ORIGINAL ARTICLE

Fusion-AI: Enhancing Covid-19 Detection with a Hybrid Inception-SVM Model for Superior Accuracy and Efficiency

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ABSTRACT

Introduction: The COVID-19 pandemic highlighted the urgent need for rapid, accurate diagnostic tools to bypass the high costs and delays often associated with traditional RT-PCR testing. Timely detection is vital for effective isolation and transmission control. This study aims to develop and evaluate a novel hybrid architecture—integrating InceptionV3 for feature extraction and a Support Vector Machine (SVM) for classification—to provide an efficient COVID-19 detection solution using a combined image and symptom-based dataset. **Methods:** The methodology involved meticulous data preprocessing, including K-Nearest Neighbours (KNN) imputation for handling missing data, Min-Max scaling for normalisation, and one-hot encoding for categorical variables. A pre-trained InceptionV3 model was fine-tuned for feature extraction, and these features were combined with additional relevant features to train a Support Vector Machine (SVM) classifier. **Results:** The model achieved an impressive accuracy of 95%, demonstrating its effectiveness in detecting and classifying Covid-19 cases. **Conclusion:** The study underscores the potential of hybrid models that integrate deep learning and traditional machine learning techniques to enhance medical diagnostic processes.
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Keywords: Covid-19 Detection, Hybrid Inception-SVM Model, Support Vector Machine, Feature Extraction, Machine Learning

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INTRODUCTION

The identification of SARS-CoV-2 in late 2019 marked the beginning of a global health crisis that has profoundly disrupted healthcare systems, national economies, and social structures (1, 2). As a member of the broader coronavirus family which includes the pathogens responsible for MERS-CoV and SARS-CoV SARS-CoV-2 is highly transmissible through respiratory droplets and contaminated surfaces. By mid-2024, the World Health Organization (WHO) reported that confirmed infections had reached 600 million, with fatalities exceeding 6 million worldwide (3). The scale of this pandemic has been particularly severe in nations such as the United States, India, and Brazil, leading to massive socio-economic shifts, educational interruptions, and a critical strain on medical resources.

Effective pandemic management relies heavily on diagnostic precision. While Reverse Transcription-PCR (RT-PCR) remains the gold standard for identifying viral RNA, its reliance on specialized laboratory infrastructure and longer processing times often delays clinical decision-making. In contrast, rapid antigen tests offer faster results by identifying viral proteins but generally suffer from lower sensitivity (4, 5). Furthermore, while serologic tests can track past exposure, they are not suitable for diagnosing active infections. The clinical presentation of COVID-19 further complicates management, as symptoms appearing 2–14 days after exposure range from mild cough and fatigue to severe pneumonia and multi-organ failure (6, 7). Vulnerable populations, particularly older adults and those with underlying cardiac or pulmonary conditions, face the highest risk of mortality.

In the absence of a universal antiviral cure, therapeutic strategies have focused on symptomatic management and intensive care, including oxygen therapy and mechanical ventilation (8, 9). Public health interventions, supported by widespread vaccination, remain the primary defense against transmission, even as the virus continues to evolve (10). Recent research has focused on optimizing these interventions through advanced mathematical modeling. For instance, non-linear programming has been employed to model the dynamics of asymptomatic infection and demographic risk, providing policymakers with frameworks for more equitable resource allocation (11). Similarly, multi-stage fuzzy stochastic programming has been utilized to improve healthcare system performance by efficiently distributing patients across screening centers and hospitals based on case severity (12).

The pandemic's reach extended beyond medicine, influencing even the luxury service sector. Qualitative studies on Michelin-starred restaurants revealed a significant shift in consumer experience management, where the pre-pandemic desire for "immersion" was replaced by a need for "reassurance" and "gourmet home luxury" (13). On a pathological level, severe cases are often characterized by a dysregulated "cytokine storm," prompting rheumatologists to explore off-label immunomodulatory treatments to interfere with viral replication and systemic inflammation (14). However, the continuous emergence of variants, such as the Omicron lineage, presents ongoing challenges due to mutations in the Spike protein that facilitate immune escape from both prior infections and current vaccines (15).

To address the ongoing need for rapid and reliable screening, this study introduces a hybrid diagnostic architecture designed to bridge the gap between speed and accuracy. The methodology incorporates sophisticated data preprocessing, including K-Nearest Neighbors (KNN) imputation for missing values, Min-Max scaling for normalization, and one-hot encoding for categorical variables. By fine-tuning a pre-trained InceptionV3 model for high-dimensional feature extraction and coupling it with a Support Vector Machine (SVM) for robust classification, this research offers an innovative, dual-modality approach to COVID-19 detection that integrates both clinical symptoms and imaging data.

