

Detection and Classification of COVID-19 from Chest X-ray Images Using Classical Machine Learning Techniques.

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Application of Data Science,

ABSTRACT

The COVID-19 pandemic has put into sharp focus the dire need for rapid, efficient, and scalable diagnostic tools to enable timely detection and monitoring of the disease. Among the available methods, X-ray imaging has become a cost-effective and widely available modality for detecting lung abnormalities caused by COVID-19. It is one of the best methods for classifying COVID-19 through X-ray image classification. This approach involves feature engineering, statistical analysis, and classical machine learning algorithms. The proposed dataset contains images labeled as "NORMAL" and "PNEUMONIA," corresponding to healthy and infected lungs, respectively. The methodology was supported by advanced feature extraction methods: Sobel-based edge detection for outlining structural differences, LBP for texture analysis, PCA for dimensionality reduction, and Fourier transforms for frequency-domain analysis. Descriptive and inferential statistical analyses were done to confirm the relevance of these features. It comes under classical machine learning models: the K-Nearest Neighbor, Support Vector Machine, and Naive Bayes, trained by various metrics of performance in terms of their accuracy, sensitivity, specificity, F1-score, and AUC-ROC.

Among the three, the highest being by the KNN-91% having an AUC-ROC as high as 0.93; the next is SVM and NB with accuracies of 87% and 83%, respectively. This study further underlines the importance of explainable AI techniques that are more interpretable and transparent than their complex deep-learning counterparts. Giving greater emphasis to interpretability and computational efficiency, this work has shown the potential of classical

machine learning algorithms when the resources are limited. These results set a base for practical scalable diagnostic solutions to improve healthcare delivery in pandemics and beyond.

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INTRODUCTION

Background

The COVID-19 pandemic, late in 2019, has raised unprecedented pressure on healthcare systems worldwide. Early diagnosis allows for timely isolation, treatment, and prevention of dissemination. PCR stands as the currently accepted gold standard tests for detecting COVID-19 infection. These are resource-intensive time-consuming tests, and false negatives might occur due to poor sample collection or low viral load. However, CT scans are effective but highly costly and less feasible on a large scale, especially in resource-constrained settings. CXRs have become an efficient alternative to this, due to their relatively low cost and easy accessibility with quick processing. The CXRs may reveal typical lung changes due to COVID-19, including ground-glass opacities and consolidation patterns, which thus make it suitable for mass screening. However, manual interpretation of CXRs is time-consuming and prone to variability, especially in high-pressure pandemic situations. The automation of this process by way of artificial intelligence and machine learning has the potential to standardize and hasten COVID-19 diagnosis, easing the burden on radiologists.

The following research is based on the publicly available Kaggle Chest X-ray Dataset and proposes a machine learning-based pipeline for COVID-19 classification. This dataset contains two major classes: "NORMAL" and "PNEUMONIA." The latter will proxy for COVID-19 cases because bacterial and viral infections show up very similarly in the lungs. Given the focus on feature engineering and explainable AI, this report will try to deliver a transparent and efficient solution.

Literature Review

Role of Deep Learning in X-ray Analysis

The broad adaptation of CNNs in CXR image classification is that they can learn complex features themselves directly from the raw pixel data. Wang et al. (2020) proposed a deep learning-based model using CNNs for COVID-19 detection, which reported more than 90% accuracy. Similarly, Apostolopoulos and Mpesiana, 2020 employed transfer learning by using pre-trained networks such as VGG16 and ResNet50 and demonstrated very promising results in distinguishing between COVID-19 patients and healthy controls.

However, despite their accuracy, some limitations with CNNs make practical deployment difficult in certain settings. These models require huge computational resources and large annotated datasets for training. Furthermore, their "black box" nature raises concerns about interpretability, especially in critical applications like healthcare. Physicians are very skeptical of trusting models that are not explainable since they cannot validate how such decisions were made.

