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Contents lists available at ScienceDirect

Informatics in Medicine Unlocked

journal homepage: www.elsevier.com/locate/imu

World Competitive Contests (WCC) algorithm: A novel intelligent optimization algorithm for biological and non-biological problems

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ARTICLE INFO

Article history:

Received 23 March 2016

Received in revised form

29 May 2016

Accepted 27 June 2016

Available online 28 June 2016

Keywords:

The motif discovery

Transcriptional factor binding sites

Optimization algorithms

World Competitive Contests

ABSTRACT

Since different sciences face lots of problems which cannot be solved in reasonable time order, we need new methods and algorithms for getting acceptable answers in proper time order. In the present study, a novel intelligent optimization algorithm, known as WCC (World Competitive Contests), has been proposed and applied to find the transcriptional factor binding sites (TFBS) and eight benchmark functions discovery processes. We recognize the need to introduce an intelligent optimization algorithm because the TFBS discovery is a biological and an NP-Hard problem. Although there are some intelligent algorithms for the purpose of solving the above-mentioned problems, an optimization algorithm with good and acceptable performance, which is based on the real parameters, is essential. Like the other optimization algorithms, the proposed algorithm starts with the first population of teams. After teams are put into different groups, they will begin competing against their rival teams. The highly qualified teams will ascend to the elimination stage and will play each other in the next rounds. The other teams will wait for a new season to start. In this paper, we're going to implement our proposed algorithm and compare it with five famous optimization algorithms from the perspective of the following: the obtained results, stability, convergence, standard deviation and elapsed time, which are applied to the real and randomly created datasets with different motif sizes. According to our obtained results, in many cases, the WCC's performance is better than the other algorithms'.

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1. Introduction

Since there are a lot of problems with the theory of computational complexities, which need more and more time for being solved, we employ meta-heuristic optimization algorithms. Most of these algorithms can result in suitable solutions with less computational complexities. An evolutionary algorithm's good performance, its stability in different types of execution with minimum errors and its elapsed time to produce acceptable results, are the main criteria that must be considered.

Many different optimization algorithms have been offered and various methods and new algorithms have been proposed to search for the motif discovery sites. Related works are examinable from two aspects: 1- proposing a new optimization algorithm aspect, and 2- the motif discovery aspect. Some of the imminent optimization algorithms which were proposed during the last decades are listed as follows. The genetic algorithm was inspired

by living organisms' evolutionary process [1]. A large number of modified genetic algorithms were proposed with a different crossover, mutation, and distinct selection operations [2]. A new optimization algorithm for a single hidden layer of feedback on a neural network, based on the genetic and convex combination algorithms, was introduced by Kwan et al. The most important characteristic of their algorithm was that it could get an acceptable answer in more reasonable time order compared with the others [3]. A new optimization algorithm, known as SOS, was introduced by Min-Yuan et al. to study living organisms. Obtained results proved the SOS's good performance [4]. A combination of imperialist competitive and bee colony algorithms which was recently introduced led to a new method for an optimization problem. Improving a global exploration of a combination of floods of bee colony algorithm is mentioned as method's goals. Moreover, it was applied to two real datasets [5]. The heat transfer optimization algorithm was inspired by both the law of heat transfer and thermodynamics [6]. Another optimization algorithm, inspired by the particle swarm optimization, was recently introduced by Gosciniaik et al. Their algorithm was not influenced by the environment, but rather by the particle swarm optimization that was employed as a model of a predator and prey. Moreover, it

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proved that their approach can be practicable in computer games [7]. The particle swarm optimization is an algorithm in which the first populations were created randomly. It is based on the social interaction among flocks of birds or schools of fish. Zhang et al. enhanced the search ability using the Bayesian techniques through exploiting past particles' positions and using a new type of mutation in order to obtain better results. Their approach is known as the BPSO method [8]. Gomez et al. introduced new optimization algorithm for spatial variability analysis and showed high improvement in the NDT measurement position [9].

The other (The second) aspect of related works is the motif discovery. Binding sites, which indicate chemical specificity and affinity, are either part of a protein or part of DNA or RNA in ligands which form a chemical bond. One of the most important components of the biomolecules' general characteristics is binding sites that can identify the other proteins. Binding sites also exist in antibodies as coded regions. A non-covalent bond between the two polypeptide chains is formed when a binding site of one protein determines another protein's surface. Transcriptional factors (TF), are proteins which bind to specific DNA sequences and control the rate of the transcription of genetic information from DNA to RNA. TF are categorized as a sequence of specific DNA binding factors that are of great importance to the regulation of a gene expression. They contain one or more DNA-binding domains that bind to specific sequences of DNA that are contiguous to the genes which they regulate. DNA binding sites are distinguishable from the other algorithms because they include the targets of the other proteins and therefore are part of DNA- in other words, are bound by DNA-binding proteins. DNA binding sites divide into several categories that are as follows: transcriptional factor binding sites, recombination sites, and restriction sites. There is a need for the evolutionary algorithms because the motif discovery problem is an NP (nondeterministic polynomial) hard problem that cannot be solved in polynomial time order. Although these algorithms are not deterministic, they can get acceptable answers in reasonable time order.

We combine the protein motif search processes with the gene discovery methods in which the discovery of human new genes of cadherin superfamily proteins is the main purpose, to identify genes' encoding protein containing specific domains [10]. Proposing a genetic algorithm for the motif discovery based on the

statistical significance of the current research is another recent study carried out, along with the above-mentioned works. After their proposed algorithm was applied to several different datasets, the obtained motifs were compared with each other [11]. Research into the Bcl-2 family protein is among subjects that relate to the present discussion. The family protein comprises several homologous proteins as well as a collection of other proteins which consists of a sequence of similarities except for a Bcl-2 homology (BH)3 motif. One of the four BH motifs is required for membership in the Bcl-2 family. Abdel et al. evaluated Bcl-2 homology motifs [12]. Determining the cellular binding motif in the case of the acute respiratory syndrome coronavirus is essential because the respiratory syndrome coronavirus threatens human lives [13]. Parkinson, Alzheimer, and some other diseases are a result of aging and stress that are among the major causes of the protean damage. According to Bonham-Carter [14], oxidation of amino acids with a high rate of motifs is due to some protean damages. Most of the solutions for bioinformatics NP_hard problems are based on ACO and PSO [15,16]. Some of the other related works that we can refer to are as follows:

Specifications of the monocyte activating motif in the mycobacterium (mycobacterial) tuberculosis [17], motifs retrieval by the Secondary Structure terns occurrences [18], and the interaction of binding motif within the nucleocapsid protein of porcine reproductive and respiratory syndrome virus and the host cellular signaling proteins [19].

2. The proposed algorithm

Proposed optimization algorithm starts with the first population of teams [20]. Every team includes several players with random values. The mentioned teams are placed into different groups based on geographical distance and begin to compete with each other in it. This stage can be considered as a local optimization. Global optimization stage which is elimination stage will begin after grouping matches. Eliminated teams will not be removed from the contests, and they will wait for new season of matches. Here is a flowchart of WCC (Fig. 1).

WCC includes several main stages:

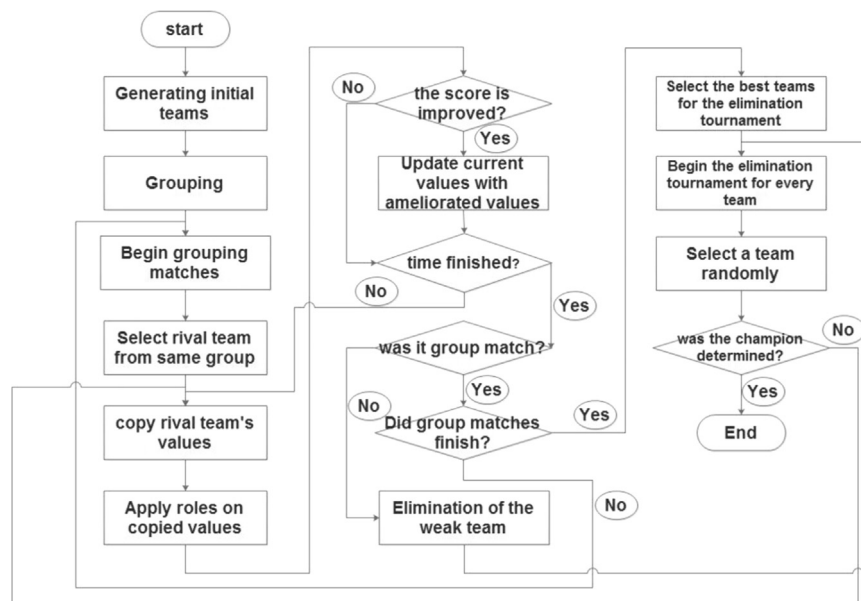


Fig. 1. The WCC flowchart.



Fig. 2. An instance of a team.

1. Generating initial teams: the number of teams that is generally generated randomly, depends on the exact nature of the problem's variables. An example of a team with 9 players has been shown in Fig. 2. A team consists of a number of players with different roles. Every player has his own role that is very important for the algorithm's good performance and convergence. Lots of various roles can be applied based on the nature of the problem. Every team which is a $1 \times (N+1)$ array, is a solution for the problem. The above-mentioned array in which N is a problem dimension and p_i is the i th player, is defined as follows

$$\text{Team} = [P_1, P_2, P_3 \dots P_N, \text{Score}]$$

2. Classifying: classification or grouping refers to organizing teams into different groups which compete against each other. A lot of methods, such as hamming distance, maximum likelihood, minimum likelihood and so many other methods, can be employed in this stage. The second stage is based on the nature of the problem. Fig. 3 represents eight groups as well as a team that has to be put into one of these groups. The values labeled on edges are resemblance rates between a team and groups. First group's matches will be held after teams are put into groups.

