Parameter Tuning of Coronavirus Herd Immunity Optimizer for Detection of Communities in Social Networks

Shikha Gupta   shikhagupta@sscbsdu.ac.in
Associate Professor (Computer Science),
Shaheed Sukhdev College of Business Studies,
University of Delhi,
India.

Priyanka Gupta   priyanka.cs.du@gmail.com
Assistant Professor (Computer Science),
Mata Sundri College for Women,
University of Delhi,
India.

Corresponding Author: Priyanka Gupta

Abstract

Community detection is an NP-Hard problem that concerns itself with partitioning a network into groups such that nodes within a partition enjoy denser network connections compared to nodes in different partitions. The capacity to locate and examine these groups can offer invaluable assistance in comprehending and illustrating the framework of networks. Since the community detection problem is inherently complex, metaheuristic optimization algorithms are extensively employed to address this problem. A recently proposed metaheuristic population-based algorithm, Coronavirus Herd Immunity Optimizer (CHIO), draws inspiration from the COVID-19 herd immunity treatment strategy. We adapt the CHIO algorithm for the problem of community detection in social networks. In this proposal, the Network Modularity value is computed to assess the quality of a community structure.

Tuning the parameters of a metaheuristic algorithm to a given problem at hand is essential for good algorithm performance and is the focus of our proposal. The parameter tuning method developed by Genichi Taguchi is utilized to fine-tune the parameters of the CHIO algorithm in the context of community detection. Experiments on real-world benchmark networks were conducted. The adapted CHIO algorithm is run with parameter values obtained after tuning. It is noticed that the proposed approach is successful in detecting community structures with a high modularity value.

Keywords: CHIO, Evolutionary algorithms, Meta-heuristic, Partitioning, Network Modularity.

1. INTRODUCTION

Network representations are useful for many complex real-world systems. Social networks, biological networks, and collaboration networks are a few examples. Networks can be illustrated as graphs, where nodes (or vertices) denote entities and edges signify their connections. Distinctive features of a network include its community structure, network transitivity, and the small-world effect.

Qualitatively, a community is defined as a group of nodes that are more tightly connected compared to their associations with nodes outside of that group. Unearthing the community structure in a network is beneficial as it provides a better understanding and visualization of the network [1]. Some notable state-of-the-art community detection methods include Fast Greedy [2], Label Propagation method [3], and Infomap [4].

Being an NP-Hard problem, several heuristic-based and non-deterministic algorithms have been proposed for detecting communities [5]. Metaheuristic algorithms exhibit high performance in exploring search space and have proven their efficiency in addressing optimization problems in different domains, such as identification of a defect in a software module, feature selection for the classification process, production forecasting, designing an authentication system, tracking of human activities, predicting wind features and its speed, partitioning of text documents, machine scheduling, cybersecurity, topic extraction, biomedical image segmentation, etc [6].

It is well accepted that the rate of advancements achieved by humans based on their behavior and evolution surpasses other nature-based systems. The introduction and application of new metaheuristic optimization algorithms across various domains is well accepted among researchers [7]. Indeed, integrating human intelligence to develop optimization techniques has been found promising in discovering solutions to real-world optimization issues [7].

Recently, metaheuristic algorithms inspired by human behavior and based on viruses' spread have been proposed. One of these algorithms, the Coronavirus Herd Immunity Optimizer (CHIO) [8], has demonstrated excellent performance in tackling optimization problems, including image segmentation, the knapsack problem, data clustering, vehicle routing problems, and more [7].

CHIO algorithm draws inspiration from the herd immunity concept as a way to control and curb the coronavirus (COVID-19) pandemic. The speed of the spread of coronavirus infection depends on how a group (community) of infected individuals directly contacts members of society (social network). This aspect of the CHIO algorithm is a motivating factor to consider for the problem of community detection.

The present work adapts the CHIO algorithm to detect communities in a social network. Because the problem of community detection is characteristically discrete in nature, CHIO has been modified to tackle this issue. The parameters for the CHIO algorithm are tuned to find their best values using a sampling method called Genichi Taguchi's Orthogonal Arrays [9]. There are two significant advantages of tuning an evolutionary algorithm. Firstly, the application of tuning algorithms leads to performance improvement, and the efforts required for tuning algorithms are minimal. Secondly, employing tuning algorithms not only leads to the acquisition of improved parameter values but also provides valuable insights into both parameter values and algorithm performance [10].

Since the experiments are performed on benchmark networks, network modularity values for the discovered community structure are compared with those of the known ground truth (label). It is seen that the proposed approach successfully detects community structures in networks with high modularity.

