10: Evolution Strategies 1

- ES overview
- ES mutation and recombination
- Self-adaptation
- Textbook Chapter 6.2, 4.4.2

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ES quick overview

Ingo Rechendberg

Hans-Paul Schewefel

- Developed: in Germany in the 1960's
- Typically applied to:
  - numerical optimization
- Attributed features:
  - fast
  - good optimizer for real-valued optimization problems
  - relatively good theoretical support
- Special:
  - self-adaption of strategy parameters

Evolution Strategies as a Scalable Alternative to Reinforcement Learning

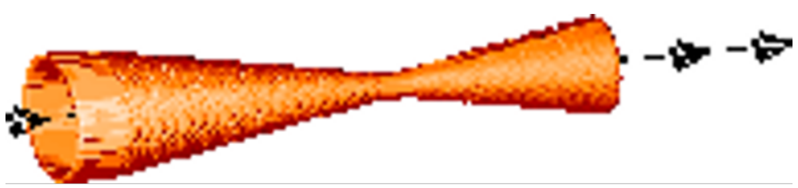
We've discovered that *evolution strategies (ES)*, an optimization technique that's been known for decades, rivals the performance of standard *reinforcement learning (RL)* techniques on modern RL benchmarks (e.g. Atari/MuJoCo), while overcoming many of RL's inconveniences.

March 24, 2017
12 minute read

https://openai.com/blog/evolution-strategies/

ES technical sketch

- Example task: to optimize the shape of a jet nozzle



Initial shape

Evolved shape

Representation	Real-valued vectors
Recombination	Discrete or intermediary
Mutation	Gaussian perturbation
Parent selection	Uniform random
Survivor selection	Deterministic elitist replacement by (μ, λ) or $(\mu + \lambda)$
Speciality	Self-adaptation of mutation step sizes

Introductory example

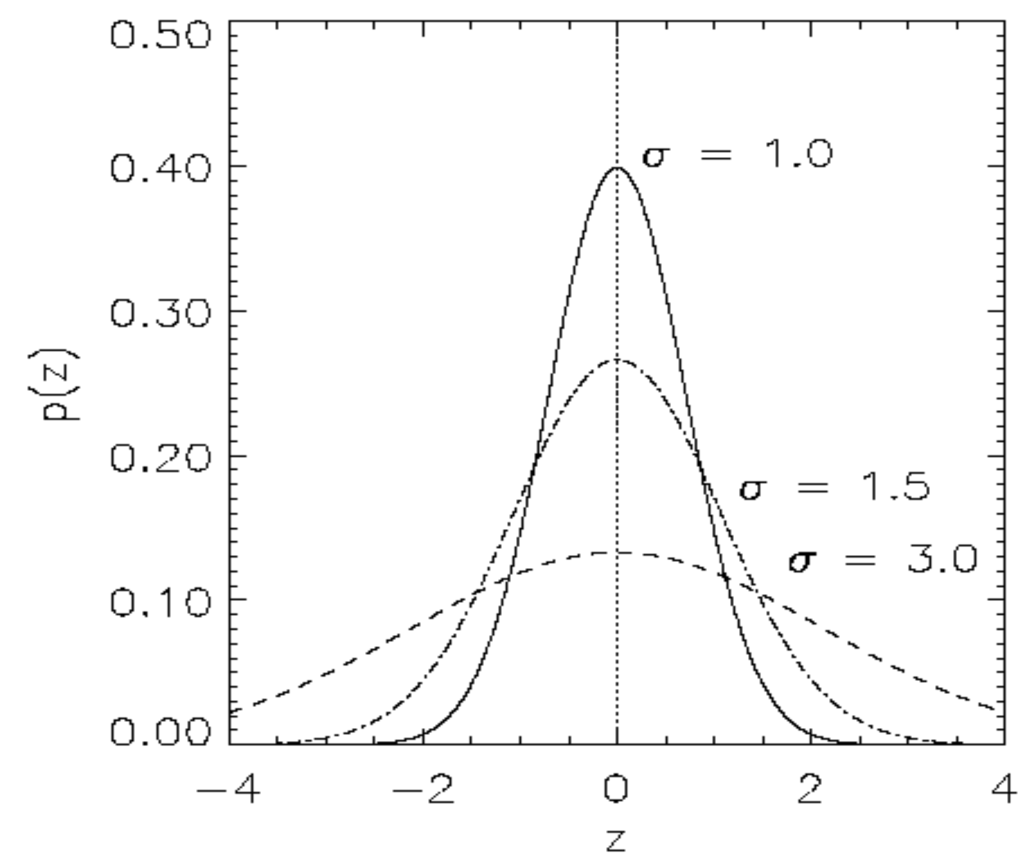
- Task: minimize $f : R^n \to R$
- Algorithm: the earliest "two-membered ES" or (1+1) ES
    - vectors from R^n directly as chromosomes
    - population size 1
    - only mutation creating one child
    - greedy selection (remove deleterious mutants)