3. Holding a match: as we know, there are a number of rules in a match, which must be followed. In this stage, how you define rules depends directly on the nature of the problem. Only do we consider one rule for the motif finding problem that is contest termination conditions. Two termination conditions are as follows: 1-time intervals, 2- the number of scoring function callings. Instead of considering "time's up" a termination

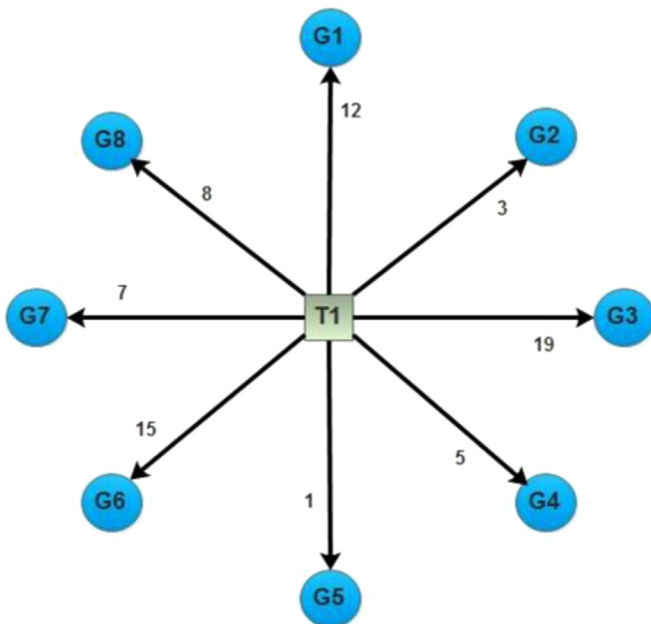


Fig. 3. Grouping.

condition, we considered "the number of scoring function callings" the termination of a contest. In a match, the rival teams usually imitate each other's values and take measures to ameliorate their status by helping their players take more active roles and score more goals. The higher score, the better status. In our proposed algorithm, there is a ball that carries a value and delivers it to the destination. A referee will call the scoring function after a player receives the ball and then he will change his value in case his score improves. The above-mentioned roles (population changes) are as follows:

1. Shooting: shooting is a process in which a player throws a ball toward the rival team's goal. In our proposed algorithm, the player who shoots throws several balls toward the rival team's goal; Ball values are considered his teammate's values. The rival team will update its players' values if obtained values improve the scoring functions; otherwise, changes cannot be applied.
2. Attacking: in the attacking role like shooting role, a player throws the balls toward the rival team with different values which are created randomly. Although attacking and shooting roles are similar in some ways, they are different in other ways. A player in the shooting role chooses his teammate's values whereas a player in the attacking role sends the randomly created values to the rival team.
3. Passing: passing is one of the main links among players. As we observed in Fig. 5, a player passes the ball to one of the randomly selected teammates and changes his value.
4. Crossing: a cross is a means of a long pass from a player to his teammate. In our proposed algorithm, a cross pass has an angle (the effect of the angle has been depicted in Fig. 4) named α . The more the α value is, the more the distance range is. We implemented the cross pass as a left rotation as it is shown in Fig. 5.

4. The scoring functions: every team can be considered as an answer to the problem. As we know, there are many teams and each team has its own merits that are different from those of another team. A score value is a value that indicates how a developed answer is close to an optimal answer. As mentioned earlier, a team is composed of some players whose values are a motif starting position in a DNA sequence. The fitness functions

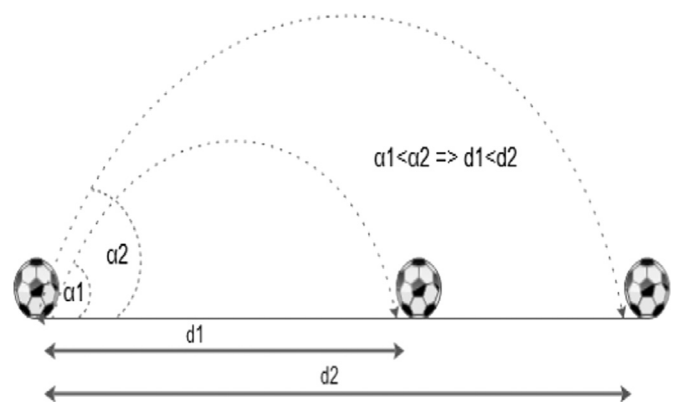


Fig. 4. The effect of an angle in a cross operation.

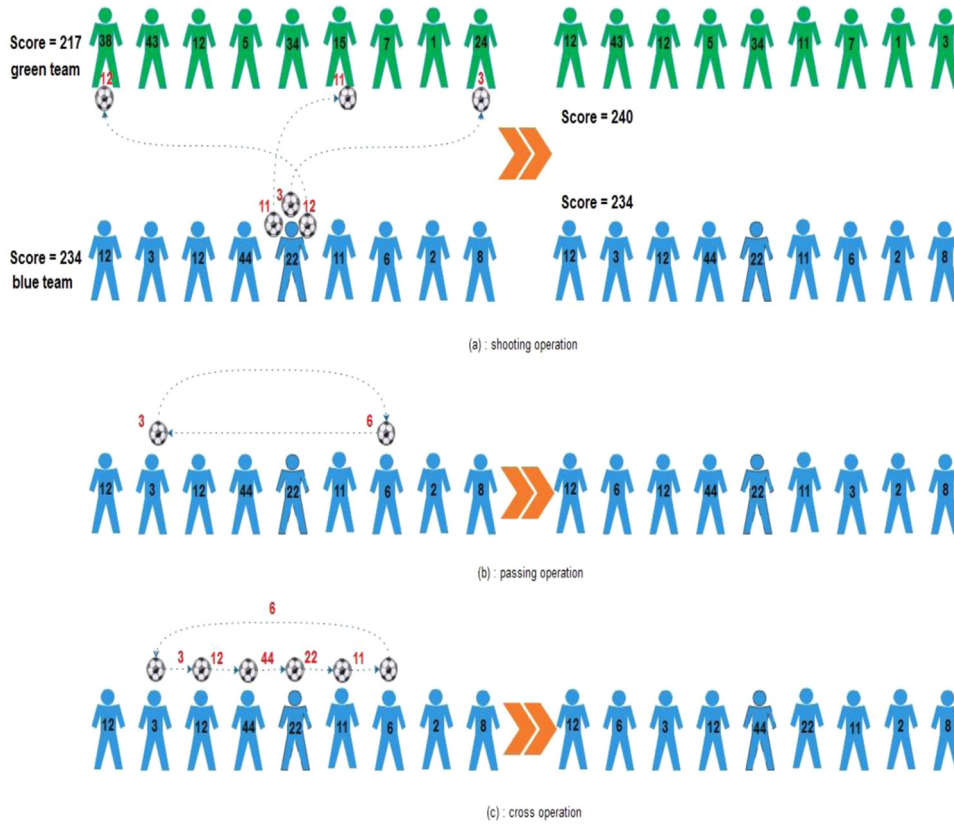


Fig. 5. An instance of a competition between the blue and green teams. (a): the status and scores of teams before a playing chance are shown on the left side and the status and scores of teams after a shooting operation are shown on the right side. (b): to apply for the pass role, we have to turn to the player with value 6. (c): the cross operation is started by the player with value 6. We implemented the cross operation as a left rotation. The cross angle is 69°.

have the main role in the convergence and correlation of an optimization algorithm and an algorithm either will converge toward a bad solution or will have difficulty in converging in case its design is not appropriate. Its speed is also an issue of the utmost importance, so it must be computed quickly. Considering the nature of the problem, the scoring functions can be defined as the maximization and minimization of the scoring functions. The scoring functions can be defined as follows

$$\text{Score (team)} = \text{score} (P_1, P_2, P_3 \dots P_N), \text{Score.}$$

For the motif discovery problem, higher score values represent the meritorious teams- in other words, the scoring functions inserted in Eq. (1), is maximization scoring functions for this problem. Fig. 6 shows how a sample of scoring is computed for the motif discovery problem.

$$\text{Score} = \sum_{i=1}^l \max(\text{count}(k, i)) \tag{1}$$

where k belongs to $\{A, T, C, G\}$, l is the length of a motif, t is the number of a sample of a sequence of DNA.

5. The elimination stages: after first group's matches are held, the elimination stages in which the most meritorious teams play each other in the final rounds, will begin. A team's face to face rivals can be determined by disparate methods such as random selection, maximum resemblance, minimum resemblance, maximum likelihood, minimum likelihood and many other methods. These stages will continue until the champion is selected. The weak teams will wait until a new season starts. The weak teams have to change their players' roles and values at the beginning of a new season. Fig. 7 depicts how an elimination tournament is held for sixteen meritorious teams.

	l							
	A	G	G	G	T	G	T	}
	C	G	G	C	G	A	C	
	A	G	G	G	T	G	C	
	A	G	C	C	T	A	C	
	A	G	G	C	T	A	C	
	C	G	A	C	C	A	A	
	A	G	G	G	G	G	T	
	A	G	A	T	G	A	A	

	A	6	0	2	0	0	5	2
	C	2	0	1	4	1	0	4
	G	0	8	5	3	3	3	0
	T	0	0	0	1	4	0	2

Consensus	A	G	G	C	T	A	C	

Fig. 6. The scoring computation [21].

