

Phymastichus-Hypothenemus-based Algorithm for Optimal Node Selection on Pinning Control of Complex Networks

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Abstract—In this article, a new optimized node selection algorithm is proposed for implementation of pinning control for complex networks. This algorithm is inspired on the biological control of berry borers by means of parasitoid agents. The algorithm optimizes node selection using a criterion to ensure searching asymptotic stability of the complex network. The objective is to determine the optimal selection of nodes for pinning control applications.

I. INTRODUCTION

The pinning control technique is used to determine a small number of controlled nodes to satisfy behavioral objectives in complex networks [1], [2]. An open problem related to this topic is to determine how many and which nodes are needed and where to place them in order to achieve the best desired performance [3]. The nodes selection on complex networks for pinning control can be optimized based on network topology, coupling strength, synchronization time, convergence time, energy consumption, key nodes to control, etc. Therefore the pinning control technique can be optimized for multiple criteria [4], [5]. The heuristic algorithms represent a viable strategy to tackle this problem, especially in optimizing criteria of large complex networks, for instance the following heuristic algorithms can be considered: PSO [6], AMO [7], ABC [8], BBO [9], WOA [10] and ACO [11]. However, the fundamental problem of determining the number of pinning nodes, which nodes and where to place them, implies nonlinear combinatorial optimization. When optimizing a multi-constraint problem with heuristic optimizers, especially the ones based on swarms, which depend strictly on a good reference of the best performance, both in initialization and in the iterative stage [12], often the swarm presents saturation at the limits of the search space, or in other cases the agents will converge to incorrect solutions [13]. The main contribution of this article is the design of a new heuristic optimizer, hereafter referred to

as the Phymastichus Hypothenemus Algorithm (PHA), which emulates the biologic control of the *Hypothenemus hampei* berry borers by the *Phymastichus coffea* wasps. This algorithm is developed to solve multi-constraint nonlinear combinatorial optimization problems for pinning control applications of complex networks, determining optimal nodes selection, and achieving simultaneously stabilization using the V-stability tool [14]. Simulation results are presented showing the performance of this new proposed algorithm, and the obtained results are also compared with the respective results using some other heuristic algorithms.

This article is organized as follows. In Section II, we introduce the pinning control for complex networks based on the V-stability concept and other mathematical tools. In Section III, we describe the proposed algorithm, and present its principles and characteristics. In Section IV, we compare PHA with other heuristic algorithms, for the stabilization of complex networks with different characteristics. Finally, we state the respective conclusions in Section V.

II. PRELIMINARIES

The preliminary concepts introduced in this section are taken mainly from [15]. Consider a network of N_n nodes, where each node is an N_s -dimensional dynamical system, as:

$$\dot{\mathbf{x}}_i = f_i(\mathbf{x}_i) + \sum_{\substack{j=1 \\ j \neq i}}^{N_n} c_{ij} a_{ij} \Gamma(\mathbf{x}_j - \mathbf{x}_i), \quad (1)$$

where $\mathbf{x}_i = (x_{i,1}, x_{i,2}, \dots, x_{i,N_s})^T \in \mathbb{R}^{N_s}$, $i = 1, 2, \dots, N_n$, are the state of the i -th node n_i , $f_i : \mathbb{R}^{N_s} \rightarrow \mathbb{R}^{N_s}$ represents the self-dynamics of n_i , constants c_{ij} are the coupling strengths between n_i and n_j , $\Gamma \in \mathbb{R}^{N_s \times N_s}$ describes the components linking for each pair of connected nodes \mathbf{x}_j and \mathbf{x}_i , and a_{ij} are the entries of the Laplacian matrix

$A \in \mathbb{R}^{N_n \times N_n}$, which represents the topological structure of the network satisfying the following conditions: if there is a connection between n_i and n_j , for $i \neq j$, then $a_{ij} = a_{ji} = 1$; otherwise, $a_{ij} = a_{ji} = 0$, for $i \neq j$; and the diagonal elements are defined by $a_{ii} = -\sum_{\substack{j=1 \\ j \neq i}}^{N_n} d_i$, $i = 1, 2, \dots, N_n$, where d_i is the connection degree of n_i .

