Developing a Comprehensive AI-Driven Decision Support System for Colorectal Cancer: Integration of Mutation Data and Web Application Implementation

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Abstract:

Colorectal cancer (CRC) is a prevalent malignancy, and early diagnosis is crucial for improving patient outcomes. With advancements in sequencing technologies, exome datasets now allow for the comprehensive analysis of genetic mutations associated with CRC. In this study, we utilize 25 colorectal cancer exome datasets containing somatic and germline mutations, categorized as either benign or malignant. To develop a decision support system (DSS) for CRC, we explore the use of various Artificial Intelligence (AI) and Machine Learning (ML) algorithms to analyze these mutations and predict the likelihood of malignancy.

Our approach begins with data preprocessing to clean and standardize the mutation data, followed by feature selection to identify key mutations/genes associated with CRC. We then implement supervised machine learning techniques such as decision trees, random forests, and support vector machines (SVM), which are known for their interpretability and effectiveness in classification problems. Additionally, we explore deep learning methods like artificial neural networks (ANNs) for more complex data patterns. These models are trained using labeled benign and malignant mutation data and validated through cross-validation techniques to assess their performance.

Once the optimal model is selected, we develop a web-based application to make the DSS accessible to clinicians. The web app integrates the trained model and allows users to input new mutation data to receive predictions on the likelihood of malignancy. This DSS has the potential to assist healthcare providers in diagnosing CRC by leveraging AI/ML models for quick and accurate mutation interpretation. The user-friendly interface ensures ease of use and integration into existing clinical workflows, contributing to personalized and timely treatment decisions for CRC patients.

Keywords:

Colorectal cancer exomes, Somatic and Germline Mutations, Supervised Learning Algorithms, Cross-Validation Techniques, Artificial Neural Networks (ANNs).