

Species Based Evolutionary Algorithms for Multimodal Optimization: A Brief Review

Jian-Ping Li, Xiao-Dong Li and Alastair Wood

Abstract—The species conservation technique is a relatively new approach to finding multiple solutions of a multimodal optimization problem. When adopting such a technique, a species is defined as a group of individuals in a population that have similar characteristics and are dominated by the best individual, called the species seed. Species conservation techniques are used to identify species within a population and to conserve the identified species in the current generation. A ‘species-based evolutionary algorithm’ (SEA) is the combination of a species conservation technique with an evolutionary algorithm, such as genetic algorithms, particle swarm optimization, or differential evolution. These SEAs have been demonstrated to be effective in searching multiple solutions of a multimodal optimization problem. This paper will briefly review its principles and its variants developed to date. These methods had been used to solve engineering optimization problems and found some new solutions.

Keywords - Species conservation technique, species optimization, evolutionary computation, genetic algorithm.

I. INTRODUCTION

Many real-world optimization problems are multimodal by nature, where many equally good solutions exist. Finding multiple solutions can help designers to understand the design space more thoroughly and to create alternative designs to satisfy design requirements.

Nature has inspired the development of many computational models, amongst which Evolutionary Computation (EC) is a good example. Even though the majority of EC algorithms are specifically designed for locating a single global optimum, there are many techniques that have been developed to solve multimodal optimization problems:

- iterative methods address the problem of locating multiple optima of a multimodal function by repeatedly applying the same optimization algorithm. Several techniques have been used to avoid iterations towards local minima, such as the tabu technique [1], the Sequential Niche technique [2] and jump techniques [3];
- explicit parallel sub-population methods attempt to produce multiple solutions to a multimodal optimization

problem by dividing a population into sub-populations that evolve in parallel, such as Multiple-National GA [4], Island Gas [5], the Adaptive Isolation Model [6], and Particle Swarm Optimization [7]. Without communications among the populations, these methods are similar to iterative methods;

- implicit parallel sub-population methods attempt to produce multiple solutions by introducing niche/speciation techniques so that a population diversity is maintained and many niches survive in a single population, such as crowding ([8], [9]), fitness sharing ([10]-[11]), restricted tournament selection [12] and species conservation techniques [13], Genetic Sampler [14]. The crowding and fitness sharing are well-known methods but cannot guarantee that all niches survive in a new population.

Species conservation is a relatively new technique for solving multimodal optimization problems [13] and has been proved to be effective to obtain multiple solutions of tested multimodal problems. In a recent work by Stoean *et al.* [15] it was shown that the species conservation algorithm can efficiently keep track of several good search space regions at once.

The aim of this paper is to introduce the basic principles of species conservation techniques and briefly review the progress of research in this area. This paper is constructed as follows: Section 2 defines the concept of species. Section 3 and 4 present some species-based evolutionary algorithms. Section 5 summarizes the performance of species conservation techniques. Finally, some conclusions are presented in Section 6.

II. SPECIES CONCEPT

A. Species with Fixed Species Distance

Species conservation techniques are based on the species concept. A species is defined as a group of individuals in a population that have similar characteristics and are dominated by the best individual, called the *species seed*. A species will depend on a parameter, called the *species distance* and denoted by σ_s

The distance between two individuals $\mathbf{x}_i = [x_{i1}, x_{i2}, \dots, x_{in}]$ and $\mathbf{x}_j = [x_{j1}, x_{j2}, \dots, x_{jn}]$ can be defined by the Euclidean distance:

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J.-P. Li is with School of Engineering, Design and Technology, University of Bradford, United Kingdom (corresponding author; tel.: +44-1274234539; e-mail: j.p.li@bradford.ac.uk).

X.-D. Li is with School of Computer Science and Information Technology, RMIT University, Australia (e-mail: Xiaodong.li@rmit.edu.au).

A.S. Wood is with School of Engineering, Design and Technology, University of Bradford, United Kingdom (e-mail: a.w.wood@bradford.ac.uk).

$$d(\mathbf{x}_i, \mathbf{x}_j) = \sqrt{\sum_{k=1}^n (x_{ik} - x_{jk})^2} \quad (1)$$

This is not the only way in which the distance between two individuals represented by vectors of real numbers can be defined. Sometimes, the distance term can be defined according to specific domain knowledge ([17]-[18]).