The pinning control technique applies local state-feedback to a small fraction of nodes in (1), which are named as pinning nodes [16]. Assuming the diffusive condition $c_{ii}a_{ii} + \sum_{\substack{j=1 \\ j \neq i}}^{N_n} c_{ij}a_{ij} = 0$, $i = 1, 2, \dots, N_n$, the network (1) can be rewritten in a compact controlled form as

$$\dot{\mathbf{x}}_i = f_i(\mathbf{x}_i) + \sum_{j=1}^{N_n} c_{ij}a_{ij}\Gamma\mathbf{x}_j + B_i\mathbf{u}_i, \quad (2)$$

where $B_i \in \mathbb{R}^{N_s \times l}$ is the input matrix, $\mathbf{u}_i \in \mathbb{R}^{N_s}$ is the control input, defined as

$$\mathbf{u}_i(\mathbf{x}_i) = \begin{cases} -K_i\mathbf{x}_i & i \in \mathcal{N} \\ 0 & i \notin \mathcal{N}, \end{cases} \quad (3)$$

where $K_i \in \mathbb{R}^{l \times N_s}$ is the gain matrix of the i -th node i , with $n_i \in \mathcal{N}$, and \mathcal{N} is the set of pinning nodes, whose cardinality N_p satisfies $1 \leq N_p \leq N_n$ [1]. Thus, the self-dynamics of the controlled nodes become

$$\dot{\mathbf{x}}_i = f_i(\mathbf{x}_i) - BK_i\mathbf{x}_i, \quad i = 1, 2, \dots, N_p. \quad (4)$$

In order to determine if the network (2) is locally asymptotically stable at the equilibrium point $\bar{\mathbf{X}}$, consider a continuously differentiable Lyapunov function

$$V_N(\mathbf{X}) = \sum_{i=1}^{N_n} \frac{1}{2} \mathbf{x}_i^T \mathbf{P} \mathbf{x}_i, \quad \mathbf{P} = \mathbf{P}^T > 0, \quad (5)$$

$$\mathbf{X} = (\mathbf{x}_1^T, \dots, \mathbf{x}_{N_n}^T)^T$$

such that

$$\begin{aligned} \dot{V}_N(\mathbf{X}) &= \sum_{i=1}^{N_n} \mathbf{x}_i^T \mathbf{P} \left(f_i(\mathbf{x}_i) + \sum_{j=1}^{N_n} c_{ij}a_{ij}\Gamma\mathbf{x}_j - BK_i\mathbf{x}_i \right) \\ \dot{V}_N(\mathbf{X}) &< \sum_{i=1}^{N_n} \mathbf{x}_i^T \mathbf{P} \left(\theta_i\Gamma\mathbf{x}_i + \sum_{j=1}^{N_n} c_{ij}a_{ij}\Gamma\mathbf{x}_j + k_i\Gamma\mathbf{x}_i \right) \end{aligned} \quad (6)$$

where $k_i \in \mathbb{R} \geq 0$ is a bound for the control gain matrix K_i and θ_i is the passivity degree of $f(\mathbf{x}_i)$. Using the Kronecker product \otimes (6) is represented as,

$$\dot{V}_N(\mathbf{X}) < \mathbf{X}^T (-\Theta + G - \mathcal{K}) \otimes \mathbf{P} \Gamma \mathbf{X}, \quad (7)$$

where $c_{ij}a_{ij}$ are the entries of $G \in \mathbb{R}^{N_n \times N_n}$, $\Theta = \text{diag}(\theta_1, \theta_2, \dots, \theta_{N_n})$, $\mathcal{K} = \text{diag}(k_1, k_2, \dots, k_{N_n})$ and $\mathbf{P} \Gamma \geq 0$. Then, according to [14], the network (1) is locally asymptotically stable about its equilibrium point if the closed-loop characteristic matrix

$$M = -\Theta + G - \mathcal{K} \quad (8)$$

is semi-negative definite. The stability so derived is called the V-stability, and based on Assumption 1 in [14], this method converts the original stability problem to the study of the negativity property of (8), which strongly depends on the selection of $V_N(\mathbf{X})$ (and of θ_i).

The optimization problem consists in the construction of the main diagonal of the matrix \mathcal{K} , whose entries k_i are elements of set \mathcal{N} of fixed cardinality $N_p > N_{\lambda^+}$, where N_{λ^+} is the number of positive eigenvalues of the matrix M when $\mathcal{K} = 0$, such that, the number of pinned nodes cannot be less than N_{λ^+} [14], k_i elements are optimized with any objective function that depends on them. The optimization problem can then be formulated as follows:

$$\begin{aligned} &\text{minimize} && f(\mathcal{U}), \\ &\text{subject to} && \mathcal{U} = \{\mathbf{u}_i \mid i \in \mathcal{N}\}, \\ &&& \max\{R_e\{\lambda\{M\}\}\} < 0, \end{aligned} \quad (9)$$

where the control law of the i -th node n_i is defined as $\mathbf{u}_i = -k_i\mathbf{x}_i$, such that

$$\mathcal{K}_{ii} = \begin{cases} k_i & i \in \mathcal{N}, \\ 0 & i \notin \mathcal{N}. \end{cases} \quad (10)$$

Let $f(\cdot)$, the selected objective function, be formulated as

$$E_{t_0}(\mathcal{U}) = \frac{1}{2} \sum_{\mathbf{u} \in \mathcal{U}} \|\mathbf{u}(t_0)\|^2 = \frac{1}{2} \sum_{i \in \mathcal{N}} \|k_i\mathbf{x}_i(t_0)\|^2, \quad (11)$$

where $E_{t_0}(\mathcal{U})$ is the energy consumed on the pinning nodes at time t_0 .

