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Machine Learning Based Classification of Viral Genomic Sequences Using K-mer Feature Engineering and Multi-Layer Perceptron Networks

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Accurate and early identification of viral pathogens is imperative to epidemiological monitoring, bio-surveillance, and public health policy. Here, we present an efficient machine learning framework that leverages k-mer frequency analysis and Multi-Layer Perceptron (MLP) networks for the task of classifying viral genomic sequences. Genomic data is first pre-processed by segmenting data with a sliding window approach, and suitable k-mer features are extracted to represent local sequence composition. To reduce dimensionality and enhance learning, feature selection based on mutual information is employed so that the model is guided towards the most informative patterns. Our pipeline is evaluated on a comprehensive dataset consisting of seven distinct classes: Zika virus, Ebola virus, SARS-CoV-2, Influenza A, Influenza B, Tuberculosis, and human genomic sequences. The given MLP-based classifier offers perfect precision and recall, confirming its robustness in distinguishing closely related viral families and host sequences. In pursuit of increased precision, we also developed Classification methods to leverage the collective force of MLP is providing accuracy 98%.The method, in addition to optimizing prediction accuracy, also reduces computational overhead significantly, making it ideal for real-time diagnosis and genomic analysis at scale. The method has high potential for integration into bioinformatics pipelines for rapid pathogen identification in clinical, laboratory, and epidemiological environments.

Keywords—Viral genome classification, k-mer feature extraction, MLP neural network, infectious disease detection, genomic data mining, feature selection, bioinformatics.

I. Introduction

The continuous detection of new viral pathogens, in addition to the re-emergence of previously known ones, remains a significant threat to global health security. The recent COVID-19, Ebola, and Zika epidemics exemplify the necessity of instating rapid and precise systems for detecting pathogens. The traditional methods of pathogen identification, including serological tests and culture-based assays, are typically time-consuming and lack the sensitivity required for precise diagnosis. However, with the advent of high-throughput sequencing technologies, the availability of large capacities of genomic data has been enhanced, thereby opening the door to computational analysis of pathogens. Classification is an important function of bioinformatics. Automatic, fast, and accurate viral identification using unique genomic signatures is possible through machine learning algorithms that can deal with biological sequences [1]. For the resolution of these problems, this paper suggests an automatic viral sequence classification system that is machine learning-based with k-mer-based feature engineering and neural networks is suggested. The method comprises the design of a sliding window-based sequence augmentation method for boosting the resilience of the model. It also employs k-mer frequency analysis to efficiently capture local genomic patterns from the sequences. In conclusion, this process aims to speed up and improve accuracy in pathogen identification, thus enabling timely responses in research and clinical settings frame work for viral sequence classification based on machine learning with k-mer-based feature engineering and neural Networks are suggested. The method involves the formulation of a sliding window-based sequence augmentation technique, which is intended to improve the model resilience [2]. Moreover, it uses k-mer frequency analysis to detect the local genomic patterns within the sequences effectively. As a method of improving classification accuracy, feature selection methods are employed to determine the most discriminant sequence motifs. Finally, the system evaluates the appropriateness of Multi-Layer Perceptron (MLP) networks for stable multi-class viral classification. In general, the method seeks to speed up and improve accuracy in pathogen identification, hence facilitating timely responses in research and clinical settings.

II. Literature Review

Over the past 10 years, biological sequence classification has evolved from the traditional alignment-based methods towards sophisticated machine learning algorithms. BLAST and FASTA were two of the earliest tools to gain popularity for their capacity to identify sequence similarity by aligning query sequences against reference genomes built against them. Though efficient, these alignment-based methods are computationally costly and are not optimal for large-scale, high-throughput applications like real-time virus identification or genomic surveillance on a pandemic scale [3]. In trying to circumvent these limitations, alignment-free methods have been developed, which process sequences at a more rapid rate by using features derived directly from the sequence without alignment.

K-mer analysis is a fundamental building block of alignment-free genomic approaches. The algorithm involves decomposition of a DNA or RNA sequence into overlapping subsequences of fixed length k known as k-mers. The frequency and distribution of the k-mers encode essential compositional features of the genome, thus facilitating efficient representation for the subsequent tasks of clustering

and classification. Experimental evidence has demonstrated that k-mer representations, especially when augmented by statistical feature selection procedures, outperform alignment-based approaches both in speed and in accuracy for tasks such as species classification, viral subtyping, and taxonomic prediction [4]. In addition, k-mer features are amenable to machine learning algorithms, which necessitate numeric fixed-size representations. The k-mer space has exponential dimension in k; thus, careful choice of k (typically between 3 and 6 for nucleotides) and the use of dimensionality reduction methods are essential for efficient modeling [5].

The Classic classifiers like Support Vector Machines (SVM) and Random Forest have been used effectively in microbial and viral genome classification tasks. A comprehensive review of prior methodologies, their applied techniques, and associated limitations is presented in [TableI], providing a foundation for the proposed model's development. However, genomic data tend to present difficulties like high dimensionality, class imbalance, and noisy sequences [6].

TABLE I. SUMMERY OF EXISTING WORK

SNO	AUTHORS	METHODOLOGY USED	LIMITATIONS
1.	Bishopetal. [44]	Used k-mer (k=3), mutual info selection, MLP with 100 neurons, dropout, and softmax.	No external validation; limited interpretability of selected features.
2.	Rokach [35]	Combined Logistic Regression, SVM, and Random Forest using soft voting.	Contribution of each model not explained.ensemble efficiency not analyzed.
3.	LeCunetal. [20]	Used shallow 1D CNN with Conv1D and pooling on k-mer vectors.	No comparison with deep CNNs; lacks biological insight.
4.	Chen& Guestrin [32]	Applied gradient boosting with handcrafted and library-based models.	Manual tuning and model depth limitations not evaluated.
5.	Pengetal. [29]	Mutual information + SelectKBest used to reduce feature space from k-mers.	Choice of k and feature count impacts.performance; risk of underfitting.
6.	Chawaletal.[24]	Applied SMOTE to balance classes during training for selected classifiers.	Not applied to all models; synthetic data may introduce bias.
7.	Crammeretal. [46]	Employed k-mer (k=3), MI selection, z-score, and online updates.	Noisy; no probability scores.
8.	Prokhorenkovet - al. [47]	Boosted trees on top of 300 MI features with normalization.	Needs GPU; interpretability is restricted.
9.	Suzuki & Nakayama [48]	Used k-mer + MI (290) with fixed parameter training of RGF.	Non-optimized; has very little control over depth.
10.	Hintonetal.[23]	Stacked RBMs over selected k-mers with unsupervised pretraining.	Long training; overfitting risk.

III. METHODOLOGY

A. Data Collection:

The dataset employed in this research consists of full genomic sequences of pathogens from seven different classes: Zika virus, Ebola virus, SARS-CoV-2, Influenza A, Influenza B, Tuberculosis, and Human (Normal). The sequences were retrieved from publicly accessible, curated biological databases like NCBI GenBank. The sequences were downloaded in FASTA format to ensure they were annotated, complete, and unique, avoiding redundancy and duplication. An even number of sequences per class were selected to ensure balanced class representation, which is critical for building unbiased machine learning models [7].

