

Genetic Algorithm-Based Optimization of Two Transfer Points (2TP) Problem in Random Graph

Abstract

This paper addresses the Two Transfer Point (2TP) problem, a critical optimization challenge in vehicle routing and ridesharing applications. The goal is to determine the optimal meeting and dropping points on a graph to minimize the total travel distance for two users with distinct origins and destinations. We propose a genetic algorithm-based approach to solve the 2TP problem efficiently. The algorithm employs binary encoding for solutions, fitness evaluation based on total travel distance, and genetic operations such as tournament selection, crossover, and mutation. Experimentation demonstrates the method's effectiveness in identifying near-optimal solutions in complete random graphs. Two experiments are conducted to compare the performance of the genetic algorithm (GA) with an exact approach: in the first, the GA operates with a fixed generation budget, while in the second, it is allowed the same time budget as the exact algorithm. Additionally, we present a practical example using a real-world road network to illustrate the algorithm's applicability.

CCS Concepts

- Theory of computation → Shortest paths; Random search heuristics.

Keywords

Two Transfer Point Problem, Vehicle routing, Ridesharing optimization, Genetic algorithm, Heuristic methods, Travel distance minimization

ACM Reference Format:

. 2025. Genetic Algorithm-Based Optimization of Two Transfer Points (2TP) Problem in Random Graph. In *Proceedings of The Genetic and Evolutionary Computation Conference 2025 (GECCO '25)*. ACM, New York, NY, USA, 7 pages. <https://doi.org/10.1145/nmnnnnnn.nmnnnnnn>

1 Introduction

In this article, we start by defining the Two Transfer Point (2TP) problem, a routing optimization challenge in which two users with distinct start and destination points seek to minimize their combined travel distance by determining the optimal meeting and dropping points. We formalize the problem mathematically and provide an exact algorithm with quadratic time complexity to solve it as well as a genetic algorithm (GA) to find near-optimal solutions.

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GECCO '25, Málaga, Spain

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<https://doi.org/10.1145/nmnnnnnn.nmnnnnnn>

However, as the problem scales with larger graphs and more dynamic constraints, exact solutions become computationally prohibitive. To address this, we propose a **Fitness Caching** Genetic Algorithm (GA) that offers an efficient heuristic for solving the 2TP problem. To the knowledge of the authors, this is the first work to formally define and address the 2TP problem—minimizing the combined travel distance for exactly two users by optimizing both a meeting and a drop-off point—within a graph-based framework. This formulation distinguishes itself from general shared mobility problems by explicitly modeling transfer point optimization for two users, supported by both an exact algorithm and a GA. The GA is not only capable of producing near-optimal solutions, but is also empirically shown to scale significantly better than the exact approach on large graphs. Furthermore, the proposed dual-method strategy allows for a comprehensive evaluation: the exact algorithm serves as a benchmark for solution quality, while the GA demonstrates practical viability for large instances where exact computation is infeasible, or very slow. This comparative analysis between solution quality and computational efficiency, tailored specifically to the 2TP problem, highlights the novelty and relevance of our approach in the context of scalable shared mobility planning.

This problem is part of the broader context of Shared Mobility Problems (SMP) [9, 17], which include carpooling, cab sharing and buspooling [9, 17], and have become a major trend in many urban cities around the world [17]. Trip sharing, as a problem 2TP, is intrinsically linked to vehicle routing and allocation challenges [9, 19], often formulated as variants of Vehicle Routing Problems (VRP) [4, 17–19], especially in dynamic and stochastic contexts [2, 4, 9, 14, 15, 17, 19]. The sources point out that ride-sharing systems are similar to other on-demand transportation services such as cabs and dial-a-ride services [2, 17]. Research in this area has explored a variety of resolution methods [2, 17], ranging from exact algorithms [2, 17], such as mixed integer programming or branch and bound [2, 4, 17], effective for small instances [2, 17] but limited due to non-polynomial complexity and scalability issues for larger problems [2, 17, 19], to heuristics and metaheuristics [2, 15, 17]. Among the latter, genetic algorithms (GA) are frequently used for their ability to quickly find good, albeit approximate, solutions for large-scale problems and in dynamic environments [2, 4, 19]. Techniques such as **clustering** [2, 9, 19], which involves grouping requests or journeys according to their spatio-temporal compatibility (including on the basis of shortest paths) [2, 19], are also used to improve the efficiency and scalability of solutions [2, 9, 19]. The evaluation of these approaches is often carried out using real data from large cities [2, 4, 9, 14, 19], simulations [2, 9, 14], or by comparing the results of heuristics with those of exact algorithms on small instances [2, 4].

