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A new pilot assignment scheme for mitigating pilot contamination in uplink massive multi-input–multi-output (MIMO) systems

Haftom Tesfay Gidena^{1*} and Kiros Siyoum Weldemichael¹

*Correspondence:
htg101mit@gmail.com

¹Department of Electronics and Communication Engineering, Mekelle Institute of Technology-Mekelle University, Mekele, Ethiopia

Abstract

Pilot contamination is a serious issue in massive multi–input–multi–output systems which significantly degrades system performance. In this paper, we investigate a new pilot assignment scheme by integrating two-dimensional genetic algorithm with Tabu-Search algorithm (TS) to mitigate the pilot contamination problem. Firstly, we design a two-dimensional genetic algorithm equipped with elitism strategy as a principal algorithm for solving the pilot assignment problem; then, aiming to enhance the convergence speed of the genetic algorithm to the ideal optimal solution, we integrate TS with the genetic algorithm. This integrated pilot assignment scheme, henceforth designated as GATS-PA, is found to be powerful in mitigating the pilot contamination problem. Numerical simulation results verify that the proposed pilot assignment scheme is very close to the ideal optimal solution with few numbers of iterations and outperforms existing methods in terms of enhancing the average uplink rate per user over a wide range of simulation parameters.

Keywords: Massive MIMO, Pilot contamination, Pilot allocation, Genetic algorithm, Tabu-search

1 Introduction

Massive MIMO has been studied as key enabling technology for 5G and future wireless systems because of significant gains in both spectral and energy efficiency [1–3]. In order to reap the full benefits of massive MIMO, acquiring the channel state information (CSI) is crucial. In time division duplex (TDD) massive MIMO, the BS can estimate the CSI from mutually orthogonal uplink pilot sequences. In multi-cell multi-user massive MIMO systems, reusing of pilot sequences in adjacent cells is unavoidable because pilot resource is practically limited. Consequently, this reusing of pilot sequences brings about an inter-cell pilot interference termed as pilot contamination [4, 5].

Various methods have been investigated to mitigate the effect of pilot contamination. In [6], a time-shifted pilot assignment method was presented which involved

asynchronous transmission of pilot signals among adjacent cells. However, this may lead to mutual interference between data and pilot.

The schemes in [7, 8] used angle-of-arrival (AOA)-based methods and relied on the fact that geographically separated users with non-overlapping AOAs do not contaminate each other even if they employ the same pilot sequences. But the assumption that small AOA spread of each user is might not be always true as long as practical wireless systems are considered. The authors in [9] proposed a blind pilot decontamination technique based on subspace partitioning approach at the cost of a large computational complexity. A weighted graph-coloring-based pilot allocation scheme was proposed in [10] to mitigate pilot contamination for massive MIMO systems. The pilot assignment problem was modeled as a graph-coloring problem in which each node in the graph represents the user terminal. This pilot allocation scheme greedily assigns different pilots to graph-connected users starting from user terminals with the highest magnitude of pilot contamination. But it has limited performance in terms of convergence to the ideal optimal solution. In [11, 12], the low-complexity Tabu-search (TS) was proposed as a pilot assignment method in cellular massive MIMO and cell-free massive MIMO systems, respectively, and outperform the random pilot assignment and the greedy pilot assignment methods. Notwithstanding its low computational complexity, TS has limited performance when it comes to comparison with the ideal optimal solution.

A one-dimensional genetic algorithm was used as a pilot assignment method in massive MIMO systems as in [13] and showed improvement in performance compared with random pilot assignment, greedy pilot assignment, and TS pilot assignment methods. However, it requires many number of iterations to converge to the ideal optimal solution. The reason for that is because it stems from random initial population and did not take advantage of elitism strategy which happens to improve the performance of genetic algorithm.

In [14], a two-dimensional genetic algorithm was investigated for aircraft scheduling problem. Therein, a two-dimensional permutation encoding along with the implementation of two-dimensional crossover and mutation operations were devised. The authors pointed out that a two-dimensional encoding approach can reflect more geographical linkage of genes and might be suitable for problems with complex structures.

Motivated by [14], in this article, we propose a two-dimensional genetic algorithm (2D-GA) for pilot assignment problem in multi-cell massive MIMO systems. We have improved the genetic algorithm by adopting an elitism strategy in order to prevent the best chromosomes from the likelihood of being destroyed by the processes of crossover and mutation operations. Moreover, aiming to increase the likelihood of convergence to the ideal optimal solution, we have integrated the meta-heuristic optimization algorithm known as Tabu-search (TS) for the purpose of generating the initial population of the two-dimensional genetic algorithm. To shed more light, we have made the following contributions.