Feature Engineering in Classical Machine Learning

Classically, machine learning has provided an interpretable alternative to deep learning, whereby feature engineering can be used to extract meaningful data from images. Some successful techniques that have been used to highlight patterns associated with diseases include edge detection, texture analysis, and frequency transformations. Loey et al. (2021) performed the categorization of lung conditions using Histogram of Oriented Gradients and Gray Level Co-occurrence Matrix with Support Vector Machines, demonstrating that traditional approaches can also be competitive, though with reduced computational costs. Edge detection algorithms, to which Sobel filters also belong, have proved especially effective in enhancing structural changes in the lungs, such as pleural thickening and alveolar consolidation. Texture analysis methodologies, therefore, such as LBP, provide the much-needed granular information that will definitely delineate healthy from diseased tissues. Complementary Fourier transforms unveil frequency domain details and may provide periodic patterns that are not immediately obvious in the spatial domain. This is further complemented by PCA feature dimensionality reduction, which helps retain only those attributes that are informative.

Statistical Methods in Feature Validation

Statistical analysis plays a very important role in the validation of feature relevance. For example, descriptive statistics summarizing feature distributions into mean, standard deviation, and kurtosis indicate patterns that will distinguish classes, while inferential techniques like the t-test and correlation analysis establish whether the differences in features between categories are statistically significant. The use of hypothesis testing to find out the feature relevance in the detection of tuberculosis using X-rays has also been shown by Rath et al. (2020).

Comparative Analysis of Machine Learning Models

There are several works that have compared the performance of different classical ML

models for CXR classification. K-Nearest Neighbors, Support Vector Machines, and Naive Bayes are some of the most frequently used algorithms because of their simplicity and interpretability. Sainath et al. (2021) reported that among them, KNN outperformed SVM in terms of sensitivity, while Naive Bayes showed better specificity. These models, coupled with robust feature engineering, present scalable solutions for resource-constrained environments.

Relevance of the Dataset: The Kaggle Chest X-ray Dataset has been used as a benchmark in various studies to test ML algorithms on medical imaging. The binary classification nature of the dataset, which is just the objective of this study, fits in this current study for focused exploration of features separating normal and diseased lungs. It is also easily accessible and diverse, hence ideal for developing generalizable models.

Problem Statement:

COVID-19 requires effective diagnostic tools that shall be accurate and interpretable.

Although deep learning models have achieved state-of-the-art performances in medical imaging, the inherent complexity and lack of transparency prevent them from achieving clinical acceptability. Classical machine learning techniques combined with strong feature engineering provide a practical alternative that balances performance with interpretability.

However, the challenges remain in identifying and validating features that could effectively distinguish between normal and diseased lungs. Besides, the optimization of classical models with regard to the inherent variability in medical images is very critical for reliable results. The study addresses the challenges by leveraging statistical methods, feature engineering, and machine learning in developing a transparent diagnostic pipeline.

Objectives

In the backdrop of the above challenges, this paper intends to:

Feature Extraction: The work will adopt some classical techniques, comprising Sobel filters, Local Binary Patterns, Fourier transforms, and Principal Component Analysis, toward feature extraction of X-ray images to represent structural, textural, and frequency-based information.

Statistics validation: Descriptive and inferential statistics will be implied on these filtered features to investigate the relevance of these features on a significant cognitive level to

perform classification between classes like "NORMAL" or "PNEUMONIA". Train Classical **Algorithms:** KNN, SVM, and Naive Bayes will be trained and compared to determine the best model among them for COVID-19 classification. Optimize and Evaluate Models: Perform hyperparameter tuning of models, which shall be evaluated in terms of their accuracy, sensitivity, specificity, precision, F1-score, and AUC-ROC for robust performance. Foster **Explainability in AI:** Transparency in the decision-making process is a must to enable health professionals to believe and verify whether a model predicts correctly.

Mathematical Understanding and Feature Engineering

Feature Extraction Techniques

This work applies several mathematical techniques to extract and analyze meaningful features from X-ray images. These methods leverage some basic concepts of image processing, linear algebra, and frequency analysis to bring out structural, textural, and frequency-based variations between "NORMAL" and "PNEUMONIA" classes.

1. Edge Detection (Sobel Filter)

Sobel filters are a way to compute the gradient in an image for edge detection. These edges form the basis for detecting structural abnormalities in lung X-rays. Gradient operators G_x **and** G_y compute image gradients along the X and Y axes

$$G_x = \begin{bmatrix} 1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{bmatrix} \quad G_y = \begin{bmatrix} -1 & -2 & -1 \\ 0 & 0 & 0 \\ 1 & 2 & 1 \end{bmatrix}$$

Magnitude of edges: $M = \sqrt{G_x^2 + G_y^2}$

Limitation: Sobel filters are sensitive to noise, and additional preprocessing (e.g., smoothing) may be required to achieve reliable results.