The 2TP problem has diverse applications beyond transportation. For example, in collaborative robotics, coordinating meeting and transfer points for robots can optimize task efficiency and energy consumption. In supply chain management, it can streamline the

transfer of goods between warehouses to reduce costs. Additionally, in disaster response, identifying optimal meeting and dropping points for rescue teams and supplies can save critical time.

The remainder of this paper provides a formal problem definition, introduces an exact algorithm alongside a **Fitness Caching** GA, assesses the GA's error relative to the exact solution, and evaluates the performance of both approaches both theoretically and empirically. The evaluation is conducted on randomly generated complete graphs as well as on small real-world road networks.

2 Two Transfer Point (2TP) Problem

Given a graph $G(V, E)$ and two paths $a - c$ and $b - d$ sharing a common segment $m - k$, the goal is to find the meeting node m and the drop-off node k , such that the pair of nodes m, k minimizes the sum of the parameters of the edges $e \in E$ of all the shortest paths SP included in this scenario. Figure 1 illustrates this problem graphically, and we can formalize this problem as in Definition 2.1.

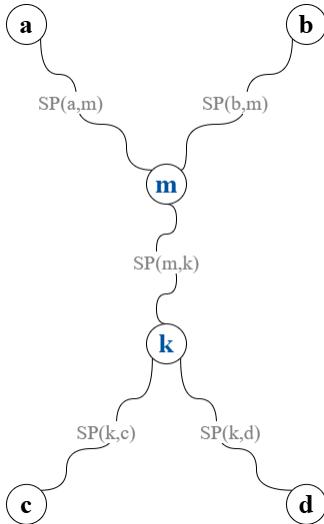


Figure 1: Two Transfer Point (2TP) problem in general graph.

Definition 2.1 (2TP Problem). Given a graph $G(V, E)$, two paths $a - c$ and $b - d$ sharing a common segment $m - k$, with $a, b, c, d \in V$, $SP(u, v)$ the shortest path between $u, v \in V$ and $\tau(u, v)$ the sum of the parameters of the edges $e \in SP(u, v)$, is there exists a pair $m, k \in V$ such that:

$$(m, k) = \min_{m, k} (\tau(a, m) + \tau(m, k) + \tau(k, c) + \tau(b, m) + \tau(m, k) + \tau(k, d))$$

In a real-world context, the sum of the edge parameters will generally be the cumulative travel time for each edge or the total travel distance, in the remainder of this article, we will use the distance parameter.

The pseudo-code (Algorithm 1) gives an exact solution for solving the 2TP problem in a general graph with an approximate worst-case time complexity of $O(n^2)$ where $n = |V|$ (cf. Section 4.2.2). This algorithm solves the 2TP problem by iterating over all possible pairs of meeting node m and dropping node k in the graph. For each pair, it computes the total travel distance for both user

using Dijkstra's algorithm [5] to find the shortest paths between the source and target nodes, as well as the meeting and dropping points. The algorithm keeps track of the minimum total distance, and at the end, it returns the optimal pair of nodes that minimizes this distance.

Modify: Put the algo with all the shortest time computed before search !!

