- Use the mutated endogenous information as parameter for the mutation operator (e.g., as step length) in order to mutate the newly created genotype

Endogeneous Adaptation

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  - $t \longleftarrow t + 1$
- **return** best solution $\tilde{x}$ discovered

- Evolution Strategies follow same basic pattern as GAs
- Put the new individuals into the population...
- ...and start the next cycle

Endogeneous Adaptation

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begin
- $t \longleftarrow 1$
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- **while** $\neg shouldTerminate$ **do**
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    - $population[i] \longleftarrow p_{new}$
  - $t \longleftarrow t + 1$
- **return** best solution $\tilde{x}$ discovered

- Evolution Strategies follow same basic pattern as GAs
- Return the best candidate solutions that were discovered

Section Outline

[A] Discrete Recombination

- Extension of uniform crossover to ρ real vectors

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- if $\rho = 2$, returns corner of hyper-cube created by parents

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- Extension of uniform crossover to ρ real vectors
- if $\rho = 2$, returns corner of hyper-cube created by parents

$\vec{g}' \longleftarrow$ recombinationDiscrete(parents)

Input: parents: the list of ρ parent individuals
Data: i: a counter variable
Data: p: a parent individual
Output: $\vec{g}'$: the offspring of the parents

begin
  for $i \longleftarrow 0$ **up to** $n-1$ **do**
    $p \longleftarrow$ parents[{randomly from $0..\rho-1$}]
    $\vec{g}'_i \longleftarrow p.g_i$
  return $\vec{g}'$

Discrete Recombination

Listing: Discrete Recombination for 2 Parents

```
public class RnBinaryDiscrete extends Rn implements
    IBinarySearchOperation<double[]> {


  public double[] recombine(final double[] parent1, final
      double[] parent2, final Random r) {

    double[] res = parent1.clone();

    for (int i = parent2.length; (--i) >= 0;) {
      if (r.nextBoolean()) {
        res[i] = parent2[i];
      }
    }

    return res;
  }
}
```

[B] Intermediate Recombination

- Extension of weighted average crossover to ρ real vectors

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- Extension of weighted average crossover to ρ real vectors
- Returns a point inside of hyper-cube defined by the parents

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- Extension of weighted average crossover to ρ real vectors
- Returns a point inside of hyper-cube defined by the parents

$\vec{g}' \longleftarrow$ recombinationIntermediate(parents)

Input: parents: the list of ρ parent individuals
Data: p: a parent individual
Output: $\vec{g}'$: the offspring of the parents

begin
  for $i \longleftarrow 0$ **up to** $n-1$ **do**
    $s \longleftarrow 0$
    for $j \longleftarrow 0$ **up to** $\rho - 1$ **do**
      $p \longleftarrow \text{parents}[j]$
      $s \longleftarrow s + p.g_i$
    $\vec{g}'_i \longleftarrow \frac{s}{\rho}$
  return $\vec{g}'$

Intermediate Recombination

Listing: Intermediate Recombination for 2 Parents

```
public class RnBinaryIntermediate extends Rn implements
    IBinarySearchOperation<double[]> {


  public double[] recombine(final double[] parent1, final
      double[] parent2, final Random r) {

    double[] res = new double[parent1.length];

    for (int i = parent2.length; (--i) >= 0;) {
      res[i] = (0.5d * (parent1[i] + parent2[i]));
    }

    return res;
  }
}
```

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Reproduction of Endogenous Parameters

- Recombination of strategy parameters $p.w$: intermediate crossover

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Reproduction of Endogenous Parameters

