A comparative study on the application of advanced bacterial foraging models to image registration

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ABSTRACT

New swarm intelligence approaches as the Bacterial Foraging Optimization Algorithm (BFOA) have recently awakened a growing interest in the evolutionary computation community. This fact is due to the promising results obtained by different variants of the latter optimization method in many real-world applications. In this work we aim to take a step ahead in the development of the discipline by introducing a large amount of BFOA variants resulting from the combination of some advanced design decisions applied on Dasgupta et al.'s self-adaptive version. Our goal is thus to achieve an improved understanding of the good properties that the BFOA approach has shown in previous contributions. We will perform an extensive experimental study considering a plethora of algorithmic variants to solve a real-world problem, image registration, a well-known and complex task in computer vision. In particular, more than fifty variants are proposed and tested tackling pairwise image registration problem instances from two different domains, namely range image registration for 3D model reconstruction and 3D medical image registration. The reported results reveal that BFOA is a versatile approach able to provide very competitive outcomes to face challenging real-world image registration problems when compared to the state-of-the-art evolutionary approaches in the field.

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1. Introduction

During the last two decades, natural swarm inspired algorithms like Particle Swarm Optimization (PSO) or Ant Colony Optimization (ACO) have proven their effectiveness in the fields of Computational Intelligence and Metaheuristics [27]. Following the same trend of swarm-based algorithms, Passino proposed the Bacterial Foraging Optimization Algorithm (BFOA) in [50]. The key idea of this novel algorithm is the application of the foraging strategy of the *Escherichia coli* bacteria in multi-optimal function optimization. The main objective of this bacteria foraging strategy is to maximize the energy obtained per unit time while searching for nutrients. Individual bacteria also communicate with others by sending signals. A bacterium takes foraging decisions after considering the two latter factors. The process, in which a bacterium moves by taking small steps while searching for nutrients, is called chemotaxis and the key idea of BFOA is mimicking the chemotactic movement of virtual bacteria in the problem search space. This swarm intelligence method has already drawn the attention of researchers because of its efficiency when solving real-world optimization problems arising in several application domains [14,37].

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Unlike the inspiration source followed by other evolutionary-based approaches, the underlying biology behind the foraging strategy of *E. coli* is emulated in an extraordinary manner and used as a simple optimization algorithm.

BFOA methods have been applied to many real world problems and proved their effectiveness over many variants of Genetic Algorithms (GA) and PSO [44]. For example, Dasgupta et al. proposed a pattern recognition application for the automatic detection of circular shapes based on BFOA [24]. Acharya et al. proposed a BFOA-based Independent Component Analysis [1] to find a linear representation of non-gaussian data where the components are statistically independent. Wan et al. presented a clustering algorithm based on the mechanism analysis of BFOA [67], which outperforms similar algorithms based on ACO and PSO. Besides, El-Abd performed a comparison between some foraging algorithms, including BFOA, and different evolutionary algorithms using a set of benchmarking functions [26].

Meanwhile, image registration (IR) [56,72] is a fundamental task in CV that aims at finding the optimal transformation between two (or more) images acquired under different conditions: using different sensors, at different time instances, from different viewpoints, or a combination of the latter situations. Such transformation estimation is formulated as an optimization problem where the degree of resemblance between images is measured by a similarity metric. The local optimization process applied by traditional IR methods, e.g. the Iterative Closest Point (ICP) algorithm [7,71], is highly influenced by image noise, discretization, and misalignment, among others. Nevertheless, evolutionary algorithms (EAs) [2,25] have demonstrated their ability to overcome some of the shortcomings of traditional IR methods, achieving a robust performance in some complex IR domains [21,57].

In order to establish a better comprehension of the BFOA optimization properties, we propose a large amount of advanced variants and study their performance to deal with IR, which is suitable for applying EAs and other real-coded metaheuristics. Thereby, we introduce and combine a set of advanced design decisions with the purpose of improving the performance of the standard BFOA proposals in the literature, specifically the self-adaptive version proposed by Dasgupta et al. [23].

Our aim is to test the different BFOA configurations performance in two different application domains, range image registration (RIR) for 3D model reconstruction, and 3D medical image registration (MIR), thus providing a general view of its behavior in these fields. To do so, we provide a broad experimentation comparing the proposed BFOA variants performance to the classical IR method, ICP, and other evolutionary and metaheuristic IR methods of the state-of-the-art.

This contribution is structured as follows. Section 2 is aimed to introduce the basis of BFOA and the two IR problem domains considered, 3D model reconstruction from range images and 3D MIR. Next, Section 3 describes the application of the different BFOA variants to tackle the latter two IR problems. Section 4 introduces the developed experimental study for RIR applications, while Section 5 presents the experimental study for MIR applications. Section 6 provides a combined analysis of the behavior of BFOA variants for both applications. Finally, Section 7 draws some conclusions and future lines.

2. Background

2.1. The bacterial foraging algorithm

The pseudocode of BFOA is described in Algorithm 1, as proposed in [50]. The method consists of the following four steps:

2.1.1. Chemotaxis
This process simulates the foraging behavior of the bacteria according to movements in two different ways. Depending on the food concentration, the bacterium will swim in the same direction or it will tumble to change its current direction for a period of time. Mathematically, $\theta^i(j, k, l)$ represents the ith bacterium in the jth chemotactic, kth reproductive, and lth elimination and dispersal phases. The tumble movement is modelled as in [50]:

$$\phi(i) = \frac{\Delta(i)}{\sqrt{\Delta(i)^T \Delta(i)}} \tag{1}$$

where Δ indicates a random vector whose direction lies in the range $[-1, 1]$. Thus, the chemotactic step is defined as:

$$\theta^i(j + 1, k, l) = \theta^i(j, k, l) + C(i)\phi(i) \tag{2}$$

where $C(i)$ represents the step size taken during the swim step.

2.1.2. Swarming
A social behavior is simulated in this stage. Those bacteria placed in locations with high amount of nutrients tend to attract other bacteria, while those placed in hazardous zones tend to repel them. This cell to cell attraction–repulsion behavior is modelled as follows:

$$J_{cc}(\theta, P(j, k, l)) = \sum_{i=1}^{S} J_{cc}(\theta, \theta^i(j, k, l))$$
$$= \sum_{i=1}^{S} \left[-d_{attract} \exp\left(-w_{attract} \Sigma_{m=1}^{p} (\theta_m - \theta_m^i)^2 \right) \right] + \sum_{i=1}^{S} \left[-h_{repell} \exp\left(-w_{repell} \Sigma_{m=1}^{p} (\theta_m - \theta_m^i)^2 \right) \right] \tag{3}$$