

A BLOOD OXYGEN LEVEL DEPENDENT (BOLD) MODEL FOR STROKE PREDICTION

Dauda F.A. ¹ Ayeni O. A. ² Marafa S I³ Amadu W B⁴

¹ Networking department, Nigerian Television Authority, Ilorin, Nigeria, Dauda F.A, fard4trust2002@gmail.com

² Department of computer science, Federal university of Technology, Akure, Nigeria; olaniyiayeni17@gmail.com

³ Department of software engineering, Nankai University, Tianjin, China; marafasalman@gmail.com

⁴ Department of software engineering, Nankai University, Tianjin, China; codewithbawurie@gmail.com

* Dauda F.A, fard4trust2002@gmail.com; Tel. :(+234- 808581 8815)

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Abstract

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Functional Magnetic Resonance Imaging (fMRI) assesses brain activity by detecting Blood-Oxygen-Level-Dependent (BOLD) signals, which are influenced by neurovascular coupling. Despite its utility, the mechanisms of neurovascular coupling remain partially understood. Motivated by prior studies with limited accuracy and small sample sizes, this research focuses on stroke prediction and early diagnosis, a critical goal given stroke's global impact as a leading cause of death and disability (WHO). The study employs Chi-square for feature selection and Convolutional Neural Networks (CNN) and Support Vector Machines (SVM) as classifiers. On the HealthCare dataset, CNN achieved 97.41% accuracy and SVM 95.70%, while on the BIDMC-PPG dataset, CNN reached 99.10% and SVM 88.28%. These results outperform benchmarks like Kallam et al. (2022), who reported 89.9% accuracy with KNN and SVM, and Lunugalage et al. (2021), who achieved 94% using similar methods.

1. Introduction

A prominent noninvasive imaging technology called magnetic resonance imaging can be used to study soft tissue in a region that contains it anatomically. Computer Tomography scan (CT-Scan) and X-ray other imaging scanning modalities. Both do not employ internal or

external radiation as a result, there are no long-term radiation effects on the people Nuclear Magnetic Resonance (NMR), which in turn makes use of the magnetic properties of the 1H ion, which is widely dispersed throughout the human body, forms the basis for how Magnetic Resonance Imaging (MRI) functions

According to research on a crucial concept in functional Magnetic Resonance Imaging (fMRI), deoxygenated hemoglobin contains paramagnetic qualities and oxygenated hemoglobin shows diamagnetic potentials in the presence of an outside magnetic field. Based on the information that the presence of paramagnetic material in blood prevents spin de-phasing and subsequently reduces T*2 parameter, Based on the blood's content of deoxygenated hemoglobin, Ogawa *et al.* (1990) developed the use of this phenomenon to evaluate brain activity. In some brain regions, an increase in neuronal activity is frequently followed by an increase in metabolic expenditure that results in vasodilation. Similarly, Bandettini *et al.* (1992), Kiviniemi *et al.* (2003) used blind foundation separation methods on BOLD fMRI data to identify activation for specific activities by temporal filtering and linking each individual voxel from an fMRI dataset to reference time chains.

1.1 Motivation

This work is motivated by the limitations observed in research of Bennett *et al.* (2019) and Kallam *et al.* (2022) which are low prediction accuracy and relatively small sample sizes.

It was found that in order to model a BOLD for stroke prediction, firing details must be extracted with configurable parameters, and prediction must be made as to which area of interest (ROI) is active at a specific point in time. Several machine learning methods have been adopted by numerous researchers working in this area (BOLD). However, additional effort must be done in the area of data enhancement to eliminate noise, redundancy, and other issues. In order to model, this study used machine learning methods Support Vector Machine, Convolution Neural Network for classification, and Chi-square were the approaches employed.

1.2 Objectives

The specific objective of this research are to design a Blood Oxygen Level Dependent (BOLD) model for prediction of stroke, Implement the model in and finally evaluate the performance of the model based on standard performance metrics.

