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An Early Stage Determination of Colon Cancer Through Deep Neural Network

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Abstract



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- I. Introduction
- II. Related Work
- III. Materials and Methods
- IV. Research Methodology
- V. Experimental Analysis

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Abstract:

Identification and prediction of Colon cancer have always been difficult and essential tasks for medical professionals. Hospitals are providing costly therapies and operations to treat the illness. So, diagnosing colon cancer at an early stage will be helpful to patients around the world. Currently, the recent improvements in medical technologies, Deep Learning techniques exhibit a major role in predicting the development of colon cancer. In this research work, the risk factors that produce colon cancer-causing genes are selected using feature selection methods such as Fisher Score Univariate Filter (FSUF) and ReliefF Multiclass Filter (RFMF), which are applied separately and integrate the selected prominent genes to minimize the dimensionality of the data. To predict colon cancer, Deep Neural Network (DNN) classifier is utilized on the reduced data and computes the classifier's performance using evaluation metrics. Finally, the outcomes of experiments are compared with two machine learning algorithms, like Independence Bayes (IB) classification model and the k-nearest neighbors (k-NN) classifier. The experimental outcomes demonstrate that the research model significantly reduces the dimension of data space and produced an accurate prediction of colon cancer when compared with other classifiers.

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☰ Contents

I. Introduction

Colon cancer is a specific type of cancer that develops in the large intestine part and represents one of the most deadly diseases among all age groups. But the progression of the disease can be reduced by proper treatment during the early stages. Global Cancer Observatory (GCO) Database 2022 examined new 1,931,590 colon cancer patients and 935,173 colon related deaths. In the human body, colon cancer develops as a result of variations in DNA within the cells that may have an impact on oncogenes and tumor suppressor genes, triggering numerous mutations in genes that may result in the colon. High-dimensional gene data based on microarray technology are primarily utilized in the analysis and detection of colon disease. [1]. In the cancer dataset, the values of the expression of genes are arranged in a matrix form, where the rows relate to the patient sample instance and the columns to different genes [2]. The gene dataset contains an excessive number of genes and relatively few samples, plenty of genes are redundant and noisy. The values in the dataset are real numbers and describe the levels of gene expression. Due to the curse of high dimensionality, attribute subset selection techniques are employed to select significant genes that cause colon cancer and to improve the accuracy of the classification task.

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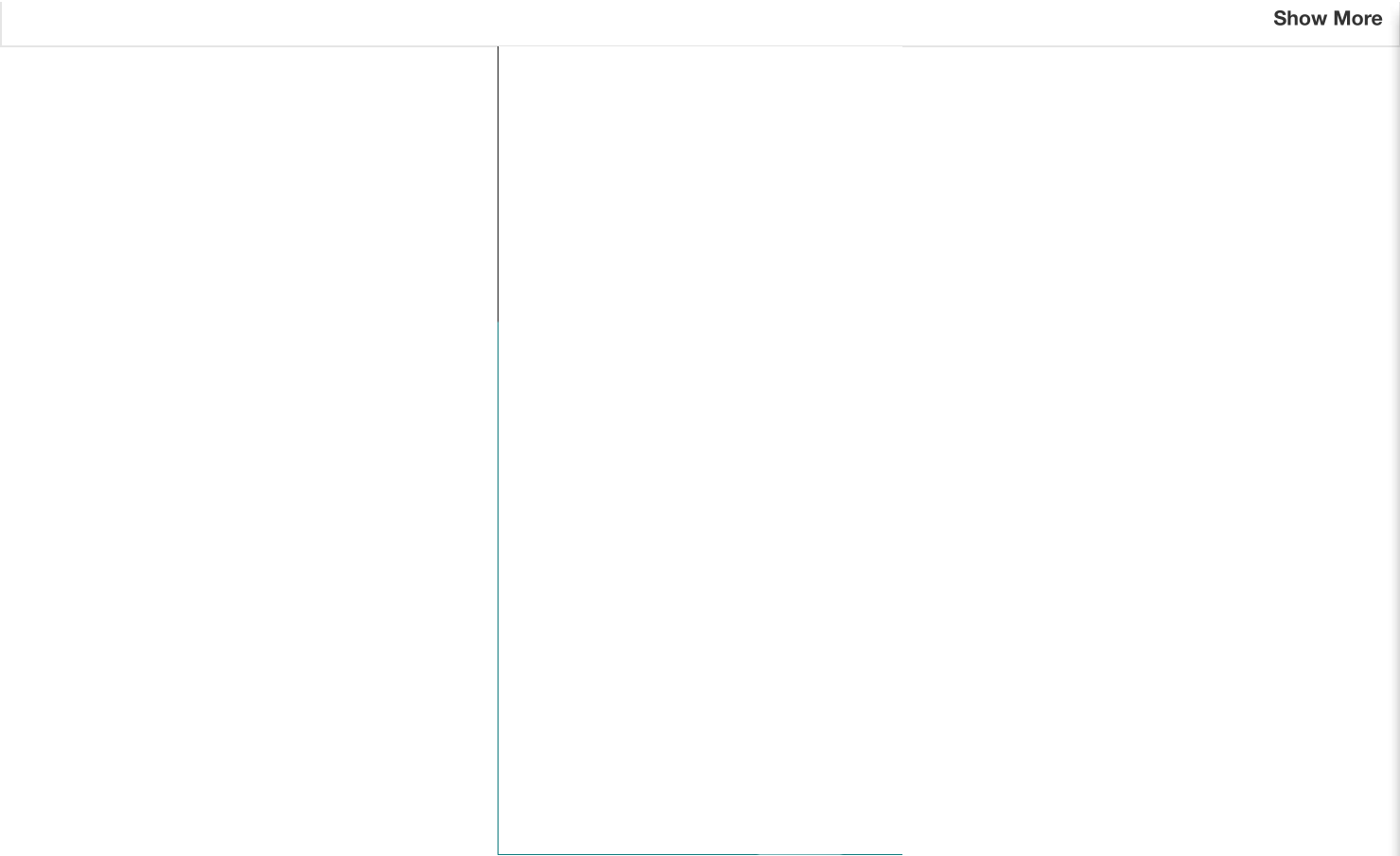
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