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REGULAR PAPER

A genetic algorithm for robust berth allocation and quay crane assignment

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Abstract Scheduling problems usually obtain the optimal solutions assuming that the environment is deterministic. However, actually the environment is dynamic and uncertain. Thus, the initial data could change and the initial schedule obtained might be unfeasible. To overcome this issue, a proactive approach is presented for scheduling problems without any previous knowledge about the incidences that can occur. In this paper, we consider the berth allocation problem and the quay crane assignment problem as a representative example of scheduling problems where a typical objective is to minimize the service time. The robustness is introduced within this problem by means of buffer times that should be maximized to absorb possible incidences or breakdowns. Therefore, this problem becomes a multi-objective optimization problem with two opposite objectives: minimizing the total service time and maximizing the robustness or buffer times.

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1 Introduction

A container terminal is an open system with three distinguishable areas (berth, container yard and landside areas) where there exist different complex optimization problems. For instance, berthing allocation or stowage planning problems are related to the berth area [20], remarshalling problem or transport optimization to the yard area, and planning and scheduling hinterland operations related to trains and trucks to the landside area [22].

In a container terminal, once a vessel arrives at the port, it waits at the roadstead until it has permission to moor at the quay. The locations where mooring can take place are called berths. These are equipped with giant cranes, known as quay cranes (QC), that are used to load and unload containers which are transferred to and from the yard by a fleet of vehicles. These QCs are mounted on the same track (or rail) and, therefore, they cannot pass each other. Two scheduling problems are considered in this paper, the berth allocation problem (BAP) and the quay crane assignment problem (QCAP). The former is a well-known combinatorial optimization problem [16], which consists in assigning berthing positions and mooring times to incoming vessels. The QCAP deals with assigning a certain number of QCs to each berthed vessel such that all required movements of containers can be fulfilled [1].

Nowadays, the point of the view for the scheduling tasks has changed. Due to the fact that the real world is uncertain, imprecise and non-deterministic, there might be unknown information, breakdowns, incidences or changes, which become the initial plans or schedules obtained invalid. Thus, there are new trends to cope these aspects in the optimization techniques. This approach is being studied within the berth allocation and the quay crane assignment problems. The uncertainty within these problems is due to the fact, among others, that engines of the QC might present a failure or the movements per time unit are lower than expected. Due to the introduction of this new objective in the scheduling optimization problem, a multi-objective optimization approach needs to be taken into consideration.

The overall collaboration goal of our group at the Universitat Politècnica de València (UPV) with the Valencia Port Foundation and the maritime container terminal Mediterranean Shipping Company S.A. (MSC) is to offer assistance and help in the planning and scheduling of tasks such as the allocation of spaces to outbound containers, to identify bottlenecks, to determine the consequences of changes, to provide support in the resolution of incidents, to provide alternative berthing plans, etc.

A comprehensive survey of BAP and QCAP is given in [1]. These problems have been mostly considered separately, with an interest mainly focused on BAP. An interesting approach for BAP is presented in [13] where a Simulated Annealing metaheuristic is compared with a mathematical model. However, there are some studies on the combined BAP + QCAP considering different characteristics of berths and cranes [6,12,15,19,24].

All the above studies do not take into consideration the uncertainty of the real world to obtain a robust scheduling. However, there are some studies that address the robust scheduling. In [10], a proactive approach for a discrete and dynamic model of the BAP is presented taking into account uncertainties in the arrival and handling times given their probability density functions. They propose a mixed integer programming model and a genetic algorithm (GA) for both problems: discrete berth allocation and QC assignment. The objective is to minimize the sum of expected value, the standard deviation of the service time and the tardiness of the incoming vessels. In [11], a robust optimization model for cyclic berthing for a continuous and dynamic BAP is studied by minimizing the maximal crane capacity over different arrival scenarios of a bounded uncertainty given by their arrival agreements.

Robust scheduling based on operational buffers has already been introduced as a proactive approach in the BAP. An approach to robust BAP is presented in [5]. They presented a feedback procedure for the BAP that iteratively improves the robustness of the initial schedule. This feedback procedure determines the time buffers for each vessel by means of adjustment rules.

In [23], another approach to the robust BAP is solved by a scheduling algorithm that integrates simulated annealing and branch-and-bound algorithms. This study introduces the robustness as an objective to maximize and an evaluation is carried out by varying the weights of these functions. The robustness is achieved by a constant buffer time assigned to all vessels.

In [25], the robust BAP problem is studied as a proactive strategy as a multi-objective optimization problem. They solved this problem with the Squeaky-Wheel optimization (SWO) metaheuristic. The first objective is to minimize the late departures and the deviation from the desired position; and, the second objective is to maximize the robustness of the schedule. They tackle the robustness measure as a diminishing return, specifically the exponential function, to capture the decreasing marginal productivity of slacks in a berthing schedule.

However, some of the above approaches consider discrete berths or previous knowledge about the uncertainty in arrival or handling times to produce robust schedules, but usually this knowledge is not available. Furthermore, other approaches propose how to obtain robust schedules by means of operational buffer times, but these buffers are set independently of the handling time of the vessels.

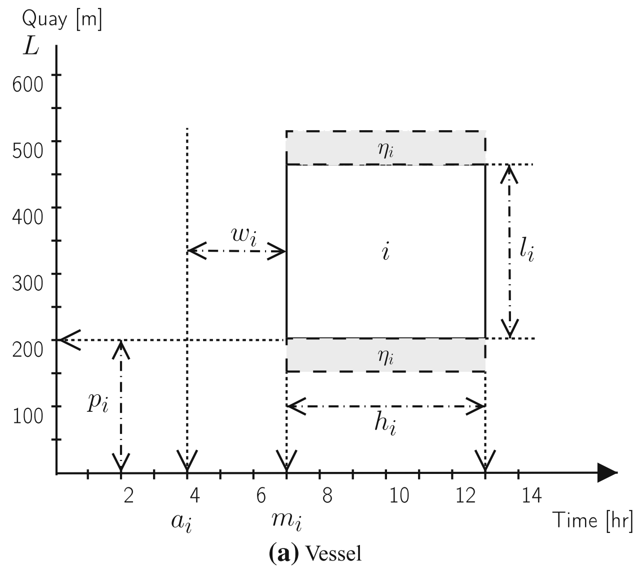
Nevertheless, in this paper, we present a formal mixed integer lineal programming (MILP) for the combined dynamic and continuous BAP + QCAP that extends the model presented in [13]. To obtain optimized solutions in an efficient way, we develop a metaheuristic GA to obtain near-optimal solutions in competitive computational times (compared with mathematical solvers). Furthermore, we assume that there is no previous knowledge about incidences, so both the MILP and the GA approaches have been adapted to tackle robustness of the BAP + QCAP as a multi-objective optimization problem using operational buffers within the schedule.

The rest of the paper is organized as follows. In the next section, we give a thorough description of the BAP + QCAP. In Sect. 3, the robustness is formalized for the BAP + QCAP. The multi-objective optimization approach to manage the two objective functions is detailed in Sect. 4. In Sect. 5, the mathematical formulation is presented. In Sect. 6, we give the details of the GA designed for the BAP + QCAP. Section 7 reports the results of the experimental study. Finally, in Sect. 8 we give the main conclusions of this work.

2 Problem description

The objective in BAP + QCAP is to obtain a schedule of the incoming vessels with an optimum order of vessels mooring and a distribution of the docks and QCs for these vessels. Figure 1b shows an example of the graphical space-time representation of a berth plan with 6 vessels. Each rectangle represents a vessel, its handling time and length.

Our BAP + QCAP case is classified, according to the classification given by [1], as:



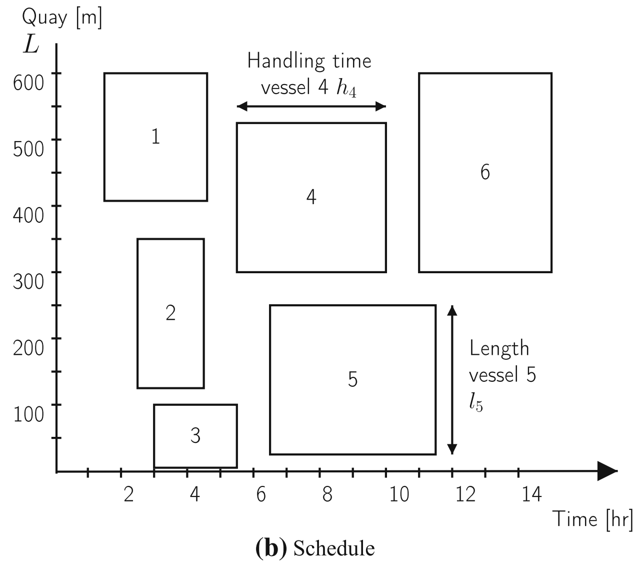


Fig. 1 Representation of the BAP + QCAP problem

– *Spatial attribute: continuous layout* We assume that the quay is a continuous line, so there is no partitioning of the quay and the vessel can berth at arbitrary positions within the boundaries of the quay. It must be taken into account that for a continuous layout, berth planning is more complicated than for a discrete layout, but it better utilizes the quay space [1].
– *Temporal attribute: dynamic arrival* Fixed arrival times are given for the vessels, so that vessels cannot berth before their expected arrival times.
– *Handling time attribute: unknown in advance* The handling time of a vessel depends on the number of assigned QCs (QCAP) and the moves required.
– *Performance measure: wait and handling times* The objective is to minimize the sum of the waiting (w_i) and handling times (h_i) of all vessels.

