Lab 9 — Austinkoster part main

start
↓
Open reference file, ifstream + Open_file + Reference
↓
Open comparison file, ifstream + Open_file + comparsionfile
↓
read id + sequence from reference
↓
convert sequence to protein sequence
↓

while (program can read comparison of sequence) {

    Convert comparison seqn to protein sequence
    ↓

    Call Needleman _ wunsch
        create _ comparison
        print _ comparison
}

return 0;

Lab 9 - anthankishi functions

above

if (row-1) ≥ 0 →yes return [(row-1), col]
↓no
else → return -1 · ((col +1)) ——→ one

Left

if (col-1) ≥ 0 →yes return [row (col-1)]
↓no
else → -1 · (row +1) ——→ end

above left

if (row-1) ≥ 0 and ((col-1)) → return [row-1, (col-1)]
else if (q = 0) → return -1 * row →
else → return -1 * col ——→ end

open_file

if if from combat open the rem → fire = ifstream f stamp
else → fin = file the fin in fals ——— d ord

got_id_cmd_sequence

if new id ≠ old → id = id , new sequre seqor = new sequence return true,
else → id r sequenc are thohanzer, return fase
end