

CSE/ECE 848

Introduction to

Evolutionary Computation

Module 3 - Lecture 10 - Part 3

Evolutionary Strategies -

Strategy Parameter Handling

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Strategy Parameters

- The strategy parameters were included on the vector so they, too, could adapt using the same methods for the values. Each value would have associated strategy parameters
- ES was the first to incorporate strategy into the overall approach to solving a problem

Strategy Parameters II

Define an individual as a combination of three vectors:

$$\vec{a} = (\vec{x}, \vec{\sigma}, \vec{\alpha})$$

\vec{x} : vector of object variables

$\vec{\sigma}$: vector of step sizes

$\vec{\alpha}$: vector of inclination angles

Strategy Settings, one σ

One σ : one stepsize for the whole population

- $a = ((x_1 \dots x_n), \sigma) \rightarrow a' = ((x'_1 \dots x'_n), \sigma')$ with
- $\sigma' = \sigma * \exp(\tau_0 * N(0,1))$ and
- $x'_i = x_i + \sigma' * N(0,1)$
- τ_0 is the learning rate

The Learning Rate τ_0

The parameter τ_0 affects the speed of step-size adaptation:

- τ_0 bigger: faster but more imprecise
- τ_0 smaller: slower but more precise
- How to choose τ_0 ?

According to recommendation of Schwefel:

(n : dimensionality of the solution vector)

$$\tau_0 = \frac{1}{\sqrt{n}}$$

Multiple σ

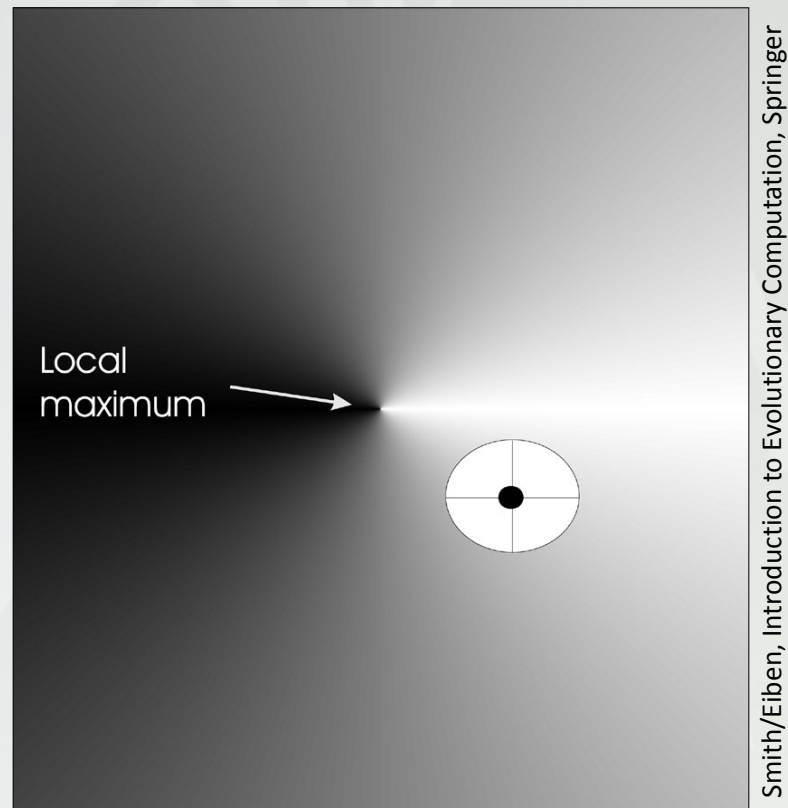
n σ values: standard mutation with individual σ_i for each parameter

- $\sigma'_i = \sigma_i \cdot \exp(\tau' \cdot N(0,1) + \tau \cdot N_i(0,1))$
- τ' is a global learning rate
 - only one realization
- τ is a local learning rate
 - n realizations