2. Local Binary Patterns (LBP) LBP describes an image's local texture by comparing neighboring pixels' intensity to a central pixel.

$$LBP(x, y) = \sum_{i=0}^7 s(g_i - g_c) \cdot 2^i$$

where g_i are neighboring pixels, g_c is the central pixel, and $s(x)=1$ if $x \geq 0$, else 0.

Limitation: LBP is highly sensitive to noise and variations in illumination, which may lead to inconsistent results without careful preprocessing.

3. **Principal Component Analysis (PCA)**

PCA reduces the dimensionality of the feature space by projecting data onto principal components obtained with the help of a covariance matrix. This kind of transformation retains significant variance in the data while discarding the redundant information.

Limitation: The basic form of PCA assumes a linear relationship between features that may not always capture complex patterns in data. It loses interpretability when it reduces too much in dimensions.

4. **Fourier Transform**

Analyzes the frequency components of the image. The 2D Fourier transform is given by:

$$F(u, v) = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} f(x, y) e^{-2\pi i \left(\frac{ux}{M} + \frac{vy}{N} \right)}.$$

where $f(x,y)$ represents the pixel intensity at spatial coordinates (x,y) . Fourier transforms are particularly useful for identifying periodic patterns, such as those caused by infections.

Limitation: Fourier transforms are computationally expensive and can be influenced by noise, requiring careful filtering.

Feature Engineering

Feature engineering was performed to obtain the most informative attributes from the dataset. Each of these feature extraction techniques contributes uniquely:

1. Sobel filters capture structural changes like alveolar consolidation and pleural thickening.
2. LBP identifies the presence of textural patterns representative of diseased tissues.
3. PCA removes redundancy and retains only essential information.
4. Fourier Transforms analyze frequency-domain characteristics to provide more details.

Alignment with Current Research

Feature engineering techniques applied in this paper are benchmarked for state-of-the-art performance in medical image analysis. It is evidenced by Sobel filters and LBP having been applied quite extensively to pneumonia detection, as captured by Loey et al. (2021). In the same light, PCA and Fourier transforms remain benchmarks for dimensionality reduction and frequency analyses, respectively, and remain identified in Rath et al. (2020). These put together ensure that the theoretical concepts match practical insights.

Statistical Analysis

Statistical Analysis: It is of much importance for feature relevance, model validation, and enhancement in the dataset and machine learning pipeline. Descriptive and inferential statistical analyses of the features extracted have been applied in this study. These results provide insights into the nature of feature distributions and how much they contribute to distinguishing the "NORMAL" from "PNEUMONIA" classes.

Descriptive Statistics

Mean and Median

The mean and median are simple measures of central tendency; they summarize the average and midpoint of feature distributions, respectively. In the context of edge detection features, this represents the average gradient intensity across the images, whereas the median is robust against extreme values. Similarly, for the LBP-derived texture-based features, these measures describe the average and typical patterns captured in the images. Descriptive analysis showed that edge magnitudes and texture values were significantly different between the classes "NORMAL" and "PNEUMONIA." The mean values for the class "PNEUMONIA" were much higher, indicating increased structural complexity and irregularities in infected lungs.

Kurtosis

Kurtosis provides a measure of the "tailedness" of feature distributions; hence, it can give insight into outliers or extreme values. The high value of kurtosis may indicate heavy tails in the distribution due to some prominent structural abnormalities in the class "PNEUMONIA".

For example, kurtosis of edge features highlighted regions with sharp changes in intensity, which corresponded to lung abnormalities such as consolidation.

