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Deep Learning Model to Evaluate Alzheimer's disease Through Multi-View Clustering

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Abstract: Early diagnosis of Alzheimer's disease (AD) plays a crucial role in the development and effectiveness of interventions, and neuroimaging stands out as an up-and-coming field for the initial identification of Alzheimer's disease. Earlier models utilized various methods to analyze images of Alzheimer's disease, such as deep learning models or unsupervised matrix factorization processes. Neither of these techniques alone can produce satisfactory results while clustering multi-view photos of Alzheimer's disease. This motivates our research to create a deep learning model for obtaining the most important Alzheimer's disease factors from MRI and classifying brain images into different stages. To achieve optimal results in multi-view clustering, the proposed model integrates a deep learning technique (Channel Boost-Convolution Neural Network) with an inverse matrix factorization method, forming an ensemble approach. The experiment analyzes several images to evaluate the implemented technique for the performance of RMSE, which are about 2.32 better than the various compared models. The results show that combining the deep learning model with Inverse matrix factorization for Alzheimer's disease multi-view image clustering works well, the Transformers can further improve multi-view clustering in deep learning.

Keywords: Alzheimer's Disease, Channel Boost-Convolution Neural Network, Decision Tree, Deep Learning, Image Classification, Image Clustering, Multi-View Assembling Approach.

1. Introduction

A number of methods for diagnosing Alzheimer's disease (AD) have previously used machine learning. Nevertheless, a large number of currently in use systems concentrate on problem classification with only two options (dementia or not), only examine data from one perspective, and necessitate human interaction to change settings. When compared to data obtained from a single view, multi-view data provides a more robust way to express features. In recent years, learning with multi-view data has received a lot of attention [1, 2]. Here, we employ nonnegative matrix factorization to precisely forecast the several phases of Alzheimer's disease development. This recommended CMC efficiently extracts data characteristics by using a multi-view learning technique to maximize the limited number of available medical pictures. It considers similarity relations between entities and resolves the issues with manual parameter setup in multi-view fusion [3, 4]. Combining shared features with complementing knowledge from several points of view is the aim of reaching a consensus representation. As the illness worsens, it might increase the accuracy of AD prediction and aid in the recognition and classification of symptoms. The effectiveness of the proposed model is demonstrated by experiments utilizing twelve perspectives of the Alzheimer's Disease brain MRI database.

Clustering the various views of Alzheimer's disease magnetic resonance imaging is essential for early disease stage identification. In the research, a model for processing two-view images—such as auxiliary and sagittal—downloaded from a reliable source is proposed. The inverse matrix factorization procedure and the channel boost-convolution neural network are used by the model to properly cluster the images based on various disease degrees.

The proposed model has the following key contributions: This reformulation highlights the practical application of the model - achieving better results in grouping MRI scans based on Alzheimer's disease, thus improved clustering accuracy for Alzheimer's diagnosis. This focuses on the technical innovation, mentioning the combination of two techniques (channel boost neural network and Inverse matrix transition factor) for analyzing the MRI data. This emphasizes the model's ability to identify different stages of Alzheimer's disease, going beyond a simple healthy/diseased classification that is Multi-stage disease classification.

If we want to specify groups of subjects or objects, we can use the information in multi-view data to find patterns or clusters. Our main objective is to analyse patients for whom we have collected biomedical and/or clinical data that describes their features. This data can be derived from a variety of diagnostic tests or molecular technologies. Patients' perspectives are shaped by the various subject features. The identification of patient groups is made easier through the integrative grouping of different viewpoints, leading to better clinical diagnostic and treatment plans.

