WATER DISTRIBUTION NETWORKS OPTIMAL DESIGN USING THE HONEY BEES MATING OPTIMIZATION ALGORITHM

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The Honey Bees Mating Optimization Algorithm (HBMOA) has been used to optimize the design of a water distribution network, meaning to obtain the least-cost design of that looped hydraulic network. HBMOA is a new evolutionary algorithm, where the search procedure is inspired by the process of mating in a real honey bee colony. The performances of two modified HBMOA forms have been analysed, by comparing our results obtained for the Hanoi water distribution network (a well known test-case), with other results obtained using other stochastic methods for combinatorial optimization (such as the Ant Colony Optimization Algorithm, the Simulated Annealing Algorithm, and various formulations based on Genetic Algorithms). Among all those methods, the 2nd modified form of HBMOA, an original form proposed here, denoted HBMOA-M2, gives the smallest cost of Hanoi network. Thus, HBMOA-M2 can be highly ranked among the most known and effective algorithms in the literature.

Keywords: Honey Bees Mating Optimization Algorithm, Hanoi water network.

1. Introduction

Evolutionary algorithms became common tools used to solve a wide range of combinatorial optimization problems in engineering, applied sciences, biology and commerce. Among them, Genetic Algorithms (GA) have been extensively and successfully implemented [1], [2]. Within the modern swarm-based approach to optimization, the search algorithm mimics the behaviour of real colonies of social insects, like ants (Ant Colony Optimization Algorithm – ACOA [$3\div5$]), bumble bees (Bumble Bees Mating Optimization Algorithm [6]), and honey bees (Honey Bees Mating Optimization Algorithm, abbreviated HBMOA [7], [8]).

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the second one, HBMOA-M2, is issued from HBMOA-M1, after improving supplementary two classical hypotheses; HBMOA-M2 proposed here is original (a new HBMOA formulation) that improves clearly the computational efficiency.

Various stochastic methods for combinatorial optimization can be applied to obtain the least-cost design of a looped water distribution network. Stochastic optimization refers to the minimization or maximization of the objective function (performance function), in the presence of randomness within the search process. By considering the Hanoi water distribution network as basic test-case, the performances of both modified HBMOA forms (mentioned above), have been compared in this paper with the performances of other stochastic methods, like ACOA, the Simulated Annealing Algorithm (SAA) [10], and various formulations based on GA. HBMOA-M2 formulation gives the smallest cost of Hanoi network.

2. Honey Bees Mating Optimization Algorithm description

Within Honey Bees Mating Optimization, the search algorithm is inspired by the process of mating in a real honey bee colony. The queen bee, drones (male bees) and brood have their own genome composed of genes. When modelling the mating process, the genome is attached to one solution (to one bee) of the studied optimization problem. One genome is mathematically described by a list of numerical values, where each value is attached to a decision variable (gene) that represents an unknown of the problem. Depending on the values of unknowns from such a list, the performance function of the problem has a greater or smaller value, so the genome of the associated solution (bee) is stronger or weaker. Within this paper, a solution (bee) has a number of unknowns (genes) equal to the total number of pipelines that form the studied hydraulic network, and the best performance means the lowest network cost *C*, the performance function *F* being defined as: $F = 10^7 C^{-1}$, with *C* in US dollars [\$].

At the first iteration, a given number of bees N_{in} (potential solutions of the problem) is generated, each with its genome (list of numerical values of the unknowns), randomly built within admissible ranges of the variables. Then, that initial population of bees is ranked decreasingly upon the performance function values, and the best solution (the one with the best performance) is selected as initial queen bee. Further, a number N_D of solutions, ranked after the queen, forms a list of drones, which may mate with the queen during the first mating-flight, while the rest of initially generated solutions are ignored. Besides its genome, which is the strongest, the queen is characterised by her speed V and/or energy E, as well as by her spermatheca capacity N_S (that is kept constant during all mating-flights, and equals the maximum number of drones that can mate with the queen during such a flight).