Let V be the set of incoming vessels. Following, we introduce the notation used for each vessel $i \in V$ (Fig. 1a). The data variables are:

– QC: Available QCs in the container terminal. All QCs carry out the same number of movements per time unit (movsQC), given by the container terminal.
– L: Total length of the berth in the container terminal.
– H: Planning horizon for this schedule. It is calculated as the last departure when the first-come, first-served (FCFS) policy is applied to the incoming vessels.
– a_i : Arrival time of the vessel i at port.
– c_i : Number of required movements to load and unload containers of i.
– l_i : Vessel length.

The decision variables are:

– m_i : Mooring time of i. Thus, waiting time (w_i) of i is calculated as ($w_i = m_i - a_i$).
– p_i : Berthing position where i moors.
– q_i : Number of assigned QCs to i.
– u_{ik} : Indicates whether the QC k works (1) or not (0) on the vessel i.

The variables derived from the previous ones are:

– h_i : Loading and unloading time at quay (handling time) of vessel i. This time depends on q_i and c_i, that is: $\left(\frac{c_i}{q_i\ \texttt{movsQC}}\right)$.
– t_{ik} : Working time of the QC k that is assigned to vessel i.
– d_i : Departure time of vessel i ($d_i = m_i + h_i$).
– s_i, e_i : indexes for the first and last QC used in vessel i, respectively.

In this study, the following assumptions are considered:

– The number of QCs assigned to a vessel do not vary along the moored time. Once a QC starts a task in a vessel, it must complete it without any pause or shift (non-preemptive tasks). Thus, all QCs assigned to the same vessel have the same working time $\left(t_{ik} = h_i, \forall k \in QC, u_{ik} = 1\right)$.
– All the information related to the waiting vessels is known in advance (arrival, priority, moves and length).
– Every vessel has a draft that is lower than or equal to the draft of the quay.
– Movements of QCs along the quay as well as berthing and departure times of vessels are not considered since it supposes a constant penalty time for all vessels.

- Simultaneous berthing is allowed, subject to the length of the berth.

And the following constraints must be accomplished:

- Moored time must be at least the same that its arrival time ($m_i \geq a_i$).
- It must be enough contiguous space at berth to moor a vessel of length (l_i).
- There is a safety distance between two moored ships. We assume that each vessel has a 2.5 % of this length at each side as a safety distance (η_i) (Fig. 1a). This safety distance is added to the length of each vessel i: $l_i := l_i + 2\eta_i$.
- There must be at least one QC to assign to each vessel. The maximum number of assigned QCs by vessel i $\left(\mathrm{QC}_i^+\right)$ depends on its length, since a safety distance is required between two contiguous QCs (`safeQC`), and the maximum number of QCs that the container terminal allows per vessel (`maxQC`). Both parameters are given by the container terminal.

Our objective is to allocate all vessels according to several constraints minimizing the total weighted waiting and handling or processing time, known as the service time, for all vessels:

$$T_s = \sum_{i \in V} (w_i + h_i) \tag{1}$$

3 Robustness in BAP + QCAP

Container terminals are uncertain and non-deterministic systems in the same way than many other real-world systems. In the BAP + QCAP problem, the initial obtained schedules might become invalid due to different reasons: breakdowns in QCs, late arrivals of the vessels, bad weather, a lower ratio of movements per QC than expected, etc.

The robustness concept means that, given a schedule, this initial schedule remains feasible when incidences occur in its actual scenario.

The usual disruptions to be considered in BAP + QCAP are the followings:

- The arrival of a vessel is delayed from its expected arrival time (a_i) assuming that the order remain unchanged.
- The handling time of a vessel is larger than its expected handling time (h_i).

In case of a delay in the arrival of a vessel, it can be modeled as the departure time of this vessel is delayed by the same amount. Therefore, an incidence related to the arrival of a vessel is represented as a larger handling time for this vessel.

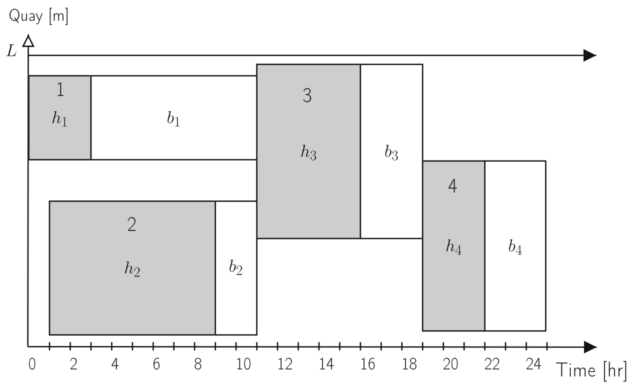


Fig. 2 Buffer times b_i given an example schedule

Given these two disruptions, we consider that a schedule is robust if a disruption in one vessel does not affect or alter the mooring times of the other vessels.

In BAP + QCAP, the robustness of a schedule might be guaranteed through two periods of time:

- The waiting time of vessels (w_i). One vessel might be late w_i time units without disrupting the schedule of the others vessels.
- The buffer times of vessels (b_i). The handling time of a vessel might be delayed b_i time units which correspond to the time between vessel i and each vessel j that shares the berth and moors just after vessel i (Fig. 2).

The schedule could absorb delays or breakdowns that do not exceed the sum of those two periods ($w_i + b_i$). Therefore, both times should be maximized to achieve the maximum robustness and ensure that there is no need to re-schedule the vessels. However, it should be kept in mind that the first objective of the BAP + QCAP is to minimize the total service time of the incoming vessels ($w_i + h_i$). Therefore, we focus on maximizing only the second period of time, buffer times (b_i), to obtain robust schedules.

The buffer time (b_i) for each vessel i is obtained by Eq. (4). We define φ_i as the set of vessels that succeed vessel i and occupy some berth space of vessel i; and, τ_{ij} is the difference between the departure time of vessel i (d_i) and the mooring time of vessel j (m_j). As example, Fig. 2 shows the buffer times (b_i) for each scheduled vessel as an empty rectangle.

$$\varphi_i = \{j \in V,\ m_j \geq d_i \wedge [p_i, p_i + l_i) \cap [p_j, p_j + l_j) \neq \varnothing\} \tag{2}$$

$$\tau_{ij} = m_j - d_i \qquad \forall i \in V,\ \forall j \in \varphi_i \tag{3}$$

$$b_i = \begin{cases} +\infty, & |\varphi_i| = 0 \\ \min_{j \in \varphi_i} \left(\tau_{ij}\right), & \text{otherwise} \end{cases} \qquad \forall i \in V \tag{4}$$

Following the concept of decreasing productivity (diminishing returns) of the buffers presented in [25], in this study it is considered that the more the handling time, the more is it likely to suffer incidences. Nevertheless, there is no need to assign a large buffer time to each vessel. For instance, in Fig. 2, Vessel 1 would not need 8 time units of buffer time (b_1) since its handling time is only 3 time units. It is not likely that this vessel would suffer a delay of that magnitude. However, Vessel 2, with a handling time of 8 time units, has only 2 time units of buffer time (b_2). In this case, it is high likely that this vessel would suffer some breakdown or delay and so becomes invalid this schedule.

It is known that the late arrivals may be due to other factors such as the travel time from its immediately origin. To simplify this study, we only consider that the magnitude of the incidence is related to the handling time.

Thus, the robustness measure is related to the buffer time b_i and the average handling time h_i^* of each vessel i. Therefore, the following objective function (Eq. 6) is proposed as a measure of the robustness of a schedule.