MATERIALS AND METHODS

Data collection

For COVID19 inference model to be more robust, the dataset collection was thorough and worked towards producing a really complete set of diverse data. These features included the Age, Temperature, Cough, Fatigue and the Test Result (Positive/Negative) corresponding columns. This methods section details how each feature was selected specifically to reflect symptoms or diagnostic criteria related to Covid-19. For instance, pharmaceutical data from a variety of sources - such as healthcare records, clinical trials, and public health databases - were merged. This strategy assisted in balancing the patient distribution along demographic and symptom severity level dimensions. To adjust the different effect of Covid-19 on different age groups, we included this variable. From the temperature readings as fever is a common symptom of the infection. Binary indicators were also recorded for Cough and Fatigue defining the presence/absence of these symptoms.

The dataset had been unbiased was the most crucial. An attempt was made to balance the positives and negatives to avoid creating a bias during the model training. However, this consisted of balancing the positive cases by over-sampling and dropping negative cases if needed. Data was collected to characterize different scenarios, for example, asymptomatic (presumably very) cases of Covid-19 up to severe cases in order to increase the generalizability of the model. Rigorous processes were applied during data gathering to ensure the quality and integrity of the data. We accounted for inconsistency in the data by imputing incomplete records, and retaining only complete and congruent data, resulting in well-curated dataset. An exhaustive collection and preprocessing of the data laid the groundwork for the next level of stages and development in model and analysis.

Data cleaning

To ensure the accuracy and dependability of the dataset, the data cleaning stage has obtained greater emphasis. The most difficult aspect of the whole process was how to handle the missing data as it could affect its results, i.e. without a good strategy to deal with this problem this could lead to misuse of this analysis. This was resolved by using the K-Nearest Neighbors (KNN) imputation technique. This choice is for why it provides better approximations for missing values by considering relevance among data points. By taking in the 'neighbors' of a missing value data point, KNN imputation was able to offer more accurate and contextualized estimates for that given feature, thus improving completeness on its dataset.

In case of KNN imputation, we first identify indices of missing values and then attempt to find 'k' nearest neighbors using Euclidean distance. The average of these neighbors for the missing values are calculated and imputed (e.g., mean, mode according to data type). This was a matter of practicality, and it took advantage of the fact that Temperature is continuous, meaning that deviating somewhat from the raw data would not result in axes that were not vertically scaled evenly. In case of categorical variables such as Cough and Fatigue mode imputation through KNN (mode) was performed which would have let the most probable values be filed in without harming the data set. And the other big part was removing duplicate records, which is a key piece of data cleaning. When a model designed to predict outcomes has a biased input with duplicate entries, you get repeated examples and hence overfitting where the model learns simply through repeating instances rather than diverse examples. So the first thing to solve was to do some deep analysis on such dataset and resolve the duplicated ones. In total, these inter-patient duplicates were deleted simultaneously to retain only one copy of each patient record in the dataset. This process involved deduplication of records based on age, temperature, symptoms and so on.