Introductory example: pseudocode

- Set $t = 0$
- Create initial point $x^t = <x_1^t, \ldots, x_n^t>$
- Assume minimization
- REPEAT until (termination condition satisfied) DO
  - Draw z_i from a normal distribution for all $i = 1,2,\ldots,n$
  - $y_i^t = x_i^t + z_i$
  - IF $f(y^t) <= f(x^t)$ THEN $x^{t+1} = y^t$
  - ELSE $x^{t+1} = x^t$
  - Set $t = t+1$

Introductory example: mutation mechanism

- *z* values drawn from normal distribution $N(\xi, \sigma)$
  - mean ξ is set to 0
  - variance σ is called **mutation step size**
- σ is varied *on the fly* by the "1/5 success rule" (Rechenberg 1973)
- This rule resets σ after *k* iterations by
  - $\sigma = \sigma$ if $p_s = 1/5$
  - $\sigma = \sigma / c$ if $p_s > 1/5$
  - $\sigma = \sigma \times c$ if $p_s < 1/5$
  - where p_s is the % of successful mutations,
  - $0.8 \leq c \leq 1$



Self adaptation

- Include the mutation step-size in the chromosome to undergo variation and selection
- Assume that under different circumstances different step sizes will behave differently: different *stages* or *spaces*
    - to adjust the mutation strategy as the search is proceeding
    - to learn and use a mutation strategy suited for the local topology

Mutation

- Net mutation effect: $< x, \sigma >$ **->** $< x', \sigma' >$
- Order is important:
  - first σ **->** σ' (see later how)
  - then x **->** $x' = x + N(0, \sigma')$
- Rational: new $< x', \sigma' >$ is evaluated on two aspects
  - primary: x' is good if $f(x')$ is good
  - secondary: σ' is good if the x' it created is good
- Reversing mutation order this would not work