Algorithm 1 Exact Algorithm for the Two Transfer Point Problem

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Require: Graph  $G$  with  $|V|$  nodes, sources nodes  $a, b$ , targets nodes  $c, d$ 
Ensure: Optimal meeting and dropping points
1: Initialize  $min_{sum} \leftarrow 0$ 
2: for each node  $m \in G$  do
3:   for each node  $k \in G$  do
4:      $sum_m \leftarrow$  Dijkstra( $a, m$ ) + Dijkstra( $b, m$ )
5:      $sum_k \leftarrow$  Dijkstra( $m, k$ )
6:      $sum_e \leftarrow$  Dijkstra( $k, c$ ) + Dijkstra( $k, d$ )
7:      $sum \leftarrow sum_m + sum_k + sum_e$ 
8:     if  $sum \leqslant min_{sum}$  then
9:        $min_{sum} \leftarrow sum$ 
10:      end if
11:    end for
12:  end for
13: return  $min_{sum}$ 

```

We hypothesize that the 2TP problem is 3SUM-hard, implying that there is no sub-quadratic algorithm for this problem. An algorithm is *sub-quadratic* if there exists an $\epsilon > 0$ such that the algorithm runs in time $O(n^{2-\epsilon})$. The 3SUM problem involves determining whether there exist three numbers within a given set that sum to zero. We can formalize this problem as in the Definition 2.2.

Definition 2.2 (3SUM Problem). Given a set S of n integers, does there exist $x, y, z \in S$ such that $x + y + z = 0$?

The 3SUM problem can be solved using a $O(n^2)$ algorithm¹ and it is generally accepted that $O(n^2)$ is the worst case lower bound as expressed in Conjecture 2.1.

Conjecture 2.1 (3SUM conjecture). *There is no sub-quadratic algorithm for the 3SUM problem [7].*

However, this conjecture has been refuted in the meantime by proving better lower bound [6, 11, 12]. Despite the fact that we are unable to show here a reduction from 3SUM to 2TP, and from 2TP to 3SUM, our intuition is that the 2TP problem in general graphs is 3SUM-HARD and that might not be the case for road graphs, although this demonstration is part of a future work. This intuition arises from the understanding that road networks deviate from the structure of classical graphs, exhibiting distinct characteristics such as Highway Dimension [1]. Consequently, specialized techniques like Hierarchical Contraction [8] can be effectively applied to optimize their analysis and representation. In the following, our focus will be directed towards classical graphs, with particular emphasis on complete graphs, due to their high connectivity, which inherently results in higher complexity.

¹By first sorting the S set, then testing each 3-tuples

3 Genetic Algorithm

GAs are a class of optimization techniques inspired by the principles of natural selection [10]. GAs operate by evolving a population of candidate solutions through selection, crossover, and mutation processes, guided by a fitness function. These algorithms are particularly effective for solving complex optimization problems where conventional methods may be computationally impractical or inefficient [16].

In the context of 2TP problem, we employ a GA to optimize the transfer points, aiming to minimize the total travel distance for both users. As before, the 2TP problem is modeled using a complete random graph $G(V, E)$ with $|V| = N$, in our experiments the number of nodes N is chosen from $\{10, 25, 50, 100\}$. The pseudo-code (Algorithm 2) provides the details of the steps in the GA process. Two users are assigned random start and destination nodes, ensuring distinct locations. The algorithm iteratively evolves candidate solutions to identify the pair of nodes, m and $k \in V$, that results in the most efficient routing for the users. Solutions are encoded as binary strings, representing the indices of the meeting and dropping points, $m, k \in V$, details are given in the Section 3.1.

Fitness is computed as the negative total travel distance for both users, ensuring minimization by maximizing fitness values. The algorithm employs tournament selection for parent selection, bitwise crossover for offspring generation, and bit-flip mutation with a 10% probability to maintain diversity. The population evolves over a predefined number of generations T , with the best-performing individuals retained, this elitist strategy prevents the loss of promising candidates and accelerates convergence toward the (near) optimal solution.

It is true that the number of possible (m, k) pairs in this problem is limited to $|V|^2$, and for small values of $|V|$, enumerating all solutions may appear tractable. However, our GA implementation leverages a *fitness caching mechanism* that stores the evaluation results of previously seen individuals, thereby avoiding redundant computation and enabling the algorithm to focus resources on exploring new regions of the solution space. In contrast to brute-force enumeration—which exhaustively and indiscriminately evaluates all combinations—the GA efficiently guides the search using evolutionary pressure toward more promising regions of the search space. Moreover, enumeration lacks the adaptive sampling and probabilistic exploration mechanisms that allow GAs to generalize across different problem settings and scale more naturally to larger instances. As a result, even when the number of evaluations is on par with the number of total possible solutions, the GA often discovers better solutions faster and with fewer redundant checks.

3.1 Encoding

Solutions in the genetic algorithm are encoded as fixed-length binary strings that represent the decision variables of the 2TP Problem, specifically the indices of the meeting and dropping points, $m, k \in V$. Each of these points is encoded using a fixed number of bits, typically one byte, resulting in a total individual length of 16 bits. This design constrains the maximum number of nodes to 256 (2^8), which is sufficient for our experiments; however, the encoding length can be increased to support larger networks.

Algorithm 2 Genetic Algorithm with Fitness Caching for the Two Transfer Point Problem

Require: Graph G with $|V|$ nodes, source nodes a, b , target nodes c, d , population size P , number of generations T

Ensure: Optimal meeting and dropping points

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1: Initialize population  $P_0$  with random binary-encoded solutions
2:  $fitness\_cache \leftarrow \emptyset$ 
3:  $best\_fitness \leftarrow -\infty$ 
4:  $best\_solution \leftarrow \emptyset$ 
5: function EVALUATEWITHCACHE(individual)
6:   if individual  $\in fitness\_cache$  then
7:     return fitness_cache[individual]
8:   else
9:     fitness  $\leftarrow$  ComputeFitness(individual)
10:    fitness_cache[individual]  $\leftarrow$  fitness
11:    return fitness
12:   end if
13: end function
14: for  $t \leftarrow 1$  to  $T$  do
15:   for each individual in population do
16:     individual.fitness  $\leftarrow$  EVALUATEWITH-
    CACHE(individual)
17:   end for
18:   Select parents using tournament selection
19:   Generate offspring using crossover and mutation
20:   for each child in offspring do
21:     child.fitness  $\leftarrow$  EVALUATEWITHCACHE(child)
22:   end for
23:   Merge offspring into the population
24:   Retain the top  $P$  individuals based on fitness
25:   if fitness of best individual in population  $> best\_fitness$ 
    then
26:     Update best_fitness and best_solution
27:   end if
28: end for
29: return best_solution with corresponding best_fitness

