A Multipopulation Differential Evolution Algorithm for Multimodal Optimization

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Outline

- Multimodal optimization
- EAs for multimodal optimization
- Multipopulation Differential Evolution
- A multiresolution variant
- Numerical results
- Conclusions

Multimodal optimization (1)

- Aim: find all optima (global and/or local) of the objective function
- Motivation:
  - give to the decision maker not a single optimal solution but a set of good solutions
  - find all solutions with local optimal behavior
- Similar with: multiobjective optimization
- Applications:
  - Systems design
  - DNA sequence analysis
  - Detecting peaks in DTA (differential thermal analysis) curves

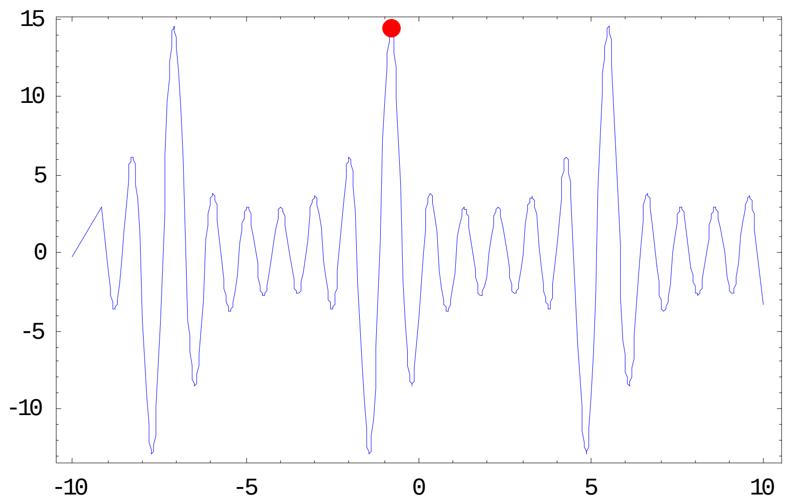
Multimodal optimization (2)

Global optimization

Aim: find a global optimum

Evolutionary approach: population concentrates on the global optima (single powerful species)

Premature convergence: bad

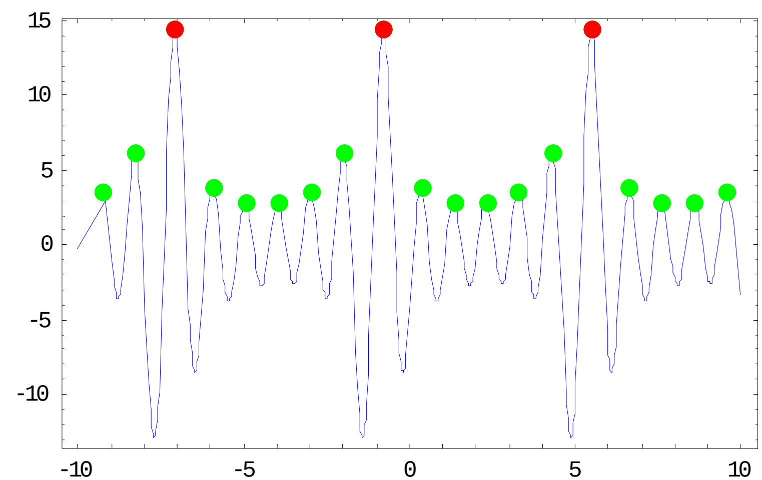


Multimodal optimization

Aim: find all (global/ local) optima

Evolutionary approach: different species are formed each one identifying an optimum

Premature convergence: not so bad



EAs for multimodal optimization (1)

- Multimodal evolutionary approaches:
  - Sequential niching models
    - Iterative application of an EA
    - At each iteration is identified an optimum
    - The fitness function is derated based on already found optima

  [Beasley et al., 1993]

  - Parallel subpopulation models
    - Divide the population into communicating subpopulations which evolves in parallel
    - Each subpopulation corresponds to a species whose aim is to populate a niche in the fitness landscape and to identify an optimum
    - Speciation is usually assured by a clustering process

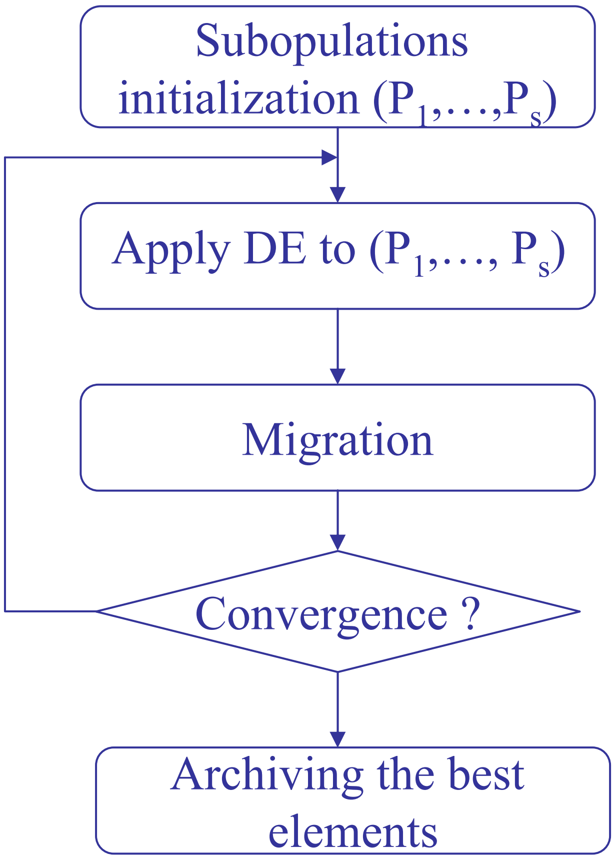
  [Bessaou et al., 2000], [Li et al., 2002]

EAs for multimodal optimization (2)

- Difficulties:
  - Finding an adequate niche radius
  - Computational cost of the clustering process (usually $O(m^2)$)

