Quantum Genetic Algorithm for Highly Constrained Optimization Problems

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Abstract—Quantum computing appears as an alternative solution for solving computationally intractable problems. This paper presents a new constrained quantum genetic algorithm designed specifically for identifying the extreme value of a highly constrained optimization problem, where the search space size _database is massive and unsorted_ cannot be handled by the currently available classical or quantum processor, called the highly constrained quantum genetic algorithm (HCQGA). To validate the efficiency of the suggested quantum method, maximizing the energy efficiency with respect to the target user bit rate of an uplink multi-cell massive multiple-input and multiple- output (MIMO) system is considered as an application. Simulation results demonstrate that the proposed HCQGA converges rapidly to the optimum solution compared with its classical benchmark.

Index Terms—genetic algorithm, quantum computing, quantum extreme value searching algorithm, blind quantum computing

I. INTRODUCTION

uantum computing technology provides efficient solutions to handle intractable computational problems that classical computers are unable to handle. This is achieved by exploiting the fundamentals of quantum nature, such as quantum superposition and quantum entanglement [1], [2]. Different communities and research organizations have used quantum computing with the promise of solving various classes of computational problems in many areas, including security and cryptography [3]–[5], networks [6]–[9], space communication [10], [11], and many other optimization fields. Quantum computing guarantees exponential speed, short running time, and high accuracy [12].

Optimal decisions with respect to certain constraints are crucial in various applications in a variety of areas, including physics, communications, and computer science. For instance, in computer networking, routing algorithms must factor in network congestion, latency, and reliability to find the best data path between devices. Similarly, in wireless communications, mobile providers must efficiently allocate radio spectrum to ensure fast and reliable connections without interference or congestion [13].

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There are two forms of constrained optimization problems: the first type refers to non-highly constrained; it means that the constraints are relatively lenient, resulting in a larger feasible set of solutions. This can make satisfying the constraints simpler, and it may also increase the number of potential solutions. The second type consists of highly constrained problems, in which constraints are stringent and limit the feasible set of solutions, which can lead finding a solution more difficult but can also lead to the

optimal and desired solution. On the other hand, in real-world optimization problems, the search space, or size of the candidate solutions for a given optimization problem, is exceedingly vast, rendering it beyond the computational capacity of both classical and quantum computers. Additionally, the search space remains unsorted, further complicating the task at hand.

The challenges presented by the highly constrained optimization problems, as well as the search space size that surpasses the computational capacities of existing classical and quantum machines, have motivated us to develop a novel quantum genetic algorithm called the highly constrained quantum genetic algorithm (HCQGA). An uplink multi-cell massive multiple-input and multiple-output (MIMO) application is utilized as a representative example for testing and validating the efficiency of the HCQGA. Note that this paper is an extension of the preceding research publications [14]–[19].

Recently, researchers have been significantly more interested in establishing various quantum genetic algorithms to solve optimization problems. The authors in [20] proposed a QGA based scheduling algorithm for heterogeneous platforms, the algorithm improves task scheduling efficiency and reduces the computational cost, but there are also communicationintensive tasks in signal processing, they reduced it by task clustering or task duplication. In [21], the authors presented a QGA with simultaneous quantum crossover on all chromosomes. They utilized two identical copies of a superposition for qubit relabeling, a complexity analysis implies that a quadratic speedup over its classical counterpart is attained in each generation's dominant factor of the run time. In [22], the authors improved the initial population stage of the genetic algorithm by employing the quantum counting algorithm to detect the number of unsuitable chromosomes in the population, the goal of this paper is to exploit a quantum algorithm faster than the classical counterparts on the optimizing performance. In [23] introduced an immigration technique that enhances the QGA by considering the most optimal qubit string in quantum chromosomes. Randomly

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transferring this highly fit qubit string to the next generation's chromosomes leads to improved mixing and overall algorithm performance.

To the best of our knowledge, there is currently no QGA available that addresses the aforementioned problem statement. This is primarily due to the limitations of most QGAs, which can only be executed on a universal quantum computer with a constrained qubit size. Consequently, in this research, we did not explore a comparison between the existing QGAs and our proposed HCQGA.