Remark 1: Taking into consideration V-stability (7) and that energy is consumed only at the pinning nodes, the maximum value of energy consumption is at time t_0 .

III. PHYMASTICHUS-HYPOTHENEMUS ALGORITHM

The general form of the optimization problem introduced in the previous section consists in determining the value and the position of the elements k_i in the main diagonal of \mathcal{K} , such that the maximum eigenvalue of M is negative. Optimizing the value of k_i implies nonlinear optimization, while its position in \mathcal{K} corresponds to combinatorial optimization. In order to solve this optimization problem, we will present a new developed heuristic algorithm, named the Phymasticus-Hypothenemus Algorithm (PHA). The PHA is inspired from the biological control of the coffee berry borer (*Hypothenemus hampei*, Fig. 1(b)), by means of the parasitoid wasp (*Phymastichus coffea*, Fig. 1(a)) [17]. Agent *Hypothenemus* optimizes the value of k and agent *Phymastichus* optimizes its position on the diagonal of \mathcal{K} .

The multi-constraint nonlinear combinatorial optimization problem and the proposed Phymasticus-Hypothenemus are described as:

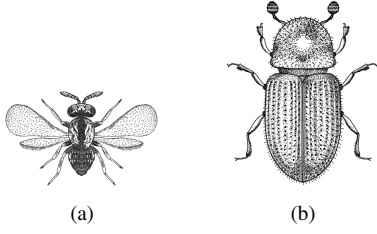


Fig. 1. (a) *Phymastichus coffea* Lasalle, (b) *Hypothenemus hampei* Ferrari.

$$\begin{aligned}
& \text{minimize} && f(\mathcal{U}) \\
& \text{subject to} && \mathcal{U} = \{H_{i,j}\mathbf{x}_j \mid j \in P_i\}, \\
& && \text{car}(P_i) = N_p, \\
& && \max \{R_e \{\lambda \{M(\Theta, G, \mathcal{K})\}\}\} < 0, \\
& && \mathcal{K}_i = \text{diag}(k_{i,1}, \dots, k_{i,j}, \dots, k_{i,N_n}), \quad (12) \\
& && k_{i,j} = \begin{cases} H_{i,j} & j \in P_i \\ 0 & j \notin P_i, \end{cases} \\
& && P_i \subseteq SS_P, \\
& && H_i \subseteq SS_H,
\end{aligned}$$

where $P_i \in \mathbb{N}^{N_p}$ and $H_i \in \mathbb{R}^{N_n}$ are the i -th agents *P. coffea* and *H. hampei* respectively, whose populations are defined as $\mathbf{P}(t) = [P_1(t)^T, P_2(t)^T, \dots, P_{N_a}(t)^T]^T$ and $\mathbf{H}(t) = [H_1(t)^T, H_2(t)^T, \dots, H_{N_a}(t)^T]^T$, N_a is the number of agents for both populations, N_p is the number of pinning nodes, $f(\cdot)$ is the objective function to be optimized for the implementation of the pinning control, $\text{car}(\cdot)$ is the set cardinality, $SS_P = [1, 2, \dots, N_n]$ is the search space of nodes (“coffee tree”) for *P. coffea* agents, n_j is the j -th node of the network, $SS_H \in \mathbb{R}^{N_n}$ is the search space for *H. hampei* agents; this search space is bounded as ${}^l\mathbf{b}_{i,j}(t) \leq SS_{H_j} \leq {}^u\mathbf{b}_{i,j}(t)$, $i \in [1, N_a]$, ${}^l\mathbf{b}(t) \in \mathbb{R}^{N_a \times N_n}$ being the lower bound and ${}^u\mathbf{b}(t) \in \mathbb{R}^{N_a \times N_n}$ the upper bound.