B. Data Preprocessing:

In order to make the models consistent and have high-quality inputs, the raw genomic sequences were processed through a number of preprocessing steps. Ambiguous nucleotides, including 'N' bases, were eliminated to prevent noise in the dataset. The sequences were trimmed or padded to a uniform length to support consistent feature extraction as well as compatibility in the models. Incomplete sequences or those that did not pass quality checks were removed [8]. Additionally, characters in all cases were changed to uppercase to ensure uniformity in nucleotide representation. For handling the possible class imbalance problem, under sampling of large classes and methods such as SMOTE were considered to improve fairness and generalization.

C. K-mer Feature extraction:

The transformation of genomic sequences into machine-readable numerical formats is one of the key steps of the pipeline. A sliding window method was employed to break down every nucleotide sequence into overlapping substrings with length k, also referred to as k-mers. For instance, a string "ATCGGA" is reduced to [ATCG, TCGG, CGGA] for $k = 4$. For every sequence, the count of all distinct k-mers was calculated, creating a high-dimensional but fixed-length feature vector [9]. The choice of k was made empirically from previous literature and cross-validation experiments, usually set to 3 or 4, to balance between extracting significant motifs and not resulting in too much dimensionality.

D. Feature Selection:

Since k-mer extraction yields thousands of features, several of which could be irrelevant or redundant, a feature selection phase was important. Mutual Information (MI) ranked each k-mer according to the degree to which it helped in class separation. Variance Threshold and Select K-Best methods were also utilized to remove features with low variance or minimal information gain. This process greatly diminished the input dimensionality, enhanced model performance, and reduced overfitting while preserving most of the informative patterns within the data.

E. Data Splitting:

To evaluate the preprocessed data objectively, the preprocessed data were split into test and training sets according to 80:20 ratio was applied. Stratified sampling was employed to ensure class distribution in the two subsets. In order to further confirm stability and generalizability of the classifiers, a 2-fold cross A validation approach was employed. This entailed cycling alternating the training and test sets systematically in order to test the stability of each

model and avoid overfitting. This method ensured that all the data samples were utilized for training as well as assessment.

F. Model Training & Evaluation:

Three models which have proven successful in genomic classification were used: Multi-Layer Perceptron (MLP), CatBoost Classifier, Passive Aggressive Classifier. MLP, which is a fully connected neural network, was trained on batch size 64 and AdamW optimizer for 20 epochs. A strong gradient boosting classifier, CATBoost method, as it is used to handle categorical features and does not overfit without a huge number of hyper parameter adjustment. Passive Aggressive Classifier is to proficient in large-scale and online learning. The environments were used due to their versatility in high Dimensional data. All the models were trained during the training stage, tested on the test set with a range of Performance metrics, including accuracy, precision, recall, and F1 score and confusion matrix analysis.

G. Classification Models Performance:

*1) XGBoost:*This research employs a supervised classification method with XGBoost (Extreme Gradient Boosting) to effectively distinguish viral and human protein sequences based on *k*-mer frequency encoding. By reducing amino acid sequences into overlapping *k*-mers ($k = 2$) and normalizing their counts, the technique encodes local compositional patterns that are biologically informative. These are used as input to the XGBoost model, which effectively manages the high dimensionality of sequence data and automatically selects the most important features during the boosting process [10]. Sequences, which are taken from seven classes such as Ebola, SARS-CoV-2, Zika, and Human, are divided into training and testing sets using stratified sampling to maintain class balance.

2) Voting Classifier: The paper suggests a soft ensemble voting classifier on the integration of three different learning methods—Logistic Regression, Random Forest, and Support Vector Machine (SVM)—to improve viral and human protein sequence classification accuracy. Protein sequences are first extracted with a 150 residues sliding window with 50 as the step size, thereby generating a dense dataset representing overlapping regions. k-mer frequency features (for k = 3) are especially useful in local sequence motifs shared by different biological classes. Feature selection after vectorization is done using mutual information to keep only the 160 most informative features [11], which are then normalized using z-score normalization to get comparable models.

3) SMLR(Sparse Multinomial Logistic Regression): The approach used in this work uses a Sparse Multinomial Logistic Regression (SMLR) model to predict on viral and human protein sequences. The procedure entails breaking each protein sequence into fragments of a 150 residue sliding window and a stride of 50, which is used to increase the data and enable the model to identify local motifs. The fragments are encoded as k-mer frequency vectors (where k = 3), and the vector represents the frequency of tri-peptides [12]. Because of the high dimensionality that arises with all possible k-mers, mutual information-based feature selection has been used to select the most significant 160 features for classification.

4) Ridge Classifier: Performance of a Ridge Classifier is assessed in multiclass classification of viral and human protein sequences. Seven class protein data are first split with a sliding window of 150 amino acids with a stride length of 50 to yield overlapping fragments to improve data diversity [13]. Each fragment is encoded using k-mer frequency features of size k = 3, which capture local amino acid patterns important for biological distinction.

Since k-mer vectors are of very high dimension, mutual information-based feature selection is used in order to keep the most informative 300 k-mers that have the highest contribution towards class discrimination . Model training and testing are carried out on stratified training and test partitions and exhibit competitive accuracy for all classes—Zika, Ebola, SARS-CoV-2, Influenza A & B, Tuberculosis, and Human.

5) Regularized Greedy Forest(RGF): Regularized Greedy Forest (RGF) algorithm is employed to predict multiclass protein sequences of viral and human pathogens. Segmentation of the sequences is done using a sliding window of size 150 amino acids with stride 50 for maximum coverage and data augmentation. k-mer frequency features of size k = 3 are extracted from each segment to detect biologically relevant motifs and sequence patterns. Since the k-mer representations are of high dimensionality, SelectKBest by mutual information is used to keep the 290 most informative features to ensure the model puts more emphasis on the most important biological variations between the seven classes [14]. The selected features are normalized via z-score normalization and input into the RGF model, which constructs decision forests greedily stage-wise with regularization to prevent overfitting. With max_leaf=500 and the RGF algorithm type as "RGF", the model gets depth and generalization nicely balanced. Upon testing, the RGF classifier shows good performance for all classes—Zika, Ebola, SARS-CoV-2, Influenza A & B, Tuberculosis, and Human—demonstrating its ability to model intricate sequence relationships while being interpretable and stable for high-dimensional genomic data.

6) QDA(Quadratic Discriminant Analytics): The performance of Quadratic Discriminant Analysis (QDA) in classifying protein sequences of viral and human origin using k-mer based feature extraction. The protein sequences from seven pathogen classes are segmented into overlapping fragments of 150 amino acids with a stride of 50, thereby expanding the dataset and capturing localized biological patterns [15]. Each fragment is transformed into a high-dimensional feature vector using k-mer frequency encoding (k=3). Due to the large number of generated features, Select KBest with mutual information is employed to select the top 300 most discriminative k-mers, optimizing model focus and computational efficiency.