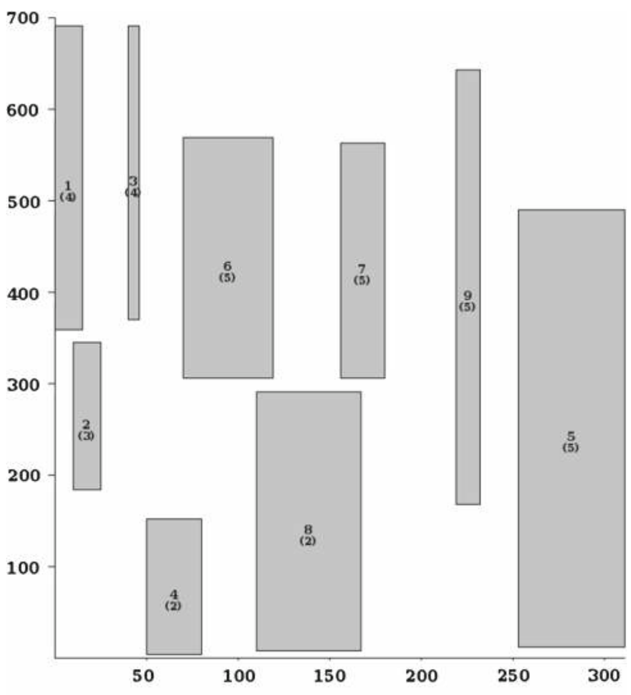
$$r_i = \min\left(1, \frac{b_i}{h_i^*}\right), \quad \forall i \in V \tag{5}$$

$$R = \sum_{i \in V} r_i \tag{6}$$

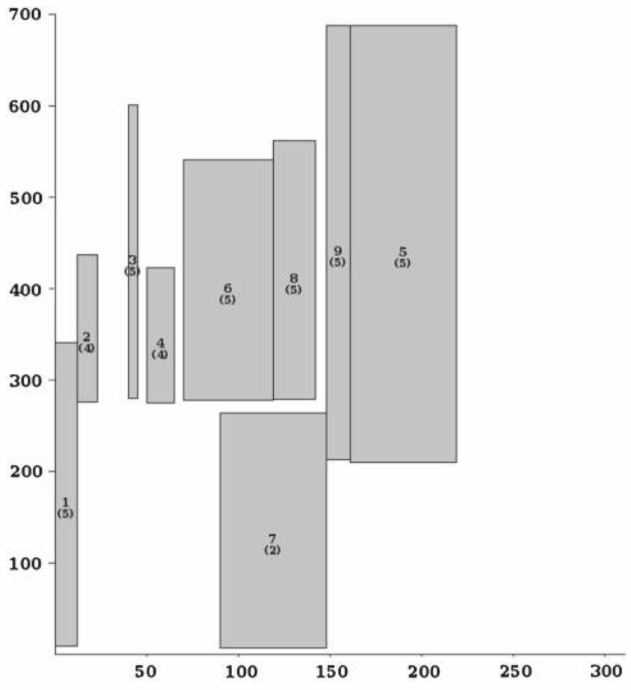
where h_i^* indicates the handling time when its possible average number of QCs $\left(\frac{1+QC_i^+}{2}\right)$ is assigned.

Let us see a simple example. Figure 3 shows two different schedules given the same set of incoming vessels. Each vessel is labeled with its vessel's ID and the assigned QC number in brackets. On the one hand, Fig. 3a represents a robust schedule since almost any incidence over any vessel could be absorbed. On the other hand, Fig. 3b shows a schedule with the optimal solution according to the objective function T_s. The latter schedule will be high likely unfeasible if any incidence occurs.

From Fig. 3a and b, it is clear that there is a trade-off between optimality and robustness. However, a robust schedule is not only achieved by extending an optimized schedule over the time. A robust schedule must also consider an optimized allocation of vessels to achieve the maximum sum of buffers with a proper distribution among them. Note that the optimality is not the makespan of the schedule, but the total service time (waiting and handling times).



(a) Robust schedule.



(b) Optimal schedule according to T_s.

Fig. 3 Two possible schedules given the same incoming vessels

4 Multi-objective approach for the BAP + QCAP

Solving the robust BAP + QCAP involves two optimization objectives: the service time (T_s) and the robustness (R). These objective functions must be normalized to apply the search process correctly. Equations (9) and (10) define the normalized service time and the normalized robustness function, respectively.

Normalizing the service time function into the interval (0, 1) implies to normalize both the waiting time (Eq. 7) and the handling time (Eq. 8). The handling time is just a linear normalization since the maximum (h_i^+) and minimum (h_i^-) times are known by assigning the minimum and the maximum number of QCs to vessel i (QC_i^+). Normalizing the waiting time requires to determine a maximum total waiting time (W_F). In this case, (W_F) value is the total waiting time of the incoming vessels when an FCFS policy is applied.

$$T_w = \frac{1}{W_F}\sum_{i\in V}(m_i - a_i) \tag{7}$$

$$T_h = \frac{1}{|V|}\sum_{i\in V}\left(\frac{h_i - h_i^-}{h_i^+ - h_i^-}\right) \tag{8}$$

$$\hat{T}_s = \frac{T_w + T_h}{2} \tag{9}$$

$$\hat{R} = \frac{R}{|V|} \tag{10}$$

Thereby, the objective function for the robust BAP+QCAP is to minimize the function F (Eq. 11). The coefficient λ ($0 \le \lambda \le 1$) assigns different weights to each component to establish an aggregate function.

$$F = \lambda\hat{T}_s - (1-\lambda)\hat{R} \tag{11}$$

In a multi-objective optimization problem, usually there is no single solution wherein all its objectives are simultaneously optimized. However, there may exist a set of Pareto optimal solutions with different tradeoffs between their objective functions. Pareto optimal solutions are defined by means of the dominance concept. Considering the robust BAP + QCAP, let x and y be two different solutions, x dominates y if at least one of the following conditions is satisfied:

$$\hat{T}_s(x) < \hat{T}_s(y) \text{ and } \hat{R}(x) \ge \hat{R}(y)$$
$$\hat{T}_s(x) \le \hat{T}_s(y) \text{ and } \hat{R}(x) > \hat{R}(y)$$

Given a set of feasible solutions D, a solution $x \in D$ is Pareto optimal (or efficient) if it is non-dominated by any other solution $x' \in D$. The Pareto optimal set is the set of all the efficient solutions.

In general, generating the Pareto optimal set is expensive computationally and is often impracticable. Therefore, algorithms try to find a good approximation of the Pareto optimal set (potentially efficient solutions). In this work, we refer to each approximation as Pareto front, which contains solutions that, although are non-dominated among them, could be dominated by other solutions not found by our algorithms.

5 Mathematical formulation

In this section, the mathematical formulations for BAP + QCAP and the robust BAP + QCAP are presented. The first MILP model (Fig. 4) solves the BAP + QCAP by minimizing

$$m_i \ge a_i \quad \forall i \in V \tag{12}$$
$$w_i = m_i - a_i \quad \forall i \in V \tag{13}$$
$$d_i = m_i + h_i \quad \forall i \in V \tag{14}$$
$$p_i + l_i \le L \quad \forall i \in V \tag{15}$$
$$q_i = \sum_{k\in QC} u_{ik} \quad \forall i \in V \tag{16}$$
$$1 \le q_i \le QC_i^+ \quad \forall i \in V \tag{17}$$
$$1 \le s_i, e_i \le |QC| \quad \forall i \in V \tag{18}$$
$$s_i \ge e_i \quad \forall i \in V \tag{19}$$
$$q_i = e_i - s_i + 1 \quad \forall i \in V \tag{20}$$
$$\sum_{k\in QC} t_{ik}\,\mathtt{movsQC} \ge c_i \quad \forall i \in V \tag{21}$$
$$h_i = \max_{k\in QC} t_{ik} \quad \forall i \in V \tag{22}$$
$$t_{ik} - M u_{ik} \le 0 \quad \forall i \in V, \forall k \in QC \tag{23}$$
$$h_i - M(1-u_{ik}) - t_{ik} \le 0 \quad \forall i \in V, \forall k \in QC \tag{24}$$
$$u_{ik} + u_{jk} + z^x_{ij} \le 2 \quad \forall i, j \in V, \forall k \in QC \tag{25}$$
$$M(1-u_{ik}) + (e_i - k) \ge 0 \quad \forall i \in V, \forall k \in QC \tag{26}$$
$$M(1-u_{ik}) + (k - s_i) \ge 0 \quad \forall i \in V, \forall k \in QC \tag{27}$$
$$p_i + l_i \le p_j + M(1 - z^x_{ij}) \quad \forall i, j \in V,\ i \ne j \tag{28}$$
$$e_i + 1 \le s_j + M(1 - z^x_{ij}) \quad \forall i, j \in V,\ i \ne j \tag{29}$$
$$d_i \le m_j + M(1 - z^y_{ij}) \quad \forall i, j \in V,\ i \ne j \tag{30}$$
$$z^x_{ij} + z^x_{ji} + z^y_{ij} + z^y_{ji} \ge 1 \quad \forall i, j \in V,\ i \ne j \tag{31}$$
$$z^x_{ij}, z^y_{ij}, u_{ik} \quad 0/1 \text{ integer} \quad \forall i, j \in V,\ i \ne j, \forall k \in QC \tag{32}$$

Fig. 4 Mathematical model for the BAP + QCAP

the function given by the Eq. (1), where M denotes a sufficiently large number (as it is used in MILP), subject to the given constraints.

The given formulation expands the model presented in [13] by adding the needed constraints to take into consideration QCs. Thereby, the handling time of vessels depends on the number of QCs and these QCs cannot pass each other when they are relocated.

