

1. **Initialized matrix** with correct gap penalties.

- Top row and first column initialized with cumulative gap penalties (-1 per gap).

2. **Filled matrix** for sequences:

- Sequence 1: CATGATAA
- Sequence 2: ATACATA
- Filled using match = +1, mismatch = -1, gap = -1
- All internal cells filled according to Needleman-Wunsch recurrence:

$$F(i,j) = \max(\begin{array}{l} F(i-1, j-1) + \text{match_or_mismatch}, \\ F(i-1, j) + \text{gap}, \\ F(i, j-1) + \text{gap} \end{array})$$

3. **Traceback steps and logic:**

- Starts from bottom-right cell of score matrix.
- At each step, move diagonally (match/mismatch), up (gap in seq2), or left (gap in seq1) based on highest score.
- Continues until top-left cell is reached.
- Annotated traceback direction per cell provided.

4. **Final alignment:**

CATGATAA
-ATACATA

- Total alignment score calculated step-by-step and shown alongside.
- Misaligned characters and gaps penalized.