# Align\_sequences.py saved in the 4. Source code folder

‘’’ This function will do the sequence alignment using **pairwise2**, which is within the **BioPython** library. The function will evaluate each sequence read from the dog\_breeds.fa file vs. the mystery sequence (mystery.fa) and calculate an alignment score. Each time a higher alignment score is calculated, both the alignment score and the corresponding sequence (best match) will be saved in a variable.

It includes the following executable steps:

**align\_sequences**: Uses pairwise2.align.globalxx() to align two sequences globally. This function compares two sequences and returns the best alignment.

**find\_best\_match**: Loops through the sequences in the database and finds the one with the highest alignment score compared to the test sequence.

‘’’

from Bio import pairwise2

def align\_sequences(seq1, seq2):

"""Align two sequences using global alignment and return the best alignment."""

alignments = pairwise2.align.globalxx(seq1, seq2) # Perform global alignment

if alignments:

return alignments[0] # Return the best alignment (highest score)

return None

def find\_best\_match(test\_sequence, database\_sequences):

"""Find the best matching sequence from the database."""

best\_match = None

best\_score = -float('inf') # Initialize with the lowest possible score

for db\_sequence in database\_sequences:

alignment = align\_sequences(test\_sequence.seq, db\_sequence.seq)

if alignment: # Check if alignment exists

score = alignment[2] # Alignment score is in index 2

if score > best\_score: # Keep track of the best match

best\_score = score

best\_match = db\_sequence

return best\_match, best\_score