HBMOA consists of the following five steps [7]:

① *Mating-flight* that represents a global iteration, during which the current queen bee Q (the best solution, which means here the selection of pipe's diameters leading to the lowest network cost) selects randomly some drones, and by mating, each drone genome is stored in her spermatheca. Before leaving the hive, the queen is initialized with some amount of speed and/or energy, randomly generated in the range $0.5\div1$. The scheme of the mating-flight process consists of:

Selecting randomly a drone D from the list of drones formed initially;

• Computing the probability of mating between that drone and the queen Q, using an annealing function of Boltzmann type, as in SAA:

$$\operatorname{Prob}(Q, D) = \exp\left(-\Delta f / V(t)\right) = \exp\left(-\left|f(Q) - f(D)\right| / V(t)\right), \quad (1)$$

where Prob(Q,D) is the probability of a successfully mating; f(Q) and f(D) are the performance functions of Q and D; V(t) is queen speed at time t. The function (1) gives greater values when queen's speed is great (at the beginning of the flight), or when drone's performance function is closed to queen's performance function;

• Generating a random number $r \in (0,1)$; if Prob(Q,D) > r, then the drone D successfully mated with the queen, and his genome is added to spermatheca;

• Even if the mating succeed or not, queen's speed and energy decay upon *t* as:

$$V(t+1) = \alpha V(t) \text{ and } E(t+1) = (E(t) - \delta E), \qquad (2)$$

where $\alpha \in [0,1]$ is a decay coefficient (usually close to 1), and δE is the amount of energy loss after each transition. In this paper, V(0)=1 and $\alpha = 0.97$;

• Iterating the above process, either until queen's spermatheca is full (maximum capacity N_s), or until her speed/energy decays down to a minimum given value, V_{min} or E_{min} . In this paper, we consider $V_{min} = 0.2$;

⁽²⁾ Creation of new brood (trial solutions), by crossovering the queen own genome with drones' genomes: after queen's return to the hive, a given number N_B of new bees appears. Thus, a drone genome is randomly selected from the spermatheca, and is combined with queen's genome, leading to the genome of a new bee. The new genome creation is made here with a single heuristic crossover operator used in GA, as:

$$B_i = Q + \operatorname{round}\left(r\left(Q - D_i\right)\right),\tag{3}$$

where the drone D_i is the solution randomly selected from the spermatheca to generate the new *i* solution (new bee B_i), and "round" refers to rounding towards the nearest integer;

③ Improvement of brood's fitness (trial solutions) by worker bees (heuristics): after creating the total number N_B of new bees, the worker bees start to take care of the brood. In this paper, workers role is implemented by a single mutation operator, which is applied to a new bee for N_M times (N_M is an imposed number of mutations, equal to the number of worker bees), thus simulating the *feeding* with royal jelly, to improve bee's performance. After selecting randomly a new bee B_i , the mutation operator chooses randomly one gene j (one variable) from bee's genome, and modifies his current value v_{ij} . We admit a non-uniform mutation operator as in GA, where the value of gene j selected for mutation is modified to:

$$v_{ij_{new}} = \text{round} \left(v_{ij} + r_2 \left(v_{ij_{max}} - v_{ij} \right) \right), \text{ if } r_1 < 0.5$$

$$v_{ij_{new}} = \text{round} \left(v_{ij} - r_2 \left(v_{ij} - v_{ij_{min}} \right) \right), \text{ if } r_1 \ge 0.5$$
 (4)

where $r_1, r_2 \in (0; 1)$ are random numbers; $v_{ij_{min}}, v_{ij_{max}}$ are limits of gene's values; (a) Adaptation of workers fitness in accordance with the amount of improvement (performance) achieved on brood. Here, the performance function of each solution modified by mutation is computed;

⑤ Replacement of the least fittest queen by a new queen (new best solution), selected among the fitter brood. If the performance of a new solution (modified by mutation) is better than the performance of the current queen, then that new solution will become new queen, replacing the old queen. In other words, after N_M imposed mutations applied on brood, the initial queen can preserve his role for the next global iteration, or it can be replaced.

The above five steps are iterated to minimize or maximize the objective function corresponding to the studied optimization problem (here, the purpose is to maximize the performance function F, meaning to minimize the hydraulic network cost C). Computations stop either when the maximum number of iterations k_{max} is reached, or before, at $k < k_{max}$, when the imposed precision criterion for queen's performance function is satisfied. When passing from the current iteration k, to the next one (k+1), there are several possible HBMOA formulations, which are extremely important with respect to algorithm's convergence. Within the classical HBMOA formulation [7], [8], all brood fed by worker bees, who failed to replace the existing queen after the current iteration k, are completely destroyed and a new list of drones (N_D new solutions) is randomly generated for the next iteration (k+1). Within the modified HBMOA forms, HBMOA-M1 [9] and the new HBMOA-M2, brood fed by worker bees and not transformed in a new queen in the current iteration k, are inserted within the list of drones for the next iteration (k+1). Even if it is far from the mating process in a real honey bee colony, that approach improves clearly the computational

efficiency of the search algorithm, because the bees already fed within the k iteration will have a greater performance at the beginning of the (k+1) iteration, than a new list of drones, fully randomly formed as in the classical approach. The original new HBMOA-M2 form proposed in this paper, is an improvement of HBMOA-M1, by adding two modifications to it, namely:

 \succ the use of tournament rule when creating new brood in step @, by selecting randomly 3 drone's genomes from the spermatheca, and combining the best of them (the one with best performance) with queen's genome. It ensures a greatest chance to available genetic material to produce better new bees;

> in step ③ (brood feeding), for each solution (new bee) randomly selected, the mutation operator chooses randomly 3 genes from bee's genome, and modifies their current values upon equations (4). It ensures to new solutions a more intensive performance improvement.

3. Numerical results

The numerical results obtained within this paper, using two modified HBMOA forms, namely HBMOA-M1 and HBMOA-M2, correspond to the Hanoi water distribution network design optimization. Hanoi network is a well-known test-case, described in 1990 by Fujiwara & Khang, and intensively studied in the literature with different stochastic methods for combinatorial optimization [10]. The first evolutionary approach using GA, by Savic & Walters in 1997, led to a cost C = 6,073,000\$ of Hanoi network. Cuhna & Sousa [10], using SAA in 1999, obtained C = 6,056,000\$. By enlarging the list of 6 pipe's diameters with two additional values, namely a smaller value: 254mm (10 in.) with 33.39\$/m, and a greater value: 1270mm (50 in.) with 450.9 \$/m, Popa & Tudor [2] obtained a cost C = 5,828,411\$ of Hanoi network using GA, while Vuță & Popa [4] obtained C = 5,443,191\$ using ACOA.

Hanoi network consists of 32 nodes and 34 main pipelines, labelled with ID numbers as in Figure 1. Data of that network are summarized in Cuhna & Sousa [10]. We enlarged here the list of pipe's diameters up to 8 values, as in Popa & Tudor [2], and we sort them increasingly, by assigning them a marker with an integer value from 1 to 8 (where marker =1 for 254mm-diameter, and marker =8 for 1270mm-diameter). Assuming that Hanoi network is flat, with 100m head at its source (node 1), and imposing a minimum head $H_{min} = 30m$ at each node, we performed the network design using both HBMOA-M1 and -M2. Head losses were computed with Darcy-Weissbach formula. The friction factor was defined by Prandtl-Nikuradse formula, for 0.2mm pipe's wall roughness.

To limit the number of possible design options, for each of those 34 pipes, we selected one among 4 successive values from diameter's list (1 of 4 successive

marker values), which leads to $4^{34} = 2.95 \cdot 10^{20}$ distinct options. We considered as decision variables (genes) of a solution (bee), the integer values of the selected markers, meaning that each solution has 34 unknowns (integers from 1 to 8).



Fig. 1. Hanoi network: node's ID from 1 to 32 (left) and pipe's ID from 1 to 34 (right)

The initial population of potential solutions (bees) has been randomly generated as following: $N_{in} = 99$ solutions for HBMOA-M1, with a maximum pressure deficit of 100m with respect to H_{min} , and $N_{in} = 96$ for HBMOA-M2, with 50m maximum pressure deficit. For both HBMOA forms, the best initial solution has been appointed queen, and the next $N_D = 40$ solutions (ranked after the queen) formed the list of drones; we imposed a spermatheca capacity of $N_S = 30$, a number $N_B = 30$ of new bees and $N_M = 40$ worker bees (mutations).

Firstly we performed 31 runs of HBMOA-M1 with $k_{max} = 1000$ iterations, to identify acceptable suboptimal solutions among the 4³⁴ distinct solutions. All 31 solutions corresponded to an unrepeatable cost of Hanoi water network, ranged from C = 5,418,790\$ to C = 5,980,587\$, with a mean cost: $\overline{C} = 5,685,926$ \$; a standard deviation: $\sigma_c = 141,097$ \$; and a 95% confidence interval for the mean cost: 5,635,435\$ < $\mu_{\overline{C}}$ < 5,736,417\$, which is substantially lower than the best solution found with GA by Popa & Tudor [2]. The cost C = 5,418,790\$ attached to the best solution obtained with HBMOA-M1 is inferior to the best solution found with ACOA by Vuță & Popa [4].