In the proposed model, there are two auxiliary variables: z^x_{ij} is a decision variable that indicates if vessel i is located to the left of vessel j on the berth ($z^x_{ij} = 1$), and $z^y_{ij} = 1$ indicates that vessel i is moored before vessel j in time (see constraint 32). Moreover, constraint 12 ensures that vessels must moor once they arrive at the terminal. Constraint 15 guarantees that a moored vessel does not exceed the length quay. Constraints 13 and 14 establish the waiting and departure times according to m_i. Constraints 16, 17, 18, 19 and 20 assign the number of QCs to the vessel i. Constraint 21 establishes the minimum handling time needed to load and unload their containers according to the number of assigned QCs. Constraint 22 assigns the handling time for vessel i. Constraint 23 ensures that QCs that are not assigned to vessel i have $t_{ik} = 0$. Constraint 24 forces all assigned QCs to vessel i working the same number of hours. Constraint 25 avoids that one QC is assigned to two different vessels

$$\sum_{i\in V}(m_i - a_i) \le W_F \tag{33}$$

$$z^t_{ij} = z^x_{ij} + z^x_{ji} + z^y_{ij} \quad \forall i,j \in V,\ i \neq j \tag{34}$$

$$\tau_{ij} = M \quad \forall i,j \in V,\ z^t_{ij} = 0 \wedge i \neq j \tag{35}$$

$$d_i + \tau_{ij} = m_j + M(1 - z^y_{ij}) \quad \forall i,j \in V,\ i \neq j \wedge z^t_{ij} = 1 \tag{36}$$

$$\tau_{ij} = M \quad \forall i,j \in V,\ z^t_{ij} = 2 \wedge i \neq j \tag{37}$$

$$b_i = \min\left(\min_{\substack{j\in V\\ i\neq j}}(\tau_{ij}),\ h^*_i\right) \quad \forall i \in V \tag{38}$$

$$r_i h^*_i = b_i \quad \forall i \in V \tag{39}$$

$$0 \le z^t_{ij} \le 2 \quad \forall i,j \in V,\ i \neq j \tag{40}$$

Fig. 5 Mathematical model for the robust BAP + QCAP

at the same time. Constraints 26 and 27 force the QCs to be contiguously assigned (from s_i up to e_i). Constraint 28 takes into account the safety distance between vessels. Constraint 29 avoids that one vessel uses a QC which should cross through the others QCs. Constraint 30 avoids that vessel j moors while the previous vessel i is still at the quay. Finally, constraint 31 establishes the relationship between each pair of vessels.

The robust BAP + QCAP model minimizes the objective function presented in Eq. (11). This model requires the 12–32 constraints presented above and the ones presented in Fig. 5. The decision variable z^t_{ij} (see constraint 40) indicates if a vessel j moors later than i and, at the same time, the vessel j intersects with the berth length occupied by vessel i (z^t_{ij}). Constraint 33 ensures that the total waiting time of the schedule does not exceed the maximum total waiting time (W_F). Constraints 34–36 assign the time between the departure time of vessel i and the mooring time of vessel j. For those vessels j that $z^t_{ij} \neq 1$, they are assigned M as a value representing an unbounded time for the robustness. Constraints 38 and 39 set the value of the available buffer time after vessel i and its robustness value, respectively.

These mathematical models have been coded in IBM ILOG CPLEX optimization studio 12.5 as detailed in the Sect. 7.

6 Genetic algorithm

In this section, we describe two implementations of genetic algorithms to solve the problems: BAP + QCAP (Fig. 4) and robust BAP + QCAP (Fig. 5), respectively.

In the first problem, the goal is to minimize the service time T_s (Eq. 1). Thus, the fitness F associated with each chromosome is the service time (T_s) of that solution.

In the second one, the goal is to find a set of non-dominated solutions (henceforth efficient set E) that is as close as to the Pareto optimal set. In this case, two objective functions are associated with each chromosome: $\hat{T}_s$ and $\hat{R}$ (see Eqs. 9 and 10, respectively), and the fitness F is computed according to the Eq. (11). Below, we describe in detail both approaches.

In both GAs, constraint-handling mechanisms based on special operators [17] have been used during the crossover and mutation operations, as well as during the creation of the initial population. This fact allows the GA to move inside the feasible region as well as to improve the quality of the solutions found.

6.1 A genetic algorithm to solve the BAP + QCAP

Algorithm 1 shows the structure of the GA we have considered herein. The core of this algorithm is taken from [8,9] and is quite similar to others generational GAs described in the literature [7] or [18]. In the first step, the initial population is generated and evaluated. Then, the GA iterates over a number of steps or generations. In each iteration, a new generation is built from the previous one by applying the genetic operators of selection, reproduction and replacement. These operators can be implemented in a variety of ways and, in principle, are independent of each other. However, in practice all of them should be chosen considering their effect on the remaining ones to get a successful overall algorithm.

The approach taken in this work is the following:

- In the selection phase, all chromosomes are grouped into pairs, and then each one of these pairs is mated or not in accordance with a crossover probability (P_c) to obtain two offspring.
- Each offspring, or parent if the parents were not mated, undergoes mutation in accordance with the mutation probability (P_m).
- Finally, the replacement is carried out as a tournament selection (4:2) among each pair of parents and their offspring.

Algorithm 1 The genetic algorithm

```
Require: A BAP + QCAP instance P
Ensure: A mooring schedule for instance P
  1. Generate the initial population;
  2. Evaluate the population;
  while No termination criterion is satisfied do
    3. Group chromosomes from the current population;
    4. Apply the reproduction operators to the chromosomes selected
    at step 3 to generate new ones;
    5. Evaluate the chromosomes generated at step 4;
    6. Apply the replacement criterion to the set of chromosomes
    selected at step 3 together with the chromosomes generated at step
    4;
  end while
  return The schedule from the best chromosome evaluated so far;
```

We consider that all chromosomes have the same number of genes N (number of vessels $|V|$), and all populations have the same number of chromosomes, popsize.

The coding schema is based on permutations of vessels, each one with a given number of QCs. So a gene is a pair (i, q_i), $1 \le q_i \le QC_i^+$, and a chromosome includes a gene like this for each one of the vessels. For example, for an instance with 5 vessels where the maximum number of QCs is 2, 3, 4, 3 and 2, respectively, two feasible chromosomes are the following ones:

chr$_1$: ((11) (21) (31) (42) (51))
chr$_2$: ((32) (12) (22) (52) (43))

Note that, the same vessel may have different number of QCs in each chromosome. In accordance with this encoding, a chromosome expresses the number of QCs that each vessel is assigned in the solution and an order for building the schedule.

The order of vessels in chromosomes is used as a dispatching rule. Hence, we use the following decoding algorithm: the genes are visited from left to right in the chromosome sequence. For each gene (i, q_i), the vessel i is scheduled at the earliest mooring time with q_i consecutive QCs available, so that none of the constraints is violated. If there are several positions available at the earliest time, that closest to one of the berth extremes is selected. Also, the QCs are chosen starting from the same extreme of the berth.

For chromosome mating, we have considered a classical crossover operator such as generalized position crossover (GPX) which is commonly used in permutation based encodings. This is a two-point crossover operator which work as follows. Let us consider two parents like:

pt$_1$: ((11) | (21) (31) | (42) (51))
pt$_2$: ((32) | (12) (22) | (52) (43))

Symbols "|" represent crossover positions 1 and 3, respectively, in this example, which are selected at random for each mating. Then, two offsprings are built taking the substrings between positions 1 and 3 in each parent and then filling the remaining positions with the genes representing the remaining vessels taken from the other parent keeping their relative order. So in this case the two offsprings are:

off$_1$: ((12) | (21) (31) | (52) (43))
off$_2$: ((31) | (12) (22) | (42) (51))

For mutation, we have implemented an operator that shuffles a random substring of the chromosome and at the same time changes the number of QCs assigned to each one of the shuffled genes at random, provided that the number of QCs is kept in between the proper limits for the vessel.

The initial population in generated at random, i.e., a random order for the vessels is chosen and each vessel i is assigned a number of QCs chosen uniformly in $\left[1, \mathrm{QC}_i^+\right]$. The termination condition is given in one of these three forms: (1) a number of generations, (2) a time limit or (3) a number of evaluations.

6.2 A genetic algorithm to solve the robust BAP + QCAP

In this section, we describe a GA that proposes a set of potentially efficient solutions E considering two optimization criteria: the service time and the robustness. The objective of this approach is to find a set E that is as close as to the Pareto optimal set of the same instance.