Massive Multiple-Input Multiple-Output (MIMO) is an advanced form of MIMO technology, featuring a large number of antennas at base stations to concurrently serve multiple users. By leveraging spatial diversity and array gain, it enhances system capacity, spectral efficiency, and energy efficiency. Massive MIMO outperforms in areas with significant population density due to its superior interference management, signal quality, and coverage extension. This technology is an integral component of 5G and 6G networks, delivering higher data rates and enhanced wireless communication performance to satisfy the expanding demands of modern connectivity [24]–[26]. Maximizing energy efficiency (EE) holds significant importance due to its potential for mitigating environmental impact, conserving finite resources, and yielding substantial cost savings [27], [28].

The EE performance of massive MIMO has been explored in the following studies: In [29], the authors proposed an energyefficient low-complexity algorithm, using Newton's methods and Lagrange's decomposition for optimal power allocation and user association in massive MIMO. In [30], an adaptive power allocation algorithm based on particle swarm optimization for enhancing energy efficiency in uplink multi-cell, multi-user massive MIMO systems was proposed. However, it does not consider the impact of Channel State Information (CSI) on this optimization in uplink multi-cell massive MIMO systems. The authors in [31] suggested a sub-optimal Dinkelbach-like algorithm to enhance energy efficiency in the downlink of a multi-cell multi-user massive MIMO system, interference limitations and maximum transmit power constraints.

The subsequent sections of this paper are organized as follows: Section II provides a comprehensive overview of the fundamental background required for the development of the HCQGA, such as the quantum extreme value searching algorithm (QEVSA), blind quantum computing (BQC), the unconstrained classical genetic algorithm (UCGA), and the unconstrained quantum genetic algorithm (UQGA). Section III introduces and extends the UQGA version into HCQGA. In Section IV, the HCQGA is applied in an uplink multi-cell massive MIMO system in order to maximize energy efficiency with respect to the desired bit rate of users. To validate the efficiency of the HCQGA, simulation experiments have been conducted in Section V. Finally, Section VI concludes the manuscript.

II. METHODS

To better comprehend the novelty of the developed HCQGA, it is essential to introduce the preliminary strategies that form its foundation. These strategies include the QEVSA, BQC, UCGA, and UQGA. By merging these strategies, the HCQGA presents a unique and innovative approach that addresses the highly constrained optimization problems, which entail search space sizes surpassing the computational capacities of existing classical and quantum machines.

A. Quantum Extreme Value Searching Algorithm

The QEVSA is designed to search for the extreme value of an unconstrained cost function or an unsorted database. It combines two distinct concepts: the classical binary searching algorithm (BSA), which utilized for identifying a specific element/item within a sorted database [32], [33], and quantum existence testing (QET) [34], which is a special case of the quantum counting algorithm. When the QET detects the presence of the searched target in the unsorted database, it returns the answer "YES" otherwise, "NO" [35]. The QEVSA is given in detail as follows:

QEVSA

- 1 We begin with step h = 0: $F_{min 1} = F_{min 0}$, $F_{max 1} = F_{max 0}$, and $\Delta F = F_{max 0} F_{min 0}$
- 2 h = h + 1
- $3 F_{med h} = F_{min h} + \left[\frac{F_{max h} F_{min h}}{2} \right]$
- 4 $flag = QET(F_{med h})$:
 - if flag = Yes, then $F_{max \, h+1} = F_{med \, h}$ $F_{min \, h+1} = F_{min \, h}$
 - Else $F_{max h+1} = F_{max h}$, $F_{min h+1} = F_{med h}$
- If $h < log_2(T)$, then go to 2, else stop and $y_{opt} = F_{med h}$

The parameter T denotes the overall number of steps required to execute the BSA embedded in the QEVSA. While the parameter F denoted the goal function, such that $F_{med\ h}$ denotes the cost function. The computational complexity of the QEVSA is $O\left(log_2(T)log_2^3\left(\sqrt{N}\right)\right)$ steps, where N denotes the overall search space.

B. Blind Quantum Computing

Blind quantum computing aims to delegate computations to untrusted quantum computes/quantum slave nodes. The BQC structure consists of one quantum server connected to several quantum computing nodes via the internet, i.e., the quantum computing nodes are accessible remotely thanks to the development of quantum communication over optical fiber.

Figure 1 illustrates the blind quantum computing architecture.

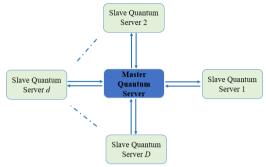


Fig. 1. Blind quantum computing architecture.

