The longest arc-preserving common subsequence problem is an NP-hard combinatorial optimization problem from the field of computational biology. This problem finds applications, in particular, in the comparison of arc-annotated Ribonucleic acid (RNA) sequences. In this work we propose a simple, hybrid evolutionary algorithm to tackle this problem. The most important feature of this algorithm concerns a crossover operator based on solution merging. In solution merging, two or more solutions to the problem are merged, and an exact technique is used to find the best solution within this union. It is experimentally shown that the proposed algorithm outperforms a heuristic from the literature.