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DRUG PREDICTION AND INTIMATION SYSTEM USING FUZZY BASED CONVOLUTIONAL NEURAL NETWORK

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Abstract: In present scenario, medical research centres have a prominent role in identifying new drugs due to the increasing ailments. There exists unique effect for each and every drug which might be either a good reaction or negative reaction. Hence there necessitates to obtain drugs impact which helps physician for prescribing replacement for the patients. The interpretations analysis stated by the drug users in online sites plays a major part in Drug reactions predictions. Modified Convolution Neural Network based Drug Prediction System (MCNN-DPS) is one of the methodology adopted earlier for the above predictions. There is no sharing of drug information in the earlier researches which might aid doctors for analysing besides replacement drugs recommendation. This research concentrates mainly on the above elucidated through an approach entitled Drug Prediction and Intimation System using Fuzzy based Convolutional Neural Network (DPIS-FCNN). The extraction of drug related posts is accomplished primarily from the online sites. Fuzzy based Convolutional Neural Network (FCNN) is greatly involved in drug reaction prediction. The logistic regression based clustering method is chiefly deployed for grouping those drugs beside with their reaction on the basis of their relevancy once prediction is done. The respective doctor receives this grouped information when they possess proper access permission. MATLAB simulation platform is greatly utilized for validating the entire research work and proved to attain improved outcome than the prevailing research works.

Keywords: Drug reaction analysis, pre-processing, grouping, access permission, fuzzy based convolutional neural network.

I. INTRODUCTION

A sort of toxicity is considered as Adverse drug reactions, still toxicity arises due to many reasons such as over ingestion effect (accidental or intentional), raised blood levels, greater drug effects that ensue in the course of proper use (eg, once drug metabolism is momentarily inhibited through a disorder or another drug) [1].The symptoms in addition to specific Poisons treatment can be mentioned for information on particular drugs toxicity [2]. A drug's unintended effects arising contained by therapeutic range is termed as side effect, an imprecise term [3]. In the

course of drug prescription risk-benefit analysis (investigating benefit likelihood vs ADRs risk) is necessitated since every drug possess potential for adverse drug reactions [4].

The ADR diagnosis is regarded as a challenging issue due to many causes [5]. There might exists symptoms like common illness which may be infrequent or unpredicted or in patients with manifold co-morbidities else being treated with several drug and no precise drug-related symptoms [6]. Healthcare specialists should be paid more attention and also to be cautious regarding drug reactions alert as a causative factor when there is an alternative clinical explanations absence for the symptoms [7]. ADR confirmation cannot be done through laboratory investigations, it necessitates suitable tools for excluding non-drug causes of the presenting symptoms or signs. As soon as ADR diagnosis is done, its categorization is dependent on management [8]. ADR type A refers to a reduction in dosage, type B signifies instant offending drug termination [9].

Adverse drug reactions might affect patients losing their self-confidence or might possess negative emotions toward their physicians besides looking for self-treatment options, which might consequently precipitate extra ADRs [10]. It is inferred that almost 5% of all the hospital admissions are due to ADR as well10%– 20% of inpatients tend to have at least one ADR for the period of their hospital visit. Sometime there exists greater ADRs actual incidence since ADRs mimic natural disease states besides remain undetected and/or unreported [11]. ADR may result in minor symptoms in some cases , some may be serious besides instigating death in as many as 0.1%–0.3% of hospitalized patients. It also greatly necessitates prompt identification and managing their detrimental effects limit on the patient.

ADR management is considered as a highly cost-effective which is irrespective of the inpatient or the outpatient setting. It also greatly demands supplementary laboratory tests or procedures for patient's symptoms cause investigation [12] since there is no clear ADR clinical diagnosis. Pharmacotherapy might be prescribed by Practitioners for ailments due to unrecognized ADR, which probably up surges costs besides additional ADRs risk. The cost may also up surge when ADR arises during the patients hospital stay due to which, prolonging of patient hospital stay may increase which upsurges the entire hospitalization cost. Apart from this, there may arise anxiety or depression and missed days of work for the patient and/or caregiver [13] which in turn encompasses indirect cost.

This research concentrates mainly on the adverse drug reaction prediction through an approach entitled Drug Prediction and Intimation System using Fuzzy based Convolutional Neural Network (DPIS-FCNN) to predict in an optimal way for obtaining drugs positive and negative reactions. The extraction of drug related posts is accomplished primarily from the online sites. Fuzzy based Convolutional Neural Network (FCNN) is greatly involved in drug reaction prediction. The logistic regression based clustering method is chiefly deployed for grouping those drugs beside with their reaction on the basis of their relevancy once prediction is done. The respective doctor receives this grouped information when they possess proper access permission.

The research work structure is as follows: Section 1 gives a brief introduction of ADR and its impacts. Section 2, describes about many prevailing research methods associated to the drug effect prediction. In Section 3, elucidates about anticipated research method. In section 4,

overall simulation results discussion has been given on the basis of analytical assessment. Lastly in section 5, conclusion is prearranged on the basis of simulation results.

II. RELATED WORKS

Cocos et al [14] suggested a methodology where words labelling are done in an input sequence through ADR membership tags by means of recurrent neural network (RNN) model. Task independent pretraining is mainly involved in forming the word-embedding vectors. Sometimes ADR detection training is also utilized for obtaining word-embedding vectors.

Tang et al [15] identified ADR mentions from social media in medicine through exploiting deep neural network (called LSTM-CRF) combining long short-term memory (LSTM) neural networks (a type of recurrent neural networks) besides conditional random fields (CRFs). The investigation is accomplished to analyse the three factors effect during ADR mention recognition.

proposed a deep neural network (called LSTM-CRF) combining long short-term memory (LSTM) neural networks (a type of recurrent neural networks) and conditional random fields (CRFs) to recognize ADR mentions from social media in medicine and investigate the effects of three factors on ADR mention recognition.

