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GEOMETRIC PATTERN OF DNA HELP IN SIGNAL PROCESSING BY USING (HMM) MODEL

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DNA sequences can be thought of as a long series of letters, four for DNA and twenty for amino acids. Aligning sequences to detect similarities is useful for finding patterns. Common patterns might give insights to common functionality of the sequences, assuming that the important functions were preserved in the genes. We introduce the alignment problem in the context of two sequences and extend to multiple sequence alignment. Three standard approaches are reviewed, comprising clustering techniques, multinomial models using sampling, and Hidden Markov Models (HMM). Deoxyribonucleic acid can be applied in signal processing that changed the way of nano –engineers. We report a new technique for measuring these rates using hidden Markov model analysis that directly incorporates the signal processing.