Uncorrelated mutation with one step size

- The same distribution is used to mutate each x_i with one σ

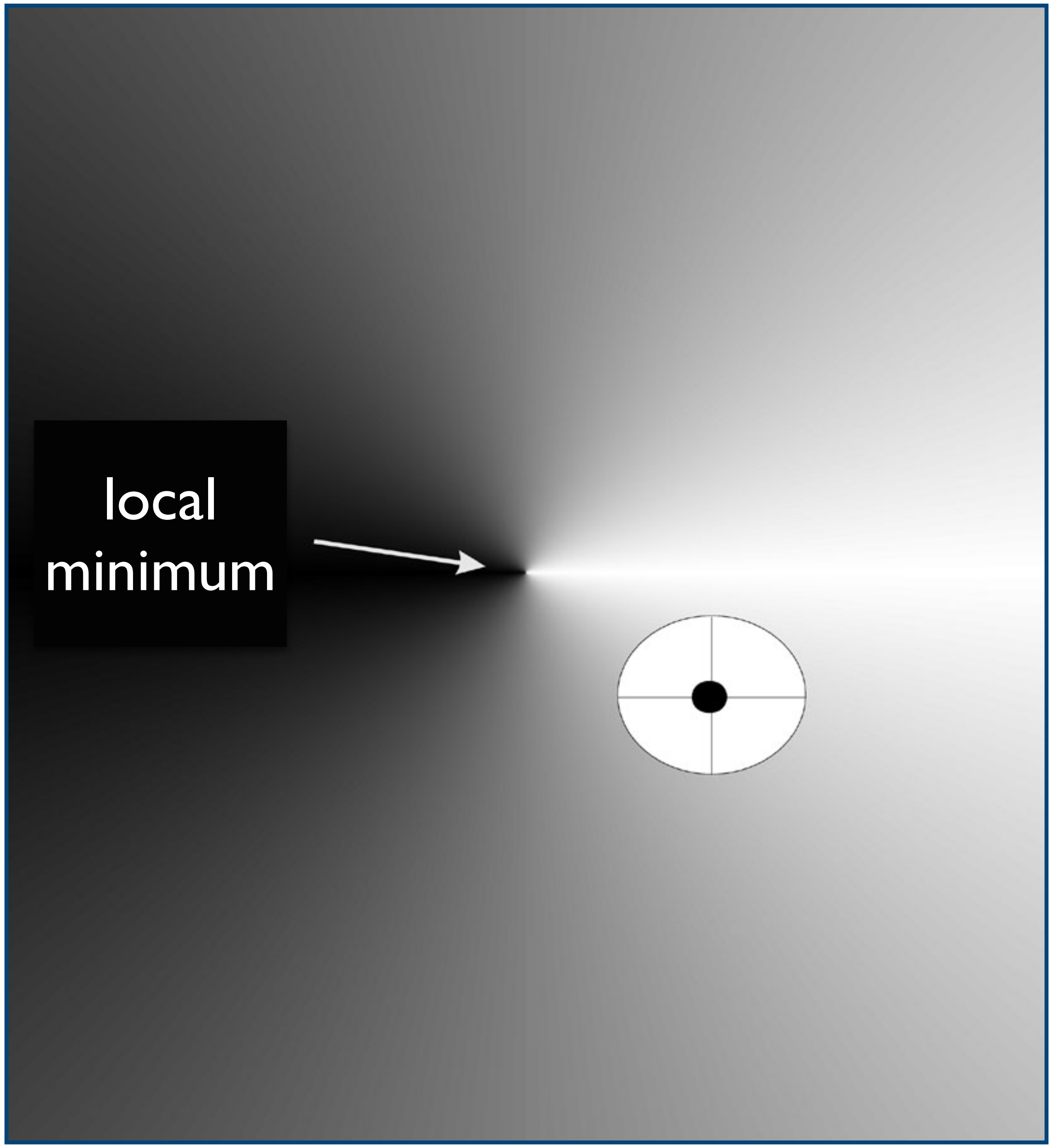
$$\sigma' = \sigma \cdot e^{\tau \cdot N(0,1)},$$
$$x_i' = x_i + \sigma' \cdot N_i(0,1).$$

- A boundary rule is used since SD very close to zero are unwanted

$$\sigma' < \varepsilon_0 \Rightarrow \sigma' = \varepsilon_0.$$

- Separate draws from the normal distribution for each variable *i*
- Learning rate $\tau \propto 1/\sqrt{n}.$

Mutants with equal likelihood and size



circle: mutants having the same chance to be created

Pros and cons with one step size

- Advantage
  - simple mechanism
  - usually fast and precise adaptation
- Disadvantage
  - poor performance on complicated contours
  - poor adaptation on widely differing objective values