Liu et al [16] presented a system for ADE relation extraction using patient-generated content in social media by utilizing semi-supervised ensemble learning framework, SSEL-ADE .This approach outperforms well in contradiction to the earlier researches. This Methodology greatly deploys various lexical, semantic, syntactic features, integrated ensemble learning besides semi-supervised learning. The effectiveness is validated through conducting series of experiments for the suggested approach.

Nguyen et al [17] exploited datas from social media, comprising Twitter, Reddit, and LiveJournal for adverse drug reactions (ADR) degree assessment for psychiatric medications. Additionally, large scale data containing of 6.4 terabytes data encompassing 3.8 billion records from all the media are processed by means of enhanced lightning-fast cluster computing. The Quantification of ADR rates is accomplished using SIDER database of drugs and side-effects plus an estimated ADR rate was created on the discussion prevalence in the social media corpora.

Yang et al [18] established a new entity recognition method on the basis of an recurrent convolutional neural network besides contrasted with recurrent neural network realized by long-short term memory architecture. It also explored techniques for medical knowledge integration as embedding layers in neural networks. In this 3 machine learning models are analysed comprising support vector machines, random forests and gradient boosting for relation classification.

Jeong et al [19] designed ML models (random forest, L1 regularized logistic regression, support vector machine, and a neural network) for utilizing CERT, CLEAR, and PACE algorithms intermediate products as inputs as well as obtaining whether a drug–laboratory event pair is related.

Casillas et al [20] deliberated a hybrid system exploiting a self-developed morpho-syntactic besides semantic analyser for medical texts in Spanish. The drugs and diseases entity recognition is performed along with adverse drug reaction event extraction. Rule-based in addition to machine learning techniques aremainly involved in event extraction phase.

Muñoz et al [21] utilized machine learning approaches which exploits drug profiles for constructing predictions 0in addition use features from multiple data sources. This method has

several limitations particularly flexibility in experimenting with different data sets and/or predictive models.

We argue that despite promising results, existing works have limitations, especially regarding flexibility in experimenting with different data sets and/or predictive models. Authors suggested to address these limitations by generalization of the key principles used by the state of the art.

Lee et al [22] outlined about the machine learning algorithm ,also suggested a potential high-performance deep learning framework for its effective applications. Deep learning plays a vital role in ADR prediction repurpose drugs and perform precision medicine.

III. DRUG PREDICTION AND INTIMATION SYSTEM

In this research, drug related posts extraction is accomplished primarily from the online sites on the basis of extracted drug names and their class labels drug dictionary. Fuzzy based Convolutional Neural Network (FCNN) is greatly involved in drug reaction prediction. The logistic regression based clustering method is chiefly deployed for grouping those drugs beside with their reaction on the basis of their relevancy once prediction is done. The respective doctor receives this grouped information when they possess proper access permission. The suggested research work flow is depicted in the following figure 1.

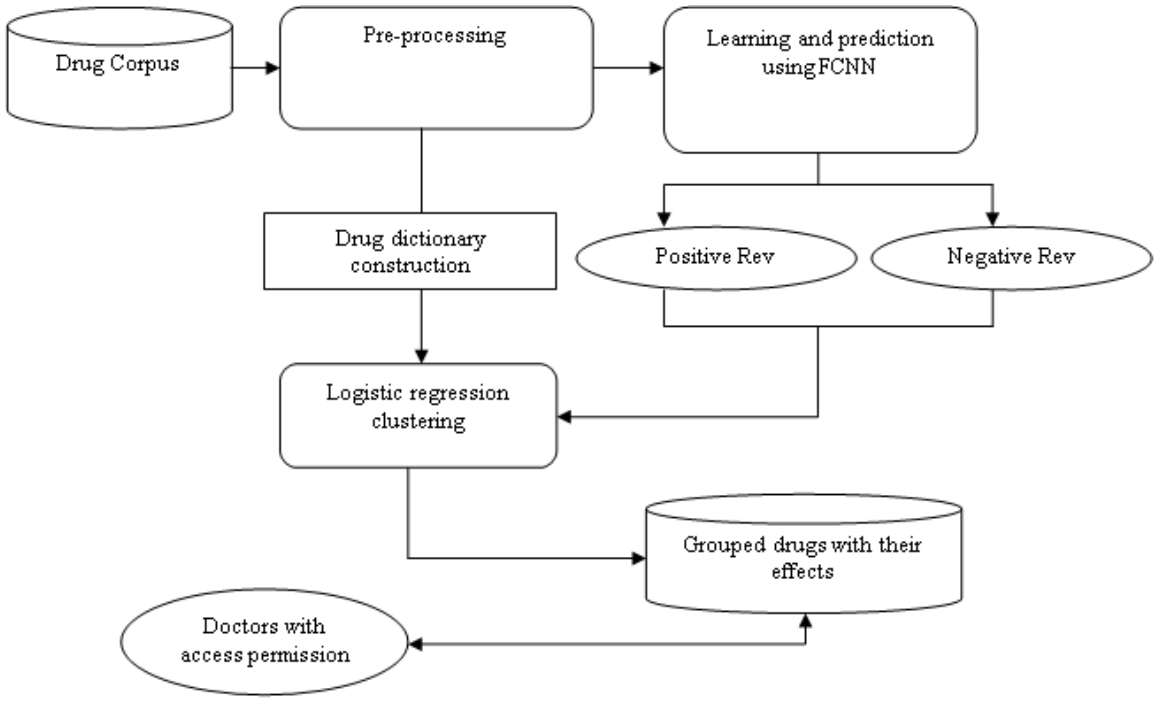


Figure 1. Processing flow of proposed research work

The recommended research technique along with comprehensive description is specified in the subsequent sub sections.

3.1. INPUT DATA COLLECTION

The drug review prediction is chiefly accomplished by utilizing two datasets: askapatient.com site,besides UCI repository(drugs.com).