Intuitively the similarity threshold specifies the upper bound on the distance between two individuals for which they are considered to be similar. In the approach the similarity threshold will also be used to determine which individuals are worth preserving from one generation to the next.

A species is defined with respect to a finite population $P_N = \{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N\}$ and the best individual in the species is called its *species seed*, which dominates all the individuals in the species. Briefly, a species S_i is centered upon its dominating individual (the species seed) \mathbf{x}^* if, for every individual $\mathbf{y} \in S_i$,

$$d(\mathbf{x}^*, \mathbf{y}) < \sigma_s / 2 \quad (2)$$

and

$$f(\mathbf{y}) \leq f(\mathbf{x}^*) \quad (3)$$

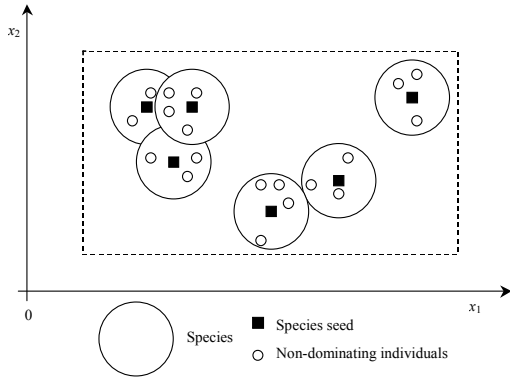


Fig. 1 A sample distribution of species in a two-dimensional domain.

Fig. 1 illustrates a sample distribution of species in a two-dimensional domain. A species is formed of actual individuals and occupies a region of the feasibility domain.

B. Adaptive Species

Without prior knowledge of a problem, it is impossible to choose a single value of niche radius/species distance for all species [2], since species in a problem will not, in general, be the same size. To overcome the dilemma of selecting a suitable species distance, some researchers are studying adaptive techniques. Bird and Li [19] used the average distance among members in a population as its ‘species’ radius so that no species radius parameter needs to be specified by users. Parmee [20] proposed a Cluster Oriented Genetic Algorithms (COGA) to identify high-performance regions of complex designs rather than to explore all solutions. Yao *et al.* [21] developed a Recursive Middling Algorithm to detect if there is a valley between two given

points, in which there are three clustering actions: *migration*, *splitting*, and *merging*. Hua *et al.* [22] proposed a Detecting Peak's Number (DPN) technique to explore new possible species by using heuristic methods to check each orthogonal direction from an individual.

Li and Wood ([23] and [24]) developed an adaptive species concept, which we will describe as follows.

Adaptive species, denoted by $\mathbf{s}(\mathbf{x}, r_x, f_x^b)$, was defined with: *species seed* (\mathbf{x}), *species radius* (r_x) and *species boundary fitness* (f_x^b). Again, a *species* is dominated by its *species seed* and is centered upon the species seed \mathbf{x} . For any points $\mathbf{y} \in \mathbf{s}(\mathbf{x}, r_x, f_x^b)$ and $\mathbf{z} \in \mathbf{s}(\mathbf{x}, r_x, f_x^b)$, we have

$$\begin{aligned} \frac{f(\mathbf{y}) + f(\mathbf{z})}{2} &< f\left(\frac{\mathbf{y} + \mathbf{z}}{2}\right) \\ f(\mathbf{y}) &\leq f(\mathbf{x}) \\ d(\mathbf{x}, \mathbf{y}) &\leq r_x \\ f(\mathbf{y}) &\geq f_x^b \end{aligned} \quad (4)$$

In this definition of species, there is one more parameter. However, the new species definition aims to develop some algorithms to automatically adjust those parameters.

It is assumed that the fitness (objective) function is symmetric to the species seed within the species domain. A typical species in one-dimensional space is shown in Fig. 2 d_x^n represents the distance between the species seed and the nearest neighbor species seed.

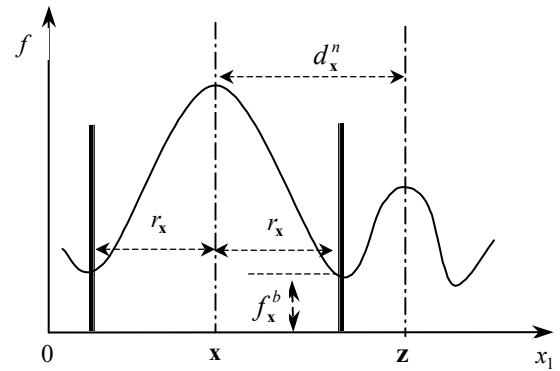


Fig. 2 Distributions of species in one-dimensional space.

