Investigating Landscape Topology for Subpopulation Differentiation in Genetic Chromodynamics

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Abstract—Evolutionary algorithms for multimodal optimization are usually radius dependent in subpopulation formation and dynamics. The appropriate setting of a value to cover such a fluctuant threshold (as a result of variously shaped attraction basins) strongly relies upon the knowledge on the problem at hand or the extensive skill in manual parameter tuning. If several thresholds model the disposal of species with the many attraction basins, radia setting significantly increases in complexity. Genetic chromodynamics is one such recent, competent technique, whose performance is practically affected by the existence of such key parameters. It is hence the purpose of present paper to present an enhanced alternative for radii maintenance within this method, which embeds a mechanism to examine the fitness landscape and detect the attractors, around which these species revolve.

I. INTRODUCTION

Belonging to the family of radii-based multimodal evolutionary frameworks, GC emerged as an efficient means in addressing optimization [2], [1]. Despite the natural differentiation into subpopulations that it achieves and the effectiveness of its application, its two parameters – the mating and merging radii – are, for some problems, hard to parameterize. A possibility to reach configurations that provide consistent results would be to resort to classical formulas to compute the value for the mating radius and try a proportional value for the merging radius. However, these cannot be expected to attain more than a medium performance. Moreover, they may either require knowledge on the problem domain or heavily depend on the user experience in parameter setting. Finally, a single radius value is not able to accurately separate several subpopulations that reside in differently sized attraction basins.

The goal of current work is to suggest a substitute for the radius parameters through a modified methodology that makes use of the landscape topology to drive the behavior of subpopulations. The discussion is constructed in the following way: The next section presents the algorithms within genetic chromodynamics, while section 3 establishes the augmented version of the paradigm. Experiments on benchmark test functions and analysis are conducted in section 4 and the final part outlines the conclusion.

II. THE GENETIC CHROMODYNAMICS FRAMEWORK

GC builds and maintains subpopulations, corresponding each to a global/local optimum of the problem, through the consideration of every individual for reproduction and the selection of a mate through a local interaction principle. Selection for replacement takes place between the resulting offspring and the current stone individual. A merging operator is used to achieve decrease in the number of individuals. The interplay between merging and mating regions strongly impacts convergence properties: a large merging radius leads to the extinction of potential mates of the surviving individuals and thus obstructs recombination. Let it be given a maximization problem and let \( f(c) \) denote the fitness evaluation of individual \( c \). The GC primary technique is outlined in (Algorithm 1): \( \text{pop\_size} \) refers to the size of the population, \( P_i(t) \) denotes the \( i \)-th individual at generation \( t \) and \( S_x \) is the set of the individuals in the merging area of \( x \).

Algorithm 1 GC original algorithm

\[
\begin{align*}
    t &= 0; \\
    &\text{initialize population } P(t); \\
    \text{repeat} & \\
    &\text{evaluate } P(t); \\
    &\text{for } i = 1 \text{ to } \text{pop\_size} \text{ do} \\
    &\quad \text{if mating region of } P_i(t) \text{ is empty then} \\
    &\quad \quad \text{mutate } P_i(t) \text{ and obtain offspring } y; \\
    &\quad \text{if } f(y) > f(P_i(t)) \text{ then} \\
    &\quad \quad \text{replace } P_i(t) \text{ with } y; \\
    &\quad \text{end if} \\
    &\quad \text{else} \\
    &\quad \quad \text{select an individual } x \text{ from the mating region of } P_i(t); \\
    &\quad \quad \text{recombine } P_i(t) \text{ and } x, \text{ obtain and evaluate one offspring } y; \\
    &\quad \quad \text{if } f(y) > f(P_i(t)) \text{ then} \\
    &\quad \quad \quad \text{replace } P_i(t) \text{ with } y; \\
    &\quad \quad \text{end if} \\
    &\quad \text{end if} \\
    &\text{end for} \\
    &\text{repeat} \\
    &\quad \text{take current existent individual } x \in P(t); \\
    &\quad S_x = \bigcup \{ m_j \} \text{ individual } m_j \text{ in the merging region of } x; \\
    &\quad \text{keep in the current population only the best individual from } S_x; \\
    &\text{until merging can not be applied at all} \\
    &t = t + 1; \\
    &\text{until stop condition}
\end{align*}
\]

A crowding mechanism (CGC) is further inserted within the standard GC approach with the goals of a better exploitation
of the search space and increased convergence speed (Algorithm 2). The selection for replacement strategy used in the enhancement is generational. In contrast to the stepping stone mechanism, the first parent is selected randomly. The offspring obtained after recombination does not replace any of the parents particularly, but the worst individual (with respect to fitness values) within its replacement radius, a new parameter of the method.

