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# Biological image processing via Chaotic Differential Search and lateral inhibition

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#### ABSTRACT

In this paper, we propose a hybrid biological image processing approach, which is based on Chaotic Differential Search (CDS) algorithm and lateral inhibition (LI) mechanism. We named this hybrid biological image processing approach as LI-CDS. Differential Search (DS) algorithm is a new bio-inspired optimization algorithm mimicking the migration behavior of an organism, and has been successfully used for solution of coordinate system transformation. The property of chaotic variable is integrated into DS to improve its search strategy so that it can escape from the local optimum. Furthermore, lateral inhibition mechanism, which is verified to have good effects on image edge extraction and image enhancement, is employed to pre-process images involved. In this hybrid biological image processing mechanism, our proposed LI-CDS method incorporates both advantages of chaos theory and lateral inhibition mechanism. Series of comparative experimental results by using LI-CDS, DS, CDS and Particle Swarm Optimization (PSO) demonstrate that the proposed LI-CDS performs better than the other three methods.

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#### 1. Introduction

As an important issue in image processing, image matching is a technique to find existence of a pattern within a given image. Image matching methods can be classified as statistics based technique and features based technique [1]. The former technique can be considered as an optimization process of finding the maximum similar degree between a pattern and a template. The later is based on the image features, e.g., border, texture, and entropy, according to specific applications. Statistics based technique is widely used in practice of matching complex images as it is independent from extensive feature extractions [2]. However, the statistic based matching process can be time-consuming since it needs to calculate the similar degree between the template and all possible positions in the original image to find a desired pattern. To address this problem, some biological image matching methods come into being.

Biological image matching is a novel multi-disciplinary field in image processing, in which bio-inspired mechanisms or algorithms are adopted. Recently, many bio-inspired computing methods have been investigated [3], and applied as the searching strategy in the

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statistics based image matching, e.g., Particle Swarm Optimization (PSO) [4], biogeography-based optimization (BBO) [5], and imperialist competitive algorithm (ICA) [6]. Inspired by the individual or social behaviors of the living beings to search the global optimal, these algorithms are successful in solving the image matching problems. However, the matching processes of these algorithms suffer from high computational complexity and long computing time.

Differential Search (DS) algorithm is a new bio-inspired optimization algorithm proposed by Pinar Civicioglu to transform geocentric Cartesian coordinates to geodetic coordinates [7], and its performance are proved to be better than all classical methods by series of comparative experiments and statistical tests. DS simulates the Brownian-like random-walk movement used by an organism to migrate. In the basic DS algorithm, a superorganism (suporg) contains large number of individuals of an organism and migrates to global optimum value of a problem. Each individual of a superorganism, representing a feasible solution, migrates from generation to generation independently until the best solution is found. DS has a successful search strategy for solution of multimodal function because it can simultaneously use huge amounts of individuals and has no inclination to correctly go toward the best possible solution [7]. Furthermore, DS has only two control parameters and it is easy to program.

Although DS has a very fast convergence speed, sometimes it may result in relapses into a local optimal situation. In this paper, chaotic search strategy is introduced into Differential Search (CDS) to improve its population diversity and exploration ability. In





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addition, lateral inhibition (LI) approach is utilized to pre-process the template and original images before using CDS for matching (LI-CDS). Lateral inhibition is firstly discovered by Hartline et al. in studying of the eyes of limulus [8]. By numerous researches, lateral inhibition mechanism has been certified to be effective in image enhancement and edge extraction, which can increase the accuracy of image matching [9,10]. The proposed LI-CDS inherits both advantages of chaotic search strategy and lateral inhibition approach, proved to perform quite well in biological image matching.

The rest of this paper is organized as follows. Section 2 introduces the basic principles of DS and its improved version CDS algorithm. The mechanism of lateral inhibition is described in Section 3. Section 4 details the implementation procedures of the hybrid biological method LI-CDS. Two groups of comparative experiments with other three algorithms are conducted in Section 5. Concluding remarks are given in the final section.

#### 2. Differential Search algorithm

#### 2.1. The basic principle of DS

DS algorithm is a new and effective bio-inspired evolutionary algorithm, inspired by seasonal migration behavior of many species of the living beings in the nature [7]. In DS algorithm, the migrating species constitute a *superorganism* containing lots of individuals, which represent a population of possible solutions of an optimization problem. Movement of a *superorganism* can be modeled as Brownian-like random walk, while capacity and fertility of each area is quantified by the fitness function depending on practical problems. During this migration, individuals of the *superorganism* test whether some randomly selected positions can meet needs of them at the moment. If such a position is tested to be suitable temporarily, they immediately settle at the discovered site and continue their migration by moving toward areas with better fitness. In this way, the *superorganism* explores the feasible solution space for the global optimum value.