```

The structure of the binary string is divided evenly: the first half encodes the meeting point and the second half encodes the dropping point. These binary segments are interpreted as unsigned integers and mapped to valid node indices using the modulo operation, ensuring all decoded values correspond to existing nodes in the graph regardless of the raw binary value. This encoding strategy allows efficient manipulation and crossover operations at the bit level. A simple example of this encoding scheme is illustrated in Figure 2, where each individual represents a unique pair of terminal points in the network.

3.2 Selection

The genetic algorithm employed in our experiments uses *tournament selection* to choose parents for crossover. This method involves randomly selecting a subset of individuals from the current population and choosing the one with the highest fitness among them to act as a parent. In the implementation, the tournament size k is defined as $\max(2, \lfloor \frac{P}{10} \rfloor)$, where P is the population size. This dynamic

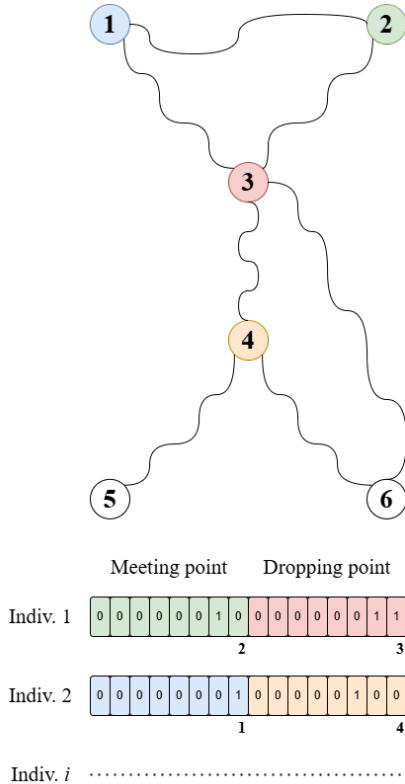


Figure 2: Two Transfer Point (2TP) individuals encoding.

sizing ensures a reasonable balance between selection pressure and population diversity, adapting to small or large populations alike.