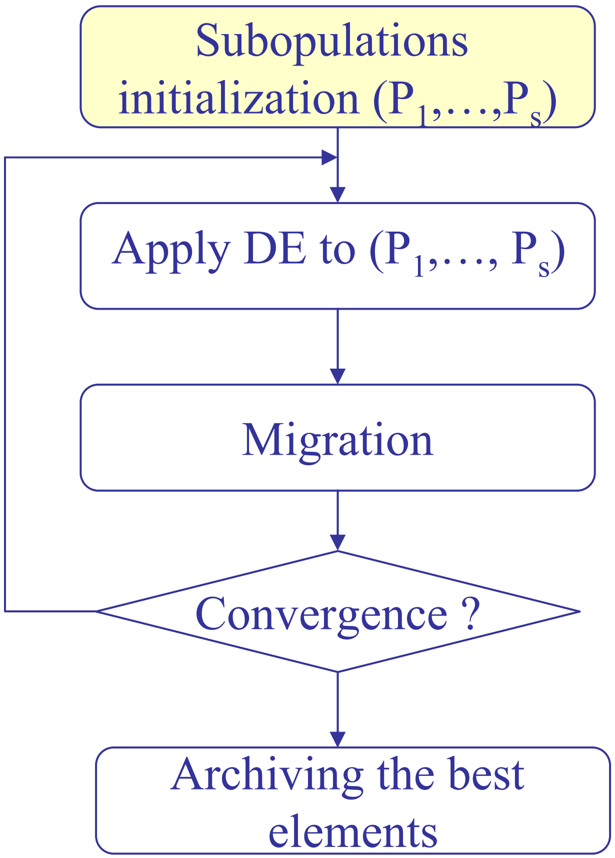
- Aim of this work:
  - Analyze the applicability of Differential Evolution to multimodal optimization
  - Develop an algorithm which:
    - Uses the fast convergence and robustness of DE
    - Uses few control parameters
    - Avoids a global processing of the entire population (clustering step)
    - Easy to be implemented in parallel

Multipopulation DE (1)



- **Population structure**
  - *s* subpopulations of fixed size *m*
- **Controlled initialization**
  - assure landscape exploration
- **DE2-type recombination**
  - fast convergence
- **Random migration**
- **Convergence ?**
  - subpopulations variance becomes small
- **Archiving**
  - collects the best elements of the subpopulations

Multipopulation DE (2)



- Problem:

  find the maxima of $f: D \subset R^n \rightarrow R$, $D=[a,b]^n$

- Resolution factor:

  $r=(b-a)/s^{1/n}$

- Subpopulation P_i is initialized in

  $D_i=[a_1^i,b_1^i] x \dots x [a_n^i,b_n^i]$

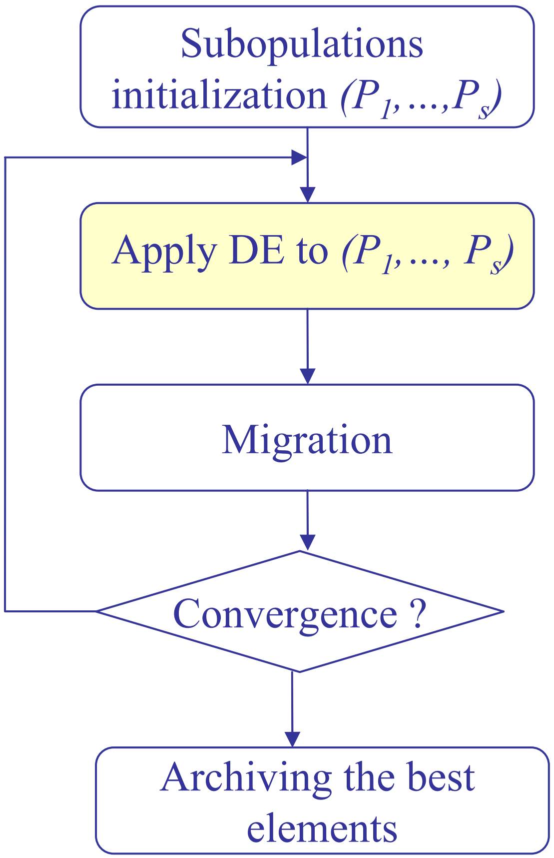
  $a_j^i=a+r\,k_j^i$, $b_j^i=a_j^i+r$

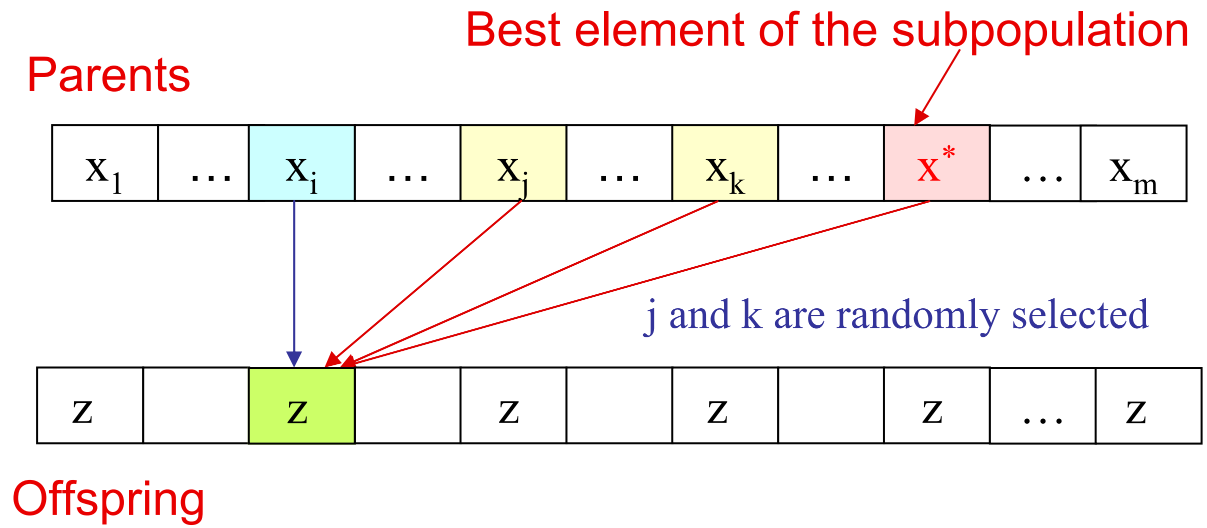
  $k_j^i \in \{0,1,\dots,[s^{1/n}]-1\}$ randomly selected

- Initially the elements of a subpopulation are relatively close to each other

- During the evolution the subpopulations can overlap

Multipopulation DE (3)



