



RESEARCH ARTICLE

HYBRID ENSEMBLE GENE SELECTION ALGORITHM FOR IDENTIFYING BIOMARKERS FROM BREAST CANCER GENE EXPRESSION PROFILES

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ABSTRACT

Breast cancer is one of the major health hazard in the world. DNA gene expression profiles plays an important role in identifying the biomarkers for cancer which not only help in accurate diagnosis of the disease, also in discovering drugs, minimizing the toxicity thus help in the effective management of the disease. In this paper we propose an algorithm for determining the biomarkers. Our hybrid ensemble gene selection algorithm was experimented over breast cancer gene expression data of 24481 genes. The algorithm selected a marker gene subset of eight genes with an accuracy and BER of 96.9% and 0.033 respectively.

Keywords: Ada boost; Correlated feature selection; Filters; Gene expression profiles; Sequential floating search algorithms; Support vector machines; Wrappers

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