

1. Read in the sequence
2. Locate all starts and stops in the genome
3. Scan all open reading frames and record numbers of G's and C's in each codon position
4. Build a frame bias model based on ORF length and G/C codon position within each ORF
5. Record the highest scoring start nodes in each frame that overlap a stop codon by ≤ 60 bp
6. Do the first pass dynamic programming, connecting nodes based on frame bias scores
7. Create a hexamer background of all 6-mers in the entire sequence
8. FOR each gene model in the dynamic programming output:
 1. Gather all hexamer statistics
9. Create log table of hexamer coding scores
10. FOR each gene model in the dynamic programming output:
 1. Calculate a coding score based on hexamer statistics
 2. Penalize the score if there is a higher scoring start upstream in the same ORF
 3. IF the gene is very long but has a negative score, THEN give it a barely positive score
11. FOR 10 iterations
 1. Build a ribosomal binding site and ATG/GTG/TTG background for all nodes
 2. FOR each gene with a score of > 35.0 :
 1. Gather its Shine-Dalgarno RBS motif data and ATG/GTG/TTG data
 3. Modify RBS and ATG/GTG/TTG weights by the observations
12. IF organism is not determined to use Shine-Dalgarno THEN run the non-SD finder
13. FOR each gene model:
 1. Assign a final score of start score + coding score
 2. Penalize the final score of genes < 250 bp
14. Do the second pass dynamic programming, connecting nodes based on hexamer coding
15. FOR each gene model in the final dynamic programming:
 1. Eliminate negative scoring models
 2. Resolve very close start pairs (≤ 15 bp from each other)
16. Print final output