The teams which fail to ascend to the elimination stages or those which are eliminated by the other teams in this stage must prepare for a new season of international contests.

6. The stop condition: as in other optimization algorithms' case, we can select one of the following options as a termination condition:
1. The ending of predefined numbers of seasons.

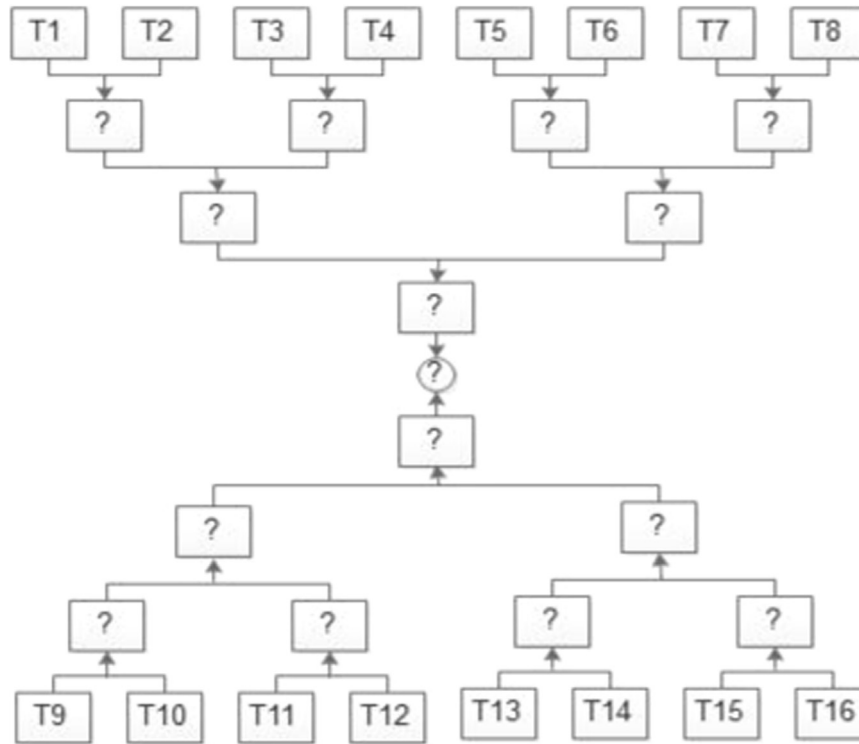


Fig. 7. The elimination stages.

2. The passing of the allocated time.
3. Reaching definite precision.
4. Keeping the best score for several seasons.
5. Calling the antiseptic numbers of scoring functions.
6. Using a combination of the above-mentioned options.

2.1. Discussion

Although our proposed algorithm (WCC), outlined above, was inspired by human sports rules, most heuristic algorithms have been inspired by nature. The present paper presents a new evolutionary algorithm. The above-mentioned optimization algorithm can be applied to various fields such as economics, computer science, engineering etc., in which the classical algorithms fail to get acceptable answers in reasonable time order. One of the main steps in determining the optimization algorithms' practical applications is classifying their models into major categories such as continuous optimization versus discrete optimization, unconstrained optimization versus constrained optimization, single-objective optimization versus multi-objective optimization, and deterministic optimization versus stochastic optimization [22]. In discrete optimization, variables often contain a subset of integer values whereas, in continuous optimization, variables contain real values. The proposed algorithm can be used as both discrete and continuous optimization algorithms. While there are some constraints on variables in the constrained category, there are no constraints on variables in the unconstrained category. Such a difference between constrained and unconstrained categories results in the placement of the proposed algorithm (WCC) on an unconstrained category. Most of the optimization algorithms which are known as single-objective optimization algorithms have single-objective functions whereas others which are known as multi-objective optimization algorithms, have multi-objective functions. WCC which is based on the nature of the problem can be applied to either multi-objective or single-objective optimization problems. It is also assumed that WCC is practical for only

deterministic optimization problems, in which the nature of problems is invariable, in contrast to stochastic optimization problems with variable natures. The main purpose of this study is to achieve good performance by reducing errors, reach a suitable convergence and appropriate stability, and get an acceptable execution time. A combination of the other optimization algorithms' dominant properties (such as being competitive in an imperialism competitive algorithm, the penalties and rewards of learning automata, and the evolutionary changes in the genetic algorithms) and the unification of them into the proposed algorithm are the other motivations behind the present paper. Creating teams with random values is the first step forward in the proposed algorithm. A team consists of some players that not only have different roles based on the exact nature of the problem but also play major roles in an algorithm's good performance. Teams that are put into different groups compete against each other. The highly qualified teams ascend to the elimination stage and continue competing depending on their players' different tasks. There is a referee who evaluates and scrutinizes teams' performance. If the end result is not acceptable or termination conditions are not fulfilled, a new season will begin. To carry out the present study, we applied WCC to the transcriptional factor binding sites (TFBS) problem which is categorized as an NP-hard problem, then compared it with several algorithms, including the genetic algorithm (GA), the imperialism competitive algorithm (ICA), the particles swarm optimization (PSO), the ant colony algorithm (ACO), and learning automata (LA) that are categorized as optimization algorithms.

Although there are some similarities between WCC and the other evolutionary algorithms, there are some important differences as well. In this section, we're going to compare WCC with the other evolutionary algorithms, so we begin with comparing WCC to the genetic algorithm in detail and indicating its terms in Table 1, along with the other algorithms' terms. The differences between WCC and the genetic algorithm are as follows:

Table 1
Parameters set for famous optimization algorithms.

Algorithm name	Population individuals	Operations on population	Evaluation function	Inspired by
WCC	Team	Shoot, pass, cross, attack	Scoring	International sport matches
GA	Chromosome	Crossover, mutation	Fitness	Natural revolution
PSO	Particle	Position and velocity update	Solution evaluation	Social of birds
ICA	Country	Absorb, revolution	Cost	Imperialism competition
ACO	Ant	Evaporation & Laying pheromone	Fitness	Behavior of Ants
LA	Stochastic automata	Set of finite actions	Computable function	Cellular automata

- All the chromosomes in the genetic algorithm are put into the current population whereas all the teams in WCC are put into different groups based on hamming distance, maximum likelihood, minimum likelihood, random grouping, and many other methods that are employed based on the exact nature of the problem.
- While there are lots of various operations such as shooting, passing, attacking, kicking and crossing in WCC, there are only two operations in the genetic algorithm, which change the chromosomes that are categorized as crossover and mutation.
- There are two types of competitions among teams in WCC: 1- the local competition and 2- the global competition. By contrast, there is not any competition among chromosomes in the genetic algorithm. The global competition guarantees that WCC does not remain in the local optimal points.
- Only the most deserved chromosomes in the genetic algorithm have a chance to pass down to the next generation whereas all the teams in WCC will get a chance to attend the next season of matches while they are trying to ameliorate their performance.
- In a generation, the genetic operations are applied with a definite rate which is categorized as crossover and mutation rates whereas all of these teams have lots of operations that can be applied in case match termination conditions are fulfilled.
- A team's values will be replaced with new values in case the newly earned score is better than the previous one. As we know, in a genetic algorithm, the fitness value for a chromosome is likely to change for the worse after crossover and mutation operations are applied.
- The genetic algorithm was inspired by natural evolution but WCC was inspired by sports rules and roles which are applied to the games.

LCA (league competition algorithm) is an optimization algorithm which is recently introduced [23]. Although it seems that WCC and LCA are the same, they are two different algorithms and have main differences that are:

- WCC is inspired by world competition and LCA is inspired by league competition, so they have difference roles and steps.
- WCC has two steps in optimization which are local optimization and then global optimization, but LCA has only one step in optimization that is global optimization.
- WCC has various operations such as shooting, crossing, passing and so on whereas there are operations like mutation and crossover in LCA.
- The scoring function is not the same in two algorithms. There is no winner and loser in WCC while winner and loser are introduced in LCA. Winner gets 3 scores and loser does not get any score. Also, scores determine to play chance in WCC whereas scores have not any influence in competition in LCA.
- A person who evaluates the player's functionality is the referee and the referee evaluates each operation of players and gives them score in WCC, but a person who evaluates team performance is a coach and evaluates team functionality overall.

- We can use from artificial intelligence methods in grouping or clustering of teams in WCC whereas there is no grouping in LCA and all teams are placed in one group and compete based on schedule table.
- There is transfer operation at the end of a season in LCA, but this operation is not available in WCC and instead of, every team tries to get some players who were not participated in the world cup and now they can proper functionality relative to current players. Then the mentioned players are superseded with the players who have not a good performance.
- There is elimination stage in WCC whereas this stage is not available in LCA.

In Table 1, the terms which are available to famous optimization algorithms are shown.

3. Experimental results

In this section, we are going to conduct two experiments in order to compare the proposed algorithm with the other famous algorithms. First, we scrutinize the TFBS problem. Then we examine the proposed algorithm's performance on standard

Table 2
Algorithms' parameters for the randomly created datasets.

Algorithm name	Parameters
WCC	Number of teams=30, number of seasons =10, number of match trying=35, number of groups=2
PSO	Number of particles=200, number of iteration=100, number of best p=5
ACO	Number of ants=200, number of iteration=60, pheromones actor=5, evaporation factor=5
LA	Size of boundary operation=10, number of iteration=8000
ICA	Number of countries=1000, number of imperialism=10, number of iteration=1
GA	Size of first population=200, number of generation=100, mutation and crossover rate=30%

Table 3
Algorithms' parameters for the real datasets.