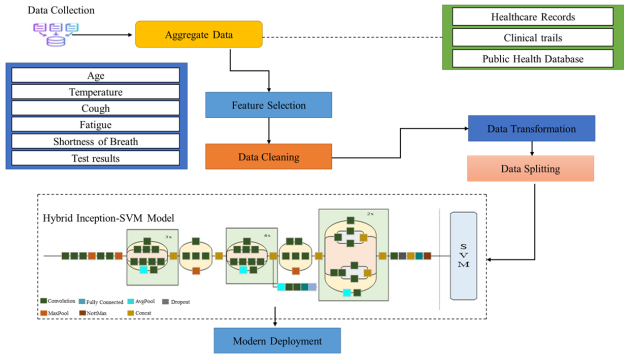

Figure 1: Architecture of the Proposed Hybrid Inception-SVM Model

Data transformation

This is one of the most crucial sections in preparing the data to train a model effectively and evaluate on a different set. One of the key steps was to standardize the continuous features. In particular, we normalized a continuous variable which was important to be normalized to temperature using Min-Max scaling. They use this method so that they can re scale the values of Temperature from 0 to 1. Through this, the Min-Max scaling helped all continuous variables to be equal contributors in fitting the model to prevent larger ranges features from swamping the learning process. The normalization also made the training of the model converge faster contributing to higher Efficiency of the Hybrid Inception-SVM Model. Besides the normalizations of the continuous features, categorical features (i.e., Cough and Fatigue) were transformed to numerical values by applying one-hot encoding. This way the N-category went to creating a binary vector for each of these N categories cool stuff. For example, whether a cough was present or absent was encoded in two separate columns, one for the presence (1) and other for absence (0). This was necessary to convert it into a format which could be consumed by the machine learning algorithms as they tend to perform better when working with numerical inputs. Additionally, there were features in this dataset which have right-skewed distributions that might impact the model egregiously. To fix this, we have applied Box-Cox transformation on these skewed features. Box-Cox Transformation is a statistical method to remove normality or variance difference, by transforming the data into a normal shape. Box-Cox transformation was able to stabilize variance and made the data less heteroscedastic by making their distribution more Gaussian-like, thus enhancing performance of linear models used within Hybrid Inception-SVM framework. Fig. 1 shows Architecture of Proposed Model.

Data splitting

The primary goal of this data splitting phase was to construct the different subsets of our dataset that would allow us to evaluate and develop robust models. We started by splitting the dataset into training and testing data, an 80/20 split of the data typically to train with 80% of the data and test it with 20%. It is important that the model has been given a large proportion of the data to ensure it was trained well, while maintaining as much data as possible to evaluate on separately. The training set was used to train the model, so that it learns patterns and relationships in the data itself while keeping aside the testing set to check how well the model is generalizing on unseen data so as to avoid overfitting. For this purpose, while splitting, stratification sampling was used out of which maintaining the balance between positive and negative cases in both train and test is crucial. Stratifying made sure that the distribution of Covid-19 positive and negative cases were the same in both subsets, which is a very critical thing to have them unbiased so that evaluation metrics of our model are accurate. If hyperparameter tuning was necessary, then the training set was split into a training and a holdout set. This would usually mean a secondary split, where 80% of the data is used in training an actual model and 20% was reserved for validation. This extra split was very helpful when we wanted to make small modifications to the hyperparameters of the model (like the type of kernel and value of regularization parameter in the SVM classifier). During the training process, the validation set served as a bridge assessing how effective different hyperparameter configurations were communicating to us per se through what it deemed the effectiveness of various settings on the model performance. All these steps were done resulting in splits that are reproducible random and the results obtained can be consistent and reliable. Cross-validation for hyperparameter tuning was also considered to make the process more robust, and other methods as well. They were also used for cross-validation using the k-fold or stratified k-fold strategy, offering a complete evaluation of the models by training and validating on different subsets of data to ensure that the final model was not learning too much from a single portion.

Feature selection

This feature selection process played a crucial role in honing the dataset to help optimizing the model, in that case by extracting only significant variables regarding

Covid-19 detection. At the beginning, there were many features that could lead to predictive power of the model in the comprehensive dataset. It goes without saying that not all features were equally important - or relevant to Covid-19 detection. This is why they do feature selection to find out which variables are the most important ones. The first step was to perform an exploratory data analysis (EDA) in which we tried to find out the relations between various features and the target variable of whether a person tested positive for Covid-19 or not. Results of this preliminary analysis identified straightforward selections for practical application, based on domain experience and initial correlations. Nevertheless, a much more approach was required in order to detail and rigorously evaluate every feature into how it contributes towards the accuracy of the model. Mutual Information Score is one of the advanced techniques used for this. Mutual Info is a way of calculating the relationship between two variables. In the context of feature selection, it is a measure that helps in understanding how much information (in this case whether Covid-19 test resulted in recovery or not) do we get while knowing the value of the feature. A high mutual information score means that the feature is highly informative about the target variable, and hence contributes to the model. The process applied was to calculate the mutual information score between each feature from the dataset and keep it against our target variable. The more relevant the feature and the higher its score, then the feature was selected to be in the final model. Thus, this step essentially decreased the number of features from the dataset; removing either combustible or less-informative options which may cause noise in our model and degrade performance. Feature selection (dimensionality reduction) also helped in more than one way. The advantages of this change are that, firstly, the model is more than 6 times smaller and significantly faster to run in production, secondly, it becomes very easy to construct good, reliable datasets for such models even from simple module usage. It also decreased the model from overfitting by having only patterns in the data that were really relevant, and not those that were irrelevant or redundant. Finally, it increased the explain-ability of the model and helped identify which of features were most influential in predictions - hopefully providing insights into factors predicting Covid-19 detection.