- *We have designed a 2D genetic algorithm tailored to the case of pilot assignment problem in massive MIMO systems. Also, we have employed an elitism strategy to prevent the best chromosomes from the likelihood of being destroyed by crossover and mutation operations and hence improve the performance of the 2D genetic algorithm.*

- To enhance the convergence speed of the genetic algorithm to the ideal pilot assignment solution, we have integrated a local-search optimization algorithm based on Tabu-Search as an initial population generator for the genetic algorithm.

Numerical simulation results confirm that, with few iterations, the performance of the proposed pilot assignment scheme is almost identical with the ideal optimal solution in terms of enhancing the uplink average rate per user.

The rest of the paper is organized as follows: Sect. 2 deals with the methodology which encompasses the model of massive MIMO system, achievable uplink (UL) rate, formulation of the optimization problem and the proposed pilot allocation scheme. Section 3 is dedicated to analyzing the computational complexity of the proposed scheme, and Sect. 4 focuses on the numerical simulation results and corresponding discussions. Finally, Sect. 5 concludes the paper.

2 Methods

2.1 System model

We consider a multi-cell, multi-user massive MIMO system with L cells operating in TDD mode, and the central BS in each cell is equipped with M antennas serving K ($K \ll M$) single-antenna users at the same time frequency resource. We assume that there are a maximum of K mutually orthogonal pilot sequences $(\phi_1, \phi_2, \dots, \phi_K)$ to be assigned to all KL users in the system. The length of each pilot sequence is considered to be one, and we assume that these pilot sequences are reused in all the L cells, but all the users in the same cell are allocated mutually orthogonal pilot sequences. The M -length channel vector between the k th user in j th cell and the BS in the i th cell can be described by [1–3].

$$\mathbf{h}_{ijk} = \mathbf{g}_{ijk} \sqrt{\beta_{ijk}} \quad (1)$$

where $\beta_{i,j,k}$ denotes the large-scale fading factor between the i th BS and the k th user in the j th cell as the result of shadow fading and path loss. It is user-dependent, but presumed constant over all M elements of the antenna array. The Symbol \mathbf{g}_{ijk} stands for the small scale fading vector of the corresponding user which follows a complex Gaussian distribution with zero mean vector and covariance matrix of \mathbf{I}_M . The large-scale fading coefficient between the k th user in the j th cell and the BS in the i th cell can be modeled as:

$$\beta_{ijk} = \frac{z_{ijk}}{(d_{ijk})^\alpha} \quad (2)$$

where $z_{i,j,k}$ is the shadow fading factor between the k th user in the j th and the BS in the i th cell which follows log-normal distribution with zero mean and standard deviation of δ_{shad} , $d_{i,j,k}$ represent the distance of the k th user in the j th cell and the BS in the i th cell, and α represents the path loss coefficient. The model of a typical multi-cell, multi-user massive MIMO system is depicted in Fig. 1 [15].

In order for the BS to acquire the CSI of its serving users, it needs pilot sequences to be transmitted which are known symbols at both transmission and reception ends. In

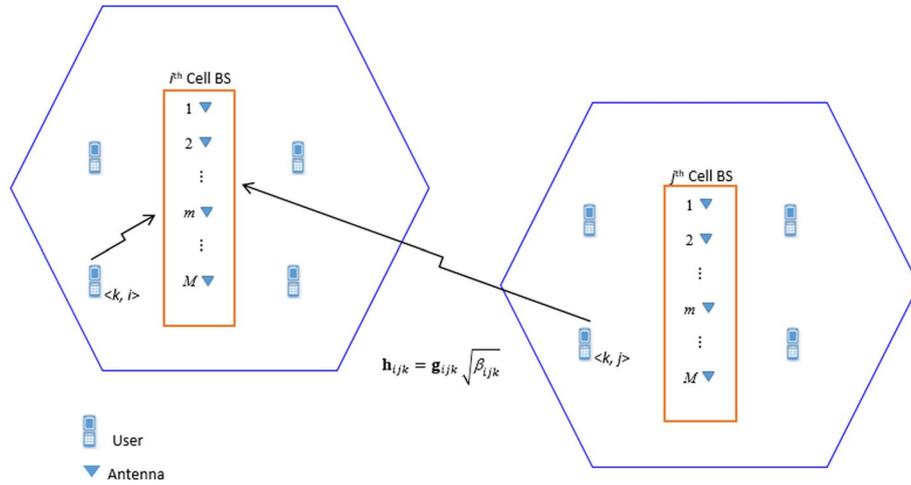


Fig. 1 Model of typical multi-cell, multi-user massive MIMO system

the dedicated uplink training phase, all user terminals transmit their corresponding pilot sequences to the BSs. Since the same K orthogonal pilot sequences are reused in every cell, the CSI is corrupted by pilot contamination from neighboring cells.

