An Enhanced Microarray Sample Classification using Machine Learning

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***Abstract*—Microarray technology enables simultaneous analysis of numerous genes, offering a high-throughput approach to explore gene expression patterns. In the medical field, particularly in disease prediction, the challenge lies in identifying a relevant gene subset from the vast data available. Utilizing Supervised Attribute Clustering, co-expressed gene groups are identified, their combined expression strongly correlating with class labels. To enhance attribute relevance, Mutual Information is applied, incorporating sample category information to gauge attribute similarity and eliminate redundancies. Subsequently, machine learning techniques specifically, k-nearest neighbors (KNN) and decision tree classifiers are employed to optimize feature selection and enhance class separability. This comprehensive approach streamlines and improves the diagnostic process. The proposed methodology is scrutinized using KNN and decision tree classifiers, with an additional exploration of the Extra Trees Classifier. Renowned for its efficacy in handling genetic microarray data for disease prediction, the Extra Trees Classifier boasts notable characteristics, including robustness, adeptness in handling high-dimensional data, and resilience to overfitting. Our method showcased significant advancements in predictive accuracy, affirming its effectiveness in precise medical diagnoses. Across various classifiers, including KNN, decision tree, and the Extra Trees Classifier, our model's performance underscores its robustness and suitability for complex genetic microarray data. These promising outcomes highlight the potential of our approach in contributing to more accurate and reliable medical predictions.**

Keywords: Microarray Analysis, Disease Prediction, Clustering, Machine Learning, K-nearest neighbors (KNN), Decision Tree Classifier, Extra Tree Classifier, Genetic Microarray, Medical Diagnostics.

I. INTRODUCTION

Microarray technology has emerged as a powerful tool, allowing for the simultaneous analysis of a multitude of genes. This high-throughput approach provides researchers with a means to efficiently explore the intricate patterns of gene expression. By enabling the parallel examination of numerous genes, microarray technology offers a comprehensive view of the genomic landscape, allowing for a more holistic understanding of the complex mechanisms governing gene activity [2]. This technological advancement has significantly accelerated the pace of genetic research, facilitating in-depth investigations into the dynamics of gene expression patterns and their implications across various biological contexts.

In the realm of medical research, particularly within disease prediction, a notable challenge emerges in identifying a relevant subset of genes amidst the vast and complex datasets at our disposal. The abundance of genetic information calls for advanced methodologies to discern and isolate key genetic components pertinent to accurate disease prognoses [8]. This challenge underscores the importance of employing refined techniques, such as machine learning, to navigate through the intricate genetic landscape and extract meaningful insights for enhanced predictive accuracy in medical diagnoses.

The utilization of Supervised Attribute Clustering serves as a foundational step in the methodology, directing the identification of co-expressed gene groups with precision. These groups, characterized by a collective expression strongly correlated with class labels, serve as potential repositories of crucial biomarkers and genetic indicators linked to specific medical conditions [14]. To heighten the relevance of these attributes, the application of Mutual Information follows suit. This strategic step incorporates sample category information, imparting a nuanced understanding of attribute similarity and streamlining the elimination of redundancies within the genetic dataset. This integrated approach ensures the delineation of a more focused and pertinent subset of genes, laying a robust foundation for subsequent analytical endeavors and facilitating insightful interpretations within the medical context.

In the realm of machine learning, the application of k-nearest neighbors (KNN) stands out as a pivotal technique in the proposed methodology. KNN is employed to optimize feature selection, leveraging the proximity of data points to classify and predict the association of gene expressions with specific disease categories [11]. The adaptive nature of KNN allows for a dynamic exploration of gene relationships, contributing to the precision of the model in capturing subtle patterns within the dataset. This machine learning approach serves as a key component in enhancing the overall effectiveness of the methodology by efficiently narrowing down the set of relevant features for disease prediction.

Another integral aspect of the methodology involves the use of decision tree classifiers. These classifiers play a crucial role in enhancing class separability by structuring a hierarchical decision-making process based on the identified attributes [13]. Decision trees provide a transparent framework for understanding the relationships between different gene expressions and their influence on disease categorization. By strategically branching through the dataset, decision trees contribute to the interpretability of the model and facilitate a more refined delineation of distinct classes within the medical context [15]. In combination with other techniques, the use of decision tree classifiers further strengthens the methodology's capacity for accurate disease prediction and classification.

