Title:A modified binary particle swarm optimization for selecting the small subset
of informative genes from gene expression data

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Abstract: Gene expression data are expected to be of significant help in the development of efficient cancer diagnoses and classification platforms. In order to select a small subset of informative genes from the data for cancer classification, recently, many researchers are analyzing gene expression data using various computational intelligence methods. However, due to the small number of samples compared to the huge number of genes (high dimension), irrelevant genes, and noisy genes, many of the computational methods face difficulties to select the small subset. Thus, we propose an improved (modified) binary particle swarm optimization to select the small subset of informative genes that is relevant for the cancer classification. In this proposed method, we introduce particles' speed for giving the rate at which a particle changes its position, and we propose a rule for updating particle's positions. By performing experiments on ten different gene expression datasets, we have found that the performance of the proposed method is superior to other previous related works, including the conventional version of bi- nary particle swarm optimization (BPSO) in terms of classification accuracy and the number of selected genes. The proposed method also produces lower running times compared to BPSO