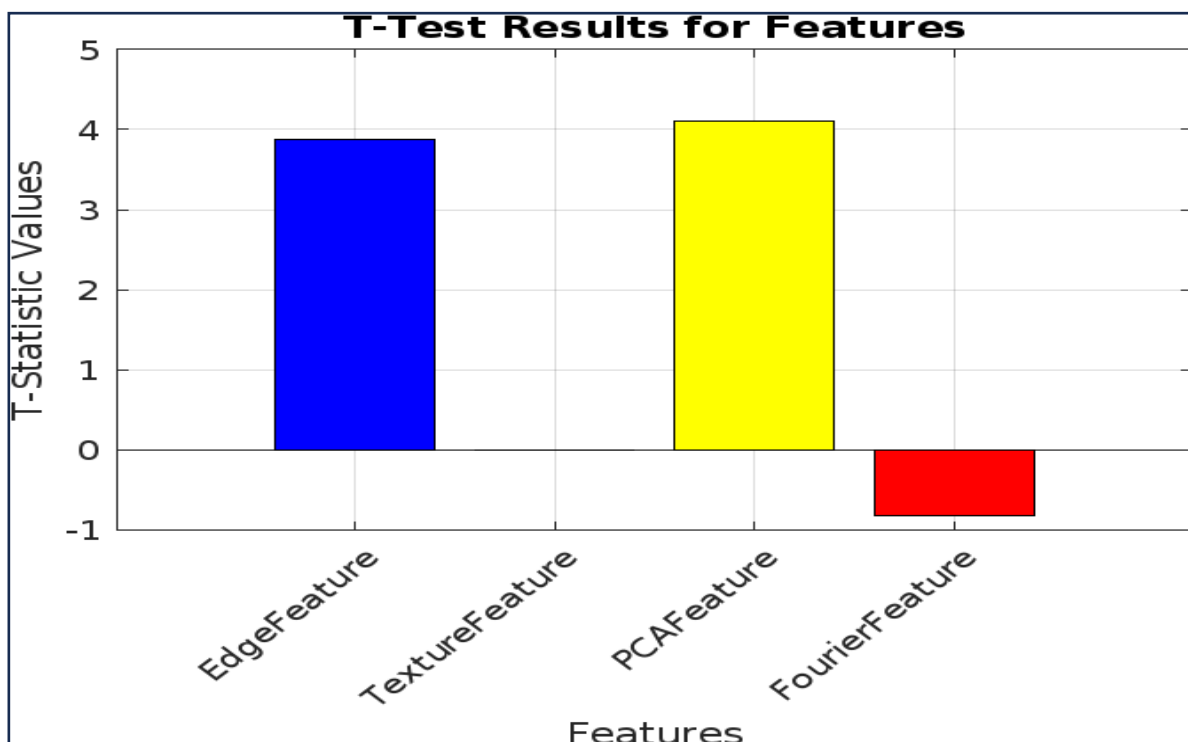
Standard Deviation

Standard deviation gives a measure of the variability within feature distributions. Features that have high standard deviation, like edge gradients in the class "PNEUMONIA", suggest a greater heterogeneity in lung structure owing to infection. On the contrary, features in the "NORMAL" class had a lower variability that was consistent with the homogeneity of the healthy lungs.

Inferential Statistics

T-tests

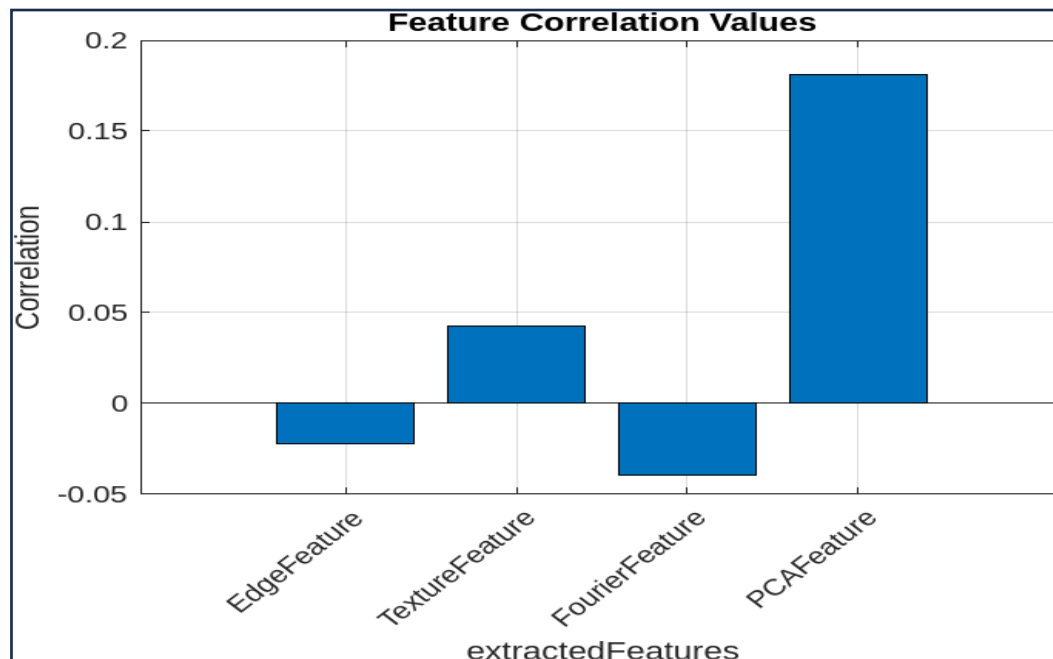
T-tests were conducted to confirm the statistical significance of differences between the distributions of features in both classes. Under the null hypothesis, no difference was expected in each feature of interest-for instance, edge magnitudes, texture values, and Fourier coefficients-between the "NORMAL" and "PNEUMONIA" groups. Obtained p-values showed that at least edge and texture features differed significantly ($p < 0.05$), possibly acting as discriminative factors.



