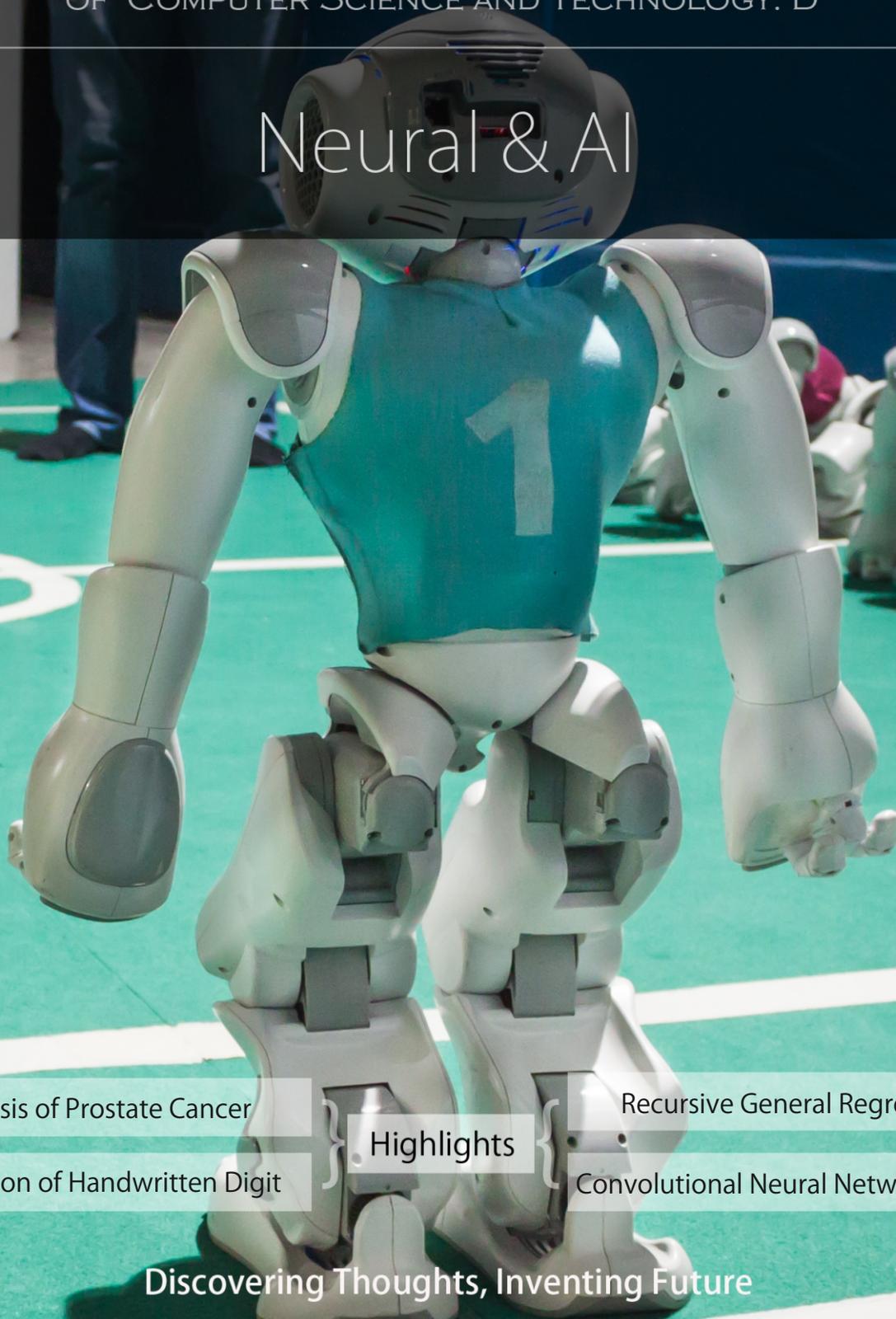


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Neural & AI



Diagnosis of Prostate Cancer

Recognition of Handwritten Digit

Highlights

Recursive General Regression

Convolutional Neural Network (CNN)

Discovering Thoughts, Inventing Future

VOLUME 19 ISSUE 2 VERSION 1.0



GLOBAL JOURNAL OF COMPUTER SCIENCE AND TECHNOLOGY: D
NEURAL & ARTIFICIAL INTELLIGENCE



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An Optimized Recursive General Regression Neural Network Oracle for the Prediction and Diagnosis of Diabetes

By Dana Bani-Hani, Pruthak Patel & Tasneem Alshaikh

State University of New York at Binghamton

Abstract- Diabetes is a serious, chronic disease that has been seeing a rise in the number of cases and prevalence over the past few decades. It can lead to serious complications and can increase the overall risk of dying prematurely. Data-oriented prediction models have become effective tools that help medical decision-making and diagnoses in which the use of machine learning in medicine has increased substantially. This research introduces the Recursive General Regression Neural Network Oracle (R-GRNN Oracle) and is applied on the Pima Indians Diabetes dataset for the prediction and diagnosis of diabetes. The R-GRNN Oracle (Bani-Hani, 2017) is an enhancement to the GRNN Oracle developed by Masters et al. in 1998, in which the recursive model is created of two oracles: one within the other. Several classifiers, along with the R-GRNN Oracle and the GRNN Oracle, are applied to the dataset, they are: Support Vector Machine (SVM), Multilayer Perceptron (MLP), Probabilistic Neural Network (PNN), Gaussian Naïve Bayes (GNB), K-Nearest Neighbor (KNN), and Random Forest (RF). Genetic Algorithm (GA) was used for feature selection as well as the hyperparameter optimization of SVM and MLP, and Grid Search (GS) was used to optimize the hyperparameters of KNN and RF. The performance metrics accuracy, AUC, sensitivity, and specificity were recorded for each classifier.

Keywords: *GRNN oracle, data mining, machine learning, genetic algorithm, diabetes, prediction model.*

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An Optimized Recursive General Regression Neural Network Oracle for the Prediction and Diagnosis of Diabetes

Dana Bani-Hani^α, Pruthak Patel^σ & Tasneem Alshaikh^ρ

Abstract- Diabetes is a serious, chronic disease that has been seeing a rise in the number of cases and prevalence over the past few decades. It can lead to serious complications and can increase the overall risk of dying prematurely. Data-oriented prediction models have become effective tools that help medical decision-making and diagnoses in which the use of machine learning in medicine has increased substantially. This research introduces the Recursive General Regression Neural Network Oracle (R-GRNN Oracle) and is applied on the Pima Indians Diabetes dataset for the prediction and diagnosis of diabetes. The R-GRNN Oracle (Bani-Hani, 2017) is an enhancement to the GRNN Oracle developed by Masters et al. in 1998, in which the recursive model is created of two oracles: one within the other. Several classifiers, along with the R-GRNN Oracle and the GRNN Oracle, are applied to the dataset, they are: Support Vector Machine (SVM), Multilayer Perceptron (MLP), Probabilistic Neural Network (PNN), Gaussian Naïve Bayes (GNB), K-Nearest Neighbor (KNN), and Random Forest (RF). Genetic Algorithm (GA) was used for feature selection as well as the hyperparameter optimization of SVM and MLP, and Grid Search (GS) was used to optimize the hyperparameters of KNN and RF. The performance metrics accuracy, AUC, sensitivity, and specificity were recorded for each classifier. The R-GRNN Oracle was able to achieve the highest accuracy, AUC, and sensitivity (81.14%, 86.03%, and 63.80%, respectively), while the optimized MLP had the highest specificity (89.71%).

Keywords: GRNN oracle, data mining, machine learning, genetic algorithm, diabetes, prediction model.

I. INTRODUCTION

According to the World Health Organization (WHO), the number of people with diabetes had quadrupled since 1980. Prevalence is increasing worldwide, particularly in low- and middle-income countries. It is estimated that medical costs and lost work and wages for people diagnosed with diabetes is \$327 billion yearly and twice as much as those who do not have diabetes (CDC, 2018). About 422 million people worldwide have the disease. It can lead to serious complications in any part of the body such as kidney disease, blindness, nerve damage, and heart

disease (Temurtas et al., 2009), and increases the risk of dying prematurely – diabetes is the seventh leading cause of death worldwide.

There are many factors to analyze to diagnose diabetes in a patient which makes the physician's job difficult. Thus, to save time, cost, and the risk of an inexperienced physician, classification models may be built to help predict and diagnose diabetes based on previous records (Polat et al., 2008). The use of machine learning in medicine has increased substantially. With the exponential growth of big data, manual efforts to analyze such data are impossible, therefore, automated techniques such as machine learning are used. Machine learning is defined as having the ability for a system to learn on its own, by extracting patterns from large raw data (Goodfellow et al., 2016).

The General Regression Neural Network Oracle (GRNN Oracle), developed by Masters et al. in 1998, combines the predictions of individually trained classifiers and outputs one superior prediction by determining the error rate for each classifier from a set of observations in order to assign weights to favor classifiers with lower error rates. The final prediction for an unknown observation is calculated by summing each classifier's prediction for that unknown observation multiplied by the classifier's weight; the classifiers with lower error rates have greater influence on the final prediction.

Because of the strong capabilities of the oracle, it has been enhanced to consist of two GRNN Oracles; one within the other. First proposed by Bani-Hani (2017), the first oracle is created through its own combination of algorithms and acts now as a classifier as it has its own predictions and error contribution to a set of unknown observations. It is then combined with other classifiers to create a new, outer oracle that has been named the Recursive General Regression Neural Network Oracle (R-GRNN Oracle). This study is applied on the Pima Indians Diabetes dataset where Genetic Algorithm (GA) is used for feature selection and hyperparameter optimization, and the proposed classifier, the Recursive General Regression Neural Network Oracle (R-GRNN Oracle), is applied along with seven other classifiers, namely Support Vector Machine (SVM), Multilayer Perceptron (MLP), Random Forest (RF), Probabilistic Neural Network (PNN), Gaussian Naïve Bayes (GNB), K-

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Nearest Neighbor (KNN), and the GRNN Oracle, for the prediction and diagnosis of diabetes. The R-GRNN Oracle was able to achieve the highest accuracy and AUC (area under the Receiver Operating Characteristic (ROC) curve) performance metrics in comparison to the other classifiers used.

The remainder of this paper is organized as follows: Section 2 presents the related work regarding this study. Section 3 explains the methodology adopted in this study. Section 4 shows the experimental analysis and results. Section 5 presents the discussion. And Section 6 presents the conclusion and future work.

II. RELATED WORK

Prediction models are vastly implemented in clinical and medical fields to support diagnostic decision-making (Zheng et al., 2015). Very few of its diagnostic applications include the prediction of Alzheimer's disease (López et al., 2009; Ramírez et al., 2013; Beheshti et al. 2017), Parkinson's disease (Gil and Manuel, 2009; Haller et al., 2012; Aich et al., 2018), and cancer such as breast cancer (Akay, 2009; Karabatak and Ince, 2009; Zheng et al., 2014; Bhardwaj and Tiwari, 2015), lung cancer (Jayasurya et al., 2010; Sun et al., 2013; Sakumua et al., 2017), and leukemia (Fang and Grzymala-Busse, 2006; Manninen et al., 2013). A plethora of studies have been carried out on the prediction of diabetes. Polat et al. (2008) used Least Square Support Vector Machine (LS-SVM) for the prediction of diabetes through Generalized Discriminant Analysis (GDA). Park and Edington (2001) applied sequential multi-layered perceptron (SMLP) with back propagation learning on 6,142 participants. The early detection of diabetes type II was conducted by Zhu et al. in 2015 in which they proposed a dynamic voting scheme ensemble. Thirugnanam et al. (2012) adopted techniques such as fuzzy logic, Neural Network (NN), and case-based reasoning as an individual approach (FNC) for the diagnosis of diabetes.

Regarding the dataset used in this study, the Pima Indian Diabetes dataset, various studies used the dataset to create prediction models for the prediction and diagnosis of diabetes. Kayaer and Yildirim (2003) applied an MLP, Radial Basis Function (RBF), and a General Regression Neural Network (GRNN) on the Pima Indian Diabetes dataset. Their highest accuracy was achieved by the GRNN at 80.21%. Carpenter and Markuzon(1998) applied several techniques on the dataset including, but not limited to, KNN, Logistic Regression (LR), the perceptron-like ADAP model, ARTMAP, and ARTMAP-IC (named for instance counting and inconsistent cases), in which the ARTMAP-IC obtained the highest accuracy at 81%. Bradley (1997) also used various classifiers on the dataset where the author's main purpose was to assess the use of the AUC as a performance metric. The author was able to

achieve the highest accuracy of 78.4% using a two-layer MLP. A hybrid of Artificial Neural Network (ANN) and Fuzzy Neural Network (FNN) was proposed by Kahramanli and Allahverdi in 2008. Their approach resulted in an accuracy of 84.2%.Lekkas and Mikhailove (2010) applied Evolving Fuzzy Classification (EFC) to two datasets including Pima Indians Diabetes dataset. They were able to reach an accuracy of 79.37%.Miche et al. (2010) presented the Optimally Pruned Extreme Learning Machine (OP-ELM) and compared its performance to a MLP, SVM, and Gaussian Process (GP) on several regression and classification datasets. Regarding the dataset concerning this study, the GP had the highest accuracy among the classifiers tested with an accuracy of 76.3%. Huang et al. (2004) was able to achieve an accuracy of 77.31% using SVM, although their paper proposed an algorithm called Extreme Machine Learning (EML). Kumari and Chitra (2013) used SVM and obtained an accuracy of 78.2%. Al Jarullah (2011) also found the accuracy to be 78.2% using Decision Trees (DTs). Bradley and Mangasarian (1998) applied Feature Selection via Concave (FSC), SVM, and Robust Linear Program (RLP) in which the RLP had the highest accuracy on the Pima Indian Diabetes dataset at 76.16%. Using a novel Adaptive Synthetic (ADASYN) sampling approach, He et al. (2008) achieved an accuracy of 68.37%.Şahan et al. (2005) proposed a new artificial immune system named Attribute Weighted Artificial Immune System (AWAIS) in which they attained a classification accuracy of 75.87%.Luukka (2011) used Similarity-Based (S-Based) classifier with fuzzy entropy measures as a feature selection method and reached an accuracy of 75.97%. Using Extreme Gradient Boosting (XGBoost), Christina et al. (2018) achieved 81% accuracy. Ramesh et al. (2017) used deep learning, more specifically Restricted Boltzmann Machine (RBM), on the dataset with 81% accuracy. Vaishali et al. (2017) applied GA for feature section with a Multi Objective Evolutionary Fuzzy (MOEF) classifier and obtained an accuracy of 83.04%.

Many other studies have been carried out on the same dataset, however, due to reporting training accuracies rather than testing and validation accuracies, they have been excluded from the literature review for several reasons including, and most importantly, overfitting, as overfitting generates higher accuracies due to fitting the model too perfectly to the training set making the model not generalized enough. The other studies that have been excluded are those that obtained high accuracies but did not mention whether they obtained it from a training set or a testing or validation set making the results questionable. It is worthy to note that this study applied 4-fold cross validation to train each classifier and were tested on a validation subset that did not take part in neither the training nor testing steps.

III. METHODOLOGY

Six individual classifiers were used in this research: SVM, MLP, RF, PNN, GNB, and KNN, in which some were used to create the GRNN Oracle, and some were combined with the first oracle to create the R-GRNN Oracle. The software and language used for this study was Python 3.6 and the hardware specifications were Intel® Core™ i7-8750H CPU @ 2.20GHz with 32.0 GB RAM.

a) Individual Classifiers

Support Vector Machine: SVM is a statistical learning method proposed by Vapnik (1995). It is a widely used supervised machine learning algorithm used for both classification and regression. SVM works by finding the hyperplane that maximizes the margin between the classes in the feature space, as seen in Figure 1. Support vectors are observations that help dictate the hyperplane. It classifies new samples based on which side of the boundary they are located on.

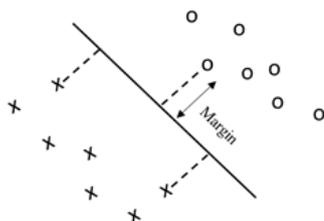


Figure 1: A simple linear SVM

Multilayer Perceptron: MLP is a feed forward artificial NN that is a modification of the standard linear perceptron. It is an algorithm that does not require a linear relationship between the independent variables and the dependent variable as it is able to solve problems that are not linearly separable through the use of activation functions located in each node. An MLP consists of an input layer, a hidden layer(s), and an output layer. It is a supervised machine learning algorithm that exploits back propagation to train itself to optimize the weights of each edge connecting two nodes. It is the most frequently used NN (Hossain et al., 2017) and is widely-used for classification, regression, recognition, prediction, and approximation tasks. Figure 2 illustrates an example of an MLP with one hidden layer with five hidden nodes.

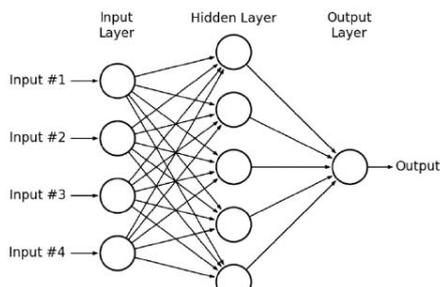


Figure 2: An MLP NN with one hidden layer (Mohamed et al. 2015)

Random Forest: RF is an ensemble created by Ho (1995) that is used for classification and regression. It has received great attention from researchers because of its simplicity and ensemble learning characteristics (Breiman, 2001). A RF is made up of many DTs where they are created through a random sampling process with replacements (Belgiu and Drăguț, 2016). RF uses the bagging technique to improve the model's performance by decreasing the model's variance without increasing the bias which helps overcome DTs' poor habit of overfitting.