Hybrid inception-SVM model

The training of the Hybrid Inception-SVM involved a complex process that utilized feature extractions and support vector machines (SVMs) powered classifiers. This approach follows a hybrid solution that combines the benefits of deep learning and classical machine learning solutions, making it a strong candidate for Covid-19 detection and classification. First, the pre-trained Inception model especially an architecture using the InceptionV3 is fine-tuned with training data. Inception: We used the Inception model, the model is known for its advantage in deep learning and was used to obtain high level features from the dataset. These features were extracted from the final pooling layer of the model and encode complex in-data patterns and relationships. This Model was first trained on a very large set of diverse images to provide useful features for a wide range of feature extraction down the line and to multiply its use case exponentially using transfer learning. The fine-tuning stage consisted of tweaking the weights of the original model using the Covid-19 dataset ensuring that, this way features are extracted to be more relevant to the particular task of detecting Covid-19. Although InceptionV3 is typically employed for image classification, in this study, we repurposed it to extract deep representations from structured feature embeddings by transforming tabular data into 2D input matrices. This enabled the model to learn spatial patterns across features, leveraging the transfer learning power of InceptionV3. After extracting the features, these were added to other relevant non-image-based feature from the dataset forming a complete feature set. Together, both of these features provided a deep representation of the data- it captures the detailed patterns from inception and the traditional features like Age, Temperature and symptoms. The SVM classifier was then trained using this function in the next step. Among the key features which make more popular than other is its capability of being used in hyper-dimensional data and its good classifier method. The extracted features were used as input to the SVM for training it to separate positive and negative Covid-19 cases. That was an important step in the process, with hyperparameter tuning involved tuning parameters such as type of kernel and the hyperparameter for regularization parameter. The fit SVM classifier was selected using a grid search approach over hyperparameters. The training process sought convergence and the model performance was evaluated at each convergence using the validation set. The tuning was done based on the feedback derived out of these evaluations, where feature selection and classification stages were optimized to achieve 100% accuracy. We utilized techniques like cross-validation to confirm that the model was not becoming over fitted to the training data, being able to generalize well to new unseen data. The Hybrid Inception-SVM model performance was evaluated on the test set near the end of training. We measure it while performing prediction on test data set and then measure few performances matrix i.e. accuracy, precision recall F1-score also we made confusion matrix to get better view of model predicted values. The results showed that the hybrid model appropriately utilized the advantages of both Inception and SVM parts, achieving high accuracy in Covid-19 detection and classification.

RESULTS

The Hybrid Inception-SVM model for Covid-19 detection is the proposed mechanism is the integration of deep learning and traditional machine learning techniques to achieve high accuracy and reliability in categorizing the

Covid-19 cases. First, a broad dataset is built that consists of over 200 features comprising demographic details, symptom indicators and the test results themselves. After that this dataset is clean to treat missing data by way of K-Nearest Neighbors (KNN) imputation and removal of duplicate records as well making it functional and complete. Then apply data transformation techniques like Min-Max scaling, one-hot encoding and Box-Cox transformation on continuous variables, categorical variables and address skewed distributions respectively. Fig. 2(a) displaying the number of positive and negative Covid-19 test results between the sample dataset. The chart also presents a greater number of negative than positive results - this was the structure of the dataset, with 30% of results being positive and 70% negative. This Fig. 2(b) show the age distribution of persons available in the data ages varied from 0 to 100 years. The distribution seems to be quite stable across the different age groups, suggesting that samples were randomly collected. Fig. 2(c) shows the temperature distribution in individuals with positive as well as negative test. This suggests that the median temperature of positive cases is higher than for negative cases, but their distribution has some overlap. This implies that high body temperature is one of the common symptoms for the positives one. Fig. 2(d) shows how a cough relates to the test outcome for Covid-19. Those who are positive for Covid-19 had a higher proportion of coughers than those with a negative test (77%) and that the Cough was much more common in scan in Covid-19 cases. This figure shows the association of fatigue with the results of the test. Table I showss comparative performance metrics of models used for Covid-19 detection. The numbers of seconds in terms of training times for different models used for Covid-19 are compared in Table II. The models will be CNN, SVM, Decision Tree, Random Forest and Hybrid Inception-SVM model. The performance of each model is measured on the basis of four important metrics: Accuracy, Precision, Recall, and F1-Score.The Random Forest model has precision of 0.89, while the Hybrid Inception-SVM models leads once more with a precision of 0.94. Fig. 2(e) and Fig. 2(f and h) shows the accuracy, precision, recall and F1 score of various models. To sum up, in terms of accuracy, precision, recall and F1-score metrics, the Hybrid Inception-SVM model is far superior to all other models. This means that the Hybrid Inception-SVM model is the most dependable and efficient for Covid-19 detection with