2.2 Achievable uplink rate

As investigated in [1–5, 10], when the number of antennas at the BS goes massive, the asymptotic SINR of the k th user in the i th cell can be formulated as:

$$\text{SINR}_{ik} \approx \frac{\beta_{iik}^2}{\sum_{j \neq i}^L \beta_{ijk}^2} \tag{3}$$

Subsequently, the asymptotic uplink rate of the k th user in the i th cell is given as

$$\text{SE}_{ik} = \log_2 \left(1 + \frac{\beta_{iik}^2}{\sum_{j \neq i}^L \beta_{ijk}^2} \right) \tag{4}$$

Exploiting only the large-scale fading coefficients, the achievable uplink system sum-rate (bits/s/Hz) is given as

$$\text{SE}_{\text{sum}} = \sum_{i=1}^L \sum_{k=1}^K \text{SE}_{ik} \tag{5}$$

2.3 Problem formulation

Given the available K mutually orthogonal pilot sequences $(\phi_1, \phi_2, \dots, \phi_K)$, there are a total of $(K!^{L-1})$ possible ways of assigning these pilot sequences to all users in all cells [10]. Considering the total uplink achievable rate of the system as an optimization target, the allocation problem can be formulated as

$$\begin{aligned}
& \max_{\{s_{ik}\} \in \{\phi_1, \phi_2, \dots, \phi_K\}} \sum_{i=1}^L \sum_{k=1}^K SE_{ik} \\
& = \max_{\{s_{ik}\} \in \{\phi_1, \phi_2, \dots, \phi_K\}} \sum_{i=1}^L \sum_{k=1}^K \log_2 \left(1 + \frac{\beta_{iik}^2}{\sum_{j \neq i}^L \beta_{ijk}^2} \right)
\end{aligned} \tag{6}$$

where s_{ik} stands for the pilot sequence assigned to the k th user in the i th cell.

2.4 Proposed pilot allocation scheme

The ideal optimal solution for the pilot assignment optimization problem in (6) is found by exhaustive-search mechanism which finds the global best pilot assignment set from all possible assignments exploiting brute-force approach, but it incurs huge cost of computational complexity for large-scale problem sizes. In this paper, we propose a 2D genetic algorithm integrated with Tabu-search (TS) to solve this optimization problem. Each scheme will be discussed separately, and the integration of the two will be finally illustrated in subsequent sections.

2.4.1 Two-dimensional genetic algorithm

We propose a two-dimensional genetic algorithm equipped with an elitism strategy as a principal solution to the pilot assignment problem. The two-dimension genetic algorithm involves 2D permutation encoding, 2D crossover operation, and 2D mutation operation. Each chromosome embodies a possible pilot assignment solution and is represented as a matrix.

A. Two-dimensional chromosome encoding

Each chromosome is encoded using two-dimensional permutation encoding with L rows and K columns, where L is the number of cells in the system and K is the number of users per cell which is equal to the number of pilots available. The chromosome representation for a system with L number of cells and K number of users is given as:

$$\begin{bmatrix} c(1,1) & c(1,2) & c(1,3) & \cdots & c(1,K) \\ c(2,1) & c(2,2) & c(2,3) & \cdots & c(2,K) \\ c(3,1) & c(3,2) & c(3,3) & \cdots & c(3,K) \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ c(L,1) & c(L,2) & c(L,3) & \cdots & c(L,K) \end{bmatrix} \tag{7}$$

$$c(x,y) \in \{\phi_1, \phi_2, \phi_K\}$$

where $c(x,y)$ stands for the gene located in row x and column y which represents the pilot assigned to the y th user in the x th cell. The population of the genetic algorithm now contains N of such 2D chromosomes, N being the number of chromosomes. Befitting this two-dimensional permutation encoding, we adopted two-dimensional crossover and mutation operations as described in [14].