Probabilistic Neural Network: PNN is a feedforward NN which is used for classification and pattern recognition problems. The probability density function (PDF) for each class is estimated using a Parzen window (kernel density estimation (KDE)) and a non-parametric function. It then uses the Baye's strategy for estimating the class probability of a new input using the PDF of each class (Karthikeyan et al., 2008). It consists of three layers: an input layer, a hidden layer, and an output layer.

Gaussian Naïve Bayes: GNB is a supervised learning algorithm that is widely used for classification problems because of its simplicity and accurate results (Farid et al., 2014). It uses Bayes theorem as its framework (Griffis et al., 2016) and has strong independence assumptions between the independent variables. One important advantage of GNB is that it could estimate the parameters necessary for classification by training on a small training set.

K-Nearest Neighbor: KNN is a non-parametric, lazy learning method for classification and regression tasks (Zhang, 2016). k is a user-set parameter that represents the number of known observations closest to the unknown observation mapped out in the feature space. For classification tasks, the class of the new observation is based on the majority class surrounding it; k is typically an odd number. For regression tasks, the new observation is taken as the average of its k neighbors.

b) Optimization Algorithms

Genetic Algorithm: GA is a population-based metaheuristic developed by John Holland in the 1970s (Holland, 1992). It is a widely used optimization technique inspired by nature, more specifically, evolution and survival of the fittest. It finds solutions throughout the search space using two main operators: crossover and mutation. Every solution is represented as a chromosome with several alleles encoded with genetic material that measure the fitness value of the objective function. Crossover produces two somewhat different chromosomes, called offspring, from two parents. The mutation operator is applied on the offspring at a given probability to create diversity in the population pool, which allows diversification in the search space.

Grid Search: GS is an exhaustive search optimization technique that works with user-set parameters for an algorithm. It is a traditional approach to manual hyperparameter tuning in which all possible combinations of the parameters selected are tested. It is guided by a performance metric and typically measured by cross validation on the training set or an evaluation on a validation subset (Hsu et al., 2003).

c) GRNN Oracle

The GRNN Oracle combines the predictive powers of several machine learning classifiers that were trained independently to form one superior prediction (Li, 2014). It determines the error rate for each classifier involved in the oracle in order to assign weights to favor classifiers with lower error rates. The final prediction for an unknown observation is calculated by summing each classifier's prediction for that unknown observation multiplied by the classifier's weight.

The steps involved in predicting a class (output) for a single observation are: first, each classifier (k) is trained on a training subset of the data and tested on another subset to obtain predictions for the observations. Second, each prediction obtained from the previous step (probability of belonging to each class) for each observation is compared to its actual prediction (actual class) and the Mean Squared Error (MSE) is calculated through Formula 1:

$$error_{i,k} = \sum_{m=1}^{num_classes} (AP_m - PP_{m,k})^2 / num_classes \quad (1)$$

where $error_{i,k}$ is the mean squared error of a known observation (i) from classifier (k), $num_classes$ is the total number of classes, AP_m is the actual probability of the known observation (i) for being class (m) and $PP_{m,k}$ is the predicted probability of being class (m) from classifier (k). Third, for a given unknown observation in the validation set (an observation that needs to be predicted), the distance between the observation and all the known samples in the testing set is calculated, and each known observation has a particular weight for the unknown observation. The distance is calculated using Formula 2 and the weight is calculated using Formula 3.

$$D(\vec{x}, \vec{x}_i) = \frac{1}{p} \sum_{j=1}^p ((x_j - x_{ij}) / \sigma_j)^2 \quad (2)$$

$$weight_i = e^{-D(\vec{x}, \vec{x}_i)} \quad (3)$$

where \vec{x} represents the vector of features belonging to the unknown observation, [feature 1, feature 2, ..., feature p], \vec{x}_i is the feature vector for the known observation, x_j is the j -th feature of the unknown observation, x_{ij} is the j -th feature of the known observation, σ_j is an adjustable sigma parameter for the j -th feature and p is the total number of features. w_k is

the weight (trust) of classifier (k) on the prediction of the unknown observation. Fourth, for the unknown observation, for each classifier (k), the predicted squared error is obtained through the MSE and weight of each known observation (Formula 4).

$$error_k(\vec{x}) = (\sum_{i=1}^n error_{i,k} * weight_i) / \sum_{i=1}^n weight_i \quad (4)$$

Fifth, each classifier (k) has an amount of trust for the final prediction of the unknown observation where the higher the weight, the more influence it has on the final prediction of the unknown observation (Formula 5).

$$w_k = (1/error_k) / (\sum_{l=1}^L 1/error_l) \quad (5)$$

$$\sum_{k=1}^L w_k = 1 \quad (6)$$

where L is the total number of classifiers, and l indicates classifier l . The sum of w_k for all classifiers (L) equals one (Formula 6). Lastly, through the amount of error each classifier (k) contributes, their trust/weight is multiplied by the unknown observation's prediction and summed up to form the final prediction for that particular unknown observation (Formula 7).

$$\hat{y} = \sum_{k=1}^L w_k * q_k \quad (7)$$

where \hat{y} is the prediction of the unknown observation outputted by the GRNN Oracle represented as a class membership vector and q_k is the predicted class membership vector for the unknown observation given by classifier (k).

d) Recursive GRNN Oracle

The best combination of classifiers that were trained and tested individually and independently was used to make the first oracle. By having predictions outputted from the oracle, it now acts as any other machine learning classifier would. The best combination of classifiers that would enhance the performance of the first GRNN Oracle is selected and this selected combination, including the first oracle, creates the second oracle, the R-GRNN Oracle. The accuracy, AUC, sensitivity, and specificity of its final predictions are taken, along with the same performance metrics of the inner GRNN Oracle and the individual classifiers for the final comparison.

IV. EXPERIMENTAL ANALYSIS AND RESULTS

a) Dataset Description

The Pima Indians Diabetes dataset was used in this study where it was originally a study conducted by the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) on the Pima Indian population near Phoenix, Arizona, in 1965 (Smith et al., 1988). There is a total of 768 observed patients where 268 of them have diabetes, which indicates the imbalanced property of the dataset. In this dataset, there are eight independent variables (features) and one dependent variable (outcome: diabetes or no diabetes), as

presented in Table 1. More detailed attributes distributions and statistical analysis are further shown in Figure 3, where the color orange signifies patients who

have diabetes. All patients recorded are females at least 21 years old of Pima Indian heritage.

Table 1: Pima Indians Diabetes dataset feature description

	Description	Type
X1	No. of Pregnancies	Discrete
X2	Plasma Glucose Concentration	Continuous
X3	Diastolic Blood Pressure	Continuous
X4	Skin Thickness	Continuous
X5	2-hr Serum Insulin	Continuous
X6	BMI	Continuous
X7	Diabetes Pedigree Function	Continuous
X8	Age	Continuous
Y	Outcome: Diabetes/No Diabetes	Discrete

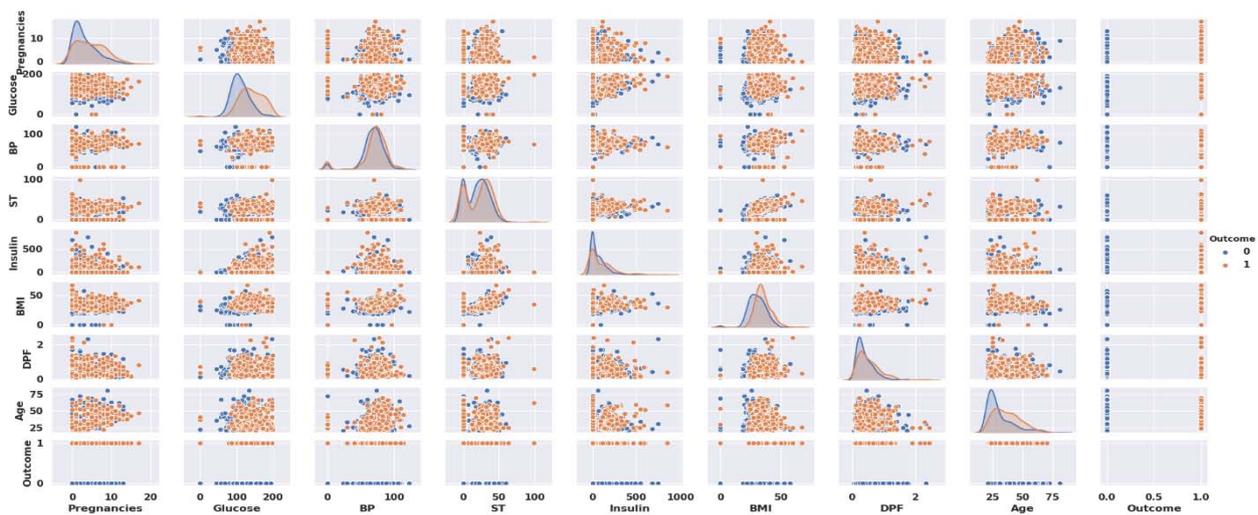


Figure 3: Attributes distributions and statistical analysis of the Pima Indians Diabetes dataset (printed in color)

b) Data Preprocessing

The first step taken in the data preprocessing phase was excluding outliers as they can drastically affect the model's predictive ability. Any point that was three standard deviations (3σ) away from the mean of any given feature was excluded. The original dataset had 768 patients, and after outlier removal, the new dataset contained 709 patients where 243 of them had diabetes. The next step was to correct the imbalanced property of the data. Since only 243 patients from the remaining 709 had diabetes, this is a class imbalance problem where those with diabetes only make up 34% of the data. Thus, an oversampling approach was applied to the minority class. Oversampling was favored over under sampling because the dataset's size concerning the number of observations was already small, and concerning how the R-GRNN Oracle works, it would not be a wise approach to remove observations, as the recursive oracle requires the dataset to be relatively large for the data subsets to be drawn. After this step, a normalization technique was applied to each independent variable in which the variable was scaled to

a range between 0 and 1; 0 indicating the lowest value in a particular feature and 1 indicating the highest. The formula of normalization is given in Formula 8 where $\min V_i$ is the minimum value in the set of values in feature V_i , and $\max V_i$ is the maximum value in feature V_i . This is performed to ensure each feature has an equal weight so that no one feature would outweigh another before the creation of the prediction model.

$$\bar{v}_j = (v_j - \min V_i) / (\max V_i - \min V_i) \quad (8)$$

c) Hyperparameter Optimization

The hyperparameters in any algorithm contributes greatly to the output of the model, therefore, determining the optimal (or near-optimal) combination of hyperparameters would yield the best result. For example, some of a NN's hyperparameters include the number of hidden layers a user sets and the number of hidden nodes in each hidden layer. Hyperparameters are defined as the properties of a model that the user can set the value to. They are different from parameters as parameters are changed internally by the model itself during training rather than set by the user before the

training process. An example to a parameter is the weights of a NN, as they are adjusted through back propagation using Gradient Decent (or any other optimizer) rather than by the user.

GA was utilized to optimize the performances of the SVM and MLP, while GS was applied on KNN and RF. The reason that GS was used instead of GA was that both KNN and RF have one parameter of interest: the number of neighbors and the number of DTs, receptively. Therefore, no combinations of hyperparameters are needed which makes it a straightforward exhaustive search. SVM and MLP however have more than one hyperparameter that need to be optimized simultaneously, which also include continuous values, this is why GA is used.

Formula 9 shows the fitness function (FV) used to evaluate each chromosome (each solution). They were evaluated based on their prediction accuracies, where TP is the true positive rate, in which it indicates those who actually have diabetes and were predicted to have diabetes, TN is the true negative rate where those who do not have diabetes were predicted not having diabetes, FP is the false positive rate in which those without diabetes were falsely predicted that they do have diabetes, FN is the false negative rate, where patients have diabetes but were falsely predicted that they don't, and K is the number of folds required for the

K -fold cross validation, in which it was set to four for this study.

$$FV = \frac{1}{K} \left[\sum_{k=1}^K \frac{TP+TN}{TP+FP+TN+FN} \right] \quad (9)$$

The hyperparameters that were included in this study relating to SVM were c and gamma (γ), where both take on continuous values, while MLP's hyperparameters included the learning rate (α), momentum, the number of hidden layers, the number of hidden nodes in each hidden layer, and the solver, where α and momentum are continuous, the number of hidden layers and nodes are integers, and the solver is categorical. Figure 4 and Figure 5 show the encoding (genotype) for the SVM and MLP parameters, respectively, where each continuous hyperparameter was encoded with a binary chromosome with a length of 15 alleles.

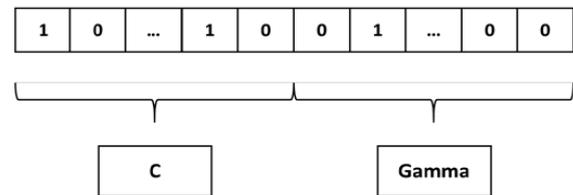


Figure 4: Chromosome encoding of the SVM parameters



Figure 5: Chromosome encoding of the MLP parameters

SVMs can handle nonlinear classifications through transforming inputs into feature vectors with the use of kernels. The SVM kernel set for this study is the Radial Basis Function (RBF) in which it is a popular Gaussian kernel function. Some of RBF's greatest advantages are its high accuracy, its fast convergence, and its applicability in almost any dimension. c is a regularization hyperparameter that determines how correctly the hyperplane between the classes separates the data. It controls the trade-off between model complexity and training error (Joachims, 2002). γ has a serious impact on the classification accuracy as it defines the influence of each training observation (Tuba and Stanimirovic, 2017), with lower values meaning "far" and higher values meaning "close". It can be thought of as the inverse of the radius of influence of observations selected by the model as support vectors. Figure 6-A shows SVM's accuracy achieved by GA in each of the 100 generations run.

With MLP, the activation function set in this study was the Rectified Linear Unit (ReLU). Activation

functions are operations which map an output to a set of inputs. They are used to impart non-linearity to the network structure (Acharya et al, 2017). Because ReLU returns a positive number, i.e. $\max(x, 0)$, the two major advantages of it are sparsity and the reduced likelihood of the "vanishing gradient" problem, as adding as many hidden layers as one would like would not cause the gradient multiplication to reach a very small number that it will likely "vanish" with more layers to add. Solvers in NNs train and optimize the weights connecting the nodes between two-adjacent layers. The two solvers considered for this study are Stochastic Gradient Decent (SGD) and Adam, a variant of SGD. The other two important hyperparameters are α and momentum. α controls how fast the network learns during training and momentum helps to converge the data (Acharya et al, 2017). They can be thought of the stepping size and direction in the search space. Figure 6-B shows MLP's accuracy achieved by GA in each of the 100 generations run.

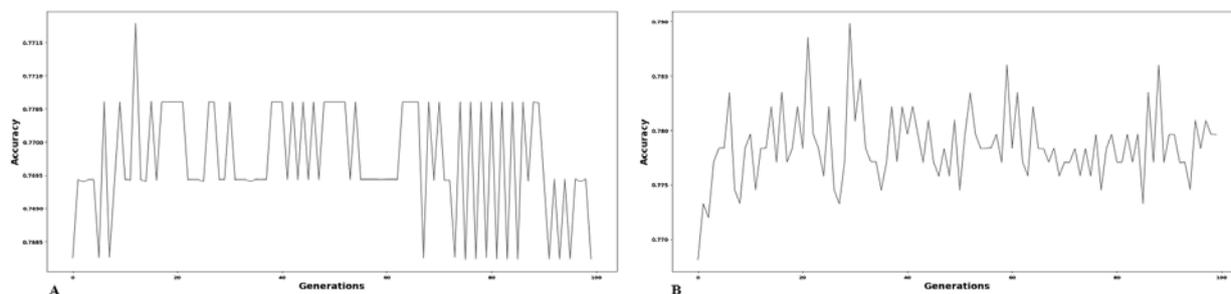


Figure 6: Prediction accuracy throughout 100 generations, A- SVM, B- MLP

d) Feature Selection

Feature selection plays an important role in classification for several reasons (Luukka, 2011). First, it can simplify the model's complexity which helps reduce computational cost, and when the model is taken for practical use fewer inputs are needed. Second, by removing redundant features from the dataset one can also make the model more transparent and more comprehensible, providing better explanation of suggested diagnosis, which is an important requirement in medical applications. Feature selection process can also reduce noise in which it may enhance classification accuracy.

GA was applied for feature selection through SVM and its optimized hyperparameters from the previous step. The solution representation for feature selection was embodied by a chromosome of eight binary values (i.e. 0's and 1's). An allele of the value 0 indicates that feature *n* was not included while an allele of 1 indicated that it was included; *n* is the *n*th feature in the dataset. To explain further, Figure 7 illustrates an example where the encoding of the selected features #1, #2, #3, and #6, out of eight features is shown. Chromosomes with a subset of features selected are then evaluated based on their accuracy. The subset of features that attained the highest accuracy was selected for further analysis. Formula 9 was also used as the fitness function for chromosome evaluation.

1	1	1	0	0	1	0	0
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Figure 7: Chromosome encoding of a selected subset of features

e) Recursive GRNN Oracle

For the first GRNN Oracle (the inner oracle), the classifiers fed into it were SVM, GNB, and RF. The accuracy and AUC for SVM were 79.72% and 85.79%, respectively. GNB had 79.09% and 85.56%, respectively, and RF at 77.50% and 81.15%. The performance of the first oracle had an accuracy of 79.54%, AUC of 85.16%, sensitivity of 59.60%, and specificity of 88.51%. MLP, PNN, and KNN were not chosen because of their inferior performances when compared to the other models. All models were run 15 times and the average of the performance metrics were taken.

For the R-GRNN Oracle, the first GRNN Oracle, which now acts as a classifier with its own predictions, was combined with SVM. Since SVM had a better performance than others, it was chosen as a match with the first oracle to create the second oracle. Figure 8 illustrates the classifiers being fed into each one of the two oracles.