UCI REPOSITORY: UCI repository drug review is greatly exploited for this research work. On the basis of specific drugs, dataset is greatly utilized for patient reviewing beside with associated circumstances. The assessment is done through 10 star rating reflecting patient satisfaction on the basis of several perspectives of online pharmaceutical review sites.

ASKAPATIENT: The drug dataset gathering is chiefly accomplished by utilizing askapatient.com.

Both the dataset attributes are as follows:

1. DrugName (categorical): name of drug

2. Review (text): patient review

3. Rating (numerical): 10 star patient rating

4. Condition (categorical): name of condition

5. Date (date): review entry date

The addition of drug names in addition to respective drug departments is done which is considered as second attribute. The drug grouping precise outcome is obtained by this approach. The construction of drug dictionary is given in excel file format. The input data format is revealed in the subsequent figure 2.

Input data

I had the expected side effects while taking the medication (upset stomach, diarrhea, loss of appetite, etc.). I was never warned about the insomnia, fatigue, or body aches, which caught me off-guard. I've been off the medication for three days and am still experiencing body aches, headache, sneezing/stuffy nose, and fairly severe fatigue. I feel like I have a bad cold or a mild case of the flu, though I have no fever or other indications that I am ill. The meds took care of the infection, which is the most important thing, and they weren't severely unpleasant to be on, though I'm quite happy to be finished with them.The lingering side-effects are almost worse than being on the medicine for me. Aside from the UTI, I felt fine a week ago, and now I feel like I need to sleep for three days straight.

Figure 2. Input data format

3.2. PREPROCESSING INPUT DATA

The Preprocessing of input data is greatly achieved through porter stemmer algorithm. The preprocessing is mainly done for obtaining document representation as a feature vector through sorting out text into distinct words. The text documents modeling as transactions are revealed in the recommended classifiers. The initial step is keyword selection for document

indexing in feature selection process. The quality is determined through classification phase which is regarded as substantial factor. The meaningful keyword is selected which is regarded as noteworthy once words not contributing the documents discrepancy is discarded. The preprocessed dataset outcome is revealed in subsequent figure 3.

The detailed explanation of this method is given in our previous research work.

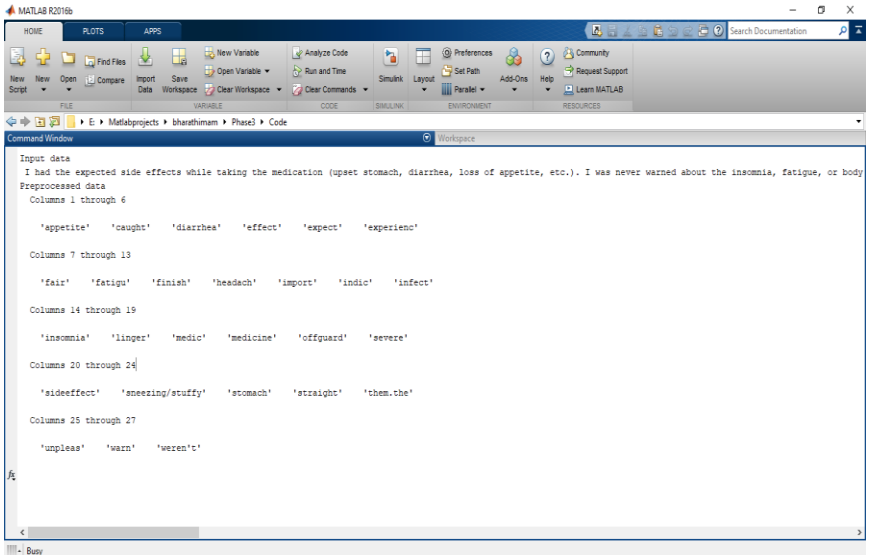


Figure 3. Pre-processed outcome

3.3. DRUG DICTIONARY CONSTRUCTION

The concept of the dictionary is to contain the words of a language (typically in alphabetical order) which can be a book/e-resource that furnishes their sense/associated terms in a several language, alongside the information, usage, pronunciation, and origin. Similarly, there necessitates the construction of the drug dictionary to facilitate the perfect scrutiny and for the prediction of drug information. For creating the drug dictionary, the existing drug details have collected from online. Following that, the URL termed http:/www.drugs.com has significantly considered to extract the drug information, as it is an optimum archive that contains numerous drug associated information.

3.4. ADVERSE DRUG REACTION IDENTIFICATION USING FUZZY CNN

Throughout this study, the strategy called Fuzzy based convolutional neural network (FCNN) has introduced to carry out the adverse drug reaction identification, in which the input feature has embedded through embedding the layer to real value matrix. Consequently, the input matrix has converted into fuzzy domain using fuzzification layer, besides the convolution of fuzzy representation has carried out in a fuzzy convolutional layer that performs as a filter to obtain high-level features from the data. Post-process of fuzzy convolutional phase, the defuzzification layer transforms the extracted feature set into crisp value. Ultimately, fully connected layer performs as output classifier for FCNN.

A weight of each feature has estimated by FCNN in order to process the adverse drug reaction identification, for which the model has fed with the input that is a sequence of words and it has processed through the layers. During the process, higher-level features have extracted through each layer, and carried to the succeeding layer. Following that, the features have extracted from the word's vector level to the adverse drug reaction. Generally, the words used in the comment should be articulated as numerical values to appropriately use the FCNN for computation. As a first step, for mapping each word in a comment to a d-dimensional vector, the word-level embedding has to be done. Hence, each comment can be converted into matrix of size m × d, in which m represents the length (the word count of the comment), and d signifies the embedded vector. Apparently, there must be a difference in the length of the comments in the dataset. To ease the function, a special word has padded at the end of the comments to same length for each comment.