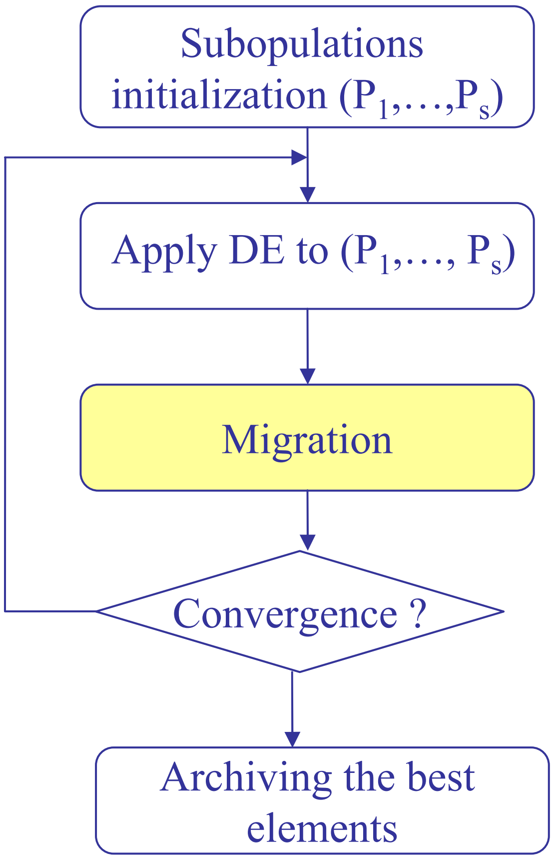


$$z_i = \begin{cases} x^* + F \times (x_j - x_k) & \text{with probability } p \\ x_i & \text{with probability } 1-p \end{cases}$$

Selection: the best one between the parent and the offspring is selected

- **Motivation:**
  - Fast convergence to an optimum (the subpopulations finds an optimum in their neighbourhood)

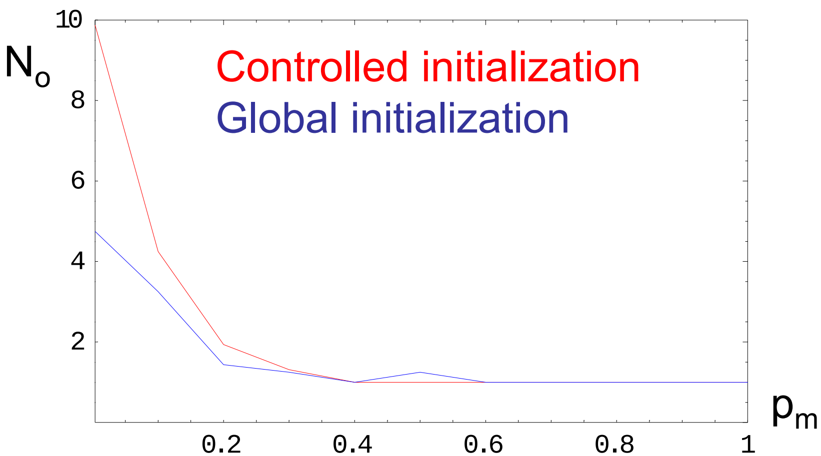
Multipopulation DE (4)

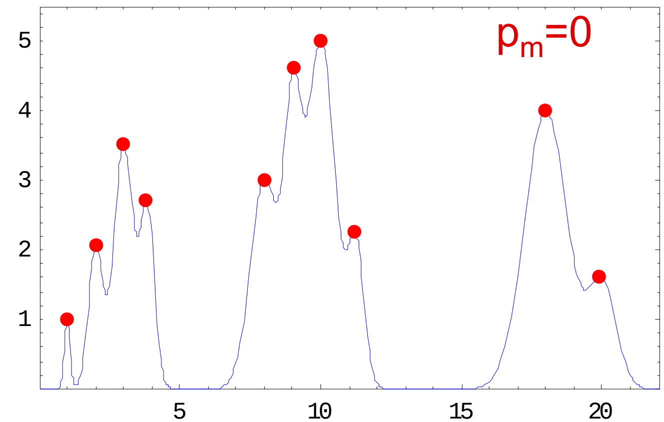


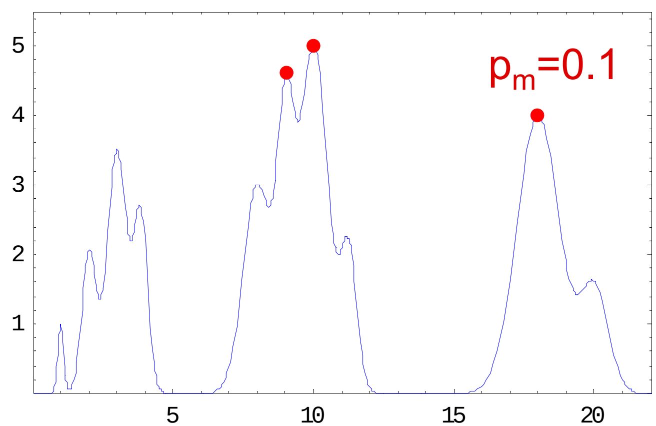
- Random migration:
  - After a given number of generations the subpopulations exchange information
  - Each element of a subpopulation can be swapped with a migration probability with a randomly selected element from a random subpopulation
- Migration effects:
  - Ensures an increase of subpopulations diversity
  - Avoid premature convergence
  - Can guide different subpopulations toward the same optimum (the subpopulations centroids migrate toward the population centroid)
- Practical remark:
  - If multiple optima have to be located the migration probability should be small

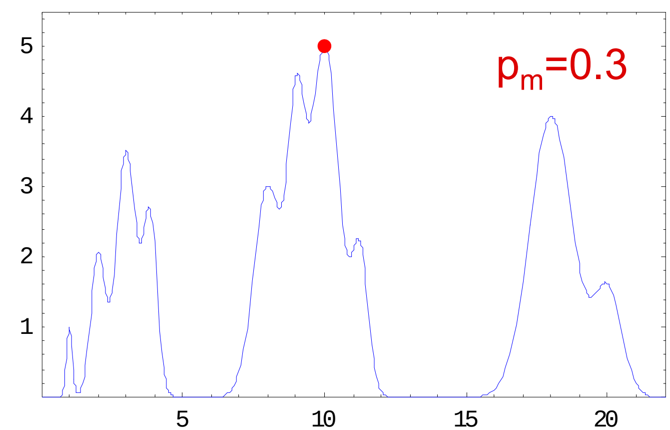
Multipopulation DE (5)