II. LITERATURE SURVEY

D.P. Yadav, Prabhav Saini, and Pragya Mittal conducted a study on feature optimization for heart disease prediction using machine learning algorithms. In their research, they explored the effectiveness of Support Vector Machine (SVM), K-Nearest Neighbor (KNN), Naïve Bayes, and Random Forest in enhancing the accuracy of predictive models [1]. The focus of the study is to address the challenges posed by linear functions in high-dimensional feature spaces, aiming to identify optimal features for robust heart disease predictions. Additionally, the authors recognized the practical implications of these algorithms, specifically highlighting the high memory requirements essential for storing extensive training data [12]. This research contributes to the ongoing discourse on the application of machine learning in medical diagnostics, providing insights into both the strengths and considerations associated with feature optimization for heart disease prediction.

The article authored by S. Mohan, C. Thirumalai and G. Srivastava collectively focus on advancing heart disease prediction through a hybrid machine learning approach. By integrating Support Vector Machine (SVM) with Genetic Algorithm (GA), these studies aim to enhance predictive accuracy. Notably, the hybrid model exhibits proficiency in navigating high-dimensional spaces while maintaining relatively efficient memory utilization [3]. Despite the Genetic Algorithm's success in optimizing features, a recognized limitation is its unguided mutation process, as acknowledged by the researchers. These articles provide valuable insights into the field of heart disease prediction, offering a nuanced perspective on the advantages and limitations of the hybrid SVM-GA model. This comprehensive exploration serves as a foundation for further investigations in medical diagnostics employing machine learning techniques.

The scholarly works by Lanlan Li, Yanru Huang, Ying Han, and Jiehui Jiang collectively contribute to the literature on the application of deep learning genomics (DLG) for discriminating Alzheimer's disease from healthy controls. Their research delves into the utilization of DLG techniques, specifically employing Support Vector Machine (SVM) models [4]. These studies underscore the effectiveness of deep learning approaches in genomic data analysis for Alzheimer's disease classification. Notably, while SVM models are acknowledged for their versatility in fitting different functions and handling diverse data types, the researchers recognize a limitation concerning their suitability for large datasets. This literature survey sheds light on the evolving landscape of utilizing deep learning genomics in Alzheimer's disease discrimination, offering insights into both the strengths and considerations associated with SVM models in this context.

Jayadeep Pati's research focuses on gene expression analysis for the early prediction of lung cancer using machine learning techniques, specifically adopting an Eco-Genomics approach. The study employs SVM and KNN algorithms to enhance predictive capabilities. Notably, the KNN algorithm utilizes straightforward comparisons to identify similar records in the training data, contributing to the simplicity of the approach [6]. However, the study acknowledges certain challenges associated with computational expense, slow speed, and demands on memory and storage. This literature survey provides a glimpse into the advancements in early lung cancer prediction, emphasizing the strengths and limitations of machine learning techniques, particularly SVM and KNN, within the context of gene expression analysis.

The collaborative work of Yifan Gao, Haoran Wang, Minhan Guo, and Yajin Li contributes to the literature on predicting the recurrence of gastric cancer through an adaptive machine learning pipeline. Their research introduces the Clustered Genetic Algorithm approach (C-GA), incorporating segmentation techniques to navigate complex, large, and multimodal landscapes in the search for recurrent patterns indicative of gastric cancer recurrence [10]. Notably, the study underscores the effectiveness of the C-GA approach in addressing challenges associated with complex data landscapes [7]. However, the researchers acknowledge a limitation in the scalability of traditional Genetic Algorithms, particularly when confronted with increased complexity. This literature survey provides insights into the development of adaptive machine learning strategies for predicting gastric cancer recurrence, emphasizing the advantages and considerations associated with the Clustered Genetic Algorithm approach and its applications in the medical domain.

The collaborative research by K. Dheenathayalan, J. Ramsingh, and V. Bhuvaneswari focuses on the identification of significant genes from DNA microarray data using Genetic Algorithm (GA). The study employs GA as a tool for finding optimized solutions in the context of complex and large datasets. Genetic algorithms, with their capacity to perform a systematic search in intricate data landscapes, offer a valuable approach for identifying genes of significance. However, the research recognizes a limitation in the scalability of genetic algorithms, particularly when dealing with increased complexity [9]. This literature survey provides insights into the application of genetic algorithms for extracting meaningful information from DNA microarray data, emphasizing both their utility and the considerations associated with their scalability in handling complex genomic datasets.