The BQC also ensures the privacy and security of data while enabling computations to be performed directly on encrypted information. The working mechanism of the QBC involves several steps, including encryption, computation on encrypted data, and decryption, to enable the processing of data while maintaining its privacy and confidentiality. Moreover, it offers significant benefits due to processing sensitive data without the need for decoding, thereby reducing the risks associated with exposure to potential threats [36].

C. Unconstrained Classical Genetic Algorithm

The UOGA is a metaheuristic strategy. It is commonly applied to solving optimization problems. There are several versions of genetic algorithms that commonly share similar working steps. The UQGA starts by randomly generating an initial population (subset from the overall set of candidate solutions). A possible candidate solution is called the chromosome. The quality of the chromosomes in a population is evaluated using a fitness function, i.e., the chromosome is assigned a fitness function value that indicates whether it approaches the optimal result or not. The present chromosomes of the population are subsequently evolved through repeated iterations, called generations (in each generation, the chromosomes undergo an evaluation process). Next, half of the chromosomes of the population with the highest fitness value are chosen for reproducing a new population (this set is named the parent set). This phase is called selection stage. Then, the selected half of the chromosomes undergo the process of crossover and mutation. The resulting new set (the second produced half of chromosomes in the population) is referred to as the offspring set. The next population is generated by merging both the parent and offspring set. The repetition of these steps for every new population aims to attain the best possible chromosome. The UCGA presents in detail as follows:

UCGA

- 1 Start with step = 0 and initialize the population size b.
- 2 Generate random population P_s .
- 3 Compute the fitness of P_s and execute a sorting algorithm to extract the parent set.

Crossover and mutation operations.

Produce P_{s+1} .

4 If the global solution J_{opt} is found, then stop, else go to 3.

D. Unconstrained Quantum Genetic Algorithm

The UQGA combines the power of the QEVSA, QBC, and UCGA to find the extreme value in a large and unsorted database, in which no classical or quantum computer can handle the search [16].

The UQGA replaces the random initialization stage and the classical selection stage with their quantum counterparts versions:

- The quantum initialization stage: This stage increases the quality of chromosomes and has a significant impact on the convergence speed of the UQGA to the optimal result to produce high quality chromosomes in a population. The quantum server selects a set of chromosomes (regions) randomly with the same sizes denoted by R. Next, the quantum server assigns every region to a quantum slave node. Then, the QEVSA is applied in every region in order to extract the initial population. The computational complexity of this stage is $O\left(log_2(T)log_2^3(\sqrt{R})\right)$ steps.
- The quantum selection stage: The procedure consists of applying $\frac{U}{2}$ times the QEVSA instead of applying the classical sorting algorithm. The computational complexity of this stage is $O\left(\frac{U}{2}.log_2(T)log_2^3(\sqrt{U})\right)$ steps.

UQGA

- Start with step = 0. Set the population and sub-database sizes, respectively U and G.
- 2 Generate the *U* regions.
- Run the QEVSA for every sub-database to create population P_{st} .
- Select the first half of the population (parent set) by applying the QEVSA $\frac{U}{2}$ times.
- 5 Crossover and mutation operations.
- 6 Produce P_{st+1} .
- If the global result F_{opt} is found, then halt, else go to 4.

III. HIGHLY CONSTRAINED QUANTUM GENETIC ALGORITHM

In this section, we extended the capability of the UQGA into the HCQGA, which can handle highly constrained optimization problems where no classical or quantum process can perform the search.

The HCQGA combines the strengths of the UQGA and penalty strategy to effectively determine the optimum extreme result of a highly constrained objective function, i.e., the algorithm specifically targets highly constrained optimization problems that are characterized by database beyond the computational power of both classical and quantum machines.

First, let's assume the task of optimizing the constrained objective function shown below,

$$\begin{aligned} & maximize(G(\boldsymbol{x})) & or & minimize(G(\boldsymbol{x})) \\ & s.t & e_y(\boldsymbol{x}) \leq 0 & \forall y = 1, ..., w , \\ & \boldsymbol{x} \in \boldsymbol{X} \end{aligned} \tag{1}$$

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The goal is to minimize (or maximize) the objective function G(x) in relation to a number of inequality constraints $e_y(x)$, where x is a w-dimensional vector with components x_1 , ..., x_i , ..., x_p that refers to the chromosome (possible candidate solution) of G(x). The parameters w and p represent the total number of selected constraint parameters and the size of the variable x, respectively. Note that $x \in X$ describes the domain constraint for each variable x_i , i.e., the lower and upper bound of each variable x_i .