From the optimization point of view, a species is an area occupied by a local optimal solution. Its species seed is the local optimal solution and so there is only one peak in a species. The maximum number of species is equal to the number of local (including global) solutions of the problem, while in the definition of adaptive species there may be more than one peak in a species, defined by using a fixed *species distance* (σ_s).

From the genetic algorithm point of view, an adaptive species is a group of individuals that have similar characteristics. Let s_1, s_2, \dots, s_k be a partitioning of a feasible region into species. Each species has its own parameters. To illustrate this, Fig. 3 shows a possible distribution of species in a two-dimensional domain. There are some intersections and spaces among species, because a species is defined by a radius. Therefore, the *union* of all species sets is part of the feasible region of a problem.

$$\bigcup s_i \in R \quad (5)$$

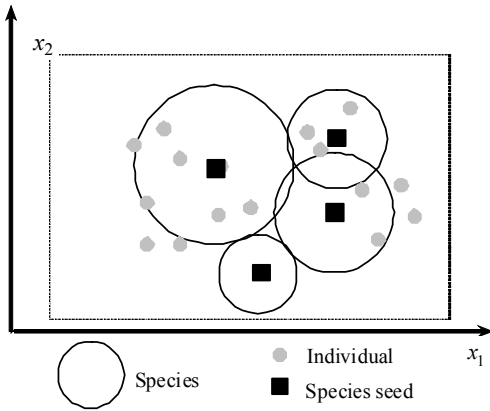


Fig. 3 Definition of a species.

III. SPECIES-BASED EVOLUTIONARY COMPUTATIONS WITH FIXED SPECIES DISTANCE

A. Species Conserving Genetic Algorithm

Begin

```

t = 0;
Initialize G(t);
Evaluate G(t);
while (not termination condition) do
    Determine species seeds Xs;
    Select G(t+1);
    Crossover G(t+1);
    Mutate G(t+1);
    Evaluate G(t+1);
    Conserve species from Xs in G(t+1);
    t = t + 1;
end (while)
Identify global optima;

```

end

Fig. 4 The structure of the SCGA

In a Species Conserving Genetic Algorithm (SCGA) [13], the population is divided into several species according to their similarity and each of these species is built around a dominating individual/species seed. Species seeds found in the current generation are conserved by moving them into the next generation. The GA using species conservation is based on the structure of a classical Simple GA (SGA) and is shown in Fig. 4 .

The only significant differences between the SCGA and the SGA are (i) that, within the generation loop, first the species seeds are determined, and (ii) that, after the genetic operators (selection, crossover, mutation) have been applied and the population evaluated, the species conservation process is performed. In the above algorithm X_s denotes the set of species seeds found in the current generation, $G(t)$.

There are three special procedures in SCGA:

- Determine species seeds: This procedure is developed to determine species seeds from a current population.
- Conserve species seeds: The new generation is constructed by applying the usual genetic operations: selection, crossover and mutation and by “copying” the found species into the population to keep its diversity.
- Identify global solutions: The global solutions are the most fit individual in X_s (the species seed set) and all the individuals in X_s that have a fitness “close to” the maximal fitness. For this purpose a *solution acceptance threshold* r_f ($0 < r_f \leq 1$) is introduced and an individual in X_s will be identified as a solution, which satisfies the following inequality:

$$f(\mathbf{x}) \geq f_{\max} \times r_f \quad (6)$$

The above SCGA has been shown to be effective to find all the global solutions of tested multimodal functions. But it is not very efficient for higher dimensional problems. Dong *et al.* [25] presented a mixed mutation strategy of five different mutations (Gaussian, Cauchy, Levy, single-point, and chaos mutation) by combining them with the SCGA to improve performance of the SCGA in searching multiple solutions. The authors claimed that this mixed mutation strategy is superior to any pure mutation strategy.

Im *et al.* [26] presented a “restricted evolution” concept and proposed a related algorithm for multimodal optimization. Actually, the restricted evolution is very similar to the above species.