The rest of the paper is organized as follows. In Section 2, we present the adapted steps for the CHIO optimizer when it is used for community detection. Section 3 outlines Genichi Taguchi's technique, which is used to tune the CHIO's control parameters. We present the results of the experiments in Section 4, followed by a discussion of the results in Section 5. In Section 6, we conclude the findings and suggest some future works.

2. CHIO FOR COMMUNITY DETECTION

In recent times, during the Coronavirus (COVID-19) pandemic, the virus spread began in December 2019, infected over 770 million lives, and caused more than 6 million deaths worldwide. COVID-19 virus is a microbe that attacks the living host's organ cells [11] and usually attacks the respiratory system.

Amidst the COVID-19 pandemic, individuals were categorized as susceptible (those at risk of contracting the virus), immune, and infected (confirmed instances) [11].

Herd immunity and social distance strategies can be applied simultaneously or independently in epidemic situations until a workable treatment is found [11]. In the case of COVID-19, both herd immunity and social distancing were found effective in containing the infection spread. Herd immunity involves reducing the death rate by increasing the immunization rate within the population, achieved through either vaccination or exposure to a natural infectious pathogen. The social distancing approach protects individuals by isolating confirmed cases and their direct contacts, resulting in protecting susceptible individuals.

The CHIO algorithm draws its inspiration from the mechanism of infection spread of COVID-19 and herd immunity & social distancing [8]. The CHIO optimization process serves as an example of a real pandemic. In this present work, CHIO is adapted for community detection.

2.1 Parameters of the Proposed Algorithm

The adapted CHIO parameters (TABLE 1), are divided into two categories: algorithmic parameters and control parameters. Algorithmic parameters are quantitative parameters that are employed as population establishment parameters such as population size, maximum number of iterations, an individual's lower and upper bounds, and problem dimension. The control parameters, on the other hand, are the parameters governing the algorithm's behavior. They include the spreading rate (or reproduction rate (BR_r)), the infected case threshold age (MaxAge), and the initial number of confirmed cases (C_0, usually set to 1).

Table 1: CHIO Parameters.

Type	Parameter	Description
Algorithmic parameters	Pop_size	Population size
	Max_Iter	Maximum number of iterations for evolution
	C_0	Number of cases infected initially, set to 1
	n	Size of an individual, set to the number of nodes in the network
Control parameters	BR_r	Spreading/Reproduction rate
	MaxAge	Maximum age amongst the infected cases

2.2 Population Generation

The proposed algorithm begins by randomly generating a population (P) of Pop_size individuals, $P = \{I_1, I_2, I_3, \ldots, I_{Pop\_size}\}$. Each individual in population P is of length n where n is the number of nodes in the given network.

2.2.1 Representation of an individual

An individual I in the population is represented using the string-based scheme [12] where it consists of n genes $\{x_1, x_2, x_3, \ldots x_n\}$. The genes of an individual correspond to the nodes of the network. We represent a social network as an undirected and unweighted graph G = (V, E) with n vertices and m edges, where V is the set of vertices (n = |V|) and E is the set of edges (m = |E|).

Given the discrete nature of the community detection problem, initially, each gene is randomly assigned a value j ∈ [0, n −1]. In the string-based representation, the ith gene (x_i) represents the community identifier of the node i ∈ G. The nodes with the same community identifier form a community structure.

Using the string-based representation, the number of communities is automatically calculated by assessing the number of unique community identifiers in each individual. For example, the network shown in FIGURE 1, consists of seven nodes named v_1 to v_7; hence an individual in the population of the proposed approach will comprise seven genes. Let us consider the following individual I:
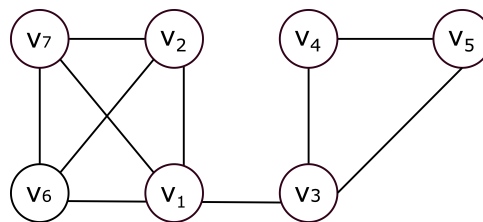
$$I = \{3, 3, 1, 1, 1, 3, 3\}$$

Figure 1: Sample Network

According to the string-based representation, the individual I is interpreted as the partition PR with two communities (shown in FIGURE 2):

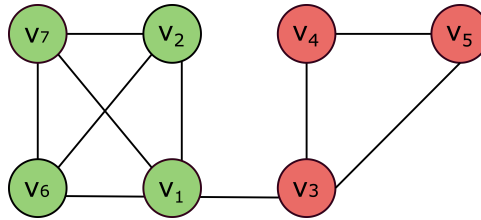$$PR = \{\{v_1, v_2, v_6, v_7\}, \{v_3, v_4, v_5\}\}$$

Figure 2: Communities for the network in Figure 1, depicted with different colors.