Tournament selection is particularly suited for problems like the 2TP problem, where the fitness landscape may contain numerous local optima and sharp discontinuities. By selecting the best individual from a random subset rather than directly based on proportional fitness, tournament selection reduces the risk of premature convergence caused by overly dominant individuals early in the search. This approach introduces a moderate degree of stochasticity, maintaining diversity in the gene pool while still favoring individuals with higher fitness. In contrast to more deterministic or proportional methods, tournament selection does not require fitness normalization and is less sensitive to the scale of the fitness values. This makes it robust in scenarios where raw fitness differences may be large or unevenly distributed across the population.

Alternative selection mechanisms such as roulette wheel selection and rank-based selection also exist, each with different trade-offs. Roulette wheel selection assigns selection probabilities directly based on relative fitness values, favoring individuals with high fitness but risking early loss of genetic diversity. Rank-based selection, on the other hand, assigns probabilities based on the ranking of individuals rather than their absolute fitness, providing smoother control over selection pressure. Although this implementation does not explicitly name elitism, an elitist strategy is effectively incorporated by preserving the top P individuals after each generation.

Following the generation of a new offspring via crossover and mutation, the population is augmented and then truncated by sorting all individuals by fitness and retaining only the best-performing subset. This ensures that the fittest solutions persist across generations, guiding the evolutionary process steadily toward optimal or near-optimal regions of the search space.

3.3 Fitness

The fitness function evaluates the quality of solutions in the GA by calculating the total travel distance for a pair of meeting and dropping points. Invalid solutions, where the meeting and dropping points are identical, are penalized with $-\infty$. For valid solutions, the fitness is the negated sum of shortest path distances, using Dijkstra, for users traveling to the meeting point $(a - m, b - m)$, between meeting and dropping points $(m - k)$, and from the dropping point to their destinations $(k - c, k - d)$. This ensures the algorithm maximizes fitness while minimizing total travel distance.

4 Results

In this section, we present the results of our experiments evaluating the performance of the GA for solving the 2TP problem. We demonstrate that the population converges to a near-optimal solution over successive generations, highlighting the algorithm's effectiveness in minimizing the total travel distance for the users. The results also include a practical example using a real-world road network, illustrating the GA's applicability to real-world scenarios. Additionally, we compare the solutions obtained by the GA (Algorithm 2) with the solutions obtained by the exact algorithm (Algorithm 1) on graphs with $|V| \in \{10, 25, 50, 100\}$, where each edge weight is a floating-point distance δ randomly drawn from the interval $[1, 10]$. In both experiments we repeated 50 random experiments with a fixed seed to enable reproducibility, the code and results are available on a [GitHub repository]. This graph structure ensures all possible routes and transfer points are represented, enabling a comprehensive evaluation of the algorithm while also reflecting the worst-case runtime scenario, as real-world road networks are typically not fully connected. In the first set of experiments, the GA operates with a fixed generation budget, while in the second, it is allocated the same time budget as the exact algorithm. Table ?? provides a summary of the GA parameters investigated and the corresponding results obtained. Finally, we analyze the theoretical running time of both algorithms and provide insights into scenarios where the GA may be preferred over the exact solution, particularly in larger or more complex instances.

4.1 Convergence

In this section, we evaluate the performance of each GA instance using the 50 instance of complete random graphs $G(V, E)$, where $|V| = 100$. The GA instances are tested with population sizes $P \in \{5, 10, 20, 50\}$ and number of generations $T \in \{250, 500\}$. The corresponding results are presented in Figures 3, and 4.

Note the total difference of distances between two user cannot be 0 since there users have to meet at an intersection (node m) and leave each other at another intersection (node k)

Difference when changing the size of the population ??

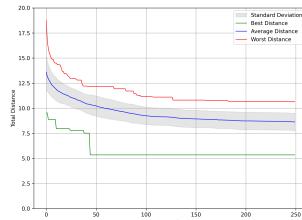
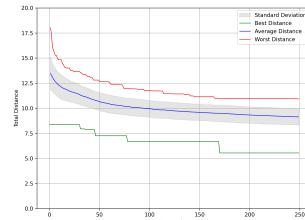
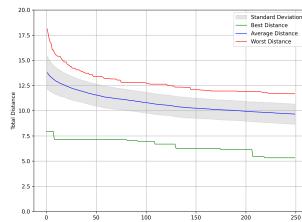
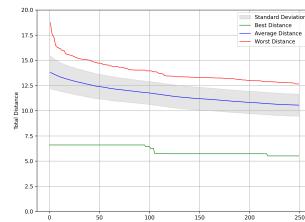
(a) GA with $P = 5, T = 250$ (b) GA with $P = 10, T = 250$ (c) GA with $P = 20, T = 250$ (d) GA with $P = 50, T = 250$

Figure 3: Evolution of the average fitness function over 50 instances of complete random graphs with $|V| = 100$ nodes for two GA configurations with $T = 250$.

