

An Improved Particle Swarm Optimization to detect the SNP Barcode for Breast Cancer Prediction

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Abstract

The analyses of disease-associated polymorphisms by genome-wide association are important studies for the detection of influences upon their interaction with other genetic factors. The gene can be examined in isolation without allowing potential interactions with other unknown factors, which might result in neglect of some disease influences. Single nucleotide polymorphism (SNP) barcodes can be applied for disease prediction and allow the detection of these influences. The particle swarm optimization (PSO) has been applied to detect the SNP barcode; however, PSO may fault to result in the non-significant SNP barcode. In this study, an improved PSO algorithm was introduced to detect the significant SNP barcodes for breast cancer prediction. A chaotic theory was applied to improve the PSO for finding the good SNP barcodes. The breast cancer datasets were simulated by using the genotype frequencies as described in the literature from steroid hormones and their signalling and metabolic pathways (96 SNPs for 8 genes) in the breast cancer association study. Two methods were used to compare with our method on finding the significant SNP barcode. Our study showed that improved PSO was robust to provide exact detection of the significant protective SNP barcode in breast cancer.

Key words: Particle swarm optimization, SNP barcode, Disease analysis.