Response to the comments of Reviewers for axioms-2640387

# Reviewer 1

## 1. Comment

I found the manuscript to be a very nice one to read, giving an appropriate balance of contextualisation, rationale, theory and results, as well as conclusions that matched the story being told throughout the manuscript. The flow of the manuscript tells the story of the work in a methodical and logical manner.

## Response

Dear reviewer, thank you for your comments and your efforts.

# Reviewer 2

## 1. Comment

The title of the manuscript is misleading as it refers to stochastic optimization methods, i.e., a more general group of methods than the genetic algorithm discussed in the manuscript. I suggest modifying the title or including a comparison with other stochastic optimization methods.

## Response

Yes, you are correct. The title has been changed to *“An intelligent technique for initial distribution of genetic algorithms”*

## 2. Comment

Introduction is informative but lacks any discussion on the state-of-the-art initialization approaches for genetic algorithms – the main topic of the manuscript

## Response

We have added references to relative works and the following paragraph has been added at the end of Introduction:

“*During the past years, many researchers have proposed variations for the initialization of genetic algorithms, such as the work of Maaranen et al [*[*gainit1*](#LyXCite-gainit1)*], where they discuss the usage of quasi-random sequences in the initial population of a genetic algorithm. Similarly, Paul et al [*[*gainit2*](#LyXCite-gainit2)*] proposed initializing the population of genetic algorithm using a Vari-begin and Vari-diversity (VV) population seeding technique. Also, in the same direction of research, Li et al proposed [*[*gainit3*](#LyXCite-gainit3)*] a knowledge-based technique to initialize genetic algorithms used mainly in discrete problems. Recently, Hassanat et al suggested the incorporation of regression techniques for the initialization of genetic algorithms.* ”

## 3. Comment

P.1, L.16: what is the reason for the differentiability requirement of the target function? Is it required by the local search step?

## Response

Yes, we have removed it. It is not necessary.

## 4. Comment

P.3, L.105-108: I am confused with the fitness calculation step. Is this an outer loop over generations,= or the loop to evaluate the fitness of chromosomes? Writing this as an algorithm will be helpful.

## Response

We have changed this step in order to be more readable.

## 5. Comment

The manuscript would benefit if the authors provide any rule of thumb for choosing the number of clusters in the k-means algorithm. This would also justify the “intelligent” part of the title.

## Response

The following phrase has been added in Subsection 3.2

“*In order to have a fair comparison between the results produced between the proposed technique and the rest, the number of centers produced by the k-means method was set to be equal to the number of chromosomes N c of the rest of the techniques. Ten times the number of initial points were used to produce the centers. In addition, through the discard process of Algorithm* [*alg:Chromosome-rejection-rule*](#alg_Chromosome_rejection_rule)*, some centers will be eliminated.* ”

## 6. Comment

What is the exact flavor of a genetic algorithm used by the authors in the OPTIMUS package? It would also be helpful to see comparisons of multiple methods for different initializations

## Response

We have added the folloging phrase in subsection 3.2:

*“The genetic algorithm variant of OPTIMUS package used in the conducted experiments was the pDoubleGenetic algorithm, that can utilize different methods for the initialization of chromosomes.”*

## 7. Comment

P.9, L.247: in “number of randomly generated chromosomes Ng”, it is my understanding that Ng is the number of generations. Please clarify

## Response

Corrected to Nc

## 8. Comment

P.3, L.101: “chromosomes in in S

## Response

Corrected.

## 9. Comment

In Algorithm 2, 3(c) “If then” seems unnecessary

## Response

Corrected.

## 10. Comment

P.8, L.235: description of column names in experimental tables (without referencing their numbers) is a bit confusing when it follows the reference to Table 1.

## Response

We have added the following phrase: *“The values in the experimental tables denote average number of function calls.”*

# Reviewer 3

## 1. Comment

The main flaw of the article is that the given description of algorithms does not allow their implementation.

## Response

The proposed method has been implemented in the OPTIMUS package and we have added the following phrase in Subsection 3.2 *“The genetic algorithm variant of OPTIMUS package used in the conducted experiments was the pDoubleGenetic algorithm, that can utilize different methods for the initialization of chromosomes.”*

## 2. Comment

Algorithm 1 does not describe the distance D(...). The right-hand side of Formula 2.(b).i depends on j, the index i is incorrectly changing from 1 to k. Its left-hand side is the index, which is proposed to be chosen as the minimum distance. It is not clear which initial centers c\_j to use, since they are only calculated in Formula 2.(d).ii. In Formula Formula 2.(d).ii, the elements from S\_j should be chosen.

