BD-MDL: BIPOLAR DISORDER DETECTION USING MACHINE LEANRING AND DEEP LEARNING

[1]R.Saranya, [2]Dr.S. Niraimathi
[1]PhD, Research Scholar, Department of Computer Science, NGM College, Pollachi
[2]Associate Professor, Department of Computer Science, NGM College, Pollachi

DOI: 10.47750/pnr.2022.13.S07.715

Abstract

About 45 million individuals all over the globe are dealing with Bipolar Disorder (BD), a mental illness that affects the brain. It's also known as manic depression because it results in drastic changes in a person's level of energy, their conduct, and their emotional state. Researchers have shown that BD is associated with significant volumetric alterations in neural networks in the brain, as opposed to those seen in a healthy individual (HP). Progress has been made in predicting using retinal vasculature, where the brain and retina have a similar biomarker structure, utilizing machine learning and deep learning, which is still the most popular method of categorization. This research proposed Bipolar disorder detection using machine learning and deep learning (BD-MDL) framework has involving to increasing the BDD accuracy rate. This study used a bipolar dataset that was scaled using a decision tree regressor with standard scalar and to choose the optimal features to use in a subsequent round of feature selection using random forest (RF) and Logistic regression (LR). Convolutional neural networks (CNN) with long short term memory (LSTM) were used throughout both training and evaluation with improved Adam optimization (IAO). Finally the classification has done with Stacking ensemble algorithm used to find the best model for predicting Bipolar Disorder.

Keywords: Convolutional neural network (CNN), Logistic regression (LR), decision tree (DT)

I.INTRODUCTION

Bipolar disorder is a mental illness that may have devastating repercussions on a person's well-being. The heritability of the risk for developing bipolar disorder is emphasized. Manic-depressive sickness is a persistent mental disorder characterized by periods of mania and depression. Only 2% of the world's population experiences any form of bipolar illness. Due to the overlap in symptoms, bipolar illness and Major Depressive Disorder (MDD) are often misunderstood. Misdiagnosis may have serious consequences in a person's daily life. The possibility of a suicide attempt increases as a result of this. Mood fluctuations, anger, depression, anxiety, and inability to sleep are all hallmarks of bipolar illness. According to some, anti-psychotic drugs are more successful in managing bipolar illness. Mental illness is best diagnosed using the criteria laid forth in the fifth edition of the Diagnostic and Statistical Manual of Mental Disorders (DSM-V) published by the American Psychiatric Association. There are a variety of factors contributing to the worrying increase in the number of individuals struggling with mental health issues. It's an added cost for healthcare providers to examine each patient thoroughly. The need for a sophisticated computer model for the analysis of mental diseases is growing. Focusing on removing the overlapping genetic link between schizophrenia and bipolar illness, this study aims to construct a highly reliable computational model to find gene biomarkers for both conditions.

Types of bipolar disorder:

Manic episodes lasting 7 days or longer, or severe mania requiring hospitalization, characterize Bipolar I illness. They may also go through a significant depressed episode that lasts for at least two weeks. A person may be diagnosed with bipolar I without ever having had an episode like this. Mania and sadness are symptoms of bipolar II condition, however the manic episodes are milder than those of bipolar I and are referred to as hypomania. A major depressive episode may occur either before or after a manic episode in a person with bipolar II. Symptoms of hypomania and sadness that persist for 2 years or more in adults and 1 year or more in children constitute cyclothymic disorder, also known as cyclothymia. These manifestations are not typical of either mania

or depression. When a person has one of these conditions, they may suffer symptoms that aren't represented in the other forms. Causes of these symptoms might be anything from drug or alcohol usage to medical issues.

The main contributions of this paper as follows

- Dataset pre-processing using standard scalar with decision tree regressor
- The best features are selected by using RF and LR
- The dataset was trained using CNN with LSTM as a DL model
- Optimization has been done with improved adam optimization
- Classification has been done with stacking ensemble algorithms

Section II analyses the current literature on BD prediction, Section III explains the BD-MDL technique, Section IV contains findings and results, and Section V discussed with conclusion and future scope.

II. BACKGROUND STUDY

Elujide et al. (2021) [5] Multilayer perception (MLP), support vector machine (SVM), random forest (RF), and decision tree (DT) were used by these authors (DT). These authors were done to find hidden patterns in patient data and categorize Psychotic Disorder Diseases like Bipolar Disorder, Vascular Dementia, Insomnia, Schizophrenia, and attention-deficit/hyperactivity disorder (ADHD) for doctors. The structures were valuable data correlation tools for iterative optimization. Deep Learning Neural Networks outperformed machine learning strategies in accuracy, actual positive rate, and false positive rate. The suggested methodologies and ensemble machine learning on the same dataset showed schizophrenia as the most accurate condition and ADHD as the least accurate. The obtained result demonstrated that the deep neural network outperformed the multilayer perception (MLP) model with a class imbalance accuracy of 75.1% against 58.44%.

Librenza-Garciaet al (2017)[9] Neuroimaging studies may help distinguish bipolar disorder (BD) from healthy controls and other psychiatric diagnoses. It may help correct BD misdiagnosis and diagnostic delay. This meta-analysis of diagnostic accuracy neuroimaging studies compared bipolar disorder patients to healthy controls. Machine learning can also access at-risk individuals, such as the children of bipolar parents. Targeted therapies may prevent high-risk prodromes from becoming full-blown diseases using machine learning. Machine learning may predict a patient's best treatment after diagnosis. Predicting treatment response can shorten depressive episodes and tailor maintenance therapy—the lack of population studies to verify most machine learning techniques.

Martinuzzi et al. (2021)[14] Identify blood biomarkers that discriminate MDD from Bipolar disorder (BD) patients when in a depressed state. We have used clinical data and serum samples from two independent naturalistic cohorts of patients with a Major Depressive Episode (MDE) who fulfilled the criteria of either BD or MDD at inclusion. The replication group froze blood samples up to three times, perhaps creating noise. Second, the replication group was observed six months following enrollment, whereas the discovery cohort was clinically assessed and sampled once.