B. Evaluation mechanism and selection strategy

To evaluate the fitness value of the population, we employed the sum of the uplink rate given in (5) as a fitness function. In every iteration of the genetic algorithm, a Roulette Wheel selection strategy is adopted to generate N populations for the next generation. Moreover, we employed an elitism strategy in which the best 5% chromosomes are selected to be passed to the next generation unaltered using the sum-rate fitness function stipulated in (5). This elitism technique allows to prevent the best chromosomes from the likelihood of being destroyed by crossover and mutation operations.

C. Two-dimensional crossover

Crossover is the kernel of genetic algorithm in which two parent chromosomes are crossed to produce an offspring for next generation with some predefined crossover probability. Befitting the two-dimensional permutation encoding, we employed a two-dimensional crossover technique which involves vertical and horizontal substring crossover operations.

D. Two-dimensional mutation

Mutation has a pivotal role in keeping the genetic diversity of the population of a genetic algorithm. Tailored to two-dimensional chromosome encoding, we applied horizontal and vertical substring mutation which correspond to the exchange of entire rows and columns, respectively, according to a random number generator and predefined mutation probability.

2.4.2 Tabu-search (TS)

TS is a meta-heuristic optimization algorithm which is widely recognized as one of the most effective local-search strategies applicable to various optimization problems. It uses a local or neighborhood search procedure to iteratively move from one potential solution to an improved solution, until some stopping criterion has been satisfied. This algorithm starts out with an initial solution vector and finds a local neighborhood around it. The algorithm exploits what is called Tabu list to get away from being stuck in the local optimum. After the termination of the iteration, the best among the solution space in all the iterations is considered as a final historical best solution vector [11]. The algorithm has the following parameters.

Neighborhood definition considering the i th cell whose pilot assignment vector is $\mathbf{s}_i = \{s_{i1}, s_{i2} \dots s_{iK}\}$, $s_{ik} \in \{\phi_1, \phi_2, \dots \phi_K\}$, the neighborhood of this pilot assignment vector is a set $\mathcal{N}(\mathbf{s}_i)$ with predefined length K , the components of which are the exchange of any two elements of \mathbf{s}_i .

Tabu list the algorithm records the solution vectors of the previous few iterations in a Tabu list, whose length is N_{tabu} , for the purpose of avoiding cycling. When the Tabu list is full, the new prohibited solution will push the first vector out of the list, and the pushed-out vector is free and added to the candidate again.

Stopping rule the search is stopped if the maximum number of iterations, I is reached.

Aspiration criterion for each search of the TS algorithm, the best state so far designated as b is defined to record the historical largest metric.

$$b = f(\mathbf{s} | \mathbf{s}_i = \mathbf{s}_i^*) \tag{8}$$

where \mathbf{s}_i^* represents the corresponding historical optimal solution of the pilot assignment vector of the i th cell, and $f(\cdot)$ is a sum-rate-based fitness function as given in (5), and \mathbf{S} is a matrix which corresponds for the pilot assignment of all cells.

2.4.3 Integrated pilot allocation scheme

In our work, we integrate TS algorithm with 2D genetic algorithm to solve the pilot assignment optimization problem. The purpose of the integration is to mitigate pilot contamination more significantly and to narrow out the performance gap with that of the ideal optimal pilot assignment solution. Here, the principal pilot assignment algorithm is the two-dimensional genetic algorithm; TS is incorporated merely to generate the initial population for the genetic algorithm. We have used TS to produce an initial pilot assignment solution which will be employed as an initial population for the genetic algorithm. In doing so, the convergence speed of the genetic algorithm to the ideal optimal solution will be enhanced due to the fact that the genetic algorithm starts out from a potential initial population instead of random initial population. The detailed algorithmic steps and implementation flowchart of the proposed scheme are illustrated in algorithm 1 and Fig. 2, respectively.