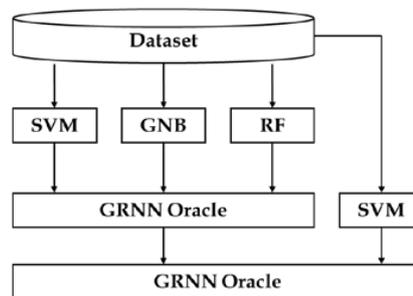


Figure 8: Overview of the Recursive GRNN Oracle

The first oracle achieved an accuracy of 79.54%, however, it was surpassed by SVM (79.72%), but the recursive model had the highest accuracy at 81.14% and highest AUC at 86.03%. Although it was able to reach the highest sensitivity too (63.80%) in comparison to the rest, MLP had the highest sensitivity (89.71%), where the recursive model came in third with 89.14% after MLP and SVM. However, since detecting TPs is of great importance (those who have diabetes), the sensitivity metric, where the R-GRNN was the highest, has a higher significance than specificity. Table 2 shows the accuracy, AUC, sensitivity, and specificity of all the classifiers: six individual classifiers (performing on their own), the GRNN Oracle, and the R-GRNN Oracle. The performances can also be seen in Figure 9 and Figure 10. Figure 9 shows the recursive model's 15 runs where the best, average, and worst performance were recorded, 86.47%, 81.14%, and 76.15%, respectively. It is worthy to mention that the dataset was shuffled each time the classifiers were run to ensure the robustness of the model, as no matter how it the data was shuffled, it always yielded better performance than the rest of the classifiers. Shuffling the data is the reason behind the high variation seen in Figure 9. Also, as a reminder to what was mentioned earlier, 4-fold cross validation was applied to train and test the models, but the actual

validation of each model was applied on a validation subset that was not involved in neither the training nor testing steps of each model.

Table 2: Performance metrics for the classifiers (average of 15 runs)

	Accuracy	AUC	Sensitivity	Specificity
SVM	79.72	85.79	58.43	89.31
MLP	76.88	80.75	49.11	89.71
RF	77.50	81.15	57.11	86.65
PNN	71.03	75.54	61.43	75.24
GNB	79.09	84.56	60.44	87.58
KNN	76.59	80.77	58.72	84.53
GRNN O.	79.54	85.16	59.60	88.51
R. GRNN O.	81.14	86.03	63.80	89.14

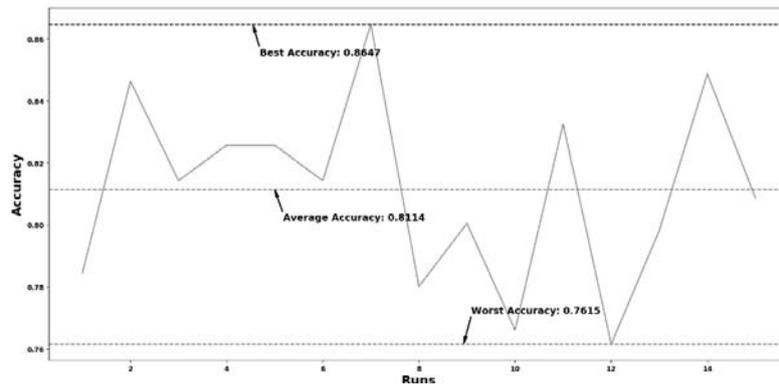


Figure 9: The best, worst, and average performances of the R-GRNN Oracle in 15 runs

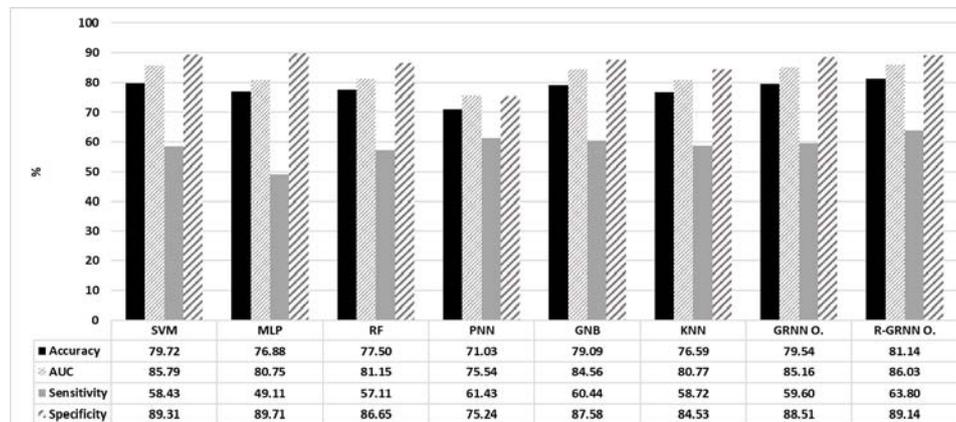


Figure 10: Graphical representation for the performance metrics for the classifiers

V. DISCUSSION

While the accuracy of the proposed model was not the highest in the literature, it still came in third when compared to all the publications studied (Table 3). It also bested the traditional oracle, SVM, MLP, RF, PNN, GNB, and KNN. However, as a slight remark, the studies did not confirm whether their accuracies were from conducting several runs and taking the average or not. As in this study, the highest accuracy achieved by the recursive model was 86.47%; one could simply report it as the highest achieved, therefore, it is wise if several runs are conducted and the average was taken.



Table 3: Comparison of the accuracy in the literature with this study

	Method	Accuracy
Kahramanli and Allahverdi (2008)	ANN and FNN Hybrid	84.20%
Vaishali et al. (2017)	MOEF	83.04%
This Study	R-GRNN Oracle	81.14%
Carpenter and Markuzon (1998)	ARTMAP-IC	81.00%
Christina et al. (2018)	XGBoost	81.00%
Ramesh et al. (2017)	RBM	81.00%
Kayaer and Yildirim (2003)	GRNN	80.21%
Lekkas and Mikhailove (2010)	EFC	79.37%
Bradley (1997)	MLP	78.40%
Al Jarullah (2011)	DTs	78.20%
Kumari and Chitra (2013)	SVM	78.20%
Huang et al. (2004)	SVM	77.31%
Miche et al. (2010)	GP	76.30%
Bradley and Mangasarian (1998)	RLP	76.16%
Luukka (2011)	S-Based	75.97%
Şahan et al. (2005)	AWAIS	75.87%
He et al. (2008)	ADASYN	68.37%

VI. CONCLUSION AND FUTURE WORK

This study presented the R-GRNN Oracle and was applied on the Pima Indians Diabetes dataset. It was applied along with seven other classifiers in which their final performances were compared. The other classifiers included are the traditional GRNN Oracle, SVM, MLP, RN, PNN, GNB, and KNN. GA was used to optimize the hyperparameters of SVM and MLP, and GS was used on RF and KNN. The models were run 15 times and the dataset was shuffled each run to ensure robustness. 4-fold cross validation was adopted as the validation method. Compared to the other models, the recursive oracle achieved the highest accuracy, AUC, and sensitivity at 81.14%, 86.03%, and 63.80%, respectively. It, however, came in third for specificity at 89.14% where optimized MLP had the highest at 89.71%.

Future research may include applying feature selection and hyperparameter optimization simultaneously rather than applying feature selection based on the optimized hyperparameters from all the features. It can also include using other metaheuristics, such as Particle Swarm Optimization (PSO) for hyperparameter optimization.

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Classification of Image using Convolutional Neural Network (CNN)

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Abstract- Computer vision is concerned with the automatic extraction, analysis, and understanding of useful information from a single image or a sequence of images. We have used Convolutional Neural Networks (CNN) in automatic image classification systems. In most cases, we utilize the features from the top layer of the CNN for classification; however, those features may not contain enough useful information to predict an image correctly. In some cases, features from the lower layer carry more discriminative power than those from the top. Therefore, applying features from a specific layer only to classification seems to be a process that does not utilize learned CNN's potential discriminant power to its full extent. Because of this property we are in need of fusion of features from multiple layers. We want to create a model with multiple layers that will be able to recognize and classify the images. We want to complete our model by using the concepts of Convolutional Neural Network and CIFAR-10 dataset. Moreover, we will show how MatConvNet can be used to implement our model with CPU training as well as less training time. The objective of our work is to learn and practically apply the concepts of Convolutional Neural Network.

Keywords: *convolutional neural network, CIFAR-10 dataset, MatConvNet, relu, softmax.*

GJCST-D Classification: *1.2.6*



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Md. Anwar Hossain^α & Md. Shahriar Alam Sajib^σ

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I. INTRODUCTION

Convolutional Neural Networks (CNN) becomes one of the most appealing approaches recently and has been an ultimate factor in a variety of recent success and challenging applications related to machine learning applications such as challenge ImageNet object detection, image classification, and face recognition. Therefore, we consider CNN as our model for our challenging tasks of image classification. We use CNN for segmentation and classification of the images in academic and business transactions. We use image recognition in different areas for example automated image organization, stock photography, face recognition, and many other related works.

a) CIFAR-10 Database

The CIFAR-10 database (Canadian Institute for Advanced Research database) is a collection of images.

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We use this dataset to train machine learning and computer vision algorithms. CIFAR-10 database is the contribution of Alex Krizhevsky and Geoffrey Hinton. This dataset has 60,000 colored images. It has ten classes, and they are an airplane, automobile, bird, cat, deer, dog, frog, horse, ship, truck. The images are of size 32x32 pixels. The dataset consists of 50,000 training and 10,000 testing examples. It is a database for people who want to try learning techniques and pattern recognition methods on real-world data while spending minimal efforts on preprocessing and formatting. We will use this database in our experiment.

b) Convolutional Neural Networks

Convolutional neural networks are deep artificial neural networks. We use CNN to classify images, cluster them by similarity (photo search), and perform object recognition within scenes. It can be used to identify faces, individual, street signs, tumors, platypuses and many other aspects of visual data. The convolutional layer is the core building block of a CNN. The layer's parameters consist of a set of learnable filters (or kernels) which have a small receptive field but extend through the full depth of the input volume. During the forward pass, each filter is convolved across the width and height of the input volume, computing the dot product, and producing a 2-dimensional activation map of that filter. As a result, the network learns about the filters. The filter activates when they see some specific type of feature at some spatial position in the input. Then the activation maps are fed into a downsampling layer, and like convolutions, this method is applied one patch at a time. CNN has also fully connected layer that classifies output with one label per node.

II. RELATED WORKS

Image recognition has an active community of academics studying it. A lot of important work on convolutional neural networks happened for image recognition [1,2,3,4]. The most dominant recent works achieved using CNN is a challenging work introduced by Alex Krizhevsky [5], who used CNN for challenge classification ImageNet. Active areas of research are: object detection [14,15,16], scene labeling [17], segmentation [18,19], face recognition, and variety of other tasks [20,21,22].

III. METHODOLOGY

Deep Learning has emerged as a main tool for self-perception problems like understanding images, the voice from humans, robots exploring the world. We aim to implement the concept of the Convolutional Neural Network for the recognition of images. Understanding CNN and applying it to the image recognition system is the target of the proposed model. Convolutional Neural Network extracts the feature maps from the 2D images by using filters. The Convolutional neural network considers the mapping of image pixels with the neighborhood space rather than having a fully connected layer of neurons. The Convolutional neural network has been proved to be a very dominant and potential tool in image processing. Even in the fields of computer vision such as handwriting recognition, natural object classification, and segmentation, CNN has become a much better tool compared to all other previously implemented tools.

a) The architecture of the Proposed Model

When one starts learning deep learning with the neural network, he realizes that one of the most supervised deep learning techniques is the Convolutional Neural Network. We design Convolutional Neural Network to recognize visual patterns directly from pixel images with minimal preprocessing. Almost all CNN architectures follow the same general design principles of successively applying convolutional layers to the input, periodically downsampling (Max pooling) the spatial dimensions while increasing the number of feature maps. Moreover, there are also fully connected layers, activation functions and loss function (e.g., cross entropy or softmax). However, among all the operations of CNN, convolutional layers, pooling layers, and fully connected layers are the most important ones. Therefore, we will quickly introduce these layers before presenting our proposed model.

The Convolutional layer is the very first layer where it can extract features from the images. Because pixels are only related to the adjacent and close pixels, convolution allows us to preserve the relationship between different parts of an image. Convolution is filtering the image with a smaller pixel filter to decrease the size of the image without losing the relationship between pixels. When we apply convolution to a 7x7 image by using a filter of size 3x3 with 1x1 stride (1-pixel shift at each step), we will end up having a 5x5 output.

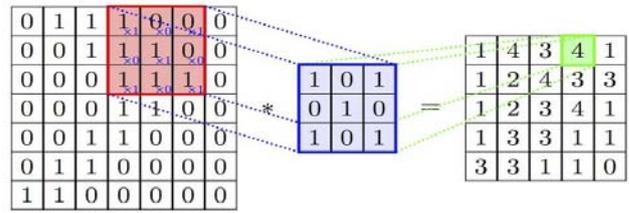


Fig. 1: Convolution Operation

When constructing CNN, it is common to insert pooling layers after each convolution layer, so that we can reduce the spatial size of the representation. This layer reduces the parameter counts, and thus reduces the computational complexity. Also, pooling layers help with the overfitting problem. We select a pooling size to reduce the amount of the parameters by selecting the maximum, average, or sum values inside these pixels. Fig.2 shows the max pooling and average pooling operation.

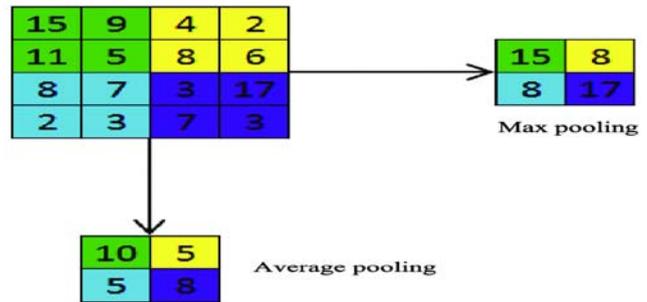


Fig. 2: Max pooling and Average pooling operation

A fully connected network is in any architecture where each parameter is linked to one another to determine the relation and effect of each parameter on the labels. We can vastly reduce the time-space complexity by using the convolution and pooling layers. We can construct a fully connected network in the end to classify our images.

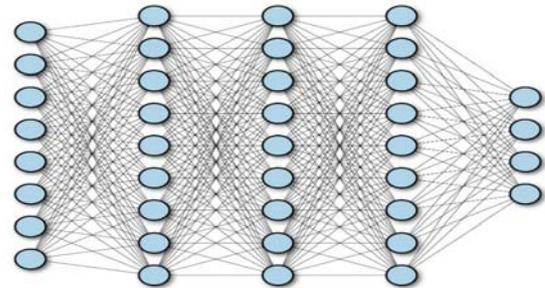


Fig. 3: Fully connected layer

Fig.4 shows the overview look of our proposed convolutional neural network. It is very much similar to the other image recognition architectures [1,2,3,4] but has changed in the number of filters, neurons and activation functions for better performance. We can divide our model into six sequences of layers.



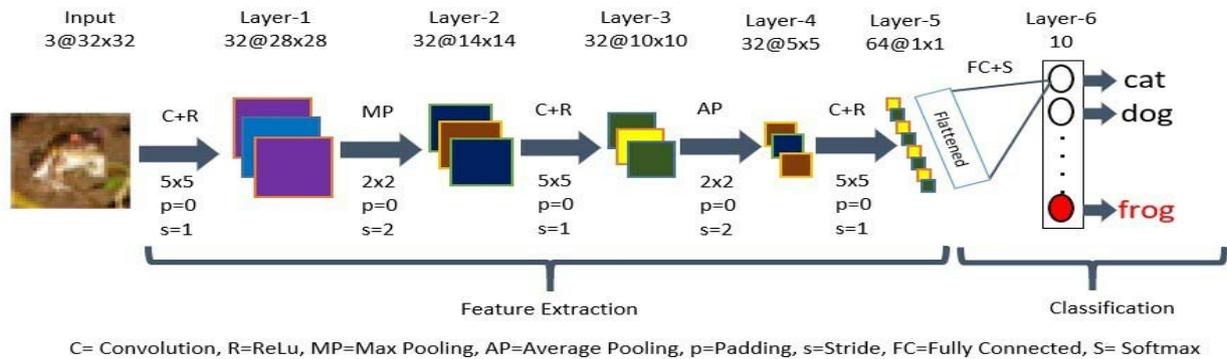


Fig. 4: The architecture of our proposed CNN

b) Explanation of the Model

A simple convolutional network is a sequence of layers. The layer transforms one volume of activations to another through a differentiable function. We use three main types of layers to build network architecture. They are a convolutional layer, pooling layer, and fully connected layer. We will stack these layers to form six layers of network architecture. We will go into more details below.

Fig.4 shows the architecture of our proposed CNN model. At first, we need some pre-processing on the images like resizing images, normalizing the pixel values, etc. After the necessary pre-processing, data is ready to be fed into the model.

Layer-1 consists of the convolutional layer with ReLu (Rectified Linear Unit) activation function which is the first convolutional layer of our CNN architecture. This layer gets the pre-processed image as the input of size $n \times n = 32 \times 32$. The convolutional filter size ($f \times f$) is 5×5 , padding (p) is 0 (around all the sides of the image), stride (s) is 1, and the number of filters is 32. After this convolution operation, we get feature maps of size $32 \times 28 \times 28$ where 32 is the number of feature maps which is equal to the number of filters used, and 28 comes from the formula $((n+2p-f)/s) + 1 = ((32+2 \times 0 - 5)/1) + 1 = 28$. Then the ReLu activation is done in each feature map.

Layer-2 is the max pooling layer. This layer gets the input of size $32 \times 28 \times 28$ from the previous layer. The pooling size is 2×2 ; padding is 0 and stride is 2. After this max pooling operation, we get feature maps of size $32 \times 14 \times 14$. Max pooling is done in each feature map independently, so we get same number feature maps as the previous layer, and 14 comes from the same formula $((n+2p-f)/s) + 1$. This layer has no activation function.