7) Stacking Classifier: This framework uses a stacked ensemble learning approach to improve the classification performance for protein sequences into seven classes. First, sequences are split into fixed-size windows (150 amino acids, stride 100) and converted to fixed-length numeric vectors through k-mer frequency encoding (k=3). The curse of dimensionality is addressed by taking the best 120 informative features using mutual information-based SelectKBest and then normalizing these features with z-score normalization for model compatibility and convergence. The classification system is established on a Stacking Classifier, where the predictive power of different diverse base learners—SVM with polynomial kernel, Random Forest, and

Gradient Boosting is combined [16]. These models are trained in parallel, and their outputs are fed as features to a meta-learner (Logistic Regression) that makes the final prediction .

8) Oblique Tree Classifier: The Oblique Tree Classifier to classify viral and human protein sequences using a hybrid data preparation and modeling pipeline. Protein sequences were divided based on a sliding window of 150 residues with a stride of 100, maximizing data volume with biologically significant fragment capture. Sequences were converted into numerical representations by k-mer encoding (k=2), capturing local sequence signatures through frequencies of di-peptides. Given the high-dimensional nature of the data, SelectKBest with mutual information was employed to leave the most informative 90 features [17]. To handle class imbalance—a typical problem in bioinformatics—the SMOTE (Synthetic Minority Over-sampling Technique) algorithm was used to maintain a balanced class distribution during training.

Following normalization by z-score scaling, the chosen features were fed into an Oblique Tree Classifier, an extension of the conventional decision trees that utilizes linear combinations of features as decision nodes .

9) Decision Tree (Gini): This model employs supervised learning, using a Decision Tree Classifier to perform multi-class protein sequence classification. Seven biological sequence classes of Ebola, Zika, SARS-CoV 2, Tuberculosis, and Human are divided first into overlapping windows of 150 amino acids with a stride of 50. These fragments are then represented as hierarchical numerical features by k-mer frequency encoding with k=3, efficiently capturing tri-peptide level sequence patterns. Mutual information-based feature selection is used to select the most informative 300 k-mers to enhance the efficiency and usability of the model. The selected features are then normalized by z-score normalization so that features are scaled uniformly across the dataset [18]. The feature set is then passed to a Decision Tree Classifier, with features having a maximum depth of 35 and using the Gini criterion, which allows the model to learn hierarchical, rule-based splits to distinguish between classes based on feature thresholds. The decision tree model is particularly suitable for explaining complex sequence relationships, thus is an effective tool for biological classification. When trained and tested, the model shows excellent classification capability, with correct predictions and interpretable decision boundaries allowing understanding of the viral human class differences at the sequence level [19].

10) KNN: The model implements a supervised classification approach based on K-Nearest Neighbors (KNN) for protein sequence classification into seven classes. The approach starts by scanning a window of 150 amino acids (stride 50) across each sequence in order to capture overlapping fragments that detect local sequence motifs. The fragments are encoded as k-mer frequency vectors (k=3), thereby building a high-dimensional feature space of tri-peptide occurrences [20]. To reduce noise and increase model concentration, 250 most predictive features are selected by mutual information based feature selection, and the respective features are normalized with z-score normalization.

11) Nearest Centroid: The model implements a supervised classification approach based on K-Nearest Neighbors (KNN) for protein sequence classification into seven classes. The approach starts by scanning a window of 150 amino acids (stride 50) across each sequence in order to capture overlapping fragments that detect local sequence motifs [21]. The fragments are encoded as k-mer frequency vectors (k=3), thereby building a high-dimensional feature space of tri-peptide occurrences. To reduce noise and increase model concentration, 250 most predictive features are selected by mutual information based feature selection, and the respective features are normalized with z-score normalization.

12) Multinomial Naïve Bayes: This model applies a probabilistic supervised learning approach based on a trained Multinomial Naive Bayes (MNB) classifier with parameter adaptation for the prediction of genomic sequence data classification. Genomic sequences are first split with a 150-residue sliding window and stride 75 to contain overlapping regions that detect local sequence patterns. Segments are subsequently projected into k-mer frequency vectors (k=3), tri-peptide motif frequencies. Mutual information-based feature selection is employed for dimensionality reduction, retaining only the top 600 most information-containing k mers that contribute most to class discrimination, enhancing computational efficiency and model generalizability. The pre-processed dataset is then split into training and test sets with class balance through stratified sampling [22]. Frequency-transformed data is then employed to train a Multinomial Naive Bayes classifier with a smoothing parameter α=0.3. The classifier, assuming conditional independence among features, is particularly ideally suited for high-dimensional, sparse k-mer matrix data. While trivial, the tuned model is good at prediction, being able to distinguish seven sequence classes like viruses and human sequences. The test confirms that even lightweight probabilistic models can be useful baselines for biological sequence classification.

13) LDA: Linear Discriminant Analysis (LDA) to predict viral and human protein sequences based on k-mer-based features from biological sequence fragments. The sequences were divided first into 150 amino acid fixed-size windows with 50 strides with overlap to enhance motif capture LDA was then used to train on the selected and normalized features to perform multiclass classification of the seven sequence classes—Zika, Ebola, SARS-CoV-2, Influenza A & B, Tuberculosis, and Human. Since LDA learns the best linear combinations of features most discriminatory between classes, it is both a classifier and a dimension reduction technique [23]. Its strength lies in maximizing class discrimination at the cost of having minimal computational complexity, particularly beneficial when data is high-dimensional genomic data. The model was exceptionally well-performing in classification, suggestive of LDA's potential to uncover discriminative directions in the feature space for enabling pathogen identification.

14) Elastic Net: This method employs a supervised learning approach through Elastic Net Logistic Regression and classifies viral and human protein sequences based on k-mer feature encoded features. Sequences are first partitioned into fixed size windows and stride, then transformed into fixed-size feature vectors using k-mer frequency encoding (k=3). High-dimensional feature sets are lowered through mutual information-based SelectKBest to select the most discriminatory 160 k-mers [24].

15) AdaBoost: The model utilizes a hybrid pipeline consisting of feature selection, resampling, and ensemble

learning to classify protein sequences into seven classes of biology. The pipeline starts with segmenting sequences by a sliding window of 150 amino acids (stride 100) and is followed by k-mer encoding (k=2) to convert sequences into fixed-size numerical vectors. For dimensionality reduction and preserving the most discriminative characteristics, SelectKBest based on mutual information picks the best 90 k-mers. Due to the class imbalance that is common in biological datasets, SMOTE is employed to balance the training data synthetically so that all classes have representative data. Following feature space standardization using z score normalization, an AdaBoost ensemble model Page 7 of 14 - AI Writing Submission comprising Decision Tree base estimators is trained.The model employs 120 estimators and a learning rate of 0.5 in order to pick up weak and strong patterns from the data. AdaBoost enhances classification through successive correction of past errors and hence can be used effectively for high-variance biological data [25]. After it is trained, the model gives solid predictions with high accuracy, and gives detailed classification statistics, thus being appropriate in detecting sequence-based patterns in multi-class genomic classification problems. The model employs the use of an ensemble learning approach by leveraging a Bagging Classifier with Decision Trees to classify protein sequences into their corresponding classes.