To solve the constrained optimization problem stated in (1), we transform it into an unconstrained one by applying the penalty strategy. Next, the process of solving (1) will be carried out in a similar manner as previously explained for UQGA.

The penalty method is a prevalent strategy utilized in genetic algorithms to address infeasible solutions to constrained optimization problems. Essentially, this method converts the constrained problem into an unconstrained one by penalizing infeasible solutions. This entails including a penalty term in the objective function for any constraint violation. For maximization problems, one writes the objective function with penalty term as,

$$eval(x) = G(x) + p(x), \tag{2}$$

where p(x) refers to the penalty function. To effectively solve maximization problems, certain criteria must be satisfied,

$$p(x) = 0$$
 if x is feasible
 $p(x) < 0$ otherwise, (3)

In addition, the following should be satisfied,

$$|p(x)|_{max} \le |G(x)|_{min},\tag{4}$$

where, $|p(x)|_{max}$ and $|G(x)|_{min}$ denote the highest of |p(x)| and lowest of |G(x)| respectively, among solutions in the current population that are considered infeasible. For minimization problems, the penalty term should satisfy the following criteria,

$$p(x) = 0 if x is feasible p(x) > 0 otherwise (5)$$

It is interesting to note that preparing the penalty term is not a straightforward task.

The HCQGA operates in a manner akin to the UQGA, albeit with a distinctive dissimilarity lying in the conversion of a constrained optimization problem into an unconstrained counterpart. An elucidating depiction of the operational process of the HCQGA can be observed in Figure 2, showcases a comprehensive flowchart.

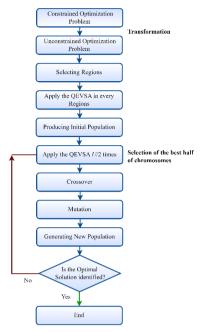


Fig. 2. Working mechanism of the HCQGA.

The complexity of both strategies (HCQGA and UQGA) has been thoroughly examined in relation to number of generations (G), population size (U) and chromosome size (C), providing a fair and comprehensive assessment. Therefore, the overall computational complexity of the algorithms is O(GUC).

By replacing quantum initialization and selection stages instead of their classical counterparts, a significant reduction in the number of executed generations can be achieved. Furthermore, during the selection stage, quantum superposition enables the reduction of larger region sizes into smaller ones. Additionally, the size of the selected regions can impact the population size. Specifically, a larger region size can lead to a reduction in population size. It is worth noting that classically, the region size is denoted by R and its processing time in classical computer is O(R), whereas in quantum computing, the region size is represented as $log_2(R)$, and its processing time on a quantum computer is $log_2^3(R)$.

The chromosome size is contingent on the total size of the search space. Consequently, a larger search space results in a larger chromosome size. Moreover, storing the population size, requires \boldsymbol{U} classical register. In contrast, from the perspective of quantum computing, the power of quantum superposition enables the utilization of only one quantum register for storing the population size.

The running time of the HCQGA is contingent upon the execution time of the quantum computer. However, due to limited access to quantum computers, our simulations were conducted on classical computers. In the following, the

expression of the total running time of the HCQGA can be written as,

$$T_{HCOGA} = U.T_R + N_q(N).T_q, (6)$$

where T_R , N_g , and T_g denote the processing time for the region R by the quantum computer, the executed generation number _which depends strongly on the overall size of the database N_{-} , and the running time required for one generation step, respectively.

IV. MASSIVE MIMO SYSTEM

This section suggests an uplink multi-cell massive MIMO, in which the aim is to maximize the energy efficiency with respect to the desired bit rate of users. Followed by investigating how to implement the HCQGA in the proposed massive MIMO.

A. Uplink Multi-Cell Massive MIMO Model

Let's consider an uplink scenario of a multi-cell system that implements massive MIMO technology. This system comprises L cells sharing the same frequency band. In each cell, there exists a base station equipped with M antennas, and K_j single-antenna active users. It is important to note that active users have specific bit rate requirements, and we categorize users based on their target bit rates. The total number of target bit rate classes is denoted by V, with each class defined as η^{ν} . Users are randomly distributed across the cells. Figure 3 illustrates the proposed uplink multi-cell massive MIMO system.