N. -F. Jie et al. (2015)[16], this author's multivariate feature selection study to classify Bipolar disorder (BD) and Major Depressive Episodes (MDD) utilizing several modalities. A forward-backwards technique was used to extract highly discriminative features from functional and structural modalities for bipolar and major depressive illnesses, resulting in excellent classification accuracy. The default mode network with atypical nodes only detected bipolar people. These data-driven discoveries suggest biomarkers for BD and MDD. Support vector machine with a forward-backwards search strategy (SVM-FoBa) found the best local solution by overcoming greedy techniques' fundamental problems. Our sample was small. Comparative research should include more participants.

Poletti et al. (2020)[20] These authors predicted mood disorder differential diagnosis by analyzing plasma levels of 54 cytokines, chemokines, and growth factors in 81 depressed bipolar patients and 127 depressed major depressive patients. Thirty-two healthy controls had clinical diagnoses predicted. The results contribute to biomarker translation into clinical practice early BD identification and novel depressive disorder therapy. Patients were selected from a single site and ethnic group, increasing population stratification and limiting generalizability. The absence of age- and gender-matched control groups may impede generalization even more. The research did not address alcohol or cigarette use.

S. Gao et al. (2017)[22] These authors used an enhanced pattern classification method to find discriminative functional connectivity patterns for Bipolar disorder (BD) and Major Depressive Episode(MDD)

diagnosis in new subjects. Our approach outperformed the original method in classification precision. Discriminative functional brain networks were found during training, and merging related independent components helped diagnose new patients. That technique's 10-fold cross-validation took 39.8 hours, which was long.

V. Vasu and M. Indiramma (2020)[23] Datasets helped study psychological disorders with the correct classifier. Electrocardiogram(ECG) data is more accurate yet not dependent on heart rate variability mode. Retinal scans predict bipolar disorder better since the brain and retina have comparable morphologies. Since many researchers used unfamiliar technologies, the analyses were less accessible. Prior probability sensitivity unstable decision trees may occur from little data changes.

III. MATERIALS AND METHODS

Bipolar Disorder detection utilizing deep learning and machine learning is discussed in this part. The proposed approach has five steps: (1) data preprocessing, (2) hybrid ML feature selection, (3) training, (4) ML classification, and (5) a comparison of ML classification methods.

3.1 Dataset:

The benchmark datasets are downloaded from Kaggle.com website https://www.kaggle.com/datasets/arashnic/the-depression-dataset. The dataset contains control and condition EEG datasets. The dataset contains 50.6 MB size.

. **3.2 Data Pre-Processing**

Data pre-processing is the most crucial phase. The majority of healthcare data has missing values and other contaminants that diminish the data's use. Data preprocessing enhances the quality and efficacy of the discoveries acquired via data mining. The use of machine learning algorithms to the dataset is essential for accurate findings and accurate prediction. The Bipolar dataset needs two levels of preprocessing.

To normalize the feature set by removing outliers and scaling the variance to one unit. Calculating the standard score is as follows:

$$Ys = z = \frac{x-\mu}{\sigma} \text{ ---------- (1)}$$

Where Ys denotes the dataset, z represents normalization, *x* denotes number attributes, μ denotes the empty attributes and σ denotes the number of rows.

Numerous ML estimators employ the standardization of a dataset as criteria; they may exhibit undesirable behavior if the individual features do not correspond to standard normally distributed data.

Classification and regression rely heavily on decision trees. The tree structure of the decision tree model represents the process of categorizing events according to their attributes. A collection of if-then rules and conditional probability distributions defined in feature and class space.

Attribute X information gain, Y denotes the normalized dataset

$$Gain(X) = Info(Y) - Info\ A(Y) \text{ ---------- (2)}$$

Pre-processing information entropy

$$Info(Y) = Entropy(Y) = -\sum_j p(j|Y) logp(j/d) \text{ --------(3)}$$

Distribution information entropy

$$InfoX(Y) = \sum_{i=1}^{v} \frac{n_i}{n} Info(Yi) \text{ --------- (4)}$$

Where eq (3) $\sum_j p(j|Y)$ the decision tree checks the left node and right node, $logp\left(\frac{j}{d}\right)$ denotes logarithm of node checking of pre-processing.

In eq (4) information entropy has filling the missing values as denotes $\sum_{i=1}^{v} \frac{n_i}{n}$