2 Related works

Glannon *et al.*, (2017) posed some hypotheses on forensic psychiatry's use of brain-based mind reading. This study examined the potential use of brain-based mind reading (BMR) in forensic psychiatry to evaluate defendants,

convicts, and perhaps even potential jurors. Techniques for structural and functional neuroimaging were used. The research showed that it would be possible to detect the content of mental states with the help of mind reading

Leuthardt *et al.*, (2016) investigated the fluctuations in the blood-oxygen-level-dependent (BOLD) signal, which provides a noninvasive measurement of blood flow, although there is no comprehensive comparison with known perfusion parameters in acute stroke. Dynamic causal modeling was used to apply P-DCM, a generative hemodynamic model of the BOLD signal that was inspired by physiological data using three different data sets, the relationship between BOLD signal temporal delay and dynamic susceptibility contrast magnetic resonance imaging (DSC-MRI) in stroke patients was investigated.

Bashar *et al.*, (2018) investigated the integration of ECG and EEG signals from low-cost devices with a number of classifiers (KNN, LDA, and ESAVM) using wavelet packet statistics feature. The combined WPS vectors from ECG and EEG data and the fused classifier have therefore produced the highest average Fscore (90.5%), when compared to single trait (ECG or EEG) with a single classifier (54.7% with ECG; 74.9% with EEG) or single trait with a fused classifier (66.0% with ECG; 87.3% with EEG).

Casson *et al.*, (2018) looked at how scalp-mounted metal electrodes may capture minute electrical potentials caused by brain activity that occurred outside of the skull. There were several modalities displayed, such as ambulatory, temporary tattoo wearable, and beyond wearable. This method offered high resolution, millisecond-level accuracy, and mobility.

Fierstra *et al.*, (2018) investigated hemodynamic failure in stroke patients. Specifically for detecting hemodynamic failure in the affected hemisphere and middle cerebral artery territory, as well as for identifying hemodynamic failure stage II, They compared BOLD fMRI cerebrovascular reactivity (CBV) and gold standard (150-) H2 O- position Emission tomography cerebral blood flow (CBF) perfusion reserve measurements. Because it may be incorporated into common clinical imaging, BOLD CVR may therefore be considered for studies estimating the risk of stroke in patients with chronic cerebrovascular steno-occlusive illness.

Nakamura *et al.*, (2018) investigated a user-friendly EEG biometric device that may be placed on the scalp and ears. Data from scalp and ear EEG recordings were used in the classification step, along with a binary class support vector

machine (SVM), combined power spectral density (PSD) and autoregressive coefficients (AR) with linear discriminant analysis (LDA), and power spectral density and autoregressive coefficients (AR) alone. The findings show that accuracy varies between 86.8% and 88.8% for scalp EEG and between 80.0% and 82.9% for ear EEG.

3.0 System Architecture

The conceptual diagram in Figure 1 illustrate designed model's system architecture. The fundamental model is composed of five important components. The first module take datasets obtained from Kaggle repository as input. These serve as input to second module which is data preprocessing. This preprocess is to remove unwelcome noise and outliers. The goal of this phase is to prevent the model's efficiency from declining, it involves dealing with missing values, handling unbalance data and label encoding of both datasets. After acquiring the pertinent datasets. Next is feature selection module using chi-square tool to ensure further clean.

Once the data are cleaned and ready to be used in the model. The purified datasets are divided into training and testing in ratio of 80% to 20%. The next module is classification, two techniques were used. These are convolution neural network (CNN) and support vector machine (SVM), s their output were evaluated using standard performance matrices. This is implemented using Python programming language. The model makes a prediction regarding whether a patient has stroke with value of (1) or none with value of (0) as shown in Figure 1

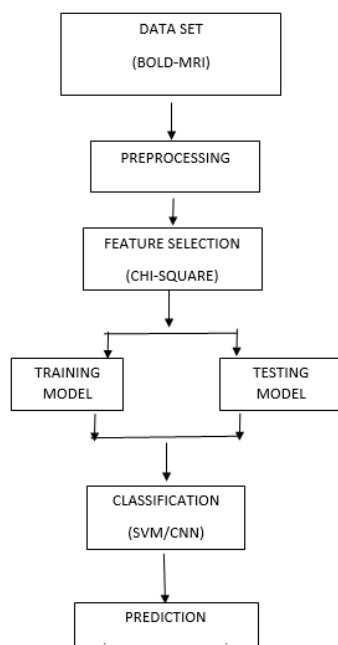


Figure 1 Model Architecture of BOLD Prediction

3.1 Data Acquisition

Dataset are integral part of the model and most source for. This study obtained two datasets from Kaggle repository namely HeathCare dataset for stroke patients and BIDMC-PPG Respiration. HealthCare dataset for stroke has 5100 rows and 12 columns. The attributes are: ID, Gender, Age, High Blood Pressure, Heart Disease, Marital Status, Work Type, Resident Type, Average Glucose Level, BMI, Smoking Status and Stroke. While BIDMC-PPG Respiration consists of MRI dataset of 120 people with ages ranging from 2 to 8 and unprocessed 750 diffusion weighted images.