P. coffea lays two eggs per host (usually one male and one female) and the best situation for the biological control of *H. hampei* is the birth of a female and a male *P. coffea*, such that a single male *P. coffea* can fertilize multiple females; however, it needs a female to bore the host abdomen to emerge [17]. The parasitization process generates the following sub-types of agents and their fitness:

Case 1: Birth of only females,

$$\tilde{f}_i(t) = \begin{cases} f_i(t) & \text{if } t = 1 \vee f_i(t) < \tilde{f}_i(t-1) \\ \tilde{f}_i(t-1) & \text{else,} \end{cases} \quad (13)$$

$$\tilde{P}_i(t) = \begin{cases} P_i(t) & \text{if } t = 1 \vee f_i(t) < \tilde{f}_i(t-1) \\ \tilde{P}_i(t-1) & \text{else,} \end{cases} \quad (14)$$

$$\tilde{H}_i(t) = \begin{cases} H_i(t) & \text{if } t = 1 \vee f_i(t) < \tilde{f}_i(t-1) \\ \tilde{H}_i(t-1) & \text{else,} \end{cases} \quad (15)$$

where $\tilde{f}_i(t)$ is the fitness of the symbiotic relationship between the best local values $\tilde{P}_i(t)$ and $\tilde{H}_i(t)$.

Case 2: Birth of a female and a male,

$$\hat{f}(t) = \begin{cases} \tilde{f}_{\min}(t) & \text{if } t = 1 \vee \tilde{f}_{\min}(t) < \hat{f}(t-1) \\ \hat{f}(t-1) & \text{else,} \end{cases} \quad (16)$$

$$\hat{P}(t) = \begin{cases} \tilde{P}_{\min}(t) & \text{if } t = 1 \vee \tilde{f}_{\min}(t) < \hat{f}(t-1) \\ \hat{P}(t-1) & \text{else,} \end{cases} \quad (17)$$

$$\hat{H}(t) = \begin{cases} \tilde{H}_{\min}(t) & \text{if } t = 1 \vee \tilde{f}_{\min}(t) < \hat{f}(t-1) \\ \hat{H}(t-1) & \text{else,} \end{cases} \quad (18)$$

where

$$\begin{aligned}
& \tilde{P}_{\min}(t), \tilde{H}_{\min}(t) \rightarrow \tilde{f}_{\min}(t) \\
& \tilde{f}_{\min}(t) = \min\{\tilde{f}_1(t), \tilde{f}_2(t), \dots, \tilde{f}_{N_a}(t)\}, \quad (19)
\end{aligned}$$

$\hat{f}_i(t)$ is the fitness of the symbiotic relationship between the best global values $\hat{P}(t)$ and $\hat{H}(t)$ and v is a $N^a \times 1$ vector of ones. If the fitness $f_i(t) > \hat{f}_i(t)$, then there are no births involving at least one female.

The wasp visits (Fig. 1(a)) different coffee berries in order to search for *H. hampei* to parasitize. The visits are memorized on the new wasp generations by inheritance of the decision vectors $w(t)$, which determine the frequency of node visits. The i -th decision vector $w_i(t) \in \mathbb{R}^{1 \times N_n}$ is defined by:

$$w_{i,j}(t+1) = \begin{cases} 1 & \text{if } t = 1 \\ w_{i,j}(t) + 1 & \text{if } \tilde{f}_i(t) < \tilde{f}_i(t-1) \\ & \wedge j \in \tilde{P}_i(t) \\ w_{i,j}(t) + 1 & \text{if } \hat{f}(t) < \hat{f}(t-1) \\ & \wedge i \in \mathcal{N}_r(t) \wedge j \in \hat{P}(t) \\ w_{i,j}(t) & \text{else,} \end{cases} \quad (20)$$

where \mathcal{N}_r is a set of uniformly distributed random nodes (without repetition).

The j -th node selected to be pinned by the i -th agent $P_i(t)$ is

$$P_{i,j}(t) = N_n + 1 - \sum_{k=1}^{N_n} S_3(\mu - W_{i,k}(t)), \quad (21)$$

where $j = 1, 2, \dots, N_p$, $W_i(t) \in \mathbb{R}^{1 \times N_n}$ is a cumulative sum of average successes of the decision vector $w_i(t)$, given by

$$W_i(t) = \left[\frac{w_{i,j}(t)}{\sum w_i(t)}, \frac{\sum_{j=1}^2 w_{i,j}(t)}{\sum w_i(t)}, \dots, \frac{\sum_{j=1}^{N_n} w_{i,j}(t)}{\sum w_i(t)} \right], \quad (22)$$

$S_3(\cdot)$ is a step function defined as: with $x = (a - b) \mid a \leq b$, $(a, b) \in \mathbb{R}$,

$$S_3(x) = \frac{1}{1 + e^{(x-\epsilon) \cdot \infty}} = \begin{cases} 0; & x > 0, \\ 1; & x < 0, \\ 1; & x = 0, \end{cases} \quad (23)$$

where ϵ is the epsilon machine “*eps*” [18], and $\mu \in [0, 1]$ is a random number with uniform distribution. If the node n_j

has been selected, its probability $w_{i,j}(t)$ during iteration t is 0, such that the node n_j is not selected again by the same *P. coffea* wasp.

