Evolution strategies

Chapter 4

ES quick overview

- Developed: Germany in the 1970's
- Early names: I. Rechenberg, H.-P. Schwefel
- Typically applied to:
  - numerical optimisation
- Attributed features:
  - fast
  - good optimizer for real-valued optimisation
  - relatively much theory
- Special:
  - self-adaptation of (mutation) parameters standard

ES technical summary tableau

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

Introductory example

- Task: minimimise f : R^n □ R
- Algorithm: “two-membered ES” using
  - Vectors from R^n directly as chromosomes
  - Population size 1
  - Only mutation creating one child
  - Greedy selection

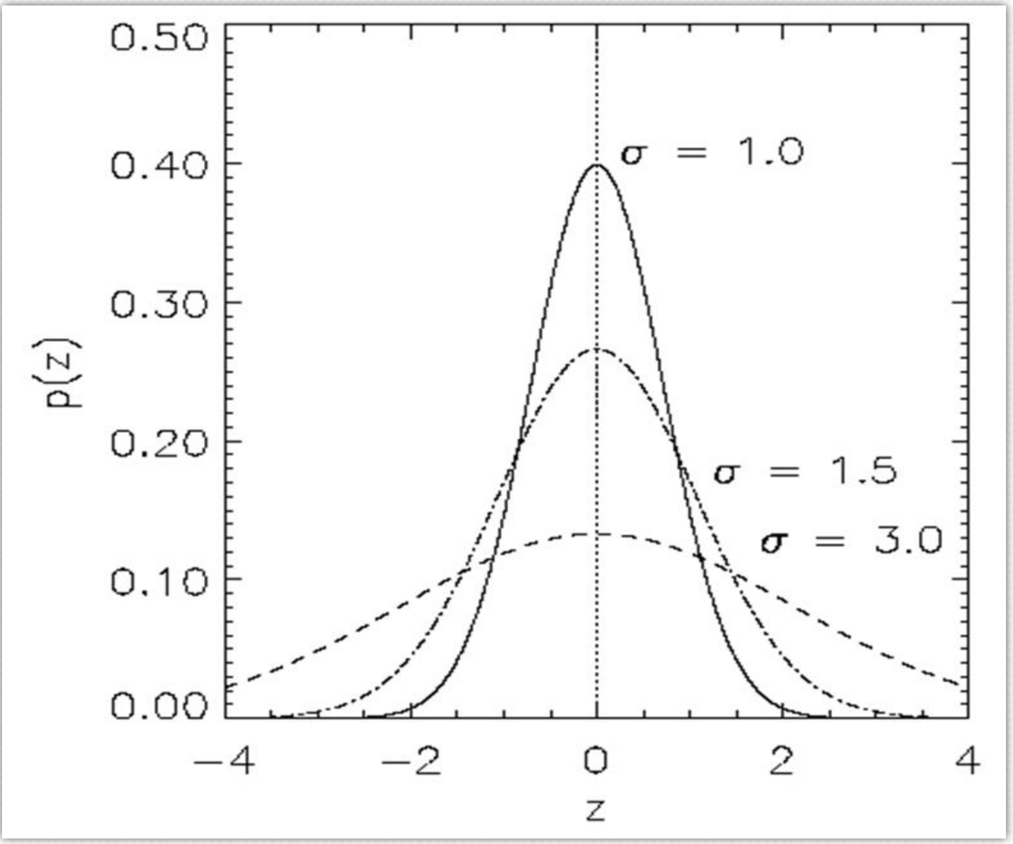
Introductory example: pseudocde

- Set t = 0
- Create initial point $x^t = \langle x_1^t,\dots,x_n^t \rangle$
- REPEAT UNTIL (*TERMIN.COND* satisfied) DO
  - Draw z_i from a normal distr. for all i = 1,…,n
  - $y_i^t = x_i^t + z_i$
  - IF $f(x^t) < f(y^t)$ THEN $x^{t+1} = x^t$
    - ELSE $x^{t+1} = y^t$
    - FI
    - Set t = t+1
- OD