Given the variety and complexity of the medical observations at our disposal, it would be inappropriate to simply integrate the results of single view clustering. Ensemble clustering may be able to circumvent some of the shortcomings of even the most cutting-edge multi-view methods. Additionally, tabular data may be better served by agglomerative clustering, but spectral clustering may be the best approach for some image-based analyses. In many cases, this holds true when patient records reveal a hierarchical structure within the disease or subtype of concern. Every view must be clustered using the optimal and most suitable approach because, in practical applications, data views come from extremely diverse input sources. As a result of the frequent retrieval of molecular data from many bio logical layers for a single set of patients, multi-view clustering algorithms find extensive use in the biomedical domain. As a step towards precision medicine, the clusters deduced from these multi-omics data allow for the sub-group classification of cancer patients.

Section 2 of this research study involves a thorough examination of prior works, known as a literature review. In section 3, the "Proposed methodology" section provides a broad outline of the process that was implemented. In section 4, results are discussed. This study concludes in section 5, which also provides opportunities for future improvements.

2. Literature Survey

In this section, we review existing research on multi-view clustering for Alzheimer's disease detection. We analyze their strengths and weaknesses to identify potential improvements for our proposed method.

Aya Gamal *et al.* [5] developed an MRI-based early Alzheimer's disease detection method that distinguishes AD, MCI, and CN. The author created a system that ignores patient visits after the first to prevent data leaking. Numerous comparative studies were performed to investigate the impact of ADNI data formats and dataset sizes. The author examined early data processing methods and evaluated their efficacy using more advanced 3D classification models. According to Mümine Kaya Keleş *et al.* [6], research work proposes the binary artificial bee colony algorithm (BABC) as a feature selector for identifying Alzheimer's disease (AD) using volumetric and statistical data from brain magnetic resonance imaging. ADNI provided an MRI. Chahd M. Chabib *et al.* [7] designed a CNN structure that uses curvelets to classify Alzheimer's disease MRI images into binary categories. DeepCurvMRI was trained and tested with Kaggle to reliably classify Alzheimer's disease phases. When MRI images are scaled and sub-banded, FCT is used. Wrapping is used. After obtaining the curvelet coefficients, kurtosis is used to process and threshold them to extract the most essential properties.

Nora Shoaip *et al.* [8] evaluate that AD is a long-lasting degenerative disease that affects the brain and causes a range of neurological disorders. This happens due to the build-up of amyloid plaques, which can impact important bodily functions. For this study, a model tree structure-powered model called ontology is used to provide the meaningful information extraction technique known as ADDO has been developed. Its purpose is to unleash an early notification to high-risk patients who are at a greater risk of developing AD The data includes demographic information, medical history, illness history, complications, medicine, and a variety of diagnostic tests; it is efficiently analyzed for patients' visit timelines.

Zongshuai Qu *et al.* [9] propose a classification framework called UNB-GCN. This framework has shown promising results in achieving improved classification performance when distinguishing in when compared to people who suffer from Alzheimer's illness. There is promising evidence that functional connectivity networks constructed using f-MRI can distinguish between healthy people and those suffering from neurological diseases.

Fazal Ur Rehman Faisal *et al.* [10] achieved optimal results by fine-tuning a CNN specifically based on ADNI data for 3D whole-brain imaging. The most accurate method they used was architecture of isotropically repeated convolutional block networks. The developed technique outperformed contemporary cutting-edge technology systems. In addition, the author's approach is completely automated, requiring no more extra data or any human interference is required, and it is incredibly efficient. This method is capable of uncovering significant patterns in data, validating existing findings from experts, assisting in diagnostic situations, and Discovering patterns that are associated with diseases other than Alzheimer's disease is a possibility.

An innovative method was utilized by Chima S. Eke *et al.* [11] to create prospective models and discover five new candidate non-amyloid biomarker panels for the early detection of Alzheimer's disease. Their findings were published in the journal Neurology. With the expertise of a data scientist, the models created using these panels were able to accurately classify prodromal AD, AD dementia, and normal controls. The sensitivity of the models was above 80%, ensuring a high rate of correctly identifying positive cases.

