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## Abstract

Recent developments in the area of genomic signal processing (GSP) reveal that this approach has important role in the analysis of genomic sequence, structure and function as well as the gene regulation of different organisms. In this paper we analyze different genomic signal processing methods used for identification of exon coding regions in DNA sequence. The gene sequences of interest are mapped to electron ion interaction potential (EIIP) values of nucleotides and these transformed numerical gene sequences are processed through different signal processing techniques like discrete Fourier transform (DFT), auto regressive (AR) and adaptive auto regressive (AAR) methods. The performance evaluation in terms of computational time is estimated and analyzed. By applying the EIIP mapped sequence to these DFT, AR and AAR methods, the effective computational time is abruptly reduced in AAR method compared to the DFT and AR methods. We tested five sequences of c-elegans) [AF099922], [FO080874. 2], [FO081434]), fruitfly [NM_170135] & homosapien (BDNF [NG_011794]).

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## Index Terms

Computer Science

Signal Processing

## Keywords

Genomic Signal Processing (GSP)   EIIP   DFT   AR and AAR