**Algorithm 2 CGC enhanced algorithm**

```
t = 0;
initialize population P(t);
repeat
    evaluate P(t);
    for i = 1 to pop_size do
        randomly choose an individual ci;
        if mating region of ci is empty then
            mutate ci and obtain d;
        else
            select an individual from the mating region of ci;
            recombine ci and c′, obtain and evaluate one offspring d;
        end if
        if f(d) > f(ci) then
            replace ci with d;
        end if
    end for
    merging on P(t);
    t = t + 1;
until stop condition
```

CGC had proven to achieve its initial goals and outperform the original GC in most of the undertaken experiments [1]. However, the additional choice of the novel replacement radius value adds more complexity to the issue of disburdening the GC framework of its radii that it is proposed to be resolved in present work.

**III. TOPOLOGICAL CROWDING GC**

A novel approach to further augment the master framework, the topological crowding genetic chromodynamics (TCGC) [3], transfers the radii-based subpopulation determination and convergence to the species adaptive movement as a consequence of the local fitness landscape. It is described in Algorithm 4, where $M_i$ represents the collection of the the mating partners of $P_i(t)$ and landscape_detect implies landscape verification.

TCGC appears with the purpose to resolve the complexity of setting appropriate values for the radius parameters involved in the dynamics and performance of CGC. The framework is endowed with mechanisms that allow subpopulation structure to be emergent and not predefined. Nevertheless, the underlying radii dependence hinders the multimodal behavior of CGC. This has offered the motivation to investigate an alternative liberated approach for subpopulations partition which is performed by means of neighboring landscape inspection.

Within proposed enhancement, the examination of the surrounding landscape essentially implies the verification of whether a pair of individuals tracks the same optimum or not. The method [4] takes a couple points as arguments and returns whether there is a valley between the two in the fitness landscape (they track different optima) or, on the contrary, they share a hill (individuals follow the same optimum). In order to reach a decision, a set of interior points between the two given variables is generated: if the fitness of all these is higher than the minimal fitness of the two tested individuals, then it is concluded that they track the same optimum. Conversely, if there exist such a point whose fitness is smaller than the minimal evaluation of the two, then it is assessed that they follow different peaks. The mechanism is described in Algorithm 3.

**Algorithm 3 Local landscape topology detection for two individuals x and y**

```
i = 1;
found = FALSE;
while i < number of gradations and not found do
    for j = 1 to number of dimensions do
        interior_j = x_j + (y_j - x_j) · gradation_j;
    end for
    if f(interior) < min(f(x), f(y)) then
        found = TRUE;
    end if
end while
return found;
```
Algorithm 4 TCGC liberated algorithm