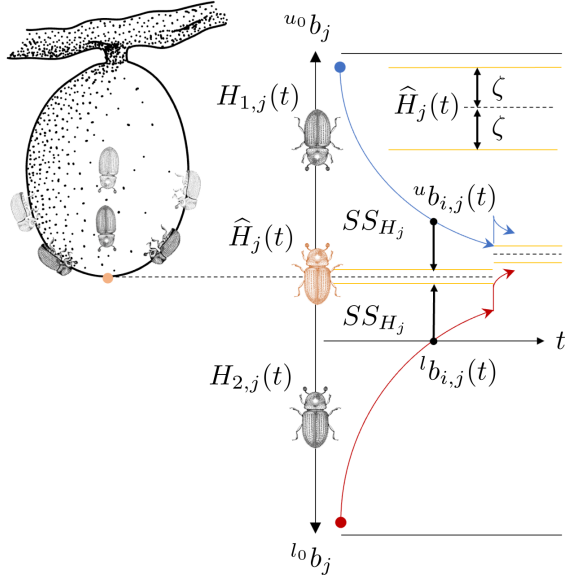


Fig. 2. The biological inspiration of the borer functions, *H. hampei* path towards the coffee berry apex.

In nature, the *H. hampei* drills berries at or near the apex, the softest area of the coffee fruit (Fig.2). The borer functions emulate this behavior by reducing the search region SS_H towards the best agents \hat{H} . The borer functions are defined as

$${}^u \mathbf{b}(t) = \left(\hat{H} - (\hat{H} - {}^{u_0} \mathbf{b} + \zeta |\hat{H}|) e^{\left(\frac{-\gamma t}{N_t} \right)} + \zeta |\hat{H}| \right) \otimes v, \quad (24)$$

$${}^l \mathbf{b}(t) = \left(\hat{H} + ({}^{l_0} \mathbf{b} - \hat{H} + \zeta |\hat{H}|) e^{\left(\frac{-\gamma t}{N_t} \right)} - \zeta |\hat{H}| \right) \otimes v, \quad (25)$$

where ${}^{u_0} \mathbf{b} \in \mathbb{R}^{1 \times N_n}$ and ${}^{l_0} \mathbf{b} \in \mathbb{R}^{1 \times N_n}$ are the initial upper and lower bounds respectively, ζ is the compression gain, N_t is the interactions number and γ is a iteration coefficient.

The behavior of the $\mathbf{H}(t)$ population is defined as

$$\Delta(t+1) = \Delta(t) + \rho_1 \eta_1 \odot (\tilde{\mathbf{H}}(t) - \mathbf{H}(t)) + \rho_2 \eta_2 \odot (\hat{H}(t) \otimes v - \mathbf{H}(t)), \quad (26)$$

$${}^u \mathbf{c}(t) = S_3({}^u \mathbf{b}(t) - \mathbf{H}(t) - \rho_3 \Delta(t)) \odot {}^u \mathbf{b}(t) \quad (27)$$

$${}^l \mathbf{c}(t) = S_4({}^l \mathbf{b}(t) - \mathbf{H}(t) - \rho_3 \Delta(t)) \odot {}^l \mathbf{b}(t) \quad (28)$$

$${}^c \mathbf{c}(t) = S_3({}^l \mathbf{b}(t) - \mathbf{H}(t) - \rho_3 \Delta(t)) \odot S_4({}^u \mathbf{b}(t) - \mathbf{H}(t) - \rho_3 \Delta(t)) \odot (\mathbf{H}(t) + \rho_3 \Delta(t)) \quad (29)$$

$$\mathbf{H}(t) = \begin{cases} ({}^{u_0} \mathbf{b} + ({}^{l_0} \mathbf{b} - {}^{u_0} \mathbf{b}) \otimes v) \odot \eta_1 & \text{if } t = 1 \\ {}^u \mathbf{c}(t-1) + {}^c \mathbf{c}(t-1) + {}^l \mathbf{c}(t-1) & \text{else,} \end{cases} \quad (30)$$