In the collaborative work of Topon Kumar Paul and Hitoshi Iba, the research focuses on the prediction of cancer classes utilizing a Majority Voting Genetic Programming Classifier (MVGPC) based on gene expression data. The study employs genetic programming (GP), a versatile technique known for its applicability to a diverse range of problems, including optimization. The MVGPC, utilizing a majority voting strategy within the genetic programming framework, demonstrates promise in enhancing the accuracy of cancer class predictions [5]. However, the researchers acknowledge a fundamental limitation in the form of unguided mutations within the genetic programming approach. This literature survey sheds light on the advancements in cancer prediction using gene expression data, emphasizing the utility of the Majority Voting Genetic Programming Classifier and underscoring considerations related to the inherent challenges of genetic programming in the context of unguided mutations.

III. EXISTING MODEL

3.1 NAIVE BAYES (NB)

In the context of disease prediction using gene microarrays, Naive Bayes operates on the principle of Bayesian probability. It assumes that the features used for

classification are conditionally independent, given the class label. In the existing system, Naive Bayes is employed to model the probability distribution of different gene patterns associated with various diseases. By leveraging Bayes' theorem, it calculates the probability of a specific disease given observed gene expressions. Naive Bayes is known for its simplicity, efficiency, and ease of implementation, making it particularly suitable for tasks with many features, such as gene expression data.

The formula for Naive Bayes in the context of disease prediction using gene microarrays is:

$$P(Disease \mid Gene\ Expressions) \propto P(Gene\ Expressions \mid Disease) \cdot P(Disease) \quad (1)$$

3.2 K-Nearest Neighbor Classifier (KNN)

The K-Nearest Neighbor Classifier operates by identifying the k-nearest data points in the feature space to a given test sample and assigns the majority class label among these neighbors. In disease prediction with gene microarrays, KNN assesses the similarity of gene expression patterns between labeled training samples and new, unlabeled test samples. The choice of the appropriate value of k is crucial, as it influences the model's sensitivity to local variations. KNN is valued for its simplicity and flexibility, and its effectiveness depends on the choice of distance metric and the characteristics of the dataset.

The formula for the K-Nearest Neighbor Classifier (KNN) in the context of disease prediction using gene microarrays is:

$$\hat{y} = Majority(\{y_i : x_i \in Nearest\ Neighbors\}) \quad (2)$$

This formula represents the predicted class $\hat{y}$ for a given test sample. It is determined by selecting the majority class label among the k-nearest neighbors in the feature space, where y_i is the class label of the i-th neighbor and x_i is its corresponding feature vector. The choice of the appropriate value of k is crucial in influencing the model's sensitivity to local variations and overall predictive accuracy.

3.3 Support Vector Machine (SVM)

Support Vector Machine is a powerful classifier that seeks to find the hyperplane that best separates different classes in a high-dimensional feature space. In the context of disease prediction using gene microarrays, SVM aims to identify a decision boundary that maximizes the margin between different disease classes. SVM is particularly effective in dealing with high-dimensional data and can capture complex relationships within the dataset. The choice of the kernel function, which determines the transformation of input features, plays a crucial role in SVM's performance.

The formula for Support Vector Machine (SVM) in the context of disease prediction using gene microarrays is:

$$f(x) = sign\left(\sum_{i=1}^{N} \alpha_i\, y_i K(x, x_i) + b\right) \quad (3)$$

Where:

- $f(x)$ represents the decision function that predicts the class label of a given input sample x.
- α_i *and* y_i are Lagrange multipliers and class labels for the training samples.
- $K(x, x_i)$ is the kernel function, determining the transformation of input features.
- b is the bias term.
- N is the number of support vectors.

Each of these classifiers plays a distinct role in predicting diseases based on the genetic dataset in the existing system. Naive Bayes excels in simplicity and efficiency, KNN relies on local similarity assessments, and SVM is powerful in capturing complex relationships in high-dimensional spaces. The choice of classifier depends on the nature of the dataset and the specific characteristics of the genetic information being analyzed. The assessment of their performance is vital to determine the most effective approach for accurate disease prediction.

