DATASET 1

a)

```
seq_1: Bacillus anthracis
seq_2: Clostridium tetani
seq_3: Escherichia coli strain
seq_4: Mycobacterium tuberculosis
seq_5: Pseudomonas aeruginosa
seq_6: Salmonella enterica
seq_7: Staphylococcus aureus
seq_8: Streptococcus pneumoniae
seq_9: Treponema pallidum
seq_10: Vibrio cholerae
```

b) Limitado a 20k chars para questao de desempenho

```
seq 1 vs seq 2: -1109
seq_1 vs seq_3: -1389
seq_1 vs seq_4: -1626
seq_1 vs seq_5: -1523
seq_1 vs seq_6: -1529
seq_1 vs seq_7: 1618
seq_1 vs seq_8: -519
seq_1 vs seq_9: -1214
seq_1 vs seq_10: -1298
seq_2 vs seq_3: -1542
seq_2 vs seq_4: -1959
seq 2 vs seq 5: -1939
seq_2 vs seq_6: -1718
seq_2 vs seq_7: -1035
seq_2 vs seq_8: -1193
seq_2 vs seq_9: -1328
seq_2 vs seq_10: -1559
seq 3 vs seq 4: -1263
seq_3 vs seq_5: -1219
seq_3 vs seq_6: -1168
seq_3 vs seq_7: -1449
seq_3 vs seq_8: -1447
seq_3 vs seq_9: -1360
seq_3 vs seq_10: -1241
seq_4 vs seq_5: -751
seq_4 vs seq_6: -1056
seq_4 vs seq_7: -1304
seq_4 vs seq_8: -1713
seq_4 vs seq_9: -1397
seq 4 vs seq 10: -1290
seq_5 vs seq_6: -1042
seq_5 vs seq_7: -1777
```

```
seq_5 vs seq_8: -1971
seq_5 vs seq_9: -1455
seq_5 vs seq_10: -1323
seq_6 vs seq_7: -1551
seq_6 vs seq_8: -1605
seq_6 vs seq_9: -1296
seq_6 vs seq_10: -1257
seq_7 vs seq_8: -751
seq_7 vs seq_9: -1178
seq_7 vs seq_9: -1178
seq_7 vs seq_10: -1279
seq_8 vs seq_9: -1237
seq_8 vs seq_10: -1329
seq_9 vs seq_10: -1294
```

c)

```
seq_1 seq_2 seq_3 seq_4 seq_5 seq_6 seq_7 seq_8 seq_9 seq_10
            -1109 -1389 -1626 -1523 -1529 1618 -519 -1214 -1298
seq_1
                  -1542 -1959 -1939 -1718 -1035 -1193 -1328 -1559
seq_2
        -1109 0
        -1389 -1542 0 -1263 -1219 -1168 -1449 -1447 -1360 -1241
seq_3
        -1626 -1959 -1263 0
                              -751 -1056 -1304 -1713 -1397 -1290
seq_4
        -1523 -1939 -1219 -751 0
                                    -1042 -1777 -1971 -1455 -1323
seq_5
        -1529 -1718 -1168 -1056 -1042 0
                                          -1551 -1605 -1296 -1257
seq_6
        1618 -1035 -1449 -1304 -1777 -1551 0
seq_7
                                                -751 -1178 -1279
        -519 -1193 -1447 -1713 -1971 -1605 -751 0
seq_8
                                                      -1237 -1329
        -1214 -1328 -1360 -1397 -1455 -1296 -1178 -1237 0
seq_9
                                                            -1294
        -1298 -1559 -1241 -1290 -1323 -1257 -1279 -1329 -1294 0
seq_10
```

d)