In DS algorithm, individuals of a *superorganism* (i.e.,  $X_i$ ,  $i = \{1, 2, 3, ..., N\}$ , where *N* is the size of a population) are defined according to the respective problem (i.e.,  $x_{i,j}$ ,  $j = \{1, 2, 3, ..., D\}$ , where *D* is the dimension of a problem). Individuals of the *superorganism* (i.e., *suporg*<sub>g</sub>, g = 1, 2, 3, ..., NCmax) are initialized easily by using Eq. (1).

$$\begin{cases} x_{i,j} = rand \cdot (up_j - low_j) + low_j \\ X_i = [x_{i,j}] \\ Suporg_g = [X_i] \end{cases}$$
(1)

where  $up_j$  and  $low_j$  are the limits of the search space. A *stopoversite* (*stopsit*) position where each randomly selected individual searches for is produced by Eq. (2).

$$stopsit = suporg + Scale \times (Donor - suporg)$$
 (2)

where *Scale* is generated by using a random number generator working in the scope of [0,1] and controls the size of the change occurred in the current position. *Donor* is defined as follows:

$$Donor = [X_{Random\_shuffling(i)}]$$
(3)

The *Random\_shuffling* function randomly changes the sequence of the elements in the set of  $i = \{1, 2, 3, ..., N\}$ , and plays an important role in DS algorithm.

One of the advantages of DS algorithm is that DS uses a large quantity of individuals in search process simultaneously. Each individual independently searches every *stopoversite* throughout the solution space, and if finds a more promising *stopoversite*, it will move there instead of the prior one. By this mechanism, the *superorganism* migrates toward the optimal solution of the problem. Structure of this algorithm is fairly simple, which is another advantage of DS. There are only two control parameters (i.e.,  $p_1$  and  $p_2$ ), which are problem dependent. The main steps involved in DS are described as follows:

**Step 1**: Initialize the parameters of the algorithm, including the size of the population N, the dimension of the problem D, control parameters  $p_1$ ,  $p_2$ , and the maximum number of generation *NCmax*. Generate a *Scale*.

**Step 2**: Produce the initial position of each individual in *superorganism* according to Eq. (1).

**Step 3**: Calculate the fitness value of each position according to the fitness function.

**Step 4**: *superorganism* starts to migrate by a Brownian-like random-walk model, which can be described as Eqs. (2) and (3). **Step 5**: If the fitness value of the searched *stopoversite* is better than the current one, update *superorganism* with *stopoversite* and continue migration toward the global maximum.

**Step 6**: If the number of current generation goes beyond the maximum number of generation (i.e., *NC* > *NCmax*), output the results. Otherwise, go to **Step 4** for the next migration.

#### 2.2. The Chaotic DS algorithm

Although the basic DS algorithm can achieve its objective and the degree of its effectiveness has been proved higher than PSO by some experiments in Section 5, there are still some constraints that handicap DS to perform very well. Sometimes, in basic DS algorithm, fast convergence may occur in the first few generations, which lead to relapses into a local optimum. In this paper, we introduce the chaotic search strategy into DS to improve its performance for image matching.

Chaos is a phenomenon that has already been observed in a variety of nonlinear dynamical systems in the laboratory. Chaos theory was epitomized by the butterfly effect in *Deterministic Nonperiodic Flow* by Edward Lorenz, then developed to what is considered as the third most important discovery in the 20th century after relativity and quantum mechanics [11]. Until now, Chaos theory has been applied to a lot of fields such as ecology, politics, and economics. Chaos is the highly unstable action of complex nonlinear deterministic systems, which are extremely sensitive to initial conditions, in finite phase space [12]. The chaotic movement ergodic characteristics are identified by the following simple and well-known nonlinear mathematical model, i.e., the logistic equation:

$$x_{n+1} = k x_n (1 - x_n) \tag{4}$$

where,  $x_n$  signifies chaotic variable, and k is the parameter can control the system states. When  $x_n$  is distributed in [0, 1], at the same time k = 4, the track of chaotic variable can be of randomness and ergodicity, and not be repeated over the whole space [13]. Chaos is a motion between certainty and randomicity, transferring from ordered state into a disordered state suddenly, but there is a delicate inherent rule in the confusion state. Therefore, in the CDS algorithm, the ergodicity and irregularity of chaotic variable is used to initialize *superorganism* and produce the control parameter *Scale* in each generation, which can help the algorithm to jump out from a local optimum and converge to the global optimum in a faster manner. So in this paper, we make use of chaotic variable to initialize the initial points of *superorganism* according to Eq. (5).

$$\begin{cases} x_{i+1,j} = 4 \cdot x_{i,j}(1 - x_{i,j}) \\ X_i = [x_{i,j}(up_j - low_j) + low_j] \\ suporg_g = [X_i] \end{cases}$$
(5)

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