Mutation Case 1: Uncorrelated mutation with one σ

- Genomes: $\langle x_1, \dots, x_n, \sigma \rangle$
- $\sigma' = \sigma \cdot \exp(\tau \cdot N(0,1))$
- $x_i' = x_i + \sigma' \cdot N(0,1)$
- Typically the “learning rate” $\tau \propto 1/n^{1/2}$
- With a boundary rule $\sigma' < \varepsilon_0 \Rightarrow \sigma' = \varepsilon_0$

Mutants with Equal Likelihood



Pros and Cons of one σ

Advantages:

- simple mechanism
- usually fast and precise adaptation

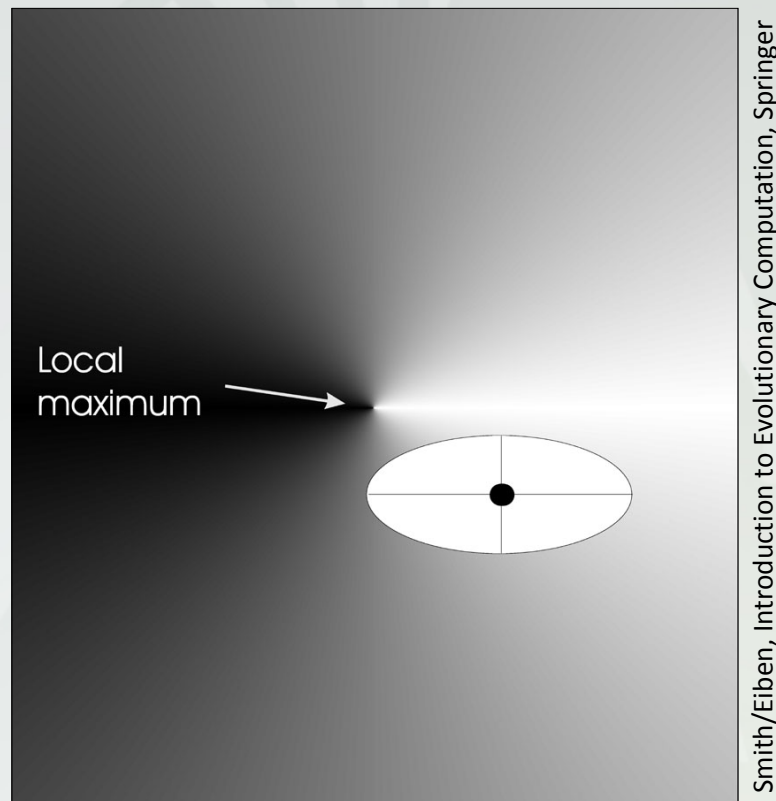
Disadvantages

- bad performances on complicated contours
- bad adaptation on widely differing objective values