- Dependence of the number of found optima on the migration probability



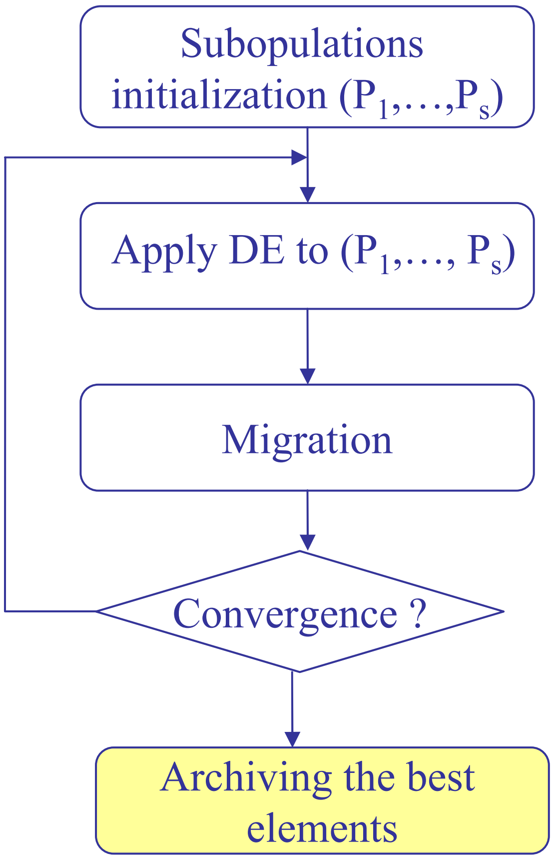






Test function: multigaussian – 10 optima

Multipopulation DE (6)



- Archiving:
  - The best element from each subpopulation is stored in an archive
- Redundancy avoiding : only the elements which:
  - are sufficiently dissimilar
  - belong to different peaks

  than those already stored are retained
- To decide if two elements belong to different peaks the hill-valley function is used

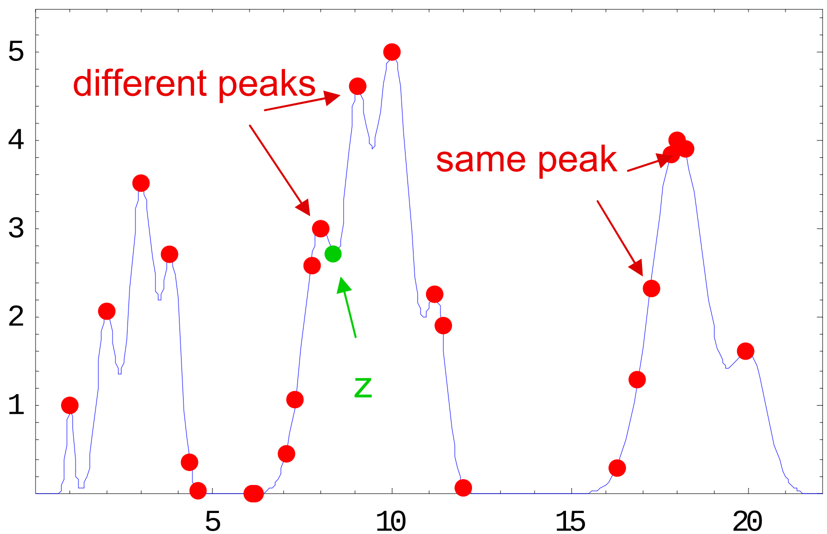
  [Ursem, Multinational Evolutionary Algorithms, 1999]

Multipopulation DE (7)

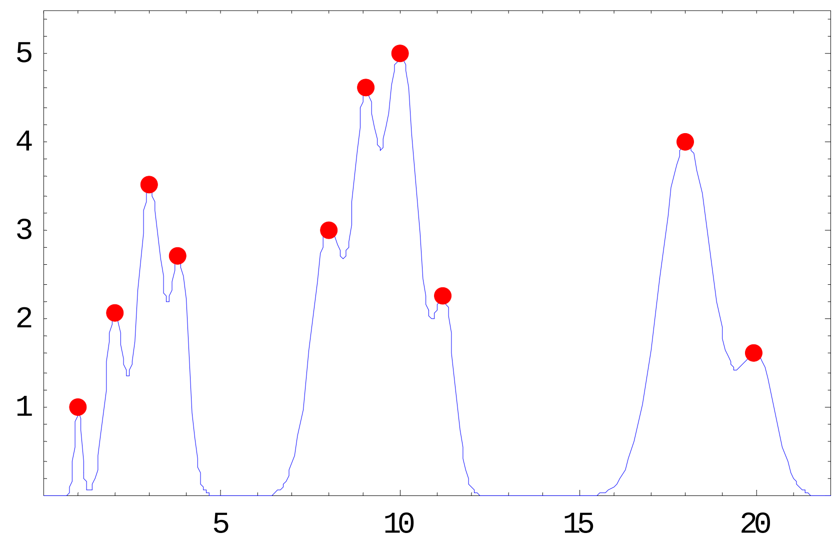
- Hill-valley function:
  - If there exists $c \in (0,1)$ such that

    $z = cx + (1-c)y$ implies $f(z) < f(x)$ and $f(z) < f(y)$

    then there exists a valley between x and y
  - The decision is based on computing z for some values of c