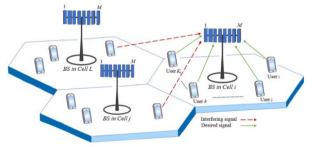


Fig. 3. A multi-cell massive MIMO system in the uplink configuration. Each cell is equipped with a single base station that has M antennas. Within each cell, there are K active users randomly distributed.

The channel gain, represented by β_{ikm} , characterizes both small and large-scale fading. Here, i, k, and m correspond to the reference cell, the reference active user, and the received antenna at the base station in the reference cell i, respectively. Pilot contamination interference is not considered in this study, assuming that channel state information (CSI) is known in advance. The transmit power of the active user k in the reference cell i is denoted as p_{ik} .

The following equation represents the uplink transmission rate for a specific user in the system denoted by *Z*.

$$Z = \frac{\sum_{m}^{M} p_{ik} \beta_{ikm}}{\varepsilon \sum_{j \neq i}^{L} \sum_{l=1}^{K} \sum_{m=1}^{M} p_{jl} \beta_{jlm}} + \underbrace{\varepsilon' \sum_{l \neq k}^{K} \sum_{m=1}^{M} p_{il} \beta_{ilm}}_{\xi_{intra}} + n_{0}', \tag{7}$$

where, the additive white Gaussian noise is denoted by n_0 . Note that ξ_{inter} describes the interference caused by users in other neighbouring cells, while ξ_{intra} refers to the interference generated by users in the reference cell i. The scaling coefficients, ε and ε' , are used to represent the interference ratios in the system, in which represent the interference ratio caused by interferer users in neighbouring cells (cells other than the reference cell i) and the interference ratio caused by interferer users within the same reference cell (cell i), respectively.

The expression of the achieved uplink transmission rate for the active user k in the reference cell i belonging to the target bit rate class v as can be written as,

$$\eta_{ik}^{v} = W.\log_2(1 + Z),$$
(8)

where, W represents the bandwidth utilized. Assuming all users share the same bandwidth W, we can determine the spectral efficiency of the reference cell i as,

$$SE_i = \frac{\sum_{k=1}^K \eta_{ik}^{\nu}}{W},\tag{9}$$

where $\eta_i = \sum_{k=1}^K \eta_{ik}^v$ correspond to the transmission rate for all users in the reference cell *i*. For the purpose of this analysis, we assume that the bandwidth occupancy of all users is similar and, therefore, it is not considered. Assuming all cells have similar circuit power P_i . One expresses the energy efficiency of the reference cell *i* as,

$$EE_i = \frac{SE_i}{\frac{1}{V}\sum_{k}^{K} p_{ik} + L.P_i},$$
(10)

where γ refers to the power amplifier efficiency coefficient. The goal of this research is to maximize the energy efficiency of cell i while satisfying the desired bit rate for the active users. The optimization problem can be formulated as follows,

$$\max_{s.t} EE_{i}$$

$$s.t \qquad \eta_{ik}^{v} \ge \eta^{v} \quad \forall i, k, v,$$

$$p_{il} \ge 0 \text{ and } p_{ik} \ge 0 \ \forall i, k, l$$

$$(11)$$

B. How to apply the HCQGA in Massive MIMO

To solve (11), we employed the penalty approach defined in Section III. The new expression of the evaluate function can be written as,

$$eval(x) = EE_i + \varphi \sum_{k=1}^{K_i} max|0, R_{ik}^v - R^v|,$$
 (12)

where, $p(\mathbf{x}) = \varphi \sum_{k=1}^{K_i} max |0, R_{ik}^{v} - R^{v}|$ refers to the global penalty term related to (12), while the parameter φ denotes a penalty coefficient. The bottleneck exists in estimating properly the value of φ in which depends on expression (12).