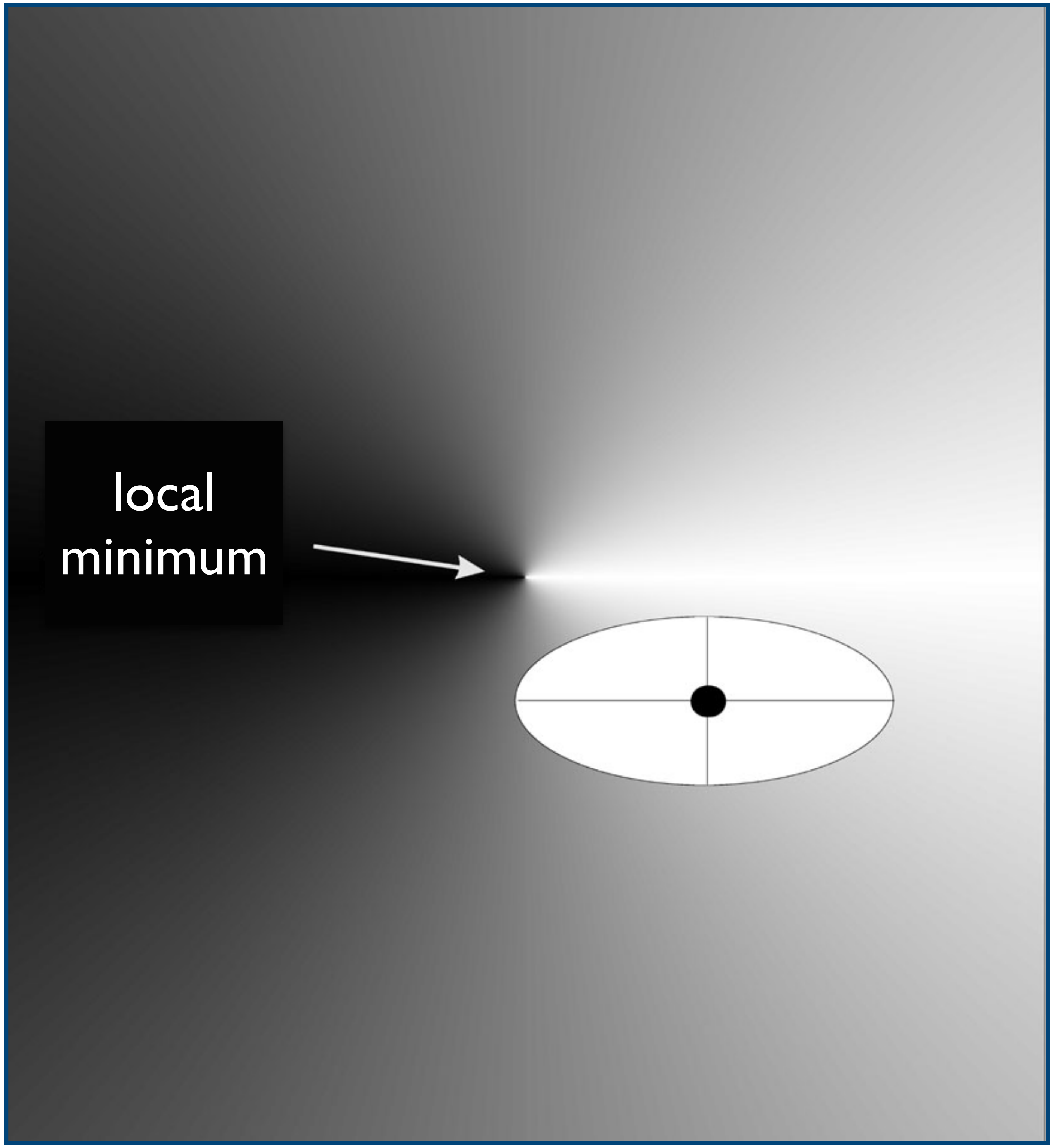
Uncorrelated mutation with *n* step size

- Use different step sizes for different dimensions
- Chromosome $\langle x_1, \ldots, x_n, \sigma_1, \ldots, \sigma_n \rangle$
- Mutation mechanism

$$\sigma_i' = \sigma_i \cdot e^{\tau' \cdot N(0,1) + \tau \cdot N_i(0,1)}, \quad \text{or} \quad \sigma_i' = \sigma_i \cdot e^{\tau \cdot N_i(0,1)},$$
$$x_i' = x_i + \sigma_i' \cdot N_i(0,1),$$

where $\tau' \propto 1/\sqrt{2n}$, and $\tau \propto 1/\sqrt{2\sqrt{n}}.$

Mutants with varying likelihood



Pros and cons with *n* step size

- Advantage
  - individual scaling
  - better global convergence
- Disadvantage
  - slower
  - cannot rotate to the coordinate system

Correlated mutations

- Allow the eclipses to have any orientation by rotating them with a rotation (covariant matrix) *C*
- Chromosome $\langle x_1, \ldots, x_n, \sigma_1, \ldots, \sigma_n, \alpha_1, \ldots, \alpha_{n\cdot(n-1)/2} \rangle$
- Mutation mechanism