Dataset 2

a)

```
seq_1: Streptococcus agalactiae
seq_2: Neisseria gonorrhoeae
seq_3: Mycobacterium tuberculosis
seq_4: Staphylococcus aureus
seq_5: Treponema pallidum
seq_6: Bacillus anthracis
seq_7: Yersinia pestis
seq_8: Acinetobacter baumannii
seq_9: Pseudomonas aeruginosa
seq_10: Helicobacter pylori
```

b)

```
seq_1 vs seq_2: -25
seq_1 vs seq_3: -14
seq_1 vs seq_4: -16
seq_1 vs seq_5: -16
seq_1 vs seq_6: -12
seq_1 vs seq_7: -24
seq_1 vs seq_8: -21
seq_1 vs seq_9: -28
seq_1 vs seq_10: -11
seq_2 vs seq_3: -18
seq_2 vs seq_4: -26
seq_2 vs seq_5: -23
seq_2 vs seq_6: -25
seq_2 vs seq_7: -14
seq_2 vs seq_8: -19
seq_2 vs seq_9: -9
seq_2 vs seq_10: -24
seq_3 vs seq_4: -23
seq_3 vs seq_5: -<u>12</u>
seq_3 vs seq_6: -16
seq_3 vs seq_7: -13
seq_3 vs seq_8: -31
seq_3 vs seq_9: -7
seq 3 vs seq 10: -20
seq_4 vs seq_5: -24
seq_4 vs seq_6: -9
seq_4 vs seq_7: -18
seq_4 vs seq_8: -22
seq_4 vs seq_9: -33
```

```
seq_4 vs seq_10: -12
seq_5 vs seq_6: -16
seq_5 vs seq_7: -5
seq_5 vs seq_8: -17
seq_5 vs seq_9: -5
seq_5 vs seq_10: -15
seq_6 vs seq_7: -17
seq_6 vs seq_8: -25
seq_6 vs seq_9: -25
seq_6 vs seq_10: -24
seq_7 vs seq_8: -25
seq_7 vs seq_9: -14
seq_7 vs seq_10: -14
seq_8 vs seq_9: -33
seq_8 vs seq_10: -15
seq_9 vs seq_10: -22
```

c)

```
seq_1 seq_2 seq_3 seq_4 seq_5 seq_6 seq_7 seq_8 seq_9 seq_10
               -25
                     -14
                           -16
                                 -16
                                       -12
                                             -24
                                                   -21
                                                         -28
                                                               -11
seq_1
          0
                                       -25
                                                               -24
          -25
                0
                     -18
                           -26
                                 -23
                                             -14
                                                   -19
                                                         -9
seq_2
                      0
                           -23
                                 -12
                                                               -20
          -14
                -18
                                       -16
                                             -13
                                                   -31
                                                         -7
seq 3
          -16
                -26
                      -23
                                 -24
                                       -9
                                             -18
                                                   -22
                                                         -33
                                                               -12
                            0
seq_4
                -23
                      -12
                            -24
                                  0
                                       -16
                                             -5
                                                   -17
                                                         -5
                                                              -15
seq_5
          -16
          -12
                -25
                      -16
                            -9
                                 -16
                                       0
                                             -17
                                                   -25
                                                         -25
                                                               -24
seq_6
                                  -5
          -24
                -14
                      -13
                            -18
                                       -17
                                              0
                                                   -25
                                                         -14
                                                               -14
seq_7
          -21
                -19
                      -31
                            -22
                                  -17
                                        -25
                                              -25
                                                    0
                                                         -33
                                                              -15
seq 8
                -9
                     -7
                                      -25
                                            -14
                                                  -33
                                                              -22
          -28
                           -33
                                 -5
                                                        0
seq 9
          -11
                -24
                      -20
                            -12
                                  -15
                                              -14
                                                          -22
seq_10
                                        -24
                                                    -15
```

```
(((((seq_3: -15.5); seq_8: -15.5): -10.625, (seq_4: -16.5, seq_9: -16.5): -10.625): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5); , seq_2: -12.5): -9.75, seq_5: -9.75): -8.3594): -7.125, seq_7: -7.125); -8.3594; (seq_1: -12.5): -9.75, seq_5: -9.75): -8.3594; (seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0, (seq_6: -12.0, seq_10: -12.0): -9.0): -8.3594, ((seq_1: -12.5): -9.0): -9.0
```