3.1.1 Data preprocessing

Duplicate and pointless data, along with noisy and untrustworthy data, are removed during this stage of the mining process. The following preprocessing techniques make mining algorithms more precise and efficient (Jiawei *et al.*, 2021).

3.1.2 Data Cleaning

The information in the data set is viewed as being untrustworthy, noisy, and inconsistent. It is essential to remove such data from the dataset as a result. Common data cleaning activities include adding missing data, decreasing noise in the data, eliminating outliers, and addressing conflicts. The binning method, clustering, and linear regression are among the approaches used to carry out various data cleaning tasks.

3.1.3 Data integration: At this stage, several, frequently disparate sources of data may be combined into a single source. It's a process for compiling and fusing various data to give them a cohesive form and framework.

3.1.4 Normalization: this is the process of adjusting attribute values to fall inside a specific range, like [-1.0, 1.0] or [0.0, 1.0]. The BOLD MRI dataset performs better thanks to this method, which also keeps data from accumulating too closely together in terms of distance measures. Three frequently used data normalization techniques are min-max normalization, z-score normalization, and decimal point normalization.

3.1.5 Min-Max Normalization: It also goes by the name of feature scaling. According to (Al-Shalabi *et al.*, 2006), the values of a numeric range of a data feature are scaled down to a range between 0.0 and 1.0 in this instance.

3.1.6 Standardization (Or Z-score normalization) When the feature's real minimum and maximum values are known, it can be used.)

There are two steps involved; Step 1: Calculate the mean/average of the distribution. It can be done using the AVERAGE () function. When the mean value is known

then proceed to Step 2: Calculate the standard deviation of the distribution which can be done using the STDEV () function

3.1.7 Decimal Point Normalization; Decimal point normalization provides range between -1 and 1. Equation 1 describe normalization

$$c' = \frac{(c) - \min(f)}{\max(f) - \min(f)} \quad (2)$$

Where min (f) represents the minimum in f, max (f) is the maximum value in f, and (c) is the value to be normalized.

3.2 Classification techniques

Two classifiers are employed, these are Convolution Neural Network (CNN) and Support vector machine (SVM)

3.2.1 CNN and its Architecture

CNN is a regulated methodology in contrast to fuzzy C-Means and ADBSCAN clustering, which are uncontrolled approaches. A Convolutional Neural Network (CNN) consists of input and output layers in addition to numerous hidden layers. These layers (short for fully-connected) come in three different varieties: CONV, POOL, and FC.

Convolutional Layer

Images are displayed as a matrix (NxNx3) that represents the height, width, and depth of the image in pixels. A depth of three is used because an image has three channels. The Convolutional Layer employs a collection of trainable filters. The input image (MxMx3), which has a reduced dimension but the same depth as the input image, is searched for specific patterns using filters. This filter is moved across the input image's width and height to produce an activation map, after which the dot product is computed. On the input image, several filters that can distinguish between various features are convolved to create activation maps, which are then delivered to the CNN's subsequent layer.

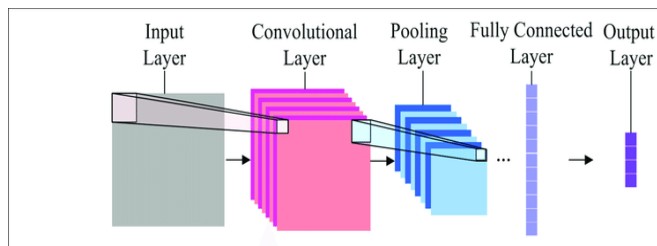


Figure 3 Structure of Simple CNN (ResearchGate.com 2021)

3.2.2 Support Vector Machine

To deal with classification and regression problems, Support Vector Machine (SVM), a supervised machine

learning technique, can be used. It is, however, typically employed to address classification problems. Each data item in the SVM technique is represented as a point in n-dimensional space (where n is the number of features), with each feature's value being its coordinate value. Finding the hyper-plane that best distinguishes the two classes is the next stage in categorization. The coordinates for each individual observation are represented by a support vector. The SVM classifier is the most effective frontier for dividing the two classes of hyper-plane and line.

