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ANALYSIS OF BIPOLAR DISORDER GENOMIC DATA TO IDENTIFY DIFFERENCES IN GENE EXPRESSION

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The main focus of the paper is the problem of correct diagnosis of bipolar disorder based on differences in gene expression present in peripheral blood leukocytes. The work was aimed at finding biomarkers that could facilitate the process of diagnosing bipolar disorder. For this purpose, data obtained from Affymetrix microarrays were analyzed. The methodology (Fig. 1) of the work involved pre-processing of the microarray data obtained from 54 patients and then performing a statistical analysis. The obtained statistically significant genes were described and compared with literature sources. The next step included hierarchical clustering and the k-means clustering methods, as well as classification using the support vector machine and linear discriminant analysis. Research has shown that some of the identified genes have been linked to bipolar disorder in literature sources. Comparing the methods used, it can be concluded that the clustering methods turned out to be more suitable for the analyzed case than the classification methods.

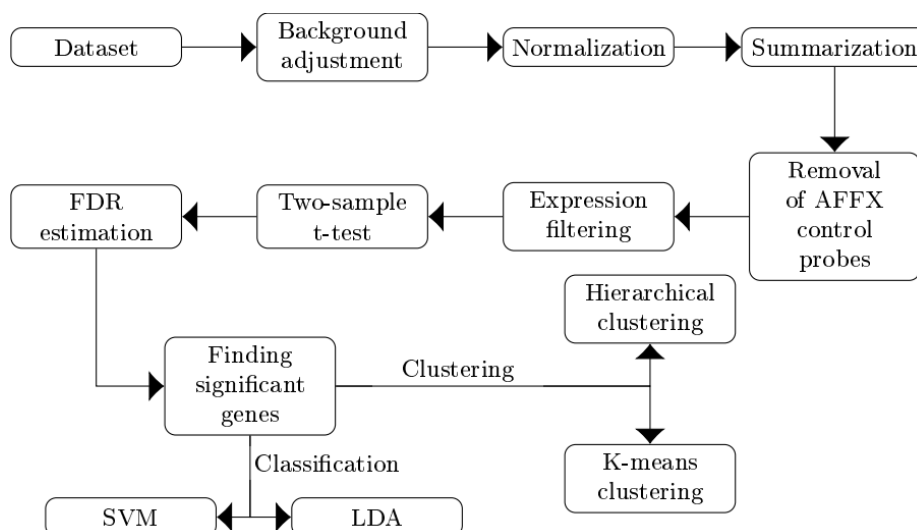


Fig. 1. The flowchart of the algorithm used in the study.