\[ t = 0; \]
\[ \text{initialize population } P(t); \]
\[ \text{repeat} \]
\[ \text{for } i = 1 \text{ to } \text{pop\_size} \text{ do} \]
\[ \text{randomly choose an individual } P_i(t); \]
\[ M_i = \Phi; \]
\[ \text{for } j = 1 \text{ to } \text{pop\_size} \text{ do} \]
\[ \text{if } P_j(t) \neq P_i(t) \text{ then} \]
\[ \text{if } \text{landscape\_detect}(P_i(t), P_j(t)) = \text{false} \text{ then} \]
\[ M_i = M_i \bigcup \{P_j(t)\}; \]
\[ \text{end if} \]
\[ \text{end if} \]
\[ \text{end for} \]
\[ \text{if } M_i \neq \Phi \text{ then} \]
\[ \text{select an individual } x \text{ from } M_i; \]
\[ \text{recombine } P_i(t) \text{ and } x, \text{ obtain one offspring } y; \]
\[ \text{find worst individual } z \text{ such that} \]
\[ \text{landscape\_detect}(y, z) = \text{false} \text{ and } f(z) < f(y) \]
\[ \text{and then replace } z \text{ with } y; \]
\[ \text{else} \]
\[ \text{mutate } P_i(t) \text{ and obtain } y; \]
\[ \text{if } f(y) > f(P_i(t)) \text{ then} \]
\[ \text{replace } P_i(t) \text{ with } y; \]
\[ \text{end if} \]
\[ \text{end if} \]
\[ \text{end for} \]
\[ \text{repeat} \]
\[ \text{take every } x \in P(t) \text{ in turn;} \]
\[ S_x = \bigcup \{m_j\} \text{ individual } m_j \text{ in the merging region of } x \]
\[ \text{and } \text{landscape\_detect}(x, m_j) = \text{false}; \]
\[ \text{keep in the current population the best individual in } S_x; \]
\[ \text{until merging cannot be applied at all} \]
\[ t = t + 1; \]
\[ \text{until stop condition} \]

result of the adaptation to the surrounding landscape topology, the interaction between individuals sufficiently close to each other but actually following different peaks is of no further concern. On the parametrization level, two radii disappear, which is important not only from the perspective of an easy tuning of the algorithm, but also, and more significantly, from the performance point of view, i.e. in terms of independence and improvement.

IV. Experimental Results

The aim of experimentation is to validate TCGC as a viable alternative to CGC. In this respect, both methods are tested against the same test problems and within similar parameter tuning environments. The test functions to be maximized and chosen as follows: Two well-known trap functions for multimodal optimization problems – Central Two-Peak (F1, 1 global and 1 central local optimum) and Five-Uneven-Peak (F2, 2 global optima), the Himmelblau function (F3, 4 global optima), the Six-Hump Camel Back function (F4, 2 global and 4 local optima) and the Schaffer function (F5, 1 global optimum among many local comparative optima).

Proportional selection, mutation with normal perturbation and intermediary recombination are used for both methods [5]. In order to make the parameter setting as objective as possible, it is tried to remove human interaction. Therefore, some reasonable bounds for the values of all parameters that appear within CGC and TCGC are established and 30 different configurations are generated by means of Latin Hypercube Sampling (LHS). For each considered parameter setting, 30 repeated runs are performed and the average results are computed. It is only the results obtained in the first configuration out of the 30 different LHS settings that are finally reported. For both methods and for all test functions, the starting population size is 200, while the stop condition for all experiments is the number of generations, which is set to 150. Three parameters are generated via LHS for TCGC: The mutation probability, the mutation strength parameter and the merging radius. The number of interior points that are used for the local landscape topology detection mechanism is set to its default and cheapest value with respect to the budget of fitness evaluation calls, that is 1. In addition to the parameters also used by TCGC, there are two additional ones to be automatically generated for the standard CGC: The mating region radius and the replacement radius of the offspring. LHS determined parameter values for the two approaches are illustrated in Table I. Note that for some of the tested functions, several well-performing configurations are found for both techniques; however only the ones that reach convergence faster, i.e. in a smaller number of generations, are reported.

<table>
<thead>
<tr>
<th></th>
<th>CGC</th>
<th>F1</th>
<th>F2</th>
<th>F3</th>
<th>F4</th>
<th>F5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mutation probability</td>
<td>0.69</td>
<td>0.69</td>
<td>0.29</td>
<td>0.6</td>
<td>0.09</td>
<td></td>
</tr>
<tr>
<td>Mutation strength</td>
<td>0.11</td>
<td>0.11</td>
<td>0.49</td>
<td>2.04</td>
<td>1.57</td>
<td></td>
</tr>
<tr>
<td>Mating radius</td>
<td>1.17</td>
<td>1.17</td>
<td>0.26</td>
<td>2.77</td>
<td>3.1</td>
<td></td>
</tr>
<tr>
<td>Replacement radius</td>
<td>0.3</td>
<td>0.3</td>
<td>2.3</td>
<td>0.56</td>
<td>1.6</td>
<td></td>
</tr>
<tr>
<td>Merging radius</td>
<td>3.06</td>
<td>3.06</td>
<td>0.87</td>
<td>0.42</td>
<td>1.25</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>TCGC</th>
<th>F1</th>
<th>F2</th>
<th>F3</th>
<th>F4</th>
<th>F5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mutation probability</td>
<td>0.9</td>
<td>0.69</td>
<td>0.65</td>
<td>0.29</td>
<td>0.79</td>
<td></td>
</tr>
<tr>
<td>Mutation strength</td>
<td>0.38</td>
<td>0.11</td>
<td>0.99</td>
<td>0.48</td>
<td>0.99</td>
<td></td>
</tr>
<tr>
<td>Merging radius</td>
<td>2.45</td>
<td>1.17</td>
<td>0.27</td>
<td>0.26</td>
<td>0.09</td>
<td></td>
</tr>
</tbody>
</table>