Layer-3 is the second convolutional layer with ReLu activation function. This layer gets the input of size $32 \times 14 \times 14$ from the previous layer. The filter size is 5×5 ; padding is 0, the stride is 1, and the number of filters is 32. After this convolution operation, we get feature maps of size $32 \times 10 \times 10$. Then ReLu activation is done in each feature map.

Layer-4 is the average pooling layer. This layer gets the input of size $32 \times 10 \times 10$ from the previous layer. The pooling size is 2×2 ; padding is 0 and stride is 2. After this max pooling operation, we get a feature map of size $32 \times 5 \times 5$.

Layer-5 is the third convolutional layer with ReLu activation function. This layer gets the input of size $32 \times 5 \times 5$ from the previous layer. The filter size is 4×4 ; padding is 0, the stride is 1, and the number of filters is 64. After this convolution operation, we get feature maps of size $64 \times 1 \times 1$. This layer acts as a fully connected layer and produces a one-dimensional vector of size 64 by being flattened.

Layer-6 is the last layer of the network. It is a fully connected layer. This layer will compute the class scores, resulting in a vector of size 10, where each of the ten numbers corresponds to a class score, such as among the ten categories of CIFAR-10 dataset. For final outputs, we use the softmax activation function.

In this way, CNN transforms the original image layer by layer from the main pixel values to the final class scores. Note that some layers contain parameters, and others don't. In particular, the convolution/fully connected layers perform transformations that are a function of not only the activations in the input volume but also of the parameters (the weights and biases of the neurons). On the other hand, the ReLu/pooling layers will implement a fixed function. We train the parameters in the convolutional/fully connected layers with stochastic gradient descent. By this process, we will prepare the trained model which will be used to recognize the image present in the test data. Thus, we can classify the images as Class- airplanes, cars, birds, cats, deer, dogs, frogs, horses, ships, trucks.

IV. IMPLEMENTATION

To implement our CNN architecture, we will use MatConvNet. MatConvNet is an implementation of Convolutional Neural Networks (CNN) for MATLAB [23]. We built our model by using MatConvNet so that our model has greater simplicity and flexibility. It exposes the building blocks of CNN as easy-to-use MATLAB functions, providing routines for computing linear

convolutions with filter banks, feature pooling and many more. In this manner, MatConvNet allows fast prototyping of new CNN architectures; at the same time, it supports efficient computation on CPU and GPU allowing to train complex models on large datasets such as ImageNet ILSVRC.

Convolutional Neural Networks (CNN) is the current state-of-art architecture for the image classification task. As shown in Fig.4 our proposed 2-D Convolutional Neural Network (CNN) model is designed using MatConvNet backend for the well known CIFAR-10 image recognition task. The whole workflow can be to preparing the data, building and compiling the model, training and evaluating the model and saving the model to disk for reuse.

Preparing the data is the first step of our approach. Before we build the network, we need to set up our training and testing data, combine data, combine labels and reshape into the appropriate size. We save the dataset of normalized data (single precision and zero mean), labels, and miscellaneous (meta) information.

Building and compiling the model is the second step. To create the CNN, we must initialize MatConvNets SimpleNN network and then define important

initialization parameters for example batch size, number of epochs, learning rate, etc.

The batch size determines the number of samples for the training phase of the CNN. The CNN will process all the training data, but only in increments of the specified batch size. We can use batch size for computational efficiency, and its value will be dependent on the user's available hardware. An epoch is a successful forward pass and a backward pass through the network. It's usually beneficial to set its value high and then to reduce it once if one is satisfied with the convergence at a particular state (chosen epoch) in the network. Learning rate is a very sensitive parameter that pushes the model towards convergence. Finding its best value will be an experimental process unless one invokes more powerful techniques such as batch normalization. In our experiment, we use batch size 60, several epochs 300 and learning rate 0.0001 for maximum accuracy.

Now we can build our CNN by creating each layer individually as shown in fig 5. Afterward, we will invoke objective and error layers that will provide a graphical visualization of the training and validation convergence after completing each epoch. MatconvNet initializes the weights by using Gaussian distribution.

```

% Block 1
net.layers(end+1) = struct('type', 'conv', 'weights', {{0.05*randn(5,5,3,32, 'single'), zeros(1, 32, 'single')}}), 'stride', [1 1], 'pad', [0 0 0 0] ;
net.layers(end+1) = struct('type', 'relu') ;
net.layers(end+1) = struct('type', 'pool', 'method', 'max', 'pool', [2 2], 'stride', [2 2], 'pad', [0 0 0 0]);

% Block 2
net.layers(end+1) = struct('type', 'conv', 'weights', {{0.05*randn(5,5,3,32, 'single'), zeros(1, 32, 'single')}}), 'stride', [1 1], 'pad', [0 0 0 0] ;
net.layers(end+1) = struct('type', 'relu') ;
net.layers(end+1) = struct('type', 'pool', 'method', 'avg', 'pool', [2 2], 'stride', [2 2], 'pad', [0 0 0 0]);

% Block 3
net.layers(end+1) = struct('type', 'conv', 'weights', {{0.05*randn(5,5,32,64, 'single'), zeros(1,64,'single')}}), 'stride', [1 1], 'pad', [0 0 0 0] ;
net.layers(end+1) = struct('type', 'relu') ;

% Block Multi-Layer-Perceptron
net.layers(end+1) = struct('type', 'conv', 'weights', {{0.05*randn(1,1,64,10, 'single'), zeros(1,10,'single')}}), 'stride', [1 1], 'pad', [0 0 0 0] ;

% Loss layer
net.layers(end+1) = struct('type', 'softmaxloss') ;

```

Fig. 5: CNN layers in MatConvNet

The third step is the training and evaluating the model. Training a CNN requires computing the derivative of the loss concerning the network parameters. We calculate the derivatives using an algorithm called back propagation which is a memory-efficient implementation of the chain rule for derivatives. We built the model and performed a random gradient descent training according to the Stochastic Gradient Descent (SGD) training algorithm. We have used SGD training algorithm to adjust the weight of the connection between neurons so that the loss reaches a minimum value or stops after several epochs. We have used CPU training. It is important to note that GPU training will dramatically help training time for CNN.

Lastly, we can begin the training of CNN by supplying the training data, the constructed model and the current batch of data. When training the CNN, only the data specified for training play a role in minimizing

error in the CNN. We feed the training data through the network for the forward pass and backward pass. The validation data is just used to see how the CNN responds to new similar data. We do not use the validation data to train the network. Afterward, we save the trained CNN and prepare for the testing phase.

During the training phase of the CNN, the simple network will produce three plots (Objective, Top1error, and Top5error) for each epoch. The top1 error is the chance that class with the highest probability is the correct target. In other words, CNN guesses the target correctly. The top5error is the chance that the true target is one of the top five probabilities. The objective for the simple network should mirror the form of the top1 and top5 error. In all the plots, we represent the training error and validation error by blue and orange respectively.

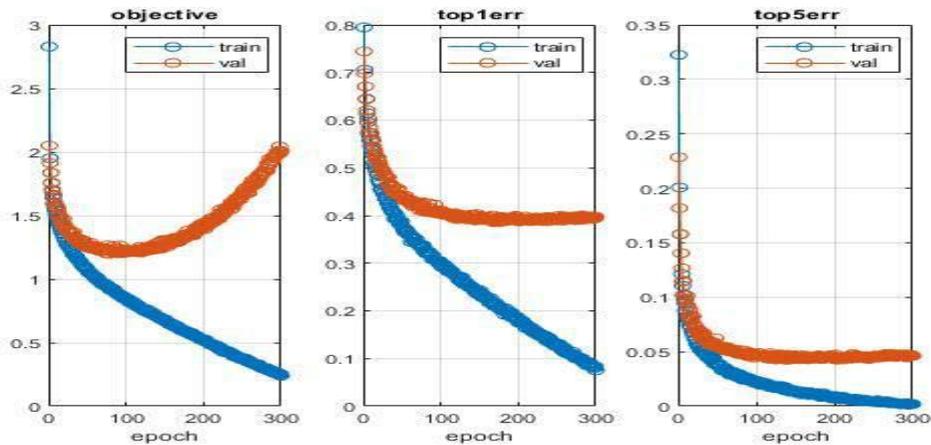


Fig. 6: Objective, Top1error, and Top5error during training

Finally, by using the testing data, we can evaluate our model. The following are an example of classification outputs from the simple network on the CIFAR-10 data.



Fig. 7: Some correct recognized outputs



Fig. 8: Some wrong recognized outputs

We can determine the test cases that show failed classifications. The model can't identify some images because of limitations in the input of standard data images. Moreover, missing pixels caused by image compression and image sharpness problems are also reasons for misclassification.

The fourth and final step is to save the model in the disk for reuse. We store the trained model in a MATLAB file format. Hence the saved model can be reused later or easily ported to other environments too.

V. RESULTS AND DISCUSSION

Among 10,118 test cases, our model misclassifies total of 661 images after three hundred epochs which correspond to 93.47% recognition rate shown in Table 1. The results are pretty good for three hundred epochs and for such a simple model with CPU training and less training time (about 3 hours).

```

Command Window
The total number of misclassified test cases = 661
Error rate=6.53%
Testing accuracy=93.47%
fx >> |
    
```

Fig. 9: Error rate and accuracy of our model.

Although there are some images which are difficult to identify, our model will be able to classify them correctly. For example, our model can recognize the following image and classify it as 'deer':



Fig. 10: Correct recognition of the bad image

Table 1: Summary of the experiment

Batch size	No. of epochs	Testing accuracy
100	250	76.82%
70	300	82.28%
60	300	93.47%

Test accuracy 93.47% implies that the model is trained well for prediction. Training set size affects the accuracy increases as the number of data increases. The more data in the training set, the smaller the impact

of training error and test error and ultimately the accuracy can be improved.

VI. CONCLUSION AND FUTURE WORK

Here we demonstrate a model which can recognize and classify the image. Later it can be extended for object recognition, character recognition, and real-time object recognition. Image recognition is an important step to the vast field of artificial intelligence and computer vision. As seen from the results of the experiment, CNN proves to be far better than other classifiers. The results can be made more accurate by increasing the number of convolution layers and hidden neurons. People can recognize the object from blurry images by using our model. Image recognition is an excellent prototype problem for learning about neural networks, and it gives a great way to develop more advanced techniques of deep learning. In the future, we are planning to develop a real-time image recognition system.

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Diagnosis of Prostate Cancer using Soft Computing Paradigms

By Samuel S. Udoh, Uduak A. Umoh, Michael E. Umoh & Mfon E. Udo

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Abstract- The process of diagnosing of prostate cancer using traditional methods is cumbersome because of the similarity of symptoms that are present in other diseases. Soft Computing (SC) paradigms which mimic human imprecise data manipulation and learning capabilities have been reviewed and harnessed for diagnosis and classification of prostate cancer. SC technique based on Adaptive Neuro-Fuzzy Inference System (ANFIS) facilitated symptoms analysis, diagnosis and prostate cancer classification. Age of Patient (AP), Pains in Urination (PU), Frequent Urination (FU), Blood in Semen (BS) and Pains in Pelvic (PP) served as input attributes while Prostate Risk (PR) served as output. Matrix laboratory provided the programming tools for system implementation. The practical function of the system was assessed using prostate cancer data collected from the University of Uyo Teaching Hospital. A 95% harmony observed between the computed and the expected output in the ANFIS model, showed the superiority of the ANFIS model over the fuzzy model. The system is poised to assist medical professionals in the domain of diagnosis and classification of prostate cancer for the promotion of management and treatment decisions.

Keywords: *prostate cancer, diagnosis, soft computing, ANFIS, fuzzy model.*

GJCST-D Classification: *F.1.1*



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Diagnosis of Prostate Cancer using Soft Computing Paradigms

Samuel S. Udoh^α, Uduak A. Umoh^ο, Michael E. Umoh^ρ & Mfon E. Udo^ω

Abstract- The process of diagnosing of prostate cancer using traditional methods is cumbersome because of the similarity of symptoms that are present in other diseases. Soft Computing (SC) paradigms which mimic human imprecise data manipulation and learning capabilities have been reviewed and harnessed for diagnosis and classification of prostate cancer. SC technique based on Adaptive Neuro-Fuzzy Inference System (ANFIS) facilitated symptoms analysis, diagnosis and prostate cancer classification. Age of Patient (AP), Pains in Urination (PU), Frequent Urination (FU), Blood in Semen (BS) and Pains in Pelvic (PP) served as input attributes while Prostate Risk (PR) served as output. Matrix laboratory provided the programming tools for system implementation. The practical function of the system was assessed using prostate cancer data collected from the University of Uyo Teaching Hospital. A 95% harmony observed between the computed and the expected output in the ANFIS model, showed the superiority of the ANFIS model over the fuzzy model. The system is poised to assist medical professionals in the domain of diagnosis and classification of prostate cancer for the promotion of management and treatment decisions.

Keywords: prostate cancer, diagnosis, soft computing, ANFIS, fuzzy model.

I. INTRODUCTION

Prostate cancer is a common disease in elderly men (Leonard, 2008; Ajape & Babatunde, 2009; Thomas, 2011). The rapid spread of prostate cancer disease stems from unawareness of its early symptoms. Early diagnosis and treatment of prostate cancer reduce the rate of fatality (Ifere & Ananaba, 2012; Ganesh *et al.*, 2013; Mfon, 2017). Some symptoms of prostate cancer observed in other diseases make it difficult to obtain precise diagnosis using traditional and hard computing methods. Soft Computing (SC) methodology offers a plausible solution to this problem. SC emulates human processing capabilities. It harnesses imprecision, uncertainty, partial truth as well as learn from previous experience to provide solution in a seemingly impossible scenario. The principal techniques of SC are – fuzzy logic, neural networks, support vector machines, evolutionary computation and probabilistic reasoning (Kurhe *et al.*, 2011). The implementation technique of SC is complementary rather than competitive. SC has been successfully applied in medical diagnosis, prediction, pattern

recognition, decision support, automotive control and infrastructure monitoring (Obot and Udoh, 2013; Agu *et al.*, 2015; Udoh, 2016; Mfon 2017; Udoh *et al.*, 2017; Arlan *et al.*, 2018). The remainder of the paper is organized in Sections. Section 2 presents related works in soft computing techniques. Section 3 addresses the design of adaptive neuro-fuzzy inference system for prostate cancer diagnosis. Implementation and discussion on the results are carried out in Section 4 while Section 5 presents the conclusion of the work and recommendation for further research.

II. RELATED WORKS

a) Fuzzy Logic

Zadeh (1965) introduced fuzzy logic (FL) as a mathematical tool for dealing with uncertainty. The FL theory provides a mechanism for representing linguistic constructs such as “many,” “low,” “medium,” “often,” “few.” It is a problem-solving methodology which provides a simple way to draw definite conclusions from vague, ambiguous or imprecise information. FL technique follows the process of fuzzification, inferencing, composition, and defuzzification (Gupta, 1995; Atınc & Kürşat, 2011; Agu *et al.*, 2015; Udoh, 2016). Ismail *et al.* (2003) presented a fuzzy logic expert system for classification of prostate cancer risk based on identified symptoms. Input parameters used were Prostate Specific Antigen (PSA), Age and Prostate Volume (PV) while Prostate Cancer Risk (PCR) served as output. The few input parameters employed hindered adequate prostate cancer risk classification. Ganesh *et al.* (2013) presented a prostate cancer hospital-based survival study to aid early diagnosis and remedy of prostate cancer. Lack of detailed clinical analysis and inclusion of intelligent tools for precise diagnosis were weaknesses of the work. Mfon (2017) investigated the intensity of prostate cancer using Mamdani reasoning mechanism of fuzzy logic. The system could diagnose and classify prostate cancer patients but lacked the cognitive ability to learn from previous data of prostate cancer patients.

b) Neural Network

Neural Network (NN) is an information processing paradigm that is inspired by the way biological nervous systems, process information and learns from previous patterns (Akinyokun, 2007; Udoh, 2016). Javed *et al.* (2001) used NN to classify cancers

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into four distinct diagnostic categories based on their gene expression signatures. The study demonstrated the potential application of NN for tumor diagnosis and identification of a candidate for therapy. Misop *et al.* (2001) studied a large series of patients with clinically localized prostate carcinoma. The clinical and pathologic data obtained at the time of prostate biopsy were used to develop a NN for prostate cancer risk classification. Bob *et al.* (2002) compared the predictive capabilities of NN and conventional statistical model. Prostate Specific Antigen (PSA) levels were employed in NN together with multivariate analysis for the detection of prostate cancer. The predictive accuracy of NN was superior to that of the statistical model. Joseph & David (2006) surveyed machine learning techniques for prostate cancer prediction. NN models performed better than decision tree models. Maysam & Feddie (2007) reported on the application of artificial intelligence technology in prostate cancer management. While most researchers focused on NN to improve the diagnosis and prognostic prediction, others explored expert systems and fuzzy modeling approaches. The lack of transparency of NN processing technique hinders global scientific community acceptance. However, this could be handled by neuro-fuzzy paradigm.

c) *Neuro-Fuzzy Paradigm*

Neuro-fuzzy model combines the capabilities of NN and FL (Akinyokun, 2007; Udoh, 2016). Benecchi (2006) proposed a neuro-fuzzy system for predicting the presence of prostate cancer. The system made use of a co-active neuro-fuzzy inference model. The predictive ability of neuro-fuzzy system performed better than that obtained by a total prostate specific antigen. Kuo *et al.* (2015) proposed a fuzzy neural network (FNN) system for prognosis of prostate cancer. The use of cluster analysis helped in the determination of the initial membership function parameters. An integration of artificial immune network and a particle swarm optimization assisted the investigation of input-output relationships. FNN algorithm gave a satisfactory prediction in prostate cancer prognosis. Cosma *et al.* (2016) proposed a neuro-fuzzy model for prediction of pathological state in patients with prostate cancer. The receiver operating characteristic (ROC) points obtained from neuro-fuzzy approach performed better than those obtained from fuzzy c-means, support vector machine (SVM) and Naïve Bayes classifiers. Mustain & Nazrul (2016) presented an ANFIS for predicting lung cancer risk. Cancer historical data were collected from hospital and preprocessed. The use of linear discriminant analysis facilitated attributes dimension reduction for cancer classification. Arlan *et al.* (2018) presented the training of the ANFIS with genetic algorithm for diagnosis of prostate cancer. The results of cancer gene profiles classification were satisfactory and superior to results obtained from neural networks.

