

Best-first search vs Beam search

Heuristics – Case: Fruit fly

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Goal of experiment:

The goal of this experiment is to compare the best-first search algorithm with the beam search algorithm; regarding the number of inversions from a genome to the solution. In addition, the breakpoints and the distance points (heuristics) are compared with each other.

Methods:

The best-first search algorithm selects the best child based on breakpoints or distance points. The beam search algorithm selects the 50 best children per layer based on the same heuristics. The algorithms are executed on the genome of *Drosophila Melanogaster*. In addition, twenty random genomes of length 25 are generated to compare the algorithms including the heuristics regarding the number of inversions to the solution.

Results:

Table1. Number of inversions needed to get to the solution with best-first search, beam search and different heuristics on *Drosophila Melanogaster* genome.

Heuristics	Best-first search	Beam search
Breakpoints	17 inversions	13 inversions
Distance Points	35 inversions	21 inversions

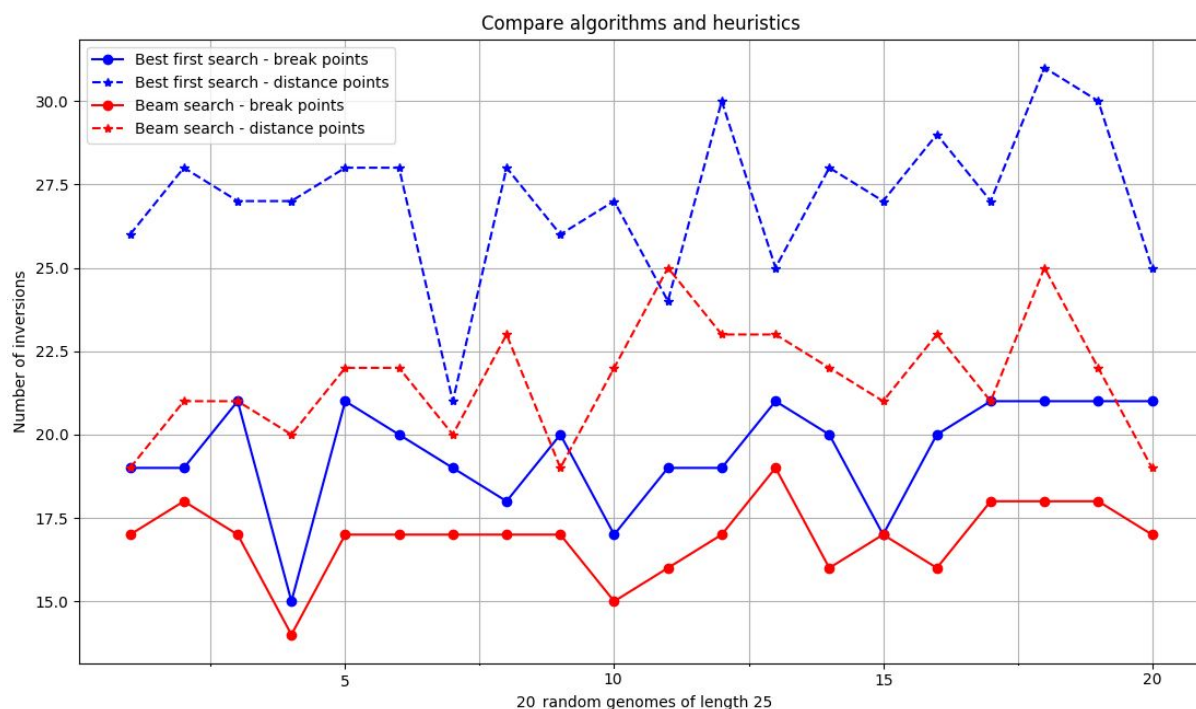


Figure 1. Comparisons between best-first search algorithm and beam search algorithm with different heuristics on 20 random genome sequences of length 25.

Discussion:

The beam search finds a solution in less steps than the best-first search. This is expected, because the best-first search prunes more than the beam search does. The heuristics based on breakpoints seems to work better than the heuristics based on distance points. The reason for this might be that the distance points do not take into account the genes that are already in a sorted order.

Conclusion:

The beam search algorithm finds a shorter path to the solution than the best-first search algorithm. The breakpoints heuristic is more reliable than the distance points heuristic.