B. Species-based Particle Swarm Optimisation

Particle swarm optimization, originally proposed by Kennedy and Eberhart [7], is inspired from the metaphor of social interaction observed among insects or animals. The population is consisted of particles. Each particle “flies” though the search space, depending on two important factors: the personal best position (pbest) \mathbf{p}_i found by the current particle and the global best position (gbest) \mathbf{p}_g identified from the entire population. The rate of position change of i-th particle is given by its velocity \mathbf{v}_i calculated by the following equation:

$$v_{id}(t) = \chi |v_{id}(t-1) + \varphi_1 [p_{id} - x_{id}(t-1)] + \varphi_2 [p_{gd} - x_{id}(t-1)]| \quad (7)$$

$$x_{id}(t) = x_{id}(t-1) + v_{id}(t) \quad (8)$$

where:

$$\chi = \frac{2}{2 - \varphi - \sqrt{\varphi^2 - 4\varphi}} \quad \text{and } \varphi = \varphi_1 + \varphi_2, \quad \varphi > 4.0$$

Using the above species conservation technique, Parrott and Li ([26]-[29]) proposed the following species-based particle swarm optimization (SPSO):

- 1) Generate the initial particles,
- 2) Evaluate all the particles in the population,
- 3) Sort the particles in descending order of their fitness values,
- 4) Determine species from the current particles.
- 5) Assign to each member of a species its 'local' gbest (ie., the species seed) to all the individuals in that species,
- 6) Adjust particle position by using equation (7) and (8),
- 7) Go back to step (2), unless the termination condition is met.

The same procedure of identifying species developed in Li *et al.* [13] is adopted. Species seed set S is initially set to ϕ . All the particles are checked in turn against the species seed found so far. If a particle does not fall within the radius r_s of all the seeds, then the particle will become a new seed. There is no need to pre-specify the number of species seeds. They are automatically generated during a run. Particles from each identified species follow a chosen neighborhood to move towards a promising region of the search space. Multiple species are able to converge towards different optima in parallel without interference.

Yuan *et al.* [30] modified the SPSO and proposed a multi-scale PSO (MPSO) algorithm in which particles are dynamically divided into several subgroups of different size in order to explore variable space using various step sizes simultaneously. This increases the possibility of finding more global solutions. In order to divide a particle into several subgroups, authors introduced another three parameters: a *minimum distance* between new seeds and the seed of subgroup, *max number and min number* of subgroups in the population, respectively *MINDIS*, *MAXSPEC* and *MINSPEC*. Özcan and Yılmaz [31] proposed a PSO with Crazyness and Hill Climbing (CPSO) using the similar idea of the MPSO. The main swarm is divided into sub-swarms of size n according to their geographical positions. The CPSO uses a random walk component and a hill climber to enhance the exploration and exploitation capabilities of PSO, respectively.

Parrott and Li [32] presented an extension to a speciation-based particle swarm optimizer (SPSO) to improve performances in dynamic environments. This improved SPSO adopted several proven useful techniques: limiting the number of particles in a species, quantum swarm, replacing the worst species and particle diversification within a species. These techniques can further improve SPSO's adaptability in maintaining a good balance between convergence and diversity within each species.

Iwamatsu [33] proposes a multi-species particle swarm optimizer (MSPSO) for locating all the global minima of multi-modal functions by spatially dividing the partial swarm into a multiple cluster, called a species, in a multi-dimensional search space. Each species explores a different area of the search space and tries to find the global solution or local solution of that area.

k -means particle swarm optimization (k PSO) [34] uses the k -means clustering algorithm to identify niches and the Bayesian information criterion to determine the number of clusters. Each sub-swarm created by the clustering process performs a local search with the same efficiency as the standard PSO. The authors claimed that k PSO is better than the SPSO, in term of the number of function evaluations needed to discover all the optima of the test functions. However, the computational cost of the clustering procedure in k PSO is higher than that of SPSO.

In order to let particles move towards different global solutions, the local best is replaced with a nearest species and the global best is replaced with a local global best, the new velocity update formula is modified and a Species Conserving Particle Swarm Optimization (SCPSO) was developed[35]. A particle's velocity is influenced by its nearest species and the nearest global solution. Numeric examples illustrate that the proposed SCPSO can comfortably outperform other related existing algorithms.