Mutation case 2: Uncorrelated mutation with n σ 's

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

Mutants with Equal Likelihood



Pros and Cons of Individual σ

Advantages

- individual scaling
- better global convergence

Disadvantages

- slower
- cannot rotate to the coordinate system

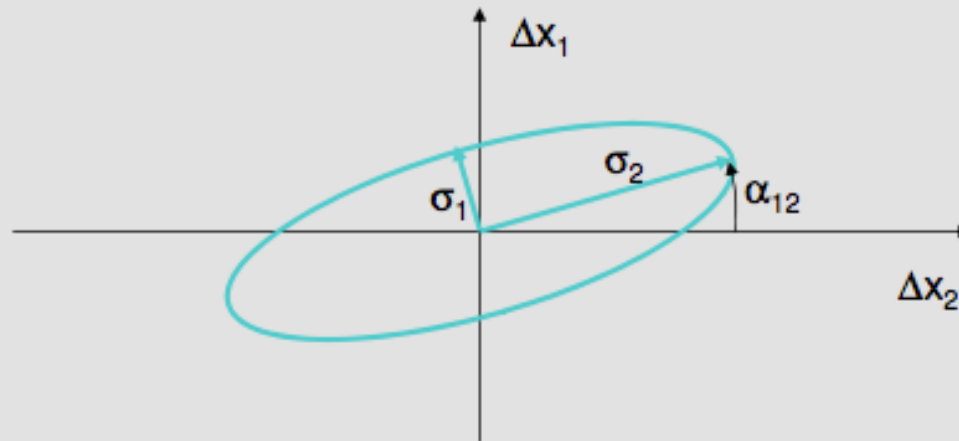
Mutation case 3: Correlated mutations

- Genomes: $\langle x_1, \dots, x_n, \sigma_1, \dots, \sigma_n, \alpha_1, \dots, \alpha_k \rangle$
- where $k = n \cdot (n-1)/2$
- with a covariance matrix C 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

Interpretation of Angles

- Interpretation of rotation angles α_{ij}
- Mapping onto covariances according to

$$c_{ij(i \neq j)} = \frac{1}{2}(\sigma_i^2 - \sigma_j^2) \tan(2\alpha_{ij})$$

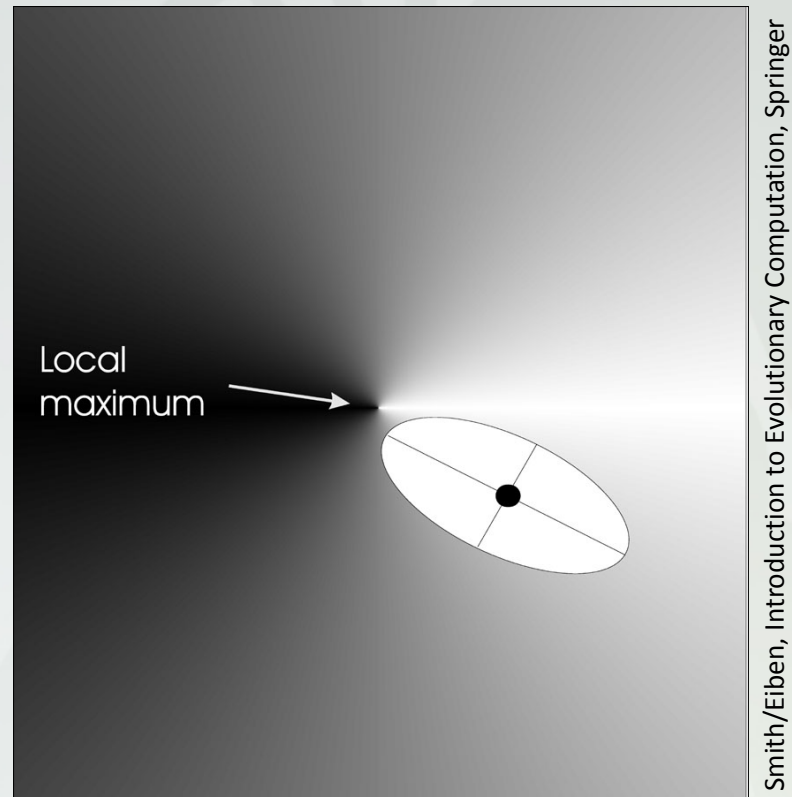


Correlated Mutations II

The mutation mechanism is then:

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

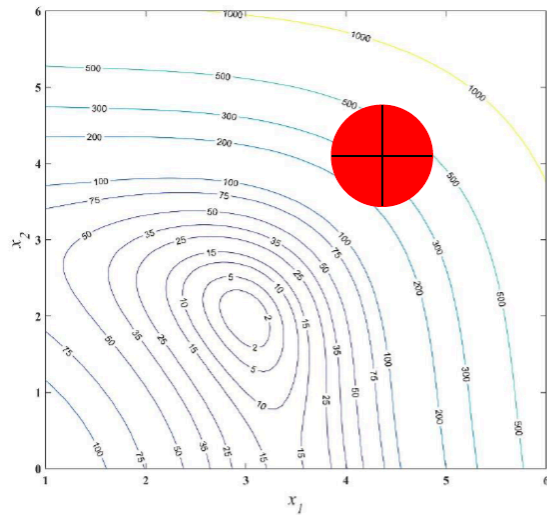
Mutants with Equal Likelihood



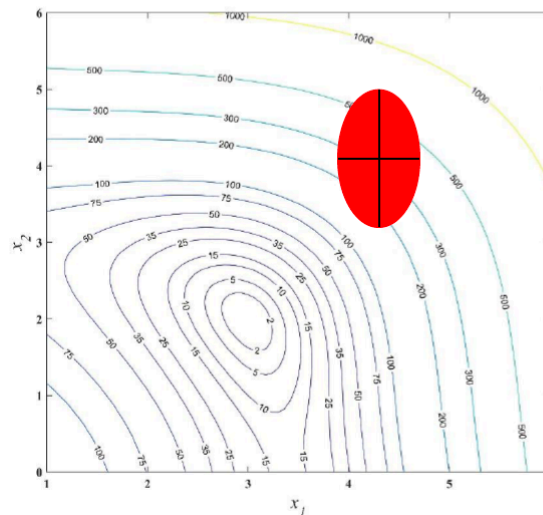
Covariance Matrix Adaptation

- Develops a covariance matrix C between the σ values:
- Modifies the shape of the distribution by modifying the covariance matrix of the individual σ . In particular, allows for rotation to deal with misaligned function.
- Mutation is based on the developed covariance matrix.

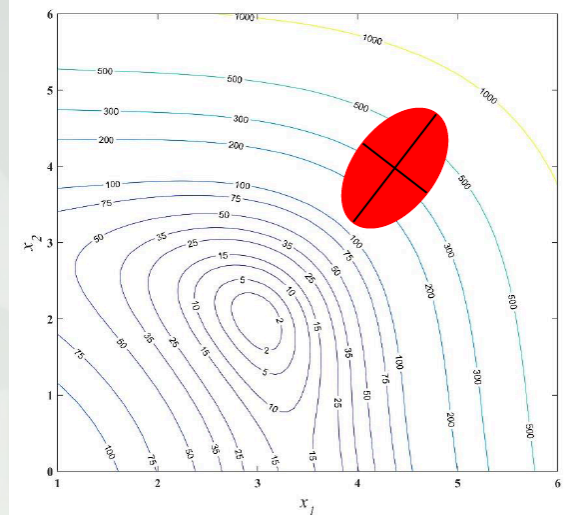
Uncorrelated with one σ



Uncorrelated with one 2σ



Correlated with one 2σ



Pros and Cons of Correlated Mutations

Advantages:

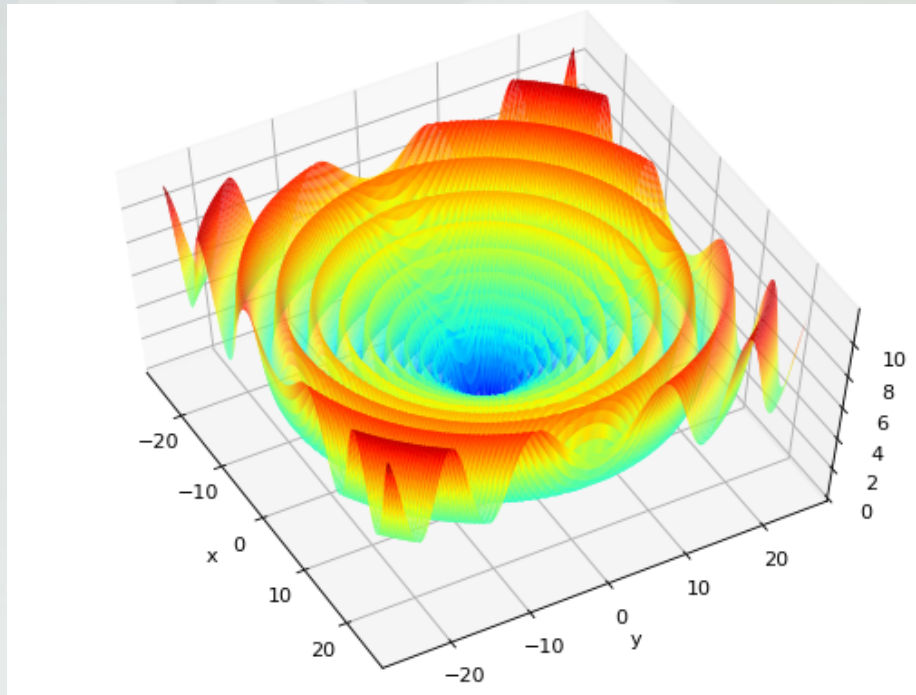
- individual scaling
- rotation
- better convergence