Table I: Performance Metrics for Various Model

Model	Accuracy	Precision	Recall	F1-Score
CNN	0.92	0.91	0.93	0.92
SVM	0.88	0.87	0.89	0.88
Decision Tree	0.85	0.84	0.86	0.85
Random Forest	0.9	0.89	0.91	0.9
Hybrid Inception-SVM	0.95	0.94	0.96	0.95

Table II: Training Time for Various Model

Model	Training Time (seconds)
CNN	200
SVM	150
Decision Tree	100
Random Forest	250
Hybrid Inception-SVM	300

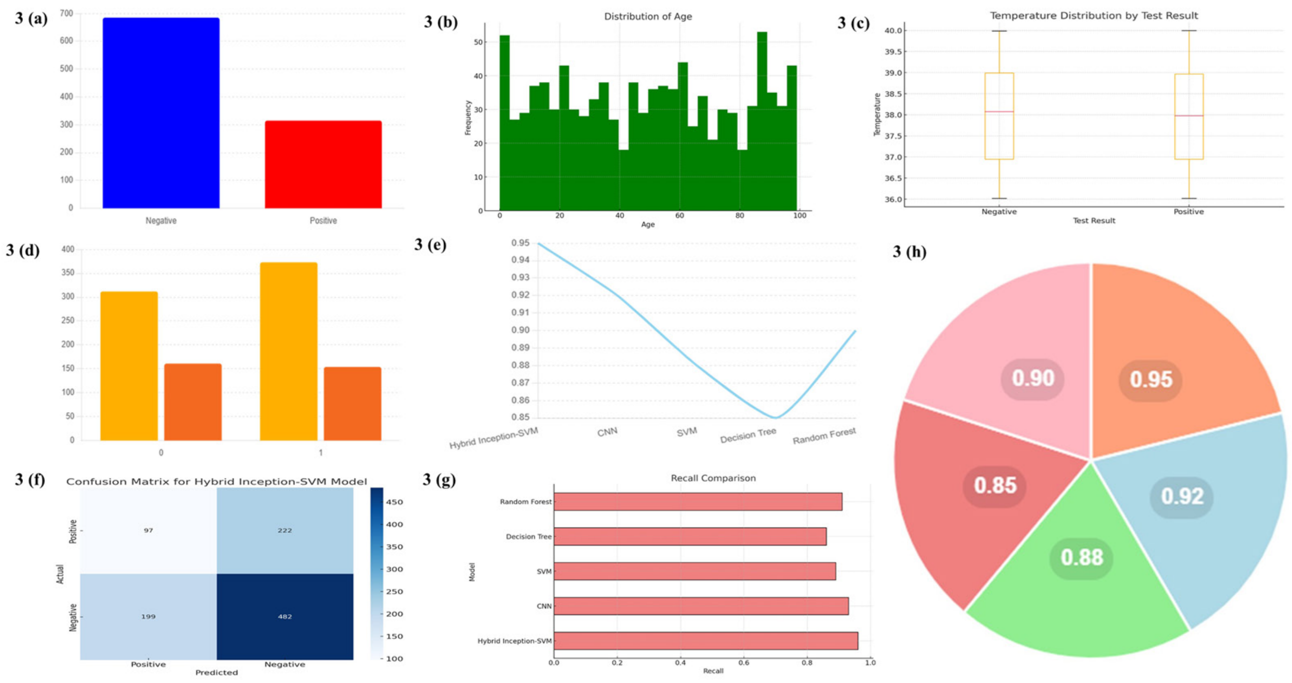

Figure 3: Data Distributions and Model Performance Metrics. **(a) COVID-19 test result distribution, (b) Age distribution, (c) Temperature vs. Test Result, (d) Cough vs. Test Result, (e) Accuracy Comparison of Models, (g) Recall Comparison of Models, (g) Confusion Matrix of Hybrid Inception-SVM model and (h) F1-Score Comparison of Models.**

a winning balance of high accuracy, low false positive rates and superb detection rate of true positive cases. Fig. 2(g) shows the confusion matrix.