C. Species-based Differential Evolution

Differential evolution (DE) is a relatively new optimization technique compared with other established evolutionary computations, such as genetic algorithm, evolutionary strategy and genetic programming. The basic differential evolution algorithm was described in [36].

In the DE initial population, each vector/ individual \mathbf{x} is generated by the sampling along each dimension of the variable vector a random value uniformly between the lower and upper bounds of the variable range. An offspring is then generated after initialization, according to the following procedure shown in Fig. 5 .

```

Randomly select parents
 $r_1, r_2, r_3 \in \{1, 2, \dots, m \mid r_1 \neq r_2 \neq r_3 \neq i\}$ 
 $j_{rand} = \text{int}[U([0,1] \cdot m) + 1]$ 
For  $j=1$  to  $m$  do
    If  $U[0,1] < CR$  or  $j = j_{rand}$  then
         $x_j^{(i,t+1)} = x_j^{(r3,t+1)} + F \cdot [x_j^{(r1,t+1)} - x_j^{(r2,t+1)}]$ 
    Else
         $x_j^{(i,t+1)} = x_j^{(i,t+1)}$ 
    End if
End for

```

Fig. 5 Differential Evolution

The above procedure is applied to all individuals of the current population for generating the next population. The

population size must be greater than 3. CR and F are user-specified control parameters, ranging from [0,1] and (0,1) respectively.

Species-based Differential Evolution (SDE) [37] which makes use of the algorithm for determining species in conjunction with a basic DE can be used effectively to solve multimodal optimization problems. The procedure can be summarized as follows:

- 1) Generate an initial population.
- 2) Evaluate all individuals in the population.
- 3) Sort all individuals in descending order of their fitness values.
- 4) Determine the species seeds for the current population.
- 5) For each species as identified via its species seed, run a basic DE.
- 6) Keep only the n fitter individuals from the combined population.
- 7) Go back to step 2, unless the termination criteria are met.

Note that in Step 5, it is possible that an identified species has less than 3 individuals. If so, some new individuals are generated randomly within the radius of species seed and added to that species so that no species has less than 3 individuals.

Due to SDE takes a long time for complicated problems to acquire all global optima, Shibasaka *et al.* [38] proposed a SDE with switching search strategies. This method switches global search and local search so that the species will not be extinguished and the stagnation of evolution will not occur.

D. Species Conservation Stochastic Optimization

The species conservation technique can be combined with a simple random optimization. This method was called as species conservation stochastic optimization (SCSO) [41] and its population size is one. The structure of the SCSO is shown as:

The results demonstrate that the proposed SCSO is able to locate all the global solutions of the test functions and seems to be more efficient than existing species conservation techniques for multimodal optimizations.

```

Begin
  Randomly initialize  $\mathbf{x}$  and  $X_s = \phi$ ;
   $X_s \leftarrow \mathbf{x} \cup X_s$ 
  while (not termination condition) do
    Randomly select  $\mathbf{x}$  from  $X_s$ ;
    Generate a random vector  $\mathbf{r}$ ;
     $\mathbf{x} \leftarrow \mathbf{x} + \mathbf{r}$ 
    Update species  $X_s$ ;
  end do
  Identify global optima;
end

```

Fig. 6 Structure of the Stochastic approach with species conservation

IV. ADAPTIVE SPECIES CONSERVATION GENETIC ALGORITHM

An adaptive species conservation [24], which can adjust the parameters (see Section II) of each found species, makes species to be adaptive to a problem and is integrated with a conventional genetic algorithm to search multiple solutions of the problem. The structure of the Adaptive Species Conservation Genetic Algorithm (ASCGA) is illustrated in Fig. 7. Users do not need to set any parameters and the programs can automatically adjust the parameters of each species, therefore, species will be adaptive to a problem. Experimental results demonstrate that this ASCGA is capable of finding the global and local optima of test multimodal optimization problems with a higher efficiency than methods from the literature.

```

Input: Optimization problem
Output: solutions
Begin
   $S(0) \leftarrow \phi$ 
  Initialise  $G(t)$ ;
  Evaluate  $G(t)$ ;
  Identify species  $S(t)$ ;
  While (not termination condition) do
    Conserve species Seeds from          Select
    Crossover  $G(t+1)$ ;
    Mutate  $G(t+1)$ ;
    Evaluate  $G(t+1)$ ;
    Identify and Update species          End (while)
  Identify global optima;
End