Algorithm name	Parameters
WCC	Number of teams=100, number of season =20, number of match trying=50, number of groups=10
PSO	Number of particles=400, number of iteration=400, number of best p=10
ACO	Number of ants=750, number of iteration=150, pheromones actor=5, evaporation factor=5
LA	Size of boundary operation=10, number of iteration=80,000
ICA	Number of countries=1000, number of imperialism=7, number of iteration=10
GA	Size of first population=400, number of generation=1000, mutation and crossover rate=30%

Table 4
obtained results from the randomly created datasets.

	Algorithm		Dataset1				Dataset2				Dataset3				Dataset4			
			Best	Worst	Avg	SD	Best	Worst	Avg	SD	Best	Worst	Avg	SD	Best	Worst	Avg	SD
Motif Length = 10	GA	FIT	57	49	52.6	7.51	91	79	85.4	10.69	126	111	118.9	13.44	152	141	148.3	11.04
		TIME	0.82	1.24	0.92	0.39	1.63	2.18	1.85	0.57	1.73	2.77	2.18	0.87	2.57	3.29	2.82	0.7
	LA	FIT	65	60	62.8	5.79	115	107	110.3	9.49	155	145	149	8.6	183	171	178	10.29
		TIME	0.98	1.16	1.09	0.17	1.49	1.93	1.77	0.39	1.57	2.36	1.99	0.76	1.78	2.98	2.4	1.1
	WCC	FIT	65	60	62.2	4.52	124	116	120.5	8.51	182	167	173.4	14.57	233	221	226.4	11.24
		TIME	0.99	1.05	1.02	0.06	1.43	1.72	1.55	0.26	1.57	1.79	1.69	0.22	1.89	2.23	2.01	0.34
	PSO	FIT	65	53	59.3	9.59	117	109	111.7	14.76	171	156	164	15.87	228	211	215.7	14.49
		TIME	1.07	1.43	1.12	0.34	1.7	2.17	1.91	0.46	1.89	2.51	2.16	0.54	2.11	2.89	2.61	0.7
	ACO	FIT	63	58	60.4	5.13	120	111	114.6	8.02	171	160	166	11.48	228	207	214	19.08
		TIME	0.97	1.04	0.98	0.14	1.69	2.13	1.86	0.38	1.83	2.38	2.13	0.51	2.45	3.04	2.75	0.45
	ICA	FIT	57	51	55.1	6.23	104	88	93.1	15.12	141	123	129.7	15.23	182	160	169.5	22.81
		TIME	1.01	1.07	1.03	0.06	1.4	1.67	1.57	0.23	1.51	1.78	1.66	0.31	1.87	2.33	1.99	0.41
Motif Length = 11	GA	FIT	62	55	58.90	8.76	100	94	98	6.92	136	130	133.10	5.37	179	163	166.80	13.76
		TIME	0.61	1.29	0.68	0.63	0.76	0.81	0.79	0.04	0.90	1.01	0.91	0.10	1.08	1.13	1.10	0.03
	LA	FIT	73	67	69.50	4.94	129	113	120.30	12.88	176	160	166.10	14.03	209	190	200.90	16.39
		TIME	0.90	1.06	0.95	0.12	1.01	1.03	1.02	11.67	1.17	1.66	1.26	0.44	1.29	1.41	1.30	0.12
	WCC	FIT	72	68	69.10	4.78	135	123	128.90	10.33	193	177	187.70	14.28	252	240	247	12.59
		TIME	0.94	0.99	0.95	0.42	1.00	1.02	1.01	0.02	1.09	1.14	1.10	0.04	1.24	1.32	1.26	0.07
	PSO	FIT	68	62	64.90	5.37	125	116	120.80	8.09	186	173	176.60	10.88	242	228	237.40	14.64
		TIME	0.87	0.98	0.89	0.94	1.02	1.03	1.02	0.01	1.16	1.20	1.17	0.03	1.36	1.40	1.37	0.03
	ACO	FIT	70	65	67	6.16	130	118	123.80	12.06	188	174	178.50	14.64	233	217	230.50	22.90
		TIME	0.66	0.86	0.74	0.15	0.93	0.99	0.95	0.06	1.18	1.25	1.22	0.06	1.29	1.40	1.35	0.09
	ICA	FIT	68	64	65.30	3.75	133	111	116.30	18.49	162	156	157.10	9.63	205	197	200.30	8.25
		TIME	0.88	0.97	0.94	0.08	0.98	1.00	0.89	0.84	0.98	1.13	1.10	0.03	1.24	1.50	1.33	0.80
Motif Length = 12	GA	FIT	65	57	62.30	8.00	114	102	106.60	13.72	150	136	142.10	15.12	189	173	179.40	19.85
		TIME	0.69	0.71	0.70	0.01	0.85	0.89	0.86	0.03	1.00	1.09	1.01	0.07	1.16	1.24	1.17	0.07
	LA	FIT	78	73	75.10	6.07	134	124	129.20	9.03	184	160	174.50	22.63	215	210	213.80	9.57
		TIME	1.01	1.29	1.04	0.25	1.10	1.11	1.10	0.01	1.20	1.22	1.21	0.02	1.34	1.36	1.35	0.02
	WCC	FIT	79	72	75	5.65	146	130	136.40	14.84	202	191	197.70	10.00	264	248	256.70	17.89
		TIME	1.03	1.07	1.04	0.03	1.13	1.17	1.13	0.03	1.22	1.24	1.22	0.01	1.34	1.35	1.34	0.01
	PSO	FIT	71	58	67.50	11.42	137	124	130.10	12.68	201	190	194.10	12.44	260	242	249.30	18.81
		TIME	0.93	1.42	1.02	0.42	1.11	1.23	1.13	0.10	1.27	1.32	1.28	0.04	1.44	1.45	1.44	0.01
	ACO	FIT	74	68	71.5	7.77	133	126	130	8.71	196	181	188.90	13.81	252	235	244.90	15.26
		TIME	0.77	0.99	0.84	0.18	1.00	1.08	1.05	0.08	1.19	1.30	1.24	0.11	1.35	1.48	1.42	0.13
	ICA	FIT	71	68	69.8	3.68	124	119	122.10	5.18	174	165	170.30	7.88	217	206	212.80	10.27
		TIME	0.95	1.00	0.95	0.04	1.05	1.62	1.11	.053	1.15	1.17	1.15	0.02	1.26	1.28	1.26	0.02
Motif Length = 13	GA	FIT	73	65	67.80	7.84	116	105	111.30	12.49	159	149	153.80	10.46	203	187	194.20	15.21
		TIME	0.73	0.75	0.73	0.21	0.89	0.90	0.89	0.01	1.04	1.54	1.11	0.46	1.20	1.28	1.22	0.06
	LA	FIT	83	76	80	6.78	141	134	137.30	7.21	199	176	184.50	23.50	232	226	227.60	12.50
		TIME	1.02	1.05	1.02	0.03	1.12	1.73	1.19	0.56	1.29	1.39	1.30	0.09	1.42	1.45	1.43	0.03
	WCC	FIT	81	75	78.80	5.96	151	142	147.60	9.61	221	207	213.10	13.67	291	265	276.80	22.35
		TIME	1.05	1.07	1.05	0.02	1.15	1.17	1.16	0.02	1.20	1.27	1.22	0.05	1.31	1.33	1.32	0.01
	PSO	FIT	84	74	76.20	9.77	145	137	140.50	7.38	210	200	205.50	12.66	277	255	265.60	20.89
		TIME	0.98	1.01	0.99	0.02	1.16	1.18	1.17	0.02	1.32	1.35	1.32	0.02	1.48	1.50	1.49	0.02
	ACO	FIT	83	72	76.70	11.04	146	135	140.20	13.09	210	198	202.90	12.20	269	256	263.40	12.74
		TIME	0.79	0.89	0.85	0.93	1.08	1.66	1.16	0.52	1.28	1.34	1.31	0.05	1.47	1.54	1.49	0.08
	ICA	FIT	77	72	74.90	4.34	138	128	132.30	8.72	190	180	183.40	8.85	237	223	229.30	13.19
		TIME	0.94	0.96	0.95	0.02	1.06	1.78	1.19	0.83	1.18	1.22	1.19	0.03	1.29	1.30	1.29	0.02

benchmark functions and compare it with FOA (Forest Optimization Algorithm), PSO (Particles Swarm Optimization), and GA (Genetic Algorithm). To carry out the study, WCC, the ant colony optimization algorithm (ACO), PSO, learning automata (LA), GA, and the imperialism competitive algorithm (ICA) are implemented in the MATLAB environment in a system with a 2.2 GH of CPU, 2 GB of RAM and WIN7 (64 bit) operating system, then four datasets are created randomly. We employ four real datasets [24] and present the obtained results in tables and diagrams. A web site is also available, "lbbwcc.ir". You can find some information about implemented algorithms and applied datasets on the web. The above-mentioned algorithms run 100 times for each dataset with a different size of the motif length. The best, the worst, and the average score values, the elapsed time (based on second), the score values standard deviation, and the elapsed time standard deviation (based on second) are determined. The standard deviation (SD) that is commonly used for algorithms' confidence, is a criterion that shows how much data scattered around the mean. The fewer SD is, the more reliable algorithms are. The algorithms' parameters for the

randomly created datasets are shown in Table 2 and the algorithms' parameters for the real datasets in Table 3. Moreover, the obtained results from both the randomly created datasets and the real datasets are shown in Tables 4 and 5, respectively. The figures are shown in Tables 4 and 5 indicate that dataset1 size is 10 × 100, dataset2 size is 20 × 200, dataset3 size is 30 × 300, and dataset4 size is 40 × 400. According to figures, all the real datasets are the same size (in a size 40 × 60). As we mentioned earlier, the conditions for all algorithms are so similar that they are compared to the same terms and conditions. The end of the predefined numbers of iterations or seasons will bring an end to the algorithms.