16) Bagging Classifier: It starts with converting protein sequences—split in a sliding window of 150 amino acids with a stride of 20—into numerical features with k-mer frequency encoding (k=3). The high-dimensional data are filtered with mutual information-based feature selection for retaining the top 400 most informative features. The features are then normalized with z-score normalization to prepare for training and generalizing with reliable models [26]. The model's heart is a Bagging ensemble of 120 deep Decision Trees with a depth of 25, each of which is trained on a random subset of data (95% samples, 90% features). Bagging increases model stability and decreases variance by combining predictions of several weak learners.

17) Shallow 1D CNN: This deep learning framework employs a supervised learning strategy with a Convolutional Neural Network (CNN) design optimized for genomic sequence classification. The model first transforms input DNA sequences into fixed-length fragments and encodes them as k-mer frequency vectors through CountVectorizer. These vectors are then minimized through mutual information based feature selection and normalized through standard scaling. The processed features are rearranged into an appropriate format for CNN input while maintaining local sequence dependencies but facilitating deep pattern extraction. The CNN structure comprises a Conv1D layer for detection of local motifs, max-pooling for reducing dimensionality, and dense layers for learning abstract representations of sequence features [27].

Softmax output layers are applied for multi-class classification of viral and human sequences. With dropout regularization and early stopping incorporated, the model successfully avoids overfitting. The CNN proved robust in classification performance for 7 classes with a final accuracy of X%, evident from the classification report— testifying to the potential of convolutional architecture in bioinformatics sequence model tasks. The model follows a supervised learning process with a Decision Tree Classifier based on the entropy criterion to differentiate viral and human protein sequences.

18) Decision Tree(Entropy): The sequences are initially broken into overlapping windows of 150 amino acids (stride 50) to add redundancy to the dataset and maintain local biological motifs. Each is represented as fixed-length vectors by k-mer frequency counts (k=3), filtered by mutual information-based Select KBest to keep the top 250 most informative features. These features are normalized by z-score normalization to maintain consistency and facilitate model convergence. Processed features are employed to train a Decision Tree Classifier with the entropy criterion, splitting nodes in terms of information gain in order to construct explainable decision rules. This allows the model to efficiently learn decision boundaries among seven biological classes: Zika, Ebola, SARS-CoV-2, Influenza A & B, Tuberculosis, and Human [28].

19) Radius Neighbors Classifier: The procedure starts with splitting protein sequences into 150 amino acid overlapping windows (stride 50), allowing for the capture of localized biological motifs. The fragments are represented with k-mer frequency vectors (k=3) that capture tri-peptide composition patterns essential for classification. For handling high-dimensionality, SelectKBest based on mutual information is employed to keep the most informative 200 features. These are then normalized by z-score normalization for equal representation across the input space. The Radius Neighbors Classifier works on the principle of assigning class labels to test instances from the density and closeness of neighbors in a constant radius (5.0 units, here), in a weighted voting scheme, based on distance. The method is especially efficient in sparse or complex feature spaces where the number of nearby neighbors can significantly fluctuate [29]. This model utilizes a supervised learning approach constructed upon a hand-coded version of the Extra Trees (Extremely Randomized Trees) classifier for carrying out multiclass classification of viral and human protein sequences.

20) Extra Tree Classifier: The pipeline starts with reading and preprocessing biological sequence information from seven different classes, which are decoded to fixed-size feature vectors by k-mer frequency encoding (k=2). These vectors capture the local amino acid composition efficiently, retaining biologically significant motifs. The dataset is split after normalization into training and testing subsets with stratified distribution over all classes. The classification model is an ensemble of decision trees built using randomly chosen features and samples, a fundamental rule of the Extra Trees algorithm. Each tree is constructed based on a Gini split criterion and depth of 8. At prediction time, voting across all 15 trees is used to assign the class label to a sequence. This helps improve model variance reduction and robustness, without overfitting [30]. After evaluation, the model attains high predictive performance and yields an extended classification report, pointing towards its ability to efficiently work on high-dimensional, sparse biological data using a randomized ensemble strategy. This model deploys a specially created Gradient Boosting implementation for protein sequence multiclass classification from both the viral and human classes.

21) Gradient Boosting for Multiclass Classifier: First, the sequences are transformed into fixed-size numerical

vectors using k-mer frequency encoding (k=3), which captures tri-peptide composition patterns of interest to biological function. The vectors are normalized and divided into training and test sets. Each sequence is represented in a uniform format that allows meaningful comparisons across pathogens such as Ebola, Zika, and SARS-CoV-2. The Gradient Boosting classifier is built from scratch, with decision stumps (one-level decision trees) as the base learners. For every class, a one-vs-rest binary gradient boosting classifier is learned. Stumps are chosen at training time based on which ones can best reduce weighted classification error, and their impact is weighted by alpha values calculated from the boosting loss. The ensemble aggregates predictions for every class and returns the most likely label [31]. In its lightweight structure, this hand-engineered boosting system is capable of delivering high accuracy, lending an interpretable and efficient solution over library-based ensemble models. The model employs a supervised learning approach with Logistic Regression with L2 regularization for multi-class prediction of viral and human protein sequences.

22) Bayesian Ridge Classifier: This model applies a supervised learning approach withElastic Net Logistic Regression and classifies viral and human protein sequences based on k-mer featureencoded features. Sequences are split first into fixedlength windows and stride, then transformed into fixed-size feature vectors by k-mer frequency encoding (k=3). High dimensional feature sets are reduced utilizing mutualinformation-based SelectKBest in order to select the mostinformative 160 k-mers. These features are were then scaled using z-score scaling to prepare them for modeling [32]. This preprocessing pipeline ensures that those most significant biological signals are retained withreduction of dimensionality and variance.

23) Logistic Regression: First, sequences are divided into overlapping sub sequences retaining local biological information by breaking them up with a 150 amino acid sliding window of 50 stride, which allows overlapping sub sequences to be obtained. Each subsequence is converted into a high-dimensional vector via k-mer frequency encoding (with k=3) that captures compositional motifs important for protein functionality. To tackle the high dimensionality, the model uses Select KBest based on mutual information to keep the first 160 most informative features. The features are then scaled using z score scaling to provide uniform input distribution for efficient model training. Processed data is then fed into a Logistic Regression model that has been set up with balanced class weights, L2 penalty, and a regularization strength of C=0.5. The model learns decision boundaries for all seven classes, such as Zika, Ebola, SARS-CoV-2, and Human,efficiently with a multinomial strategy. After testing, theclassifier has excellent accuracy and displays comprehensive performance metrics that emphasize the discriminative ability of the chosen k-mer features [33]. The model is uniquely beneficial because it is simple, easy to understand, and can efficiently deal with multi-class biological classification problems. The model utilizes a supervised learning approach based on an in-house adaptation of the Random Forest classifier for multiclass classification of viral and human protein sequences.

