**Peer Review of *Genetic Algorithm-Based Solver for Very large Multiple Jigsaw Puzzles of Unknown Dimensions and Piece Orientation***

In this paper, the authors propose a new jigsaw puzzle solver that leverages a genetic algorithm to search the vast space of possible puzzle solutions. The proposed chromosome representation and crossover technique form the major algorithmic difference between this work and previous research. The new representation and operator allow the authors to discard previously required a-priori knowledge about the puzzle to be solved. Specifically, the algorithm no longer requires knowledge of the image dimensions and the correct geometric orientation of the pieces in the puzzle. They also show that their revised algorithm is capable of solving “mixed-bag” puzzles, in which they feed the algorithm the pieces to several distinct puzzles at the same time. The algorithm is not completely free of simplifying assumptions however. The dissimilarity measure used is designed with rectangular images in mind. Also the chromosome design and crossover operator only work for square puzzle pieces, all having exactly the same dimensions. The authors provide many references to papers in other fields where they believe their work may find applications, and also note that computational jigsaw puzzle research doesn’t need much justification because solving puzzles is intriguing in its own right; a claim that I and perhaps most computer scientists would agree with.

To the best of the authors’ knowledge and to the best of my own based on my brief research into the subject, the algorithm presented in this paper made some impressive and novel improvements over the previously state-of-the-art jigsaw puzzle solvers. Prior to this algorithm, the best solver that operated without knowledge of the original image dimensions and correct piece orientation could solve 9600 piece puzzles in 23.5 hours. The algorithm presented in this paper managed to more than double the number of pieces to 22,755 while decreasing the solving time to just 3.5 hours. However, there are a few gaps in the paper’s description of the algorithm that the authors should revise.

The first glaring problem with this paper is its failure to be specific about the implemented algorithm. The paper goes through sufficient detail on their chromosome representation, measure of piece edge dissimilarity, and how dissimilarity is used to compute chromosome fitness. However there seems to be some gaps in the description of the crossover and mutation operators, as well as the process used to evolve the population from generation to generation.

The new crossover operator, which is the crux of the proposed algorithm, is described well enough to grasp the idea after multiple readings; however its description could use some clarifying elaboration to improve reader understanding. Also, the paper doesn’t include any details of how the operation was implemented, which would be extremely beneficial to researchers, both to verify the results of the paper and to help drive development in this area of research, especially if it works as well as the paper suggests. If I understood the crossover operation correctly, the “until…do” loop shown in figure 6 seems to be an abuse of notation and should be replaced by more descriptive pseudocode that captures that fact that each step is its own loop that continues until it can no longer make progress, and the outer “until…do” loop shown will never iterate more than once.

There is one sentence in the algorithm’s description in section 3.3.2 that mentions that a mutation process is used and can cause an edge assignment to fail during the crossover operation. However, this mutation process is never described. Leaving the readers completely in the dark about the nature of this operation and when it takes place in the crossover process.

Finally, the paper does not explicitly say how the population for the next generation is constructed and what kind of replacement strategy is used. They provide the population size used, they note that a fitness proportional roulette wheel is used for selection, and that the crossover operator occurs between two selected parents. The only hint towards the algorithm’s population evolution and replacement technique provided is “In each generation we start by copying the best four chromosomes.” This seems to imply they are going to take a generational approach in which an entirely new population, except for those four most fit individuals, is generated during each generation by repeated applications of the crossover operator. Even if this can be implied by researchers somewhat familiar with genetic algorithms and the difference between steady-state and generations GAs, its bad practice to leave any of the core genetic operators up to the readers’ implications. Also, it’s a somewhat abnormal procedure to explicitly retain the best individuals of the population from generation to generation as it can limit the exploration ability of the GA, thus the authors should describe briefly their reasoning behind this choice. At the very least the authors should add some pseudocode for the algorithm as a whole to show readers the framework within which they are working.

In addition to providing a vague description of the algorithm, the authors do not mention how many runs of the GA were performed on each puzzle to get the numbers shown, but they do say that the accuracies shown are the averages over the runs performed. Also, the authors incorrectly reference [18]saying that the paper solved puzzles with 22,755 pieces, when in [18] the value was 22,834, and the algorithm did not solve any of the 22,834 piece puzzles to 100% completion. More concerning is the fact that the 22,834 piece puzzle shown in figure 1 c-d of [18] is the exact image shown in figure 4 a-f of the paper in discussion, and the image doesn’t have a citation or explicit indication that it is the same puzzle explored in [18]. There may be several possible explanations for this, but as it stands this leaves readers open to think that maybe the authors purposefully removed problematic pieces to allow their algorithm to correctly solve the puzzle to completion.

Finally, as a suggestion for a more complete results section, it would have been nice to compare against the results of [17]as seen in [18]. Most likely the authors only compared against [9] because they wanted to focus on the improvement compared to algorithms that don’t know the dimensions of the image or piece orientation. However, I still think it would be valuable and more comprehensive to provide tables showing this algorithm against the greedy approach taken in [17] that requires knowledge of piece orientation.

As a whole the paper presents an algorithm that shows great promise and certainly has the potential to be the new state-of-the-art jigsaw puzzle solver. The English is generally very well-written, relatively easy to follow, and I didn’t notice any spelling or grammar issues. However, the authors need to revise their paper to add the missing details of their algorithm and their experiment listed above. Also the authors need to be sure that they are being consistent when referencing their sources. If there is a legitimate reason behind the piece number discrepancy described above, they need to state that explicitly when citing the source. Also they need to explicitly cite the source of their images if they are taken from previous research. Finally, I recommend the authors add more comparison data to the results section as mentioned above. It would be nice to provide future researchers with benchmark comparison data in one convenient place, especially if this is to become the new state-of-the-art algorithm for this problem. My recommendation is that the authors address all of the issues I’ve laid out above, and then resubmit for another peer review.