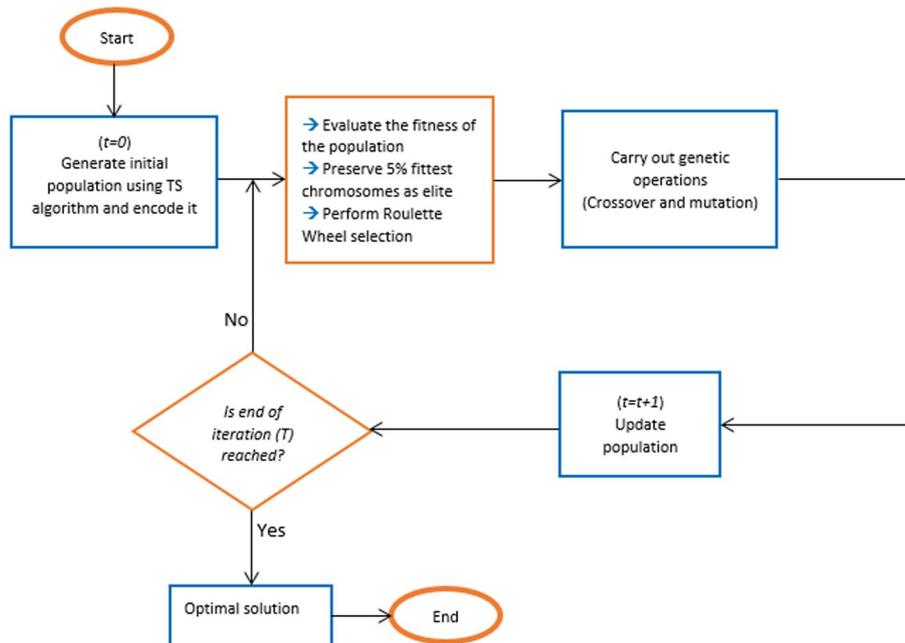


Fig. 2 Flowchart of the proposed scheme

Input: population size, N , number of iterations for 2D-GA, T , number of iterations for TS, l , and K pilot sequences $\{\phi_1, \phi_2, \dots, \phi_K\}$