## Response

Thank you for your comment,

1) We have defined D(x,y) as the Euclidean distance of (x,y)

2) We have changed the index in 2.i

3) We have clarified in 2.d.ii that the elements from S\_j would be chosen

## 3. Comment

In addition, there is no explanation whether some sets S\_j can be empty after applying Algorithm 1. At Step 3 it is proposed to calculate s\_j, then \sigma\_j appears in Formula. I can assume that s\_j = \sigma\_j, however these parameters are not used in Algorithm 1. How does the function f affect the centers c\_j?

## Response

Yes, you are correct. We have removed the calculation of s\_j, since they are not used in the main algorithm.

## 4. Comment

The stop condition in Algorithm 1 is: “no change in centers”, but further after Algorithm 1 this condition becomes more vague: “no change significantly in centers”.

## Response

Corrected.

## 5. Comment

Apparently the number of centers should coincide with the number of chromosomes, but the authors use different notations without providing details. This can only be guessed from the context.

## Response

We have changed the notations and also we have modified the paragraph about the number of centers to the following:

“*In order to have a fair comparison between the results produced between the proposed technique and the rest, the number of centers produced by the k-means method was set to be equal to the number of chromosomes N c of the rest of the techniques. Ten times the number of initial points were used to produce the centers. In addition, through the discard process of Algorithm* [*alg:Chromosome-rejection-rule*](#alg_Chromosome_rejection_rule)*, some centers will be eliminated.* ”

## 6. Comment

It is better to use “multivariable function” instead of “multi-dimensional function” (line 1).

## Response

Corrected.

## 7. Comment

The condition of continuity and differentiability for the function f is necessary for gradient-type methods. For the evolution methods under consideration, it is not required at all (line 16).

## Response

Yes, we have removed it.

## 8. Comment

The function domain definition uses the symbol \otimes (tensor product). Here we need the symbol \times (Cartesian, or direct, product).

## Response

Corrected.

## 9. Comment

GPU processing units = graphics processing unit processing units (line 31).

## Response

Corrected.

## 10. Comment

Line 101: N\_c should be instead of N\_C, and “in S” should be instead of “in in S”.

## Response

Corrected.

## 11. Comment

Line 106: N\_c should be instead of N\_g (?).

## Response

Corrected.

## 12. Comment

There is no explicit step for chromosome updating in Genetic Algorithm (lines 98-128). According to notations, the initial chromosomes g\_i are formed and then they do not change (there is no update formula with notations g\_i).

## Response

Thank you for this comment.

1) We have added the Step “Replacement procedure” to indicate how the chromosomes with the worst fitness values are replaced by offsprings.

2) We have extended the mutation procedure to clarify what element is altered through mutation

## 13. Comment

Genetic Algorithm (lines 98-128) does not indicate the distribution law for random variables a\_i and r. The pair (z,w) does not contain indices.

## Response

We have clarified in the revised text that i=1,..,n for the pair (z,w). Also, we have noted that the a\_i is a set of random numbers.

## 14. Comment

In Algorithm 2 it is enough to check the norms ||c\_i-c\_j|| for i > j only (or for i < j only) due to symmetry.

## Response

Yes, this has been corrected to the revised version.

## 15. Comment

The authors propose to find the centers (Algorithm 1, which is incorrect), and then some of them are removed by Algorithm 2. This does not correspond to Step 1.(a) in Genetic Algorithm, at which the number of chromosomes is fixed at the beginning.

## Response

Yes you are correct, there is a some missunderstanding here. We have added the following text at Step 1.a of genetic algorithm to clarify this:

*“**In most implementations of genetic algorithms, the chromosomes will be selected using some random number distribution. In the present work, the chromosomes will be selected using the sampling technique described in subsection* [*subsec:The-proposed-sampling*](#subsec_The_proposed_sampling)*. ”*

## 16. Comment

It is advisable to describe parameters \epsilon and \sigma (line 209).

## Response

The following phrase was added: *“**Also, for the conducted experiments the values \epsilon =1,\sigma= 1 were used.”*

## 17. Comment

It is advisable to add \cite{...} for the triangular distribution (line 240).

## Response

Added.