

Spacing Memetic Algorithms

- using distances to control population “spacing” -

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Motivation

Standard Memetic Algorithm: a genetic algorithm that generates offspring

via: parent selection → recombination → **local search**

- all individuals are local optima w.r.t. the local search neighborhood, higher quality pressure
- systematic local search can easily lead to basins of attraction, big valleys, plateaux (even in one generation), higher risk of losing diversity

Spacing Memetic Algorithms: Use a search space distance to **strictly** control population **spacing**—a specific type of diversity

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Spacing Memetic Algorithms: Use a search space distance to **strictly** control population **spacing**—a specific type of diversity

Spacing Concepts 1

Consider a (discrete) optimization problem and denote:

\mathbb{S} the search space, all candidate solutions

N the local search neighborhood relation, i.e. set
 $\{(l_1, l_2) \in \mathbb{S} : l_1 \text{ is a neighbour of } l_2\}$

(\mathbb{S}, N) the search space graph

Search Space Distance

The distance $d : \mathbb{S} \times \mathbb{S} \rightarrow \mathbf{R}_+$ is the shortest path function in (\mathbb{S}, N) .

- $d(l_1, l_2) = n \iff$ at least n local search steps needed to link l_1 and l_2
- Examples: **the Hamming distance** for a bit flip neighborhood, **edit distance** for a deletion/insertion neighborhood

This **correlation with the local search** gives the “semantic” of the distance

- the local search does not walk a long distance in a few steps.

Spacing Concepts 2

Given a population P containing individuals l_1, l_2, \dots, l_n :

- 1 The **minimum spacing** is the smallest distance in the population

$$\min\{d(l_i, l_j) : l_i, l_j \in P, i \neq j\}$$

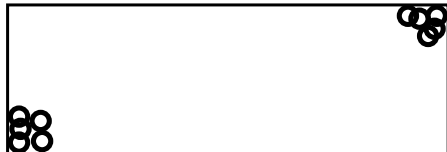
- 2 The **average spacing** is the average distance among individuals

$$\frac{\sum_{1 \leq i < j \leq |P|} d(l_i, l_j)}{\frac{1}{2}|P| \cdot (|P| - 1)}$$

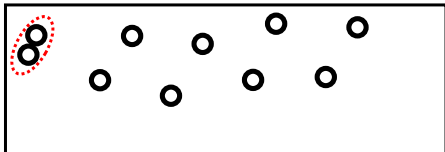
We use the word “diversity” to point to these clearly-defined indicators (**no** entropy, **no** statistical dispersion, **no** gene frequencies, **no** other measures except distances)

Objectives

A) Inappropriate population
Average spacing: **quite high**



B) Acceptable population
Minimum Spacing: **very low**



⇒ **Only one spacing indicator not enough** to describe the quality of the spatial distribution ⇒ We propose **two objectives**:

Objective 1 Keep the minimum spacing above a specific threshold

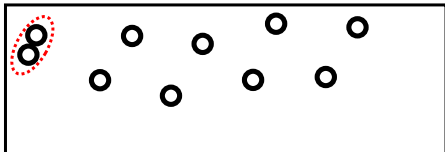
Objective 2 Maximize the average spacing (subject to Objective 1)

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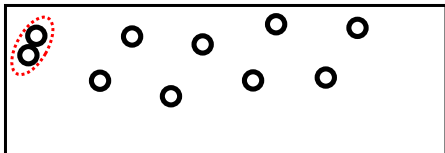
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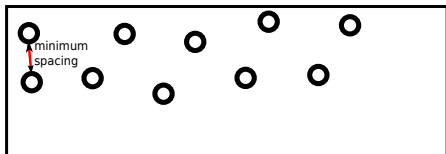
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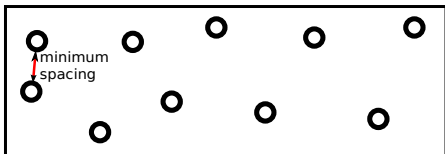
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Objective 1 Keep the minimum spacing above a specific threshold

Objective 2 Maximize the average spacing (subject to Objective 1)



Good minimum spacing, **good** pop.



Higher average spacing, **better!**

Summary

- 1 Description of Spacing Memetic Algorithms (SMA): SMA is a MA with changes at two levels:
 - Fitness-distance replacement
 - Offspring acceptance and rejection
- 2 Related Work (MA|PM, niching, geometric genetic algorithms, etc.)
- 3 Numerical Validations (NK-Model, clique, coloring) and Conclusions

Survival and Replacement

Case 1 Minimum spacing **lower** than the threshold defined by **Objective 1**:

- Pick up the closest two individuals (closer than the threshold)
- Eliminate the worst

Case 2 Minimum spacing **higher** than the threshold defined by **Objective 1**:

- Select a first candidate I using the original replacement (tournament selection, roulette wheel, etc)
- Second candidate J =the closest individual to I
- The worst ranked of I and J is eliminated

The rule of **Case 2** has the advantage or **re-using the original selection**. If one does not require **re-using** this selection, other variants are available.

Offspring acceptance test

Suppose offspring O is **too close** to existing individual I :

- Reject offspring O
 - O brings NO new genetic material to the population
 - Exception: “aspiration criterion”, i.e. if O is better than the best-known visited individual
- Repeat the offspring generation process

“ O too close to I ” means:

$$d(O, I) < T$$

where T is **the minimum spacing threshold** (noted R in the paper)

Number of rejections

If offspring O is rejected, the offspring generation process is repeated.



Question: **how many times** can this process be repeated?