where $\Delta(t)$ is the position increment of the population $\mathbf{H}(t)$, $\eta_1 \in \mathbb{R}^{N_a \times N_n}$ and $\eta_2 \in \mathbb{R}^{N_a \times N_n}$ are uniformly distributed random matrices, ρ_1 is the influence constant for the births of two females, ρ_2 is the influence constant for the births of one female and one male, ρ_3 is the inertial constant, ${}^u \mathbf{c}(t)$, ${}^c \mathbf{c}(t)$ and ${}^l \mathbf{c}(t)$ are the upper, center and lower clipping functions respectively, which prevent agents *H. hampei* from exceeding the search space, \odot is the Hadamard product [19], and S_4 is a step function defined as, with $x = (a - b) \mid a \geq b, (a, b) \in \mathbb{R}$,

$$S_4(x) = 1 - \frac{1}{1 + e^{(x+\epsilon) \cdot \infty}} = \begin{cases} 1 & x > 0 \\ 0 & x < 0 \\ 1 & x = 0. \end{cases} \quad (31)$$

Algorithm 1 and Fig. 3 present the pseudo code and the flow chart of the proposed Phimastychus-Hypothenemus Algorithm, respectively. Some stopping criteria for the algorithm are: number of iterations, error tolerances and null variations of the decision matrix ω . Starting with N_p values close to N_n and large control gains \mathcal{K} increases the possibility of starting with healthy populations (seeds of good initialization).

Algorithm 1 Phimastychus-Hypothenemus Algorithm.

Data: $N_n, N_p, N_a, {}^{l_0} \mathbf{b}, {}^{u_0} \mathbf{b}, \zeta, \gamma, \rho_1, \rho_2$ and ρ_3 .

Result: \hat{P} : Best agent *P. coffea*, \hat{H} : Best agent *H. hampei*, \hat{f} : Best fitness.

- 1: Initialization:
 - 2: $t \leftarrow 1$
 - 3: $(\mathbf{P}, \tilde{\mathbf{P}}, \mathbf{H}, \tilde{\mathbf{H}}, \Delta) \leftarrow [0]^{N_a \times N}$
 - 4: $(\mathbf{f}, \tilde{\mathbf{f}}) \leftarrow [0]^{N_a \times 1}$
 - 5: $\omega \leftarrow [1]^{N_a \times N}$
 - 6: **while** $t \leq N_t$ **do**
 - 7: $\mathbf{H}(t) \leftarrow$ by the Eq.(30)
 - 8: **for all** $i \in [1, N_a]$ **do**
 - 9: $\omega \leftarrow w_i(t)$ save to decision vector
 - 10: **for all** $j \in [1, N_p]$ **do**
 - 11: $P_{i,j}(t) \leftarrow$ by the Eq.(21)
 - 12: $w_{i,P_{i,j}}(t) \leftarrow 0$
 - 13: **end for**
 - 14: $w_i(t) \leftarrow \omega$ update the decision vector
 - 15: $f_i(t) \leftarrow$ (12) is evaluated
 - 16: $\tilde{P}_i(t) \leftarrow$ by the Eq.(14)
 - 17: $\tilde{H}_i(t) \leftarrow$ by the Eq.(15)
 - 18: $w(t+1) \leftarrow$ by the Eq.(20)
 - 19: $\tilde{f}_i(t) \leftarrow$ by the Eq.(13)
 - 20: **end for**
 - 21: $\hat{P}(t) \leftarrow$ by the Eq.(17)
 - 22: $\hat{H}(t) \leftarrow$ by the Eq.(18)
 - 23: $w(t+1) \leftarrow$ by the Eq.(20)
 - 24: $\hat{f} \leftarrow$ by the Eq.(16)
 - 25: $t = t + 1$
 - 26: **end while**
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IV. SIMULATIONS RESULTS

The following experiments are carried out to compare the performances of the proposed PHA algorithm with other

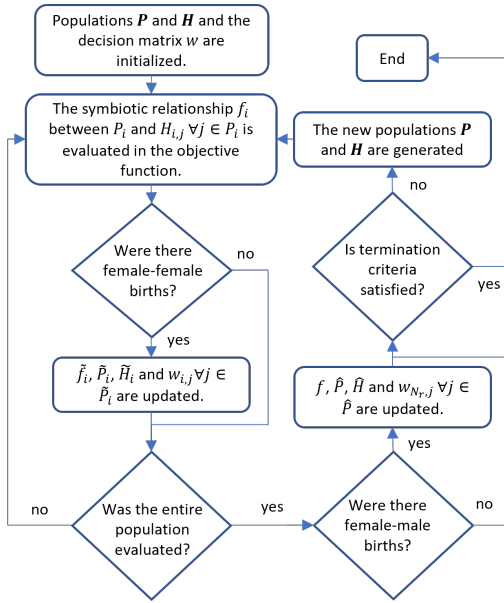


Fig. 3. The flow chart of PHA.