Thus, we have modified the Algorithm 1 in the following issues:

– The initial population is constructed in such a way a percentage of this population is at least, as good as the solution that the FCFS policy would propose.
– For each generation and for each chromosome, a pair of random weights that sum 1 are assigned to each objective function.
– Gene representation changes. The initial berthing position is added to the pair (i, q_i). Thus, each gene is represented by (i, q_i, p_i), where q_i and p_i are feasible values for vessel i.
– Before performing crossover, mutation and replacement, daughter and son inherits mom and dad weights, respectively. Therefore, the replacement operation compares daughter and mom, and son with dad. The two best chromosomes pass to the following generation.
– In the decoding process to evaluate each chromosome, the initial berthing position is given by each gene. Therefore, this value is not computed by the decoding process. A mooring time should be assigned to vessel i so that it is feasible, taking into account that vessel i must be berthed at quay from position p_i with q_i QCs without breaking any of the problem constraints.
– Once the population of the next generation is obtained, the efficient set E is updated.

Following, we describe in detail the issues that have been modified with respect to the single-objective GA.

Representation Structure of each chromosome is similar to the structure that is used in single-objective GA (Sect. 6.1). However, the gene has been modified to consider the initial berthing position as part of its data. Thus, this value is assigned by the GA instead of being computed by the decoding function. Structure of each gene and each chromosome is shown in Fig. 6.

It should be noted that each gene must be composed by feasible values with respect to vessel i. That is, according to the problem constraints, each vessel i can be assigned at most QC_i^+ cranes. Therefore, $1 \le q_i \le \mathrm{QC}_i^+$. Likewise, if the berth length is L, then $\eta_i \le p_i \le L - l_i - \eta_i$.

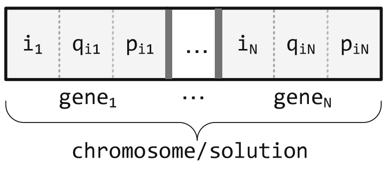


Fig. 6 Chromosome representation

Algorithm 2 shows an outline of the multi-objective GA. Variable O indicates the number of objective functions that are considered by the algorithm.

Below, we describe the main steps of this algorithm.

Initialization Construction of initial population is performed so that the service time of a percentage of the initial population (GA parameter) is at least as good as the solution provided by the policy FCFS. The other chromosomes are constructed by instantiating each gene in the following way:

- Vessel identifier (i): an integer, between 1 and N is chosen randomly. Two genes of the same chromosome cannot have the same vessel identifier.
- Number of QCs: an integer, between 1 and QC_i^+, is chosen randomly.
- Initial position: an integer p_i, between η_i and $L - l_i - \eta_i$, is chosen randomly.

Each chromosome x in the initial population is considered to update the efficient set E. Following, we describe how is performed this operation [2].

Update of efficient set E According to the concept of dominance defined above, updating set E with a new solution x consists of:

- Adding x to E if there is no other solution $y \in E$ such that y dominates x,
- Removing from set E all solutions dominated by x.

Generations After the initial population has been generated, the algorithm constructs a new generation of population for each iteration, until some stop criterion is fulfilled.

Algorithm 2 multi-objective genetic algorithm

```
Require: A BAP + QCAP instance $P$, $popsize$, $N$,$O$
Ensure: $E$: set of non-dominated solutions
  $pop_0 \leftarrow$ generate_the_initial_population($popsize$,$N$, $O$)
  $t \leftarrow 0$
  while No termination criterion is satisfied do
    assign_weights($pop_t$,$N$,$O$)
    $pop_{t+1} \leftarrow$ construct_next_generation($popsize$,$N$, $O$)
    $t \leftarrow t + 1$
  end while
  return schedule for each element of efficient set $E$
```

Algorithm 3 construct_next_generation

```
Require: $pop_t$,$popsize$,$N$,$O$
Ensure: $pop_{t+1}$
  $i \leftarrow 0$
  assign_weights($pop_t$,$N$,$O$)
  $i \leftarrow 0$
  while $i < popsize$ do
    $m \leftarrow$ random integer between 1 and $popsize$, which has not been selected yet in the current loop.
    $d \leftarrow$ random integer between 1 and $popsize$, which has not been selected yet, in the current loop.
    $p \leftarrow$ random real between 0 and 1
    $daughter.weights \leftarrow chromosome_m.weights$
    $son.weights \leftarrow chromosome_d.weights$
    if $p \leq$crossover probability $P_c$ then
      crossover($chromosome_m$,$chromosome_d$,$daughter$,$son$)
    else
      $daughter \leftarrow chromosome_m$
      $son \leftarrow chromosome_d$
    end if
    $p \leftarrow$ random real between 0 and 1
    if $p \leq$ mutation probability $P_m$ then
      mutation($daughter$)
    end if
    $p \leftarrow$ random real between 0 and 1
    if $p \leq$mutation probability $P_m$ then
      mutation($son$)
    end if
    if $daughter \neq chromosome_m$ then
      evaluate $daughter$
      $E \leftarrow$ update_efficient_set($daughter$)
    end if
    if $son \neq chromosome_d$ then
      evaluate $son$
      $E \leftarrow$ update_efficient_set($son$)
    end if
    if $daughter.fitness \leq chromosome_m.fitness$ then
      $pop_{t+1} \leftarrow pop_{t+1} \cup \{daughter\}$
    else
      $pop_{t+1} \leftarrow pop_{t+1} \cup \{chromosome_m\}$
    end if
    if $son.fitness \leq chromosome_d.fitness$ then
      $pop_{t+1} \leftarrow pop_{t+1} \cup \{son\}$
    else
      $pop_{t+1} \leftarrow pop_{t+1} \cup \{chromosome_d\}$
      $i \leftarrow i + 2$
    end if
  end while
```

Let pop_t be the population obtained in the generation t, Algorithm 3 shows how each generation is constructed.

Crossover Crossover operation is performed using the same operator that is used by the single-objective GA (GPX). However, some differences there exist and these are explained in the following.

The crossover receives one pair of chromosomes (mom and dad), which are in the current population pop_t and have been selected randomly. The objective of this operator is to construct two offspring chromosomes (daughter and son). For that, each time the crossover operation is performed, the following steps are made:

1. Two cross points are chosen randomly, k_1 and k_2 ($1 \leq k_1 < k_2 \leq N$). Figure 7a and b show an example, where $N = 8$, $k_1 = 3$ and $k_2 = 6$.
2. Each gene in chromosome mom and dad, which is in position p, $k_1 \leq p < k_2$ is copied to the same position in chromosomes daughter and son, respectively.
3. Each gene in chromosome mom/dad, which is in position p, $1 \leq p < k_1$ is copied to the same position in chromosome son/daughter.
4. Each gene in chromosome mom/dad, which is in position p, $k_2 \leq p \leq N$ is copied to the same position in chromosome son/daughter.

Figure 8 shows the position of genes that will be copied from the chromosome mom to the offspring son. The same procedure is made for the chromosome dad and the offspring daughter.

One chromosome cannot have two genes with the same vessel identifier. Therefore, if the vessel identifier in the gene that will be copied already exists in the offspring (daughter/son), the vessel identifier in the new chromosome must be modified.

The new value (i') is obtained from the first gene in the chromosome parent (mom/dad) that has a vessel identifier that does not exist in the offspring. Because the original vessel identifier has been modified, it is necessary to ensure that the number of QCs and the initial position in the gene are feasible with respect to the new vessel identifier (i'). If the number of QCs or the initial position in the gene is higher than the maximum value that is allowed for vessel (i'), these values are also modified, by the maximum values corresponding to vessel (i').

Figure 9 shows an example where the identifier 6 must be changed by the identifier 2, because the vessel 6 already exists in the offspring. Once the identifier is modified by 2, the procedure must verify the number of QCs and initial position in the same gene are feasible, with respect to the vessel 2. In this case, the maximum initial position of vessel 2 is 400. Therefore, the value 473 in the same gene must be modified to 400.

Mutation Mutation operation is performed on one chromosome, following these steps:

1. Two positions (k_1 and k_2) of the chromosome are chosen randomly ($1 \leq k_1 < k_2 \leq N$).
2. Positions of genes that are between k_1 and k_2, both included, are modified randomly.
3. The number of QCs in each gene that is between k_1 and k_2, both included, is modified by a feasible random value with respect to the vessel in the same gene.
4. The initial position in each gene that is between k_1 and k_2, both included, is modified by a random value that is feasible with respect to the vessel that is in the same gene.

Figure 10 shows how the offspring son, which has been obtained after the crossover operation, is mutated. First, two values $k_1 = 2$ and $k_2 = 4$ are selected randomly. Then, all genes between both positions are shuffled. The gene 2 is moved to position 4, the gene 3 to position 2 and gene 4 to position 3. Finally, the number of QCs and the initial position of each gene in position p, $2 \leq p \leq 4$ are modified by selecting feasible random values for each one.

Evaluation of one chromosome/solution Function that evaluates each objective function of one chromosome and its fitness (evaluate in Algorithm 3) is the responsible of assigning a valid mooring time to each vessel. For that, it processes each vessel in the same order that it appears in the chromosome. For each gene g in the chromosome, this procedure assigns the mooring time most near to the arrival time of the vessel $g.i$, such that all the problem constraints are fulfilled, considering the initial position of the vessel i must be $g.p_i$ and the number of QCs that must be available at this time is at least $g.q_i$.