Disadvantages:

- much slower
- mutation effort scales quadratically
- because of speed, self-adaptation slow

Schaffer Test Function

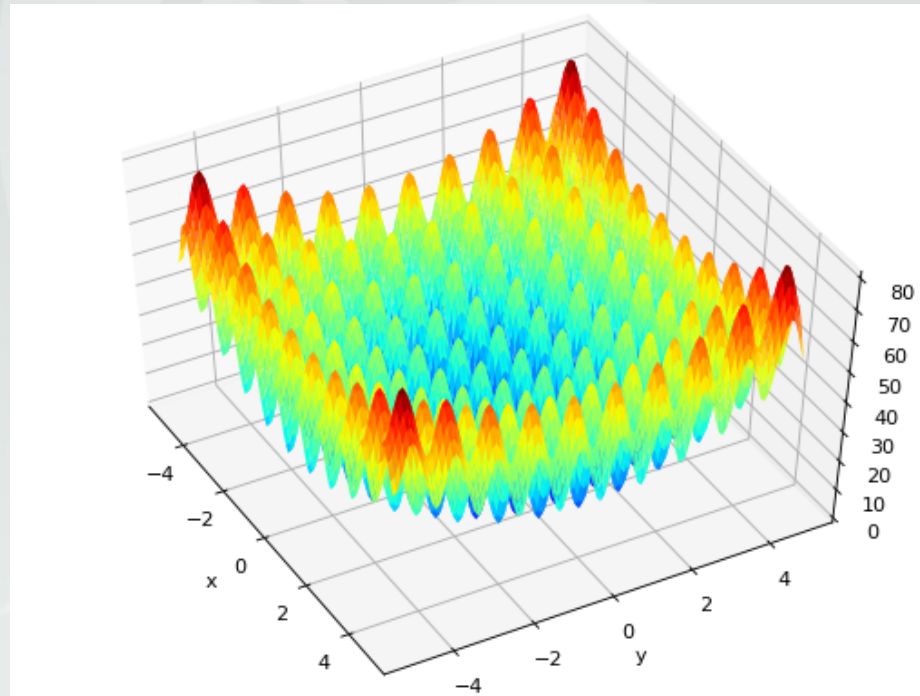
Type	minimization
Range	$x_i \in [-100, 100]$
Global optima	$x_i = 0, \forall i \in \{1 \dots N\}, f(\mathbf{x}) = 0$
Function	$f(\mathbf{x}) = \sum_{i=1}^{N-1} (x_i^2 + x_{i+1}^2)^{0.25} \cdot [\sin^2(50 \cdot (x_i^2 + x_{i+1}^2)^{0.10}) + 1.0]$