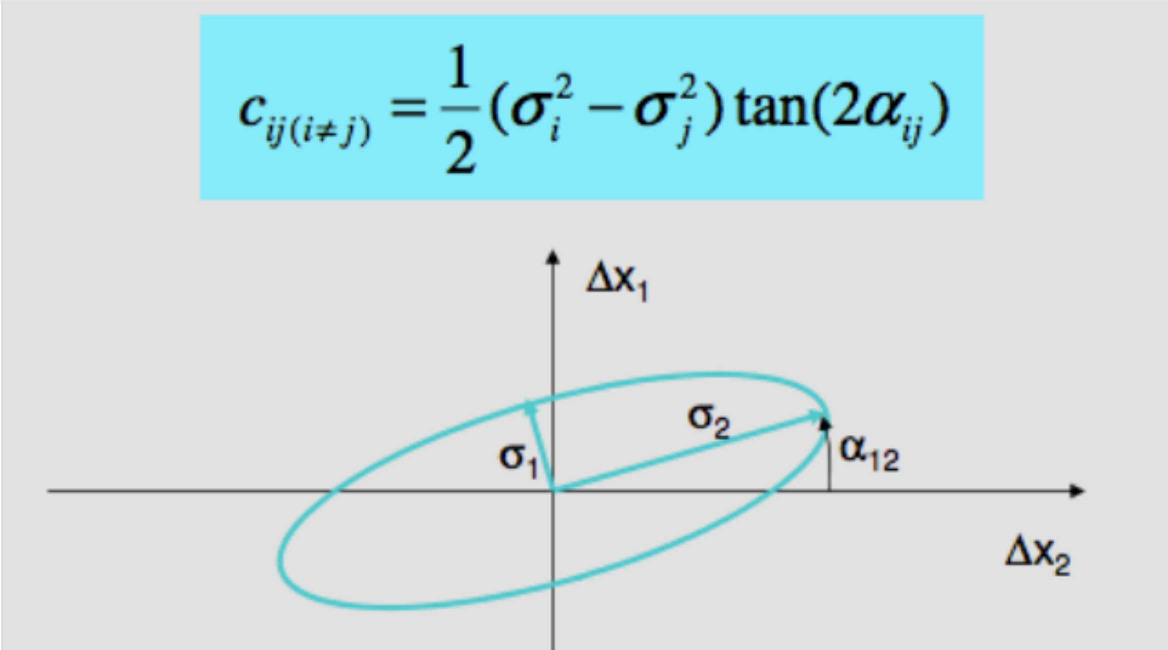
$$\sigma_i' = \sigma_i \cdot e^{\tau' \cdot N(0,1) + \tau \cdot N_i(0,1)}$$
$$\alpha_j' = \alpha_j + \beta \cdot N_j(0,1),$$
$$\overline{x}' = \overline{x} + \overline{N}(\overline{0}, C'),$$

where $n_\alpha = \frac{n\cdot(n-1)}{2}$, $j \in 1, \ldots, n_\alpha$, and $\tau \propto 1/\sqrt{2\sqrt{n}}$, $\tau' \propto 1/\sqrt{2n}$, and $\beta \approx 5^o$.