Figures 3b and 3c illustrate the impact of population size on the convergence behavior of the GA. Specifically, a larger population size ($P = 20$ in Figure 4d) requires more generations to achieve the similar fitness value compared to a smaller population size ($P = 10$ in Figure 3b). This slower convergence occurs because larger populations provide greater genetic diversity, which increases the search space and delays premature convergence. While this delay can result in slower progression towards the optimal solution, it also reduces the likelihood of becoming trapped in suboptimal solutions, highlighting a trade-off between exploration and convergence speed.

Difference when after two times more generation ?

A comparison of Figures 3b and 4d reveals that the population may converge prematurely to a suboptimal solution. For example, this phenomenon can be seen in Figure 4d where the GA remains stagnant between approximately generation 200 and generation 340 before converging on a better solution. This issue can be mitigated by employing a larger population size, as demonstrated in Figure 4d, allocating a higher computational budget, or increasing the bit-flip mutation probability. Each of these approaches enhances exploration within the search space, reducing the likelihood of premature convergence.

4.2 Mean Relative Error

In this section, we evaluate the solutions obtained by the GA (Algorithm 2) with different size of population to the solutions obtained by the exact algorithm (Algorithm 1) on the same 50 random instance of complete random graphs with $|V| \in \{10, 25, 50, 100\}$, first with a fixed budget of generation for the GA and then with an execution time budget equal to the one required by the exact algorithm.

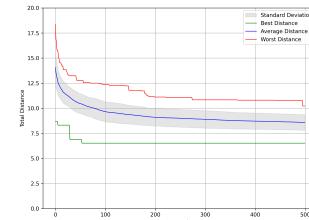
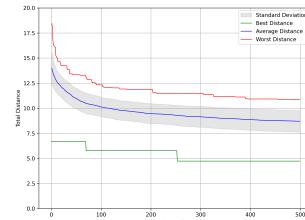
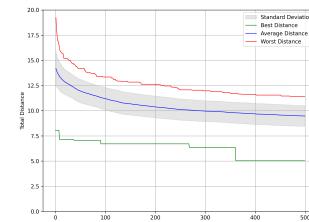
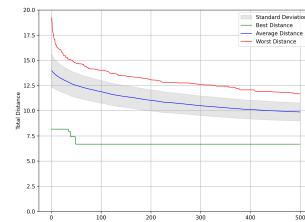
(a) GA with $P = 5, T = 500$ (b) GA with $P = 10, T = 500$ (c) GA with $P = 20, T = 500$ (d) GA with $P = 50, T = 500$

Figure 4: Evolution of the average fitness function over 50 instances of complete random graphs with $|V| = 100$ nodes for two GA configurations with $T = 500$.

The Mean Relative Error (MRE) is calculated by first determining the relative error for each instance. This is defined as the percentage difference between the total distance obtained by the GA and the exact solution, normalized by the exact solution's distance. The MRE is then computed as the arithmetic mean of these relative errors across all evaluated instances, providing a measure of the GA's average deviation from the optimal solution. In the followign the MRE is expressed in %, meaning that the solution found by the GA deviate by X% from the correct solution

4.2.1 With fixed generation budget. The left the better, choose $T = 500$ as first test given the better average results show in the previous section

MRE depend on the graph size, the larger the graph, the larger the Error

$P = 20$ is the one for which the % of error if the smallest on average for the tested size of graphs and a fixed number of generations, better than $P = 50$ when the graph is large