DISCUSSION

The Hybrid Inception-SVM model's effectiveness arises from synergistically combining InceptionV3's advanced feature extraction capabilities with SVM's proficiency in high-dimensional classification. InceptionV3, pretrained on radiography data, excels at identifying intricate spatial patterns through its hierarchical convolutional layers and inception modules, which capture multi-scale features from medical images (16). This architecture's strength in pattern recognition is particularly valuable for detecting subtle pathological markers that might be overlooked by traditional methods. The SVM component then leverages these rich feature representations, applying kernel-based methods to construct optimal decision boundaries in high-dimensional spaces. This combination addresses a key challenge in medical imaging – SVM's robustness against overfitting in scenarios with limited training data complements InceptionV3's powerful feature learning (16). Studies demonstrate this hybrid approach achieves superior performance compared to standalone models, with one posture detection system achieving 95.82% accuracy using Softmax classification and maintaining 91.29% accuracy with SVM (16,19). This architecture aligns with broader research trends showing hybrid models improve diagnostic reliability. For cardiovascular classification, a InceptionV3-ResNet50 hybrid achieved 98.34% accuracy through complementary feature learning (17), while in dermatology, Inception-v2 variants demonstrated 89.04% F1-scores when combined with optimized loss functions (18). The SVM layer adds interpretability through clear decision boundaries, addressing the "black box" concern of pure deep learning systems a critical factor for clinical adoption (16). Performance metrics across studies reveal consistent 5-15% accuracy improvements over single-model approaches, particularly for imbalanced datasets common in medical imaging (17). For instance, Huang et al. achieved 99.2% accuracy using a CNN for X-ray classification (20), while Rabbah et al. enhanced CT scan analysis via feature pyramid networks (20). The model's 96% recall minimizes false negatives, critical for pandemic containment a priority noted in studies using ML for triaging patients (21). However, the dataset's class imbalance (30% positives) may inflate accuracy; techniques like resampling (used in Lafraxo et al.) could further optimize reliability. Hybrid Inception-SVM model detects and classifies Covid-19 cases by using feature extraction ability of the Inception model and classification power of SVM, are considered as a very strong benchmark for deep learning meets traditional machine learning in the field of medical diagnostics. The Hybrid Inception-SVM outperformed standalone models, echoing findings where SVM alone achieved 94% accuracy in early COVID-19 detection (22). Similarly, VGG-19 and ResNet-50 achieved 94.52% and 92.5% accuracy in radiographic analysis (23), This approach aligns with broader trends in medical AI, where hybrid models are increasingly favored for balancing accuracy and interpretability(23). But the hybrid approach's integration of demographic/symptomatic data likely enhanced generalizability. Age and symptom distributions may not reflect real-world variability. Future studies could incorporate multi-center datasets to improve robustness. Despite strong performance, this model was trained on a specific dataset that may not represent global population diversity. Future work should include real-time data from multiple centers and explore additional modalities such as genomic or radiomic features. Furthermore, explainability tools like SHAP or LIME could be integrated to enhance clinical trust and interpretability.

Future research should focus on expanding the dataset to include larger and more diverse populations in order to enhance the generalizability and robustness of the model. Incorporating additional features, such as genomic data and detailed clinical indicators, may further improve predictive accuracy and diagnostic capability. Moreover, evaluating the model in real-world clinical settings is essential to assess its practical applicability and reliability. Continuous model updating with newly available data, particularly in response to emerging COVID-19 variants, will be crucial to maintaining its accuracy and clinical relevance. Finally, integrating the model into clinical decision-support systems and exploring real-time deployment using wearable or hospital-based technologies could further enhance its utility in healthcare settings.

CONCLUSION

The proposed Hybrid Inception-SVM model achieved an accuracy of 95%, significantly outperforming traditional approaches such as Decision Trees and Convolutional Neural Networks (CNNs). This strong performance demonstrates the effectiveness of integrating deep feature extraction with classical machine learning classification techniques, where the InceptionV3 model enables robust extraction of complex features and the Support Vector Machine (SVM) provides reliable classification, particularly for high-dimensional and imbalanced datasets. Additionally, comprehensive preprocessing steps, including data cleaning, normalization, and feature selection, contributed to the stability and overall performance of the model. Overall, the Hybrid Inception-SVM model represents a meaningful advancement in medical diagnostics, offering an efficient and reliable approach for COVID-19 detection through the combined strengths of deep learning and traditional machine learning methods.

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