and in this way avoids overlaps. For the backtrack table, the corresponding row or column is filled with a different symbol so that the alignment stops when it hits the symbol, avoiding overlaps from alignments started outside of the region as well. In addition, the upper right and lower left quadrants of both tables must be masked to avoid aligning multiple subsequences that are not arranged linearly and therefore could not exist together.

The masking process is shown here for the alignment of TTTGGCGAAA with TTTACCTAAA and with score inputs of indel = -2, match = 1, mismatch = -2 (using scores that will return highly conserved alignments to show the example on a small scale). When TTT is aligned with TTT, the corresponding columns and rows are altered.

For the alignment table, the values are changed to a low number, in this case -1:

For the backtracking table, the symbol 'x' is substituted in:

Once the tables are masked accordingly, the same process can be repeated, each time using the updated tables to

With this design, the algorithm will never return alignments that overlap. For some biological questions, this may be a helpful feature. However, it must be noted that this algorithm prioritizes highest scored alignments. If there was a more biologically relevant alignment, but it had a lower alignment score, it could be masked in this process. In this scenario, modifying an algorithm to return every possible alignment within a certain score range may be more useful. Instead, this algorithm would be most relevant for preliminary comparisons of sequences that are intended for finding general areas of similarity, not any specific subsequence. Additionally, the function of this new algorithm has only been tested on a small scale and with formulated strings that do not have a directly biological basis, but would presumably still capture the function.