Output: the best K pilot assignment set

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1 Initialization: generate initial population using TS algorithm,  $t=0$ 
2 while  $t < T$  do
3     - Compute fitness values of the population using the sum-rate in (5)
4     - Parents  $\leftarrow$  Roulette Wheel Selection (population)
5     - Elite  $\leftarrow$  the best 5% parents
6     - Offspring  $\leftarrow$  2D crossover (parents)
7     - Update offspring  $\leftarrow$  2D mutation (offspring)
8     - Update population  $\leftarrow$  parents  $\sqcup$  update offspring  $\sqcup$  elite
9     -  $t \leftarrow t+1$ 
10 end while
11 return the best  $K$  pilot assignment set

```

Algorithm 1 GATS-PA

3 Complexity analysis

According to [11], the order of computational complexity of TS-PA is $\mathcal{O}(LK^3)$. The order of computational complexity of the pilot assignment using 2D-GA can be estimated as $\mathcal{O}(NTLK)$. Therefore, the order of computational complexity of the proposed scheme is estimated to be $\mathcal{O}(NLK^3) + \mathcal{O}(NTLK)$, where N is population size, and T is the number of iterations of the genetic algorithm. The computational complexity of all the pilot assignment algorithms is summarized in Table 1.

The computational complexity of RPA is negligible in relation to the other schemes. In fact, RPA has the lowest computational complexity of any possible pilot assignment that optimizes a given objective function. But it has the poorest performance in terms of mitigating pilot contamination. The exhaustive-search pilot assignment, EX-PA, performs the best of all in mitigating pilot contamination but has an exponential order of complexity which makes it infeasible in practice. All but EX-PA has a polynomial order of complexity.

Table 1 Computational complexity

Algorithm	Order of complexity
TS-PA	$\mathcal{O}(LK^3)$
GATS-PA	$\mathcal{O}(PLK^3) + \mathcal{O}(PLK^2), T = K$
EX-PA	$\mathcal{O}(K^{l-1})$

Since the proposed scheme is an integration of TS-PA and 2D-GA, it stands to reason that it has higher computational complexity than TS-PA and 2D-GA taken individually. But the proposed scheme outperforms both TS-PA and 2D-GA in mitigating pilot contamination. Moreover, in comparison with EX-PA, the computational complexity of the proposed scheme can be considered negligible. For instance, for $L=7$ and $K=10$ massive MIMO system, the complexity of the proposed scheme with $T=K$ iterations and $N=20$ initial populations is 1.62×10^{34} times lower than that of EX-PA. So, the proposed scheme is able to achieve an efficient trade-off between system performance and computational complexity.

4 Numerical results

4.1 Simulation setup

In this section, numerical simulation is conducted considering a typical massive MIMO system with L hexagonal cells and K single-antenna users uniformly distributed in their respective cells with a distance not less than 30m from BS. The radius of the cell is set to 500 m. The number of pilot sequences is equal to K , which is the number of users per cell. Accordingly, the loss of spectral efficiency due to uplink pilot transmission is set as $\mu_0=0.05$ [10]. The performance of the proposed pilot assignment scheme, GATS-PA is compared with the following three existing pilot assignment schemes. *Random pilot assignment (RPA)*, *TS-based pilot assignment (TS-PA)* and *Exhaustive-search pilot assignment (EX-PA)*. The results are obtained by averaging from 2000 independent channel realizations. All the system parameters employed in this simulation are summarized in Table 2.

4.2 Results and discussion