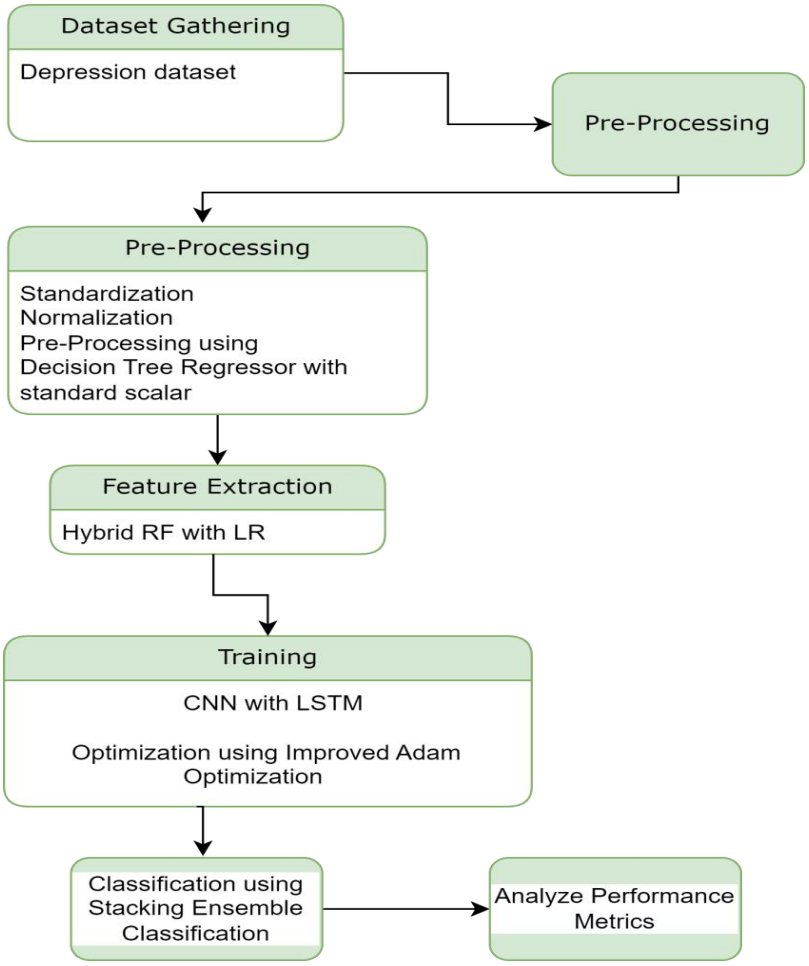


Figure 1:Architetcure Diagram for BD-MDL Model

3.3 Hybrid Feature Selection

Random Forest

Sample dataset Ds is included in the M-dimensional feature space X. A random forest is utilized to choose numerous excellent P trees; from these P trees, the number of Q uncorrelated good trees is then calculated. The five steps illustrate constructing an enhanced random forest with X and Q uncorrelated high-performance trees.

Step 1: Using the bagging technique, randomly sample D with replacement to generate K in-of-bag data subsets IOB1, IOB2,..., IOBK.

Step 2: Create a tree classifier for each IOBi subset of in-of-bag data and give it an evaluation value. This procedure should be repeated until all trees have been harvested;

Step 3: Sort these K trees by the area under the curve in increasing order (AUC);

Step 5: Enhanced random forest construction: relationships are detected between the projected probabilities of various P trees.

Logistic Regression

The logistic regression model is explained as follows.

P_i may be represented in terms of the explanatory variables x_{ij}, x_{i2}. . . , $x_{i\ and}$ k denote the number of features.

$$Pi = \frac{1}{1+exp(\sum_{j=1}^{k} \beta_i x_{ij})} \text{ ------- (5)}$$

In eq (6), get a linear connection between logit (p_i) and the explanatory variables when applying the logit transformation to (eq 6)

$$logit(p_i) = \log(\frac{p_i}{1-p_i}) \text{ --------- (6)}$$

The model's logit form is sometimes denoted by the equation (6). logit (pi) is the log odds (or the logarithm of the probabilities) of success for the explanatory variables xi,1, xi,2,..., xi k.

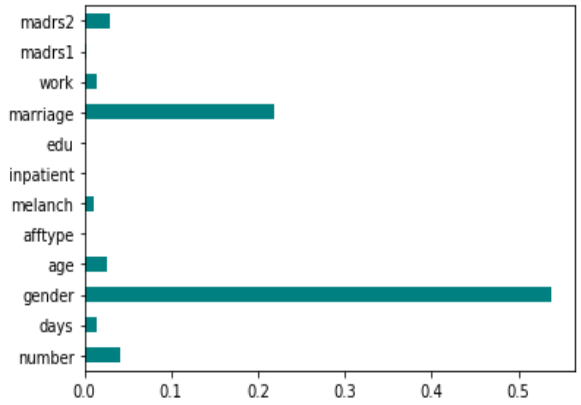


Figure 2: Feature importance Chart

The feature characteristics compared bipolar disorder with ages. We can also include days, edu, inpatient etc.

3.4 Training using CNN with LSTM

According to interconnected layer takes its name from the fact that each neuron in one layer is coupled to each neuron in the layer above. Typically, the final layers of a CNN consist of two to three wholly linked layers. Fully linked layers are enabled after an affine transformation, including matrix manipulation and the addition of bias values. The layers preceding the fully linked layer are responsible for feature extraction. With promising outcomes, it is heartening to see academics using CNN's potential computer vision breakthroughs for BD prediction. Consequently, we have presented a hybrid network for anticipating blood cell cancer that incorporates CNN and LSTM. CNN is one of the most important nodes in this network. LSTM recognizes and analyses the CNN output sequence after the CNN layer. To extract temporal features from BD variables, the CNN network aids the process. As a result, the LSTM network is more accurate in predicting BD. The convolutional and pooling layers are hidden layers in CNN on past training models. The Kaggle repository's "BD Data Set" is used in the proposed technique. The network mentioned above's convolutional layers will minimize spectral dispersion. CNN's local connections and weight-sharing features allow the model to discover local patterns with fewer tuning parameters. Some translation invariance is included in CNN with RESNet150 to its "local and global pooling" layers.

$h^{(s)} = f_h\left(A_{hh}h^{(s-1)} + A_{ih}x^{(s)}Wish(s) + b_h\right)$ ---------- (7)

$y^{(s)} = f_0\left(A_{ho}h^{(s)} + bo\right)$ -------- (8)

Where

X^s - the input data

h^s - the hidden layer units

y^s - the output

$A_{ih'}, A_{hh}\ and\ A_{ho}$ - the transformation matrices between $X^{(s)}\&\ h^{(s)}, h^{(s-1)}\&h^s\ \ and\ h^{(s)}\&y^s$

$b_h\ and\ b_o$ - the constant bias terms

$f_h\ and\ f_o$ - the no-linear activation function

Some function of this net input is the activity or state of RCL, which is given by

$z_{ijk}(t) = f(g(X_{ijk}))$ ---------- (9)

Where g, the rectified linear activation function is defined by $g((x_{ijk}(t)) = \max(x_{ijk}(t), 0)$ and f is the local response normalization (LRN) function defined by

$$f\left(g(x_{ijk})\right) = \frac{g(x_{ijk}(t))}{\left(1+\frac{a}{n}\sum_{k'=\max\left(0,k-\frac{n}{2}\right)}^{k'=\min\left(K,k+\frac{n}{2}\right)}(g(x_{ijk'}(t)))^2\right)\beta}$$ ------- (10)

Here k is the total number of feature maps in the current layer α, and β are constants of normalization.