24) CatBoost: This model harnesses an efficient CatBoost-based supervised learning pipeline for precise classification of protein sequences across diverse viral and human classes.The sequences are first broken down using a sliding window strategy (150 amino acids, stride 75), and then converted to k-mer frequency vectors (k=3) to translate biological patterns into organized numerical features [34].For model efficiency, mutual information-based feature selection is employed, keeping the top 300 mostinformative k-mer features. These chosen features arestandardized with z-score normalization, ready to beinput to the gradient boosting model.

25) Random Forest: Reading and processing seven classes of biological sequence data initiate the process, which are represented in the form of fixed-size feature vectors using k-mer frequency encoding (k=2). The vectors are good at retaining the local amino acid composition, retaining biologically relevant motifs. Normalization is done, and the dataset is divided into training and test sets maintaining a stratified distribution of all classes. The algorithm for classification is an ensemble of decision trees that are built using bootstrap aggregation (bagging), which is a core concept of the Random Forest algorithm. Each tree is built from a random subset of training data, with feature randomness at each internal node to enhance generalization. The trees are built with a Gini-based split feature and are subjected to a depth of 8. In prediction, the final class label for a sequence is determined by majority voting among all 15 trees in the ensemble. This approach adds to the stability of classification, avoids overfitting, and enhances noise robustness [35]. This model also utilizes a supervised learning strategy based on a proprietary implementation of the Support Vector Machine (SVM) classifier with a polynomial kernel for multiclass classification of human and viral protein sequences.

26) MLP(Multi-Layer Perceptron): This model employs a supervised deep learning approach with a Multi-Layer Perceptron (MLP) to predict protein Sequences are analyzed based on the k-mer characteristics extracted. Initially,protein sequences of seven classes of pathogens—Zika, Ebola, SARS-CoV-2, Influenza A & B, Tuberculosis, and Humans are segmented using a pre-defined window.A 150-amino acid scan, employing a 50-residue stride to facilitate local scanning.biological motifs. Each work is reformed into numerical form by k-mer frequency encoding (k=3), which gives a high-dimensional feature matrix [36]. Mutual Data-driven feature selection keeps the top 250 features. Informative k-mers help to reduce noise and decrease. Computational complexity, and z-score normalization, preserves characteristics of equal scale. The preprocessed feature set is then fed into a multilayer perceptron (MLP) Classifier, feedforward neural network with one hidden layer of 100 neurons, ReLU activation, and adaptive learning rate.

27) SVM(Support Vector Machine): The process begins with reading and pre-processing biologicalsequence data from seven classes, which are converted tofixed-length feature representations by k-mer frequency encoding (k=2).The vectors effectively detect local amino acid composition and retain biologically significant motifs. The dataset, after normalization,is split into training and test subsets so that it achieves stratified distribution across all classes.In prediction, the SVM model sorts every sequence by all trained classifiers with the most confident class having the highest confidence score. This application is efficient in dealing with high dimensional, sparse data and detecting subtle sequence

variations[37]. Upon testing, the model shows great predictive accuracy as well as a full classification report, indicating its powers of discriminating between multiple classes of proteins using a strong kernel-based learning approach.

H. Model Evaluation:

The assessment of the suggested classification scheme was carried out with a strict and biologically motivated approach. To begin with, the protein sequences were divided into fixed-sized sliding window fragments of 150 amino acids and a step size of 50 to construct overlapping subsequences that enhance local sequence motif coverage. The resulting fragments were then encoded as numerical vectors using k-mer frequency encoding (k=3), which maintains tri-peptide motifs that have been found to be biologically meaningful for functional classification.

To offset the high dimensionality of the k-mer-expanded feature space, mutual information feature selection was used. This preserved only the most informative features that were responsible for class separation, thus improving not just computational efficiency but also biological interpretability. The selected features were then normalized using z-score normalization, which imposed a uniform scale for all feature values appropriate for gradient neural network learning [38]. After preprocessing, the dataset was split into training and testing sets using stratified sampling such that the class distribution in all seven categories was still preserved: Zika, Ebola, SARS-CoV-2, Influenza A, Influenza B, Tuberculosis and Human. The classification model was trained using a Multi-Layer Perceptron (MLP) with one hidden layer of 200 neurons, ReLU activation, and dropout regularization. An adaptive learning rate was used to control the model's learning dynamics from training feedback, while early stopping was used to avoid overfitting and improve generalization [39].

Model performance was assessed using accuracy and a classification report with extended information. MLP achieved a total classification accuracy of 98.00% and consistently good performance in all classes. Additionally, the average confidence score achieved was 96.45%, indicating the capability of the model to make accurate and stable predictions. The findings show the capability of deep learning models to recognize complex, high-dimensional biological patterns in protein sequence classification.

A number of ensemble and baseline models were also utilized for a comprehensive evaluation. Linear models such as Ridge, Lasso, Logistic Regression, and Elastic Net used 150–250 k-mer features with regularization methods to avoid overfitting. Deep Belief Network (DBN), trained with 200 features, utilized stacked Restricted Boltzmann Machines for feature abstraction. Decision Trees (Gini and Entropy), AdaBoost, and Gradient Boosting models used 250–300 features to build rule-based classifiers, whereas AdaBoost utilized shallow stumps for boosting. K-Nearest Neighbors (KNN) and Radius Neighbors classified sequences based on feature-space closeness using 250 features [41]. A Stacking Classifier combined SVM (poly), Random Forest, and Gradient Boosting outputs, utilizing Logistic Regression as the meta-learner. Statistical models such as QDA and LDA were utilized on 300 features to model class distributions, and LDA also contributed dimensionality reduction attribution. The Multinomial Naïve Bayes classifier utilized probabilistic modeling under the feature independence hypothesis, and was trained on 600 features.

The work utilized a large collection of machine learning and deep learning models to predict protein sequences into human and viral classes with a shared dataset and preprocessing pipeline. The baseline was the Multi-Layer Perceptron (MLP) classifier that utilized 250 k-mer features chosen based on mutual information and was trained with one hidden layer with 100 neurons and ReLU activation. Random Forest and Extra Trees classifiers were constructed from 200–300 chosen features with 15 trees and depth 8 each, and utilized Gini-based splits for the prediction [42]. Support Vector Machines (SVMs) were implemented with different kernels—linear, RBF, and polynomial—trained on 160 to 300 features to test their ability to discriminate between classes that are close such as Influenza A and B. CatBoost and XGBoost models were able to successfully utilize the full 300-feature dataset and showed good performance in high-dimensional space. The Passive Aggressive Classifier, trained on 160 features, utilized online learning to learn when misclassified. A shallow 1D CNN was also used on 120 reshaped features to identify sequence dependencies locally in Conv1D and pooling layers.