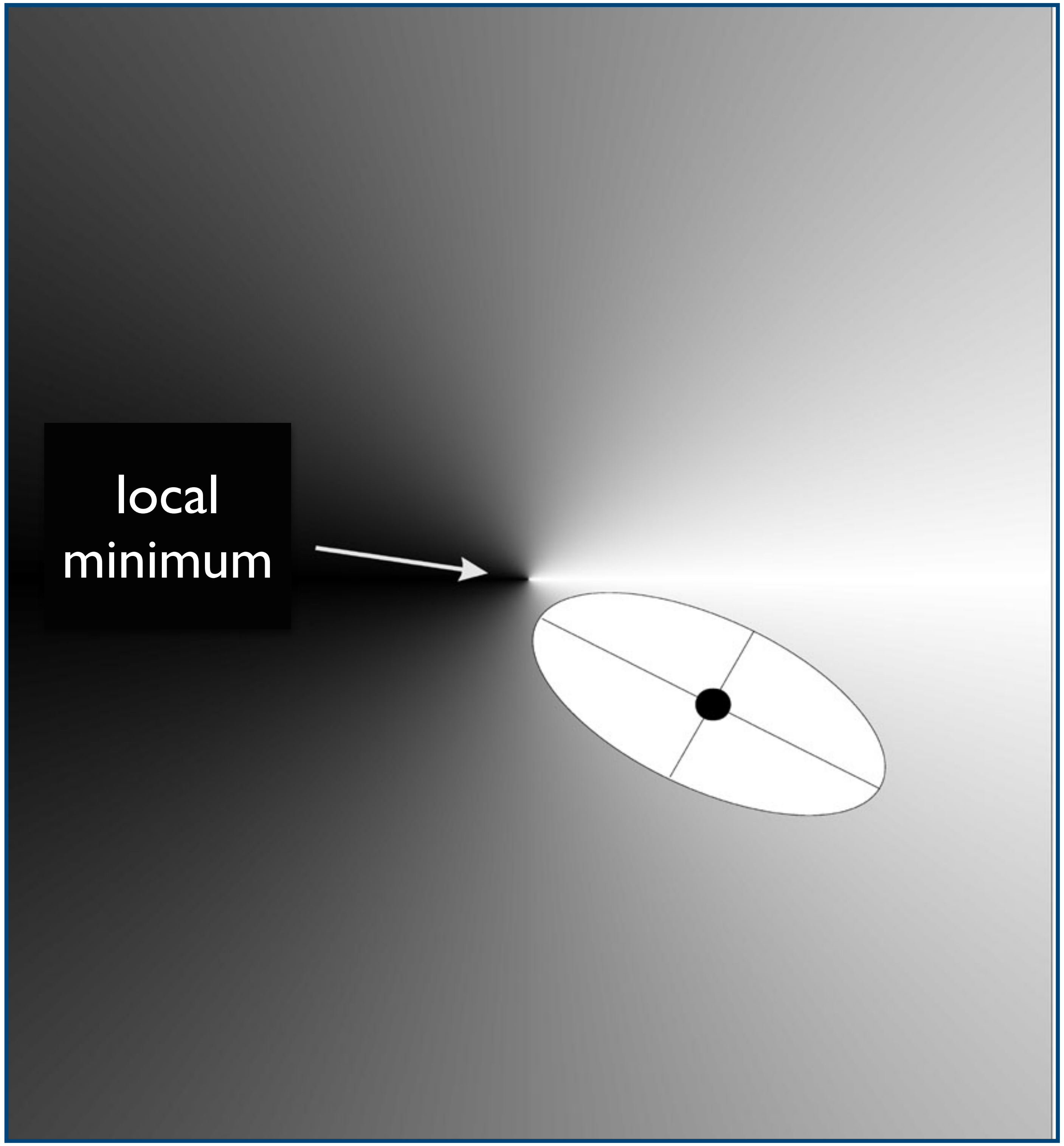
Correlated mutations

- The covariance matrix C is defined as

$$c_{ii} = \sigma_i^2,$$
$$c_{ij,i\neq j} = \begin{cases} 0 & \text{no correlations,} \\ \frac{1}{2}(\sigma_i^2 - \sigma_j^2)\tan(2\alpha_{ij}) & \text{correlations.} \end{cases}$$



Mutants with varying likelihood and direction



Pros and cons with correlated mutations

- Advantage
    - individual scaling
    - rotation
    - better global convergence
- Disadvantage
    - much slower
    - mutation effort scales quadratically
    - because of speed, self-adaptation slow