It is interesting to observe that the newly proposed TCGC reaches the solutions in a faster manner: The average number of optima detected out of the 30 repeated runs of the same parameter setting, in each generation and for each of the two compared methods, were computed to prove it and Figure 1 plots the obtained results. Function F1 is the only one for which CGC reaches the two actual optima quicker than TCGC, although the latter had a better start in the initial generations. However, for F2, CGC finds only 4.66 out of the 5 optima, while TCGC reaches all of them and, at any generation during the entire evolution, it takes the lead. The same situation happens for function F3, where the four optima seem to be detected more rapidly by the newly adopted method (in less than 100 generations, while for CGC about 140 are necessary). Very important differences can be noticed for F4, where none of the two methods finds all the 6 optima, given the parameter constraints that are imposed for this experiment: However, TCGC undoubtedly dominates CGC during the
Fig. 1. Number of optima detected by CGC and TCGC from the first
generations to the last, computed in average for the most prolific configuration.

whole evolutionary process and it finally reaches 5.2 solutions,
while the latter discovers only 3.33. However, by increasing
the amount of interior points up to 14, the results of TCGC
were significantly improved (Figure 2 and Figure 1). Both
approaches find the desired solution for the last function,
again with an advantage on the TCGC side with respect to
convergence speed.

Fig. 2. Number of solutions found for $F_4$ when different number of interior
points are considered for investigating the space topology within TCGC.

Figure 3 shows how the population size shrinks over the
generations for $F_3$ and $F_5$, where the trend was not similar
for both approaches: It has been again computed as an av-
erage over 30 repeated runs of the same parameter setting.
It drastically decreases for CGC in the initial generations
and then remains constant until the stop condition is met.
By confronting the sections corresponding to function $F_3$ in
Figures 1 and 3, it may be concluded that a better equilib-
rium is maintained within the population for TCGC; besides
the required similarity below the given threshold, merging
takes place only after the verification of the membership of
all individuals to the attraction basin of the same optimum
is performed. The fact that recombination takes place only
between individuals that track a common peak may also have
an important influence upon population dynamics. Conversely,
a potential high value for the mating radius within CGC
conducts towards the recombination of different individuals,
regardless of the fact that they follow the same optimum or
not. At the same time, the population size tends to come closer
to the desired number of solutions for TCGC, and that can be
observed especially for $F_5$ in Figure 3.

Fig. 3. Population dynamics over the generations for $F_3$ and $F_5$ functions.

V. CONCLUSIONS

There are several significant aspects of the novel proposed
topological alternative to crowding genetic chromodynamics.
The mating region of an individual is now determined by a
pool of points that are found to lie in the same attraction basin
as the current one. Therefore, regardless of the sizes of the
basins of attraction of the different optima or the existence of
plateaus in the fitness landscape, TCGC prevents the establish-
ment of more subpopulations connected to the same peak on
the one hand, and of having a subpopulation with individuals
that track different peaks, on the other hand. The replacement
area of an offspring is represented by the individuals that
are verified to follow the same peak as the descendent. This
inhibits the eventuality that the descendent might migrate to
an adjacent subpopulation. Merging is further supported by
an additional confirmation that all envisaged individuals track
the same optimum. Only inhabitants of the same attraction
basin can be united and thus neighboring subpopulations may
further diverge. The complexity of parametrization is consid-
erebly reduced and performance dependence on appropriate
parameters is also resolved.

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