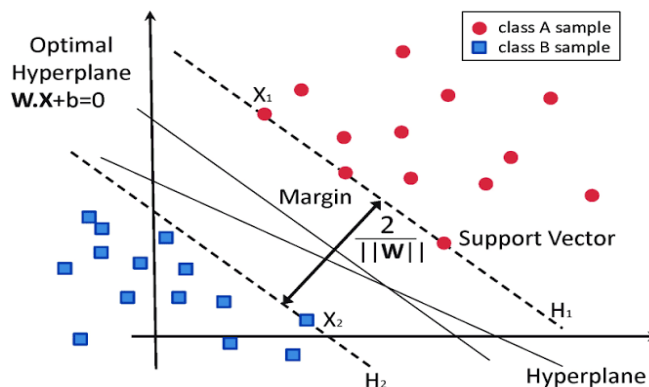


Figure 2: SVM hyper-plane (ResearchGate.com 2021)

There are different types of SVM, this model employed Bi-class SVM for its model as shown in Figure 2 above.

The following equations (4) to (10) are adapted for SMV and the hyper plane is equally illustrated in Figure 3.3

$$\frac{w}{\|w\|} (x - y) = \text{width} = \frac{2}{\|w\|} \quad (5)$$

$$W \cdot x + b = 1 \quad (6)$$

$$w \cdot y + b = -1 \quad (7)$$

$$w \cdot x + b - w \cdot y - b = 1 - (-1) \quad (8)$$

$$w \cdot x - w \cdot y = 2 \quad (9)$$

$$\frac{w}{\|w\|} (x - y) = \frac{2}{\|w\|} \quad (10)$$

Where w is weight and b is the hyper plane, which is likewise a vector and should always be greater than zero, and x is a vector point on the x axis and y is a vector point on the y axis. The algorithm 1 illustrated SVM algorithm

Algorithm 1 Support Vector Machine (Sunil ray, 2017)

candidateSV = {closest pair from opposite classes}

while there are violating points do

Find a violator

candidateSV = candidateSVU violator

If any $ap < 0$ due to addition of c to S then

candidateSV = candidateSV \ p

repeat till all such points are pruned

end if

end while

3.3 Standard Performance Metrics

3.3.1 Accuracy

A common performance indicator for classification algorithms is accuracy. This is defined total number of accurate forecasts divided by the total number of predictions this formula can be used to easily calculate accuracy from the confusion matrix:

$$\text{Accuracy} = \frac{\text{Number of correct predictions}(T_p+T_n)}{\text{Total population}(T_p+F_p+F_n+T_n)}$$

Where: T_p stands for True Positive. T_n stands for True Negative.

F_p stands for False Positive. F_n stands for False Negative.

3.3.2 Recall or Sensitivity

Recall, also known as sensitivity, is defined as the total number of correct positive predictions divided by the sum of correct positive forecasts and incorrect positive predictions. The recall value is between 0 and 1.

$$\text{Recall} = \frac{\sum T_p}{(\sum T_p + \sum F_n)} \tag{12}$$

3.3.3 Specificity

Specificity, is defined as the sum of all correct negative predictions divided by the total of both correct and incorrect negative predictions. The specificity value is between 0 and 1.

$$\text{Specificity} = \frac{\sum T_n}{\text{ConditionNegative}(\sum F_p + \sum T_n)} \tag{13}$$

3.3.4 Precision

Precision is defined as the sum of all accurate positive forecasts divided by the total of all accurate positive and negative predictions. The precision value is a number between 0 and 1.

$$\text{Precision} = \frac{\sum T_p}{\sum T_p + \sum F_p} \tag{14}$$

3.3.5 F1-Score

The harmonic mean of a system's precision and recall values is known as the F-score. The following equation can be used to determine it: $2 \times [(\text{Precision} \times \text{Recall}) / (\text{Precision} + \text{Recall})]$.

$$\text{F1-Score} = \frac{2T_p}{(2T_p + (T_p + F_n))} \tag{15}$$

$$= \frac{T_p}{(T_p + 1/2(T_p + F_n))} \tag{16}$$

F-score can be as high as 1 which denotes perfect precision and recall, or as low as 0, which implies both precision and recall are zero.

