

Question1E

- If a gene ends with a codon that has a low frequency of appearance in my table then it is very likely my predictor will stay in the intergenic region and completely miss that gene.

- If the genes have lots of nucleotides forming a stop codon in the intergenic region then it will mislead my predictor during traceback to assume there was a gene before when there wasn't.

Similarly if the genes have lots of start codons in their sequence but that do not lead to a Start state (ie they are just part of the genic region) then it would lead my predictor to wrongly assume the beginning of a genic session and thus ending my genic region while it should have continued . Therefore I have many genes but of too short size.