Once a valid mooring time has been assigned to each gene g, the two normalized objective functions: service time (Eq. 9) and robustness (Eq. 10) are computed; and, the fitness assigned to the chromosome is computed according to the Eq. (11).

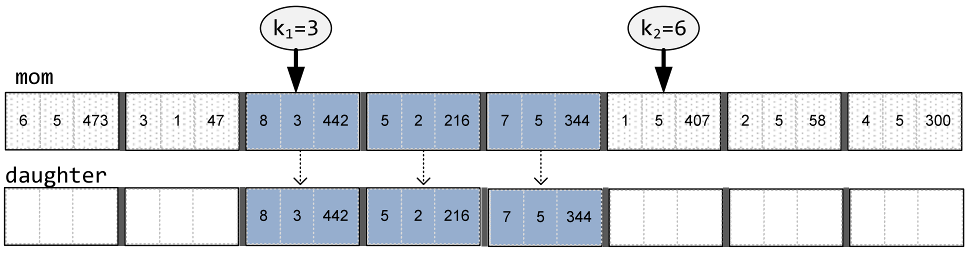
7 Evaluation

The experiments were performed in a corpus of 100 instances randomly generated, where parameters (`maxQC`, `safeQC`, etc.) follow the suggestions of container terminal operators. Thus, these instances correspond to configurations in real-world scenarios. Each one is composed of a queue from 5 to 20 vessels. These instances follow an exponential distribution for the inter-arrival times of the vessels ($\beta = 20$). The number of required movements and length of vessels are uniformly generated in [100, 1,000] and [100, 500], respectively. In all cases, the berth length (L) was fixed to 700 m; the number of QCs was 7 (corresponding to a determined MSC berth line) and the maximum number of QCs per vessel was 5 (`maxQC`); the safety distance between QCs (`safeQC`) was 35 m and the number of movements that QCs carry out was 2.5 (`movsQC`) per time unit.

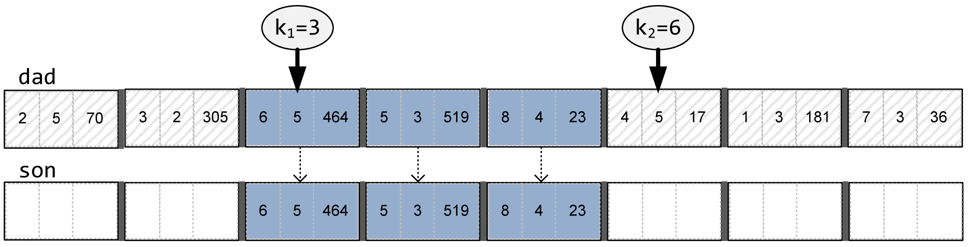
The two approaches developed in this paper, the GA and the MILP model, were coded using C++ and the IBM ILOG CPLEX optimization studio 12.5, respectively. They were solved on a Core 2 Quad 2.83 Ghz with 4 Gb RAM.

In the GA, the population size was 500. Mutation and crossover probabilities were $P_m = 0.1$ and $P_c = 0.8$, respectively. Due to the stochastic nature of the GA process, each instance was solved 30 times and the results show the average obtained values.

Fig. 7 Crossover points applied to the parents



(a) Chromosome *mom*



(b) Chromosome *dad*

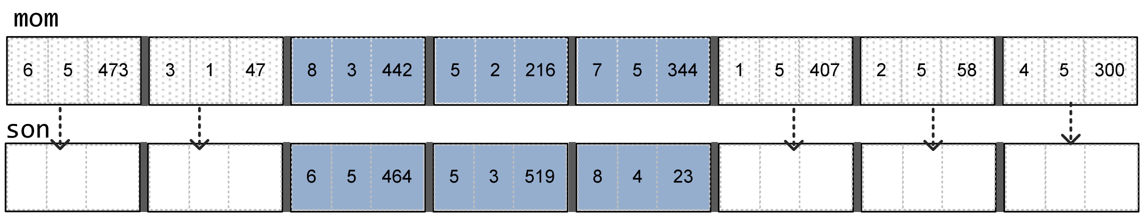
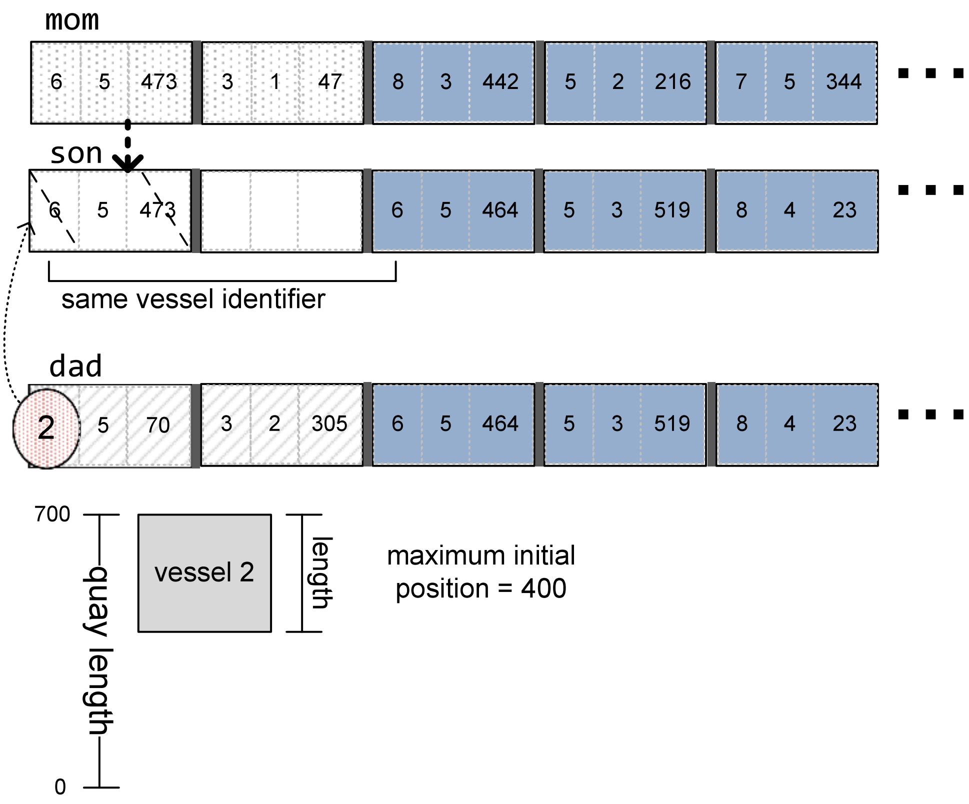


Fig. 8 Copy of genes to complete the offspring

Fig. 9 Ensure offspring feasibility



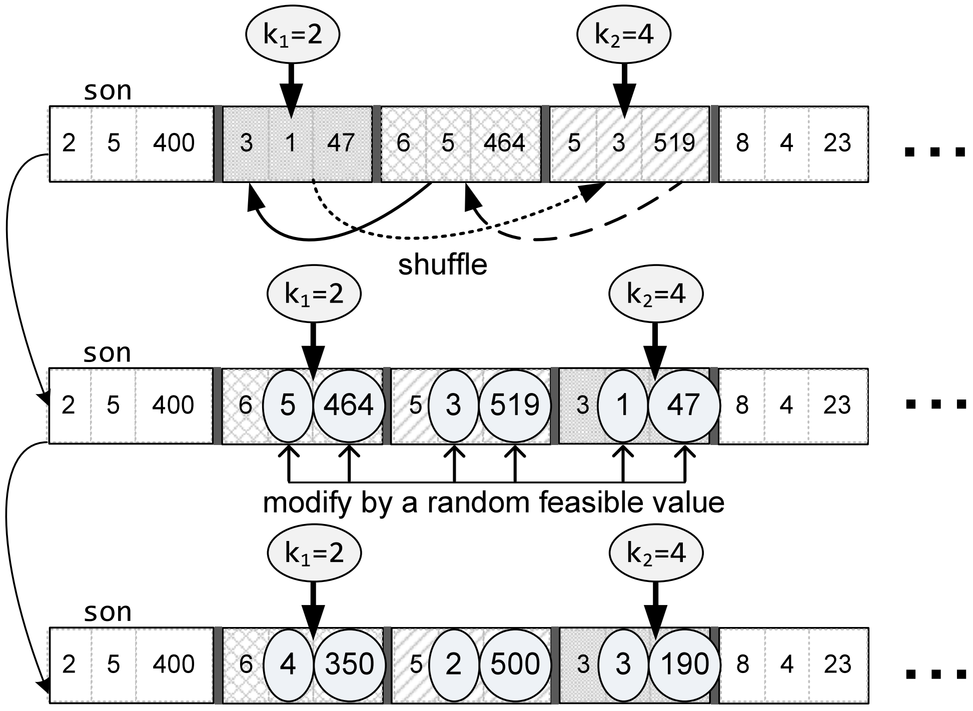


Fig. 10 An example of mutation operation

7.1 BAP + QCAP

Table 1 shows the average results for CPLEX and GA for each group of 100 instances with the same number of vessels (5–20). The timeout was 10 s. For CPLEX, the reported values are the average value of T_s for the solutions reached (Avg T_s), the number of instances solved to optimality (#Opt) and the number of instances solved without certify optimality (#NOpt). The last two columns show the best and the average values of the solutions obtained by the GA in 30 runs, respectively. Obviously, in all cases, the objective function (T_s) increases as the number of incoming vessels increases from 5 up to 20.

