

MGAlign Pseudocodes

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01 initialize 5'_hits and 3'_hits as empty arrays
02 do
03   for position = 0 to length(mRNA_Sequence) - wordsize - 1
04     initialize tempArray as an empty array
05     do
06       hit_position = search_from_5'_end(position, Genome_Sequence)
07       if extend_hit(hit_position) == true
08         tempArray.append(hit_position)
09       while hit_position < length(mRNA_Sequence)
10         if length(tempArray) <= 10
11           append tempArray to 5'_hits
12           break
13       end for
14     for position = 0 to length(mRNA_Sequence) - wordsize - 1
15       initialize tempArray as an empty array
16       do
17         hit_position = search_from_3'_end(position, Genome_Sequence)
18         if extend_hit(hit_position) == true
19           tempArray.append(hit_position)
20         while hit_position < length(mRNA_Sequence)
21           if length(tempArray) <= 10
22             append tempArray to 3'_hits
23             break
24         end for
25       possible_pairs = get_possible_pairs(5'_hits, 3'_hits)
26     while length(possible_pairs) > 0
27       initialize all_alignments as an empty array
28     foreach possible_pair in possible_pairs
29       internal_matches = search_for_internal_matches(possible_pairs)
30       alignment = select_alignment_from_internal_matches(internal_matches)
31       alignment = search_for_small_internal_exons(alignment)
32       alignment = search_for_flanking_exons(alignment)
33       alignment = select_best_splice_site_motif(alignment)
34       append alignment to all_alignments
35     end foreach
36     report_best_alignment(all_alignments)
```