Figs. 9 and 8 depict Tables 4 and 5 as diagrams with over 100 times of independent execution. The horizontal pivot represents amounts of execution and the vertical pivot represents the fitness values. The best, the worst, the average and the standard deviation which is inserted in Tables 3 and 4, are obtained from over 100 times of independent execution for each algorithm with different motif sizes. Bold values for every group in Tables 3 and 4 indicate the best results compared with the other algorithms. Fig. 8 shows

Table 5
Obtained results from the real datasets.

	Algorithm	Dataset5				Dataset6				Dataset7				Dataset8				
		Best	Worst	Avg	SD	Best	Worst	Avg	SD	Best	Worst	Avg	SD	Best	Worst	Avg	SD	
Motif Length = 17	GA	FIT	218	202	210.90	17.28	224	203	213.30	17.55	223	205	213.80	17.13	232	207	218.60	24.38
		TIME	29.34	30.58	29.84	1.09	29.02	30.30	29.62	1.56	29.07	29.89	29.47	0.62	28.37	29.91	29.18	1.24
	LA	FIT	303	280	293.30	22.62	314	268	287	40.37	285	266	272.50	18.88	298	267	279.30	26.98
		TIME	15.56	15.93	15.82	0.38	15.47	16.31	15.94	0.83	16.57	17.04	16.72	0.44	15.65	18.19	17.43	2.54
	WCC	FIT	312	295	303	19.69	314	284	301.90	26.43	294	277	283.40	15.11	305	278	294.20	21.39
		TIME	17.27	18.29	17.62	0.88	16.75	17.55	17.06	0.87	17.13	17.43	17.25	0.30	17.15	17.43	17.27	0.27
	PSO	FIT	279	263	273.70	15.03	299	257	271.70	35.72	269	258	263.60	10.50	286	262	271.40	24.86
		TIME	14.08	14.57	14.35	0.57	14.05	15.03	14.46	0.84	14.23	14.78	14.39	0.58	14	14.22	14.10	0.19
	ACO	FIT	314	284	298.90	31.25	307	278	294	25.37	286	264	275.40	19.08	298	276	286.50	19.50
		TIME	15.57	16.33	15.96	0.88	15.84	17.01	16.31	0.87	15.17	16.35	15.79	1.00	15.59	17.42	16.27	1.94
	ICA	FIT	285	269	278.70	15.23	289	261	275.10	25.51	264	251	258.80	10.75	280	263	269.70	17.94
		TIME	15.82	16.53	16.22	0.72	15.98	16.39	16.25	0.39	16.72	18.64	17.82	1.98	16.48	17.08	16.78	0.53
Motif Length = 18	GA	FIT	246	215	230.20	34.63	237	223	227.30	14.14	234	212	222.30	19.13	239	213	225.40	26.61
		TIME	30.79	32.81	31.83	2.85	30.47	32.31	31.47	1.74	30.83	31.29	31.11	0.41	29.60	30.61	30.19	1.17
	LA	FIT	325	286	303.60	34.26	314	268	287	40.37	304	270	289.90	29.10	318	277	291.90	37.07
		TIME	16.10	16.74	16.42	0.62	15.47	16.31	15.94	0.83	16.74	17.41	17.01	0.60	16.22	16.81	16.44	0.53
	WCC	FIT	343	306	323.10	36.26	326	302	313.60	28.04	305	284	295.70	19.90	316	296	307.50	16.50
		TIME	17.23	17.81	17.44	0.79	17.75	18.65	18.07	0.81	17.37	17.76	17.58	0.31	17.17	17.62	17.42	0.45
	PSO	FIT	291	269	281.70	21.07	297	272	284.70	21.02	291	266	279.30	21.91	290	259	278.20	26.75
		TIME	14.60	15.72	15.14	1.05	14.66	15.33	14.93	0.70	14.75	14.98	14.87	0.22	15.49	15.75	15.66	0.13
	ACO	FIT	338	296	317.30	37.63	333	298	314.50	33.86	301	276	289.80	21.39	314	291	301.10	19.61
		TIME	16.30	17.41	17.05	1.00	16.01	16.93	16.35	1.02	16.14	16.94	16.48	0.74	15.69	16.51	16.14	0.65
	ICA	FIT	295	279	288.80	16.84	297	280	288	16.43	279	264	273.50	16.62	286	270	279	15.93
		TIME	16.34	16.76	16.56	0.38	16.40	16.66	16.54	0.25	16.91	17.64	17.16	0.74	15.44	16.11	15.66	0.24
Motif Length = 19	GA	FIT	253	227	236	25.33	243	229	235.80	14.95	247	229	237.20	20.82	259	228	239.50	31.44
		TIME	32.57	33.81	32.00	1.33	31.89	32.72	32.21	0.73	31.88	32.93	32.24	0.92	31.65	34.01	32.61	2.11
	LA	FIT	330	312	320.60	18.61	334	306	317.50	32.03	310	294	301.10	15.96	318	290	303.90	22.69
		TIME	16.77	17.48	17.23	0.58	16.73	17.50	17.32	0.68	17.10	18.22	17.39	1.10	16.62	16.93	16.79	0.33
	WCC	FIT	344	316	332.90	24.67	342	314	329.10	25.94	322	303	309.90	19.41	331	306	320.40	22.72
		TIME	18.05	18.57	18.26	0.53	17.93	18.50	18.17	0.53	17.97	18.76	18.24	0.70	17.84	18.88	18.35	1.04
	PSO	FIT	330	288	305.70	39.75	310	289	299.80	22.96	297	273	285.60	24.78	305	278	290	27.89
		TIME	15.56	16.03	15.66	0.41	15.10	16.05	15.38	0.96	15.54	16.19	15.73	0.57	14.72	15.88	15.09	1.15
	ACO	FIT	342	316	331.60	23.88	353	316	332.50	38.34	311	289	302.60	22.36	323	294	307.30	26.26
		TIME	17.30	18.14	17.71	0.97	17.07	17.94	17.45	0.86	17.70	18.14	17.87	0.49	16.52	17.41	16.95	0.88
	ICA	FIT	315	289	301.70	19.85	315	296	304.70	19.18	294	284	288.20	11.11	298	286	291.20	13.91
		TIME	15.19	16.94	15.90	0.28	16.78	17.16	16.98	0.32	17.30	17.81	17.63	0.46	16.75	17.69	17.14	0.88
Motif Length = 20	GA	FIT	264	249	253.50	13.05	264	245	251.60	17.56	256	238	247.20	18.69	262	230	248.20	29.93
		TIME	34.12	35.73	34.76	1.46	33.51	34.10	33.81	0.59	32.97	34.21	33.33	1.13	31.74	33.41	32.48	1.76
	LA	FIT	355	325	337.40	33.38	348	319	329.50	29.87	322	307	313.20	17.13	326	309	320.20	17.19
		TIME	16.76	17.58	17.30	0.86	16.98	17.69	17.42	0.84	17.66	18.81	18.16	1.20	17.84	18.34	18.03	0.50
	WCC	FIT	359	332	346	23.74	364	332	345.90	26.66	336	313	320.40	19.29	341	316	333.60	23.71
		TIME	18.90	19.15	18.99	0.23	18.06	18.85	18.46	0.78	18.53	19.29	18.02	0.52	17.63	18.02	17.79	0.44
	PSO	FIT	336	308	321.20	26.03	338	297	314.20	36.70	308	291	302.70	17.20	325	296	306.90	25.43
		TIME	16.21	16.49	16.33	0.28	15.69	16.10	15.56	0.45	15.56	16.59	15.76	0.91	16.14	17.28	16.65	1.11
	ACO	FIT	335	333	341.80	23.99	362	323	340.70	36.02	320	304	314.60	17.15	343	308	324	29.15
		TIME	18.04	19.16	18.46	1.02	17.55	18.63	17.93	1.10	17.42	18.08	17.71	0.75	17.21	17.97	17.60	0.79
	ICA	FIT	321	309	314.10	10.04	328	308	316.30	21.16	308	295	301.10	12.76	316	297	305.40	17.09
		TIME	16.22	16.38	16.30	0.15	16.33	16.63	16.51	0.28	16.99	17.62	17.27	0.72	16.26	17.03	16.58	0.92

the average stability of algorithms for all randomly created and all real datasets by implementing over 100 times of individual execution. Algorithms' stability which indicates a fluctuation in the current outcome compared with the previous and subsequent outcomes, is one of the main criteria for a comparison between meta-heuristic algorithms. From this point of view, an algorithm whose results are in a straight forward line with maximum fitness values and a minimum undulation is considered as a proper algorithm [25]. The error bars which indicate the validity of the algorithms are represented in Fig. 8. The above-mentioned criterion determines how similar or different measurements are. The error bars with a minimum height show the suitability of an algorithm as the benchmark that can be used in scientific papers with experimental results shown on graphs [26].