From these results, it can be observed that CPLEX was not able to reach any optimal solution by the given timeout in at least 25 % of the instances with 8 vessels or more. In addition, it cannot get any optimal solution from 18 up to 20 vessels with this timeout. Regarding GA, all instances were solved and it can be observed that the average values were better than those from CPLEX, the differences being in direct ratio with the number of vessels. Here, it is important to remark that GA reached approximately 1,000 generations in 10 s. However, the GA was able to converge in lower times.

Figure 11 shows the GA convergence for one representative instance of 20 vessels indicating for each generation the average of the best value [Avg(Best)] and the average of the entire population [Avg(Pop)], so that near-optimal values were obtained after 150 generations, taking about 1.5 s.

Considering the previous test case, the binomial sign test for a single sample [4,21] has been employed to show that

Table 1 Comparison CPLEX with GA (timeout 10 s)

$\|V\|$	CPLEX			GA	
	Avg T_s	#Opt	#NOpt	Best T_s	Avg T_s
5	267.08	100	0	267.08	267.08
6	339.25	97	3	339.21	339.21
7	417.52	88	12	416.70	416.80
8	501.41	74	26	497.70	497.98
9	585.94	58	42	575.36	576.22
10	690.91	38	62	667.15	669.55
11	797.15	24	76	758.12	762.88
12	927.85	18	82	852.99	860.78
13	1,065.32	12	88	947.88	959.54
14	1,212.86	6	94	1,049.60	1,064.61
15	1,406.21	3	97	1,154.58	1,172.50
16	1,610.21	2	98	1,268.47	1,291.39
17	1,796.58	1	99	1,372.89	1,402.45
18	2,101.27	0	100	1,486.20	1,523.05
19	2,333.46	0	100	1,605.74	1,651.37
20	2,603.36	0	100	1,733.20	1,788.23

the average fitness from generation 253 has a similar quality to that obtained with a higher number of generations.

Thirty experiments have been performed on the GA. For each one, the average fitness per generation g ($1 \leq g \leq 500$) has been computed. Then, the results given by the process with g and 500 generations have been compared and classified into two categories: (1) number of times that the average fitness obtained with 500 generations was better than that obtained with g generations; (2) the opposite case. Table 2 shows the number of experiments that correspond

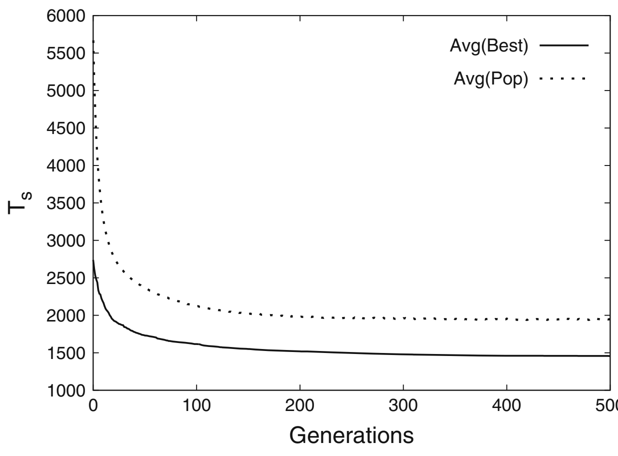


Fig. 11 Convergence of the genetic algorithm

Table 2 Model for binomial sign test for a single sample

Generations (g)	Category 1	Category 2	Total
400	15	15	30
350	16	14	30
300	17	13	30
270	16	14	30
253	20	10	30
100	30	0	30
20	30	0	30

Table 3 Probability of obtaining x or more experiments

Generations (g)	Category 1 (x)	Category 2 ($N-x$)	$P(\geq x)$
400	15	15	0.572
350	16	14	0.427
300	17	13	0.292
270	16	14	0.427
253	20	10	0.049
100	30	0	9.313e−10
20	30	0	9.313e−10

to each category, considering a total of 30 experiments, and $g = \{400, 350, 300, 270, 253, 100, 20\}$.

Within a binomially distributed population, the likelihood that an experiment will fall in category 1 will equal π_1, and the likelihood that an experiment will fall in category 2 will equal π_2. To apply the statistical test, $H_0 : \pi_1 = 0.5$ has been specified as the null hypothesis.

$$P(\geq x) = \sum_{r=x}^{n} \binom{n}{r} (\pi_1)^r (\pi_2)^{(n-r)} \qquad (12)$$

Equation (12) is employed to compute the probability that a number of experiments equal to or greater than x out of a total of n experiments will fall in one of the two categories. These probabilities are shown in Table 3.

Table 4 Average T_s for 20 vessels setting different timeouts

Timeout (s)	CPLEX	Best GA	Avg GA
5	3,187.01	1,743.04	1,799.87
10	2,603.36	1,735.56	1,787.54
20	2,406.16	1,729.53	1,779.44
40	2,251.88	1,726.79	1,773.20
60	2,126.56	1,725.57	1,770.19

Given that a nondirectional alternative hypothesis has been employed ($\pi_1 \neq 0.5$), the null hypothesis can be rejected if $P(\geq x) \leq \alpha/2$ [21]. According to the results in Table 3, if $\alpha = 0.05$, the null hypothesis cannot be rejected for the values $g = \{400, 350, 300, 270, 253\}$ because the probabilities are >0.025. However, the null hypothesis is rejected for the other cases. There exists a considerable difference between the average fitness that is obtained with a number of generations lower than 253, and the average fitness that is obtained with 500 generations. Then, it means that with $g \geq 253$ is possible to obtain an average fitness with similar quality to that obtained with 500 generations.

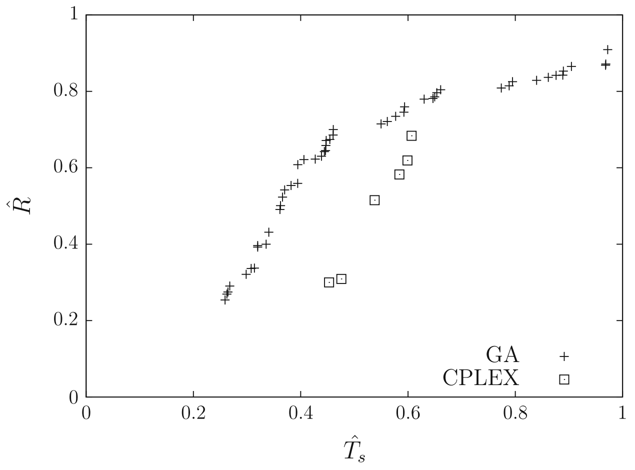
Table 4 shows how the average T_s for 20 vessels decreases as more computation time was allowed. In this experiment, the timeout was set from 5 to 60 s. It can be observed, the GA approach does not require a large timeout (the improvement is lower than 1 % beyond 5 s). Moreover, CPLEX was given a timeout up to 300 s and it obtained an average T_s (1,876.27) greater than the one obtained by the GA after 5 s (1,743.04).

7.2 Robust BAP + QCAP

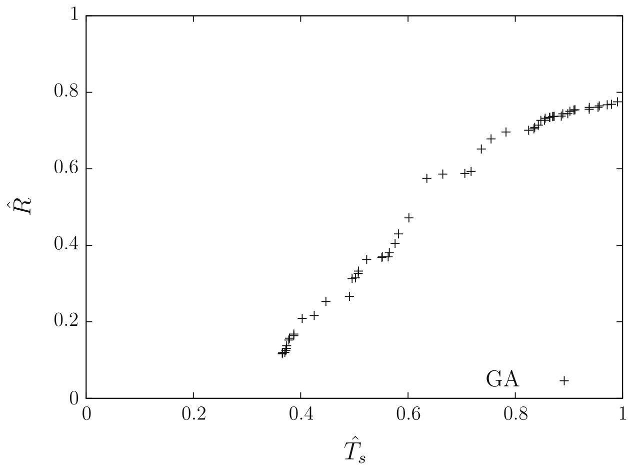
Table 5 shows the results of the CPLEX and the GA for the robust BAP + QCAP for each group of 100 instances with the same number of vessels (5–20) and the same weights $\lambda \in \{0, 0.2, 0.5, 0.8, 1\}$. The timeout was set to 10 s. For CPLEX, the reported values were the average value of F for the solutions reached (Avg F), the number of instances solved to optimality (#Opt), the number of instances solved without certify optimality (#NOpt) and the number of instances for which no solution was reached by the timeout (#NSol). Note that CPLEX was not able to reach the optimal solution even for instances with five vessels (e.g., $\lambda = 0.2$). Furthermore, for instances with more than eight vessels, CPLEX was not able to reach a feasible solution for all instances while robust GA always obtains feasible solutions for all instances. Note that robust GA was able to get better solutions (lower F values) for instances with more than ten vessels. CPLEX solver was not able to find feasible solutions to most instances due to the fact that the addition of the robustness objective function and the variables related to it makes this problem much harder.