Tetiana Habuza *et al.* [12], it was analyzed that various tests, including psychophysiological and cognitive assessments, along with other functional studies, have the potential to identify early stages of dementia before symptoms become apparent. By combining structural data with cognitive tests, NDs can be diagnosed more reliably, making it a powerful multimodal diagnostic tool. Goal. The author aims to enhance dementia screening by investigating the correlation between brain structure and function. This innovative approach opens up new possibilities for identifying markers of neurodegeneration. This exemplified typical aging. Similar to how a data scientist would analyze the situation, a significant fluctuation from the designed process indicates a heightened possibility of rapid cognitive decline.

In a recent study by Yu Zhang *et al.* [13] proposed a novel approach to predicting the progression of Alzheimer's disease at various time points. Their method, which is based on tensor decomposition, aims to address the challenges of variability and instability in prediction accuracy. Using an author's framework, a prediction model is created by analyzing correlations in spatio-temporal morphological variation trends among biomarkers. This particular model makes use of tensor latent components to construct multi-task interactions and transfer knowledge, which finally results in the generation of correct prediction outcomes. Additionally, to merge temporally continuous MRI recordings, the method that has been suggested makes use of the gradient-boosting ensemble learning technique.

Gargi Pant Shukla *et al.* [14] analyzed novel pre-processing techniques that offer valuable insights. These early procedures are crucial for increasing the precision of classification algorithms. Furthermore, the suggested techniques enhance the decrease in training time needed for current learning algorithms, resulting in a more efficient and practical diagnostic process. Similar to what a data scientist would do, a dataset from the ADNI was used for the study's objectives. The dataset was converted from a four-dimensional format to a two-dimensional version to enable further analysis.

An evaluation and development of a multi-feature selection model was carried out by Luyun Wang and colleagues [15]. The graph measurements and machine learning techniques were applied by this model to determine which characteristics were the most appropriate for the classification of HC, EMCI, LMCI, and AD. To arrange the proper brain working some parameters need to be put in for each single scenario, the author employs the J-HCPMMP brain parcellation methodology. After that, a model is developed in a manner that is analogous to the work of a data scientist to determine which attributes are the most advantageous by utilizing dual graph measurements.

Chen-Chen Fan *et al.* [16] evaluate the GRM, a method that can be seamlessly integrated into current AD detection models to enhance their performance. To accomplish this, it simulates the hidden connection that exists between locations that are geographically separated. As demonstrated by the results of the experiments, the overall accuracy of Alzheimer's disease classification may be greatly enhanced by more than 4.3% with the incorporation of GRMs into existing CNN-based characterization models. Pusparani, Yori, *et al.* [17] research article proves the theory of selection slices that can enhance the performance of machine learning. Specifically, the selection of slices in MRI images has been found to considerably enhance the accuracy of Alzheimer's disease (AD) categorization. Additionally, the author's findings indicate that the accuracy of the coronal view results surpasses that of the axial and sagittal views. In addition to this, the author observed that the LeNet model performed exceptionally well when it came to the classification of Alzheimer's sickness. After that, the results of the multiclass classification can be applied to evaluate the significance of each category in the classification of Alzheimer's disease (AD).

Abdulaziz Almohimeed *et al.* [18] proposed a multi-level stacking model to scientists. This model uses CS sub-scores and ADNI dataset sub-scores to increase AD prediction accuracy. Problem formulation considers two classes (AD, CN) and three classes (AD, CN, MCI) of complexity. The unique multi-level stacking method uses level-based heterogeneous models with homogeneous and heterogeneous modalities. Wu *et al.* [19] observed abnormal gamma oscillations in the left and right hippocampus and prefrontal cortex during short-term memory in APP/PS1 transgenic Alzheimer's mice. The researchers also examined how gamma transcranial afferent stimulation (tACS) affected Alzheimer's mice and its mechanism. According to the author, reduced field potentials and abnormal hippocampus-prefrontal cortex connection may cause short-term memory loss in Alzheimer's rats. This link is inappropriate since the hippocampus resides in the frontal cortex.