3.5 Improved ADAM Optimization

Adam is an optimization approach for stochastic gradient descent training model replacement in deep learning. Adam could be able to lose weight. As a result, we enhanced the Adam optimization method to reduce model weights.

3.6 Stacking Ensemble classification

Embedding the SVM with DT, LR and GNB is arranged as stacking ensemble classification

//Pseudocode: bipolar disorder prediction

Begin

Bipolar attributes ($\sum_{n=1}^{20} f(i)$)

Input:

1: $F_0 \ldots F_{14}$

2: R←Pre-Processed set x←indiviudal features total ← No.of Outcome U←Matrix of features u_{ij}← individual feature

3: **Initialize**

4: comment1=0; date2=0; likes1=0; dislikes2=0; I=0; U(0)

5:Begin

6: For N in 1 to 1024

7: If (is empty f(i))

8: if(isnumeric f(i))

9: If (isnan f(i))

10: R← {F(1)…F(n)}

11: End for

12:Repeat

13: For f(i)€N

14: Calculate the feature importance f(i) C(k)=[C_{ij}] with U(k)

15: Selecting the importance feature set Update u_{ij} =[C_{ij}] U(k)

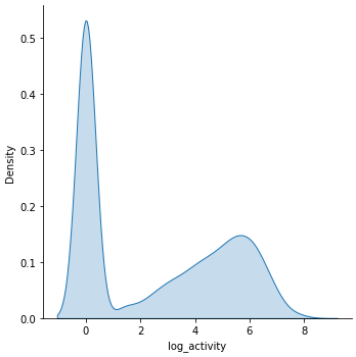
16: Classification done with DT+ LR+SVM+NB

17: Analyze classification performance metrics like accuracy, precision, recall, fmeasure

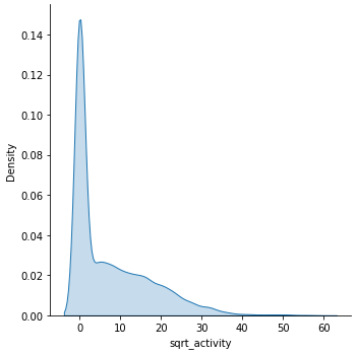
18: comparative analysis of Classification algorithms

IV. IMPLEMENTATION RESULTS

The implementation has done by using python programming language.