4.2.2 With equal time budgets. The exact algorithm (Algorithm 1) systematically evaluates all possible pairs of meeting and dropping points in the graph. Its complexity can be expressed as:

$$O(|V|^2) + O(|E| + |V| \log |V|)$$

where $O(|E| + |V| \log |V|)$ is the time complexity of Dijkstra's algorithm for a graph with $|V|$ nodes and $|E|$ edges. Since Dijkstra's algorithm is only once at the beginning, the complexity of The exact algorithm (Algorithm 1) can therefore be simplified into:

$$O(|V|^2)$$

the overall complexity scales quadratically with $|V|$, making the exact algorithm computationally expensive as the graph size increases. The GA is therefore particularly advantageous for very

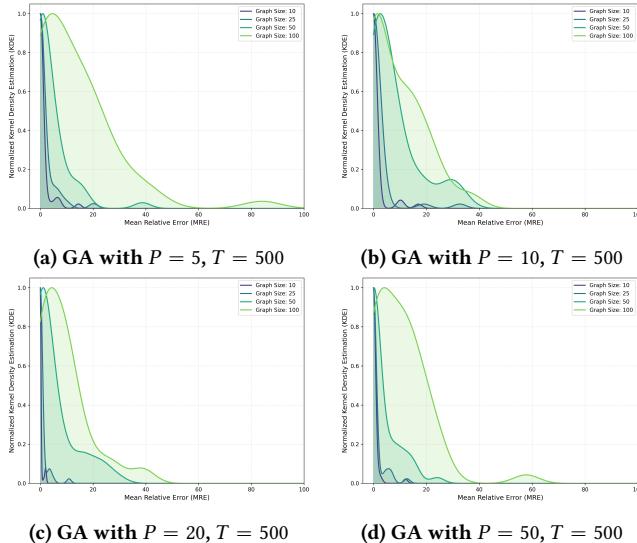


Figure 5: Normalized Kernel Density Estimation (KDE) of the Mean Relative Error (% MRE) for GA with fixed number of generations $T = 250$ and variable population size P over 50 instances of complete random graphs.

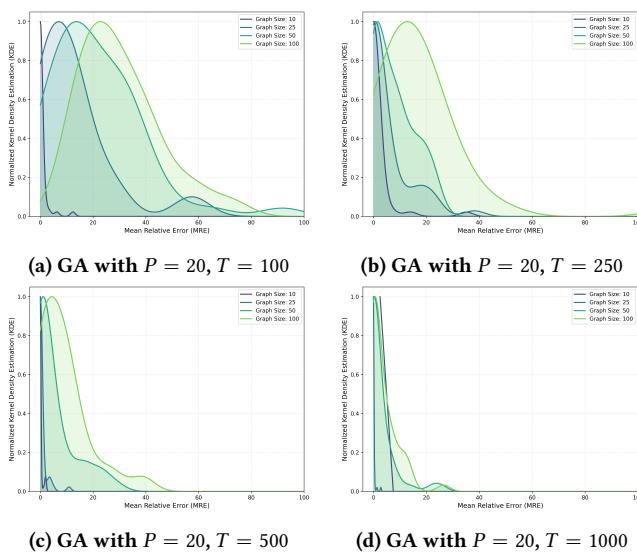


Figure 6: Normalized Kernel Density Estimation (KDE) of the Mean Relative Error (% MRE) for GA with fixed population size $P = 20$ and variable number of generations over 50 instances of complete random graphs.

large graph instances. While the exact algorithm provides guaranteed optimal solutions, its computational cost becomes prohibitive for large graphs due to its dependence on the quadratic scaling of node pairs. In contrast, the GA efficiently balances computational effort with solution quality, making it a practical choice for large-scale problems where exact solutions are infeasible.

Smaller graph mean smaller running time for the GA so less generation to converge

On our experimental setup, the table 1 give the time τ taken by the Exact Algorithm (EA) for each size $|V|$ of the tested graph

Table 1: Average running time of the the Exact Algorithm (EA) on the complete random graphs

Graph Size $ V $	τ
10	0.001s
25	0.003s
50	0.020s
100	0.157s
200	1.239s
400	11.675s