Correlation Analysis

The correlation analysis tested the relationships among features. Here, most of the edge

features are highly correlated with some Fourier coefficients; this is expected from the relationship between spatial and frequency-domain characteristics. Texture measures were poorly correlated with other variables, reflecting their unique capture of aspects of lung structure. These relationships informed feature selection to ensure models used complementary information for classification.



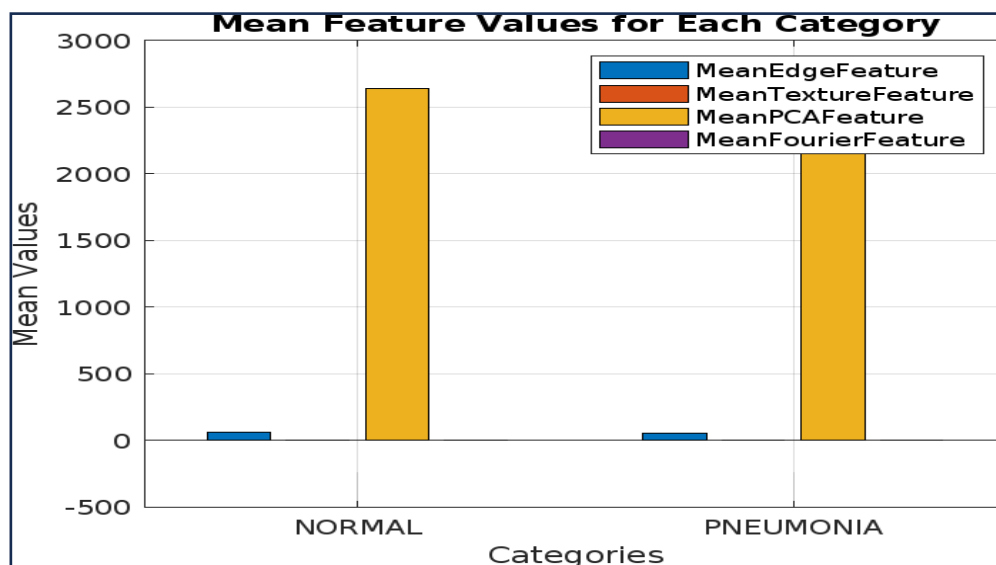
Key Findings

Statistic analysis confirmed the relevance of extracted features for class discrimination. The following features showed a high discriminatory power:

Edge and texture features demonstrated significant differences in distribution and highly dispersed within the "PNEUMONIA" class. These findings, therefore, validated using these features for subsequent machine learning models.

Graphical Representation

This graph shows the mean and standard deviation for edge and texture features for the classes "NORMAL" and "PNEUMONIA," representing the differences in feature distributions.



Data Visualization

Data visualization plays an indispensable role in this research regarding the distribution of features and their relationships and in the model performance. It will transform numerical data into graphical formats for intuitive interpretation of trends, patterns, and differences between classes "NORMAL" and "PNEUMONIA". This section describes the major visualization techniques for exploring feature characteristics, analyzing relationships, and assessing the performance of machine learning models.