(a) Log activity



(b) Sqrt Activity

Figure 3: Activity with Density diagram

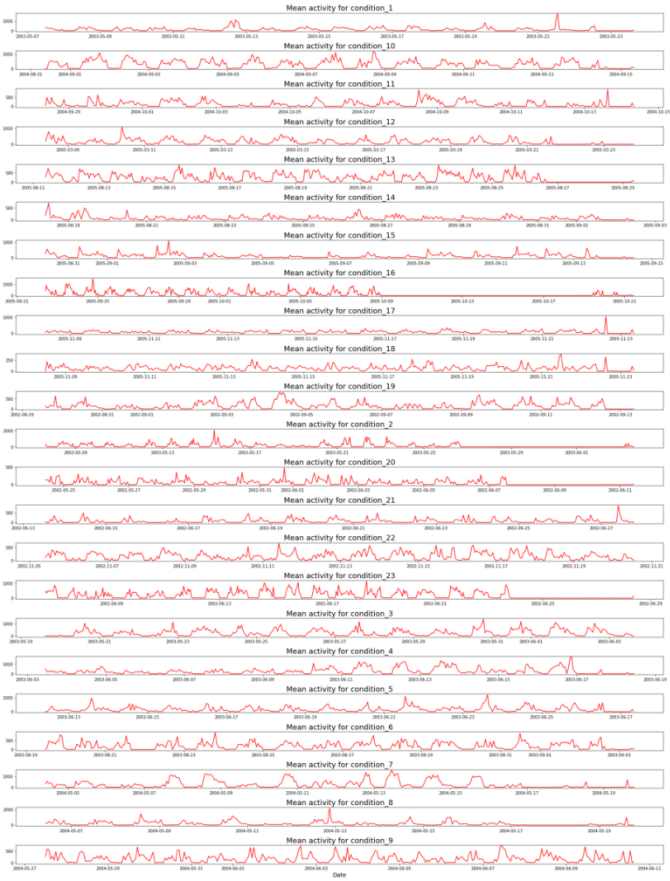


Figure 4: Mean activity control and condition chart

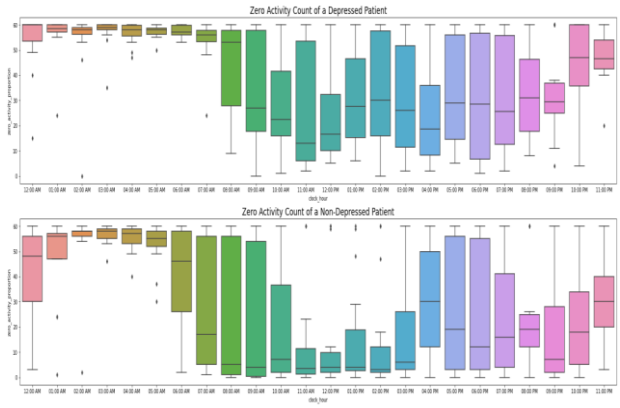


Figure 5: Zero activity Count of a Depressed and Non depressed Patient

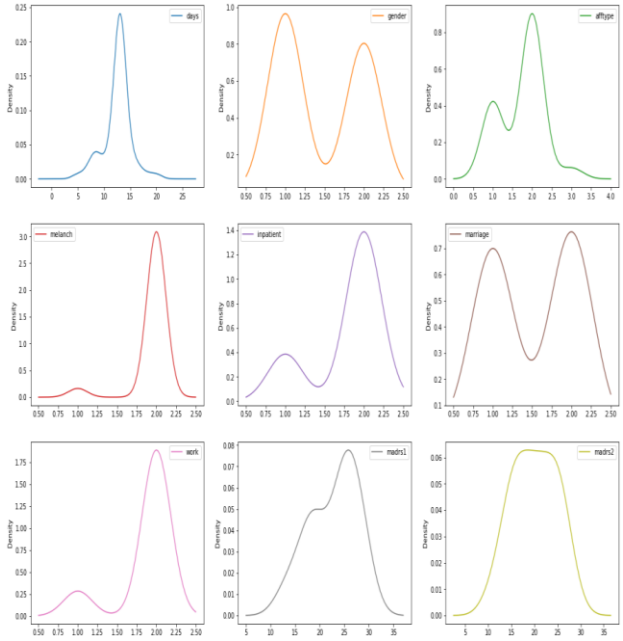


Figure 6: Depressed data flow as different parameters

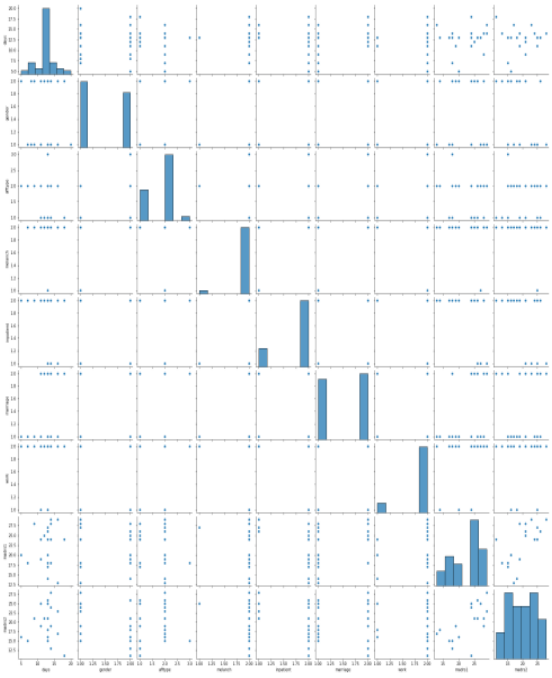


Figure 7: Depressed scatter flow diagram

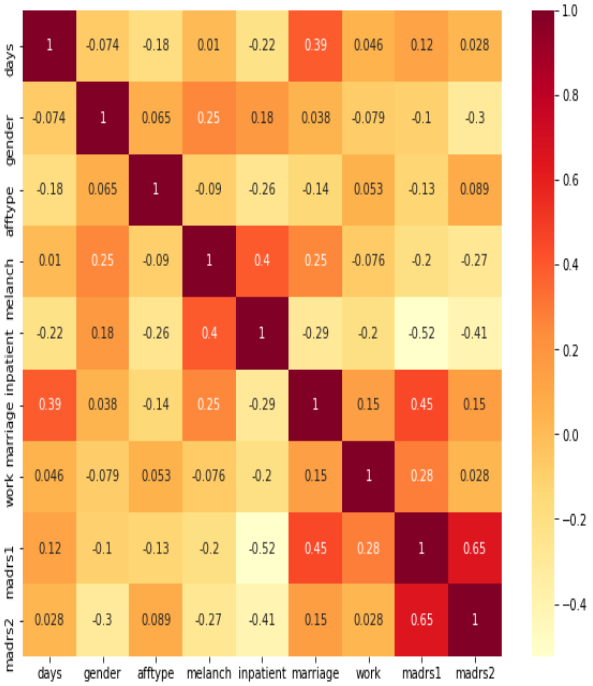


Figure 8:Correlation matrix

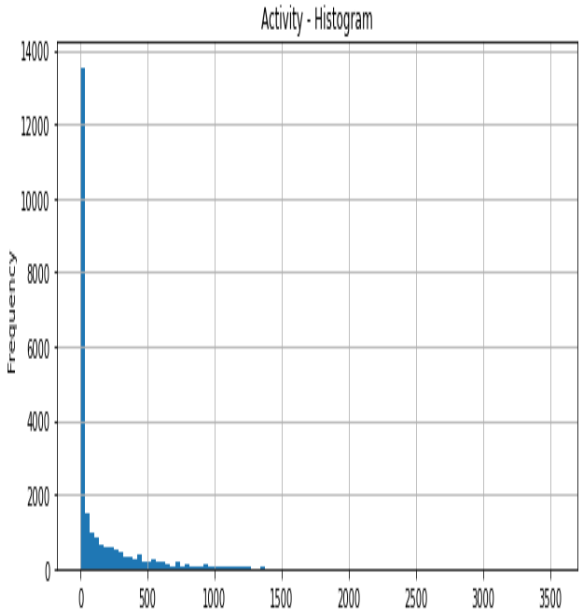


Figure 9: Activity histogram

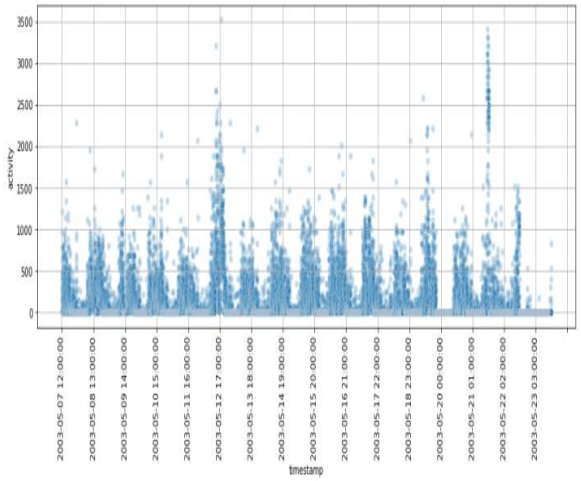


Figure 10: Timestamp activity plot

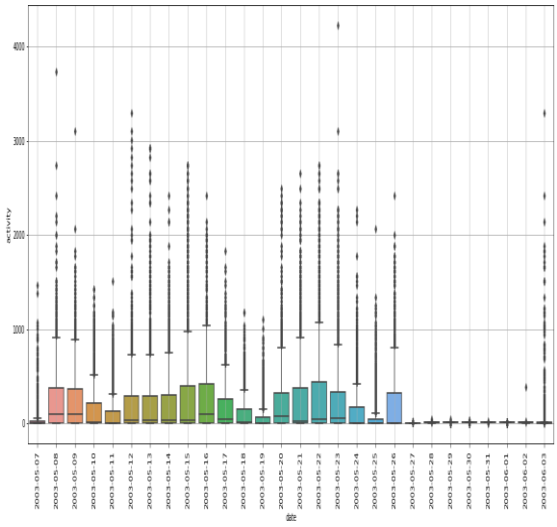


Figure 11: Patients activity with date

V. RESULTS AND DISCUSSION

The Implementation has been accomplished using the programming language Python. DT, SVM, LR, and GNB are embedded with stacking classification algorithms that have been developed and evaluated..

- True Positives (TP): TP is a legitimate, recognized, and approved class value.
- True Negatives: TN is an erroneous value assigned to an improper class.
- False Positives: FP is an incorrect value that has been mislabeled as an acceptable class
- False Negatives: FN is a valid value improperly designated as an unsuitable class..

$ACCURACY = \frac{(TP+TN)}{(TP+FP+FN+TN)}$ -------- (11)

The precision parameter sets the maximum number of valid values

$Precision \frac{TP}{TP+FP}$ ---------- (12)

