

Figure captions

1. MCTS algorithm steps.
2. Decision and objective spaces in a MOP with two variables (x_1 and x_2) and two objectives (f_1 and f_2). In the objective space, yellow dots are non-optimal objective vectors, while blue dots form a non-dominated set. From [17].
3. HV(P) of a given Pareto-front P.
4. r_x^p is the projection of the r_x value on the piecewise linear surface (discontinuous line). The shadowed surface represents HV(P). From [31].
5. Environment of the Deep Sea Treasure (from [26]): grey squares represent the treasure (with their different values) available in the map. The black cells are the sea floor and the white ones are the positions that the vessel can occupy freely. The game ends when the submarine picks one of the treasures.
6. Optimal Pareto Front of the Deep Sea Treasure, with both objectives to be maximized.
7. Example of two different sequences of actions (R: Right, D: Down) that lie in the same position in the map, but at a different node in the tree.
8. Sample MO-PTSP map.
9. Results in DST: percentages of each optima found during 100 games played with different weight vectors. Scalarization approaches converge to the edges of the optimal front, whereas Pareto approaches are able to find all optimal solutions. The proposed algorithm, MO-MCTS, finds these solutions significantly more often than NSGA-II.

Table captions

- I. MO-PTSP averages (plus standard error) with different weight vectors. Results in bold obtained an independent t-test p-value < 0.01 .
- II. Results in MO-PTSP: Each cell indicates the triplet (D, \emptyset , d), where D is the number of maps where the row algorithm dominates the column one, \emptyset is the amount of maps where no dominance can be established, and d states the number of maps where the row algorithm is dominated by the column one. All the algorithms followed the same route (order of waypoints and fuel canisters) in every map tested.
- III. MO-PTSP Results with different weights. The last column indicates if the evolved individual dominates (\leq) or not (\emptyset) each one of the base genomes for that particular map.

*Note: For table III, the symbol \leq corresponds to the latex symbol \preceq : \preceq