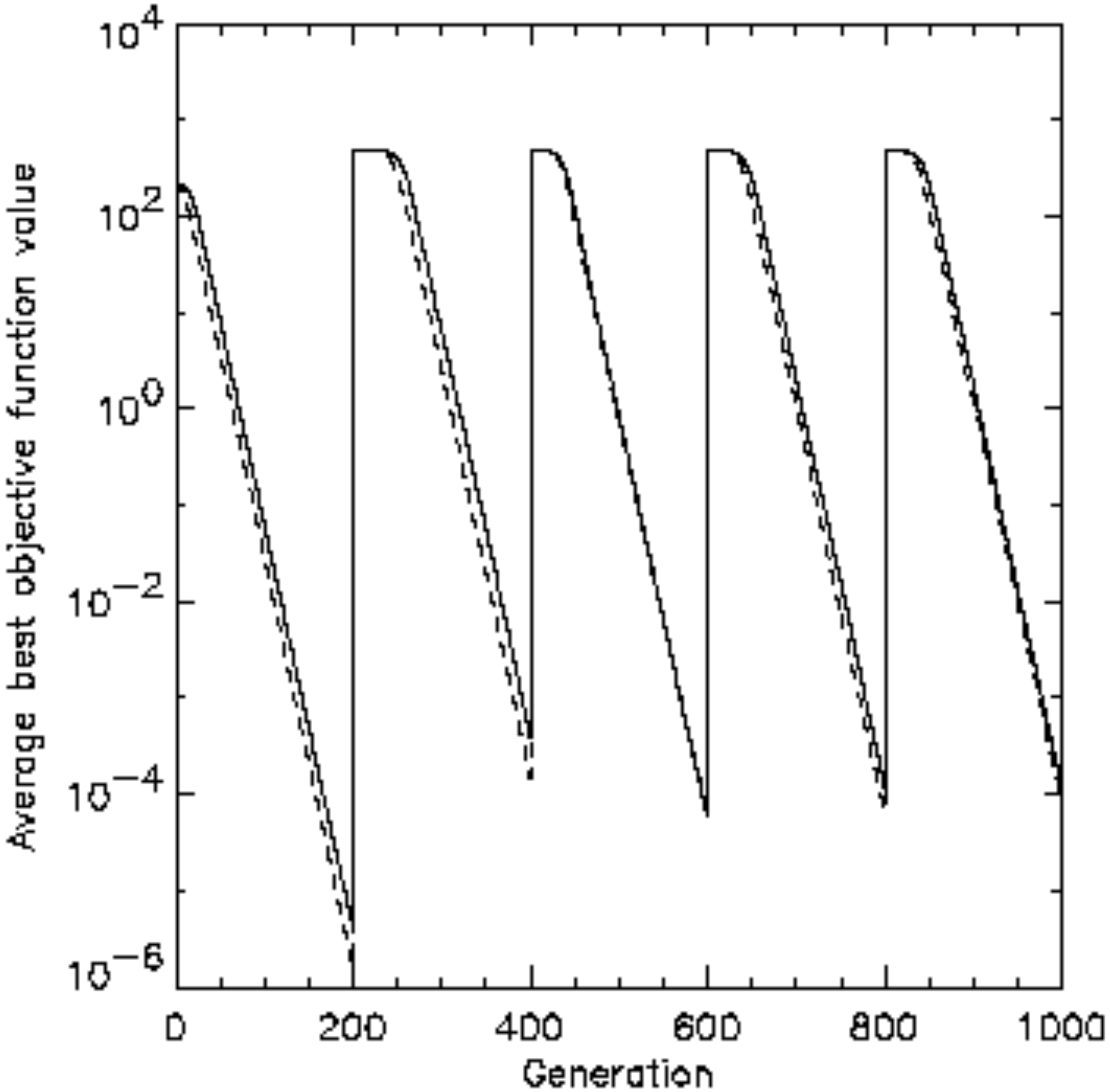
Structures of individuals for different mutations