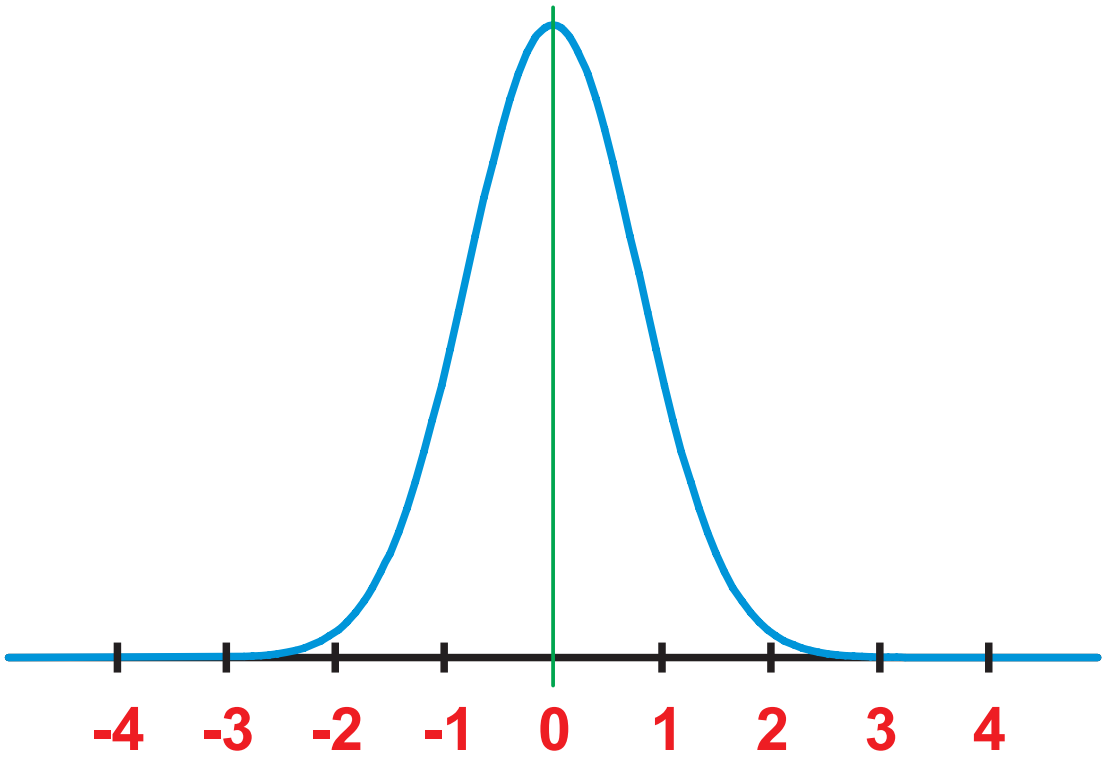
- Recombination of strategy parameters $p.w$: intermediate crossover
- Mutation is different from mutation of a genotype: we mutate a mutation strength
- Mutation means to mutate the degree with which a candidate solution should be changed
- Here, not the absolute value (1, 7, 1.5, etc.) is interesting...
- ...but more the scale, i.e., 1, 10, 0.1, 10000, 0.001, ...

Reproduction of Endogenous Parameters

- Recombination of strategy parameters $p.w$: intermediate crossover
- So we are concerned about the scale

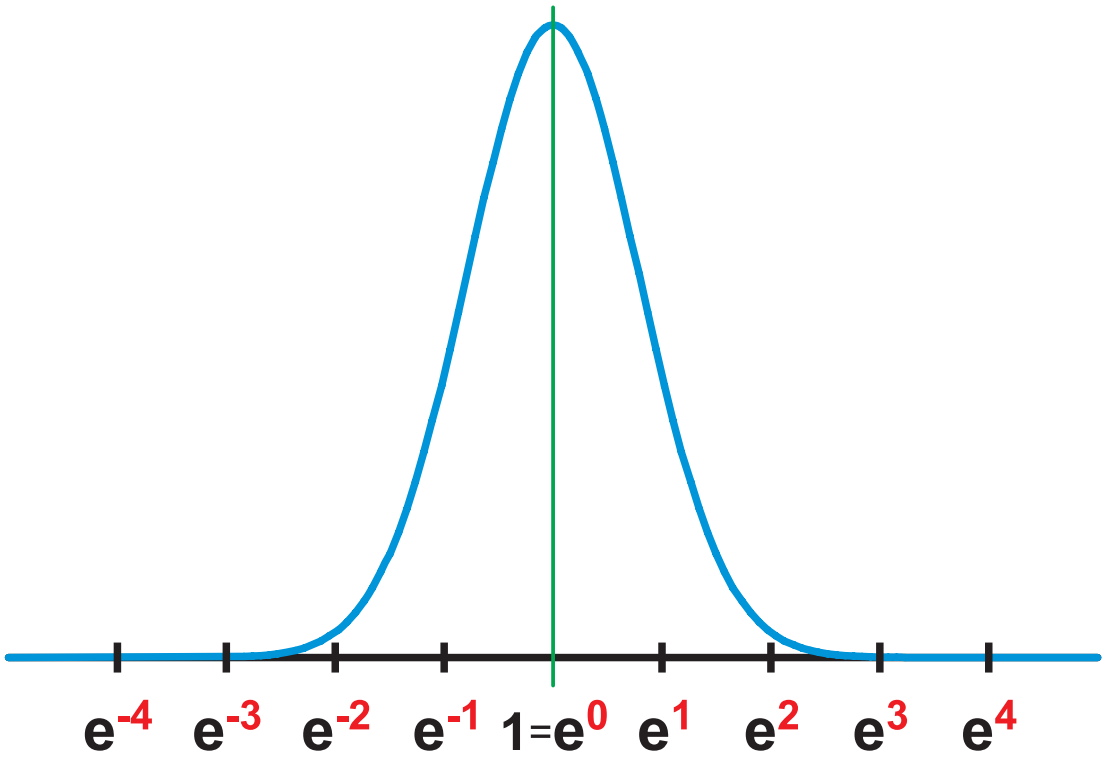
Reproduction of Endogenous Parameters

- Recombination of strategy parameters $p.w$: intermediate crossover
- So we are concerned about the scale
- Normal distribution produces values of approximately same scale around its center



Reproduction of Endogenous Parameters

- Recombination of strategy parameters $p.w$: intermediate crossover
- So we are concerned about the scale
- Log-Normal distribution produces values of difference scale