For every comment containing of M words (w_1, w_2, ...,w_m, ..., w_M), the w_m words in the comment will be transformed into a vector $u_m = [u_1, u_2, ..., u_D]$. A fixed size V dictionary, so we have embedding matrix $D \in R(d \times |V|)$. The mapping of w_m to the vector u is obtained through Equation (1).

$$u_m = Dv^w \quad (1)$$

wherev^w denotes vector dimension |V| which has a value of 1 in the index w and 0 in the remaining positions. w represents word w_m index in the dictionary V. Initially the matrix D is randomly initiated, then its values are trained in the course of model training.

The embedding of every input to a matrix X is done on the basis of assigning of membership functions to multiple linguistic labels for every element in the input matrix.A linguistic variable is a linguistic expression (one or more words) labeling an information granular. For example, a membership function is labeled by expressions like "hot temperature" or "rich customer". It means in this work linguistic variables will be drug or non drug only. Fuzzy rules will be formed with the extracted features of this work in If and then else format, based on rule outcome linguistic variable for each fuzzy rule will be declared. The fuzzy model defined in our work is shown in the following figure 4.

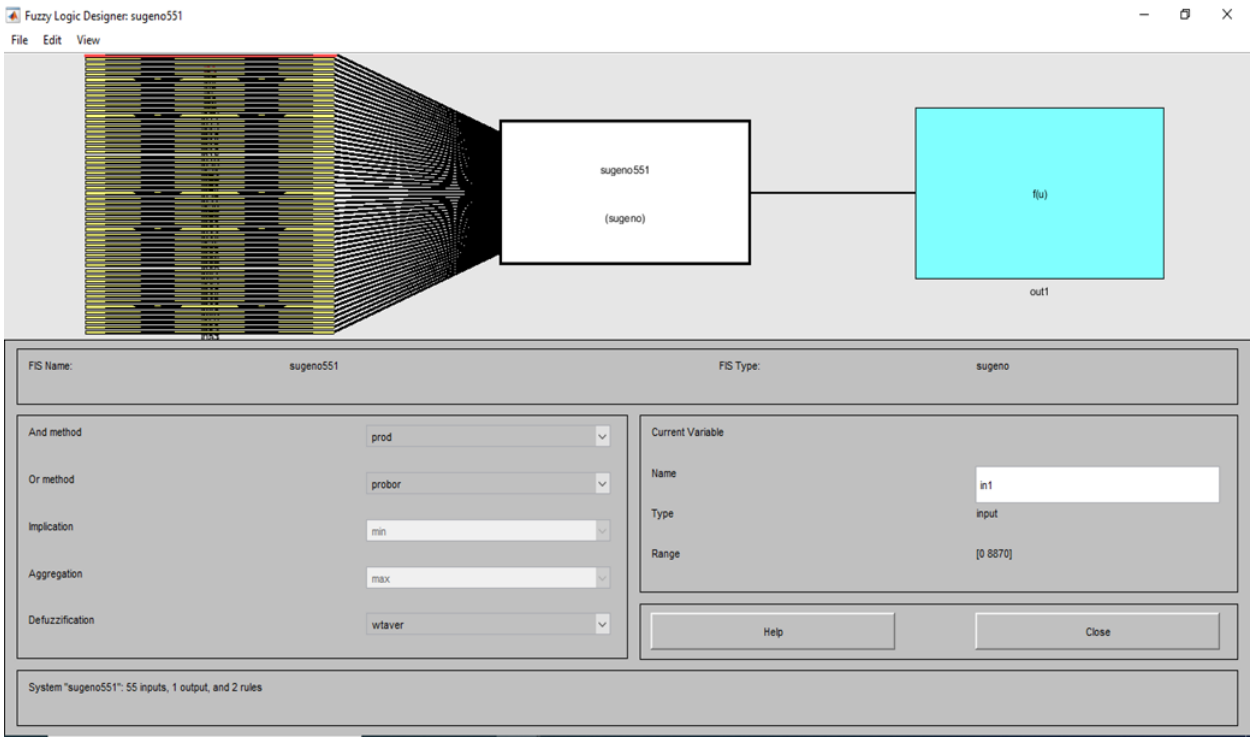


Figure 4. Fuzzy logic designer

In this work Gaussian membership function is exploited. The computation of grade is done through fuzzy membership function elucidating input node membership to a particular fuzzy set. The fuzzy sets $\widehat{\widehat{X}}$ in Equation (2) is acquired by Equation (3) that estimates through max product operation. Those are considered as likelihoods that input besides output data belong to the predefined reference fuzzy numbers $\widehat{MF_{ij}}$ in the universe of discourse.

$$\widehat{X} = \text{fuzzification}\left(x_{ij}\middle|cx_{ij}\right) \tag{2}$$

Where i, j are element indices x in input matrix X, in addition to input fuzzy membership function center cx.

$$x_{ij} = \text{possibility}\left(x_{ij}\middle|\widehat{MF}_{ij}\right) = \max_{x\in X}(\widehat{MF}_{ij}\delta(x - x_{ij})) \tag{3}$$

Where $\delta(x - x_{ij})$ is the kronecket delta function.

There are two processing stages in each fuzzy convolution layer, namely fuzzy convolution stage, besides pooling stage. The fuzzy convolutional stage is a process of applying fuzzy convolutional filters to original 1D data as in Equation (4) in which computation of fuzzy convolutional filters W_μ is done through Equation (5) with W is original convolution filter.

$$x_i = b_i + \sum_{a=0}^{m-1} W_\mu x_{(i+a)} \quad (4)$$

$$W_\mu = \text{fuzzification } (W) \quad (5)$$

Equation (6) is acquired output from fuzzy convolution stage which is regarded as a non-linear transformation. The latter stage o operation called pooling which is nearby results summarystatistics after feature extraction stage. This stage helps the representation to be invariant to translation of input, and meanwhile, input size to next fuzzy convolutional layer might be reduced. In this work Relu function layer is applied in pooling layer. The Rectified Linear Unit is generally used activation function in deep learning models. The function returns 0 if it receives any negative input, but for any positive value xx it returns that value back.

$$f(x) = \max(0, x) \quad (6)$$

where f(x) - convolution layer activation function .

