

Identification of miRNA Biomarkers for Inflammatory Bowel Disease Using a Machine Learning Approach

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Background:

The integration of bioinformatics, machine learning, and molecular biology enables the identification of biomarkers for disease diagnosis and prognosis. We present a work focused on Inflammatory Bowel Disease (IBD), characterized by variable clinical manifestations and associations with epigenetic molecules, such as microRNAs.

Methods and Results:

This work aims to use supervised machine learning to identify biomarkers for early prediction and diagnosis of IBD. We collected microarray datasets from the Gene Expression Omnibus, including miRNA profiles from patients with Ulcerative Colitis, Crohn's Disease, and healthy controls. An initial statistical analysis identified differentially expressed miRNAs. Various classification models—Logistic Regression, Support Vector Machines, Random Forest, and Extreme Gradient Boosting—will be evaluated using several classification metrics. SHAP analysis will be used to study the miRNA's influence on patient stratification, while enrichment analysis will connect findings to biological mechanisms related to inflammation and oxidative stress.

Conclusions and Significance:

This study showcases machine learning's potential in discovering biomarkers for IBD. By identifying predictive miRNAs, we aim to enhance patient diagnosis, stratification and management. Insights from SHAP and enrichment analyses will deepen our understanding of biological mechanisms and support the development of targeted therapies to improve patient outcomes.

Keywords:

Biomarkers, Inflammatory Bowel Disease, Machine Learning, MicroRNAs, Patient Stratification.

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