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Data: i: a counter variable
Output: $\vec{\sigma} \in \mathbb{R}^n$: the new mutation strength vector

begin
- $\nu \longleftarrow e^{\tau_0\{\text{Gaussian random number}\}}$
- $\vec{\sigma} \longleftarrow \vec{0}$
- **for** $i \longleftarrow 0$ **up to** $n-1$ **do**
  - $\vec{\sigma}_i \longleftarrow \nu * e^{\tau\{\text{Gaussian random number}\}} * \vec{\sigma}'_i$
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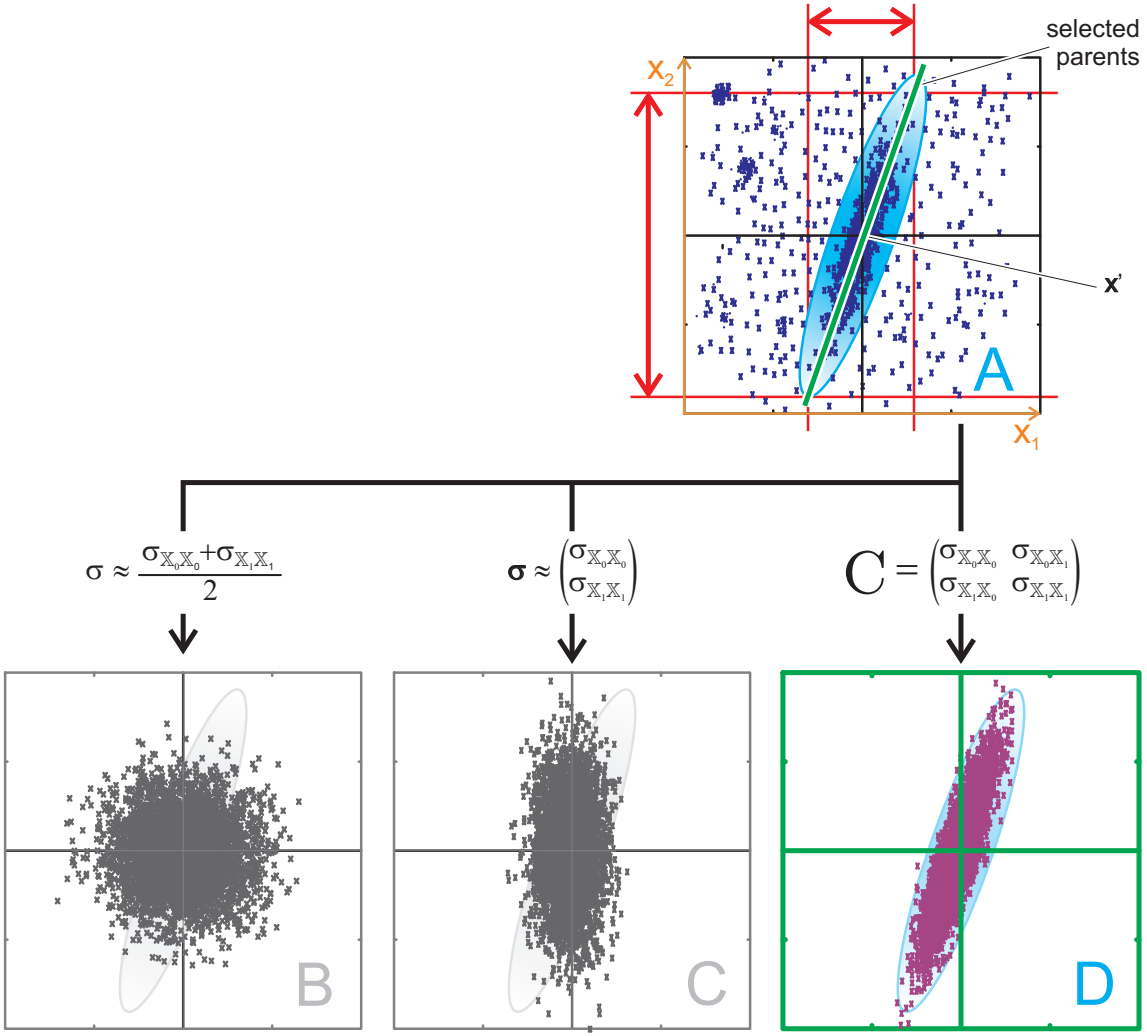

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- Both are exogenous parameters maintained centrally and updated by the algorithm
  - The center μ of the distribution is set to the weighted average of the selected parent points
  - Covariance matrix is *updated* in each iteration with information from the selected parets
- New population is sampled from normal distribution, parent individuals are discarted (no traditional mutation/crossover)

CMA-ES: Invariances

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- We want this! (Remember: Roulette-Wheel Selection versus Truncation Selection)

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- When doing numerical optimization, this is the way to go!

Section Outline

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谢谢

Thank you

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Caspar David Friedrich, “Der Wanderer über dem Nebelmeer”, 1818
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