Several approaches are used to compute the penalty coefficient [37]–[40]. The choice of approach depends on the optimization problem and the required computational resources. Often, the fixed penalty coefficient method, which consists of setting up the penalty value manually and is easy to use and quick but lacks adaptability to data, is applied [37]. Another method is called the penalty parameter estimation strategy, which aims to estimate the penalty coefficient automatically based on the problem's characteristics. It is data-driven and improves generalization but can be computationally costly and assumption-dependent [39]. In addition to an adaptive penalty coefficient, which consists of modifying the penalty coefficient iteratively during the optimization process, it reduces the risk of regularization but requires complex implementation and tuning to avoid instability [40].

V. SIMULATION RESULTS

In this section, we demonstrated the efficiency of the HCQGA in maximizing the energy efficiency of massive MIMO and reducing the computational complexity of the system through simulation evaluation. The classical constrained genetic algorithm (CCGA) was considered as a benchmark.

It is interesting to highlight that the overall number of active users and transmit power set _different possible power values that are considered as candidate values for transmitting a signal_ affect the overall search space, i.e., if the number of active users or the transmit power set increase, the database size also rises. For this sake, we constructed two simulation experiments, where each simulation analyzes the effect of each variant on the performance of the HCQGA and CCGA, i.e., the variant can be the overall number of active users or transmit power set.

A. Simulation 1

To ensure the validity of our results, we implemented a well-established simulation framework. The simulation setup of the massive MIMO system consisted of one reference cell with a scaling factor of $\varepsilon'=0.01$, surrounded by six neighboring cells. Each neighboring cell had an identical scaling factor of $\varepsilon=0.00015$.

It is important to note that all cells, including the reference cell, contained only one base station with a fixed number of antennas, M = 128. The energy efficiency and the number of generations executed were computed for varying numbers of active users within the reference cell, ranging from 5 to 11 (denoted as K).

The study considers three distinct target bit rate classes, as indicated in Table 1. It should be noted that, for every given number of active users in the reference cell (K_{ref}) , the total user population is randomly divided into two groups, each assigned to a specific target bit rate class. Furthermore, it is important to highlight that the computation of energy efficiency remains unaffected by the target bit rate of active users in the six neighboring cells.

In light of what has already been discussed, we concluded that converting the constrained objective function into an

TABLE I SIMULATION PARAMETERS SETTINGS

B bandwidth 1 MI	Hz
the concentration of the conce	
static circuit power of BS 1 W	
p_c circuit power per antenna 0.2	
target bit rate class 1 100 l	Mbit/s
R ² target bit rate class 2 130 l	Mbit/s
target bit rate class 3 150 l	Mbit/s

unconstrained one and selecting the appropriate penalty coefficient depend tightly on the application, i.e., our suggested massive MIMO. In our investigation, we chose to select the optimal penalty coefficient manually. In order to approximate an appropriate setup for the penalty coefficient, we conducted a third simulation in parallel, using classical constrained exhaustive search (CCES) to identify the best optimal scenarios that maximizes the energy efficiency with the given target bit rate classes of the massive MIMO model. Since the CCES can handle small-scale databases, we employed a small number of users.

Figure 4 illustrates the energy efficiency utilized by the HCQGA and CCGA algorithms for different scenarios with varying numbers of total active users. As clearly shown in Figure 4, the energy efficiency usage with respect to the target bit rates is equal for both HCQGA and CCGA, across different numbers of active users. This demonstrates that both algorithms perform equally in maximizing energy efficiency while considering the target transmission rate of massive MIMO.

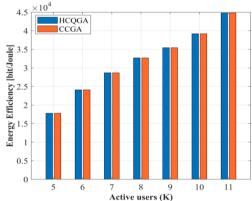


Fig. 4. Energy efficiency usage for different number of active users by the CCGA and HCQGA.

Figure 5 presents the average number of generations performed by the HCQGA and CCGA for different scenarios with varying numbers of total active users. In the comparison between the HCQGA and CCGA algorithms, it is noticeable that the CQGA exhibits a lower average number of generations performed compared to the CCGA. As a result, the computational complexity of the HCQGA is reduced in comparison to the CCGA. Furthermore, as the overall number of active users (database size) increases, the HCQGA consistently maintains a lower computational complexity in comparison to the CCGA.

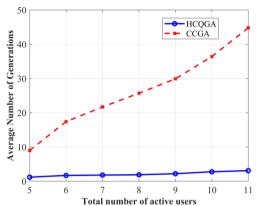


Fig. 5. Average number of generations executed by the CCGA and HCQGA.