Introductory example: mutation mechanism

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

Illustration of normal distribution



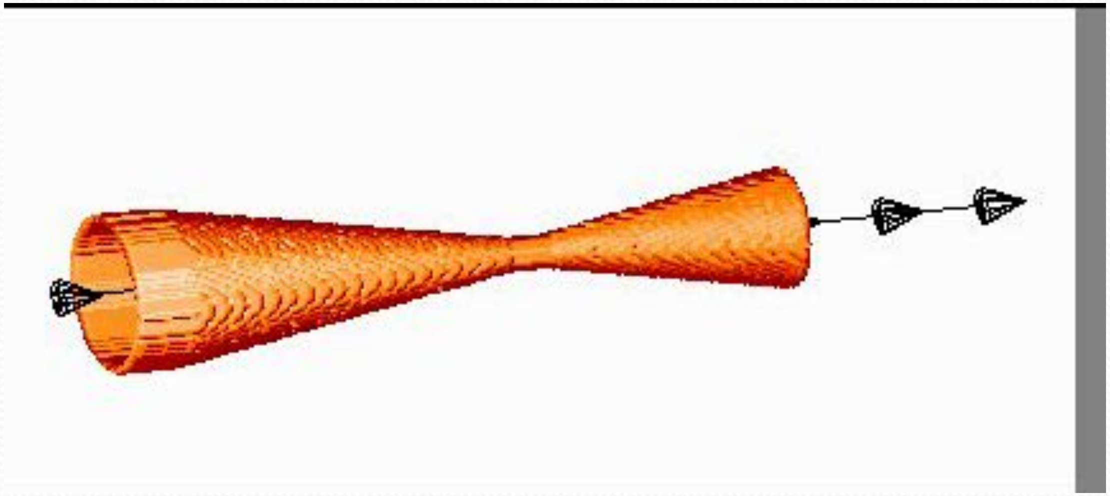
Another historical example: the jet nozzle experiment

Task: to optimize the shape of a jet nozzle
Approach: random mutations to shape + selection

Initial shape

Final shape

The famous jet nozzle experiment (movie)



Representation

- Chromosomes consist of three parts:
  - Object variables: $x_1,\ldots,x_n$
  - Strategy parameters:
    - Mutation step sizes: $\sigma_1,\ldots,\sigma_{n\sigma}$
    - Rotation angles: $\alpha_1,\ldots, \alpha_{n\alpha}$
- Not every component is always present
- Full size: $\langle\, x_1,\ldots,x_n, \sigma_1,\ldots,\sigma_n ,\alpha_1,\ldots, \alpha_k \,\rangle$ where $k = n(n-1)/2$ (no. of i,j pairs)

Mutation

- Main mechanism: changing value by adding random noise drawn from normal distribution
- $x'_i = x_i + N(0,\sigma)$
- Key idea:
  - σ is part of the chromosome $\langle x_1,\ldots,x_n, \sigma \rangle$
  - σ is also mutated into σ' (see later how)
- Thus: mutation step size σ is coevolving with the solution x