4.0 Result and Discussion

The research was conducted by extracting relevant features from the datasets, as outlined in the methodology, using chi-squared. However, before we train the data into Machine Learning Algorithm, we need to input the Label Encoder. Subsequently, Data preprocessing was done to clean the data set in order to make it compatible to use. However, the machine learning algorithm used to build this stroke prediction model in this research is CNN and SVM classifier and the performance evaluation were determined. Anaconda3.6 (Python Distribution), Tensor flow PyCharm Community Editor 2021 was used as the development environment.

4.1 Confusion Matrix

Confusion Matrix Classification of Chi-Square with CNN.

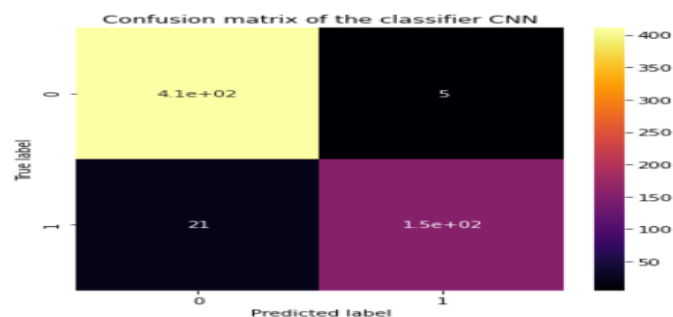


Figure 4 Classification of Chi-Square with CNN (TP = 411, TN = 154, FN = 21, FP = 5).

Performance	Chi-Square + SVM (%)	Chi-Square + CNN (%)
Sensitivity	98.10	95.14
Specificity	92.42	96.86
Precision	95.37	98.80
Accuracy	95.91	95.60
F1 score	96.71	96.93

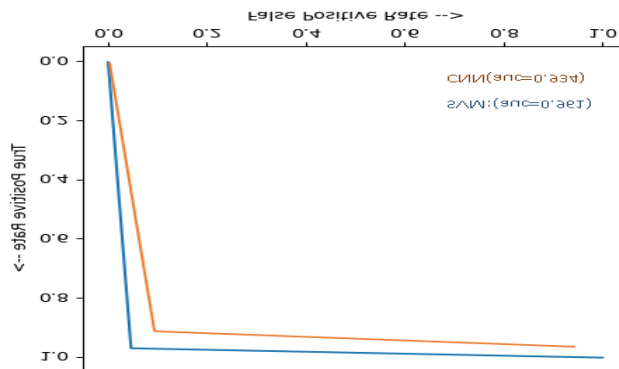


Figure 7 ROC curve for Chi-square with SVM

Table 1. Standard Performance Matrix for Stroke/HealthCare dataset

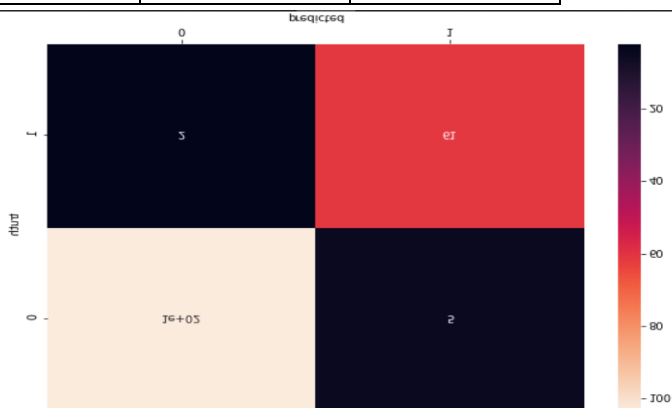


Figure 5 Classification Chi-Square with SVM (TP = 103, TN = 61, FP = 5, FN = 2).