The feature reduction is primarily achieved through auto encoder which is meant for learning efficient data coding in an unsubstantiated mode and regarded as a sort of artificial neural network. The main objective of autoencoder is studying a dataset representation (encoding) classically for dimensionality reduction. The reconstructing side is also learnt along with reduction side, where the condensed encoding generation presentation ought to be as near as probable to its original input. An autoencoder mainly comprises of encoder and decoder, which is defined as transitions Φ and ψ such that:

$$\Phi : X \to F$$

$$\Psi: F \to X$$

$$\Phi, \Psi = \underset{\Phi, \Psi}{\arg\min} \|X - (\Psi \circ \Phi)X\|^2$$

Let us assume a single hidden layer in which an autoencoder encoder stage results the input $x \in R^d = X$ in addition maps it to $h \in R^p = F$

Consider a single hidden layer in simple , the encoder stage of an autoencoder ensues the input $x \in R^d = X$ and maps it to $h \in R^p = F$

$$h = \sigma(Wx + b)$$

The fully connected layer of the FCNN is working as a classifier with input features being the crisp value z_i fetched from the defuzzification process with center of gravity method in Equation (7),

where C_y - defuzzification membership function center .

$\hat{\hat{y}}_i$ - classifier output and

W_{fc} - fully connected layer weight matrix .

$$z_i = \text{defuzz}\,(x_i) = \frac{\sum C_y x_i}{\sum x_i} \tag{7}$$

$$\hat{y}_i = W_{fc} z_i \tag{8}$$

The output error evaluation is done through Cross entropy which refers the loss function as revealed in Equation (9), where y represents target, ˆy denotes classifier output ,N notates number of sample.

$$E = -\frac{1}{N}\sum_{n=1}^{N}[y_n \log(\hat{y}_n) + (1 - y_n)\log\,(1 - \hat{y}_n)] \tag{9}$$

The conventional back-propagation learning algorithm is greatly utilized along cross-entropy loss function with for training model parameters. The weight update as presented in Equation (10).

$$W_{fc}(k+1) = W_{fc}(k) - \alpha_{fc}\frac{\partial E}{\partial W_{fc}} \tag{10}$$

The updating of defuzzification membership functions centers $C_y(k)$ is performed through Equation (11), where a_{Cy} denotes updating center learning rate, y_{k+1} and $\hat{\hat{y}}_{k+1}$ are, output target and model's actual output respectively,.

$$C_y(k+1) = C_y(k) + a_{cy}\nabla C_y \tag{11}$$

Equations (12)–(15) is mainly utilized for Center value C_w assessment in addition to fuzzification membership function variance σ of convolution layer's weight through learning rate αC_w.

Centervalue C_w and variance σ of fuzzification membership function of convolution layer's weight are calculated by with learning rate αC_w.

$$C_w(k+1) = C_w(k) + \alpha_{cw}(k) + \alpha_{C_w}\nabla W_\mu \quad (12)$$

And

$$\sigma_{C_w}(k+1) = \sigma_{cw}(k) + \alpha_{C_w}\nabla W_\mu \quad (13)$$

Where

$$\delta_k = \left(W_{\mu k}\right)^T \delta_k^{(3)} f'(x_k) \quad (14)$$

$$\nabla W_{\mu k} = \sum y_{ij} * \text{rot } 180\ (\delta_k) \quad (15)$$

Equations (16) and (17) is utilized for mean and variance of fuzzification layer's membership function updating, where α_{cx} denotes fuzzification layer learning rate.

$$C_x(k+1) = C_x(k) + \alpha_{cx}\nabla C_x \quad (16)$$

$$\sigma_{C_x}(k+1) = \sigma_{cx}(k) + \alpha C_x \nabla C_x \quad (17)$$

The fuzzy CNN architecture is revealed in the subsequent figure 5.

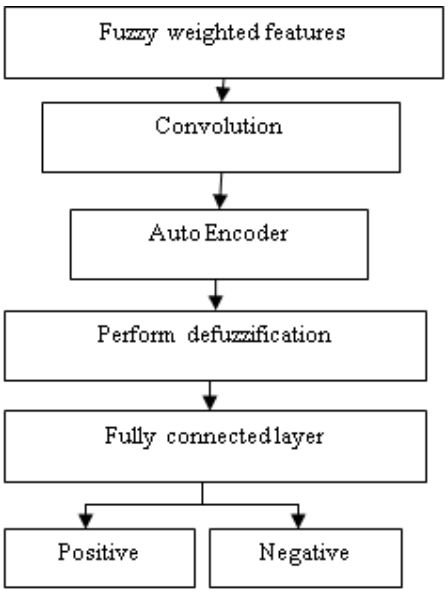


Figure 5. Fuzzy CNN architecture

Algorithm:

Step 1: Initialize the network with convolution layer, pooling layer, auto encoder layer as well as softmax layer. Initialize the network parameters such as bias, variance, learning rate and so on

Step 2: Choose training data

Step 3: Compute fuzzy weight for input features using equation 2 and 3

Step 4: Apply 1D convolution to get convoluted input features using equation 4

$$x_i = b_i + \sum_{a=0}^{m-1} W_\mu x_{(i+a)}$$

Step 5: Calculate Relu function on convoluted input features using equation 6

$$f(x) = \max(0, x)$$

Step 6: Reduce the number of features through auto encoder

$$\Phi, \Psi = \underset{\Phi, \Psi}{\arg\min} \|X - (\Psi \circ \Phi)X\|^2$$

Step 7: Accomplish defuzzification on outcome retrieved from auto encoder

Step 8: Use fully connected layer to merge outcomes and produce final result

Step 9: Choose another training data besides repeat the processes from step 3 to step until all the training data has been trained