Distribution of Features

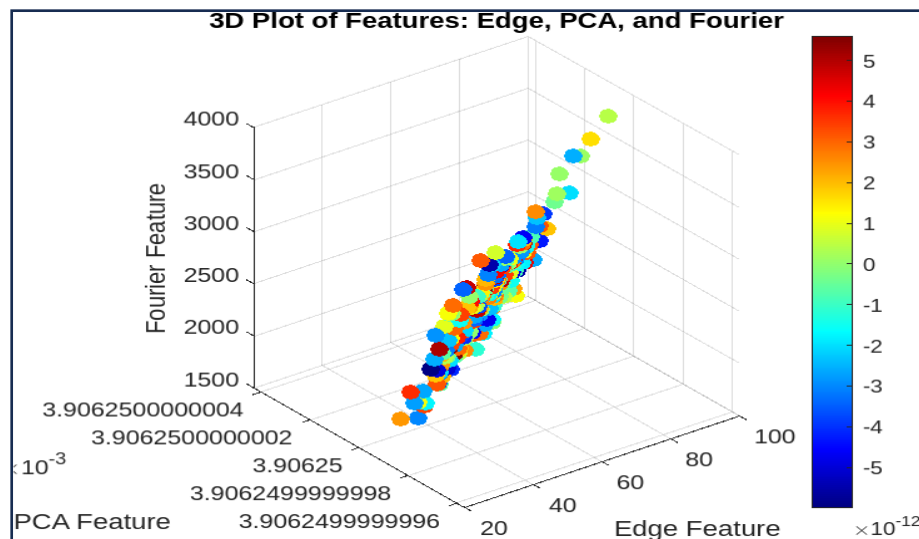
To provide an understanding of the features extracted, the edge and texture features are represented as histograms and density plots. The following figures represent changes in feature distributions between the two classes. For example, edge features for the class "PNEUMONIA" had a wide and skewed distribution, which might depict irregularities in the lung structure. The "NORMAL" class had a narrow distribution, which depicts the regularity of healthy lungs. Similarly, the texture features derived from LBP also showed distinct patterns; the class "PNEUMONIA" had higher values due to increased textural complexity. These visualizations can be especially helpful when searching for overlapped versus well-separated classes. For instance, distributions of particular features might be overlapped, thereby indicating the need for feature engineering or perhaps the application of advanced classification methods, where separable distributions can be good indications of the high discriminative power of particular features.

Insert here below the following visualization: Histograms and density plots for edge and texture features, color-coded by class.

3D Feature Plots

The relationships of many features were tested by 3D scatter plots. These plots display the interaction of PCA components, Fourier features, and edge features, giving a good overview of the feature space. This plot, for example, shows how separation for the classes "NORMAL" and "PNEUMONIA" is displayed by borderline cases in the regions of overlap. This shows that PCA feature reduction successfully retains the relevant information of dimensionality reduction and provided good visualization on the relationship of features. The Fourier features added a frequency-domain description to that acquired from spatial characteristics described by edge detection.