Figure 3 depicts the CDF of the average uplink rate for the four algorithms when $L=3$, $K=5$, and $T=1$. Obviously, RPA performs lowest of all as it does not consider an optimization target. TS performs way better than RPA, but lower than the proposed scheme. Specifically, when CDF reaches 0.5, the average uplink rates per user achieved by RPA, TS-PA, and GATS-PA are 9.82 bps/Hz, 10.55 bps/Hz, and 10.9 bps/

Table 2 System simulation parameters

Parameters	Value
Number of cells, L	3, 4, 7
Number of BS antennas per cell, M	128
Number of users per cell, K	4, 5, 6
Log normal shadow fading, δ_{shad}	8 dB
Cell radius, R	500 m
Path loss exponent, α	3.8
Population size of GA, N	20
Number of iterations of GA, T	K
Number of iterations of TS, I	K
Mutation probability, p_m	0.1
Crossover probability, p_c	0.9
Loss of spectral efficiency factor, μ_0	0.05

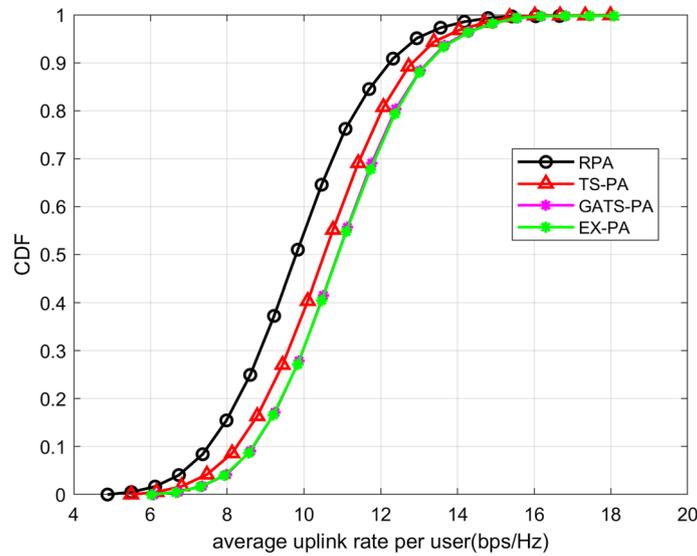


Fig. 3 CDF of average uplink rate per user with $L=3, K=5, M=128$

Hz, respectively. The performance gap between RPA and TS is 0.73 bps/Hz and the performance gap between TS-PA and GATS-PA is 0.35 bps/Hz. As can be observed from the figure, the performance of the proposed scheme and that of the exhaustive-search method is almost identical that it is difficult to tell them apart. This is because the 2D genetic algorithm starts out from a potential initial pilot assignment solution obtained by the TS algorithm. To shed more light, when CDF reaches 0.5, the performance gap between GATS-PA and EX-PA is only 0.01 bps/Hz. This means with one iteration of the genetic algorithm, GATS-PA is almost identical to the ideal optimal solution and hence mitigates pilot contamination significantly.

Figure 4 demonstrates the CDF of average uplink rate per user achieved by three algorithms RPA, TS-PA, and GATS-PA, when the number of cells is increased to 7 and the number of users is increased to 6. Overall, it can be observed that the average uplink rate achieved by all the schemes decreased due to the simultaneous increase in the number of users and cells, but the performance gap between RPA and the rest gets wider. Here, RPA performs the worst, and the proposed scheme performs the best. Particularly, when CDF is 0.5, RPA, TS-PA, and GATS-PA achieve 7.93 bps/Hz, 8.85 bps/Hz, and 9.26 bps/Hz, respectively. In this case, the performance gap between TS-PA and RPA is 0.92 bps/Hz, and the performance gap between TS-PA and GATS-PA is 0.41 bps/Hz.

Figure 5 depicts the significance of integrating TS algorithm with the 2D-GA in reducing the number of iterations to reach convergence for $L=3$ and $K=4$ massive MIMO system. As can be observed from the figure, if the 2D-GA-based pilot assignment (equipped with elitism) starts off from random initial population, it reaches convergence to the ideal optimal solution after 30 iterations. On the other hand, when TS algorithm is leveraged as an initial population generator for the genetic algorithm, the number of iterations required by GATS-PA to reach convergence to the ideal optimal solution is reduced to one. This is because in lieu of random initial population

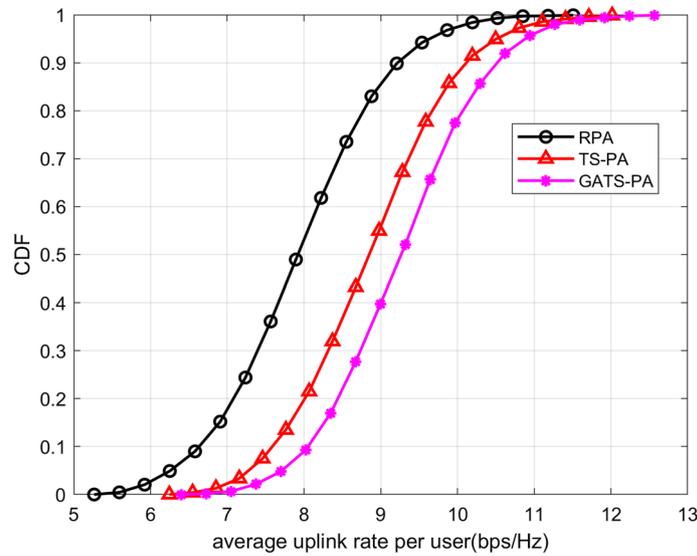


Fig. 4 CDF of average uplink rate per user with $L = 7, K = 6, M = 128$

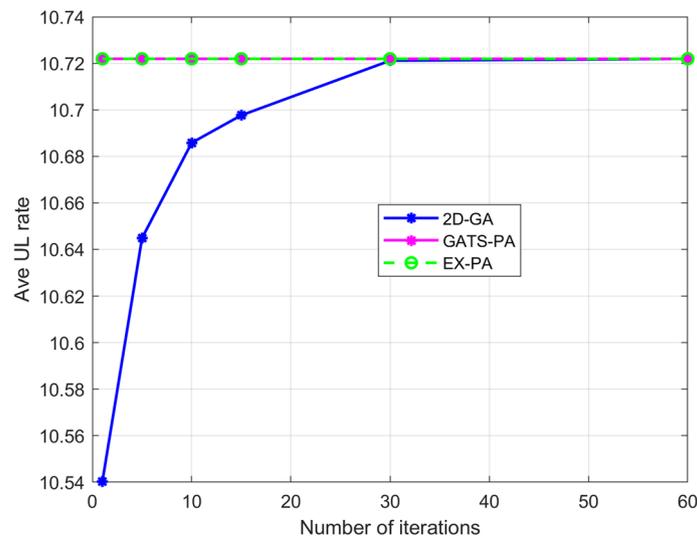


Fig. 5 Convergence analysis for $L = 3, K = 4, M = 128$

the genetic algorithm avails an enhanced initial population obtained by TS, and these enhanced initial pilot assignment solutions are preserved by the elitism strategy from the likelihood of being destroyed by the crossover and mutation operations.

Similarly, the convergence of the proposed scheme with $L = 4, K = 4$ massive MIMO system is depicted in Fig. 6. Even from the first iteration, the performance of the proposed scheme is almost identical to the ideal optimal solution. In this case, the proposed scheme converges to the ideal optimal solution after 4 iterations. However, it has to be noted that as the problem size (as the number of cells and/or the number of users) increases, the number of iterations required by the proposed scheme to reach convergence also increases.

