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]).
Computational Study and Performance Evaluation of Different Genomic Signal Processing Methods for Identification of Protein Coding Regions (Exon Regions) of DNA Sequence

- Achuthsankar S. Nair, Sivarama Pillai Sreenadhan A coding measure scheme employing electron-ion interaction pseudopotential (EIIP), ISSN 0973-2063,2006, Bioinformation.
- Sitanshu Sekhar Sahu, Ganapati Panda, An efficient signal processing approach in eukaryotic gene prediction. Vol. 1-2010/Iss. 2, pp. 75-79, IJSIP
- T. K. Attwood and D. J. Parry-Smith, An Introduction to Bioinformatics, Addison Wesley Longman
- David W. Mount, Introduction to Bioinformatics, Cold Spring Harbor Press.
- Vinay K. Ingle, John G. Proakis, Digital Signal Processing Using MATLAB.

Index Terms
Keywords
Genomic Signal Processing (GSP)  EIIP  DFT  AR and AAR