Step 10: Output the result

3.5. DRUG REACTION GROUPING USING LOGISTIC REGRESSION BASED CLUSTERING METHOD

Logistic regression model has significantly utilized during this study to carry out the drug grouping process in accordance with respective department. It is known to be a statistical approach for forecasting the correlation within the group of independent variables (x_s) and a dependent variable (y). Besides, it possesses the ability to forecast the probability of the mode choice and evaluate the marginal effect of every explanatory variable. The estimation of the probability of each result has obtained by employing a binary logistic regression model for every individual cluster of the regression and classification tree. Defined the target variable as y=1 for drug; whereas y=0 for non-drug. For describing the correlation between explanatory variables and target variable, the explanatory variable coefficient and Odds Ratio (OR) can be exploited, during which the maximum likelihood estimation method takes place for the estimation. The OR represents the odds that an outcome will occur given a particular exposure, compared to the odds of the outcome occurring in the absence of that exposure. The impacts of xs on the y has measured as OR.

A convex partition of the features spaces have performed by the logistic regression. Prior to the modification made by the trainer a clustering algorithm has enforced in the feature space, in way the partition is not necessarily convex in the initial features. Generally, Logistic regression has known to be a supervised classification algorithm. Only discrete values for provided set of features (or inputs), X have taken by the target variable (or output), y in a classification problem. Apart from general thought, logistic regression IS a regression model, which has the capability to construct a regression model for predicting the probability that a given data entry belongs to the category numbered as "1". Similar to Linear regression assumes that the data follows a linear function, Logistic regression models the data using the sigmoid function.

$$g(z) = \frac{1}{1 + e^{-z}} \tag{18}$$

By bringing a decision threshold into the limelight, it is possible to make Logistic regression to be a classification method. Relying on the classification problem, defining the threshold value is a significant perspective of Logistic regression, during which the values of precision and recall play a vital role while defining the threshold value. Preferably, it is necessary that both precision and recall to be 1, but this seldom is the case.

Our model algorithm consists of 2 sub-stages. During the first stage, the drugs that use K-means will get clustered in order to tackle the outliers and eliminate the inappropriately classified data, if any. Then, the data which has appropriately clustered and classified will be taken as the input for our supervised classification with the help of logistic regression.

3.5.1. LOGISTIC REGRESSION ALGORITHM

In several domains like biological sciences, the application of the Logistic regression model has considered to be significant. At the time of classifying the data items into categories, the Logistic regression algorithm has necessitated. In general, the target value in logistic regression is binary, as it classifies the data as either 1 or 0. Accordingly, a drug has signified as positive or negative (for adverse reaction) in our model. Our logistic regression algorithm tends to discover the best fit, which is rational in diagnostic aspect for defining the correlation within our target variable and the predictor variables. The following equation formulates the linear regression-based logistic regression algorithm.

$$y = h_\theta(x) = \theta^T x \tag{19}$$

Since the aforementioned expression is inadequate for predicting our binary values ($y(i) \varepsilon \{0, 1\}$), presented the subsequent function in order to forecast the probability that a given drug belongs to the "1" (positive) class versus the probability that it belongs to the "0" (negative) class.

$$P(y = 1|x) = h_\theta(x) = \frac{1}{1 + \exp(-\theta^T x)} \equiv \sigma(\theta^T x) \quad (20)$$

$$P(y = 0|x) = 1 - P(y = 1|x) = 1 - h_\theta(x) \quad (21)$$

We have enabled to retain the value of $\theta^T x$ between the range of 0, 1, by performing the following function (called as a sigmoid function). Subsequently, in search of the value of θ, the probability P (y=1|x) = $h_\theta x$ is greater if x belongs to the "1" class; and lesser if x belongs to the "0" class (that is to say, P (y=0|x) is large).

$$\sigma(t) = \frac{1}{(1 + e^{-t})} \quad (22)$$

3.5.2. K MEANS CLUSTERING

K-means is significant among the effective unsupervised classification algorithms, and it can be implemented with ease. It is most prominent clustering method that performs on the basis of partitioning, which tends to identify a user defined cluster quantity that has denoted by the respective centroids. It has considered to be an archetypal example for distance-based clustering algorithm that considers the distance as a measure of similarity (the least distance within objects represents the higher similarity). The implementation steps of k-means clustering can be described as follows,

Step 1: Initialize k value

Step 2: Next is to determine for each input data the cluster center that it is nearest to by using equation

$$S_i^{(t)} = \{x_p : \left\| x_p - m_i^{(t)} \right\|^2 \leq \left\| x_p - m_i^{(t)} \right\|^2 \forall_j, 1 \leq j \leq k\} \quad (23)$$

Step 3: Revise the cluster centres through re-computing the mean of each input data, which has designated to the clusted

$$m_i^{(t+1)} = \frac{1}{\left| S_i^{(t)} \right|} \sum_{x_j \in S_i} x_j \quad (24)$$

Step 4: Loop through step (2) and (2) till the k-means cluster converged with the mean value of the clusters, in order to bring k-means cluster to a stop

Subsequently, our k-means cluster has cleaned through eliminating the inappropriately clustered data, by which the identification of our new dataset has concluded for classification. At the instance of the size of new data exceeds 75%, the supervised classification process can be initiated, otherwise the k-means step will be iterated until converged with appropriate size.