2.2.2 Repair function

In the context of evolutionary algorithms, it is common practice to enhance convergence and reduce unnecessary iterations by introducing a biased population initialization instead of a purely random one [13]. To introduce the bias, the repair process randomly selects a gene, say, x_l^q, $l \in [1, n]$ of an individual I_q, $q \in [1, \text{Pop\_size}]$. The community identifier of x_l^q is assigned to all its neighbors. The proposed method involves applying the repair process for 40% of an individual's genes [13].

2.3 Fitness Computation

Network Modularity is a quality metric used by researchers to measure the strength of the particular division of a network [14]. In the literature, many EA-based meta-heuristic optimization algorithms have sought to maximize the Network Modularity (Q) value to uncover the underlying community structure in a network [12].

Network Modularity (Q) [15] for an undirected and unweighted graph G = (V, E) with n = |V| vertices and m = |E| edges is defined as:

$$Q = \frac{1}{2m} \sum_{i,j=1}^{n} \left(A_{ij} - \frac{k_i k_j}{2m} \right) \delta(c_i, c_j) \tag{1}$$

In the above equation, A is the adjacency matrix of Graph G, k_i denotes degree of node i. Kronecker delta function $\delta(c_i, c_j)$ is defined as follows:

$$\delta(c_i, c_j) = \begin{cases} 1, & c_i = c_j \\ 0, & c_i \neq c_j \end{cases}$$

Where, c_i and c_j denote the community identifiers of node i and j respectively. $c_i, c_j \in \{1, 2, 3, \cdots, N_c\}$, N_c denotes the number of communities in graph G.

In this study, we used Network Modularity (Q) to measure the quality of the community structure. The Q metric ranges from 0 to 1, including both endpoints. Value of Q close to 0 indicates that the

edges inside communities are not significantly different from the random case, while a value of Q close to 1 indicates strong community structure (good divisions of a network into communities). A modularity value above 0.3 signifies a robust community structure in a network [16].

2.4 Main Loop

The proposed algorithm improves the initial population of individuals by employing the CHIO evolutionary mechanism [8], aiming to attain an optimal solution. After an iteration of the improvement process, each gene of an individual either remains the same or is affected based on the three cases of social distancing, namely Infected case, Susceptible case, and Immuned case [8]. The algorithm maintains two additional data structures, namely the status vector (S) and the age vector (A).

The status vector $S = \{S_1, S_2, S_3, \cdots, S_{Pop\_size}\}$ keeps track of the current status (susceptible or infected) of individuals. Each element in S is initialized to either zero (susceptible) or one (infected). Note that, the initial number of ones in S is equal to C_0.

The age vector $A = \{A_1, A_2, A_3, \cdots, A_{Pop\_size}\}$ is also maintained where A_q represents the age of a person denoted by node q in the graph G. The elements in A are initialized to zeros. A_q increases by 1 if an individual I_q remains infected.

FIGURE 3 depicts the flowchart of the proposed algorithm. The pseudocode of the adapted CHIO algorithm for community detection is given in the Algorithm 1.

3. PARAMETER TUNING FOR ADAPTED CHIO

CHIO's sensitivity is based on two control parameters BR_r (Basic Reproduction Rate) and MaxAge (Maximum infected cases age) [8]. BR_r value affects the herd immunity and represents the expected number of individuals that will be infected. MaxAge limits the maximum iterations for which the infected solutions may not show improvement [8]. These two parameters are tuned using Genichi Taguchi's technique for experiment designs, an effective and robust problem-solving tool enhancing process efficiency and productivity [9]. The main objective of the Taguchi technique is to build high-quality products with a significant reduction in time and cost.

Fei et al. [17] performed an extensive review of the literature on approaches for parameter tuning. According to the authors of [17], Taguchi's contribution to processing optimization has been extensive, since it aims to acquire the optimal combination set of factors/levels with the lowest cost solution to meet product quality standards.