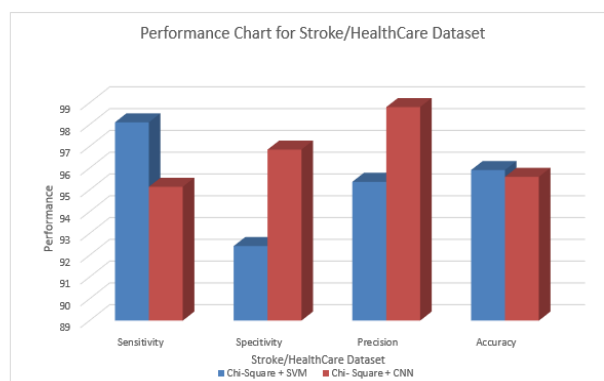


Figure 8: Performance of the Model on Stroke/HealthCare dataset

4.2 Scatter Plot

This shows relationship that exist between two or more variables. Data visualization techniques like scatter plots can be used to display a trend. The scatter plot can be seen in Figure 6.

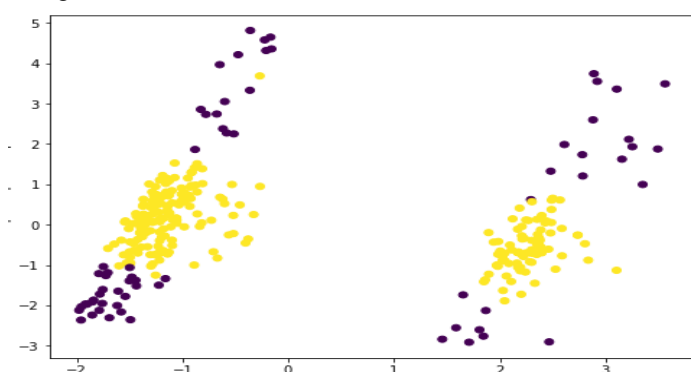


Figure 6 Scatter plot

4.3 The Receiver Operating Characteristics

The (ROC) Curve for Chi-Square with SVM is shown in Figure 7. The effectiveness of the categorization threshold is displayed by the ROC Curve. The real positive rate versus the false positive rate on the curve.

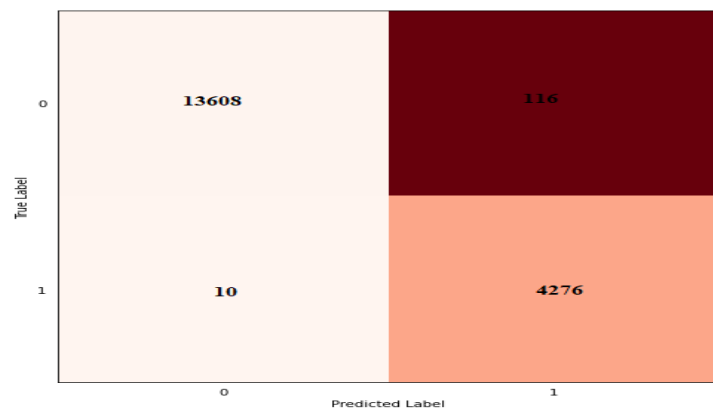


Figure 9: Classification of CNN with Chi-Square (TP = 13608, TN = 4276, FP = 3259, FN=10).

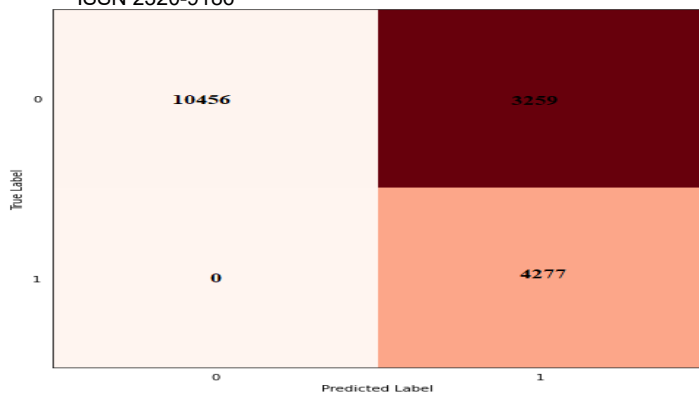


Figure 10: Classification of SVM with Chi-Square (TP = 10456, TN = 4277, FP = 3259, FN=0).