Weijia Liu *et al.* [20] presented a framework for estimating brain age and predicting the risk of longitudinal AD conversion. The CRES, for example. The results indicated that the CRES uncovered noteworthy patterns in AG among various clinical groups, providing a solid basis for subsequent analysis of AD conversion risk. The author uses advanced statistical models and visualization tools to forecast the chance of moderate cognitive impairment (MCI) patients getting Alzheimer's disease. We can also learn about Alzheimer's disease progression in mild cognitive impairment (MCI) patients and identify those at risk. It may produce early interventions with a big impact.

AmnaAl-Sayed et al [21], In clinical data, you can often find a variety of data formats. The quality and accuracy of the output may suffer when machine learning algorithms are applied to mixed data. Modeling and processing mixed data with an application in heart disease detection is the focus of this research, which presents a hybrid model combining unsupervised and supervised learning techniques. Collaborative clustering and decision-combining (the ensemble approach) are the two primary parts of the model. Because several types of clustering algorithms are used to process different perspectives, the mixed data clustering problem is also known as a multi-view clustering problem. A new collaborative framework was suggested to facilitate the clustering process by allowing the various clustering algorithms to exchange information. This allows for the production of expert models that represent different feature spaces within the data set, as each algorithm operates on a separate space. By improving the collaboration term representing entropy, the expectation maximization algorithm ensures outstanding convergence characteristics and forms the foundation for this optimization process. An ensemble method like the stacking method was employed. To train the expert model's prediction findings and then utilize them to forecast the final output, the logistic regression model was employed as a meta-classifier. The outcomes of various clustering algorithms and meta-classifiers are optimized by this collaborative technique, as shown by the findings.

Guoqing Chao *et al* [22], Two main categories of multi-view clustering algorithms, generative and discriminating, have been covered in this study. As a result of the wide variety of discriminative methods, we have categorized them into five broad groups according to the views they integrate. The first three groups share commonalities, such as specific structures across views. The fourth group includes methods that combine views directly, and the fifth group includes methods that combine views after projections. In comparison to discriminative methods, generative methods have not progressed nearly as far. In order to have a deeper understanding of multi-view clustering, we clarify the connections between MVC and a number of related learning techniques. Along with highlighting some intriguing and difficult future paths, we have also presented numerous real-world uses of MVC.

Sally El Hajjar *et al* [23], In terms of COVID-19 diagnosis, our suggested technique has a number of significant benefits. It improves diagnostic accuracy by capturing a complete picture of the disease through the integration of many data views. It is practical for usage in the real world due to its unsupervised nature, which does not necessitate a large amount of labeled data. Better clustering results, possibly even better than previous unsupervised approaches, are the consequence of the addition of constraints, such as a smoothing term for cluster indices and an orthogonality requirement for the non-negative embedding matrix. Its robustness and generalizability have been proven by rigorous experiments on different datasets, which implies that it could have larger applications.On the other hand, there are additional difficulties, such as complicated unsupervised models, hyperparameter sensitivity, data views' availability and relevance, and data views' complexity. Additional study and validation are necessary to assess our approach's practical relevance in a clinical setting and to solve these shortcomings, even though it presents intriguing solutions.

The above-mentioned methods have discussed deep learning techniques for Alzheimer's disease and some issues. To overcome the issues, the purpose is to provide high accuracy in multi-view clustering of Alzheimer's MRI images for the sagittal and auxiliary view images. It is the hybridization of the channel boost neural network and the Inverse matrix transition factor to form seven clusters based on Alzheimer's disease stages. The detailed proposed model is described below section.

3. Proposed Model

The proposed methodology for multi-view clustering of Alzheimer's disease is visually represented in Figure 1 and 2 below.

The model is deployed by following a set of steps.

