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Invention Title	A NOVEL APPROACH TO DNA SEQUENCE CLASSIFICATION: MACHINE LEARNING AND PATTERN MATCHING
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Abstract:

The present invention introduces a pioneering approach to DNA sequence classification through the integration of machine learning and advanced pattern matching. The system begins by extracting informative features from DNA sequences, including nucleotide composition and structural characteristics. Utilizing a diverse set of machine learning algorithms, such as neural networks and support vector machines, the models are trained on labeled datasets to learn intricate genomic patterns. A distinctive lies in the incorporation of advanced pattern matching algorithms, ensuring precise classification through validation and refinement. The invention further adapts to genomic landscapes with an adaptive learning component, continuously updating models based on new data. Two additional embodiments, a parallel processing architecture enhanced computational efficiency and a hybrid model integration approach for increased classification accuracy, highlight the system's versatility. Overall, this innovative sequence classification system offers a comprehensive, efficient, and adaptable solution with implications for genomics, molecular biology, and various related fields

Complete Specification

Description:The present invention pertains to the field of bioinformatics and computational biology, specifically addressing the automated classification of DNA sequences. More particularly, the invention relates to a novel approach that combines machine learning techniques and advanced pattern matching algorithms for the accurate efficient categorization of DNA sequences based on their inherent biological features and characteristics. The application of this invention finds utility in various fields including genomics, molecular biology, medical diagnostics, and other disciplines reliant on the analysis and interpretation of DNA sequences.

BACKGROUND OF THE INVENTION
The following description of related art is intended to provide background information pertaining to the field of the disclosure. This section may include certain aspects the art that may be related to various features of the present disclosure. However, it should be appreciated that this section be used only to enhance the understanding the reader with respect to the present disclosure, and not as admissions of prior art.

Advancements in genomics and the rapid increase in DNA sequencing data have underscored the importance of efficient and accurate methods for classifying DNA sequences. Traditional approaches to DNA sequence classification often involve manual curation and expert analysis, which are resource-intensive, time-consuming susceptible to human error. As the volume of genomic data continues to grow exponentially, there is a pressing need for automated and scalable solutions that can large datasets while maintaining high accuracy.

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