An algorithm's convergence is considered another criterion for a comparison between evolutionary algorithms. When the number of seasons, iterations or generations are augmented or when the allocated time to algorithms is augmented, the heuristic algorithms have to approach an optimal answer. An examination of the

above-mentioned algorithms' convergence proved that these algorithms have a proper convergence. Since the number of generations or the number of iterations is not identical for the algorithms, we have to employ the allocated time (or the number of fitness functions callings) to compare different algorithms. The convergence of algorithms for all randomly created datasets as well as all real datasets is depicted in Fig. 9. In Fig. 9, the horizontal pivot represents the number of fitness functions callings and the vertical pivot represents the fitness values. Dash lines in Fig. 9 relate to the mean values of algorithms. The algorithms which are at the top of the dash lines are definitely better than the algorithms which are at the bottom of the dash lines.

In conclusion, we'd like to refer to some practical results of the present paper:

1. Table average values shown in Table 6 which depict the mean values of all randomly created and all real datasets provide a solid base for the proposed algorithm's good performance. Two bold values in every column indicate the best state.

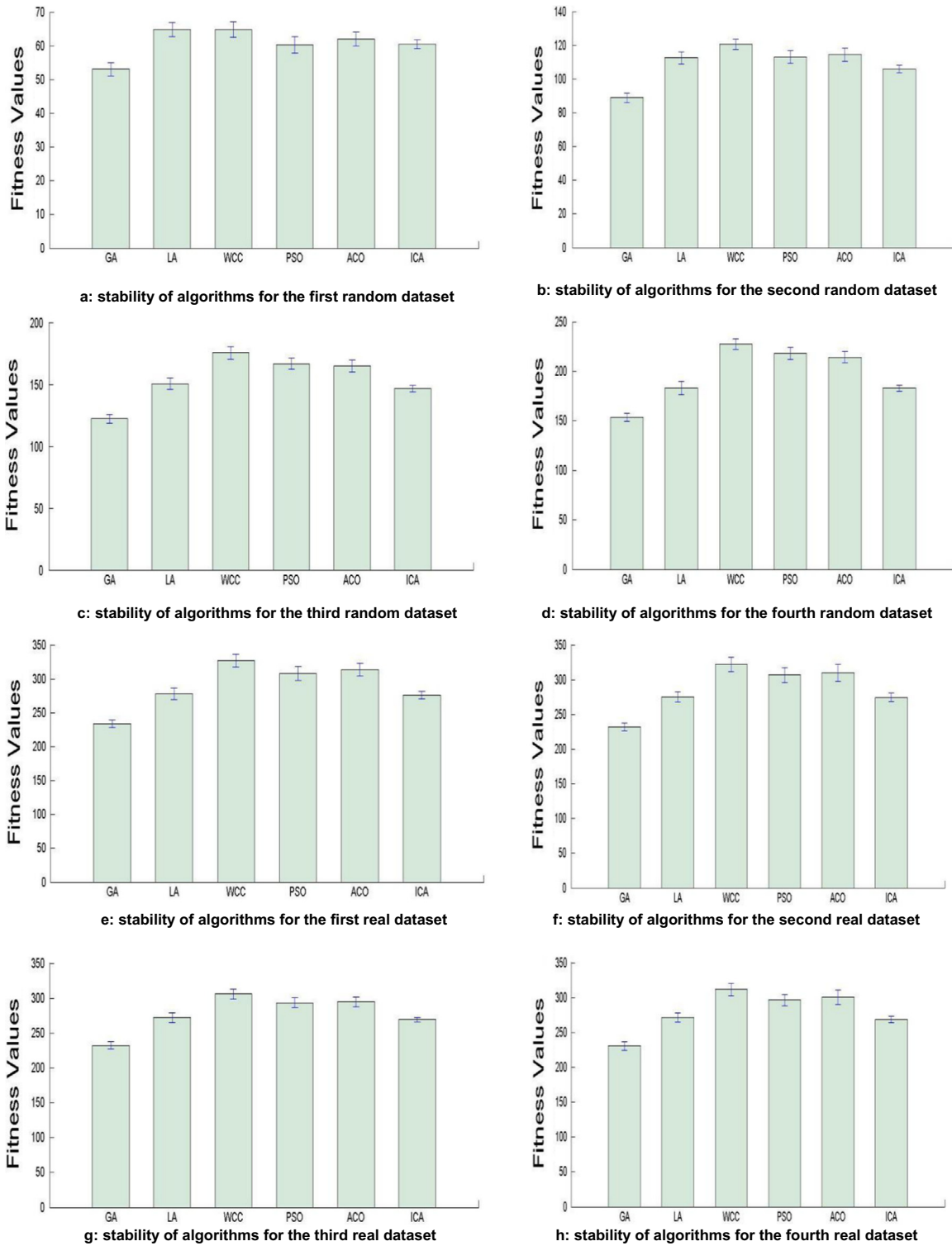


Fig. 8. The stability of algorithms for the randomly created datasets: the randomly created datasets are represented in diagrams *a* through *d*, and the obtained real datasets in diagrams *e* through *h*. The motif length is considered 10 for the randomly created datasets, and 20 for the real datasets.

2. The GA algorithm is of great research value because it provides a solid base for the other evolutionary algorithms' good performance. However, its results are worse than the others'.
3. Although LA has good performance for small datasets and lies at the top of the dash lines, it is not suitable for big datasets because it lies at the bottom of the dash lines.
4. ICA is better than GA, although it does not have proper performance compared with the other algorithms. As we observed earlier, it lies at the bottom of the dash lines.
5. There is a close competition among ACO, PSO, and WCC and all of them are at the top of the dash lines. WCC is better than two others and ACO is relatively better than PSO.

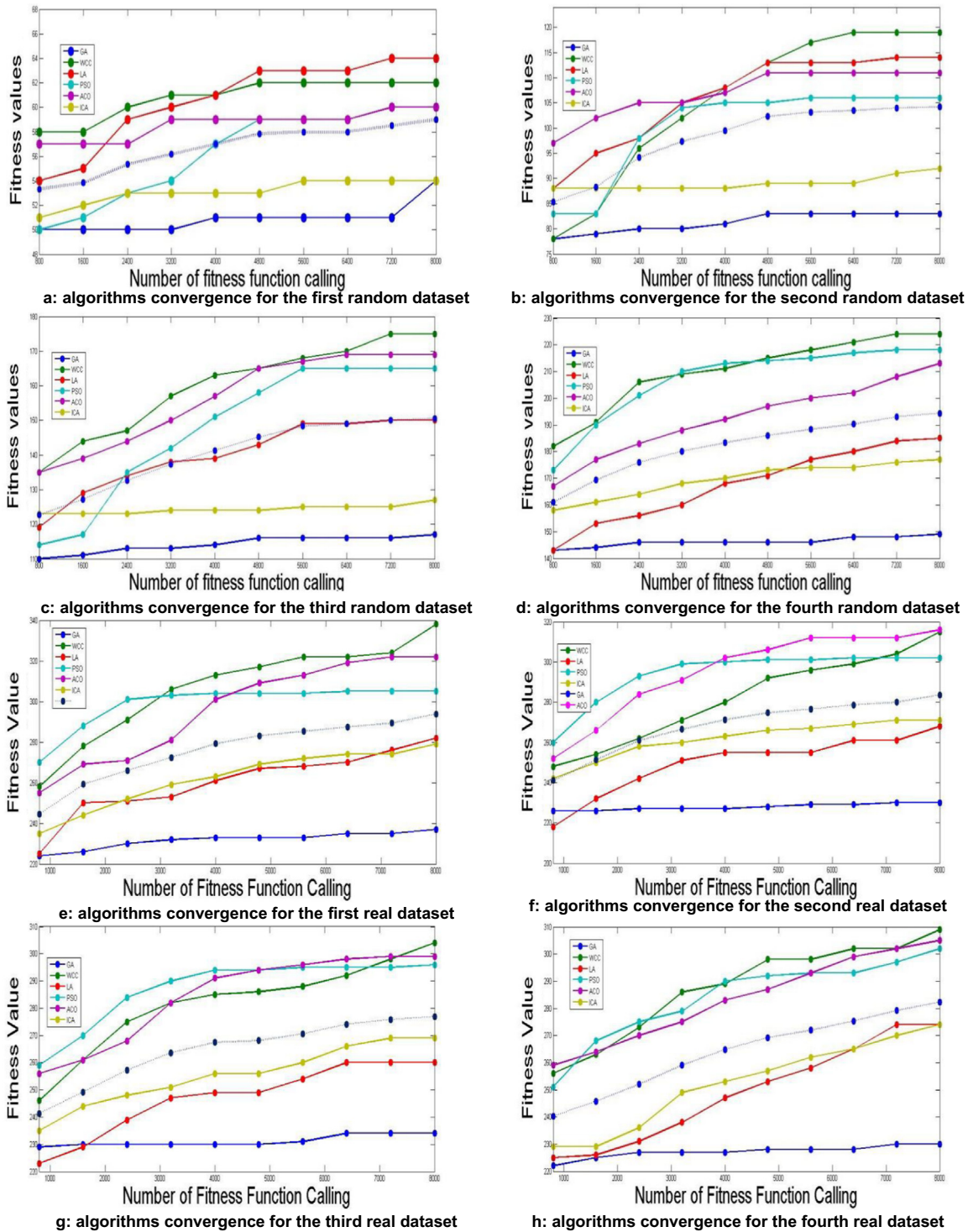


Fig. 9. Algorithms' convergence for the randomly created datasets: the randomly created datasets are represented in diagrams a through d, and the obtained real datasets in diagrams e through h. The motif length is considered 10 for the randomly created datasets, and 20 for the real datasets.