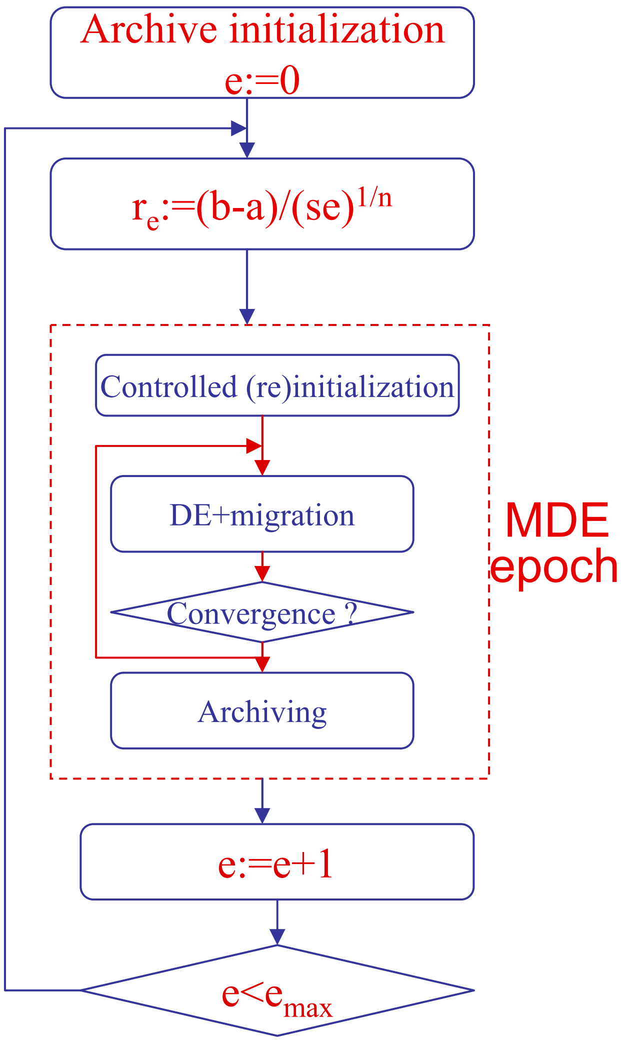


Archive before valley detection



Archive after valley detection

A multiresolution variant (1)



- Motivation:
  - When many optima have to be found, MDE needs many subpopulations
  - If the optima are unequally spaced some of them could be missed
- Basic idea:
  - Apply repeatedly the MDE for different resolution factors
  - Hybridization between the sequential and parallel niching methods
- (Re)initialization:
  - Based on the resolution factor and on the archive content
- Communication between different epochs:
  - Through the archive

A multiresolution variant (2)

- Idea of controlled (re)initialization
  - At each new epoch *e*, the elements of subpopulation P_i are selected from a subdomain

$$D_i=[a_1^i,b_1^i] \times \ldots \times [a_n^i,b_n^i]$$

$$a_j^i=a+r_e k_j^i,\ b_j^i=a_j^i+r_e, \qquad r_e=(b-a)/(se)^{1/n}$$

$k_j^i \in \{0,1,\ldots,[s^{1/n}]-1\}$ randomly selected

  - A random element from D_i is accepted with the probability

$$P_a(x)=\frac{1}{1+\sum_{i=1}^{k}\sigma(x,a_i)}, \qquad \sigma(x,a)=\begin{cases}1-\dfrac{d(x,a)}{r_e/2} & \text{if } d(x,a)<r_e/2\\ 0 & \text{otherwise}\end{cases}$$

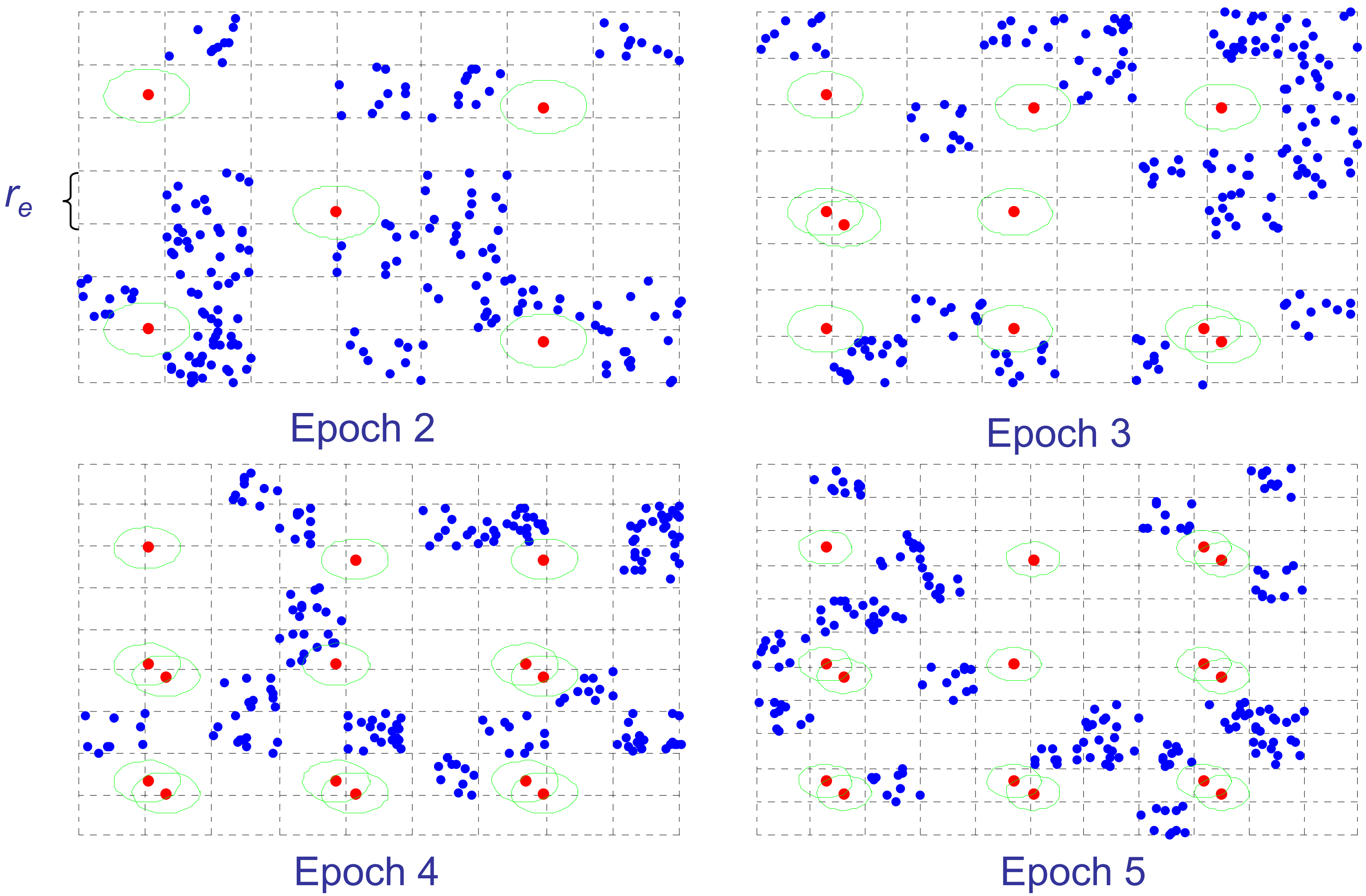
$A=\{a_1,\ldots,a_k\}$ – the archive

- The selection of elements from D_i is based on a non-uniform distribution obtained by modifying the uniform distribution by using a sharing function