Case 1 Until an offspring O is accepted

OR

Case 2 Until a number of failed tries (*maxRejects*) is reached

In Case 2 the offspring is mutated and accepted

- mutations introduce random genetic material → “artificial” diversity

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Setting the quality and spacing pressures

Higher or lower maxRejects?

- low maxRejects → low quality pressure
 - The search makes appeal to mutations very quickly
- high maxRejects → high quality pressure
 - SMA goal: “diversity without quality sacrifices”
 - mutations only used after a **very high** threshold of maximum failed (maxRejects) tries

Higher or lower minimum spacing threshold?

- small T → low diversity pressure
- large T → high diversity pressure

Detecting and avoiding search space traps

Using T and $maxRejects$ to escape search space traps.

- The history of the distance distribution can detect stagnation
- Even if the minimum spacing is higher than T the population can be trapped, e.g.
 - All distances are less than $2 \times T$ (but higher than T —many small plateaux in a “big valley” or “well”)
 - Many mutations needed over many iterations to maintain a minimum spacing of T
- In case of trap detection, apply **reactive dispersion routine**:
 - 1 more diversity pressure (higher T)
 - 2 less quality pressure (lower $maxRejects$)
 - 3 the above change is kept until the population distribution is back to normal (the population is supervised)

Related Research

- MA|PM Memetic Algorithms with Population Management [Sorensen and Sevaux, 2006]
 - If the new individual does not satisfy the diversity criterion, it is mutated (i.e. maxRejects is 0)
 - SMA: different maxRejects values, reactive dispersion, new spacing replacement operators
- Multi-modal optimization: “niching” methods are used to locate all “peaks” (global optima) of a function:
 - population divided in sub-populations exploiting niches
 - crowding [De Jong, 1977; Mahfoud, 1995; Smith, Forrest; Cedeno, Vemuri] induces niches by forcing new individuals to replace similar individuals (using distances or genomic similarities)
 - SMA: stable subpopulation, niches or clusters are **discouraged**
- Geometric operators (crossover/mutation) [A. Moraglio] , distance-preserving crossover [Mertz, TSP]
 - SMA does not aim at modifying existing operators

Other ideas in the literature

- Multi-objective optimization distances (e.g., crowding distance)
 - calculated in the **objective function** space
- Diversity-guided/controlling genetic algorithms choose the genetic operators using distances
 - distances are not essential, any general diversity indicator is useful
- Scatter Search

Results

Results are reported on four discrete problems:

- Artificial problems (One-Max-Plateaux and *NK*-model) using the **Hamming distance**
- The clique problem using the **Hamming distance**
- Graph *k*-coloring using the **partition distance**

Similar trends are observed:

- **Objective 1** is essential, **Objective 2** is very useful
- without spacing strategies, the average spacing can become 0

→ We describe next the impact of the main SMA ideas on *k*-coloring.

Impact of Main Spacing Ideas

<i>k</i> -coloring instance: G, k	Full SMA #hits	Obj. 1 OFF #hits	Obj. 2 OFF #hits	React OFF #hits	Spacing OFF #hits
dsjc500.1, 12	50/50	21/50	49/50	50/50	15/50
dsjc1000.1, 20	50/50	3/50	30/50	49/50	0/50
dsjr500.1c, 85	46/50	2/50	10/50	1/50	3/50
flat1000.76, 82	42/50	33/50	33/50	42/50	9/50
le450.25c, 25	47/50	2/50	23/50	29/50	3/50
r250.5, 65	49/50	4/50	24/50	25/50	4/10

SMA The complete version of SMA has **very high success rates**

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Obj1 OFF Without keeping a minimum distance threshold, SMA does not attain high (stable) success rates; the average spacing becomes ≈ 0 at the end of failed runs;

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Obj2 OFF By disabling **Objective 2**, SMA does not reach a wide covering of the search space, and so, it **can not be very robust**;

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React OFF Without reactive dispersion (i.e. R and $maxRejects$ fixed) the search can not be unlocked from special search space “traps”. In certain cases, this can make a important difference: **46/50** vs **1/50**;

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Spacing OFF With no spacing strategy at all, SMA finds few solutions.

Conclusions

Distances can be a simple-but-effective tool to control diversity:

- All spacing components can be inserted into an existing algorithm with no modifications on the original memetic operators
- The computational overhead can be very limited
 - The local search is usually much more time consuming (small populations)
 - A fast distance calculation method is recommended

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Clique

Graph	opt	SMA			<i>Spacing OFF</i>			<i>Obj. 1 OFF</i>			<i>Obj. 2 OFF</i>	
		bst(#b)	avg(std)	min	bst(#b)	avg(std)	min	bst(#b)	avg(std)	min	bst(#b)	avg(st
C125.9	34	34 (3)	33.1 (0.8)	31	32 (2)	29.9 (1.4)	28	32 (2)	31.0 (0.6)	30	33 (4)	32.2 (0
brock200_2	12	11 (2)	9.9 (0.7)	9	10 (1)	9.0 (0.4)	8	10 (3)	9.2 (0.6)	8	11 (2)	10.1 (0
brock200_4	17	16 (1)	14.4 (0.8)	13	15 (1)	13.3 (0.9)	12	14 (3)	13.1 (0.7)	12	15 (3)	14.3 (0
gen200_p0.9_44	44	40 (1)	36.3 (1.3)	35	37 (1)	33.7 (1.3)	32	36 (1)	34.7 (0.8)	33	39 (1)	36.2 (1
gen200_p0.9_55	55	55 (1)	40.2 (5.8)	35	43 (1)	36.8 (2.6)	34	46 (1)	36.4 (3.6)	33	53 (1)	41.8 (5

Comparison SMA on Cliques