Taguchi method determines optimal settings of numerous process variables with a minimal set of experiments. The method suggests replication of the experiment to achieve improved accuracy of the results. Taguchi L8 orthogonal array (OA) design containing 8 experimental runs is used. We have experimented with four levels (0.01, 0.02, 0.03, 0.04) and two levels (50, 100) of variations for BR_r and MaxAge respectively.
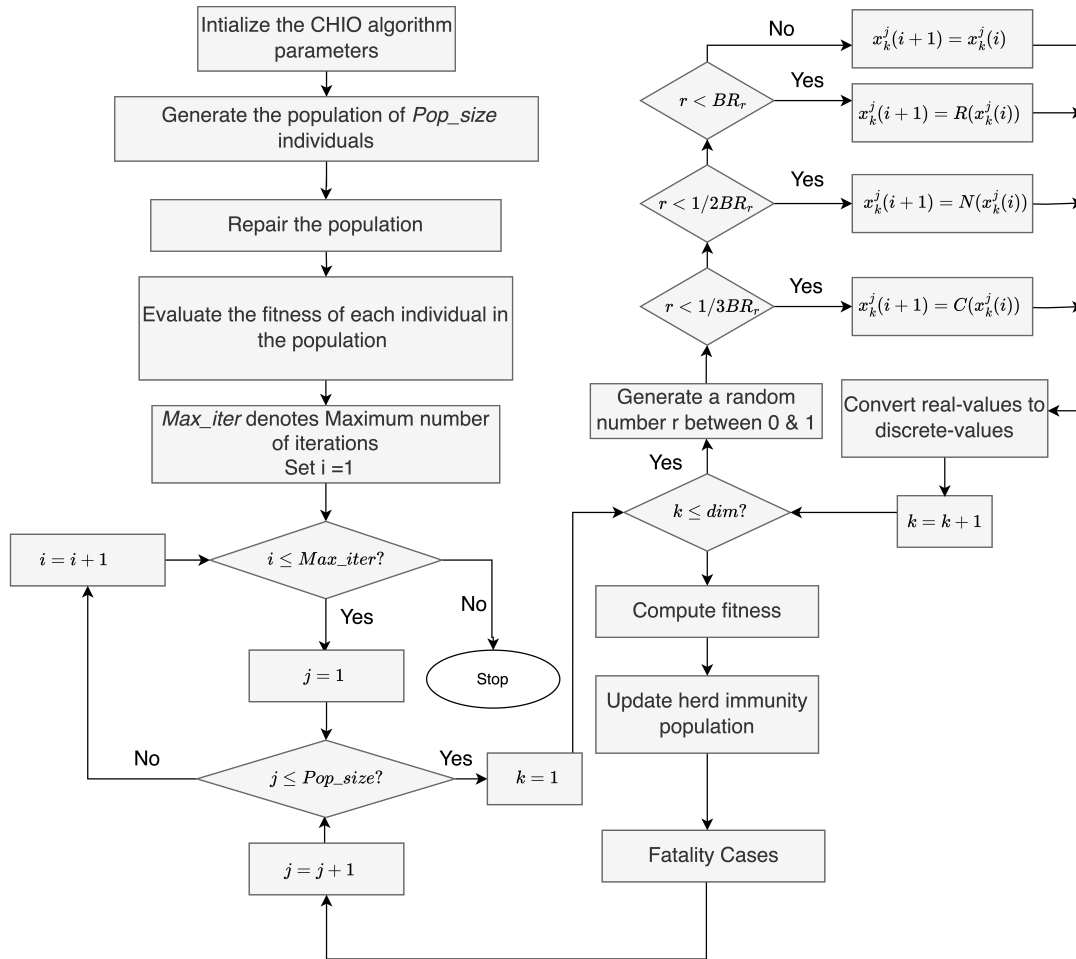
Figure 3: The flowchart of the proposed adapted CHIO algorithm.

The objective functions utilized for optimization in parameter tuning are signal-to-noise ratios (S/N). S/N is the log function of the desired output. Since the proposed algorithm aims at maximizing the network modularity (fitness function), 'the larger the better' quality characteristic is chosen when computing the S/N ratio as follows:

$$S/N = -10 * \log \left(\sum (1/Y^2)/n \right)$$

This expression is large when all of the individual response values are large. We have tuned the parameters of the adapted CHIO using the Dolphin network. The adapted CHIO is run 10 times for each combination of BR_r & MaxAge and an average of modularity value is recorded. TABLE 2 and FIGURE 4, illustrate the results of parameter tuning.

The Basic Reproduction Rate (BR_r) governs CHIO operators by facilitating the spread of the virus pandemic among individuals.

The influence of the basic reproduction rate (BR_r) on the performance of the proposed adapted CHIO algorithm is assessed using values 0.01, 0.02, 0.03, and 0.04. While a higher value of BR_r

---

Algorithm 1 Adapted CHIO algorithm for Community Detection

Input:

Population $P = \{I_1, I_2, \ldots, I_{Pop\_size}\}$, Population size: Pop_size

Maximum number of iterations: Max_iter, Number of nodes in a network: n

Dimension of an individual: n

Spreading/Reproduction rate: BR_r, Maximum age amongst the infected cases: C_0 (initially, set to 1)