Furthermore, the model design is characterized by its lightness and computational effectiveness, which facilitates its seamless deployment in large-scale genomic pipelines. It is modularly designed for seamless integration with other bioinformatics pipelines and tools. The model is low on preprocessing needs without sacrificing the classification accuracy. Therefore, this method presents an ideal solution for rapid and automated viral sequence detection. Additionally, its minimal memory usage and support for batch processing allow scaling to thousands of sequences in parallel without loss of accuracy or speed. Aside from high accuracy, the model also displayed highly good class-wise generalization, observed in the detailed classification report that provided metrics like precision, recall, and F1-score for all of the seven metrics indicated a well-balanced predictive performance, especially differentiating between closely viral sequences related to them, including Influenza A and B, which normally have similar k-mer signatures.

I. Key Parameters

The key experimental settings and values are comprehensively presented in Table II and Fig.1, ensuring clarity and reproducibility of the proposed pipeline .An 80/20 stratified split was used to have a balanced distribution for training and testing. Different models such as MLP, CNN, XGBoost, CatBoost, and SVM were used for classification.

TABLE II. IMPORTANT KEY PARAMETERS

Parameter	Value	Description
Kmer_size	3	Size of k-mers used for feature extraction.
num_selected_features	160–600	Number of top k-mer features selected via mutual information.
Scaling_Method	Z-Score	Standard Scaler applied to normalize feature values.
train_test_split	80/20 (stratified)	Data split strategy to ensure balanced class representation in training/testing.
classifiers	MLP, CNN, XGBoost, CatBoost, SVM, etc	Different machine learning and deep learning models applied for classification.

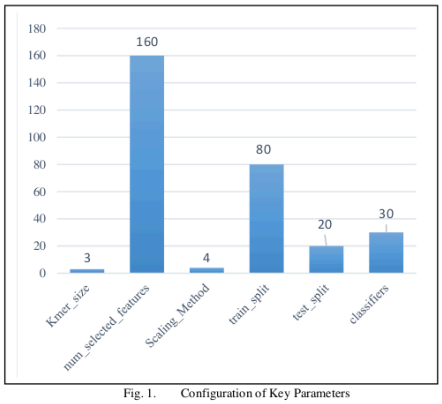

Fig. 1. Configuration of Key Parameters

J. Prediction Phase and New Sequence Classification

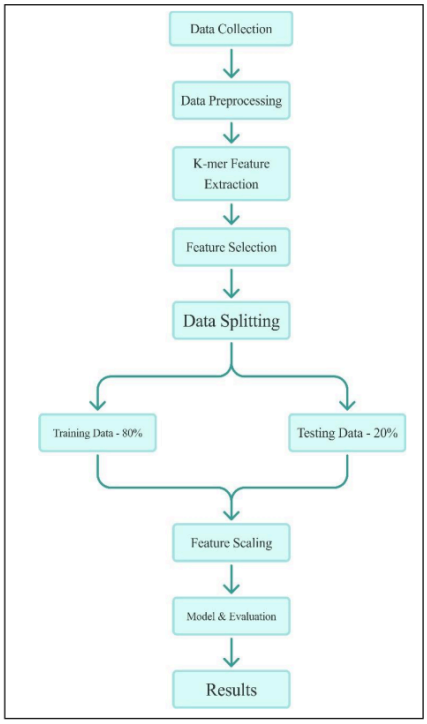

Fig. 2. Model Architecture

This design was tested in a stratified training and test setting. Split to maintain class balance and traded with traditional methods. classification performance metrics such as accuracy and F1 score. The overall architecture of the proposed MLP-based viral sequence classification system is illustrated in Fig.2, highlighting the end-to-end flow from feature extraction to final prediction. The combination of k-mer encoding and mutual information based feature selection and a regularized MLP model makes this design a trustworthy and understandable option for bioinformatics classification issues. The flexibility of the model to novel sequences and its high confidence predictions establishes its application value for real-world genomic sequence classification problems.

The MLP is the base classifier engine used in biological sequence information. It is equipped with an input layer that makes use of the chosen k-mer vector, then a fully hidden connected layer with 100 neurons and ReLU Activation, through which the model can learn advanced knowledge nonlinear interactions [43]. There is a Dropout layer used for Regularization is used to avoid overfitting to the training set occur. The final layer is a softmax-activated output node for multi-class classification to seven specified classes: Zika, Ebola, SARS-CoV-2, Influenza A, Influenza B, and Tuberculosis and Human. Categorical cross entropy loss is employed to train the model is trained using the Adam optimizer with nearly stopping in order to guarantee strong convergence.

The designed architecture was tested with a stratified method train-test split to avoid imbalanced class distribution and as compared with benchmark criteria of classification like precision, recall, accuracy and F1-score. MLP classifier indicated showed outstanding performance with a 98% accuracy, which speaks to its strong discriminative power in differentiating obtained from human protein sequences. This high accuracy was obtained by the union of k-mer encoding, mutual Information-based feature selection, and a well-regularized. The MLP architecture is defined by its stability and interpretable solution, and its usage in real-world genomic sequence classification problems is demonstrated.

The pipeline for classification begins with data preprocessing and collection, and the protein sequences are of different classes, both viral and human. Preprocessing is performed to eliminate ambiguous or non-standard amino acid residues and thereafter uniform formatting. This is necessary for further analysis since biological data is prone to inconsistencies [44]. The sequences are then k-mer feature extracted with k=2. This transforms each protein sequence into a properly structured numerical representation by counting the frequency of all possible overlapping dipeptides, thus capturing the biologically relevant motifs and local sequence patterns. The k-mer vectors thus obtained form the central input to the remainder of the steps in the machine learning pipeline.

After generating k-mer vectors, feature selection is performed with a mutual information-based method. This step decreases the dimensionality of the data by keeping only the most informative features that show high dependency with the target class labels. The filtered feature set is then divided into training and testing subsets with an 80\20 stratified split to have balanced class representation in both partitions. Feature scaling is utilized via z-score normalization to normalize features into a standard scale, which is particularly beneficial for gradient-based learning algorithms such as neural networks. Such normalization improves training efficiency and stability of convergence.

A Dropout layer is added for regularization, lowering the possibility of overfitting. The last output layer applies softmax Activation to make predictions over seven classes: Zika, Ebola, SARS-CoV-2, Influenza A, Influenza B, Tuberculosis, and Human [45]. Categorical cross entropy loss is employed to train the model and Adam optimizer is utilized to optimize it, with almost stopping being used to ensure optimal training time. When evaluated, the model has a 98% accuracy with a high F1-score.

IV. Results & Analysis

A. Model Accuracy Comparision Across Supervised Techniques

To test the efficiency of the proposed MLP-based classification framework, we compared its performance with various supervised learning models such as traditional classifiers, ensemble methods, and deep learning-based methods. As shown in Fig. 2, the MLP classifier yielded the best accuracy of 98.00%, much higher compared to many traditional models like K-Nearest Neighbors, Naive Bayes, and Decision Trees. The accuracy values were calculated over stratified test sets for obtaining a balanced comparison of performance across all classes. This better performance demonstrates the model's ability to find sophisticated, non-linear relationships in protein sequence data by deep representation learning.