III. METHODOLOGY

The method followed for prostate cancer diagnosis in this work is depicted in Figure 1. It comprises four major stages namely: 1. Data collection and preprocessing; 2. ANFIS design and training 3; ANFIS parameters checking and 4. Prostate Cancer Diagnosis.

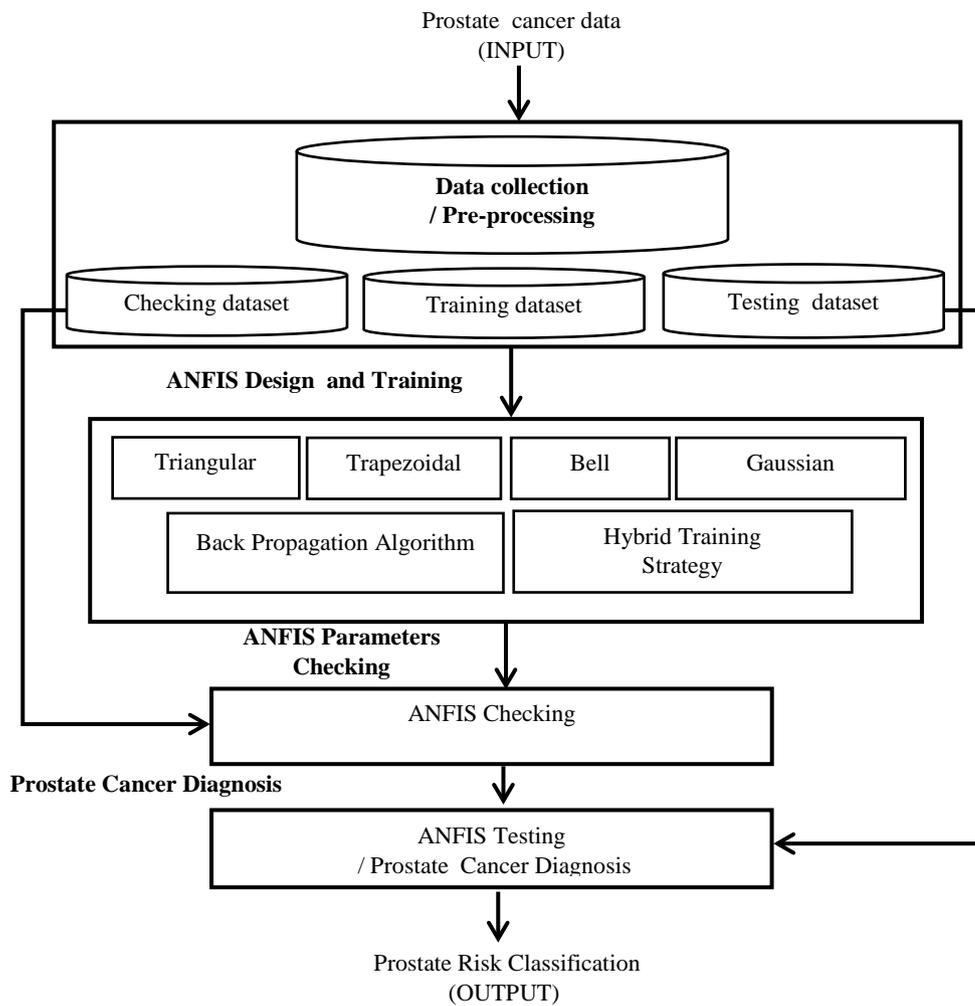


Figure 1: Block Structure of Stages in Prostate Cancer Diagnosis

a) Data Collection and Processing

A collection of 510 prostate cancer dataset within nine months (July 2017 to March 2018) from the University of Uyo Teaching Hospital, Uyo, (UUTH), Nigeria, assisted the assessment of the practical function of the system. The attributes: Age of Patient (AP), Pain in Urination (PU), Frequent Urination (FU), Blood in Semen (BS) and Pains in Pelvic (PV) served as input while Prostate Risk (PR) served as output. The splitting of the dataset in the ratio of 8:1:1, translated into 408, 51 and 51 datasets for system training, checking and testing respectively.

b) ANFIS Design and Training

ANFIS design consists of five layers. The first and the fourth layers consist of adaptive nodes which have parameters to be learned while the second, third and fifth layers are fixed nodes and contain no learning parameters. The system employed Sugeno inference mechanism whose reasoning methodology shows the output of each rule as a sequential combination of each rule input variable plus the constant term as shown in Equation 1.

$$\text{IF } a \text{ is } X_1 \text{ AND } b \text{ is } Y_1 \text{ AND... AND } c \text{ is } Z_1 \text{ THEN } f_1 = p_1a + q_1b + \dots + r_1c + s_1 \tag{1}$$

where a, b, c are the inputs or antecedent parameters, X, Y, Z are the fuzzy sets of inputs parameters, f is the fuzzy set of output parameters and $p, q, r,$ and s are consequent parameters.

Layer 1 is the input layer. It has AP, PU, FU, BS, and PP as inputs. Every node i in layer 1 has a node function

$$O_i^1 = \mu X_i(a) \tag{2}$$

where a is the input to node i , and X_i is the linguistic label (Low, Moderate and High) associated with this node function. O_i^1 is the membership function of X_i , and it specifies the degree to which the given input satisfies the quantifier X_i . Different Types of Membership functions such as Triangular, Bell,

Gaussian and Trapezoidal are employed in ANFIS. The general form of a triangular membership function is shown in Equation 3.

$$\mu_x(a) = \begin{cases} 1 & \text{if } a = y \\ \frac{a-x}{y-x} & \text{if } x \leq a < y \\ \frac{z-a}{z-y} & \text{if } y \leq a < z \\ 0 & \text{if } z \leq a \end{cases} \quad (3)$$

where x, y, z are the parameters of the membership function (MF) governing triangular shape, X_i is the linguistic variable, a is prostate cancer input, x and y are the parameters of the membership function such that $x \leq a < y$. Layer 2 is the rule node. Every node in layer 2 computes the firing strength of each rule as given in Equation 4. Layer 3 is the normalization layer. Every node in layer 3 calculates the ratio of the ith rule's firing strength to the sum of all rules's firing strengths as shown in Equation 4. Layer 4 is the defuzzification layer which consists of consequent nodes for computing the contribution of each rule to the overall output as shown in Equation 6. Layer 5 is the output layer (a single node that computes the overall output, Prostate Risk (PR). The output as shown in Equation 7 is computed as summation of prostate cancer signals.

$$O_i^2 = w_i = \mu X_i(a) * \mu Y_i(b) * \mu Z_i(c) \quad (4)$$

$$O_i^3 = \bar{w}_i = \frac{w_i}{\sum_{l=1}^n w_l} \quad (5)$$

$$O_i^4 \equiv \bar{w}_i f_i = \bar{w}_i (p_i a + q_i b + \dots + r_i c + s_i) \quad (6)$$

$$O_i^5 = \sum_i \bar{w}_i f_i = \frac{\sum_i w_i f_i}{\sum_i w_i} \quad (7)$$

The training and parameters adjustments in ANFIS are facilitated either by hybrid learning algorithm or the back propagation algorithm. The hybrid learning algorithm converges faster than the traditional back propagation method. It comprises the combination of least square method in the forward pass and back propagation gradient descent procedure in the backward pass. In the forward pass, the node output goes forward until layer 4 and the consequent parameters are updated by least square method. In the backward pass, the error signal propagates backwards and the premise parameters are updated by gradient method. (Udoh *et al.*, 2017).

IV. RESULTS AND DISCUSSION

The system as shown in Figure 2 was implemented in an environment characterized by MatLab 2015a programming tools. Prostrate cancer data samples of sizes 408, 51 and 51 records facilitated system training, checking and testing respectively. Figures 3 and 4 depict the loading of training and checking data as well as training and checking error interface respectively. The results of training and checking errors carried out in 20 iterations using hybrid learning process with Triangular, Trapezoidal, Bells or Gaussian membership functions are presented in Table 1.

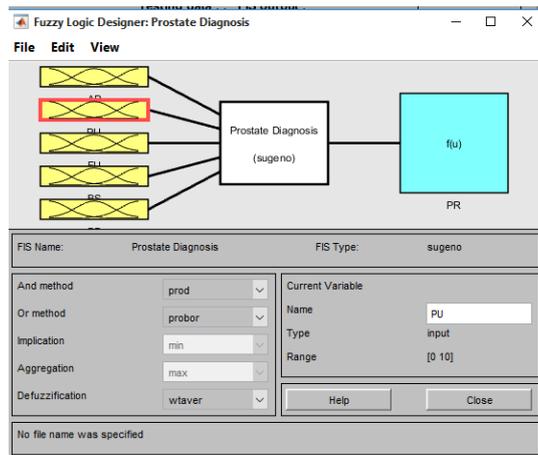


Figure 2: Prostate Cancer Diagnosis Implementation

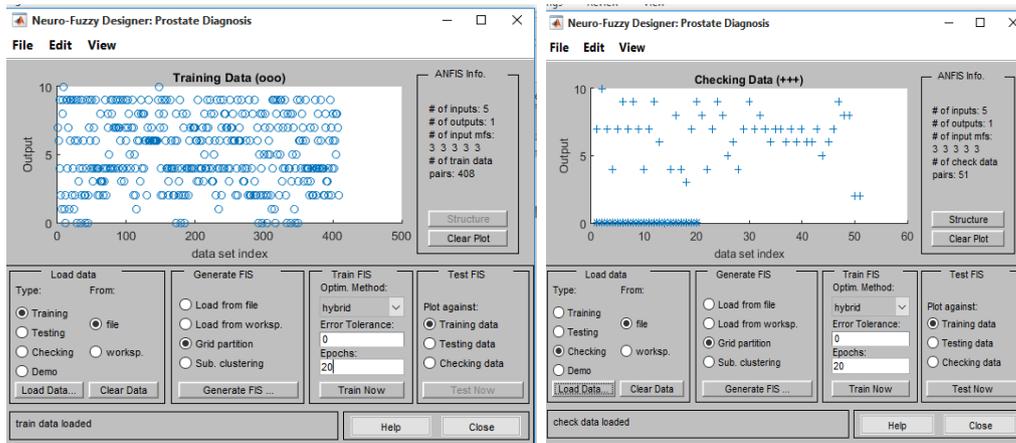


Figure 3: Loading of Training and Checking Data

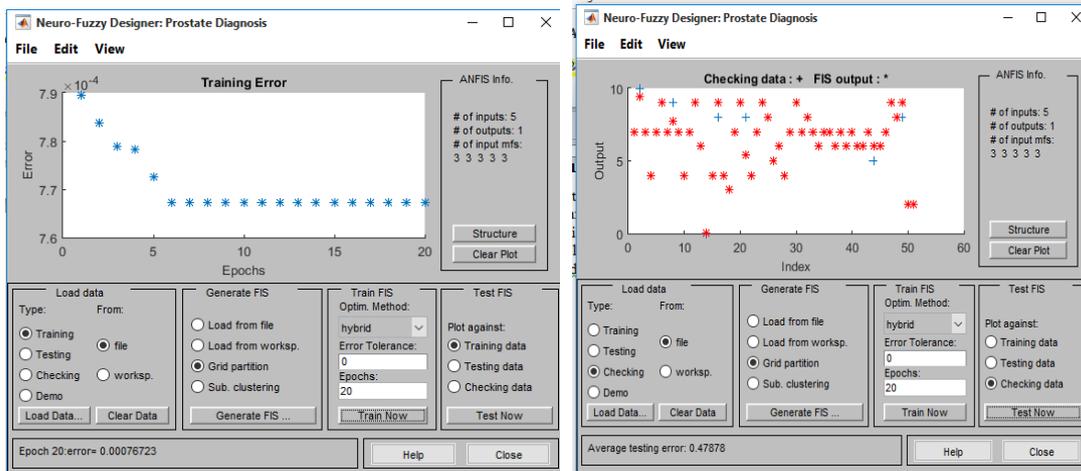


Figure 4: Training and Checking Error Interface

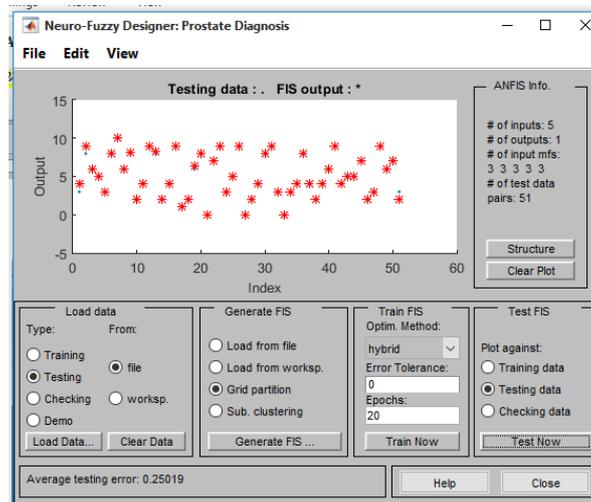


Figure 5: Testing Error Interface

As shown in Figure 5. The 51 testing data samples were loaded to ascertain the functionality of the trained and checked ANFIS. An average testing error of 0.25019 was observed between the computed and the expected output. The testing and checking errors

derived from the experiment using different membership functions are depicted in Table 1.

Table 1: Training and Checking Errors Based on Different Membership Functions

Iteration No.	Triangular MF		Trapezoidal MF		Bells MF		Gaussian MF	
	Training Error	Checking Error						
1	0.000148	0.531080	0.197052	1.020400	0.002829	0.619600	0.001827	0.606912
2	0.000145	0.530330	0.197007	1.014800	0.002764	0.679068	0.001760	0.612429
3	0.000141	0.529580	0.196963	1.009600	0.002699	0.745846	0.001696	0.617943
4	0.000138	0.528840	0.196919	1.004500	0.002635	0.819051	0.001633	0.623423
5	0.000135	0.528110	0.196815	0.999700	0.002571	0.897450	0.001572	0.628843
6	0.000132	0.527370	0.196831	0.995100	0.002508	0.979547	0.001514	0.634181
7	0.000129	0.526650	0.196786	0.990700	0.002445	1.063660	0.001458	0.639416
8	0.000127	0.525920	0.196742	0.986400	0.002382	1.148020	0.001403	0.644531
9	0.000124	0.525200	0.196697	0.982300	0.002320	1.230880	0.001352	0.649510
10	0.000121	0.524490	0.196653	0.978400	0.002260	1.310590	0.001302	0.654341
11	0.000119	0.523770	0.196608	0.974600	0.002200	1.385740	0.001255	0.659013
12	0.000116	0.523070	0.196564	0.970900	0.002143	1.455150	0.001209	0.663518
13	0.000114	0.522360	0.196519	0.967400	0.002087	1.517930	0.001166	0.667850
14	0.000112	0.521660	0.196475	0.964000	0.002034	1.573510	0.001125	0.672004
15	0.000110	0.520960	0.196430	0.960685	0.001983	1.621590	0.001086	0.675976
16	0.000108	0.520270	0.196385	0.957500	0.001935	1.662100	0.001048	0.679766
17	0.000105	0.519580	0.196341	0.954400	0.001889	1.695200	0.001012	0.683374
18	0.000104	0.518895	0.196296	0.951390	0.001846	1.721220	0.000978	0.686801
19	0.000102	0.518220	0.196251	0.948500	0.001805	1.740570	0.000945	0.690049
20	0.000098	0.517540	0.196207	0.945600	0.001767	1.753790	0.000914	0.693122

Triangular MF gave the best results in terms of training and checking errors, followed by Gaussian MF. The worst checking errors were observed in Bells MF. The results of prostate cancer diagnosis using the ANFIS and the fuzzy paradigms are depicted in Figure 6. The data points in the ANFIS diagnosis matched the expected output more precisely than those in the fuzzy diagnosis. Out of the 20 data points used in the

experiment, 19 data points matched with the expected output in the ANFIS model, whereas the fuzzy model had 14 similar data points. In the first instance of the diagnosis, using the ANFIS model the patient with serial number 1 had a high degree of prostate cancer. This corresponds to the expected output from domain experts.