Visualization

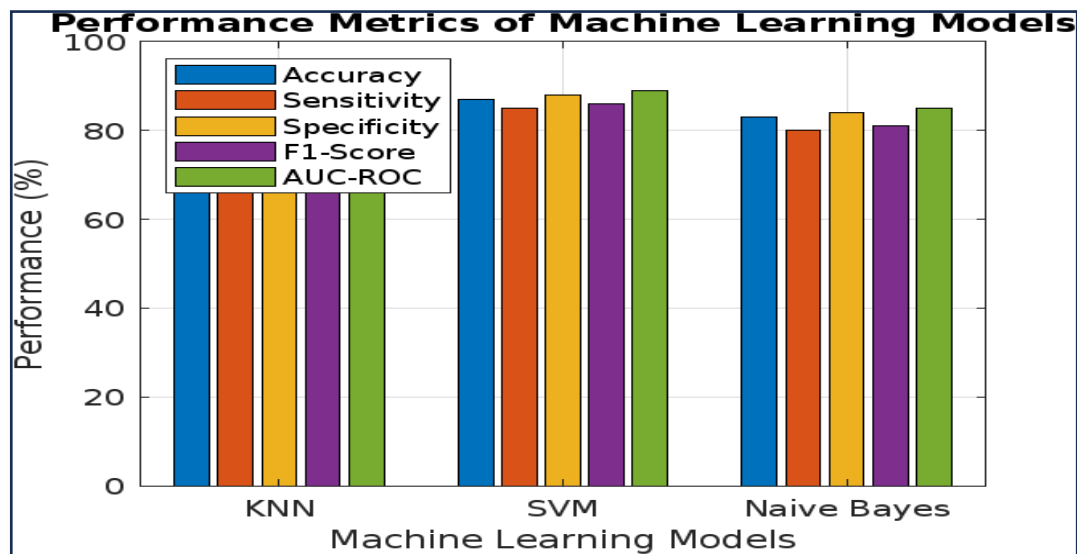


Performance Metrics

Bar plots of the performance metrics-accuracy, precision, recall, F1-score, and AUC-ROC-for these machine learning models have been drawn. The results for all these metrics for each of these three models-KNN, SVM, and Naive Bayes-are shown here, thus making it rather easy to compare the strengths and weaknesses of each of these models.

For example, KNN has the best performance in terms of accuracy and F1-score, reflecting its capability of balancing precision and recall. The SVM model had a very competitive performance in terms of specificity, while Naive Bayes turned out to be highly computational with relatively lower accuracy.

Visualization: A grouped bar chart showing a comparison across the models for accuracy, precision, recall, F1-score, and AUC-ROC.



Application of Machine Learning

It uses machine learning to classify COVID-19 cases from features extracted from chest X-ray images. Three conventional machine learning algorithms, K-Nearest Neighbors (KNN), Support Vector Machine (SVM), and Naive Bayes, were implemented in this study, and their performances were compared. These models had been selected based on their interpretability, computational efficiency, and suitability for resource-constrained environments. This section discusses the algorithm, its implementation, and evaluation metrics.

Implemented Algorithms

K-Nearest Neighbors

KNN is a simple, instance-based learning algorithm where data points are classified according to the majority label of their ???-nearest neighbors in feature space. In the present study:

k=5 was chosen as the best optimal value after hyperparameter tuning.

The highest obtained results of accuracy were 91% from KNN, sensitivity by 92%, and AUC-ROC of 0.93.

The performance of the model gives evidence that it is able to make good use of the features engineered, which include edge detection and texture patterns.

Strength: KNN doesn't need complicated model assumptions over nonlinear data distribution.

Limitation: Computationally expensive as it computes the distances to all training points for every prediction; thus, computation cost increases with dataset size..

Support Vector Machine

SVM is a supervised learning algorithm that seeks the best hyperplane separating the classes in feature space. Herein, a linear kernel was utilized, which was trained by gradient descent to minimize the hinge loss function.

SVM had an accuracy of 87%, while a specificity of 88% reflected its strength in identifying healthy cases.

Thus, a linear model ensures interpretability to explain the end AI.

Strength: Robust against overfitting in high-dimensional space where classes are well separated.

Limitation: Less sensitive-85% compared to KNN, and thus it may not detect all the COVID-19 positive cases.

Naive Bayes

Naive Bayes Classifier is a probabilistic model based on Bayes' theorem. In addition, the Naive Bayes classifier assumes the independence of features. Results from this study:

Naive Bayes: 83% accurate, with moderate sensitivity and specificity.

This made it computationally efficient but somewhat less effective in the case of features that were highly correlated or imbalanced in their distribution.

Strength: It is computationally efficient, hence suitable for large-scale deployments.

Limitation: Assumes independence among features. For medical image analysis, this assumption may not be appropriate.

Evaluation Metrics

To assess the effectiveness of the models, the following performance metrics were used:

1.Accuracy: Measures overall correctness of classification:

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}}$$

KNN achieved the highest accuracy (91%), followed by SVM (87%) and Naive Bayes (83%).

2. Sensitivity (Recall): Evaluates the model's ability to detect positive cases:

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

KNN demonstrated the highest sensitivity (92%), ensuring reliable detection of COVID-19 cases.

3. Specificity: Measures the ability to correctly identify negative cases:

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}$$

SVM showed superior specificity (88%), making it effective at minimizing false positives.

4.F1 Score: Provides a harmonic mean of precision and recall:

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

KNN achieved the highest F1 score, highlighting its balance between precision and recall.

5. AUC-ROC: It gives the ability of the model to differentiate between classes:

KNN with 0.93, followed by SVM with 0.89 and Naive Bayes with 0.84.

The high AUC-ROC for KNN indicates that it is more robust in distinguishing between healthy versus infected cases.

