Abstract

In the field of health DNA microarrays are widely used to predict cancer, in which cancer cells can experience abnormalities in expressing their genes. This DNA microarray makes it possible to determine the stages of development of cancer cells by looking at the level of gene expression. Analysis of gene expression data in the form of microarrays can facilitate medical experts in detecting and diagnosing whether a person has cancer or not. Microarray data itself has large dimensions so that it can affect the process and classification accuracy. Therefore, to do the classification process in microarray data, it is necessary to do a process that is dimension reduction. This dimension reduction aims to reduce redundancy and increase the relevance of the data owned. In this case, the author uses the Minimum Reduction Maximum Relevance (MRMR) method which is optimized using the Genetic Algorithm (GA) method. In short MRMR is a technique used to identify a set of genes that has high relevance to class attributes but has low redundancy between attributes. MRMR seeks to overcome this problem by removing the subset of attributes that are considered unnecessary. Then the Functional Link Neural Network (FLNN) algorithm with Legendre Polynomial base is used for the classification process in microarray data. In the GA MRMR test with the Functional Link Neural Network (FLNN) classification we found an increase in the accuracy of the Colon Tumor data of 5.55% - 16.66%, in the Lung data of 2.78 - 5.56% and in the Ovarian data of 2 % - 2.67%.