WROCŁAW UNIVERSITY OF SCIENCE AND TECHNOLOGY
FACULTY OF FUNDAMENTAL PROBLEMS OF TECHNOLOGY
INTRODUCTION TO BIOINFORMATICS

TASK #2
QUANTITATIVE MATCHING OF SEQUENCE PAIRS

Deadline: April 30, 2025

Prepare a properly functioning program for quantitative comparison of pairs of protein or DNA coding sequences using **the Needleman-Wunsch global matching algorithm**

The program should control the correctness of the input data, generate correct results, as well as be concise, legible (with comments) and consistent with the style rules of the programming language used.

Requirements:
1. Ability to load sequences:
   - manually
   - from a FASTA file

2. Ability to select scores for match and mismatch and penalties for gaps.

3. Generating one optimal matching pathway
   - displaying together with program parameters, scoring, matching length, percentage of identical positions and gaps
   - saving the result to a text file

4. Graphical display of the scoreboard along with the optimal path.

The report should include:

1. Algorithm code with description of individual functionalities

2. Estimation of computational complexity

3. User instructions (how to use your program)

Additional task

Generating all optimal matching paths.