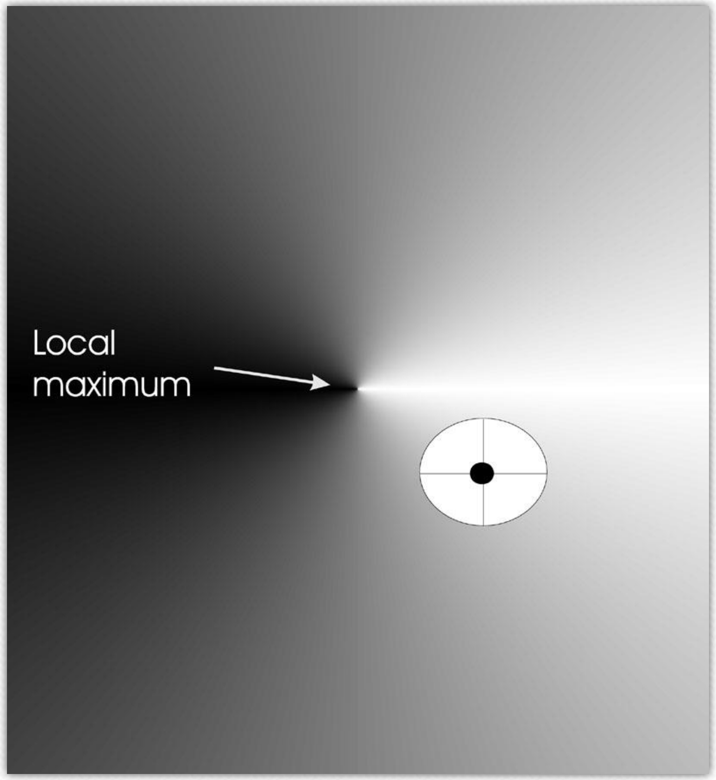
Mutate σ first

- Net mutation effect: 〈 x, σ 〉 □ 〈 x', σ' 〉
- Order is important:
  - first σ □ σ' (see later how)
  - then x □ x' = x + N(0,σ')
- Rationale: new 〈 x' ,σ' 〉 is evaluated twice
  - Primary: x' is good if f(x') is good
  - Secondary: σ' is good if the x' it created is good
  - Step-size only survives through "hitch-hiking"
- Reversing mutation order this would not work

Mutation case 1: Uncorrelated mutation with one σ

- Chromosomes: $\langle x_1,\ldots,x_n, \sigma \rangle$
  - $\sigma' = \sigma \cdot \exp(\tau \cdot N(0,1))$
  - $x'_i = x_i + \sigma' \cdot N(0,1)$
- Typically the "learning rate" $\tau \propto 1/ n^{½}$
- And we have a boundary rule $\sigma' < \varepsilon_0 \Rightarrow \sigma' = \varepsilon_0$

Mutants with equal likelihood

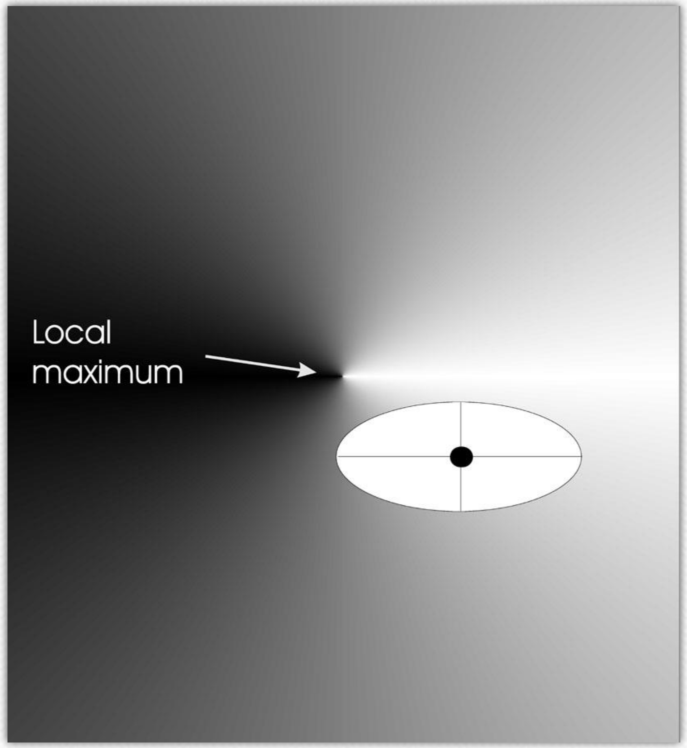


Circle: mutants having the same chance to be created

Mutation case 2: Uncorrelated mutation with n σ's

- Chromosomes: $\langle x_1,\ldots,x_n, \sigma_1,\ldots, \sigma_n \rangle$
  - $\sigma'_i = \sigma_i \cdot \exp(\tau' \cdot N(0,1) + \tau \cdot N_i(0,1))$
  - $x'_i = x_i + \sigma'_i \cdot N_i(0,1)$
- Two learning rate parameters:
  - τ' overall learning rate
  - τ coordinate wise learning rate
- $\tau \propto 1/(2n)^{½}$ and $\tau \propto 1/(2n^{½})^{½}$
- Boundary rule: $\sigma_i' < \varepsilon_0 \Rightarrow \sigma_i' = \varepsilon_0$

