Abstract

Diverse high throughput genomic data is available in public domain. However, no single source data analysis technique is available even today which can fully reveal the function of genes. Therefore fusion of multiple data source using Bayesian algorithm is proposed here for prediction of genes. Amino acids sequence of proastate, colon, breast, gastric genes from National Health Informatics site are taken as source data for prediction. The spectrum of genes is fused successfully using Bayesian algorithm to screen out cancer gene from healthy gene and validated the approach with the existing DSP based prediction method.
Bayesian Fusion in Cancer Gene Prediction

References

- S. Achuthsankar Nair and S. Pillai Sreenadhan, "A coding measure scheme employing electron-ion interaction pseudopotential (EIIP)", ISSN 0973-2063, Bioinformation 1(6): pp. 197-202

**Index Terms**

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**Keywords**

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