Further, we performed 10 runs of HBMOA-M2 for $k \le k_{max} = 500$ iterations, with an alternative stop condition after reaching the imposed maximum

value of the performance function: $F_{max} = 1.835$ (meaning C = 5,450,000\$). All runs started from the same initial bees' population, with the performance function of initial queen: F = 1.515 (C = 6,599,310\$); each run yielded a different result. Nine solutions corresponded to a cost from C = 5,401,236\$ to C = 5,446,029\$. For a single run among 10, the convergence condition hasn't been achieved for $k = k_{max}$ iterations, the final cost being C = 5,461,949\$. The solution of run no. 2 converged within only k = 21 iterations (for that solution, C = 5,446,029\$). The solution of run no. 5, with the smallest cost of Hanoi network: C = 5,401,236\$ (with final performance function F = 1.851), becomes the *optimal solution of the studied problem*, the attached cost being inferior to any previous result, obtained with any other method! In Table 1, we present the pipe diameters D, volumetric flow rates Q_v and heads H within Hanoi network, for the above optimal solution, together with other network data (pipe lengths L and water demand Q_d at each node). At node 30 of that network we obtained the minimum head: 30.39m.

Table 1	
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pe	L [m]	D [mm]	pe	L [m]	D [mm]	pe	L [m]	D [mm]	ode	Q_d [m ³ /h]	ode	Q_d [m ³ /h]	ode	Q_d
Ŀ	$Q_v [m^3/h]$		Pi	$Q_{\nu} [\text{m}^3/\text{h}]$		Ŀ	$Q_{\nu} [\text{m}^{3}/\text{h}]$		ž	<i>H</i> [m]	Ň	<i>H</i> [m]	ž	<i>H</i> [m]
1	100 199	100 1270 19940.0		800 508 1525.8		25	1300 609.6 2480.0		1	-19940 100	13	940 31.40	25	170 37.76
2	1350 190	1270 50.0	14	500 406.4 910.8		26	850 10	508 84.9	2	890 99.00	14	615 42.56	26	900 34.77
3	900 833	1016 35.8	15	550 406.4 630.8		27	300 254 184.9		3	850 86.63	15	280 38.59	27	370 33.63
4	1150 1016 8205.8		16	2730 254 [∞] 135.7 [∞]		750 18	254 35.1	4	130 81.59	16	310 36.50	28	290 44.87	
5	1450 1016 7480.8		17	1750 304.8 729.3		29	1500 69	406.4 95.0	5	725 75.36	17	865 30.88	29	360 30.75
6	450 647	1016 75.8	18	800 508 2074.3		30	2000	304.8)5.0	6	1005 68.82	18	1345 70.93	30	360 30.39
7	850 512	762 25.8	19	400 508 2134.3		31	1600	254 5.0	7	1350 67.30	19	60 81.20	31	105 32.06
8	850 457	762 75.8	20	2200 77	1016 /30.0	32	150 31	254 5.0	8	550 59.26	20	1275 76.04	32	805 33.51
6	800 762 4050.8		21	1500 14	406.4 15.0	33	860 42	406.4 20.0	9	525 52.85	21	930 47.32		
10	950 200	609.6 00.0	22	500 4	245 85.0	34	950 12	508 25.1	10	525 48.12	22	485 34.18		
11	1200 150	609.6 00.0	23	2650 50	762 40.0				11	500 43.74	23	1045 51.80		
12	3500 508 940.0		24	1230	762 00.0				12	560 40.63	24	820 46.97		

Hanoi water distribution network data, for the optimal solution (5th run of HBMOA-M2)

The mean cost of Hanoi network, $\overline{C} = 5,437,037$, obtained by using HBMOA-M2, is lower with almost 200,000\$ than the 95% confidence interval for the mean cost obtained using HBMOA-M1.

All computations were performed with our own numerical code, written in Pascal. Then, all data from Table 1, excepting the flow rate values, were inserted in EPANET network map, to plot the flow direction from Figure 1.

4. Conclusions

The Honey Bees Mating Optimization Algorithm has been implemented to Hanoi network design optimization, using a modified form of classical HBMOA, denoted HBMOA-M1, and an original new HBMOA form that improves clearly the computational efficiency, denoted HBMOA-M2. We tested the performance of our algorithms on Hanoi hydraulic network, because it is a well-known testcase, intensively studied in literature, since 1990, with various stochastic methods for combinatorial optimization. The optimal solution found with HBMOA-M2 corresponds to 5,401,236\$ cost of Hanoi water distribution network, which is inferior to any previous cost, obtained with any other method! That allows us to claim that HBMOA-M2 formulation can be highly ranked among the most known and effective algorithms in the literature.

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