In another experiment, in order to examine the real quality of the proposed algorithm, we employ eight benchmark functions listed in Table 7 [27,28]. Benchmark functions' names, variable ranges, optimum target values, benchmark functions equations, and the number of variables are all presented in Table 7. These functions can be used either as maximization or as minimization problems. We consider them to be minimization problems.

F1, shown in Fig. 10, is a benchmark function with a minimum value $f = -18.5547$ for $x = 9.0389$ and $y = 8.6678$.

First, we list the results of test functions, then describe F1 in detail. We select 10 teams, 40 playing chances in a match, 4 groups and 9 sessions for WCC, along with roles that we mentioned earlier. Fig. 11 depicts not only teams' numerical values but also how players' values are changing. In Fig. 11, there is a table next to each picture; every table shows the exact value of a player. In addition, scores values are available. The best team is bolded after a session. The obtained values are considerable after 1026 callings of the scoring functions.

Table 6
The average results of all randomly created datasets and all real datasets.

Algorithm		All random datasets				All real datasets				All datasets			
		Best	Worst	Avg	SD	Best	Worst	Avg	SD	Best	Worst	Avg	SD
GA	FIT	123.25	112.25	117.46	11.26	243.81	222.18	231.92	21.41	191.15	174.16	181.94	17.00
	TIME	1.10	1.38	1.18	0.26	31.11	32.41	31.63	1.29	17.08	17.91	17.39	0.82
LA	FIT	148,018	137.00	142.43	11.23	319.00	290.25	302.99	27.28	243.56	222.69	232.18	20.10
	TIME	1.23	1.51	1.33	0.98	16.51	17.33	16.96	0.80	9.38	9.96	9.67	0.92
WCC	FIT	168.18	156.37	162.33	11.29	328.37	303.37	316.28	23.09	258.54	239.35	249.19	17.91
	TIME	1.22	1.30	1.25	0.10	17.67	18.28	17.87	0.59	9.99	10.36	10.12	0.36
PSO	FIT	161.68	149.25	154.95	12.48	303.18	276.62	289.40	24.85	241.91	221.58	231.21	19.44
	TIME	1.30	1.50	1.38	0.23	15.02	15.68	15.25	0.63	8.63	9.08	8.79	0.45
ACO	FIT	160.37	148.81	154.58	12.13	323.75	296.62	310.78	26.55	252.17	231.98	242.39	20.17
	TIME	1.24	1.46	1.33	0.24	16.57	17.52	17.00	0.93	9.42	10.03	9.69	0.61
ICA	FIT	142.50	131.93	136.33	10.10	298.12	281.31	289.64	16.27	229.62	215.41	222.03	13.69
	TIME	1.17	1.36	1.22	0.23	16.36	17.06	16.70	0.57	9.28	9.74	9.48	0.42

Table 7
Test functions.

Function	Name	Equation	Search range	Dimension	Optimum
F1	Ghaemi	$x\sin(4x) + 1.1y\sin(2y)$	$0 < x, y < 10$	2	-18.5547
F2	Griewangk	$\frac{1}{4000} \sum_{i=1}^n x_i^2 - \prod_{i=1}^n \cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$	$-600 \leq x_i \leq 600$	5, 10	0
F3	SODPF	$\sum_{i=1}^n x_i ^{i+1}$	$-1 \leq x_i \leq 1$	5, 10	0
F4	Rastrigin	$10n + \sum_{i=1}^n [x_i^2 - 10 \cos(2\pi x_i)]$	$-5.12 \leq x_i \leq 5.12$	5, 10	0
F5	step	$\sum_{i=1}^n (x_i + 0.5)^2$	$-100 \leq x_i \leq 100$	5, 10	0
F6	Schwefel's p2.22	$\sum_{i=1}^n x_i + \prod_{i=1}^n x_i $	$-10 \leq x_i \leq 10$	5, 10	0
F7	Quadric noise	$\sum_{i=1}^n ix_i^4 + rand(0, 1)$	$-1.28 \leq x_i \leq 1.28$	5, 10	0
F8	quadric	$\sum_{i=1}^n (\sum_{j=1}^i x_j)^2$	$-100 \leq x_i \leq 100$	5, 10	0

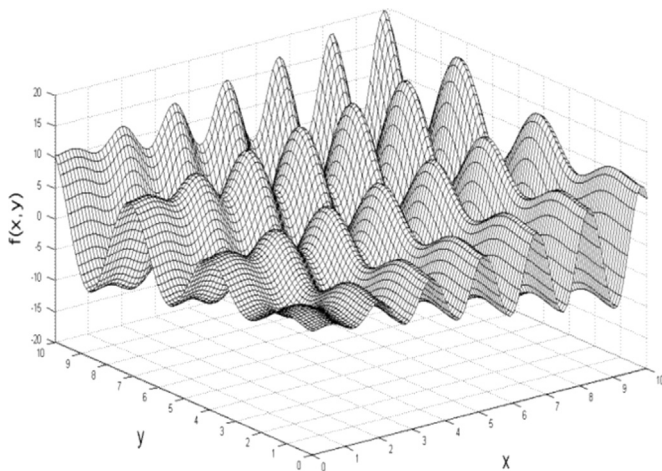


Fig. 10. 3D diagram of F1 [29].

GA, PSO [30] and the forest optimization algorithm (FOA) [31], are among algorithms which have been compared to WCC in the second experiment. The experimental results obtained from over 30 separate execution, are listed in Table 7 as follows: benchmark functions' alias names, the number of variables, algorithms' names, the first population, the level of acceptable accuracy, the number of fitness functions callings in which an algorithm reaches a definite level of accuracy at its worst, at its best, and its average states, the average of obtained results, the average of obtained

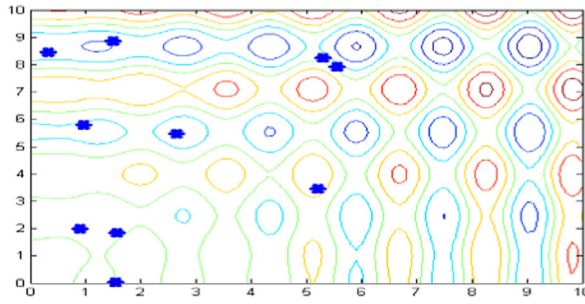
results and the elapsed time in which an algorithm is successful in reaching the level of accuracy. Reaching definite accuracy is considered a stop condition (Table 8).

In order to compare the above-mentioned algorithms, we will use $F_k(i)$, where K is the number of benchmark functions and i is a dimension or the number of variables. As you can see in Table 3, GA does not have proper performance, so it is not comparable with the other algorithms. Since there is a close competition among WCC, PSO, and FOA, they can be compared in two ways:

First, we compare the algorithms with an average number of evaluation functions callings. The results are as follows: FOA is better than the others for F1(2), F2(10), F3(5), F4(5), F5(5) and F7(5); PSO is better than the other algorithms for F2(5) and F7(10); and WCC is better than the others for F3(10), F4(10), F5(10), F6(5), F6(10), F8(5) and F8(10).

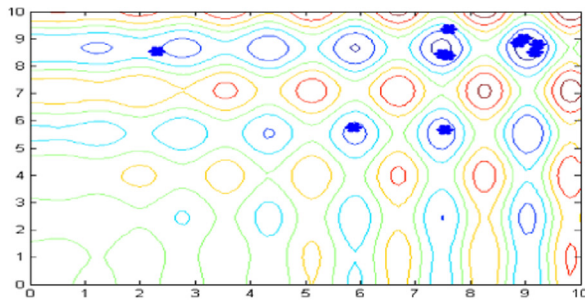
Then we compare the algorithms with an average number of the elapsed time, with the result that GA is better than the others for F2(5); PSO is better than the others for F3(10), F5(10), F6(5) and F7(10); and WCC is better than the others for F5(5), F6(10), F7(5), F8(5) and F8(10). FOA is better than the others for only F3(5) due to the local and global seeding time.

In conclusion, we have to pay attention to a kind of trade between the elapsed time and the number of evaluation functions callings. The first method is appropriate for problems that need more time for evaluation functions, and the second method is appropriate for problems that need less time for evaluation functions.



