

## **Abstract**

Ulcerative colitis (UC) is an inflammatory bowel disease in humans resulting from the improper activation of the intestinal mucosa, which is triggered by a combination of genetic, immunological, and environmental factors. Unfortunately, despite the availability of numerous therapeutic alternatives depending on the severity of the disease, UC is still considered an incurable condition. According to the United States Census data in 2016, an estimated 451,776 adults in the United States were living with ulcerative colitis. The diagnosis of UC is made through clinical symptoms along with stool examination, colonoscopy, and biopsy to confirm colitis and rule out infection. However, early detection with endoscopy and histology does not always accurately diagnose ulcerative colitis. Therefore, one alternative method that can be used to detect ulcerative colitis is by implementing machine learning on gene expression data. This study aims to identify features in the design of a predictive model for ulcerative colitis using the cuckoo search algorithm and support vector machine method, with gene expression data as its basis. To enhance the model's results, hyperparameter tuning was used with three kernels, i.e. RBF, polynomial, and linear. Based on our results, the performance of the SVM method with a Polynomial kernel was the best, achieving an accuracy of 0.78 and an F1 score of 0.82.

**Keywords:** Ulcerative colitis, Microarray, SVM, Cuckoo Search Algorithm

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