Table 2: Standard Performance Matrix for the BIDMC-PPG Dataset

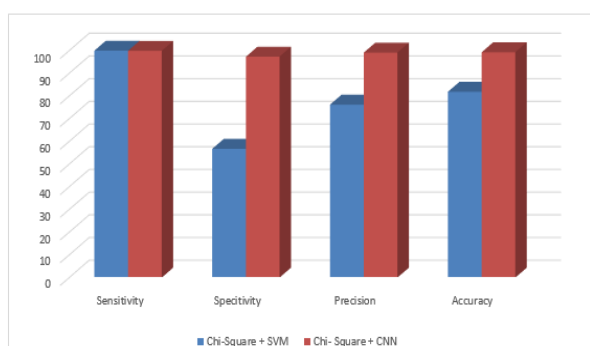


Figure 11: Performance of the Model on BIDMC-PPG dataset

Table 3 Summary of the two datasets (HealthCare and BIDMC-PPG)

Standard Performance Metrics	Chi-Square + SVM Health Care Dataset %	Chi-Square + CNN Health Care dataset %	Chi-Square + SVM BIMDC-PPG Dataset %	Chi-Square + CNN BIMDC-PPG Dataset %
Sensitivity	98.1	98.14	100	99.93
Specificity	92.42	96.86	56.75	97.65
Precision	95.37	98.80	76.24	99.15
Accuracy	95.91	95.60	81.89	99.30
F1 score	96.71	96.93	86.52	99.54

Performance	Chi-Square + SVM	Chi-Square + CNN
Sensitivity	100	99.93
Specificity	56.75	97.36
Precision	76.24	99.15
Accuracy	81.89	99.30
F1 score	86.52	99.54

The figure 12 above shows the Comparison of Stroke/HealthCare Dataset and BIDMC-PPG Dataset based on standard performance metrics,

4.5 Comparison of the Findings

Table 4: Summary of the Model Findings

Author	Technique	Dataset	Result(Average)
Kallam et al., 2022	KNN + SVM	Stroke/HealthCare	89.9%
Lunugala et al.,2021	KNN + SVM	Stroke/Healthcare	94%
2024 model	Chi-Square + SVM	Strike/HealthCare	95%
2024 model	Chi-Square + CNN	Stroke/HealthCare	96.7%

5.0 Summary and Conclusion

This study examines the interaction between magnetization transfer (MT) and blood oxygen

level-dependent (BOLD) contrast in functional magnetic resonance imaging (fMRI), focusing on higher blood oxygenation leading to reduced magnetization transfer ratio (MTR), particularly in brain tumor regions. Using datasets from Kaggle, the research employed chi-square for feature selection and deep learning classifiers CNN and SVM to predict BOLD abnormalities with standard performance evaluation metrics. Results were compared with previous findings, emphasizing the need for more precise detection of BOLD abnormalities, particularly in early development stages. It is important to stress that the methods used are meant to enhance the development of stroke prediction model. A larger dataset is recommended for further research in order to extend the model's range of applicability. Dimensionality reduction methods that offer the best precision among the two algorithm such as CNN and SVM should also be considered.

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Author's brief profile

Dauda .F.A (M.Tech) is an engineer at the Nigerian Television Authority, His research focus spans along machine learning, cyber security and optimization of telecommunication networks. He can be reached via (+234)-8085818815 and by email-fard4trust@gmail.com

Ayeni O.A is a senior lecturer at federal university of Technology, Akure Nigeria. His research interest are machine learning, software engineering. His email is olaniyiayeni17@gmail.com and can be reached via +234-8034311198

Marafa .S. I (B.Tech) is currently a master's student at the department of software engineering, Nankai University,

Tianjin China. His research areas include fault tolerance, Machine Learning, Optimization and software engineering. He can be reached by phone on (+86)-13752034504 and via email-marafasalman@gmail.com.

Amadu W.B (B.Sc.) is currently a master's student at the department of software engineering, Nankai University, Tianjin China. His research areas includes human computer interaction and software engineering. He can be reached by phone on (+86)-15922144231 and via email-codewithbawurie@gmail.com

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