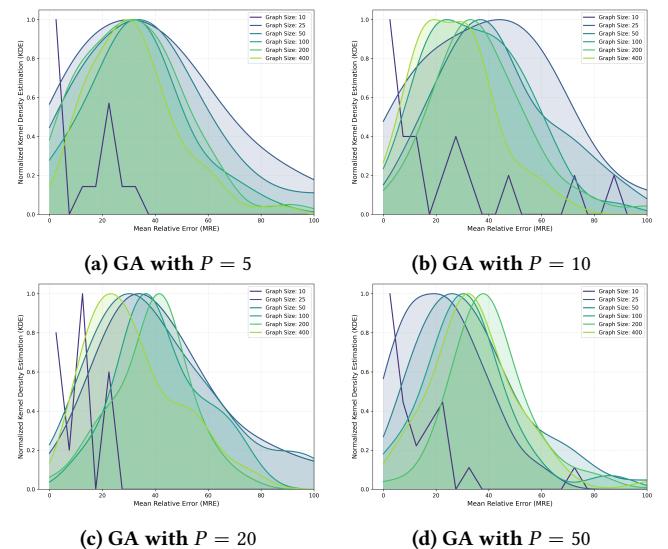


Figure 7: Normalized Kernel Density Estimation (KDE) of the Mean Relative Error (% MRE) for GA with T linked to τ and variable population size P over 50 instances of complete random graphs.

When there no enough time for the GA to complete an evolution, we took the first solution found, as it is the case for graph with $|V| = 10$, which explain the strange curves. Also for small instance of graph, the probability to find relatively good solution on first try are higher, this is why all variant of the GA in the figure 7 have low MRE for the G with $|V| = 10$

When the same budget of time is allocated to both algorithms, GA and EA, it seem that on average larger population ($P = 50$) perform better -> Explain why

But when $|V| = 400$ in the complete random graphs, so large graph instance, GA with $20 > P > 10$ perform better

4.3 Real Road Network Case

Talk about MRE and most importantly running time

4.3.1 With fixed generation budget.

4.3.2 With equal time budgets. Trade-off !

5 Future Works

Future work could investigate further enhancements to the GA applied to the 2TP problem. One potential direction is the exploration of adaptive GAs, where parameters such as population size, mutation rate, and crossover probabilities adjust dynamically throughout the optimization process. Additionally, alternative selection mechanisms, such as rank-based or tournament selection with elitism, could be explored to improve convergence and prevent premature stagnation. Implementing an early stop criterion could also be beneficial, halting the algorithm when no significant improvement in fitness is observed over a number of generations, thus saving computational resources. Further, combining GAs with local search methods, such as hill-climbing or simulated annealing, could refine the solutions by intensifying the search around promising individuals. Another avenue for future research is to assess the performance of the GA on larger graphs, investigating its scalability and efficiency in solving 2TP problems in more complex scenarios. Finally, exploring multi-objective GAs to optimize additional criteria, such as minimizing travel time or balancing load between users, could provide more nuanced solutions for real-world applications.

Note that, in addition to the exact solution and GAs, other methods can be employed to solve the 2TP problem. Heuristic approaches, such as greedy algorithms, can be used to iteratively select candidate meeting and dropping points based on local optimizations, though they may not guarantee global optimality. In earlier research, a heuristic approach was proposed to optimize meeting points in ride-sharing scenarios within extensive multi-modal road networks [3], demonstrating its ability to find near-optimal solutions efficiently. Meta-heuristic methods, like simulated annealing or particle swarm optimization, offer alternative search strategies that balance exploration and exploitation, potentially providing near-optimal solutions with reduced computational complexity. Furthermore, approximation algorithms could be applied to provide efficient solutions with bounded error in cases where exact solutions are too costly to compute. Further research could focus on extending the 2TP problem to include more than two users [13], as well as developing an exact algorithm that can compute solutions in subquadratic time.

6 Conclusion

Trade-off ! This paper introduced a genetic algorithm (GA) to address the Two Transfer Point (2TP) problem, a critical optimization challenge in vehicle routing and ride-sharing. The GA demonstrated its ability to find near-optimal solutions for smaller problem instances and acceptable solutions for larger instances, efficiently handling scenarios where the exact algorithm becomes computationally intractable. The GA's iterative population-based approach balances exploration and exploitation, effectively navigating the solution space while ensuring scalability. These results highlight the GA's potential as a practical heuristic for solving the 2TP problem, though further research is necessary to fully evaluate its applicability and effectiveness in real-world scenarios.

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