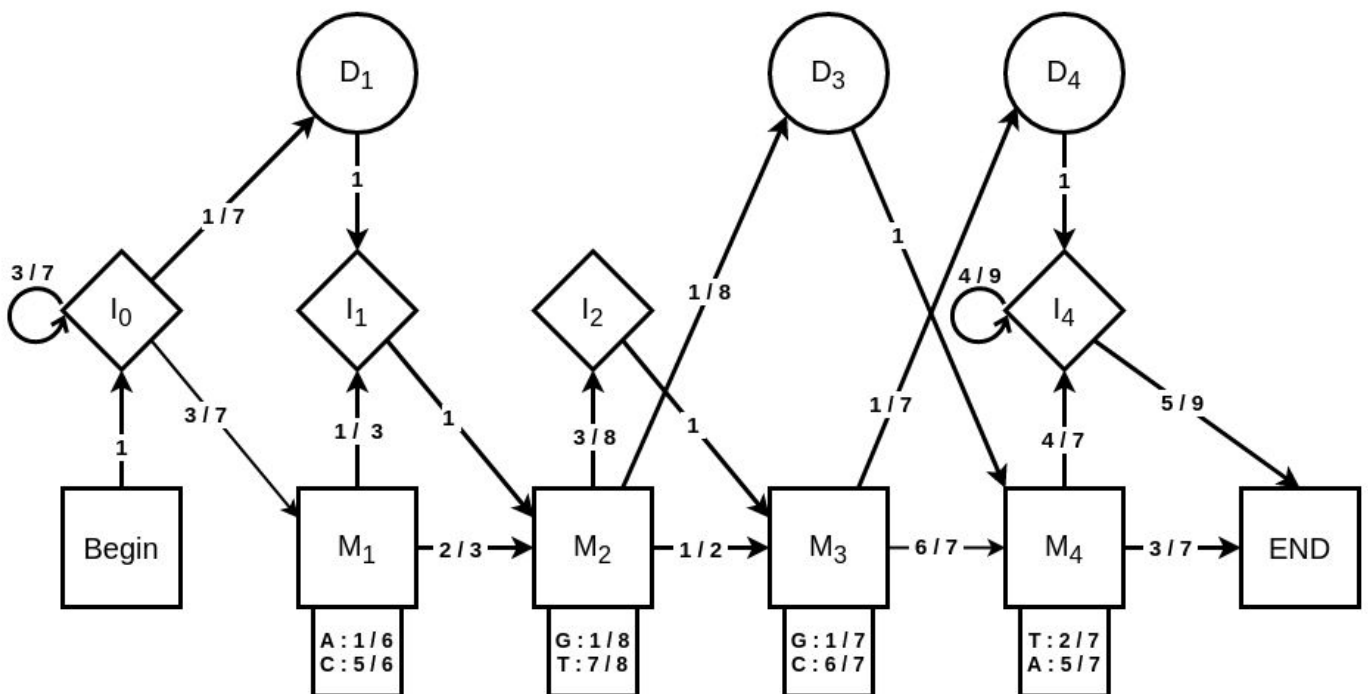


CENG 465
Introduction to Bioinformatics
Assignment #2

Part A:
The profile Hidden Markov Model (pHMM);



Part B:

Alignment of the sequence “CTCTGA” to the profile HMM using the Viterbi algorithm;

	-	C	T	C	T	G	A
Begin	1	0	0	0	0	0	0
I₀	0	0.25	2.68 E-2	2.87 E-3	3.08 E-4	3.3 E-5	3.54 E-6
I₁	0	0	8.93 E-3	9.58 E-4	7.98 E-4	1.1 E-5	1.18 E-6
I₂	0	0	0	0	0	5.23 E-4	9.36 E-6
I₄	0	0	0	0	0	0	1.43 E-5
D₁	0	3.57 E-2	3.83 E-3	4.10 E-4	4.4 E-5	4.71 E-6	5.06 E-7
D₃	0	0	0	0	6.98 E-4	1.25 E-5	0
D₄	0	0	0	0	0	5.7 E-5	0
M₁	0	0	0	9.57 E-3	0	0	2.36 E-6
M₂	0	0	0	0	5.58 E-3	9.98 E-5	0
M₃	0	0	0	0	0	3.99 E-4	0
M₄	0	0	0	0	0	0	2.44 E-4
End	0	0	0	0	0	0	1.05 E-4

Best Path is;

Begin -> I₀ -> I₀ -> M₁-> M₂ -> M₃ -> M₄ -> End

the probability associated with the best path is 1.05E-4.