Mutants with equal likelihood



Ellipse: mutants having the same chance to be created

Mutation case 3: Correlated mutations

- Chromosomes: $\langle x_1,\ldots,x_n, \sigma_1,\ldots, \sigma_n, \alpha_1,\ldots, \alpha_k \rangle$ where $k = n \cdot (n-1)/2$
- Covariance matrix C is defined as:
  - $c_{ii} = \sigma_i^2$
  - $c_{ij} = 0$ if i and j are not correlated
  - $c_{ij} = \frac{1}{2} \cdot (\sigma_i^2 - \sigma_j^2) \cdot \tan(2 \alpha_{ij})$ if i and j are correlated
- Note the numbering / indices of the α's

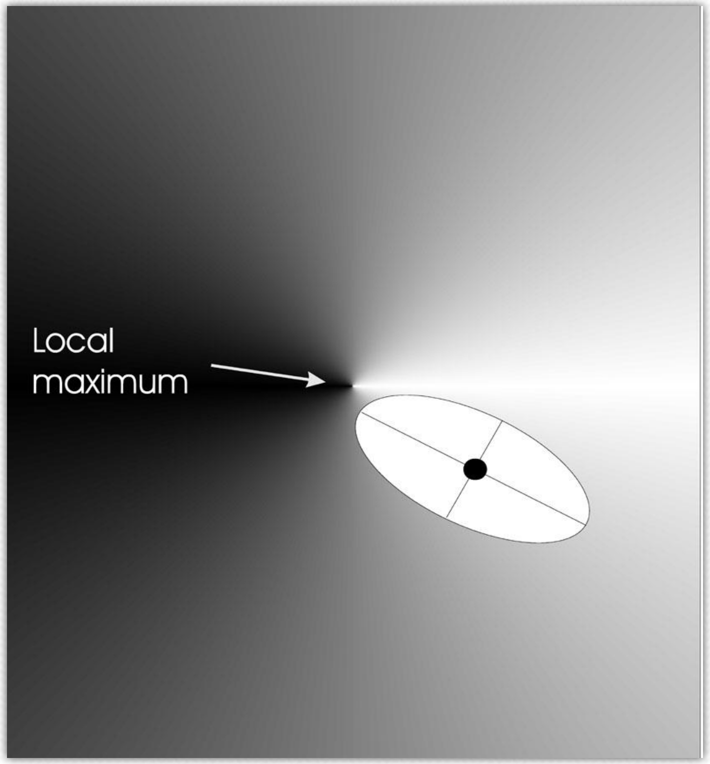
Correlated mutations cont'd

The mutation mechanism is then:

- $\sigma'_i = \sigma_i \cdot \exp(\tau' \cdot N(0,1) + \tau \cdot N_i(0,1))$
- $\alpha'_j = \alpha_j + \beta \cdot N(0,1)$
- $\boldsymbol{x}' = \boldsymbol{x} + \boldsymbol{N}(\boldsymbol{0}, \boldsymbol{C}')$
  - $\boldsymbol{x}$ stands for the vector $\langle x_1, \ldots, x_n \rangle$
  - $\boldsymbol{C}'$ is the covariance matrix $\boldsymbol{C}$ after mutation of the α values
- $\tau \propto 1/(2n)^{½}$ and $\tau \propto 1/(2n^{½})^{½}$ and $\beta \approx 5°$
- $\sigma_i' < \varepsilon_0 \Rightarrow \sigma_i' = \varepsilon_0$ and
- $|\alpha'_j| > \pi \Rightarrow \alpha'_j = \alpha'_j - 2\pi \, \mathrm{sign}(\alpha'_j)$

- NB Covariance Matrix Adaptation Evolution Strategy (CMA-ES) is probably the best EA for numerical optimisation, cf. CEC-2005 competition