From DEAP Documentation

Rastrigin Test Function

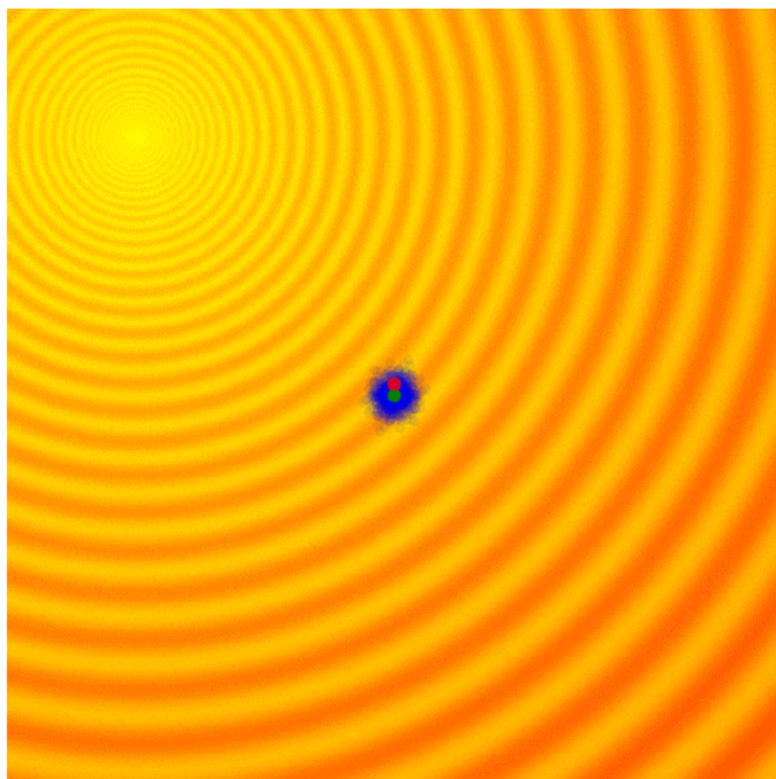
Type	minimization
Range	$x_i \in [-5.12, 5.12]$
Global optima	$x_i = 0, \forall i \in \{1 \dots N\}, f(\mathbf{x}) = 0$
Function	$f(\mathbf{x}) = 10N + \sum_{i=1}^N x_i^2 - 10 \cos(2\pi x_i)$