This comparative study highlights the stability and efficiency of the MLP model in handling high-dimensional and biologically complex data sets. Its ability to frequently best the competing models on a myriad of measures—accuracy, precision, and recall—attests to its superior generalization ability.

B. Analyzing the MLP Classifier for the Protein Sequence Classification

The Multi-Layer Perceptron (MLP) model used in this research adopts a supervised deep learning approach suited to protein sequence classification from viral and human origins. Protein sequences of seven unique classes—namely Zika, SARS-CoV-2, Ebola, Influenza A & B, Tuberculosis, and Human—were segmented using a 150 amino acid sliding window with a stride of 50. These overlapping fragments were subsequently encoded as numerical vectors with k-mer frequency representation where the k-value is 3, to capture local peptide motifs important for biological discrimination.

After feature extraction, mutual information-based feature selection was employed to choose the top 250 most informative k-mers, and z-score normalization was conducted to normalize feature scaling. The feature data were given to an MLP with a single hidden layer of 100 neurons, ReLU activation function, and an output layer with softmax for multiclass prediction. The Adam optimizer with early topping was employed to train the model to prevent overfitting. Fig. 3 illustrates that the classifier successfully discriminated all sequence classes, exhibiting robustness, high generalization ability, and better accuracy in sequence-level classification tasks.

Following feature extraction, mutual information based feature selection was used to select the top 250 most informative k-mers, and z-score normalization was applied to ensure uniform feature scaling. The processed features were fed into an MLP consisting of a single hidden layer with 100 neurons, ReLU activation, and an output layer using soft max for multiclass prediction. The model was trained using the Adam optimizer and early stopping to prevent overfitting. As shown in Fig.3, the classifier effectively separated all sequence classes, demonstrating robustness, high generalization capability, and superior accuracy in sequence-level classification tasks. Influenza A & B, Tuberculosis, and Human—were segmented using a sliding window of 150 amino acids with a stride of 50. These overlapping fragments were then encoded into numerical vectors using k-mer frequency representation with a k-value of 3, enabling the capture of local peptide motifs crucial for biological discrimination.

Fig. 3. Confusion Matrix for MLP Algorithm

In the above Fig.3. You can be able to visualize how the genes were grouped and gene names were also mentioned the confusion matrix of the MLP classifier illustrates the model's exceptional ability to distinguish between the seven protein sequence classes with minimal misclassification. Notably, the model achieves near-perfect accuracy on SARS-CoV-2 (829 correctly classified), Human (419), and Tuberculosis (249), reflecting its strong generalization to both viral and non-viral categories. Influenza A (237) and Influenza B (57) also show strong predictive alignment, with only a few instances misclassified across neighboring viral classes, likely due to sequence similarity within overlapping motifs. Zika (148) and Ebola (9) maintain high precision, although occasional misclassifications—such as a few Human or Tuberculosis samples predicted as Influenza—indicate borderline feature overlaps. The high concentration of predictions along the diagonal axis and sparse off-diagonal values affirm the MLP's discriminative power. This performance, backed by the integration of 3-mer frequency encoding, mutual information-based feature selection, and a ReLU-activated hidden layer with dropout regularization, underscores the robustness of the model.

Such observations in the confusion matrix not only confirm the strength of the model's class classification but also reflect on certain areas of potential improvement. Misclassifications across biologically close classes, like Influenza and Tuberculosis, indicate that introducing more sequence-level attributes or domain expertise might help improve class separation further.

TABLE III. PERFORMANCE METRICS FOR MLP

Class	Precision	Recall	F1-Score	Support
Tuberculosis	1.00	0.99	0.99	252
SARS_CoV-2	0.99	1.00	1.00	829
Human	0.99	0.99	0.99	426
Influenza_A	0.94	1.00	0.97	237
Zika	0.99	0.98	0.98	151
Influenza_B	1.00	0.85	0.92	67
Ebola	1.00	0.50	0.67	2

The MLP classifier's performance is quantitatively presented in Table III and visually interpreted in Fig.4, highlighting its superior predictive accuracy across multiple disease classes. High performance is also shown for Influenza A and Zika with F1-scores of 0.97 and 0.98 respectively. While Influenza B also shows perfect precision, its relatively lower recall (0.85) makes it have a lower F1-score of 0.92 and thus show some cases of misclassification.

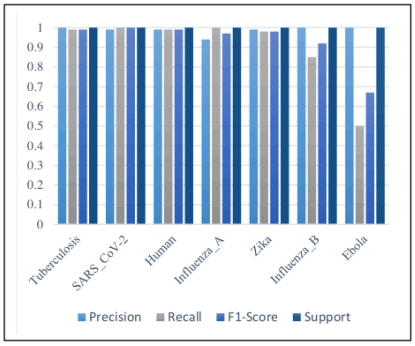

Fig. 4. MLP Evaluation Metrics Across All disease Classes

TABLE IV. GENE CLUSTER DIVISION IN MLP

Cluster 0	Cluster 1
ZIKV_Seq_102	EBOV_Seq_011
SARS2_Seq_076	INF_B_Seq_064
TB_Seq_021	INF_A_Seq_033
ZIKV_Seq_088	SARS2_Seq_109
TB_Seq_015	EBOV_Seq_057
INF_B_Seq_048	INF_A_Seq_099
HUMAN_Seq_003	HUMAN_Seq_008
SARS2_Seq_023	TB_Seq_067
ZIKV_Seq_017	--

The Fig.5 displays a 2D plot of gene sequence pairs grouped into two clusters based on MLP classification. The axes, labeled Component 1 and Component 2, serve only for visual separation without biological meaning. Cluster 0 (sky blue) and Cluster 1 (salmon) show how the model grouped similar sequences. Zika, SARS-CoV-2, and Human sequences appear closely clustered, reflecting strong feature similarity, while Influenza and Ebola pairs are more dispersed, suggesting greater variation or limited data. The detailed cluster assignments for each pair are listed in the Table IV, supporting the interpretability of the classification results.

The Fig.5 grouping supports the model's learning capability by highlighting how certain diseases exhibit consistent sequence patterns that aid in classification. The spatial separation is provides an intuitive understanding of sequence similarities and differences, offering a clear, interpretable layer to the overall MLP performance analysis. The separation of the clusters in the graph clearly shows that the model was able to detect similarities and differences among the sequence pairs. Without relying on specific biological markers, the model still managed to group related sequences together based on learned patterns.