The recall parameter specifies the number of relevant values that have been determined. Divide the true positive value by the total of the true positive and false negative values to get the recall value:

$Recall \frac{TP}{TP+FN}$ ---------- (13)

These are the greatest methods for determining measurement outcomes, but choosing the right one is challenging with this technique. As a result, the F-measure now has a uniform unit for measuring results. The F-measure method improves both accuracy and memory by determining the harmonic mean of both.:

$F - Measure \frac{2\,x\,(precision\ x\ recall)}{preceision+recall}$------(14)

Table 1: Training and testing accuracy, loss comparison table

Epochs	Training Loss	Training Accuracy	Val (Testing) Loss	Testing Accuracy
1	0.0047	0.9984	0.0632	0.9863
2	0.0041	0.9986	0.0579	0.9855
3	0.0020	0.9994	0.0550	0.9880
4	0.0032	0.9990	0.0596	0.9870
5	0.0025	0.9992	0.0697	0.9861
6	0.0024	0.9992	0.0642	0.9863
7	0.0031	0.9991	0.0612	0.9874
8	0.0026	0.9991	0.0728	0.9866
9	0.0027	0.9999	0.0717	0.9871
10	0.0038	0.9988	0.0748	0.9870

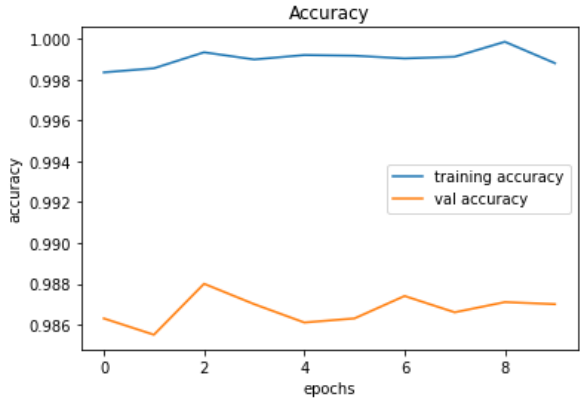


Figure 12: training and validation Accuracy Comparison

Figure 6 depicts the DL Model training and validation accuracy comparison. The X-axis represents Epochs. The Y-axis represents the proportion of accuracy.

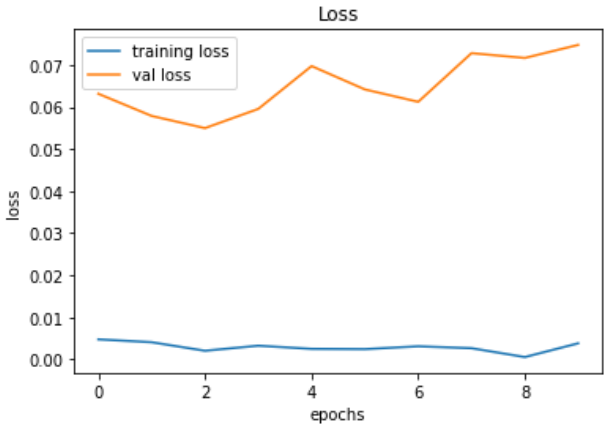
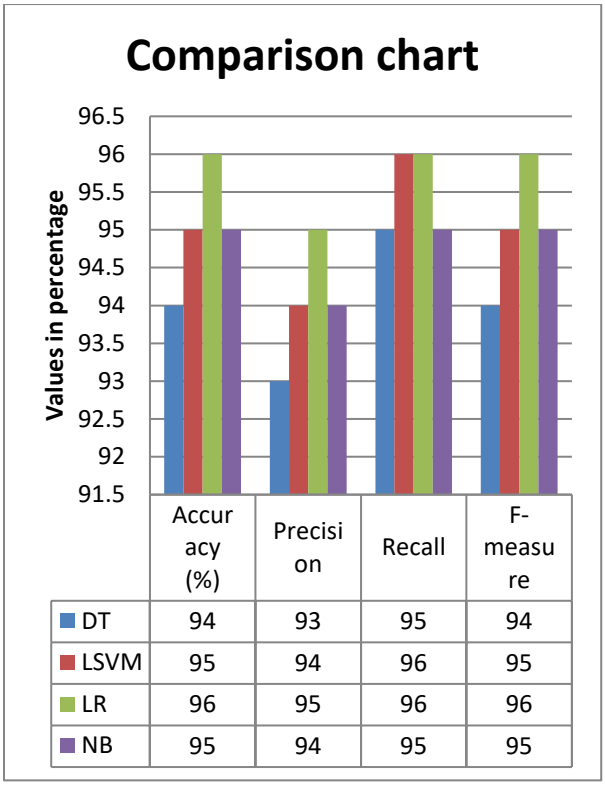


Figure 13: training and testing Loss Comparison

Figure 13 shows a comparison of training and testing loss. The suggested DL model's Training loss and Validation loss are compared between epochs and Loss. Eras are represented on the X-axis. Loss is shown on the Y-axis.