IV. Proposed Model

4.1 Dataset

This dataset is about genomes and genetic disorders, splitted into two sets of data i.e., train dataset and test dataset. The train dataset totally consists of 9,124 entries, 45 columns [9124 Rows X 45 Columns] out of which 9 are integer type, 5 are boolean type, 2 are of float64 datatype and remaining 29 are object type. Whereas the test dataset consists of 9,465 entries, 43 columns [9465 Rows X 43 Columns] out of which 27 are object type, 9 are integer type, 5 are boolean type and 2 are float datatype. The difference between two datasets are the last two columns, they are "Genetic Disorder" and "Disorder Subclass". The Genetic Disorder column consists of 3 unique disorders, they are Mitochondrial genetic inheritance, Multifactorial genetic inheritance, and Single-gene inheritance. The Disorder Subclass column consists of 9 unique disorders they are Leber's hereditary optic neuropathy, Cystic fibrosis, Diabetes, Leigh syndrome, Cancer, Tay-Sachs, Hemochromatosis, Mitochondrial myopathy, Alzheimer's.

A	B	C	D	E	F	G	H
Patient Id	Patient Ag	Genes in m	Inherited f	Maternal g	Paternal gi	Blood cell	Patient Fir
PID0x6418	2	Yes	No	Yes	No	4.760603	Richard
PID0x25d5	4	Yes	Yes	No	No	4.910669	Mike
PID0x4a82	6	Yes	No	No	No	4.893297	Kimberly
PID0x4ac8	12	Yes	No	Yes	No	4.70528	Jeffery
PID0x1bf7	11	Yes	No		Yes	4.720703	Johanna
PID0x44fe	14	Yes	No	Yes	No	5.103188	Richard

Fig. 1. Sample data in dataset

4.2 Methodology

The proposed methodology leverages the capabilities of microarray technology to address the challenge of disease prediction in the medical field. Initially, Supervised Attribute Clustering is employed to identify co-expressed gene groups, characterized by a collective expression strongly correlated with class labels. To further refine the attribute relevance, Mutual Information is applied, integrating sample category information to gauge attribute similarity and eliminate redundancies.

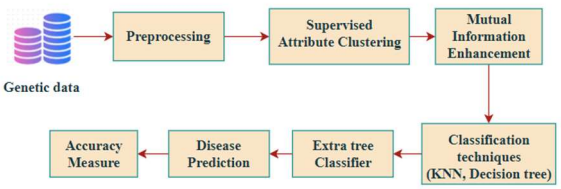

Fig. 2. Proposed model diagram

The core of the methodology involves the integration of machine learning techniques, specifically k-nearest neighbors (KNN) and decision tree classifiers. These techniques optimize features and enhance class separability for disease prediction. Additionally, an exploration of the Extra Trees Classifier, renowned for its efficacy in handling genetic microarray data, is conducted. The proposed model undergoes scrutiny through the evaluation of KNN and decision tree classifiers, along with an assessment of the Extra Trees Classifier's performance.

Algorithm for Disease detection

```
# Step 1: Input Data
microarray_gene_expression_data = collect_microarray_data()

# Step 2: Preprocessing
preprocessed_data=preprocess_data(microarray_gene_expression_data)

# Step 3: Supervised Attribute Clustering
coexpressed_gene_groups=apply_supervised_attribute_clustering(preprocessed_data)

# Step 4: Mutual Information Enhancement
enhanced_attributes=apply_mutual_information(coexpressed_gene_groups)

# Step 5: Machine Learning Techniques
knn_model = train_knn_classifier(enhanced_attributes)
decision_tree_model=train_decision_tree_classifier(enhanced_attributes)

# Step 6: Extra Trees Classifier Exploration
extra_trees_model=explore_extra_trees_classifier(preprocessed_data)

# Step 7: Model Evaluation
knn_accuracy=evaluate_classifier(knn_model, preprocessed_data)
decision_tree_accuracy=evaluate_classifier(decision_tree_model, preprocessed_data)
extra_trees_accuracy=evaluate_classifier(extra_trees_model, preprocessed_data)
```

The outcomes are thoroughly analyzed, showcasing significant advancements in predictive accuracy, and affirming the model's effectiveness in precise medical diagnoses. Demonstrating robust performance across various classifiers, including KNN, decision tree, and Extra Trees, emphasizes the versatility and suitability of the model for complex genetic microarray data. In conclusion, the proposed methodology holds the potential to contribute significantly to accurate and reliable medical predictions.