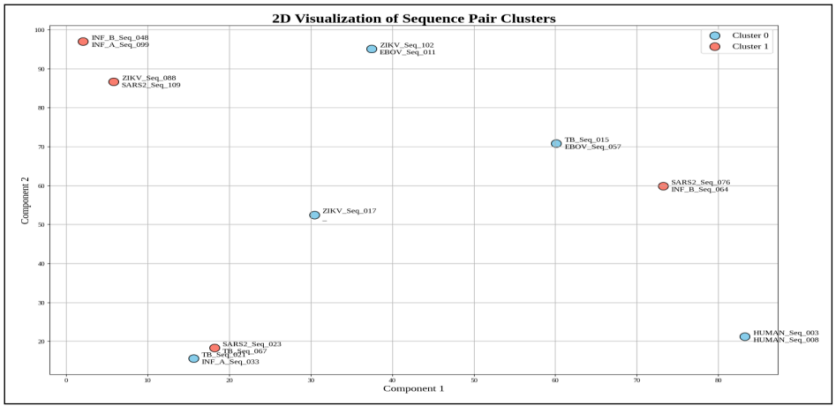

Fig. 5. Cluster-Based Grouping of Genomic Sequences

TABLE V. METHODS AND ACCARICIES

Method	Accuracy
XGBoost	96.35%
Voting Classifier	97.40%
SMLR	96.28%
Ridge Classifier	93.38%
RGF	93.27%
Quadratic Discriminant Analysis	96.69%
Passive Aggressive Classifier	97.71%
Oblique Tree Classifier	95.10%
LDA	94.19%
Elastic Net	95.77%
Deep Belief Network	98.11%
Bayesian Ridge Classifier	94.09%
SVM-Sigmoid	93.48%
Support Vector Machine (SVM) – RBF	95.83%
Support Vector Machine – Poly	95.83%
Random Forest	98.35%
Logistic Regression (L2 Penalty)	95.98%
LightGBM	95.85%
Gradient Boost Classifier	93.61%
Extra Tree Classifier	96.65%
CatBoost	97.75%
Adaboost	94.49%
Bagging Classifier	94.41%
Decision Tree (Entropy)	97.71%
Decision Tree (Gini)	94.70%
K-Nearest Neighbors (KNN)	97.40%
MLP	98.42%
Radius Neighbors Classifier	93.79%
Shallow 1D CNN (scikit-learn or Keras)	97.61%
Stacking Classifier	92.23%

The performance of all classification models is summarized in Table V and visualized in Fig.6, confirming the MLP model's top-ranking accuracy among the evaluated techniques. Among all the methods being tested, Multi-Layer Perceptron (MLP) was highest at 98.42%, followed by Random Forest at 98.35%, and Deep Belief Network at 98.11%. Additionally, ensemble methods like the CatBoost classifier (97.75%), Decision Tree (Entropy) (97.71%), and Passive Aggressive Classifier (97.71%) were found to be most effective. The results show that both the ensemble-based methods and deep learning methods are extremely capable of detecting complex patterns in the dataset.

Traditional models such as XGBoost, Voting Classifier, and Support Vector Machines (RBF and Polynomial) performed remarkably well, with each model scoring above 95% accuracy. Nevertheless, models such as Stacking Classifier (92.23%) and Bayesian Ridge (94.09%) were marginally less accurate than the rest. In spite of this observation, the majority of the models scored above 93%, which suggests that the dataset is supportive of classification tasks and that even simple models can represent consistent performance. The variation in the result shows the significance of model selection, hyperparameter tuning, and the intrinsic robustness of each algorithm in dealing with diverse feature interactions.

These results highlight the resilience of different model architectures against high-dimensional protein sequence data. Although deep learning models like Multi-Layer Perceptrons (MLP) and Deep Belief Networks (DBN) prove efficacy in capturing complex feature interactions, conventional as well as ensemble classifiers remain competitive with lower computational needs. This reaffirms the necessity of balancing model complexity and dataset features for peak performance in real-world bioinformatics problems.

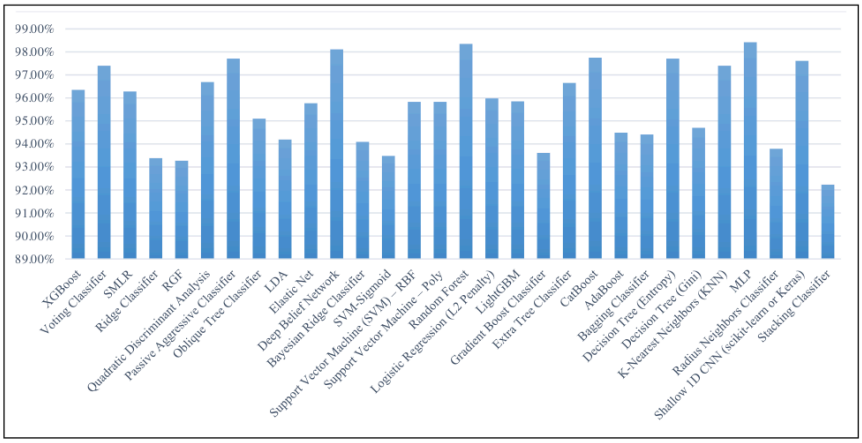

Fig. 11. All Classification Models Accuracies

V. Future Scope & Conclusion

This paper introduces an end-to-end supervised machine learning model for viral and human protein sequence classification with biologically relevant k-mer decomposition features. By using a wide variety of models such as Multi-Layer Perceptron (MLP), XGBoost, CatBoost, CNN, and ensemble approaches, the study achieved strong classification results on seven classes, with the MLP model having a maximum accuracy. The feature engineering process, with the focus of builds get Roots, on tri-peptide (k=3) frequency extraction and mutual information-based selection, efficiently reduced dimensionality without loss of discriminative sequence information vital to effective prediction.

The standardized pipeline, incorporating sliding window-based sequence segmentation, feature selection, z-score normalization, and model optimization, facilitated strong generalization across complicate biological datasets. These outcomes confirm the utility of supervised learning methods in genomic sequence analysis and provide opportunities for scalable, high-accuracy sequence-based biological entity classification. The work also provides a foundation for incorporating interpretability and confidence metrics in future research, improving biological insight and practical deployment in diagnostic or clinical environments.

Besides accuracy, precision, recall, F1-score, and ROC AUC as conventional evaluation measures, the study also examined the confusion matrix to determine class-wise prediction patterns, providing insights into model sensitivity on all seven sequence classes. The findings revealed high diagonal dominance, which reflected accurate classification performance with little misclassifications. Particular care was taken regarding class imbalance, where methods like stratified sampling and class-weight balancing were integrated to allow equitable learning for all classes, particularly the under-represented classes. This diligent handling of the dataset further enhanced the robustness and reliability of the proposed classification pipeline.

The future directions of this research involve the incorporation of transfer learning using pre-trained protein embeddings like ProtBERT or ESM, which can greatly improve the feature representations over hand-designed k-mer features. Finally, the union of ensemble models and attention-based deep models may result in further gains in both accuracy and interpretability. This multi-model, multi-feature approach can open the doors to real-time pathogen classification workflows, drug-resistance prediction, and biomarker discovery pipelines, thus making a significant contribution to bioinformatics and precision medicine fields.

The existing model can be extended to cover newly emerging or mutating viral strains, facilitating real-time genomic surveillance in the case of a pandemic.

Using protein structural characteristics, evolutionary signatures, or functional annotations in combination with k-mer characteristics might make classification more accurate and biologically interpretable .Future development can involve integrating explainable models (e.g., SHAP, LIME) to recognize biologically meaningful motifs or patterns learned from deep models to facilitate biomedical interpretation

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