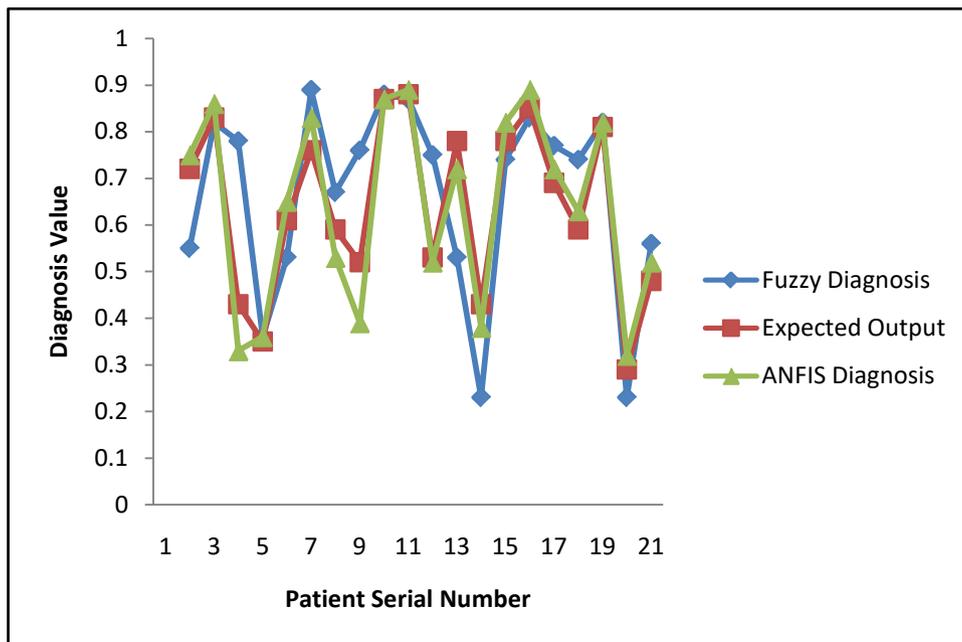


Figure 6: Graph of Prostate Cancer Diagnosis

However, using the same sets of input variables on the fuzzy model presented in (Mfon, 2017), the same patient had a moderate prostate cancer which

disagrees with the expected output from domain experts. The summary of the prostate cancer diagnosis results is shown in Table 2.

Table 2: Summary of Prostate Cancer Diagnosis Results

Patient Serial Number	Patient ID Number	Fuzzy Diagnosis Value (Mfon, 2017)	Fuzzy Diagnosis Label	Expected Diagnosis Output	Expected Diagnosis Label	ANFIS Diagnosis Value (Current Study)	ANFIS Diagnosis Label	Class Grade
1	012	0.57	Moderate	0.72	High	0.75	High	A
2	121	0.80	High	0.83	High	0.82	High	A
3	300	0.78	High	0.43	Low	0.33	Low	C
4	705	0.23	Low	0.35	Low	0.36	Low	C
5	131	0.53	Moderate	0.61	Moderate	0.65	Moderate	B
6	125	0.89	High	0.76	High	0.83	High	A
7	171	0.67	Moderate	0.59	Moderate	0.53	Moderate	B
8	165	0.76	High	0.52	Moderate	0.39	Low	C
9	234	0.88	High	0.87	High	0.87	High	A
10	126	0.87	High	0.88	High	0.89	High	A
11	191	0.75	High	0.53	Moderate	0.52	Moderate	A
12	192	0.53	Moderate	0.78	High	0.72	High	B
13	158	0.23	Low	0.39	Low	0.38	Low	C
14	144	0.74	High	0.78	High	0.82	High	A
15	124	0.83	High	0.85	High	0.89	High	A
16	171	0.77	High	0.70	High	0.72	High	B
17	193	0.74	High	0.60	Moderate	0.63	Moderate	A
18	987	0.82	High	0.82	High	0.82	High	A
19	865	0.23	Low	0.29	Low	0.32	Low	C
20	166	0.56	Moderate	0.50	Moderate	0.51	Moderate	B

Both ANFIS and fuzzy models gave high diagnosis in the second instance of the diagnosis. This is in agreement with expected output from domain experts. Nevertheless, the diagnosis value of the ANFIS model was observed to be closer to that of domain experts than the one from the fuzzy model. Investigation showed that 14 out of 20 instances (70%) gave accurate prediction in the fuzzy model while 19 out of 20 instances (95%) gave accurate predictions in the ANFIS model. The results of the experiment shown in Table 2, demonstrated the precision of ANFIS model over fuzzy model in the task of prostate cancer diagnosis.

V. CONCLUSION AND RECOMMENDATION

This paper presented a review of prostate cancer diagnosis using soft computing models. Practical function of the ANFIS paradigm was assessed in an environment characterized by matrix laboratory programming tools. The data of prostate cancer patients collected from the University of Uyo teaching hospital, Uyo, Nigeria, was used for system training and testing. A comparison of the results, showed the accuracy of the ANFIS model over the fuzzy model in the task of prostate cancer diagnosis. Future works would employ

evolutionary computations and support vector machine for further investigations.

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Recognition of Handwritten Digit using Convolutional Neural Network (CNN)

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Abstract- Humans can see and visually sense the world around them by using their eyes and brains. Computer vision works on enabling computers to see and process images in the same way that human vision does. Several algorithms developed in the area of computer vision to recognize images. The goal of our work will be to create a model that will be able to identify and determine the handwritten digit from its image with better accuracy. We aim to complete this by using the concepts of Convolutional Neural Network and MNIST dataset. We will also show how MatConvNet can be used to implement our model with CPU training as well as less training time. Though the goal is to create a model which can recognize the digits, we can extend it for letters and then a person's handwriting. Through this work, we aim to learn and practically apply the concepts of Convolutional Neural Networks.

Keywords: *convolutional neural network; MNIST dataset; MatConvNet; ReLu; softmax.*

GJCST-D Classification: 1.2.6



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Md. Anwar Hossain^α & Md. Mohon Ali^σ

Abstract- Humans can see and visually sense the world around them by using their eyes and brains. Computer vision works on enabling computers to see and process images in the same way that human vision does. Several algorithms developed in the area of computer vision to recognize images. The goal of our work will be to create a model that will be able to identify and determine the handwritten digit from its image with better accuracy. We aim to complete this by using the concepts of Convolutional Neural Network and MNIST dataset. We will also show how MatConvNet can be used to implement our model with CPU training as well as less training time. Though the goal is to create a model which can recognize the digits, we can extend it for letters and then a person's handwriting. Through this work, we aim to learn and practically apply the concepts of Convolutional Neural Networks.

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I. INTRODUCTION

Recently Convolutional Neural Networks (CNN) becomes one of the most appealing approaches and has been an ultimate factor in a variety of recent success and challenging machine learning applications such as challenge ImageNet object detection image segmentation and face recognition. Therefore, we choose CNN for our challenging tasks of image classification. We can use it for handwriting digits recognition which is one of high academic and business transactions. There are many applications of handwriting digit recognition in our real life purposes. Precisely, we can use it in banks for reading checks, post offices for sorting letter, and many other related works.

a) MNIST database

The MNIST database (Modified National Institute of Standards and Technology database) is a handwritten digits dataset. We can use it for training various image processing systems [11]. The database is also widely used for training and testing in the field of machine learning. It has 60,000 training and 10,000 testing examples.

Each image has fixed size. The images are of size 28*28 pixels. It is a database for people who want to try learning techniques and pattern recognition methods on real-world data while spending minimal efforts on preprocessing and formatting. We will use this database in our experiment.

b) Convolutional Neural Networks

Convolutional neural networks are deep artificial neural networks. We can use it to classify images (e.g., name what they see), cluster them by similarity (photo search) and perform object recognition within scenes. It can be used to identify faces, individuals, street signs, tumors, platypuses and many other aspects of visual data. The convolutional layer is the core building block of a CNN. The layer's parameters consist of a set of learnable filters (or kernels) which have a small receptive field but extend through the full depth of the input volume. During the forward pass, each filter is convolved across the width and height of the input volume, computing the dot product, and producing a 2-dimensional activation map of that filter. As a result, the network learns when they see some specific type of feature at some spatial position in the input. Then the activation maps are fed into a down sampling layer, and like convolutions, this method is applied one patch at a time. CNN has also fully connected layer that classifies output with one label per node.

II. RELATED WORK

Handwriting digit recognition has an active community of academics studying it. A lot of important work on convolutional neural networks happened for handwritten digit recognition [1,6,8,10]. There are many active areas of research such as Online Recognition, Offline recognition, Real-Time Handwriting Recognition, Signature Verification, Postal-Address Interpretation, Bank-Check Processing, Writer Recognition.

III. METHODOLOGY

Deep Learning has emerged as a central tool for self-perception problems like understanding images, a voice from humans, robots exploring the world. We aim to implement the concept of Convolutional Neural Network for digit recognition. Understanding CNN and applying it to the handwritten digit recognition system is the target of the proposed model. Convolutional Neural Network extracts the features maps from the 2D images.

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Then it can classify the images using the features maps. The convolutional neural network considers the mapping of image pixels with the neighborhood space rather than having a fully connected layer of neurons. The convolutional neural network is a powerful tool in signal and image processing. Even in the fields of computer vision such as handwriting recognition, natural object classification, and segmentation, CNN has been a much better tool compared to all other previously implemented tools. The broader aim may be to develop a machine learning model that could recognize people's handwriting.

a) *The Architecture of the Proposed Model*

When one starts learning deep learning with a neural network, he realizes that CNN is an important tool for image classification. Convolutional Neural Networks are a special kind of multi-layer neural networks designed to recognize visual patterns directly from pixel images with minimal preprocessing. Almost all CNN architectures follow the same general design principles of successively applying convolutional layers to the input, periodically downsampling (Max pooling) the spatial dimensions while increasing the number of feature maps. Moreover, there are also fully connected layers, activation functions and loss function (e.g., cross entropy or softmax). However, among all the operations of CNN, convolutional layers, pooling layers, and fully connected layers are the most important ones. Therefore, we will quickly introduce these layers before presenting our proposed model.

The convolutional layer is the first layer which can extract features from the images. Because pixels are only related to the adjacent and close pixels, convolution allows us to preserve the relationship between different parts of an image. Convolution is filtering the image with a smaller pixel filter to decrease the size of the image without losing the relationship between pixels. When we apply convolution to the 5x5 image by using a 3x3 filter with 1x1 stride (1-pixel shift at each step), we will end up having a 3x3 output (64% decrease in complexity).

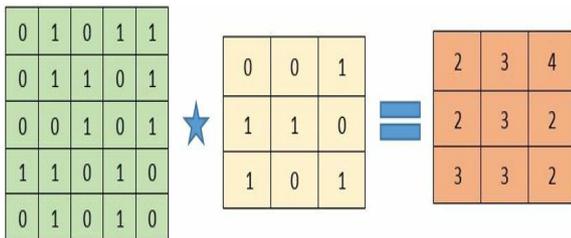


Fig. 1: Convolution operation

When constructing CNN, it is common to insert pooling layers after each convolution layer to reduce the spatial size of the features maps. Pooling layers also help with the overfitting problem. We select a pooling

size to reduce the amount of the parameters by selecting the maximum, average, or sum values inside these pixels. Max Pooling, one of the most common pooling techniques, may be demonstrated as follows:

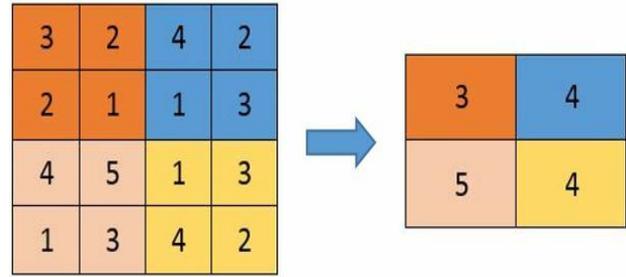


Fig. 2: Max pooling operation

A fully connected network is in any architecture where each parameter is linked to one another to determine the relation and effect of each parameter on the labels. Since convolution and pooling layers reduce time-space complexity, we can construct a fully connected network in the end to classify the images.

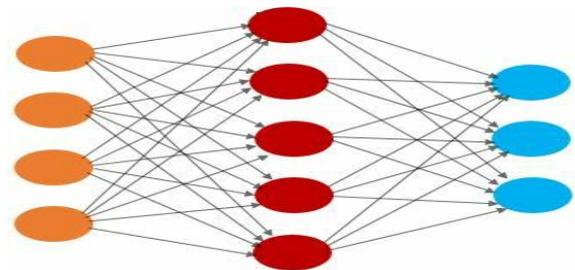


Fig. 3: Fully connected layers

Now we think, it is time to share an overview look of our proposed convolutional neural network. It has similarity with other handwritten digit recognition architectures [1,6,8,10,11] but has changed in a number of filters, neurons and activation functions for better performance. It has seven layers.

b) *Explanation of the Model*

A simple convolutional neural network is a sequence of layers, and every layer transforms one volume of activations to another through a differentiable function. We use three main types of layers to build the network. These are convolutional layers, pooling layers and fully connected layers. We will stack these layers to form our network architecture. We will go into more details below.

Fig.4 shows the architecture of our proposed CNN model. At first, we need some pre-processing on the images like resizing images, normalizing the pixel

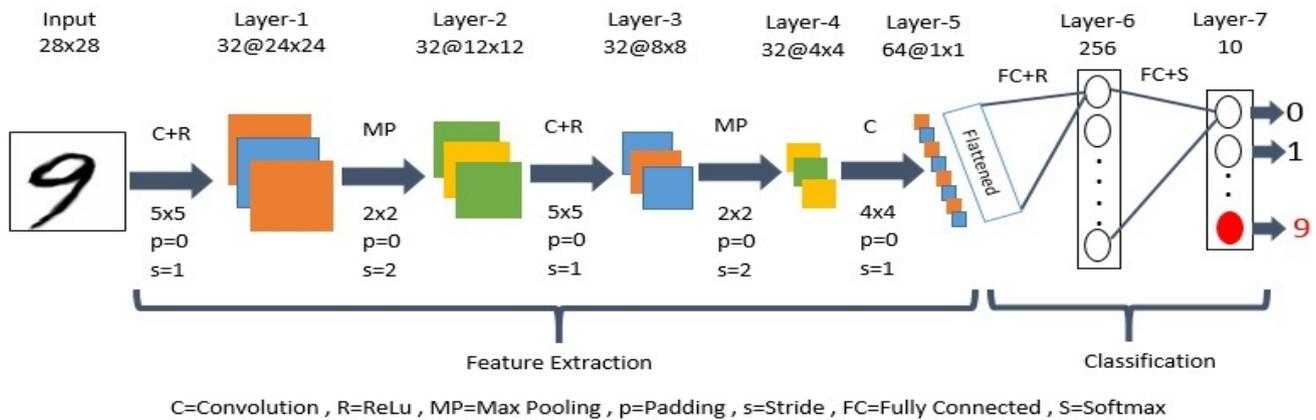


Fig. 4: The architecture of our proposed CNN

values, etc. After the necessary pre-processing, data is ready to be fed to the model.

Layer-1 consists of a convolutional layer with ReLu (Rectified Linear Unit) activation function. It is the first convolutional layer of our CNN architecture. This layer gets the pre-processed image as the input of size $n*n=28*28$. The convolution filter size ($f*f$) is $5*5$; padding (p) is 0 (around all the sides of the image), stride (s) is 1 and the number of filters is 32. After this convolution operation, we get feature maps of size $32@24*24$ where 32 is the number of feature maps which is equal to the number of filters used, and 24 comes from the formula $((n+2p-f)/s)+1=((28+2*0-5)/1)+1=24$. Then the ReLu activation is done in each feature map.

Layer-2 is the max pooling layer. This layer gets the input of size $32@24*24$ from the previous layer. The pooling size is $2*2$; padding is 0 and stride is 2. After this max pooling operation, we get feature maps of size $32@12*12$. Max pooling is done in each feature map independently, so we get same number feature maps as the previous layer, and 12 comes from the same formula $((n+2p-f)/s)+1$. This layer has no activation function.

Layer-3 is the second convolutional layer with ReLu activation function. This layer gets the input of size $32@12*12$ from the previous layer. The filter size is $5*5$; padding is 0, the stride is 1 and the number of filters is 32. After this convolution operation, we get feature maps of size $32@8*8$. Then ReLu activation is done in each feature map.

Layer-4 is the second max pooling layer. This layer gets the input of size $32@8*8$ from the previous layer. The pooling size is $2*2$; padding is 0 and stride is 2. After this max pooling operation, we get a feature map of size $32@4*4$.

Layer-5 is the third convolutional layer without ReLu activation function. This layer gets the input of size $32@4*4$ from the previous layer. The filter size is $4*4$; padding is 0, the stride is 1 and the number of filters is 64. After this convolution operation, we get feature maps of size $64@1*1$. This layer acts as a fully connected

layer and produces a one-dimensional vector of size 64 by being flattened.

Layer-6 is the fully connected layer. This layer takes an input one-dimensional vector of size 64 and outputs a one-dimensional vector of size 256. It has ReLu activation function.

Layer-7 is the last layer of the network. It is also fully connected layer. This layer will compute the class scores, resulting in a vector of size 10, where each of the ten numbers corresponds to a class score, such as among the ten categories of MNIST dataset. It has softmax activation function for final outputs.

In this way, CNN transforms the original image layer by layer from the original pixel values to the final class scores. Note that some layers contain parameters and others don't. In particular, the convolution / fully connected layers perform transformations that are a function of not only the activations in the input volume but also of the parameters (the weights and biases of the neurons). On the other hand, the ReLu / pooling layers will implement a fixed function. The parameters in the convolutional / fully connected layers will be trained with stochastic gradient descent algorithm so that the class scores are consistent with the labels in training set for each image. The algorithm will prepare the trained model which will be used to classify the digits present in the test data. Thus, we can classify the digits presents in the images as: Class-0,1,2,3,4,5,6,7,8,9.

IV. IMPLEMENTATION

To implement our CNN architecture, we will use MatConvNet. MatConvNet is an implementation of Convolutional Neural Networks (CNN) for MATLAB [12]. It exposes the building blocks of CNN as easy-to-use MATLAB functions, providing routines for computing linear convolutions with filter banks, feature pooling and many more. In this manner, MatConvNet allows fast prototyping of new CNN architectures; at the same time, it supports efficient computation on CPU and GPU allowing to train complex models on large datasets such as Image Net ILSVRC.

Convolutional Neural Networks (CNN) are the current state-of-art architecture for the image classification task. Our proposed 2-D Convolutional Neural Network (CNN) model is designed using MatConvNet backed for the well known MNIST digit recognition task. The whole workflow can be to preparing the data, building and compiling of the model, training and evaluating the model and saving the model to disk to reuse.

Preparing the data is the first step of our approach. Before we build the network, we need to set up our training and testing data, combine data, combine labels and reshape into the appropriate size. We save the dataset of normalized data (single precision and zero mean), labels, and miscellaneous (meta) information.