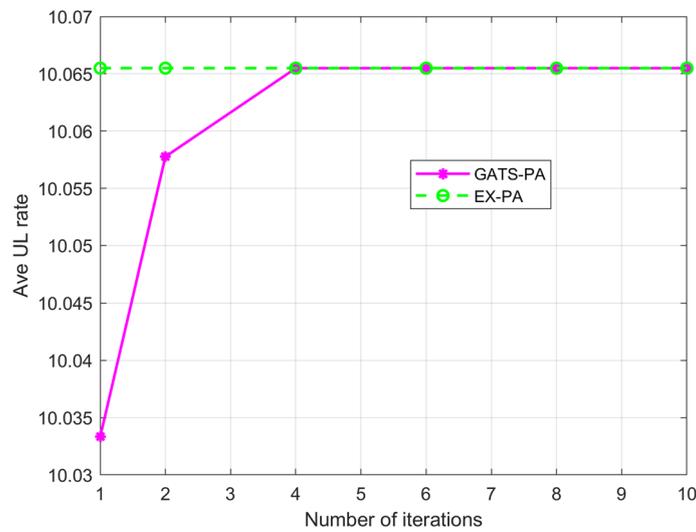


Fig. 6 Convergence analysis for $L=4, K=4, M=128$

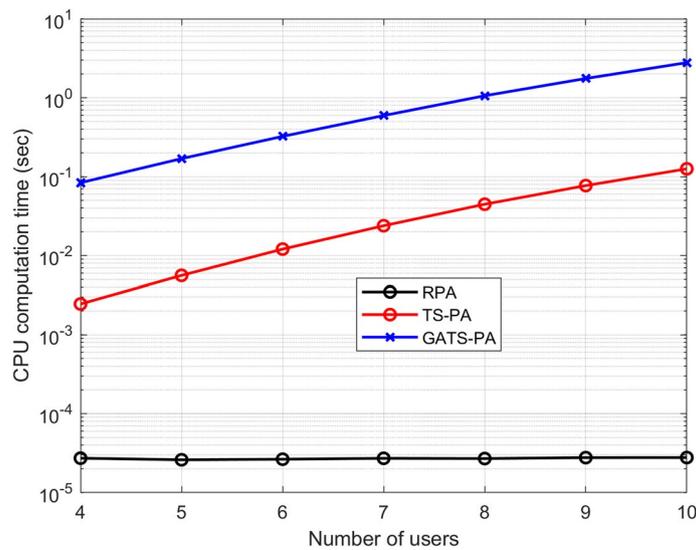


Fig. 7 CPU computation time comparison

The computational complexity can also be analyzed using CPU computation time in seconds. Accordingly, when $L=7$, the CPU computation time for RPA, TS-PA and GATS-PA with respect to the variation in the number of users is illustrated in Fig. 7. The simulation is conducted using MATLAB R2018a installed in a personal computer with an Intel(R) Core™ i5 and Windows operating system. For GATS-PA, K iterations and $N=20$ initial populations are utilized. From this figure, the CPU computation time required by RPA more or less stays constant irrespective of the increase in the number of users and is the lowest computation time. Although RPA achieves the lowest CPU computation time, its performance in terms of mitigating pilot contamination is the poorest. For TS-PA and GATS-PA, the computation time increases with

the increase in the number of users. As it can be observed the GATS-PA takes more CPU computation time in comparison with TS-PA. Although the CPU computation time of GATS is higher than that of TS-PA, its performance in terms of mitigating pilot contamination is better than TS-PA. Moreover, its computational complexity is far more negligible in comparison with the ideal optimal pilot assignment solution which have exponential order of complexity.

5 Conclusion

In this paper, a new pilot assignment method designated as GATS-PA, which integrates two-dimensional genetic algorithm with Tabu-search, has been proposed as a pilot assignment scheme to mitigate the pilot contamination problem in massive MIMO systems. Numerical simulation is conducted to assess the performance of the proposed scheme in relation to existing schemes. The simulation results and corresponding performance analysis confirm that the proposed pilot assignment scheme enhances the uplink average rate per user and mitigates pilot contamination more significantly in comparison with existing methods. Moreover, with few number of iterations, the proposed scheme is found to be almost identical to the ideal optimal solution when the problem size is small.

Albeit negligible in comparison with that of the exhaustive-search method, the computational complexity of the proposed scheme is still considerable. In the future, while keeping the high performance achieved by the proposed scheme in enhancing the uplink average rate of users, improving the complexity of the genetic algorithm and/or the TS algorithm might be considered a plus in order to account for very large problem sizes.

Abbreviations

BS	Base station
CDF	Cumulative distribution function
CSI	Channel state information
EX-PA	Exhaustive-search pilot assignment
GA	Genetic algorithm
MIMO	Multi-input multi-output system
TDD	Time division duplex
RPA	Random pilot assignment
TS-PA	Tabu-search pilot assignment
2D	Two-dimensional
GATS-PA	Two-dimensional genetic algorithm integrated with Tabu-search

Author contributions

HG is the main contributor of this manuscript. He wrote the manuscript, carried out simulations, and undertook analysis of the results. KW revised the manuscript and provided an invaluable guidance in the documentation. All authors have read and approved the final manuscript.

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Availability of data and materials

Data sharing is not applicable to this article as no datasets were generated or analyzed during the current study.

Declarations

Competing interests

The authors declare no competing interests.

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