Table 5 Average F values obtained by CPLEX with robust BAP + QCAP model

$\|V\|$	λ	Robust CPLEX				Robust GA	
		Avg F	#Opt	#NOpt	#NSol	Best F	Avg F
5	0	−0.723	100	0	0	−0.715	−0.696
	0.2	−0.481	99	1	0	−0.465	−0.455
	0.5	−0.141	97	3	0	−0.096	−0.090
	0.8	0.150	99	1	0	0.229	0.230
	1	0.324	100	0	0	0.436	0.437
6	0	−0.698	82	18	0	−0.708	−0.674
	0.2	−0.450	83	17	0	−0.437	−0.420
	0.5	−0.106	86	14	0	−0.066	−0.059
	0.8	0.180	90	10	0	0.283	0.284
	1	0.346	92	8	0	0.419	0.426
7	0	−0.684	53	47	0	−0.719	−0.669
	0.2	−0.438	48	52	0	−0.435	−0.409
	0.5	−0.091	57	43	0	−0.050	−0.043
	0.8	0.184	70	30	0	0.272	0.275
	1	0.342	83	17	0	0.428	0.428
8	0	−0.637	27	73	0	−0.712	−0.648
	0.2	−0.391	29	70	1	−0.417	−0.386
	0.5	−0.059	34	65	1	−0.031	−0.021
	0.8	0.217	42	57	1	0.272	0.274
	1	0.368	60	40	0	0.414	0.414
9	0	−0.612	15	80	5	−0.709	−0.631
	0.2	−0.353	14	81	5	−0.407	−0.368
	0.5	−0.019	16	81	3	−0.019	−0.008
	0.8	0.254	27	70	3	0.283	0.287
	1	0.404	40	58	2	0.435	0.436
10	0	−0.549	9	80	11	−0.699	−0.616
	0.2	−0.294	6	80	14	−0.390	−0.350
	0.5	0.019	12	74	14	−0.006	0.003
	0.8	0.310	14	79	7	0.297	0.300
	1	0.454	24	68	8	0.440	0.440
15	0	−0.461	0	17	83	−0.644	−0.530
	0.2	−0.167	0	15	85	−0.316	−0.268
	0.5	0.103	0	17	83	0.032	0.044
	0.8	0.372	0	16	84	0.291	0.294
	1	0.546	1	18	82	0.406	0.407
20	0	–	0	0	100	−0.564	−0.449
	0.2	−0.035	0	1	99	−0.246	−0.204
	0.5	0.243	0	1	99	0.066	0.074
	0.8	0.520	0	1	99	0.297	0.299
	1	–	0	0	100	0.417	0.417



(a) 10 vessels.



(b) 20 vessels.

Fig. 12 Pareto front for representative instances

The evaluation of the robust BAP + QCAP model presented in Sect. 3, as a multi-objective optimization problem, requires the study of the dominance of solutions as well as the Pareto front. Thus, for each instance, a set of non-dominated solutions after a timeout of 10 s was obtained. Figure 12 shows the Pareto front for two representative instances of 10 and 20 vessels, respectively. This Pareto front is an important tool for the decision maker (the container terminal operators) to assess the trade-off between $\hat{T}_s$ and $\hat{R}$ of the different schedules obtained according to their preferences. The Pareto front of the CPLEX consists of the non-dominated solutions obtained by solving the mathematical model with different λ values ranging from 0 to 1 in steps of 0.1. Note that the GA obtained a large set of solutions over the Pareto front. Moreover, in the case of ten vessels, the solutions obtained by the GA dominates the ones obtained by CPLEX (Fig. 12a). Figure 12b shows the Pareto front for a representative schedule of 20 vessels. In this case, CPLEX was not able to reach feasible solutions.

The performance (robustness) of the schedules obtained by the GA with a timeout of 10 s was evaluated by generating actual scenarios with some incidences in the actual handling time of the vessels. An incidence over a vessel i is modeled as a delay d in the handling time of this vessel i. An incidence is absorbed if there is enough buffer time behind the vessel i so as to not alter the mooring time of the subsequent vessels. For each instance, the vessels that vary their handling times were uniformly chosen among all the vessels.

In this experiment, 100 instances of 20 vessels were evaluated. For each instance, four different schedules were chosen from the set of efficient solutions of the multi-objective

Table 6 Average of incidences absorbed in schedules of 20 vessels

Range	R_m	R_1	R_2	R_M
$d \in [1,\ 0.2\ h_i]$	29.37	45.67	60.71	71.95
$d \in [1,\ 0.5\ h_i]$	26.25	43.10	59.14	71.29
$d \in [1,\ 0.8\ h_i]$	22.44	37.53	54.63	66.55
$d \in [1,\ 1.0\ h_i]$	20.42	37.17	53.53	65.50
$d \in [1,\ 1.2\ h_i]$	19.49	35.15	50.79	62.79

GA according to their robustness: the one with the minimum robustness (R_m), the one with the maximum robustness (R_M) and two intermediate robust schedules (R_1 and R_2).

The incidences (delays, d) introduced were randomly chosen from a range. This range varies from a minimum value (1) to a maximum value, which is related to the handling time (h_i) of the vessel affected by the incidence (first column of Table 6). For each range, 100 incidences were uniformly created and applied to the four schedules (R_m, R_1, R_2 and R_M) of each instance.

Table 6 shows the percentage of incidences absorbed by each type of schedule. It can be observed that the more the robust schedule, the more are the incidences absorbed. For instance, with delays $d \in [1, 0.5\ h_i]$, the R_m schedule only absorbed 26.25 % of incidences on average, but the R_M schedule absorbed up to 71.29 %. Note that as the delay became larger, fewer schedules can absorb the incidences. With delays between ranges of $[1, 0.2\ h_i]$, the R_M schedule can absorb 71.95 % of incidences on average. However, with larger ranges, the incidences absorbed decreased down to 62.79 % on average.

8 Conclusions

The competitiveness among container terminals causes the need to improve the efficiency of each one of the subprocesses that are performed within them. However, this efficiency is affected by the uncertainty of the environment such as bad weather, breakdowns of the engines, delays, etc. This paper focuses on two of the main related problems, the berth allocation and QCAP, in an integrated way. To this end, a mixed integer lineal programming model and a GA were developed in a dynamic and continuous BAP + QCAP. The MILP model was unable to get optimal solutions when a reasonable timeout is set or when the problem becomes harder (more than ten vessels). Moreover, many of the instances were solved but without any guarantees of being the optimal ones since the timeout was reached. However, the GA approach was able to obtain near-optimal solutions in lower computational times and it also maintained a rapid convergence of the results even with large vessel queues. From these results, it is concluded the adequacy of a metaheuristic approach based on GA for solving the BAP + QCAP problem.

These two approaches, the MILP model and the GA, were extended as a multi-objective optimization problem to cope the uncertainty by obtaining robust schedules. The robustness of a schedule is related to the operational buffer times between the vessels. This new problem (robust BAP + QCAP) becomes harder and even instances of 5 vessels were not optimally solved by the MILP model in a reasonable time. Since the two objectives considered in this study, 'service time' and 'robustness', are opposite, there is no single optimal solution for these scheduling problems such that it is necessary to evaluate the trade-off between these objectives functions. Thereby, the multi-objective GA was able to obtain a set of efficient solutions and a study of the Pareto front was presented. Visualizing this Pareto front helps to the container terminal operators to decide which schedule is better depending on the actual state.

The robustness, that is tackled in this study, is related to the use of berth as resource. This is a clear contribution to the adequate resolution of robust BAP + QCAP. From this point, since there is no previous knowledge about incidences, it could be analyzed how to distribute the operational buffer times among the vessels equally. To this end, other evolutionary multi-objective algorithms, such as NSGA-II [3] or SPEA2+ [14], might be employed to introduce this new objective function into the model. Furthermore, robustness related to shared QCs is an interesting problem to be studied. When QCs are considered for robustness, a delay in the arrival or handling time of a vessel might be propagated to those vessels with QCs in common although they do not occupy the same berth space. In this case, a further analysis is needed to re-allocate the QC correctly, which gives rise to a new re-scheduling problem.

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