Output: Community structure I_{best} with the best modularity value

---

1: Randomly initialize each individual $I_q = \{x_1, x_2, ..., x_n\}$ of the population P, $1 \leq q \leq Pop\_size$
2: Repair each individual I_q of the population P, $1 \leq q \leq Pop\_size$ /* Section 2.2.2 */
3: Evaluate the fitness of each individual I_q, $1 \leq q \leq Pop\_size$ /* using Equation 1. */
4: **for** $i = 1 \rightarrow$ Max_iter **do**
5:     **for** $j = 1 \rightarrow$ Pop_size **do**
6:         **for** $k = 1 \rightarrow$ n **do**
7:             Generate a random number r between 0 an 1
8:             **if** $r < \frac{1}{3}BR_r$ **then** //**Infected Case**
9:

$$x_k^j(i+1) = x_k^j(i) + r \times (x_k^j(i) - x_k^c(i))$$

10:             *Note: The value $x_k^c(t)$ is chosen from infected individual $I_c(i)$ such that $S_c = 1$*
11:             **else if** $r < \frac{1}{2}BR_r$ **then** //**Susceptible Case**
12:

$$x_k^j(i+1) = x_k^j(i) + r \times (x_k^j(i) - x_k^m(i))$$

13:             *Note: The value $x_i^m(t)$ is chosen from infected individual $I_m(i)$ such that $S_m = 0$*
14:             **else if** $r < BR_r$ **then** //**Immuned Case**
15:

$$x_k^j(i+1) = x_k^j(i) + r \times (x_k^j(i) - x_k^v(i))$$

16:             *Note: The value $x_i^v(t)$ is chosen from best immuned case $I_v(t)$ based on the status vector(S) s.t.*

$$f(I_v) = arg \min_{s \sim \{(t|S_t=2)\}} f(I_s)$$

17:             **else**//no change
18:

$$x_k^j(i+1) = (x_k^j(i))$$

19:             **end if**
20:         **end for**
21:         Transform the individual $I_j(i + 1)$ from real domain to discrete domain using Transformation function

$$T : X \rightarrow Y, \text{ defined as}$$

$$y_k = T(x_k) = \begin{cases} \lfloor x_k \rfloor & if \ x_k - \lfloor x_k \rfloor < 0.5 \\ \lceil x_k \rceil & if \ x_k - \lfloor x_k \rfloor \geq 0.5 \end{cases} \quad \forall k = 1, 2, \ldots, n$$

22:        Compute the fitness value f of an updated individual $I_j(i+1)$
23:        **if** $f(I_j(i+1)) > f(I_j(i))$ **then**
24:           Replace the individual $I_j(i)$ with individual $I_j(i+1)$.
25:        **else**
26:          **if** $S_j == 1$ **then**
27:            $A_j = A_j + 1$.
28:          **end if**
29:        **end if**
30:        Status (S_j) is updated for the new individual $I_j(i+1)$ using the following equation[4]:
31:

$$S_j = \begin{cases} 1, if f(I_j(i+1)) < \frac{f(I)^j(i+1)}{\Delta f(I)} \wedge S_j = 0 \wedge is\_Corona(I_j(i+1)) \\ \\ 2, if f(I_j(i+1)) \geq \frac{f(I)^j(i+1)}{\Delta f(I)} \wedge S_j = 1 \end{cases}$$

32:

$$is\_Corona(I_j(i+1)) = \begin{cases} 1, \text{if } I_j(i+1)) \text{ becomes infected} \\ 0, \text{Otherwise} \end{cases}$$

33:

$$\Delta f(I) = \frac{\sum_{q=1}^{Pop\_size} f(I_q)}{\Delta f(I)}$$

34:        **if** $(S_j == 1 \wedge A_j > MaxAge)$ **then** //**Fatality Case**
35:           Remove $(I_j(i+1))$ from the population
36:           Randomly generate the new individual $I_j(i+1)$
37:           Repair newly generated individual $I_j(i+1)$ /* Section 2.2.2 */
38:           Set age (A_j) and status (S_j) of newly generated individual $I_j(i+1)$ to zero.
39:        **end if**
40:    **end for**
41: **end for**
42: Return the best individual so far I_{best}

---

indicates a larger exploration area, it also indicates a larger time to convergence. A good value for BR_r will achieve a balance between exploration area and convergence rate.

The influence of the maximum age of the infected individuals (MaxAge) on the performance of the adapted CHIO algorithm is evaluated using values 50, and 100. MaxAge is the allowed age after which non-improving infected cases will be replaced by new solutions.

FIGURE 4 indicates that compared to the MaxAge, BR_r exhibits a stronger influence on the quality of detected partitions.

The results demonstrate that adapted CHIO performs well when the control parameters BR_r and MaxAge are set to 0.03 and 100, respectively. These values are used to assess how well adapted CHIO performs on other datasets (networks).