Mutants with equal likelihood



Ellipse: mutants having the same chance to be created

Recombination

- Creates one child
- Acts per variable / position by either
  - Averaging parental values, or
  - Selecting one of the parental values
- From two or more parents by either:
  - Using two selected parents to make a child
  - Selecting two parents for each position anew

Names of recombinations

	Two fixed parents	Two parents selected for each i
$z_i = (x_i + y_i)/2$	Local intermediary	Global intermediary
z_i is x_i or y_i chosen randomly	Local discrete	Global discrete

Parent selection

- Parents are selected by uniform random distribution whenever an operator needs one/some
- Thus: ES parent selection is unbiased - every individual has the same probability to be selected
- Note that in ES “parent” means a population member (in GA’s: a population member selected to undergo variation)

Survivor selection

- Applied after creating λ children from the μ parents by mutation and recombination
- Deterministically chops off the “bad stuff”
- Two major variants, distinguished by the basis of selection:
  - (μ,λ)-selection based on the set of children only
  - (μ+λ)-selection based on the set of parents and children:

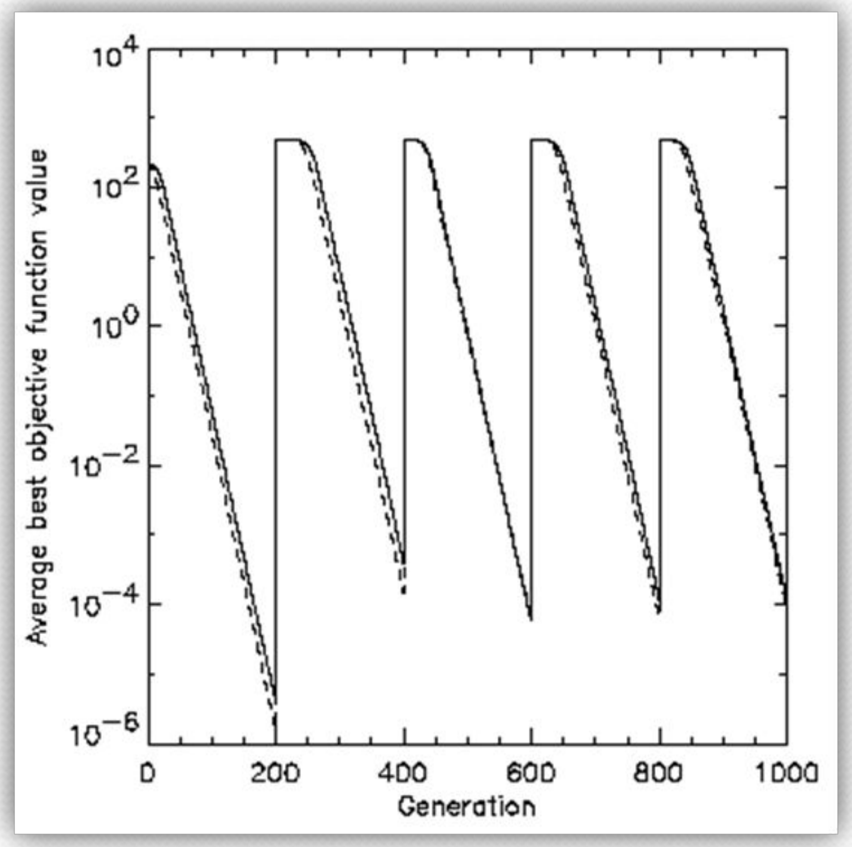
Survivor selection cont'd

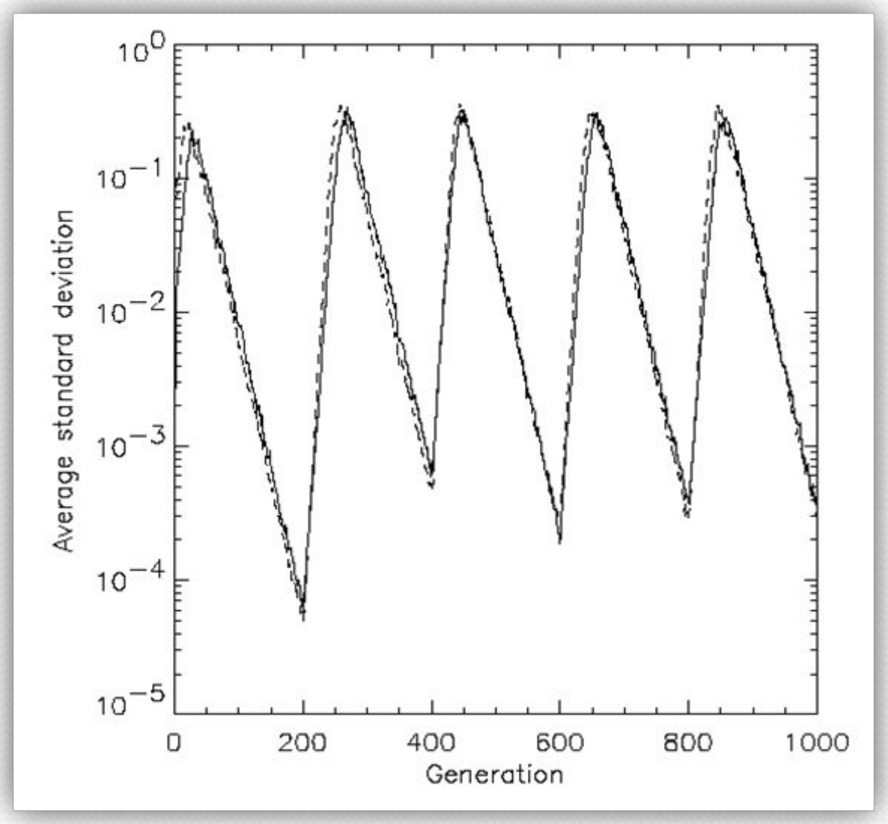
- ($\mu+\lambda$)-selection is an elitist strategy
- (μ,λ)-selection can "forget"
- Often (μ,λ)-selection is preferred for:
  - Better in leaving local optima
  - Better in following moving optima
  - Using the + strategy bad σ values can survive in $\langle x,\sigma \rangle$ too long if their host x is very fit
- Selective pressure in ES is high compared with GAs,