```

Fig. 7 Structure of the ASCGA

V. PERFORMANCE AND ANALYSIS

A. Capability in searching multiple solutions

All the above species-based evolutionary algorithms have been reported to be capable of finding multiple global solutions of a multimodal problem. It is conjectured that the n -dimensional Shubert function where $|x_i| \leq 10$ has $n \cdot 3^n$ unevenly distributed global optima and a lot of local solutions. SCGA was able to successfully obtain all the global solutions for 1, 2 and 3-dimensional Shubert functions.

Stoan *et al.* [15] compared the species conservation technique and multinational algorithms, and said that the species conservation algorithm efficiently keeps track of several good search space regions at once, and can give better solutions than multinational algorithms ([39], [40]).

The two-dimensional Shubert function [42] is defined by

$$f(\mathbf{x}) = \prod_{i=1}^2 \sum_{j=1}^5 j \cos[(j+1)x_i + j] \quad (9)$$

where $-10 \leq x_i \leq 10$ for $i=1,2$. It is estimated to have 760 local minima, 18 of which are global minima with the objective function value of -186.73. It is very interesting to

notice that the ASCGA with the population size of 1000 found all 761 solutions within 1005 generations, shown in Fig. 8 The ASCGA has the capability of finding global and local solutions for tested functions.

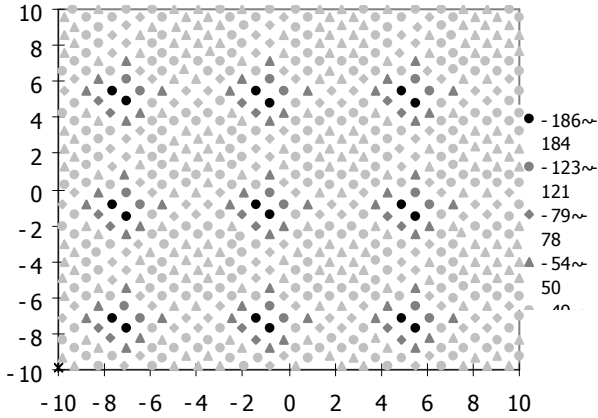


Fig. 8 Distribution of species for the 2-D Shubert function.

B. Effects of selection of species distance

The performance of species-based evolutionary computations depends upon the selection of the species distance (σ_s):

- smaller species distance leads to an increase in the number of species and a decrease in the efficiency of the algorithm. For an n -dimensional problems, the maximum number of species seeds [43] will be:

$$N_{ns} = \prod_{k=1}^n \left(1 + \text{int} \left[\frac{x_k^u - x_k^l}{d_k} \right] \right) \quad (10)$$

where

$$d_{k+1} = \frac{\sigma_s}{2} \sqrt{1 - \frac{\sigma_s^2}{16d_k^2}}, \quad d_1 = \sigma_s, \quad \text{and } x_k^u, x_k^l \text{ are the upper and lower limit of the } k\text{th variable.}$$

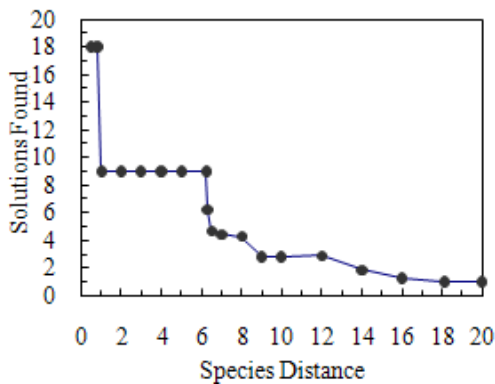


Fig. 9 Variation in the average number of solutions found with species distance for the two-dimensional Shubert function.

- Larger species distance results in the algorithm being unable to find all global solutions of the test problems. Fig. 9 illustrates that as the species distance is increased, the numbers of global solutions found decreases when SCGA [13] is used to solve the 2-dimensional Shubert function.

C. Different species definitions

An artificial problem ([17], [18], [44]) is used to demonstrate how the SCGA is able to explore the design space for multiple meaningful solutions that are significantly different in a domain-specific sense.

