## **EX2 Report – Shon Cohen**

1. Viterbi algorithm with first sequence from yeastGenes.fasta and p = 0.003. We can see 13 appearances of the motif.

 

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- 2. **Forward algorithm** the log likelihood of the first sequence in yeastGenes.fasta: -869.610408405
- **3. Posterior decoding** vs Viterbi:

 

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4. Motif learning: as we can see, the model converged successfully.