Building and compiling of the model is the second step. To create the CNN, we must initialize MatConvNets DagNN (Directed acyclic graph neural network) network and then define important initialization parameters.

Batch size determines the number of samples for the training phase of the CNN. The CNN will process

all the training data, but only in increments of the specified batch size. We use batch size for computational efficiency, and its value will be dependent on the user's available hardware. An epoch is a successful forward pass and a backward pass through the network. It's usually beneficial to set its value high. Then we can reduce the value once if one is satisfied with the convergence at a particular state (chosen epoch) in the network. Learning rate is a very sensitive parameter that pushes the model towards convergence. Finding its best value will be an empirical process unless one invokes more powerful techniques such as batch normalization. In our experiment, we use batch size 40, a number of epochs 8 and learning rate 0.001 for maximum accuracy.

Now we can build our CNN by creating each layer individually as shown in Fig.5. Afterward, we will invoke objective (log loss) and error (classification loss) layers that will provide a graphical visualization of the training and validation convergence after completing each epoch. After building the network layers, we initialize the weights. MatConvNet does this with Gaussian distribution.

```

% Layer-1 and Layer-2 ( Convolution + ReLu and Max Pooling )
net.addLayer('conv1', dagnn.Conv('size', [5 5 1 32], 'hasBias', true, 'stride', [1 1], 'pad', [0 0 0 0]), {'input'}, {'conv1'}, {'conv1f' 'conv1b'});
net.addLayer('relu1', dagnn.ReLU(), {'conv1'}, {'relu1'}, {});
net.addLayer('pool1', dagnn.Pooling('method', 'max', 'poolSize', [2 2], 'stride', [2 2], 'pad', [0 0 0 0]), {'relu1'}, {'pool1'}, {});

% Layer-3 and Layer-4 ( Convolution + ReLu and Max Pooling )
net.addLayer('conv2', dagnn.Conv('size', [5 5 32 32], 'hasBias', true, 'stride', [1 1], 'pad', [0 0 0 0]), {'pool1'}, {'conv2'}, {'conv2f' 'conv2b'});
net.addLayer('relu2', dagnn.ReLU(), {'conv2'}, {'relu2'}, {});
net.addLayer('pool2', dagnn.Pooling('method', 'max', 'poolSize', [2 2], 'stride', [2 2], 'pad', [0 0 0 0]), {'relu2'}, {'pool2'}, {});

% Layer-5 ( Convolution acts as Fully Connected and Flattened )
net.addLayer('conv3', dagnn.Conv('size', [4 4 32 64], 'hasBias', true, 'stride', [1 1], 'pad', [0 0 0 0]), {'pool2'}, {'conv3'}, {'conv3f' 'conv3b'});

% Layer-6 ( Fully Connected + ReLu )
net.addLayer('fc1', dagnn.Conv('size', [1 1 64 256], 'hasBias', true, 'stride', [1 1], 'pad', [0 0 0 0]), {'conv3'}, {'fc1'}, {'conv5f' 'conv5b'});
net.addLayer('relu5', dagnn.ReLU(), {'fc1'}, {'relu5'}, {});

% Layer-7 ( Fully Connected + Softmax )
net.addLayer('classifier', dagnn.Conv('size', [1 1 256 10], 'hasBias', true, 'stride', [1 1], 'pad', [0 0 0 0]), {'relu5'}, {'classifier'}, {'conv6f' 'conv6b'});
net.addLayer('prediction', dagnn.SoftMax(), {'classifier'}, {'prediction'}, {});

% Loss
net.addLayer('objective', dagnn.Loss('loss', 'log'), {'prediction', 'label'}, {'objective'}, {});
net.addLayer('error', dagnn.Loss('loss', 'classerror'), {'prediction', 'label'}, {'error'});
    
```

Fig. 5: CNN layers in MatConvNet

The third step is the training and evaluating the model. Training a CNN requires computing the derivatives of the loss concerning the network parameters. We use back propagation algorithm for computing derivatives. It is a memory-efficient implementation of the chain rule for derivatives. We have use Stochastic Gradient Descent (SGD) training algorithm to adjust the weight of the connection between neurons so that the loss reaches a minimum value or stops after several epochs. Only log loss is used to adjust weights. We have used CPU training. It is important to note that GPU training will dramatically help training time for CNN.

Lastly, we can begin the training of CNN by supplying the training data, the constructed model and the current 'batch' of data. When training the CNN, only the data specified for training plays a role in minimizing error in the CNN. The algorithm uses training data for the forward and backward pass. The algorithm uses

validation data to see how the CNN responds to new similar data, so it only is fed through the forward pass of the network. Afterward, we save the trained CNN and prepare for the testing phase.

During the training phase of the CNN, each epoch will produce up to two plots (error and objective) shown in Fig.6. For the DagNN network, MatConvNet minimizes the loss, while the error plot allows one to compute more statistical inference. The blue curve represents the training error and the orange represents the validation error of our CNN model during training.

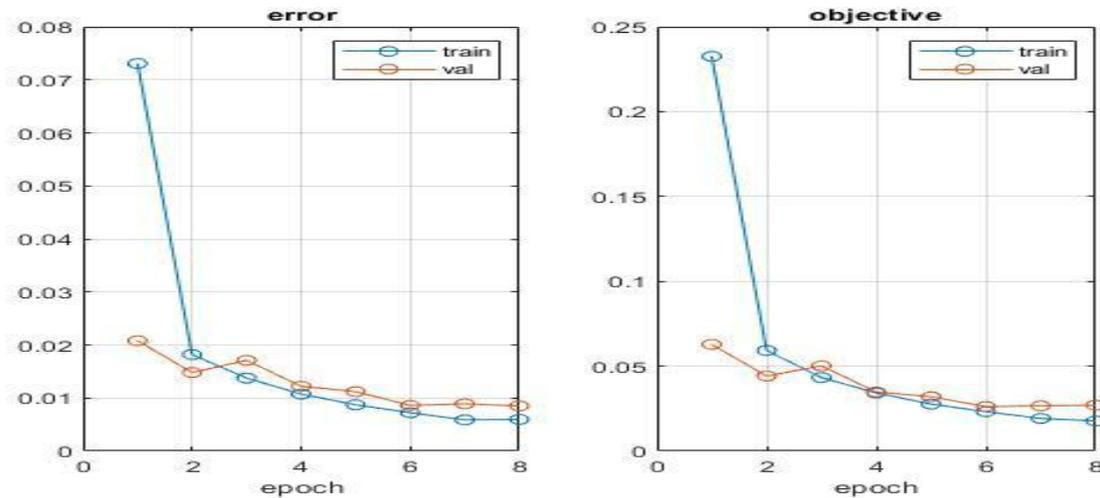


Fig. 6: Classification loss (error) and log loss (objective) during training

Finally, by using the testing data, we can evaluate our model. The following are example classification outputs from our model during testing.

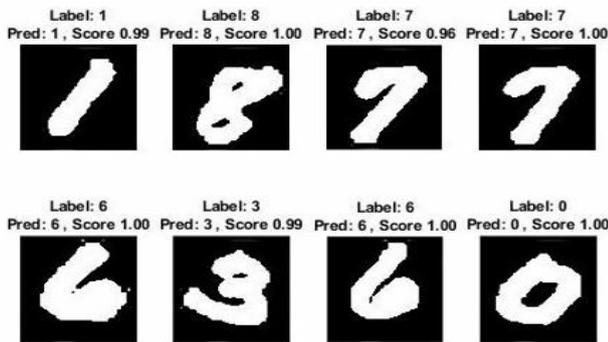


Fig. 7: Some correct recognized output

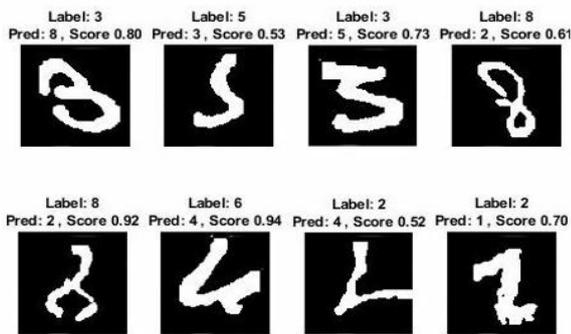


Fig. 8: Some wrong recognized output

We can find these test cases that show failed classifications. But we think most patterns can be solved by increasing the training set and increasing the standard number pattern. Moreover, missing pixels caused by image compression and image sharpness problems are also reasons for misclassification.

The fourth and final step is to save the model in the disk for reuse. We can store the trained model in a

Matlab file format. Hence the saved model can be reused in later or easily ported to other environments too.

V. RESULTS AND DISCUSSION

Among 10,000 test cases, our model misclassifies total 85 digits after eight epochs which correspond to 99.15% recognition rate shown in Table 1. The results are pretty good for such a simple model with CPU training and less training time (about 30 minutes).

```

Command Window

ans =

    ' total_number_of_misclassified_test_cases = 85
      error_rate = 0.85%
      testing_accuracy = 99.15% '

fx >>
    
```

Fig. 9: Error rate and accuracy of our model

Although there are some digits which are not a good handwriting, our model will be able to classify them correctly. For example, our model classifies the following image as '2'.



Fig.10: Correct recognition of bad handwriting

Table 1: Summary of the experiment

Batch size	No. of epochs	Accuracy
80	15	98.80%
60	8	99.14%
40	8	99.15%

Testing accuracy 99.15% implies that the model is trained well for prediction. Training set size affects the accuracy and accuracy increases as the number of data increases. The more data in the training set, the smaller the impact of training error and test error, and ultimately the accuracy can be improved.

VI. CONCLUSION AND FUTURE WORK

Here we demonstrate a model which can recognize handwritten digit. Later it can be extended for character recognition and real-time person's handwriting. Handwritten digit recognition is the first step to the vast field of Artificial Intelligence and Computer Vision. As seen from the results of the experiment, CNN proves to be far better than other classifiers. The results can be made more accurate with more convolution layers and more number of hidden neurons. It can completely abolish the need for typing. Digit recognition is an excellent prototype problem for learning about neural networks and it gives a great way to develop more advanced techniques of deep learning. In future, we are planning to develop a real-time handwritten digit recognition system.

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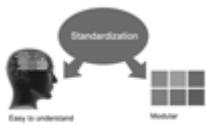
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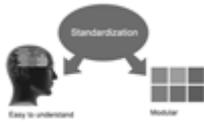


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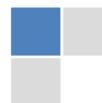
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- Electronic material
- Any other original work

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2. Drafting the paper and revising it critically regarding important academic content.
3. Final approval of the version of the paper to be published.

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Appealing Decisions

Unless specified in the notification, the Editorial Board's decision on publication of the paper is final and cannot be appealed before making the major change in the manuscript.

Acknowledgments

Contributors to the research other than authors credited should be mentioned in Acknowledgments. The source of funding for the research can be included. Suppliers of resources may be mentioned along with their addresses.

Declaration of funding sources

Global Journals is in partnership with various universities, laboratories, and other institutions worldwide in the research domain. Authors are requested to disclose their source of funding during every stage of their research, such as making analysis, performing laboratory operations, computing data, and using institutional resources, from writing an article to its submission. This will also help authors to get reimbursements by requesting an open access publication letter from Global Journals and submitting to the respective funding source.

PREPARING YOUR MANUSCRIPT

Authors can submit papers and articles in an acceptable file format: MS Word (doc, docx), LaTeX (.tex, .zip or .rar including all of your files), Adobe PDF (.pdf), rich text format (.rtf), simple text document (.txt), Open Document Text (.odt), and Apple Pages (.pages). Our professional layout editors will format the entire paper according to our official guidelines. This is one of the highlights of publishing with Global Journals—authors should not be concerned about the formatting of their paper. Global Journals accepts articles and manuscripts in every major language, be it Spanish, Chinese, Japanese, Portuguese, Russian, French, German, Dutch, Italian, Greek, or any other national language, but the title, subtitle, and abstract should be in English. This will facilitate indexing and the pre-peer review process.

The following is the official style and template developed for publication of a research paper. Authors are not required to follow this style during the submission of the paper. It is just for reference purposes.



Manuscript Style Instruction (Optional)

- Microsoft Word Document Setting Instructions.
- Font type of all text should be Swis721 Lt BT.
- Page size: 8.27" x 11", left margin: 0.65, right margin: 0.65, bottom margin: 0.75.
- Paper title should be in one column of font size 24.
- Author name in font size of 11 in one column.
- Abstract: font size 9 with the word "Abstract" in bold italics.
- Main text: font size 10 with two justified columns.
- Two columns with equal column width of 3.38 and spacing of 0.2.
- First character must be three lines drop-capped.
- The paragraph before spacing of 1 pt and after of 0 pt.
- Line spacing of 1 pt.
- Large images must be in one column.
- The names of first main headings (Heading 1) must be in Roman font, capital letters, and font size of 10.
- The names of second main headings (Heading 2) must not include numbers and must be in italics with a font size of 10.

Structure and Format of Manuscript

The recommended size of an original research paper is under 15,000 words and review papers under 7,000 words. Research articles should be less than 10,000 words. Research papers are usually longer than review papers. Review papers are reports of significant research (typically less than 7,000 words, including tables, figures, and references)

A research paper must include:

- a) A title which should be relevant to the theme of the paper.
- b) A summary, known as an abstract (less than 150 words), containing the major results and conclusions.
- c) Up to 10 keywords that precisely identify the paper's subject, purpose, and focus.
- d) An introduction, giving fundamental background objectives.
- e) Resources and techniques with sufficient complete experimental details (wherever possible by reference) to permit repetition, sources of information must be given, and numerical methods must be specified by reference.
- f) Results which should be presented concisely by well-designed tables and figures.
- g) Suitable statistical data should also be given.
- h) All data must have been gathered with attention to numerical detail in the planning stage.

Design has been recognized to be essential to experiments for a considerable time, and the editor has decided that any paper that appears not to have adequate numerical treatments of the data will be returned unrefereed.

- i) Discussion should cover implications and consequences and not just recapitulate the results; conclusions should also be summarized.
- j) There should be brief acknowledgments.
- k) There ought to be references in the conventional format. Global Journals recommends APA format.

Authors should carefully consider the preparation of papers to ensure that they communicate effectively. Papers are much more likely to be accepted if they are carefully designed and laid out, contain few or no errors, are summarizing, and follow instructions. They will also be published with much fewer delays than those that require much technical and editorial correction.

The Editorial Board reserves the right to make literary corrections and suggestions to improve brevity.



FORMAT STRUCTURE

It is necessary that authors take care in submitting a manuscript that is written in simple language and adheres to published guidelines.

All manuscripts submitted to Global Journals should include:

Title

The title page must carry an informative title that reflects the content, a running title (less than 45 characters together with spaces), names of the authors and co-authors, and the place(s) where the work was carried out.

Author details

The full postal address of any related author(s) must be specified.

Abstract

The abstract is the foundation of the research paper. It should be clear and concise and must contain the objective of the paper and inferences drawn. It is advised to not include big mathematical equations or complicated jargon.

Many researchers searching for information online will use search engines such as Google, Yahoo or others. By optimizing your paper for search engines, you will amplify the chance of someone finding it. In turn, this will make it more likely to be viewed and cited in further works. Global Journals has compiled these guidelines to facilitate you to maximize the web-friendliness of the most public part of your paper.

Keywords

A major lynchpin of research work for the writing of research papers is the keyword search, which one will employ to find both library and internet resources. Up to eleven keywords or very brief phrases have to be given to help data retrieval, mining, and indexing.

One must be persistent and creative in using keywords. An effective keyword search requires a strategy: planning of a list of possible keywords and phrases to try.

Choice of the main keywords is the first tool of writing a research paper. Research paper writing is an art. Keyword search should be as strategic as possible.

One should start brainstorming lists of potential keywords before even beginning searching. Think about the most important concepts related to research work. Ask, "What words would a source have to include to be truly valuable in a research paper?" Then consider synonyms for the important words.

It may take the discovery of only one important paper to steer in the right keyword direction because, in most databases, the keywords under which a research paper is abstracted are listed with the paper.

Numerical Methods

Numerical methods used should be transparent and, where appropriate, supported by references.

Abbreviations

Authors must list all the abbreviations used in the paper at the end of the paper or in a separate table before using them.

Formulas and equations

Authors are advised to submit any mathematical equation using either MathJax, KaTeX, or LaTeX, or in a very high-quality image.

Tables, Figures, and Figure Legends

Tables: Tables should be cautiously designed, uncrowned, and include only essential data. Each must have an Arabic number, e.g., Table 4, a self-explanatory caption, and be on a separate sheet. Authors must submit tables in an editable format and not as images. References to these tables (if any) must be mentioned accurately.



Figures

Figures are supposed to be submitted as separate files. Always include a citation in the text for each figure using Arabic numbers, e.g., Fig. 4. Artwork must be submitted online in vector electronic form or by emailing it.

PREPARATION OF ELETRONIC FIGURES FOR PUBLICATION

Although low-quality images are sufficient for review purposes, print publication requires high-quality images to prevent the final product being blurred or fuzzy. Submit (possibly by e-mail) EPS (line art) or TIFF (halftone/ photographs) files only. MS PowerPoint and Word Graphics are unsuitable for printed pictures. Avoid using pixel-oriented software. Scans (TIFF only) should have a resolution of at least 350 dpi (halftone) or 700 to 1100 dpi (line drawings). Please give the data for figures in black and white or submit a Color Work Agreement form. EPS files must be saved with fonts embedded (and with a TIFF preview, if possible).

For scanned images, the scanning resolution at final image size ought to be as follows to ensure good reproduction: line art: >650 dpi; halftones (including gel photographs): >350 dpi; figures containing both halftone and line images: >650 dpi.