Table 2: Experimental results for Network Modularity (over 10 runs) as per Taguchi L8 Orthogonal Array

BR_r	MaxAge	Network Modularity	S/N Ratio
0.01	50	0.5055	-5.925
0.01	100	0.5026	-5.9764
0.02	50	0.5178	-5.7176
0.02	100	0.5142	-5.7769
0.03	50	0.5151	-5.7623
0.03	**100**	**0.5184**	**-5.7068**
0.04	50	0.5124	-5.8084
0.04	100	0.5167	-5.7364
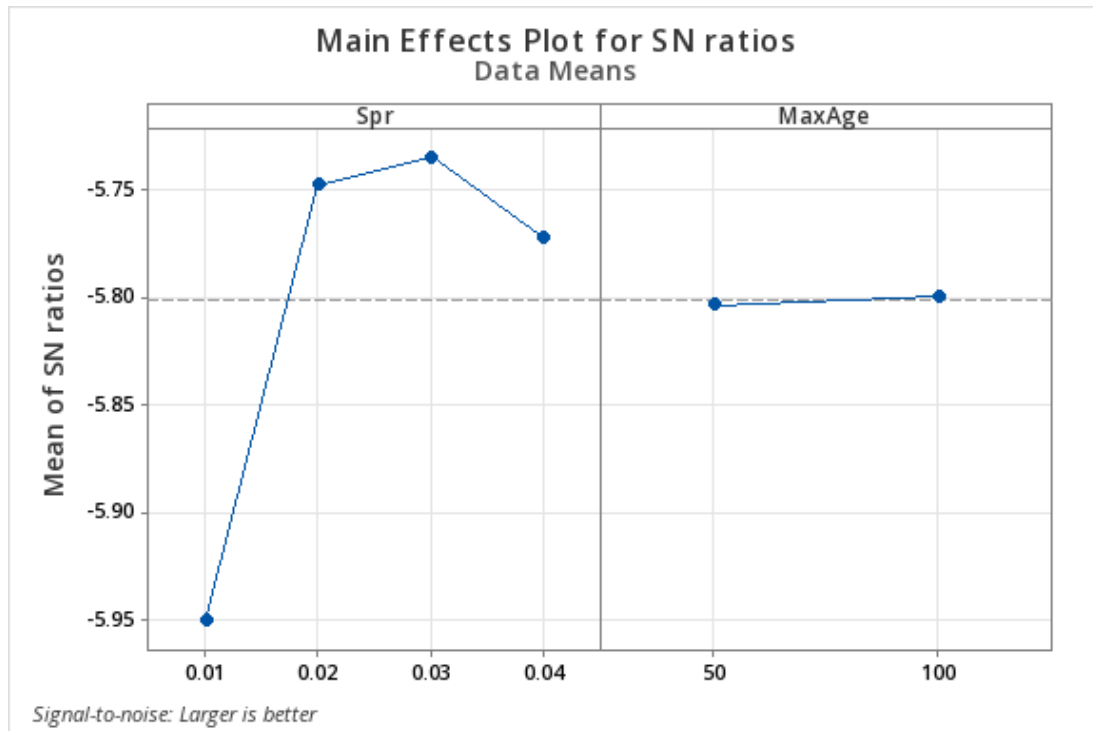
Figure 4: SN Ratio Graph. Spr denotes Spreading Rate (BR_r)

4. EXPERIMENTS

We have evaluated the performance of the adapted CHIO method and its tuned parameters for real-world benchmark networks. The benchmark networks have known label (ground truth) community structure. The networks under consideration are unsigned, undirected, unweighted, and static (the connections between entities remain unchanged over time), and feature non-overlapping communities.

The experiment was carried out with a population size Pop_size of 30 individuals, and for 1 lakh iterations, as specified for the original CHIO algorithm [8]. Tuned parameters BR_r and MaxAge values are 0.03 and 100 respectively (as decided through the parameter tuning process). For statistical significance, each experiment was repeated 30 times. The proposed algorithm optimizes the Network Modularity (Q) value.

4.1 Karate Club Network

Karate club network [18], compiled by W Wayne Zachary, is a friendship network of members of a club at a university in United states of America. This network consists of 34 nodes and 78 edges. Nodes denote the members of a club. Edges represents the friendships among the members.

4.2 Bottlenose Dolphin Network

The Bottlenose Dolphin Network, compiled by Lusseau [19], is an undirected network of frequent associations among the bottlenose dolphins residing in Doubtful Sound, New Zealand. There are 62 nodes and 159 edges in a network. The network was split into two groups due to the absence of a significant participant [20].

4.3 American College Football Network

The American College Football network [21] has 115 nodes and 616 edges. Nodes in the network symbolize the teams and edges, represent games played between the teams. The network was organized into conferences, with eight to twelve teams in each conference. Each team played more games with other teams in same conferences than the teams in different conferences.