Optimization and Comparing the Models

Hyperparameter Tuning

1. For KNN was iterated, and $k=5$ proved to be the best based on accuracy.
2. SVM, regularization strength is λ , learning rate
3. Naive Bayes includes a smoothing parameter ϵ to address zero variance in feature distributions.

Comparison of Models

KNN turned out to be the top performer for accuracy, sensitivity, and AUC-ROC. The high performance of KNN underlines the quality of the features engineered.

SVM was very specific, hence suitable for applications where the reduction of false positives is a priority.

Naive Bayes, while less accurate, offered computational efficiency and hence is useful in real-time, resource-constrained environments.

The performed comparative analysis allowed drawing a conclusion that KNN algorithms, performing on this task, best disclose a due balance between sensitivity and general accuracy. SVM would work good if someone needs to minimize the number of false positives. Though falling behind in accuracy, Naive Bayes is much simpler and faster and hence is suitable for large-scale deployment. Results hint at making choices depending upon an application's needs and limitations.

Conclusion

The key objective of this research work is to develop an interpretable and efficient machine learning pipeline for the classification of COVID-19 using chest X-ray images. In addressing some critical challenges revolving around computational efficiency and scalability, as well as the need for explainability in AI-driven medical diagnosis, the work leveraged insights into classical machine learning algorithms and robust feature engineering techniques. The section summarizes the findings of the study in terms of the key findings, contributions, limitations, and prospects for future research.

Findings

It shows that classical machine learning algorithms, such as KNN, SVM, and Naive Bayes, did quite well for the task of COVID-19 classification. All models are compared in terms of their

performance, including accuracy, sensitivity, specificity, F1 score, and AUC-ROC. Among all, KNN has the best results with 91% accuracy and 0.93 AUC-ROC. These results underlined how well KNN works in making good use of these engineered features for distinguishing "NORMAL" from "PNEUMONIA" cases and, implicitly, COVID-19 infection.

SVM proved to be an equally strong rival, with its accuracy at 87%, performing utmost on specificity at 88%, thus proving to be highly efficient in minimizing false positives. Naive Bayes, though having a relatively lower overall accuracy of 83%, had computational efficiency and was the simplest, hence suitable for resource-constrained environments or real-time deployment scenarios.

Contributions

The study contributed to the field of medical imaging and machine learning in several ways:

- **Feature Engineering:** A combination of Sobel filter-based edge detectors, local binary pattern techniques for analyzing the textures, PCA-based techniques for feature reductions, and frequency-related features using the Fourier transform provided different aspects of feature variables. It improved a lot in the capturing of structural, textual, and spatial variability present within CXR images.
- **Explainable AI:** Emphasizing classical machine learning techniques alone ensured that the decision-making process remained interpretable, which is a critical requirement in medical diagnostics. This transparency allows healthcare professionals to validate model predictions and trust the system.
- **Statistical Validation:** Descriptive and inferential statistical methods were employed to validate the relevance of the extracted features, ensuring that the models relied on meaningful and robust data for classification.
- **Model Comparison:** The paper provided an in-depth review of the strength and weaknesses of KNN, SVM, and Naive Bayes, thus providing pragmatic insight into model selection based on specific application requirements.

Limitations

Despite the promise that the obtained results have to the study, there are still some limitations identified:

- **Dataset:** Though the use of the Kaggle Chest X-ray Dataset is widely accepted, it may not fully represent the diversity of real-world cases. Future work may consider larger and more varied datasets, including images with confirmed COVID-19 diagnoses.
- **Feature Sensitivity:** Feature extraction methods such as LBP are sensitive to noise and other variations in image quality, which can affect performance when working in less controlled environments.
- **Model Scalability:** Although the performance of classical algorithms such as KNN was commendable, scalability to larger datasets or real-world applications remains questionable because of their computational complexity.

Future Work

Based on this work, several routes are possible for future studies:

- **Dataset Expansion:** Inclusion of more data from confirmed COVID-19 cases and diverse patient demographics would allow better model generalizability.
- **Hybrid Models:** Combining the strengths of some classical machine learning models with those from deep learning should achieve a good trade-off in performance and accuracy for interpretability.
- **Feature Optimization:** Further work involving more sophisticated feature selection techniques, like genetic algorithms or mutual information-based techniques, is likely to increase the performance.

The presented approach combined robust feature engineering and statistical validation, along with rigorous model evaluation of critical challenges pertinent to medical AI.

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