	Accuracy (%)	Precision	Recall	F-measure
DT	94	93	95	94
LSVM	95	94	96	95
LR	96	95	96	96
NB	95	94	95	95

Figure 14: Performance metrics as accuracy, precision, recall, F-measure

Figure 14 is a response to the comparison chart. The ML algorithm outperforms the SVM, GNB, and LR as bipolar disorder prediction models in terms of accuracy for existing ML algorithms.

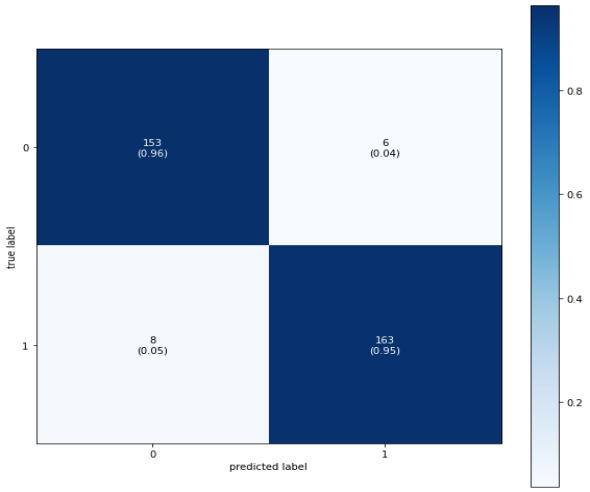


Figure 15: confusion matrix

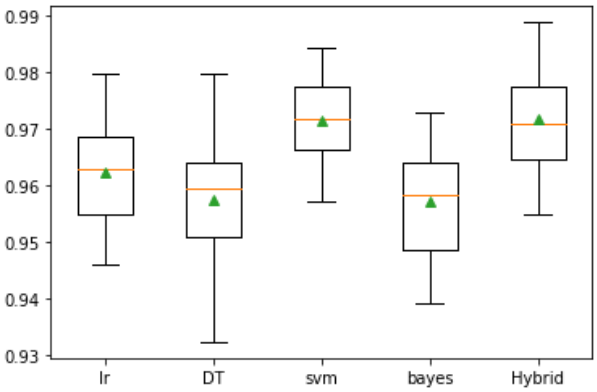


Figure 16: Stacking ensemble classification accuracy comparison chart

V. CONCLUSION

Due to the lack of identified biomarkers, distinguishing between bipolar disorder (BD) and major depressive disorder (MDD) is a significant clinical difficulty; hence, a deeper knowledge of their aetiology and brain abnormalities is urgently required. We proposed BD-MDL approaches to detect bipolar disorder, while combining the DL and ML for higher accuracy when the dataset size is too heterogeneous. Hybrid techniques like preprocessing, and feature selection are used to develop the suggested model. CNN with LSTM and the IAO aided with the training. To classify the data, many ML algorithms were deployed. Stacking ensemble has a 97.2% accuracy rate when compared to the other algorithms.

VI. REFERENCES

1. A. Chalehchaleh and A. Khadem, "Diagnosis of Bipolar I Disorder using 1 D-CNN and Resting-State fMRI Data," 2021 5th International Conference on Pattern Recognition and Image Analysis (IPRIA), 2021, pp. 1-5, doi: 10.1109/IPRIA53572.2021.9483574.
2. Antosik-Wójcińska, A. Z., Dominiak, M., Chojnacka, M., Kaczmarek-Majer, K., Opara, K. R., Radziszewska, W., … Święcicki, Ł. (2020). Smartphone as a monitoring tool for bipolar disorder: a systematic review including data analysis, machine learning algorithms and predictive modelling. International Journal of Medical Informatics, 104131. doi:10.1016/j.ijmedinf.2020.104131
3. Ceccarelli, F., & Mahmoud, M. (2021). Multimodal temporal machine learning for Bipolar Disorder and Depression Recognition. Pattern Analysis and Applications. doi:10.1007/s10044-021-01001-y
4. D. Fitriati, F. Maspiyanti and F. A. Devianty, "Early Detection Application of Bipolar Disorders Using Backpropagation Algorithm," 2019 6th International Conference on Electrical Engineering, Computer Science and Informatics (EECSI), 2019, pp. 40-44, doi: 10.23919/EECSI48112.2019.8977102.
5. Elujide, I., Fashoto, S. G., Fashoto, B., Mbunge, E., Folorunso, S. O., & Olamijuwon, J. O. (2021). Application of deep and machine learning techniques for multi-label classification performance on psychotic disorder diseases. Informatics in Medicine Unlocked, 23, 100545. doi:10.1016/j.imu.2021.100545
6. H. B. Evgin et al., "Classification of fNIRS Data Using Deep Learning for Bipolar Disorder Detection," 2019 27th Signal Processing and Communications Applications Conference (SIU), 2019, pp. 1-4, doi: 10.1109/SIU.2019.8806435.
7. K. -Y. Huang, C. -H. Wu, M. -H. Su and C. -H. Chou, "Mood disorder identification using deep bottleneck features of elicited speech," 2017 Asia-Pacific Signal and Information Processing Association Annual Summit and Conference (APSIPA ASC), 2017, pp. 1648-1652, doi: 10.1109/APSIPA.2017.8282296.
8. Karthik, S., & Sudha, M. (2020). Predicting bipolar disorder and schizophrenia based on non-overlapping genetic phenotypes using deep neural network. Evolutionary Intelligence. doi:10.1007/s12065-019-00346-y
9. Librenza-Garcia, D., Kotzian, B. J., Yang, J., Mwangi, B., Cao, B., Pereira Lima, L. N., … Passos, I. C. (2017). The impact of machine learning techniques in the study of bipolar disorder: A systematic review. Neuroscience & Biobehavioral Reviews, 80, 538–554. doi:10.1016/j.neubiorev.2017.07.004
10. Liu, Y. S., Chokka, S., Cao, B., & Chokka, P. R. (2021). Screening for bipolar disorder in a tertiary mental health centre using EarlyDetect: A machine learning-based pilot study. Journal of Affective Disorders Reports, 6, 100215. https://doi.org/10.1016/j.jadr.2021.100215
11. M. Ebrahim, M. Al-Ayyoub and M. Alsmirat, "Determine Bipolar Disorder Level from Patient Interviews Using Bi-LSTM and Feature Fusion," 2018 Fifth International Conference on Social Networks Analysis, Management and Security (SNAMS), 2018, pp. 182-189, doi: 10.1109/SNAMS.2018.8554886.
12. M. Margarette Sanchez et al., "A Machine Learning Algorithm to Discriminating Between Bipolar and Major Depressive Disorders Based on Resting EEG Data," 2022 44th Annual International Conference of the IEEE Engineering in Medicine & Biology Society (EMBC), 2022, pp. 2635-2638, doi: 10.1109/EMBC48229.2022.9871453.
13. M. S. Salman, E. Verner, H. J. Bockholt, Z. Fu and V. D. Calhoun, "Machine Learning Predicts Treatment Response in Bipolar & Major Depression Disorders," 2021 IEEE 21st International Conference on Bioinformatics and Bioengineering (BIBE), 2021, pp. 1-6, doi: 10.1109/BIBE52308.2021.9635339.
14. Martinuzzi, E., Barbosa, S., Courtet, P., Olié, E., Guillaume, S., Ibrahim, E. C., … Belzeaux, R. (2021). Blood cytokines differentiate bipolar disorder and major depressive disorder during a major depressive episode:

Initial discovery and independent sample replication. Brain, Behavior, & Immunity - Health, 13, 100232. doi:10.1016/j.bbih.2021.100232

15. N. Agnihotri and S. K. Prasad, "Predicting the Symptoms of Bipolar Disorder in Patients using Machine Learning," 2021 10th International Conference on System Modeling & Advancement in Research Trends (SMART), 2021, pp. 697-702, doi: 10.1109/SMART52563.2021.9676247.
16. N. -F. Jie et al., "Discriminating bipolar disorder from major depression using whole-brain functional connectivity: A feature selection analysis with SVM-FoBA algorithm," 2015 IEEE 25th International Workshop on Machine Learning for Signal Processing (MLSP), 2015, pp. 1-6, doi: 10.1109/MLSP.2015.7324352.
17. O. Cigdem et al., "Diagnosis of Bipolar Disease Using Correlation-Based Feature Selection with Different Classification Methods," 2019 Medical Technologies Congress (TIPTEKNO), 2019, pp. 1-4, doi: 10.1109/TIPTEKNO.2019.8895232.
18. P. J. Moore, M. A. Little, P. E. McSharry, J. R. Geddes and G. M. Goodwin, "Forecasting Depression in Bipolar Disorder," in IEEE Transactions on Biomedical Engineering, vol. 59, no. 10, pp. 2801-2807, Oct. 2012, doi: 10.1109/TBME.2012.2210715.
19. Perez Arribas, I., Goodwin, G. M., Geddes, J. R., Lyons, T., & Saunders, K. E. A. (2018). A signature-based machine learning model for distinguishing bipolar disorder and borderline personality disorder. Translational Psychiatry, 8(1). doi:10.1038/s41398-018-0334-0
20. Poletti, S., Vai, B., Mazza, M. G., Zanardi, R., Lorenzi, C., Calesella, F., … Benedetti, F. (2020). A peripheral inflammatory signature discriminates bipolar from unipolar depression: A machine learning approach. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 110136. doi:10.1016/j.pnpbp.2020.110136
21. R. Jadhav, V. Chellwani, S. Deshmukh and H. Sachdev, "Mental Disorder Detection : Bipolar Disorder Scrutinization Using Machine Learning," 2019 9th International Conference on Cloud Computing, Data Science & Engineering (Confluence), 2019, pp. 304-308, doi: 10.1109/CONFLUENCE.2019.8776913.
22. S. Gao et al., "Discriminating bipolar disorder from major depression based on kernel SVM using functional independent components," 2017 IEEE 27th International Workshop on Machine Learning for Signal Processing (MLSP), 2017, pp. 1-6, doi: 10.1109/MLSP.2017.8168110.
23. V. Vasu and M. Indiramma, "A Survey on Bipolar Disorder Classification Methodologies using Machine Learning," 2020 International Conference on Smart Electronics and Communication (ICOSEC), 2020, pp. 335-340, doi: 10.1109/ICOSEC49089.2020.9215334.
24. Wu, M.-J., Mwangi, B., Bauer, I. E., Passos, I. C., Sanches, M., Zunta-Soares, G. B., … Soares, J. C. (2017). Identification and individualised prediction of clinical phenotypes in bipolar disorders using neurocognitive data, neuroimaging scans and machine learning. NeuroImage, 145, 254–264. doi:10.1016/j.neuroimage.2016.02.016
25. Z. Xiong, X. Zhang, M. Zhang and B. Cao, "Predicting Features of Human Mental Disorders through Methylation Profile and Machine Learning Models," 2020 2nd International Conference on Machine Learning, Big Data and Business Intelligence (MLBDBI), 2020, pp. 67-75, doi: 10.1109/MLBDBI51377.2020.00019.