4.4 Books on American Politics

The network, compiled by Krebs [22], encompasses 105 nodes and 441 edges. Nodes denote the political books released in 2004 and available for purchase on the e-commerce platform Amazon.com. Edges denote frequently bought books by the same customers. The network was organized into three groups based on political orientation of books: conservative, liberal, and centrist or unaligned, as outlined in [23].

4.5 Les Miserables Network

The network, curated by Victor Hugo [24], illustrates the interactions between 77 characters in the novel of the same title. The novel's characters are depicted as nodes, and connections (edges) link any two characters who appear together in the same chapter of the novel.

5. RESULTS AND DISCUSSION

To validate the efficacy of the proposed approach, we ran the adapted CHIO algorithm 30 times for each considered network and computed the Network Modularity (Q) value for the discovered community structure. The best value of Q over 30 runs was noted for each network. TABLE 3 shows the values of Network Modularity (Q) and the number of communities (N_c) identified by the proposed algorithm using the tuned parameter values. It is noted that in each case, the proposed method successfully detects the communities with a network modularity value that is higher than the ground truth.

Table 3: Network Modularity (Q) and Number of communities (N_c) for various datasets (networks) by the adapted CHIO algorithm

Network	Ground Truth		Result	
	Q	N_c	Q	N_c
Karate	0.37	2	**0.42**	4
Dolphin	0.4	2	**0.53**	5
Football	0.55	12	**0.58**	8
Books on American Politics	0.41	3	**0.53**	4
Les Miserables	0.54	11	**0.56**	9

As shown in TABLE 4, we also compare the performance of the proposed algorithm with well-known state-of-the-art community detection algorithms, namely Fast Greedy, Label Propagation method, and Infomap. The results for state-of-the-art algorithms are noted from a recent study performed by authors of [25]. It is noted that compared to the state-of-the-art algorithms, the proposed algorithm extracts a higher quality community structure indicated by a higher network modularity value. For the Football network, while the proposed approach achieves higher modularity than that of the ground truth, Infomap algorithm show the best modularity value. For the Football network, the number of communities identified by the adapted CHIO is less than those in the label, possibly due to the resolution limit exhibited by network modularity. The resolution limit states that communities that are smaller than a scale cannot be resolved [26].

Table 4: Network Modularity (Q) for various datasets (networks) by the adapted CHIO algorithm and the state-of-the-art algorithms for community detection

Algorithm	Karate	Dolphin	Football	Books on American Politics	Les Miserables
Fast greedy	0.38	0.49	0.54	0.5	0.5
Label Propagation	0.37	0.37	0.59	0.51	0.48
Infomap	0.4	0.52	**0.60**	0.52	0.55
Adapted CHIO	**0.42**	**0.53**	0.58	**0.53**	**0.56**

6. CONCLUSION AND FUTURE SCOPE

The present work adapts a novel optimization algorithm called Coronavirus Herd Immunity Optimizer (CHIO), which draws inspiration from human-based behaviors. The adapted CHIO is successfully applied to the complex problem of community detection, a discrete-valued optimization problem encountered in real-life social networks. The optimal parameter values for CHIO are determined using Genichi Taguchi's method for parameter tuning.

The evaluation of the tuned and adapted CHIO's performance is carried out on real-life networks, with a focus on Network Modularity as a crucial metric. The research employs benchmark networks to compare the discovered community structures' modularity values with those of the known ground truths, demonstrating CHIO's ability to successfully detect community patterns in networks exhibiting high modularity.

In essence, the research underscores the efficacy of the proposed approach, that is, the adapted CHIO algorithm as an optimization algorithm for community detection in real-life networks, showcasing its potential to unearth meaningful community structures by leveraging nature-inspired principles.

In the future, we plan to test the proposed algorithm on other types of networks, such as signed networks, multi-dimensional networks, and dynamic networks. While the quality of tuned parameters can only be demonstrated empirically, based on the good quality results obtained in the present work, and since the parameter tuning is independent of the type of considered network, it is expected that the proposed approach would generalize to other types of networks.

The proposed approach can be advantageous in real-world applications that benefit from the detection of densely linked (higher modularity) communities in a network. For instance, finding the population areas that are more susceptible to a virus spread, determining high-impact authors from citation networks, and detecting individuals in online social networks that are possibly involved in anti-social activities.

7. FUNDING

8. CONFLICT OF INTEREST

The Authors have no conflicts of interest on this article to declare.

References

[1] Gong M, Ma L, Zhang Q, Jiao L. Community Detection in Networks by Using Multiobjective Evolutionary Algorithm With Decomposition. Phys A. 2012;391:4050-4060.