$$\text{new size} = \frac{\text{left data}}{\text{total sum}} \tag{25}$$

Post-cleaning the clustered data, the appropriately clustered drugs have procured for being designated as input, which trains the logistic regression algorithm. The ensuing Figure 6 depicts the results of drug grouping process.

```
Similar grouping words
  Columns 1 through 6
    'No Synonyms Found!'    'abdomen'    'achieve'    'acute'    'adequate'    'alert'
  Columns 7 through 10
    'appearance'    'appetite'    'as the crow flies'    'bring in'
  Columns 11 through 14
                        'bring to an end'    'caution'    'come to an end'    'consecutive'
  Columns 15 through 20
    'contaminate'    'conventional'    'desire'    'directly'    'drug'    'end'
  Columns 21 through 27
    'endure'    'fine'    'frank'    'harsh'    'honest'    'hunger'    'imagine'
  Columns 28 through 32
    'in the right posi…'    'introduction'    'just'    'kill'    'length of track'
  Columns 33 through 38
    'pale'    'plain'    'polish'    'remain'    'require'    'result'
  Columns 39 through 43
    'significance'    'sleeplessness'    'surface'    'tidy'    'trade event'
  Columns 44 through 47
    'traveling fair'    'undiluted'    'wait for'    'wedged'
```

Figure 6. Grouping similar drugs outcome

3.6. DOCTORS ACCESS PERMISSION

It is necessary to register the details of each doctor, those who require to get access to the drug information. Accordingly, they have provided with the login credentials (user name, password), which has to be submitted to obtain permission to access. If users (doctors) submit the valid login credentials, they are authorized to access the drug information that are associated to their corresponding field, through which they are enabled to know the drug names and their adverse reactions; if the credentials are invalid, they would be revoked from further access. The ensuing Figure 7, 8 and 9 represent the access permission requests and permission process.

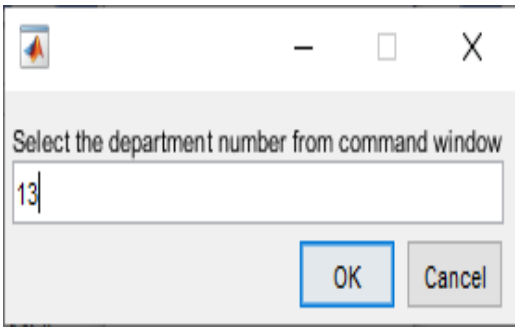


Figure 7.Asking department number to retrieve contents

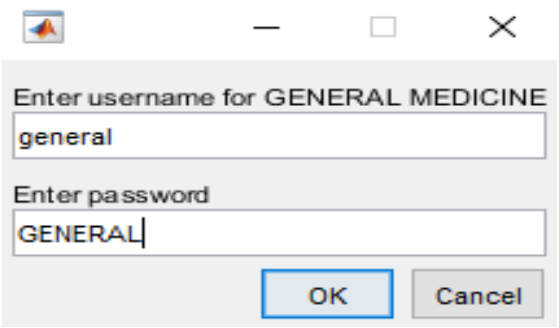


Figure 8. Asking login details

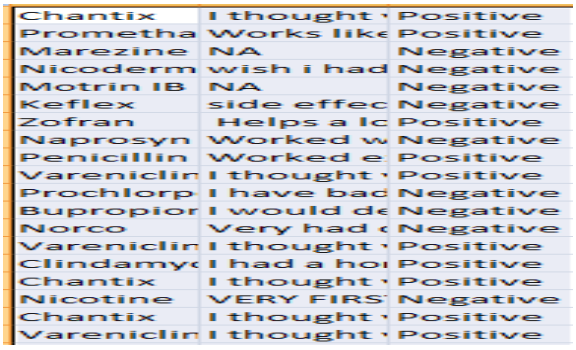


Figure 9. Retrieved outcome

IV. RESULTS AND DISCUSSION

In accordance with several parameters, the proposed framework has numerically evaluated in this segment, concerning the scrutiny of the performance enhancement of both the proposed and prevailing technologies. The implementation of the proposed approach has carried out under the simulation environment of MATLAB by considering the parameters, such as Accuracy, Precision, Recall and F-Measure. During the evaluation, the MCNN-DPS, SDRPS and the existing ADRMine approaches have taken as the benchmark technologies to compare and evaluate the efficiency of the proposed DPIS-FCNN approach.

ACCURACY: It refers to the number of appropriately identified drug names existed over the tweets, which has the reduced rate of false positive. Accordingly, the accuracy of the proposed approach must be higher than every other methods (e.g. ADRMine). Hence, considering the values of true positive, false positive, true negative and false negative, the accuracy rate of drug prediction framework has estimated, as expressed by the following equation

$$\text{Accuracy} = \frac{T_p + T_n}{(T_p + T_n + F_p + F_n)} \tag{26}$$

PRECISION: It defines the fraction of relevant instances obtained, among overall instances

$$\text{Precision} = \frac{|\{\text{relevant drug name}\} \cap \{\text{Predicted drug names}\}|}{|\{\text{Predicted drug names}\}|} \tag{27}$$

RECALL: It refers to the fraction of the overall quantity of actually retrieved relevant instances

$$\text{Recall} = \frac{|\{\text{relevant drug name}\} \cap \{\text{Predicted drug names}\}|}{|\{\text{relevant drug names}\}|} \quad (28)$$

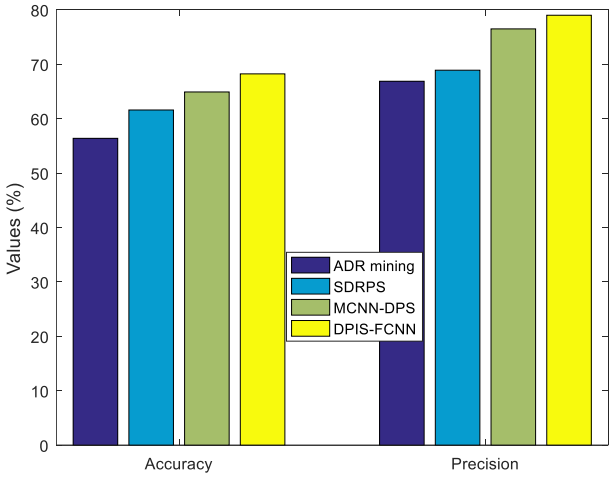
F-MEASURE: It represents (F-score/F1-score) the accuracy metric of a test, which has described as the weighted harmonic mean of the precision and recall of the test

$$F = 2 . \frac{\text{Precision} .\text{Recall}}{\text{Precision}+\text{Recall}} \quad (29)$$

There are two types of datasets (i.e. a benchmark drug dataset and the data obtained from askapatient, an open access web archive) have involved during this study, concerning the comparison. Table 1 compares the obtained values of performance parameters.