- $\lambda \approx 7 \cdot \mu$ is a traditionally good setting (decreasing over the last couple of years, $\lambda \approx 3 \cdot \mu$ seems more popular lately)

Self-adaptation illustrated

- 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 illustrated cont'd





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

Prerequisites for self-adaptation

- $\mu > 1$ to carry different strategies
- $\lambda > \mu$ to generate offspring surplus
- Not "too" strong selection, e.g., $\lambda \approx 7 \cdot \mu$
- (μ,λ)-selection to get rid of misadapted σ's
- Mixing strategy parameters by (intermediary) recombination on them

Example application: the cherry brandy experiment

- Task: to create a colour mix yielding a target colour (that of a well known cherry brandy)
- Ingredients: water + red, yellow, blue dye
- Representation: $\langle$ w, r, y ,b $\rangle$ no self-adaptation!
- Values scaled to give a predefined total volume (30 ml)
- Mutation: lo / med / hi σ values used with equal chance
- Selection: (1,8) strategy

Example application: cherry brandy experiment cont'd

- Fitness: students effectively making the mix and comparing it with target colour
- Termination criterion: student satisfied with mixed colour
- Solution is found mostly within 20 generations
- Accuracy is very good

Example application: the Ackley function (Bäck et al '93)

- The Ackley function (here used with n =30):

$$f(x) = -20 \cdot \exp\left(-0.2\sqrt{\frac{1}{n} \cdot \sum_{i=1}^{n} x_i^2} \right) - \exp\left(\frac{1}{n} \sum_{i=1}^{n} \cos(2\pi x_i) \right) + 20 + e$$

- Evolution strategy:
  - Representation:
    - $-30 < x_i < 30$ (coincidence of 30's!)
    - 30 step sizes
  - (30,200) selection
  - Termination : after 200000 fitness evaluations
  - Results: average best solution is $7.48 \cdot 10^{-8}$ (very good)