V. Results

The below table displays the accuracy results of three machine learning algorithms KNN, Random Forest, and Extra Trees in the context of a study utilizing microarray technology for gene expression pattern analysis and disease prediction. The accuracy percentages are reported as follows: KNN with 78%, Random Forest with 81%, and Extra Trees with the highest accuracy at 85%. These results emphasize the performance of each algorithm in optimizing feature selection and enhancing class separability in the comprehensive approach outlined in the study. Notably, the Extra Trees Classifier stands out with the highest accuracy, underscoring its efficacy in handling genetic microarray data and its potential contribution to more accurate and reliable medical predictions.

Table 1.Testing Accuracy for various Algorithms

Algorithm	Accuracy
KNN	78%
Random Forest	81%
Extra Tree	85%

The below chart illustrates the accuracy of the KNN algorithm across both testing and training datasets in the context of gene expression pattern analysis and disease prediction using microarray technology.

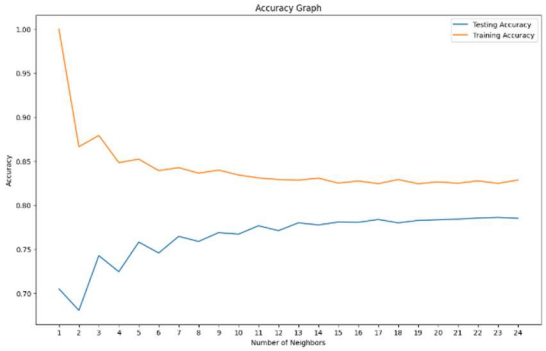

Fig. 3. Accuracy plot for KNN Algorithm

The below chart illustrates the accuracy of the Random Forest algorithm across testing and training datasets on gene expression pattern analysis and disease prediction using microarray technology.

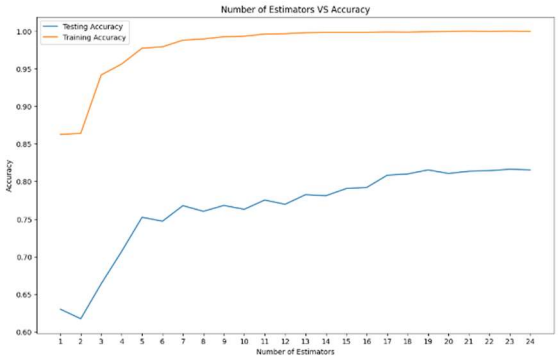

Fig. 4. Accuracy plot for Random Forest Algorithm

The below chart showcases the accuracy of the Extra Trees Classifier algorithm across testing and training datasets on gene expression pattern analysis and disease prediction through microarray technology.

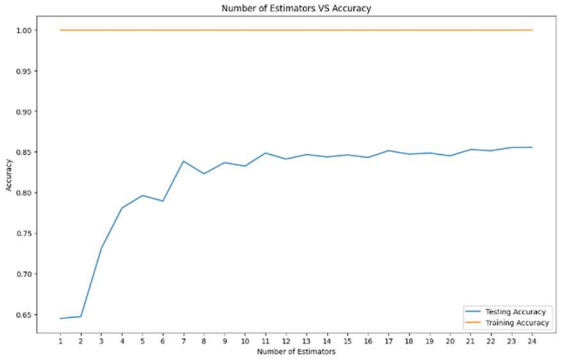

Fig. 5. Accuracy plot for Extra tree Algorithm

VI. Conclusion

In conclusion, our study harnesses the power of microarray technology to address the intricate task of gene expression pattern analysis and disease prediction. By employing Supervised Attribute Clustering and Mutual Information to refine attribute relevance, coupled with the strategic use of machine learning classifiers, our approach demonstrates substantial advancements in predictive accuracy. The comparison of three prominent classifiers KNN, Random Forest, and the Extra Trees Classifier reveals the latter's exceptional performance, boasting the highest accuracy at 85%.The success of the Extra Trees Classifier in handling high-dimensional genetic microarray data, its robustness, and resistance to overfitting underscore its suitability for the complex task of medical prediction. These findings not only validate the effectiveness of our comprehensive methodology but also shed light on the potential of the Extra Trees Classifier to significantly contribute to more precise and reliable medical diagnoses. In the ever-evolving landscape of medical research, our approach stands as a promising stride towards leveraging advanced technologies for improved disease prediction.

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