CN	CN_1	CN_2	CN_3
N_n	30	40	60
N_e	224	383	876
m	5	21	33
\bar{k}	14.93	19.15	29.2
$\min\{k\}$	10	12	19
$\max\{k\}$	20	24	38
\bar{c}	9.53	-11.35	-4.64
I_c	$[-2, 20]$	$\begin{bmatrix} -40 \\ 20 \end{bmatrix}$	$\begin{bmatrix} -24 \\ 16 \end{bmatrix}$
$\bar{\theta}$	45.93	-6.31	-7.69
I_θ	$\begin{bmatrix} -4 \\ 80 \end{bmatrix}$	$\begin{bmatrix} -23 \\ 8 \end{bmatrix}$	$\begin{bmatrix} -56 \\ 35 \end{bmatrix}$
\bar{x}_0	$\begin{bmatrix} -0.01 \\ 2.02 \end{bmatrix}$	$\begin{bmatrix} 2.02 \\ 2.21 \end{bmatrix}$	$\begin{bmatrix} 23.83 \\ 26 \\ 31.85 \end{bmatrix}$
I_{x_0}	$\begin{bmatrix} -8 \\ 9 \end{bmatrix}$	$\begin{bmatrix} -2 \\ 7 \end{bmatrix}$	$\begin{bmatrix} -23 \\ 80 \end{bmatrix}$
SS	$\begin{bmatrix} 1E+2 \\ 1E+7 \end{bmatrix}$	$\begin{bmatrix} 1E+4 \\ 1E+6 \end{bmatrix}$	$\begin{bmatrix} 1E+7 \\ 1E+9 \end{bmatrix}$
N_p	15	37	54

TABLE I
COMPLEX NETWORK DATA.

heuristic optimization algorithms, such as: ALO [20], TLBO [21], GWO [22], AMO [7], PSO [6], ABC [8], GSK [23], BBO [9], WOA [10] and ACO [11]. The parameter settings used in the simulations for these algorithms are the following: ALO, WOA and TLBO: no special parameters; GWO: $a = 2 - 2(g/\max_g)$; AMO: 5 animals in each group; PSO: $\omega = 0.6$, and $c_1 = c_2 = 2$; ABC: abandonment criteria = 25; GSK: $P = 0.1$, $k_f = 0.5$, $k_r = 0.9$, and $K = 10$; BBO: habitat modification probability = 1, immigration probability bounds per gene = $[0,1]$, step size for numerical integration of probabilities = 1, maximum immigration and migration rates for each island = 1, and mutation probability = 0.1; ACO: initial pheromone value = $1E-6$, pheromone update constant = 20, exploration constant = 1, global pheromone decay rate =

CN	$\bar{F}(x)$	$\bar{f}(x)$	$\bar{G}(x)$	$t/50$
ALO				
CN_1	$3.7E+71$	$1.4E+16$	4.4	19.0
CN_2	$1.3E+73$	$1.5E+14$	34.0	32.0
CN_3	$2.3E+73$	$4.2E+22$	47.0	46.0
TLBO				
CN_1	$8.3E+71$	$9.7E+15$	8.6	2.3
CN_2	$2.6E+73$	$1.4E+14$	51.0	3.3
CN_3	$3.9E+73$	$4.0E+22$	62.0	6.0
GWO				
CN_1	$8.0E+71$	$8.9E+15$	7.6	1.0
CN_2	$2.3E+73$	$1.2E+14$	47	1.7
CN_3	$3.4E+73$	$3.1E+22$	58.0	3.0
AMO				
CN_1	$2.2E+15$	$2.2E+15$	0	2.7
CN_2	$1.4E+72$	$2.0E+14$	11.0	4.9
CN_3	$4.7E+72$	$4.7E+22$	21.0	8.1
PSO				
CN_1	$2.8E+72$	$1.4E+16$	17.0	0.85
CN_2	$33E+73$	$1.6E+14$	57.0	1.3
CN_3	$4.7E+73$	$4.8E+22$	69.0	2.5
ABC				
CN_1	$1.4E+70$	$1.7E+13$	0.33	0.57
CN_2	$4.4E+71$	$4.8E+11$	5.3	1.1
CN_3	$2.2E+73$	$1.2E+19$	45.0	2.0
GSK				
CN_1	$6.1E+72$	$1.2E+16$	24.0	6.2
CN_2	$4.2E+73$	$1.5E+14$	65.0	25.0
CN_3	$4.8E+73$	$4.3E+22$	69.0	67.0
BBO				
CN_1	$5.0E+70$	$1.7E+16$	1.2	2.4
CN_2	$2.4E+72$	$1.6E+14$	13.0	5.0
CN_3	$3.5E+72$	$4.1E+22$	17.0	7.8
WOA				
CN_1	$1.6E+72$	$1.1E+16$	12.0	0.92
CN_2	$2.4E+73$	$1.4E+14$	49	1.5
CN_3	$3.5E+73$	$4.2E+22$	58.0	2.8
ACO				
CN_1	$8.2E+73$	$4.9E+13$	91.0	1.2
CN_2	$1.7E+74$	$4.4E+12$	130	2.3
CN_3	$1.8E+74$	$1.6E+21$	140.0	7.1
PHA				
CN_1	$8.3E+15$	$8.3E+15$	0	1.2
CN_2	$7.9E+13$	$7.9E+13$	0	2.4
CN_3	$3.3E+22$	$3.3E+22$	0	4.4