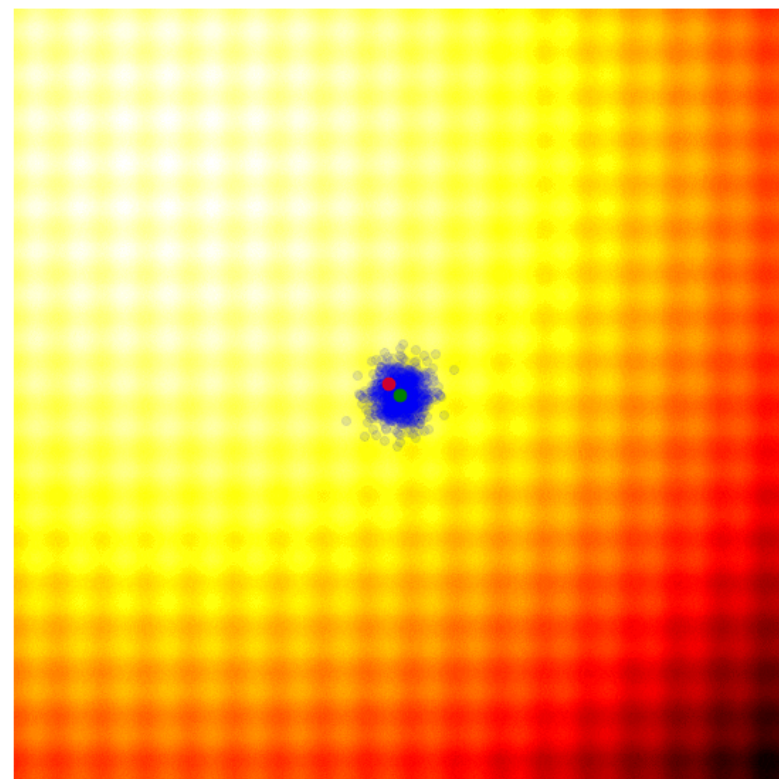
From DEAP Documentation

Simulation of Simple ES (without adaptation), adopted from otoro.net

Schaffer Function



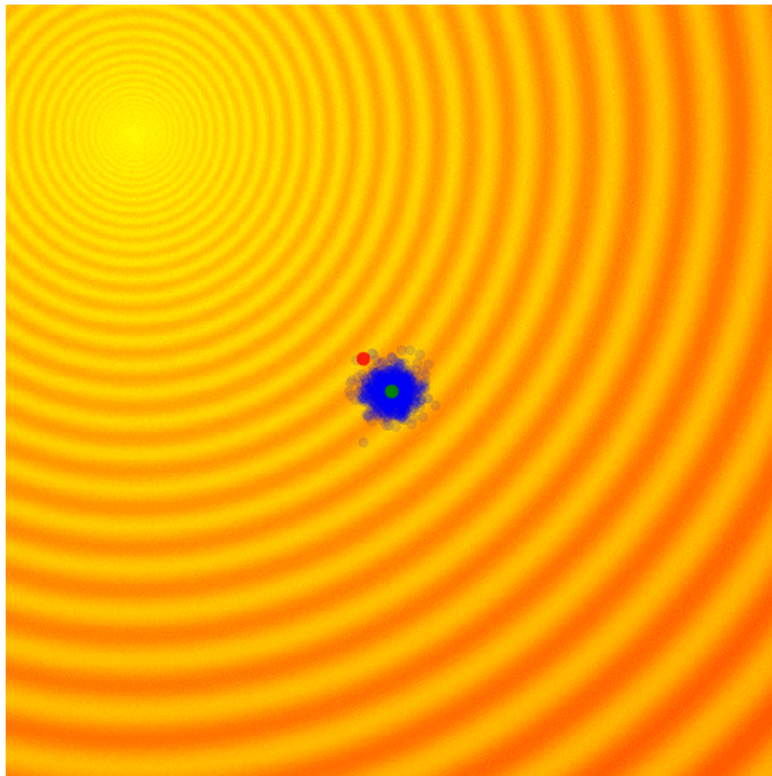
Rastrigin Function



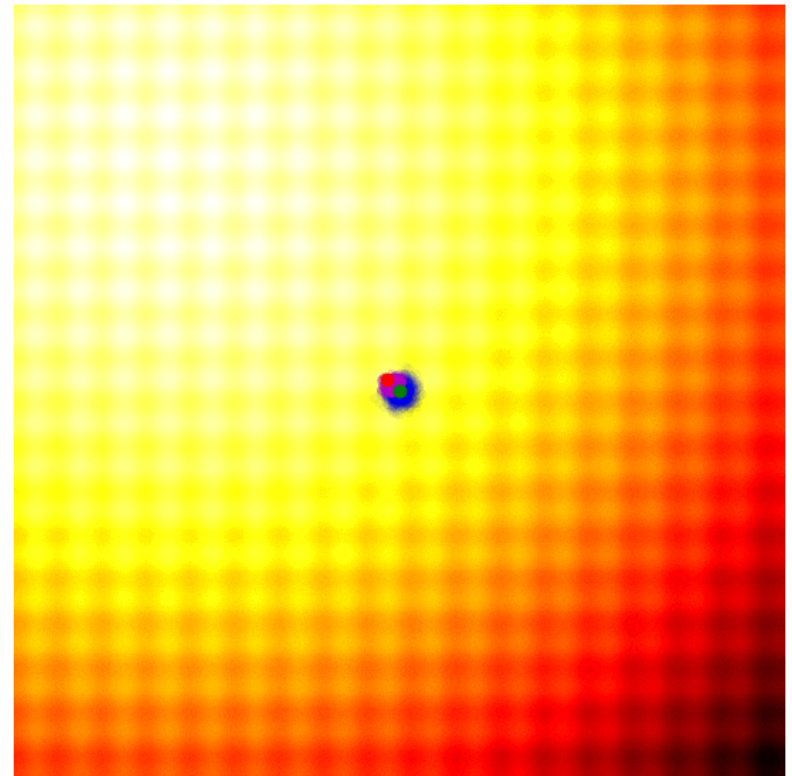
Red dot: Best so far — Green dot: Average of population

Simulation of CMA ES, adopted from otori.net

Schaffer Function



Rastrigin Function



Red dot: Best so far — Green dot: Average of population