Color charges: Authors are advised to pay the full cost for the reproduction of their color artwork. Hence, please note that if there is color artwork in your manuscript when it is accepted for publication, we would require you to complete and return a Color Work Agreement form before your paper can be published. Also, you can email your editor to remove the color fee after acceptance of the paper.

TIPS FOR WRITING A GOOD QUALITY COMPUTER SCIENCE RESEARCH PAPER

Techniques for writing a good quality computer science research paper:

1. Choosing the topic: In most cases, the topic is selected by the interests of the author, but it can also be suggested by the guides. You can have several topics, and then judge which you are most comfortable with. This may be done by asking several questions of yourself, like "Will I be able to carry out a search in this area? Will I find all necessary resources to accomplish the search? Will I be able to find all information in this field area?" If the answer to this type of question is "yes," then you ought to choose that topic. In most cases, you may have to conduct surveys and visit several places. Also, you might have to do a lot of work to find all the rises and falls of the various data on that subject. Sometimes, detailed information plays a vital role, instead of short information. Evaluators are human: The first thing to remember is that evaluators are also human beings. They are not only meant for rejecting a paper. They are here to evaluate your paper. So present your best aspect.

2. Think like evaluators: If you are in confusion or getting demotivated because your paper may not be accepted by the evaluators, then think, and try to evaluate your paper like an evaluator. Try to understand what an evaluator wants in your research paper, and you will automatically have your answer. Make blueprints of paper: The outline is the plan or framework that will help you to arrange your thoughts. It will make your paper logical. But remember that all points of your outline must be related to the topic you have chosen.

3. Ask your guides: If you are having any difficulty with your research, then do not hesitate to share your difficulty with your guide (if you have one). They will surely help you out and resolve your doubts. If you can't clarify what exactly you require for your work, then ask your supervisor to help you with an alternative. He or she might also provide you with a list of essential readings.

4. Use of computer is recommended: As you are doing research in the field of computer science then this point is quite obvious. Use right software: Always use good quality software packages. If you are not capable of judging good software, then you can lose the quality of your paper unknowingly. There are various programs available to help you which you can get through the internet.

5. Use the internet for help: An excellent start for your paper is using Google. It is a wondrous search engine, where you can have your doubts resolved. You may also read some answers for the frequent question of how to write your research paper or find a model research paper. You can download books from the internet. If you have all the required books, place importance on reading, selecting, and analyzing the specified information. Then sketch out your research paper. Use big pictures: You may use encyclopedias like Wikipedia to get pictures with the best resolution. At Global Journals, you should strictly follow here.



6. Bookmarks are useful: When you read any book or magazine, you generally use bookmarks, right? It is a good habit which helps to not lose your continuity. You should always use bookmarks while searching on the internet also, which will make your search easier.

7. Revise what you wrote: When you write anything, always read it, summarize it, and then finalize it.

8. Make every effort: Make every effort to mention what you are going to write in your paper. That means always have a good start. Try to mention everything in the introduction—what is the need for a particular research paper. Polish your work with good writing skills and always give an evaluator what he wants. Make backups: When you are going to do any important thing like making a research paper, you should always have backup copies of it either on your computer or on paper. This protects you from losing any portion of your important data.

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10. Use proper verb tense: Use proper verb tenses in your paper. Use past tense to present those events that have happened. Use present tense to indicate events that are going on. Use future tense to indicate events that will happen in the future. Use of wrong tenses will confuse the evaluator. Avoid sentences that are incomplete.

11. Pick a good study spot: Always try to pick a spot for your research which is quiet. Not every spot is good for studying.

12. Know what you know: Always try to know what you know by making objectives, otherwise you will be confused and unable to achieve your target.

13. Use good grammar: Always use good grammar and words that will have a positive impact on the evaluator; use of good vocabulary does not mean using tough words which the evaluator has to find in a dictionary. Do not fragment sentences. Eliminate one-word sentences. Do not ever use a big word when a smaller one would suffice.

Verbs have to be in agreement with their subjects. In a research paper, do not start sentences with conjunctions or finish them with prepositions. When writing formally, it is advisable to never split an infinitive because someone will (wrongly) complain. Avoid clichés like a disease. Always shun irritating alliteration. Use language which is simple and straightforward. Put together a neat summary.

14. Arrangement of information: Each section of the main body should start with an opening sentence, and there should be a changeover at the end of the section. Give only valid and powerful arguments for your topic. You may also maintain your arguments with records.

15. Never start at the last minute: Always allow enough time for research work. Leaving everything to the last minute will degrade your paper and spoil your work.

16. Multitasking in research is not good: Doing several things at the same time is a bad habit in the case of research activity. Research is an area where everything has a particular time slot. Divide your research work into parts, and do a particular part in a particular time slot.

17. Never copy others' work: Never copy others' work and give it your name because if the evaluator has seen it anywhere, you will be in trouble. Take proper rest and food: No matter how many hours you spend on your research activity, if you are not taking care of your health, then all your efforts will have been in vain. For quality research, take proper rest and food.

18. Go to seminars: Attend seminars if the topic is relevant to your research area. Utilize all your resources.

19. Refresh your mind after intervals: Try to give your mind a rest by listening to soft music or sleeping in intervals. This will also improve your memory. Acquire colleagues: Always try to acquire colleagues. No matter how sharp you are, if you acquire colleagues, they can give you ideas which will be helpful to your research.



20. Think technically: Always think technically. If anything happens, search for its reasons, benefits, and demerits. Think and then print: When you go to print your paper, check that tables are not split, headings are not detached from their descriptions, and page sequence is maintained.

21. Adding unnecessary information: Do not add unnecessary information like "I have used MS Excel to draw graphs." Irrelevant and inappropriate material is superfluous. Foreign terminology and phrases are not apropos. One should never take a broad view. Analogy is like feathers on a snake. Use words properly, regardless of how others use them. Remove quotations. Puns are for kids, not grunt readers. Never oversimplify: When adding material to your research paper, never go for oversimplification; this will definitely irritate the evaluator. Be specific. Never use rhythmic redundancies. Contractions shouldn't be used in a research paper. Comparisons are as terrible as clichés. Give up ampersands, abbreviations, and so on. Remove commas that are not necessary. Parenthetical words should be between brackets or commas. Understatement is always the best way to put forward earth-shaking thoughts. Give a detailed literary review.

22. Report concluded results: Use concluded results. From raw data, filter the results, and then conclude your studies based on measurements and observations taken. An appropriate number of decimal places should be used. Parenthetical remarks are prohibited here. Proofread carefully at the final stage. At the end, give an outline to your arguments. Spot perspectives of further study of the subject. Justify your conclusion at the bottom sufficiently, which will probably include examples.

23. Upon conclusion: Once you have concluded your research, the next most important step is to present your findings. Presentation is extremely important as it is the definite medium through which your research is going to be in print for the rest of the crowd. Care should be taken to categorize your thoughts well and present them in a logical and neat manner. A good quality research paper format is essential because it serves to highlight your research paper and bring to light all necessary aspects of your research.

INFORMAL GUIDELINES OF RESEARCH PAPER WRITING

Key points to remember:

- Submit all work in its final form.
- Write your paper in the form which is presented in the guidelines using the template.
- Please note the criteria peer reviewers will use for grading the final paper.

Final points:

One purpose of organizing a research paper is to let people interpret your efforts selectively. The journal requires the following sections, submitted in the order listed, with each section starting on a new page:

The introduction: This will be compiled from reference matter and reflect the design processes or outline of basis that directed you to make a study. As you carry out the process of study, the method and process section will be constructed like that. The results segment will show related statistics in nearly sequential order and direct reviewers to similar intellectual paths throughout the data that you gathered to carry out your study.

The discussion section:

This will provide understanding of the data and projections as to the implications of the results. The use of good quality references throughout the paper will give the effort trustworthiness by representing an alertness to prior workings.

Writing a research paper is not an easy job, no matter how trouble-free the actual research or concept. Practice, excellent preparation, and controlled record-keeping are the only means to make straightforward progression.

General style:

Specific editorial column necessities for compliance of a manuscript will always take over from directions in these general guidelines.

To make a paper clear: Adhere to recommended page limits.



Mistakes to avoid:

- Insertion of a title at the foot of a page with subsequent text on the next page.
- Separating a table, chart, or figure—confine each to a single page.
- Submitting a manuscript with pages out of sequence.
- In every section of your document, use standard writing style, including articles ("a" and "the").
- Keep paying attention to the topic of the paper.
- Use paragraphs to split each significant point (excluding the abstract).
- Align the primary line of each section.
- Present your points in sound order.
- Use present tense to report well-accepted matters.
- Use past tense to describe specific results.
- Do not use familiar wording; don't address the reviewer directly. Don't use slang or superlatives.
- Avoid use of extra pictures—include only those figures essential to presenting results.

Title page:

Choose a revealing title. It should be short and include the name(s) and address(es) of all authors. It should not have acronyms or abbreviations or exceed two printed lines.

Abstract: This summary should be two hundred words or less. It should clearly and briefly explain the key findings reported in the manuscript and must have precise statistics. It should not have acronyms or abbreviations. It should be logical in itself. Do not cite references at this point.

An abstract is a brief, distinct paragraph summary of finished work or work in development. In a minute or less, a reviewer can be taught the foundation behind the study, common approaches to the problem, relevant results, and significant conclusions or new questions.

Write your summary when your paper is completed because how can you write the summary of anything which is not yet written? Wealth of terminology is very essential in abstract. Use comprehensive sentences, and do not sacrifice readability for brevity; you can maintain it succinctly by phrasing sentences so that they provide more than a lone rationale. The author can at this moment go straight to shortening the outcome. Sum up the study with the subsequent elements in any summary. Try to limit the initial two items to no more than one line each.

Reason for writing the article—theory, overall issue, purpose.

- Fundamental goal.
- To-the-point depiction of the research.
- Consequences, including definite statistics—if the consequences are quantitative in nature, account for this; results of any numerical analysis should be reported. Significant conclusions or questions that emerge from the research.

Approach:

- Single section and succinct.
- An outline of the job done is always written in past tense.
- Concentrate on shortening results—limit background information to a verdict or two.
- Exact spelling, clarity of sentences and phrases, and appropriate reporting of quantities (proper units, important statistics) are just as significant in an abstract as they are anywhere else.

Introduction:

The introduction should "introduce" the manuscript. The reviewer should be presented with sufficient background information to be capable of comprehending and calculating the purpose of your study without having to refer to other works. The basis for the study should be offered. Give the most important references, but avoid making a comprehensive appraisal of the topic. Describe the problem visibly. If the problem is not acknowledged in a logical, reasonable way, the reviewer will give no attention to your results. Speak in common terms about techniques used to explain the problem, if needed, but do not present any particulars about the protocols here.



The following approach can create a valuable beginning:

- Explain the value (significance) of the study.
- Defend the model—why did you employ this particular system or method? What is its compensation? Remark upon its appropriateness from an abstract point of view as well as pointing out sensible reasons for using it.
- Present a justification. State your particular theory(-ies) or aim(s), and describe the logic that led you to choose them.
- Briefly explain the study's tentative purpose and how it meets the declared objectives.

Approach:

Use past tense except for when referring to recognized facts. After all, the manuscript will be submitted after the entire job is done. Sort out your thoughts; manufacture one key point for every section. If you make the four points listed above, you will need at least four paragraphs. Present surrounding information only when it is necessary to support a situation. The reviewer does not desire to read everything you know about a topic. Shape the theory specifically—do not take a broad view.

As always, give awareness to spelling, simplicity, and correctness of sentences and phrases.

Procedures (methods and materials):

This part is supposed to be the easiest to carve if you have good skills. A soundly written procedures segment allows a capable scientist to replicate your results. Present precise information about your supplies. The suppliers and clarity of reagents can be helpful bits of information. Present methods in sequential order, but linked methodologies can be grouped as a segment. Be concise when relating the protocols. Attempt to give the least amount of information that would permit another capable scientist to replicate your outcome, but be cautious that vital information is integrated. The use of subheadings is suggested and ought to be synchronized with the results section.

When a technique is used that has been well-described in another section, mention the specific item describing the way, but draw the basic principle while stating the situation. The purpose is to show all particular resources and broad procedures so that another person may use some or all of the methods in one more study or referee the scientific value of your work. It is not to be a step-by-step report of the whole thing you did, nor is a methods section a set of orders.

Materials:

Materials may be reported in part of a section or else they may be recognized along with your measures.

Methods:

- Report the method and not the particulars of each process that engaged the same methodology.
- Describe the method entirely.
- To be succinct, present methods under headings dedicated to specific dealings or groups of measures.
- Simplify—detail how procedures were completed, not how they were performed on a particular day.
- If well-known procedures were used, account for the procedure by name, possibly with a reference, and that's all.

Approach:

It is embarrassing to use vigorous voice when documenting methods without using first person, which would focus the reviewer's interest on the researcher rather than the job. As a result, when writing up the methods, most authors use third person passive voice.

Use standard style in this and every other part of the paper—avoid familiar lists, and use full sentences.

What to keep away from:

- Resources and methods are not a set of information.
- Skip all descriptive information and surroundings—save it for the argument.
- Leave out information that is immaterial to a third party.



Results:

The principle of a results segment is to present and demonstrate your conclusion. Create this part as entirely objective details of the outcome, and save all understanding for the discussion.

The page length of this segment is set by the sum and types of data to be reported. Use statistics and tables, if suitable, to present consequences most efficiently.

You must clearly differentiate material which would usually be incorporated in a study editorial from any unprocessed data or additional appendix matter that would not be available. In fact, such matters should not be submitted at all except if requested by the instructor.

Content:

- Sum up your conclusions in text and demonstrate them, if suitable, with figures and tables.
- In the manuscript, explain each of your consequences, and point the reader to remarks that are most appropriate.
- Present a background, such as by describing the question that was addressed by creation of an exacting study.
- Explain results of control experiments and give remarks that are not accessible in a prescribed figure or table, if appropriate.
- Examine your data, then prepare the analyzed (transformed) data in the form of a figure (graph), table, or manuscript.

What to stay away from:

- Do not discuss or infer your outcome, report surrounding information, or try to explain anything.
- Do not include raw data or intermediate calculations in a research manuscript.
- Do not present similar data more than once.
- A manuscript should complement any figures or tables, not duplicate information.
- Never confuse figures with tables—there is a difference.

Approach:

As always, use past tense when you submit your results, and put the whole thing in a reasonable order.

Put figures and tables, appropriately numbered, in order at the end of the report.

If you desire, you may place your figures and tables properly within the text of your results section.

Figures and tables:

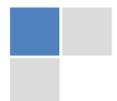
If you put figures and tables at the end of some details, make certain that they are visibly distinguished from any attached appendix materials, such as raw facts. Whatever the position, each table must be titled, numbered one after the other, and include a heading. All figures and tables must be divided from the text.

Discussion:

The discussion is expected to be the trickiest segment to write. A lot of papers submitted to the journal are discarded based on problems with the discussion. There is no rule for how long an argument should be.

Position your understanding of the outcome visibly to lead the reviewer through your conclusions, and then finish the paper with a summing up of the implications of the study. The purpose here is to offer an understanding of your results and support all of your conclusions, using facts from your research and generally accepted information, if suitable. The implication of results should be fully described.

Infer your data in the conversation in suitable depth. This means that when you clarify an observable fact, you must explain mechanisms that may account for the observation. If your results vary from your prospect, make clear why that may have happened. If your results agree, then explain the theory that the proof supported. It is never suitable to just state that the data approved the prospect, and let it drop at that. Make a decision as to whether each premise is supported or discarded or if you cannot make a conclusion with assurance. Do not just dismiss a study or part of a study as "uncertain."



Research papers are not acknowledged if the work is imperfect. Draw what conclusions you can based upon the results that you have, and take care of the study as a finished work.

- You may propose future guidelines, such as how an experiment might be personalized to accomplish a new idea.
- Give details of all of your remarks as much as possible, focusing on mechanisms.
- Make a decision as to whether the tentative design sufficiently addressed the theory and whether or not it was correctly restricted. Try to present substitute explanations if they are sensible alternatives.
- One piece of research will not counter an overall question, so maintain the large picture in mind. Where do you go next? The best studies unlock new avenues of study. What questions remain?
- Recommendations for detailed papers will offer supplementary suggestions.

Approach:

When you refer to information, differentiate data generated by your own studies from other available information. Present work done by specific persons (including you) in past tense.

Describe generally acknowledged facts and main beliefs in present tense.

THE ADMINISTRATION RULES

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CRITERION FOR GRADING A RESEARCH PAPER (COMPILATION)
BY GLOBAL JOURNALS INC. (US)

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Topics	Grades		
	A-B	C-D	E-F
<i>Abstract</i>	Clear and concise with appropriate content, Correct format. 200 words or below	Unclear summary and no specific data, Incorrect form Above 200 words	No specific data with ambiguous information Above 250 words
<i>Introduction</i>	Containing all background details with clear goal and appropriate details, flow specification, no grammar and spelling mistake, well organized sentence and paragraph, reference cited	Unclear and confusing data, appropriate format, grammar and spelling errors with unorganized matter	Out of place depth and content, hazy format
<i>Methods and Procedures</i>	Clear and to the point with well arranged paragraph, precision and accuracy of facts and figures, well organized subheads	Difficult to comprehend with embarrassed text, too much explanation but completed	Incorrect and unorganized structure with hazy meaning
<i>Result</i>	Well organized, Clear and specific, Correct units with precision, correct data, well structuring of paragraph, no grammar and spelling mistake	Complete and embarrassed text, difficult to comprehend	Irregular format with wrong facts and figures
<i>Discussion</i>	Well organized, meaningful specification, sound conclusion, logical and concise explanation, highly structured paragraph reference cited	Wordy, unclear conclusion, spurious	Conclusion is not cited, unorganized, difficult to comprehend
<i>References</i>	Complete and correct format, well organized	Beside the point, Incomplete	Wrong format and structuring



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