[2] Clauset A, Newman ME, Moore C. Finding Community Structure in Very Large Networks. Phys Rev E Stat Nonlin Soft Matter Phys. 2004;70:066111.

[3] Raghavan UN, Albert R, Kumara S. Near Linear Time Algorithm to Detect Community Structures in Large-Scale Networks. Phys Rev E Stat Nonlin Soft Matter Phys. 2007;76:036106.

[4] Rosvall M, Bergstrom CT. Maps of Random Walks on Complex Networks Reveal Community Structure. Proceedings of the national academy of sciences, 2008;105:1118–1123.

[5] Moradi M, Parsa S. An Evolutionary Method for Community Detection Using a Novel Local Search Strategy. Phys A. 2019;523:457-475.

[6] Makhadmeh SN, Al-Betar MA, Awadallah MA, Abasi AK, Alyasseri ZAA, et al. A Modified Coronavirus Herd Immunity Optimizer for the Power Scheduling Problem. Mathematics. 2022;10:315.

[7] Rai R, Das A, Ray S, Dhal KG. Human-Inspired Optimization Algorithms: Theoretical Foundations, Algorithms, Open-Research Issues and Application for Multi-Level Thresholding. Arch Comput Methods Eng. 2022;29:5313-5352.

[8] Al-Betar MA, Alyasseri ZAA, Awadallah MA, Abu Doush I. Coronavirus Herd Immunity Optimizer (Chio). Neural Comput Appl. 2021;33:5011-5042.

[9] G. Taguchi, Yokoyama Y. Taguchi Methods: Design of Experiments.ASI Press; Japanese Standards Association, Dearborn, MI, Tokyo, Japan. 1993.

[10] Eiben AE, Smit SK. Parameter Tuning for Configuring and Analyzing Evolutionary Algorithms. Swarm Evol Comput. 2011;1:19-31.

[11] Randolph HE, Barreiro LB. Herd Immunity: Understanding COVID-19. Immunity. 2020;52:737-741.

[12] Cai Q, Gong M, Ma L, Ruan S, Yuan F, et al. Greedy Discrete Particle Swarm Optimization for Large-Scale Social Network Clustering. Inf Sci. 2015;316:503-516.

[13] Tasgin M, Herdagdelen A, Bingol H. Community Detection in Complex Networks Using Genetic Algorithms. 2007. ArXiv preprint: https://arxiv.org/pdf/0711.0491.pdf

[14] Khan BS, Niazi MA. Network Community Detection: A Review and Visual Survey. 2017. ArXiv preprint: https://arxiv.org/ftp/arxiv/papers/1708/1708.00977.pdf

[15] Newman MEJ, Girvan M. Finding and Evaluating Community Structure in Networks. Phys Rev E Stat Nonlin Soft Matter Phys. 2004;69:026113.

[16] Newman MEJ. Fast Algorithm for Detecting Community Structure in Networks. Phys Rev E Stat Nonlin Soft Matter Phys. 2004;69:066133.

[17] Fei NC, Mehat NM, Kamaruddin S. Practical Applications of Taguchi Method for Optimization of Processing Parameters for Plastic Injection Moulding: A Retrospective Review. Int Sch Res Not. 2013;2013:1-11.

[18] Zachary WW. An Information Flow Model for Conflict and Fission in Small Groups. J Anthropol Res. 1977;33:452-473.

[19] Lusseau D. The Emergent Properties of a Dolphin Social Network. Proc R Soc Lond B. 2003;270:S186-S188.

[20] Lusseau D, Schneider K, Boisseau OJ, Haase P, Slooten E, et al. The Bottlenose Dolphin Community of Doubtful Sound Features a Large Proportion of Long-Lasting Associations. Behav Ecol Sociobiol. 2003;54:396-405.

[21] Girvan M, Newman MEJ. Community Structure in Social and Biological Networks. Proc Natl Acad Sci U S A. 2002;99:7821-7826.

[22] https://public.websites.umich.edu/~mejn/netdata/polbooks.zip

[23] Newman MEJ. Finding Community Structure in Networks Using the Eigenvectors of Matrices. Phys Rev E Stat Nonlin Soft Matter Phys. 2006;74:036104.

[24] Knuth DE. The Stanford Graphbase: A Platform for Combinatorial Computing. New York ACM Press. 1993;1.

[25] Saoud B. Modularity Maximization to Find Community Structure in Complex Networks. In: Conference proceedings ICCSA'. 2021;2021:42.

[26] Fortunato S, Barthélemy M. Resolution Limit in Community Detection. Proc Natl Acad Sci U S A. 2007;104:36-41.