A multiresolution variant (3)

- Illustration of controlled (re)initialization $f(x,y)=\sum_{j=1}^{5} j(\cos(j+1)x+j)\sum_{j=1}^{5} j(\cos(j+1)y+j)$

(Shubert function (2D) on $[-10,10]^2$ – 18 global optima)



Population elements

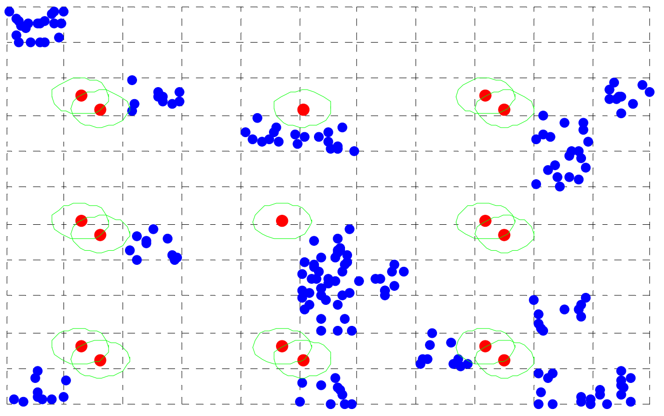
Current archive

Restricted area around found optima

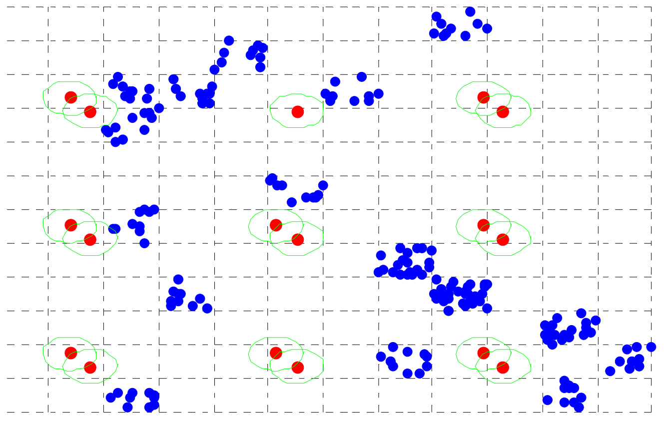
MDE parameters:
m=10
s=20
p_m=0.1
100 generations
t_m=10

A multiresolution variant (4)

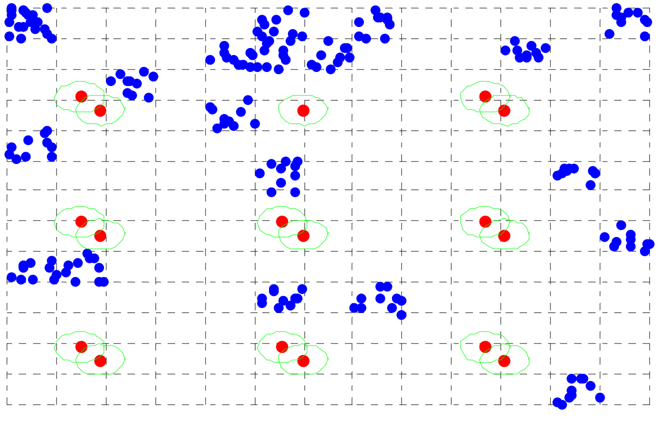
- Illustration of controlled (re)initialization (Shubert function (2D) – 18 global optima)



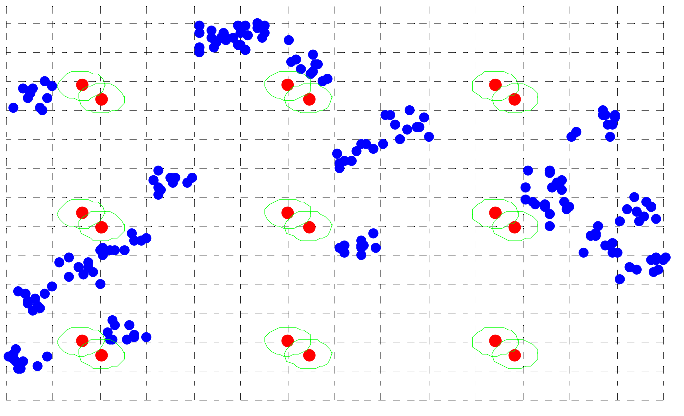
Epoch 6



Epoch 7



Epoch 8



Epoch 9

Population elements

Current archive

Restricted area around found optima

MDE parameters:
m=10
s=20
p_m=0.1
100 generations
t_m=10

Numerical results (1)

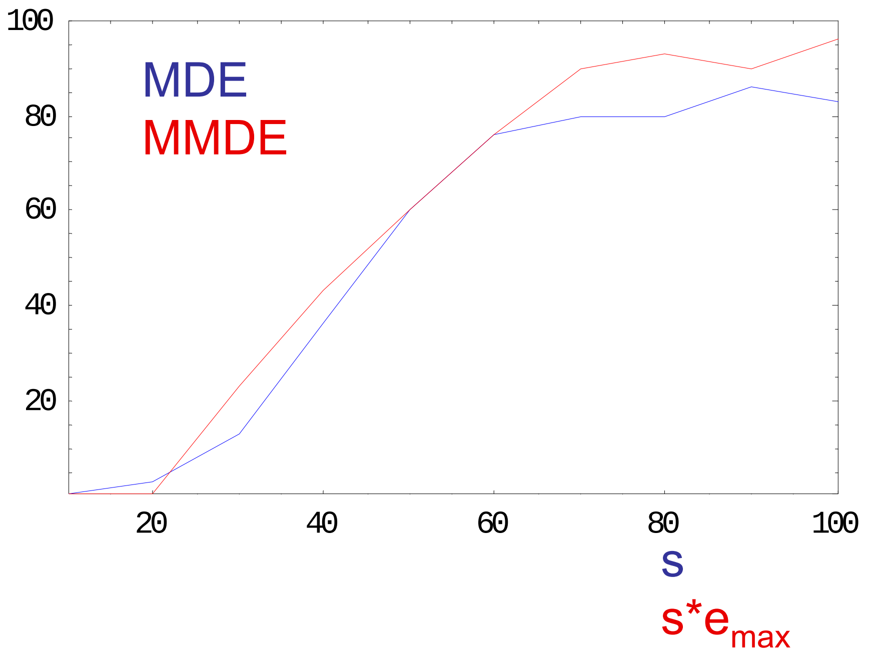
- Aim of experiments:
  - Analyze the ability of MMDE to locate multiple optima
  - Compare MMDE with other multimodal evolutionary techniques
- Experimental setup:
  - The population is divided into *s* subpopulations of fixed size *m*
  - DE convergence for a subpopulation: $Var(X(g))<10^{-5}$
  - Migration: random
  - DE parameters:
    - p=1
    - F adaptive:

$$F(g)=\sqrt{\frac{c(g)-(m-1)/m}{2}}, \qquad c(g)=\frac{Var(X(g-1))}{Var(X(g))}$$

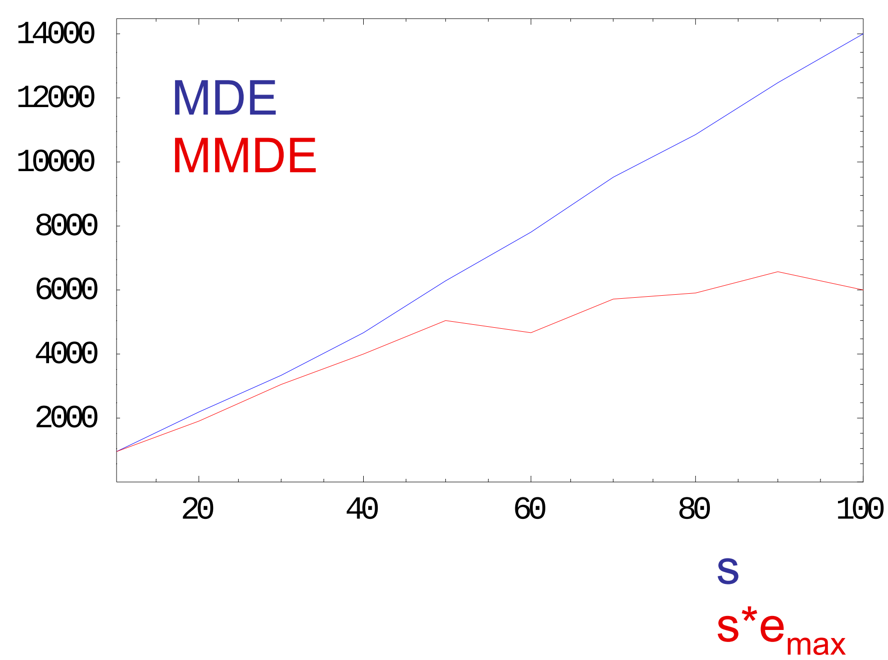
Numerical results (2)

- Comparison between MDE and MMDE:
- Test function: multigaussian

Succes rate (%)



Function evaluations

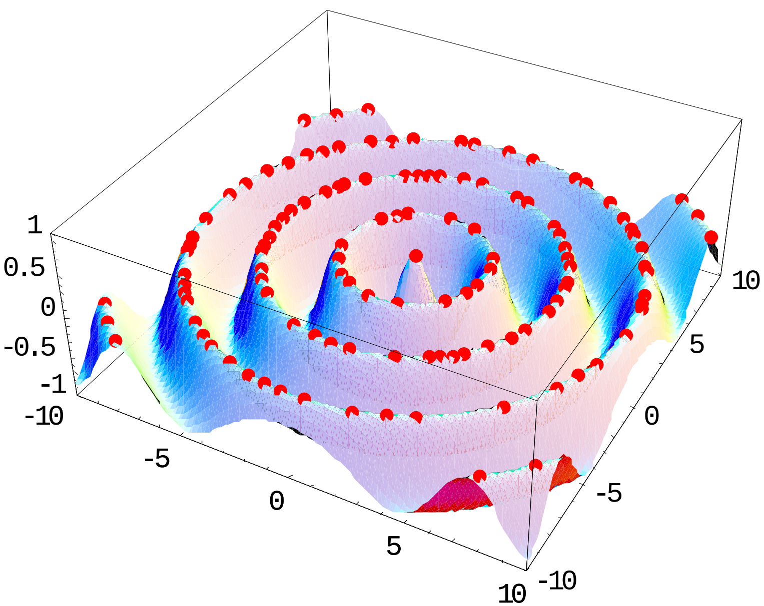


m=5, g=50

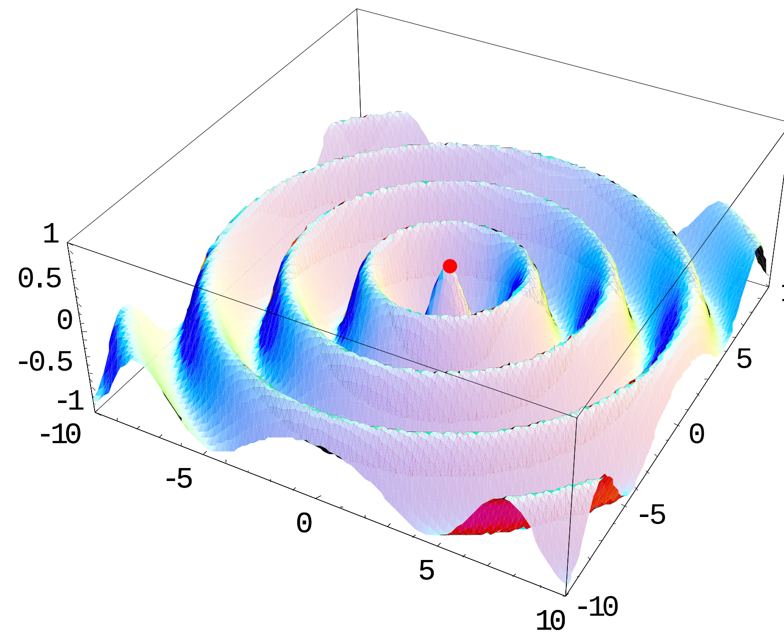
Numerical results (3)