TABLE II
SIMULATIONS RESULTS OF ALO, TLBO, GWO, AMO, PSO, ABC, GSK, BBO, WOA, ACO AND PHA.

0.9, local pheromone decay rate = 0.5, pheromone sensitivity = 1 and visibility sensitivity = 5; PHA: $\rho_1 = 0.5$, $\rho_2 = 0.6$, $\rho_3 = 0.7$, $\zeta = 0.02$ and $\gamma = 10$; for all algorithms the population size is 50 and the iterations number is 500.

The tests consist in minimizing the objective function (12) for three different complex networks, whose characteristics are presented in Table I, where N_e is the number of edges, m is the number of positive eigenvalues in (8), \bar{k} is the average connection degree, \bar{c} is the average coupling strength, $\bar{\theta}$ is the average passivity degree, \bar{x}_0 is the average initial condition, I_{c,θ,x_0} is the distribution interval and SS is the search space for bounds of the control gains. The dimensions of the search space for each algorithm are $D = 2N_p$, where the dimensions from 1 to N_p represent the set of nodes selected to apply pinning control, and the other half is used for bounds of control gains.

The penalty function is defined as $F(x) = f(x) + qG(x)$, where $F(x)$ indicates the new objective function to be optimized, q is a penalty parameter for $G(x) = \max[0, g(x)]^\beta$, β is 1 or 2, $f(x)$ and $g(x)$ are respectively the objective function and its constraint previously defined in (12).

The simulation runs on a computer with the following characteristics: 16.0 GB installed RAM (15.8 GB usable), 11th Gen Intel(R) Core(TM) i5-11400H @ 2.70GHz 2.69 GHz Processor, and MATLAB R2022a. Each simulation for every complex network runs 50 times independently, whose average results are displayed in Table II, where blue numbers indicate best performance with guaranteed network stability and red numbers generate positive definite matrix M . The complexity O of each algorithm is represented by the processing time $t/50_{\text{samples}}$ (seconds). From the comparison results obtained via simulations, it can be seen that the proposed algorithm almost always fulfill stability conditions (8), mainly for large size complex networks, while some of the other tested algorithms may not fulfill (8). For small networks, the AMO algorithm usually has better performance than the PHA, because, in animal migration, the agents do not occupy the same place, thus avoiding repeating nodes. However, this advantage disappears for large networks or networks with a large number of combinations of pinning nodes. The closer N_p is to N_n , the easier it is to find stability in the network, since almost all nodes are controlled, however, this implies a high number of permutations for the heuristic algorithms of fixed and ordered dimensions, producing poor performance or edge locks, which causes most heuristic algorithms not to find sets of control gains that guarantee $M \leq 0$.

V. CONCLUSIONS

The PHA algorithm was developed to solve a specific problem: the optimal node selection on pinning control of complex networks, which, as mentioned, implies nonlinear combinatorial optimization with multi-criteria. The set of fixed cardinality pinning nodes is proposed arbitrarily by the user, and when this cardinality is close to the total number of nodes in the network it is easier to guarantee the network stability, however, this implies a high number of permutations for the heuristic algorithms of dimensions fixed and ordered, producing poor performance or border locks, while the PHA algorithm agents interpret the permutations as combinations, drastically reducing the computational complexity, avoiding the repetition of nodes. Another important aspect in the PHA algorithm is that with the borer functions, agents are encouraged to visit new search areas, giving time to make decisions in safe areas. Comparing the PHA algorithm with other heuristic algorithms is possible if and only if the optimization problems in question consist of the same problems for which the PHA algorithm was developed. For the above, the PHA algorithm is a useful tool for pinning control of complex networks; mainly when the network size is considerably large. This algorithm can be applied, regardless of the network size, the dynamics of the nodes, the topology of the network, and the strength of its connections. For future work, it is interesting to study

the case of a PHA algorithm with the minimum number of pinning nodes, which can guarantee stabilization for complex networks.

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