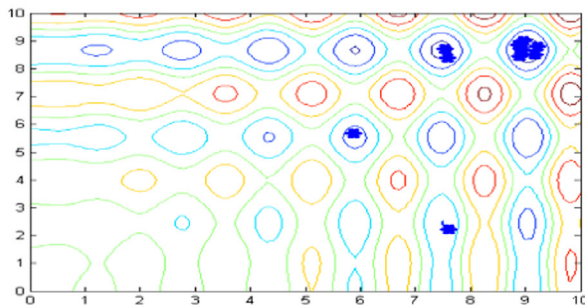
P1	P2	Score
0.9048	1.9597	-1.9284
5.5542	7.9049	-2.1280
5.2086	3.4503	6.96530
2.6671	5.4486	-8.4902
0.9868	5.7701	-6.1402
1.5889	1.8360	-0.9069
1.5565	0.0118	-0.0888
1.5002	8.8374	-9.3867
5.3096	8.2439	-2.7466
0.3330	8.4251	-8.1064

a: randomly generated values



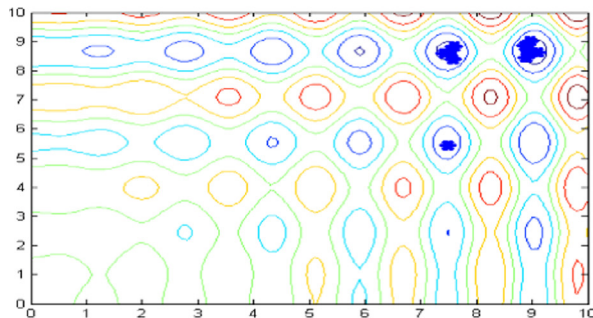
P1	P2	Score
7.6037	9.3280	-8.37540
9.1780	8.4878	-16.5698
7.6018	8.3885	-14.5217
9.2203	8.7835	-15.9905
2.3173	8.5285	-8.79200
5.8766	5.7574	-11.3660
7.5371	5.6705	-13.0618
8.8860	8.8334	-16.4057
8.9829	8.9773	-16.5140
7.4904	8.4251	-15.8695

b: positions and values of teams at the end of 3th session



P1	P2	Score
7.6037	2.2152	-8.74310
9.1780	8.4878	-16.5698
7.6018	8.3885	-14.5217
9.2203	8.7835	-15.9905
8.9486	8.6694	-17.9731
5.8766	5.6500	-11.7969
7.5371	8.7068	-16.6833
8.8860	8.8334	-16.4057
8.9829	8.9773	-16.5140
8.9118	8.4251	-16.3294

c: positions and values of teams at the end of 6th session



P1	P2	Score
7.6037	8.8196	-15.4805
9.1175	8.6147	-18.0554
7.6018	8.3885	-14.5217
7.4260	8.5864	-16.7442
8.9486	8.6694	-17.9731
7.5019	5.4253	-13.3086
7.5371	8.7068	-16.6833
8.8860	8.8334	-16.4057
8.9829	8.9773	-16.5140
8.9118	8.4251	-16.3294

d: positions and values of teams at the end of 9th session

Fig. 11. The location and values of teams for some of the iterations.

Table 8
Experimental results for benchmark functions.

Function	Dim	Algorithm	Population	Worst	Best	Num_eval	Acc	Result	Iter	el.time
F1	2	WCC	10	33,723	13,301	23,558.1	0.001	-18.5546	7	0.4929
F1	2	FOA	30	3281	368	1092.9	0.001	-18.5545	141.6	2.995
F1	2	PSO	30	31,862	12,567	22,258.31	0.001	-18.5546	104	0.5217
F1	2	GA	30	62,937	24,823	43,966	0.001	-18.5543	1523.5	0.9199
F2	5	WCC	40	9172	1804	4547.5	0.5	0.0312	2	0.4437
F2	5	FOA	30	19,043	4400	8847.1	0.5	0.3900	1402.3	0.8086
F2	5	PSO	30	10,440	2640	4320.72	0.5	0.3906	71	0.3887
F2	5	GA	30	11,613	4806	9911.3	0.5	0.4111	324.53	0.3250
F3	5	WCC	10	1147	64	357	0.001	0.0003	1.4	0.2271
F3	5	FOA	30	881	108	351.9	0.001	0.0003	44.9	0.0951
F3	5	PSO	30	3680	660	1756	0.001	0.0005	29.26	0.2143
F3	5	GA	30	1550	601	720.3	0.001	0.0001	24.8	0.0803
F4	5	WCC	15	6775	3261	4747	0.1	0.0011	2.22	0.2823
F4	5	FOA	30	5516	2655	3865.4	0.1	0.0011	610.73	0.2299
F4	5	PSO	30	52,410	25,227	36,722	0.1	0.0011	611.01	2.1838
F4	5	GA	30	22,720	10,936	15,919	0.1	0.0459	551.87	0.9467
F5	5	WCC	15	3150	2950	3060	0.001	0.0001	1.85	0.0227
F5	5	FOA	30	6517	793	2186.6	0.001	0.0001	944.55	0.2696
F5	5	PSO	30	7200	1740	3828	0.001	0.0001	62.8	0.0269
F5	5	GA	100	7959	4961	6202.8	0.001	0.0001	71	0.3846
F6	5	WCC	10	2387	1686	2218.9	0.01	0.0002	5	0.2809
F6	5	FOA	30	4065	1129	2220.6	0.01	0.0067	651.80	0.3501
F6	5	PSO	30	12,180	6000	8331	0.01	0.0084	137.85	0.2039
F6	5	GA	100	20,787	8409	13,443	0.01	0.0047	155.5	0.9385
F7	5	WCC	15	824	51	433.75	0.01	0.0049	1	0.0561
F7	5	FOA	30	455	200	266.15	0.01	0.0046	44.45	0.1091
F7	5	PSO	30	23,160	2400	15,501	0.01	0.0030	257.35	0.1430
F7	5	GA	100	45,151	7212	25,031	0.01	0.0093	404.5	0.6031
F8	5	WCC	10	4413	3284	4441.9	0.1	0.0644	2.15	1.2968
F8	5	FOA	30	69,225	6472	28,011	0.1	0.0656	8305.5	2.8129
F8	5	PSO	30	12,360	4740	8001	0.1	0.0706	132.35	1.1747
F8	5	GA	1000	25,403	17,534	20,612	0.1	0.0262	23.5	2.2699
F2	10	WCC	10	9019	6980	8257.3	0.5	0.2564	2.25	0.4520
F2	10	FOA	30	1407	2231	7510.5	0.5	0.3906	173	0.6633
F2	10	PSO	30	7880	15,440	12,057	0.5	0.3906	199.95	0.1895
F2	10	GA	30	44,788	4820	19,566	0.5	0.1124	677.57	3.5848
F3	10	WCC	10	2481	241	801.42	0.001	0.0005	1.28	0.1171
F3	10	FOA	30	2544	60	924.4	0.001	0.0005	27.6	0.1852
F3	10	PSO	30	4900	1680	3432	0.001	0.0005	57.02	0.1135
F3	10	GA	30	2701	1451	2045.7	0.001	0.0010	70.7	0.2038
F4	10	WCC	15	28,271	17,402	23,310	0.05	0.0278	3.85	1.76
F4	10	FOA	30	29,184	17,964	24,063	0.05	0.001	820.5	1.8169
F4	10	PSO	30	84,898	52,258	70,000	0.05	0.004	1160	3.2853
F4	10	GA	30	63,643	39,175	52,475.1	0.05	0.0448	1818.5	3.9621
F5	10	WCC	15	3150	2950	3050	0.001	0.0001	1.85	0.0486
F5	10	FOA	30	15,465	3876	10,667	0.001	0.0001	1288.7	0.2059
F5	10	PSO	30	8040	1980	3714	0.001	0.0001	60.9	0.0113
F5	10	GA	1000	58,465	46,448	52,329	0.001	0.0001	60	6.5164
F6	10	WCC	10	7556	5062	6037.3	0.01	0.0035	5	0.4102
F6	10	FOA	30	18,135	3909	11,512.2	0.01	0.0076	3521.8	0.9298
F6	10	PSO	30	13,440	5880	8604	0.01	0.0086	142.4	0.4254
F6	10	GA	1000	80,018	50,413	59,809	0.01	0.0099	68.75	6.6464
F7	10	WCC	5	4716	673	2558.3	0.1	0.0807	1.3	0.2300
F7	10	FOA	30	1501	761	1338	0.1	0.0851	597.75	0.4900
F7	10	PSO	30	1020	420	663	0.1	0.0550	10.05	0.1355
F7	10	GA	100	15,807	11,478	13,016	0.1	0.0928	14.75	1.9884
F8	10	WCC	5	9679	6487	8874.3	0.5	0.3307	3.65	0.1485
F8	10	FOA	30	22,358	1407	9978	0.5	0.3605	2945.7	0.8480
F8	10	PSO	30	13,500	4200	9215	0.5	0.2235	119.25	0.1654
F8	10	GA	1000	106,815	46,279	67,488	0.5	0.4985	77.5	12.4106

4. Conclusion

In the current study, a new evolutionary algorithm, known as WCC, which was inspired by human sports rules was introduced. As we know, there are lots of interesting events such as competitions, award ceremonies, victory parties and so many others in sports. Every team has a set of rules and some players who are put into different groups; every player performs a different task. Different teams compete against each other and qualified ones ascend to the next stage and continue their competition. At the

end of a season, a champion is introduced and the other teams prepare for a new season. We evaluated the performance of the proposed algorithm on a motif discovery problem and eight benchmark functions. Moreover, we compared WCC with GA, ICA, PSO, ACO and LA, based on the above-mentioned problems. The experimental and numerical results indicated that the proposed algorithm's performance was better than the other algorithms' performance. The proposed algorithm had reasonable execution time, acceptable precision, and more satisfactory results in comparison to the other algorithms. According to our results, WCC was

better than the others and from the perspective of the elapsed time standard deviation, it was better than all the other algorithms. The WCC's elapsed time was a little longer than the others', except GA, however if we consider the WCC's elapsed time a termination condition for the other algorithms, its obtained results will be better than those of the others, too. The ICA's results standard deviation was the best in comparison to the others', but as we observed earlier, its best result was worse than the ACO's and WCC's. The WCC's obtained results standard deviation was also better than the ACO's. A trade discovery between WCC parameters that are as follows: playing chances, the number of groups, the number of teams and the number of seasons is an important topic for future research or combining WCC with the other metaheuristic algorithms and applying it to different optimization problems can be considered an interesting topic for research.

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