- Test function: Schaffer 2D

$$f(x,y) = 0.5 + \frac{\sin^2(\sqrt{x^2+y^2}) - 0.5}{(1+0.001(x^2+y^2))}, \quad x,y \in [-10,10]$$



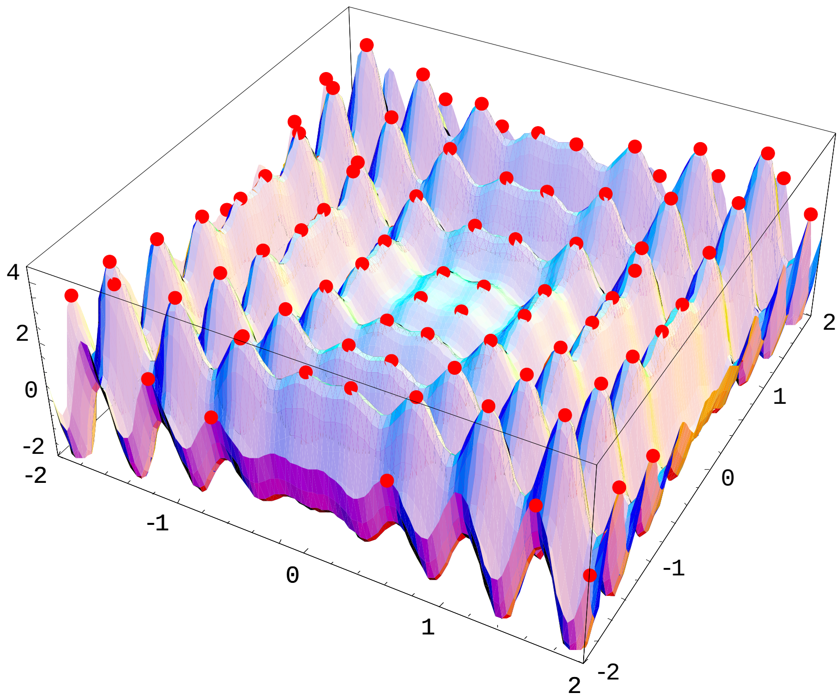
m=10, s=20, g=50, e=10, p_m=0



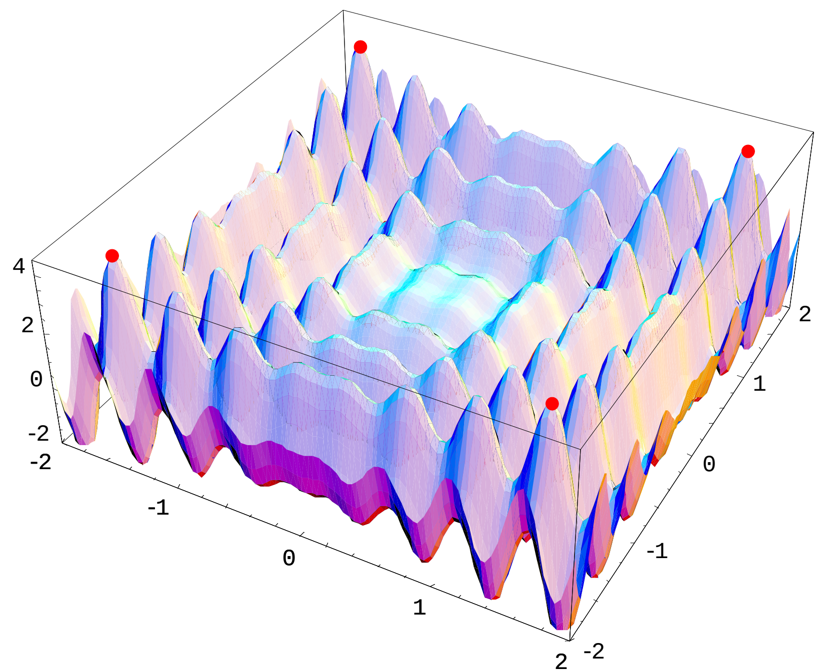
m=10, s=20, g=10x10, e=10, p_m=0.5

Numerical results (4)

- Test function: multi-peaks $f(x,y) = x\sin(4\pi x) - y\sin(4\pi y + \pi),\ x,y \in [-2,2]$



m=5, s=50, g=50, e=20, p_m=0
(91 elements in the archive)



m=5, s=50, g=10x10, e=20, p_m=0.5
(4 elements in the archive)

Numerical results (5)

- Comparative results

Test function: Himmelblau

MMDE ($m=5, s=10, e_{max}=2, p_m=0$) Sequential niching [Beasley, 1993] ($m=26$)

Fct.eval.	Succes rate	RMS error	Fct.eval.	Succes rate	RMS error
2665	96%	0.1	5500	76%	0.2

Test function: multi-peaks [de Castro, 2002]

MMDE ($m=5, s=50, e_{max}=20, p_m=0$) Opt AI-net (20 cells, 10 clones, 451 gen.)

Fct. eval.	No. of optima	Fct. eval.	No. of optima
76630	88.16	90200	61

Numerical results (6)

- Comparative results

Test function: Shubert 2D

MMDE (m=10,s=50,e_{max}=10,p_m=0)		SCGA [Li et al., 2002] (m=300)	
Fct. eval.	No. of optima	Fct. eval.	No. of optima
39463	17.26	35747	18

Test function: Schaffer 2D

MMDE (m=40,s=10,e_{max}=1,p_m=0.5)		Island model+speciation [Bessaou et al., 2000] (m=10, s=50)	
Fct. eval.	Succes rate	Fct. eval.	Success rate
26253	90%	18000	100%

Conclusions

- Characteristics of MMDE:
  - Exploration ensured by a multi-resolution approach and a controlled (re)initialization of subpopulations
  - Exploitation ensured by a adaptive DE2 variant
  - Preservation of good solutions by a controlled archiving
  - Small subpopulations
  - Migration introduce flexibility:
    - high migration probability: locate one global optima
    - small migration probability: locate all global optima
    - no migration: identify all global/local optima
  - No niche radius
  - No global clustering
  - Easy to parallelize
  - Sensitivity to the number of subpopulations and to the number of epochs