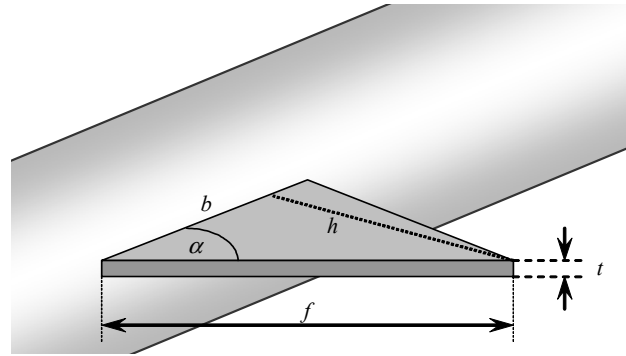


Fig. 10 A simple wing design (b = base – fixed size, f = front edge length, α = angle of attack, t = thickness).

The problem is to design a triangular wing of the shape given in Fig. 10. The wing has a fixed length base (b) of 10 m and its design is defined by three real-valued attributes: the *front edge length* ($0 \leq f \leq 20$ m), the *angle of attack* ($0 \leq \alpha \leq \pi$ radians), and the *thickness* ($0 \leq t \leq 20$ cm). It was supposed that the fitness of a wing $F(f, \alpha, t)$ can be evaluated as

$$F(f, \alpha, t) = h(f) \cdot h(20\alpha/\pi) \cdot h(t) \quad (11)$$

using a modified version of the 3-D Shubert function with

$$h(x) = \sum_{j=1}^5 j \cos[(j+1)x + j] \quad (12)$$

Table 1 shows the effects of different practical species definitions on solutions. Using Euclidean distance, SCGA can find all the global solutions (81), but this definition has no practical meaning. When some practical species definitions are applied, such as different in wing length, the SCGA can find 6 global solutions. Therefore, users can define some meaningful measurement of species distance based on design requirements and let a SCGA obtain required solutions.

VI. CONCLUSIONS

Species-based evolutionary algorithms (SEAs) are one of several niching techniques for finding multiple solutions of complex optimization problems. This method is based on the

notion of species, which defines a group of individuals that have similar characters. All individuals within each species are dominated by the best individual in the species, commonly referred to as species seed. Species are naturally emerged to the population after applying evolutionary operations, such as selection, mutation and crossover in a genetic algorithm.

TABLE I. EFFECTS OF SPECIES DEFINITIONS

Distance	Distribution of global solutions/(species)	solutions
Euclidean distance $d(\mathbf{w}_1, \mathbf{w}_2) = \sqrt{(f_1 - f_2)^2 + (\alpha_1 - \alpha_2)^2 + (t_1 - t_2)^2}$		81
Difference in wing length $d(\mathbf{w}_1, \mathbf{w}_2) = f_1 \sin(\alpha_1) - f_2 \sin(\alpha_2) $		6
Difference in wing surface area $d(\mathbf{w}_1, \mathbf{w}_2) = \frac{b}{2} f_1 \sin(\alpha_1) - f_2 \sin(\alpha_2) $		7
Difference in weight $d(\mathbf{w}_1, \mathbf{w}_2) = \frac{b}{2} t_1 f_1 \sin(\alpha_1) - t_2 f_2 \sin(\alpha_2) $		6
Difference in shape $d(\mathbf{w}_1, \mathbf{w}_2) = \alpha_1 - \alpha_2 $		3

Species conservation techniques have been applied to different evolutionary algorithms to develop related SEAs, such as species conservation genetic algorithm, species-based particle swarm optimization and species-based differential evolution. Those SEAs have been demonstrated to be effective in searching all the global solutions of tested multimodal functions.

Species distance/radius is an important control parameter in a species-based evolutionary algorithm and has large effects on their performances. Choosing a very small species distance may decrease an SEA's efficiency, while a very large species distance could result in the SEA being unable to distinguish the several possible solutions.

Euclidean distance is a common way to measure species distance. It may not be, however, meaningful in some application domains. Some specific measurement of species distance should be applied to obtain meaningful solutions in solving practical problems.

Adaptive species evolutionary algorithms can automatically adjust species parameters.

For higher dimensional problems, the species-based evolutionary computations are not as effective as other niching techniques. More work should be done in improving efficiency so that they can be used in real-world engineering problems.

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