Trident Algorithm

Algorithm 1: Calculate microRNA, double strand DNA triplex forming potential

1: for all —query_sequence— do
2:   for all —reference_sequence— do
3:     for all —match_types— do
4:       run do_alignment
5:     end for
6:   end for
7: end for

Algorithm 2: do_alignment

1: for query_sequence i = 1..N do
2:   if i is in end region then
3:     open ← −9
4:     ext ← −4
5:   else
6:     open ← −36
7:     ext ← −16
8: end if
9: for reference_sequence j = 1..M do
10:   if weighted_region then
11:     nt_nt_score_{i,j} ← score5p(i, j)
12:   else
13:     nt_nt_score_{i,j} ← score(i, j)
14: end if
15: maxv(x, y, z) ≡ max(x, y, z, 0)
16: A(i, j) ≡ score(i, j) + maxv(A(i − 1, j − 1))
17: B(i, j) ≡ max(A(i, j − 1) + open, B(i, j − 1))
18: C(i, j) ≡ \begin{cases} 
    \text{max}(C(i − 1, j) + ext, A(i − 1, j) + open) & \text{if in weighted region} \\
    -1 & \text{else}
\end{cases}
19: best_{i,j} ← \text{max}(A(i, j), B(i, j), C(i, j))
20: if best\_{i,j} is within allowed score ranges then
21:   retain hit struct
22: end if
23: end for
24: end for
25: Remove overlapping hit structs
26: Sort hit structs by score, DNA position and MicroRNA position
27: for all Hit structs do
28:   for all Positions in MicroRNA - DNA alignment, i and j, respectively do
29:     if best_{i,j} = A(i, j) then
30:       Label base pairs as bonded
31:     else if best_{i,j} = B(i, j) then
32:       Mark microRNA, i, as a gap

else
Mark DNA, j, as a gap
end if
end for
end for