Table 1. Performance metric values

Metrics	Benchmark dataset				Aska patient dataset			
	ADRMine	SDRPS	MCNN-DPS	DPIS-FCNN	ADRMine	SDRPS	MCNN-DPS	DPIS-FCNN
Accuracy	56	61	65	68.2464	57	60	69	70.8108
Precision	64	68	77	79.0210	68	69	74	92.5620
Recall	70	75	75	75.3333	70	74	77	71.3376
F-Measure	69	70	75	77.1331	68	70	76	80.5755



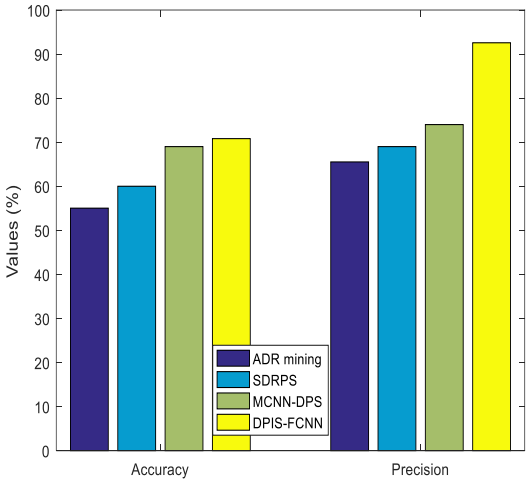


Figure 10. Accuracy and precision of bench mark data Figure 11. Accuracy and precision for askapatient

Figure 10and 11 individually compare the performance of both the proposed approach and the prevailing ADRMINE technique for two different datasets, in which the proposed approach establishes its ability to surpass the existing methods. During the comparison for benchmark

dataset, the accuracy of the suggested DPIS-FCNN method proves to be 3.24%, 7.24%, and 12.24% higher than MCNN-DPS, SDRPS, and ADRMine, respectively. Besides, obtains 2.021%, 11.021%, and 15.021% of superior precision values than MCNN-DPS, SDRPS, and ADRMine, respectively. Under the comparison for askapatient dataset, the proposed method acquires 1.81%, 10.81%, and 13.81% more accuracy; whereas, attains 18.562%, 23.562%, and 24.562% higher precision values when compared to MCNN-DPS, SDRPS, and ADRMine methods, correspondingly.

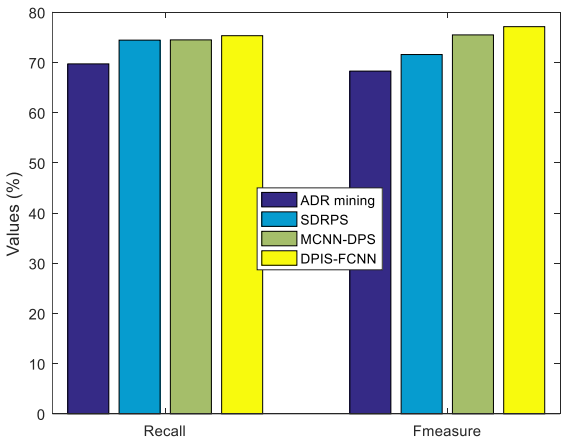


Figure 12.Recall and F-Measure of benchmark data

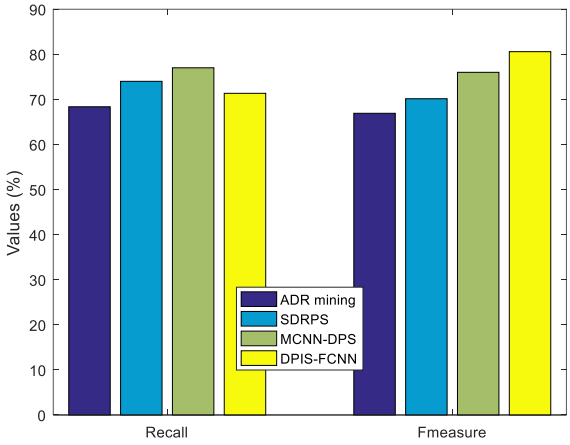


Figure 13. Recall and F-Measure of askapatient

Figure 12 and 13 individually compare the performance of both the proposed approach and the existing ADRMINE method for two different datasets, in which the proposed approach proves to be efficient than the existing methods. In the comparison for benchmark dataset, the suggested DPIS-FCNN method obtains 0.33%, 0.33%, and 5.33% higher recall rates; besides, secures 2.13%, 7.13%, and 8.13% of superior F-measure values than MCNN-DPS, SDRPS, and ADRMine, respectively. During the comparison for askapatient dataset, the proposed method obtains 5.66% and 2.66% lesser recall when compared to MCNN-DPS, and SDRPS, whereas procures 1.33% higher recall rate than ADRMINE; besides, secures 4.57%, 10.57%, and 12.57% more F-measure values when compared to MCNN-DPS, SDRPS, and ADRMine methods, correspondingly.

V. CONCLUSION

In initial phase of this study, the information regarding the drugs have gathered from online (such as, social media, open access archives). Subsequently, the Fuzzy based Convolutional Neural Network (FCNN) has employed to deal with the prediction of drug reaction, besides the logistic regression-based clustering approach takes place to cluster the associated reaction of those drugs in terms of their correlation. Following that, the clustered information would have furnished to the respective physicians if they require appropriate access permission. Since this work tends to surpass the present works, the entire work has simulated under the simulation environment of MATLAB.

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