These findings highlight the computational advantages of the HCQGA algorithm in scenarios with a larger number of active users.

B. Simulation 2

The parameter setup of this simulation environment follows the previously described configuration in simulation 1. The objective of this simulation is to examine the influence of the transmit power set size on both the energy efficiency usage of the massive MIMO and the number of generations executed by the HCQGA and CCGA algorithms. The energy efficiency and the number of generations executed were computed for transmit power set size, ranging from 24 dBm to 42 dBm. The value of *M* equals 128, while the value of *K* equals 6.

Figure 6 shows the energy efficiency usage by the HCQGA and CCGA algorithms for different scenarios with varying transmit power set size. As seen from Figure 6, the energy efficiency usage with respect to the target bit rates, is found to be equal for both the HCQGA and CCGA algorithms across various transmit power set sizes. This observation affirms that both algorithms exhibit comparable performance in optimizing energy efficiency while accounting for the target transmission rate of the active users in massive MIMO.

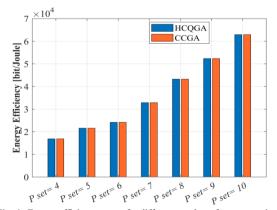


Fig. 6. Energy efficiency usage for different number of power set size for both the CCGA and HCQGA.

Figure 7 displays the average number of generations executed by the HCQGA and CCGA algorithms across different scenarios, considering various transmit power set sizes. In comparing the HCQGA and CCGA algorithms, it is evident that the HCQGA achieves a lower average number of generations performed compared to the CCGA, even when confronted with significant increases in transmit power set sizes. Consequently, the HCQGA exhibits a reduced computational complexity compared to the CCGA. Moreover, as the transmit power set sizes (database size) increases, the HCQGA consistently maintains a lower computational complexity relative to the CCGA.

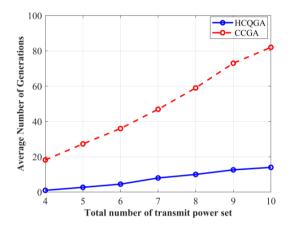


Fig. 7. Average number of generations executed by the CCGA and HCQGA.

C. Simulation 3

In the light of what have been discussed in the previous sections, it has been demonstrated that the quality of chromosomes during the initialization stage has a significant impact on the convergence speed of the genetic algorithm to the optimal result. This simulation investigates the effect of the coverage ratio $\frac{U.R}{N}$ on the runtime of the initialization stage of the HCQGA.

Figure 8 depicts the runtime required for various coverage values (%) during the quantum initialization stage of the HCQGA, when employing either classical or quantum computers. It is evident that as the coverage increases, the runtime of classical computers exhibits an exponential growth.

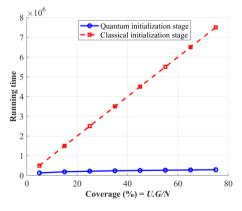


Fig. 8. The running time of the quantum and classical initialization stages.

In contrast, the quantum computer demonstrates significantly lower running times compared to the classical counterpart, while also maintaining consistently low runtimes despite increasing coverage.

Furthermore, Figure 9 illustrates the relationship between the region size and the average number of generations performed by the HCQGA. It is observed that as the region size increases, the number of executed generations drops.

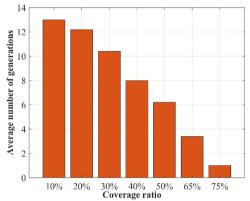


Fig. 9. The effect of increasing the region size on the executed average number of generations for the HCQGA.

VI. CONCLUSION

This paper introduces the highly constrained quantum genetic algorithm (HCQGA) as a novel approach for finding the extreme value with respect to certain constraints in a vast and unsorted database, which surpasses the computational capacity of current available classical and quantum computers. To test the efficiency of this quantum strategy. We have investigated the maximization of the energy efficiency of an uplink multicell massive MIMO system with respect to the target bit rate of users. The HCQGA demonstrated accelerated convergence towards optimal maximum energy efficiency, outperforming the constrained classical genetic algorithm (CCGA) in terms of computational efficiency.

In future work, we are planning to extend the classical massive MIMO framework into a quantum counterpart, where entanglement-assisted quantum channels are considered for improving the performance of the overall bit rate and energy efficiency. Followed by demonstrating the theoretical results by building extensive simulations.

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