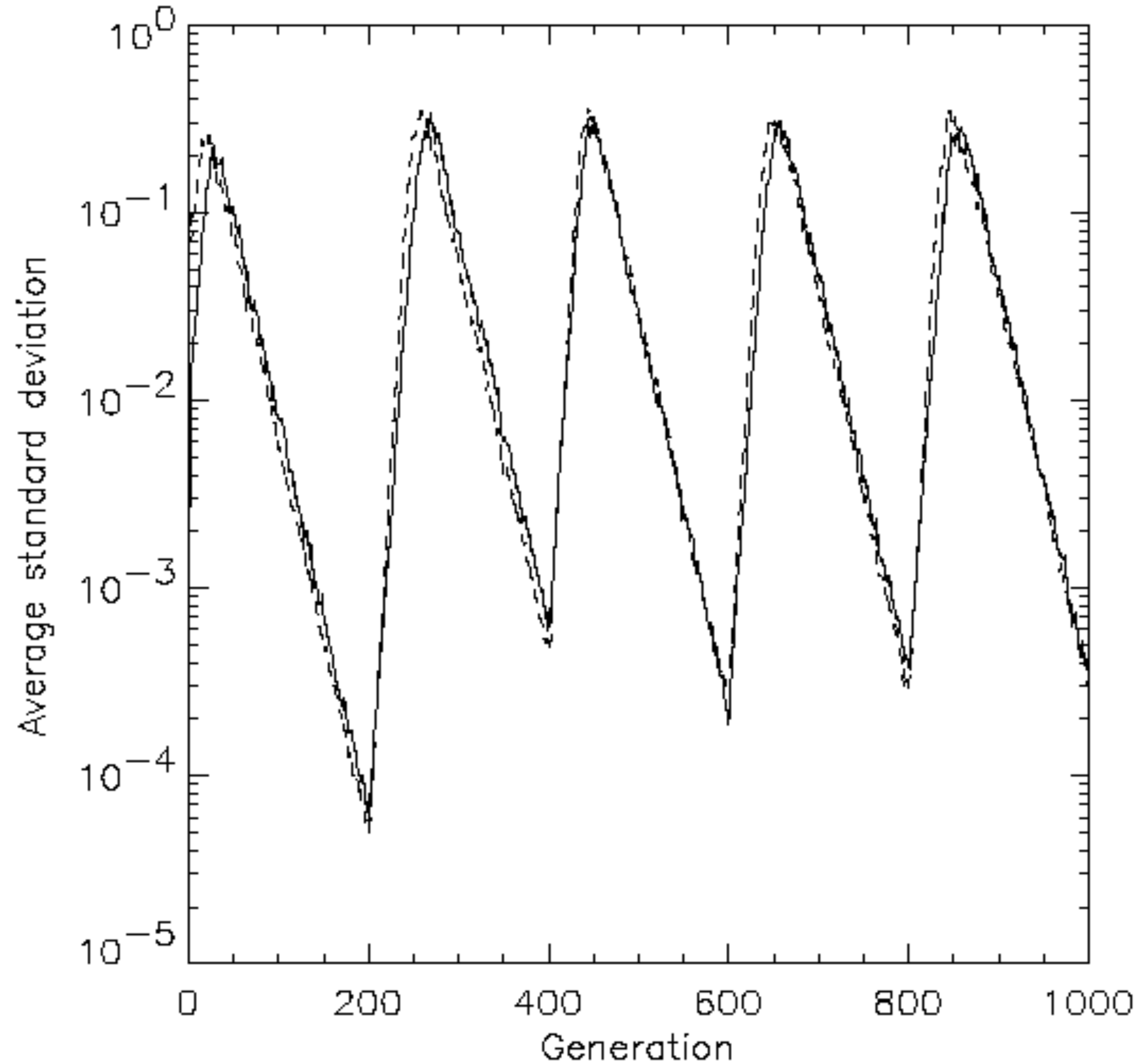
n_σ	n_α	Structure of individuals	Remark
1	0	$\langle x_1, \dots, x_n, \sigma \rangle$	Standard mutation
n	0	$\langle x_1, \dots, x_n, \sigma_1, \dots, \sigma_n \rangle$	Standard mutations
n	$n \cdot (n-1)/2$	$\langle x_1, \dots, x_n, \sigma_1, \dots, \sigma_n, \alpha_1, \dots, \alpha_{n \cdot (n-1)/2} \rangle$	Correlated mutations

Self-adaptation

- Theoretically and empirically, σ must decrease over time, exploration -> exploitation
- Given a dynamically changing fitness landscape (optimum location shifted every 200 generations)
- Self-adaptive ES is able to
    - follow the optimum and
    - adjust the mutation step size after every shift!

Self-adaptation





Changes in the fitness values (left) and the mutation step sizes (right)