Step 1: Dataset Collection and Preprocessing - This is the first phase in the deployed method, Here the image datasets for the auxiliary and sagittal views were downloaded. By registering, users can download these images from the Alzheimer's Disease Neuroimaging Initiative (ADNI) website at [24]. Datasets that are available to the public for use in research projects can be found at this URL [24]. The two sets of MRI data represent the view sagittal and auxiliary contain all six subjects that correspond to each stage of Alzheimer's disease progression. These subjects are as follows: Control Normal (CN), which represents stage 1 of the progression of Alzheimer's disease; Subjective Memory Consider (SMC), which represents stage 2 of the progression of Alzheimer's disease; Early Mild Cognitive Impairment (EMCI), which represents stage 3 of the progression of Alzheimer's disease; Mild Cognitive Impairment (MCI), which represents stage 4 of the progression of Alzheimer's disease; Lately Mild Cognitive Impairment (LMCI)—which represents stage 5 of the progression of Alzheimer's disease; and confirmed Alzheimer's disease (AD), which represents stage 6 of the progression of Alzheimer's disease.

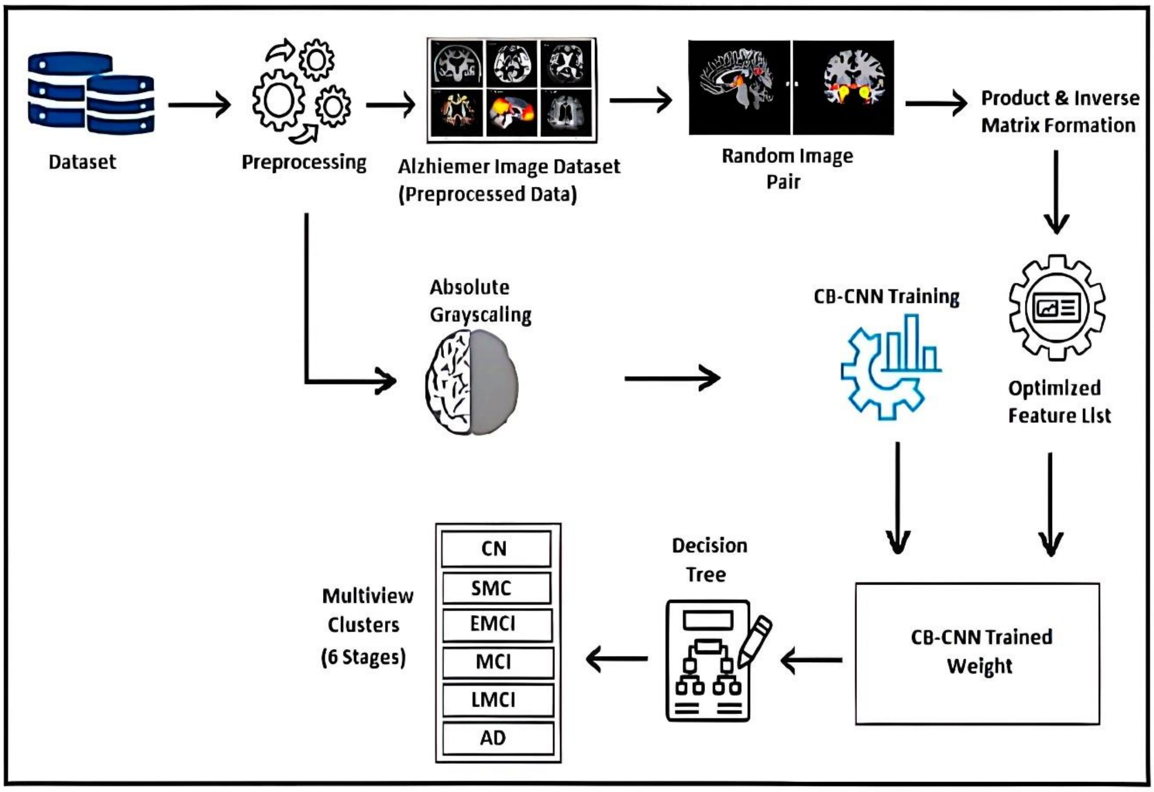

Figure 1. Overview of the proposed model

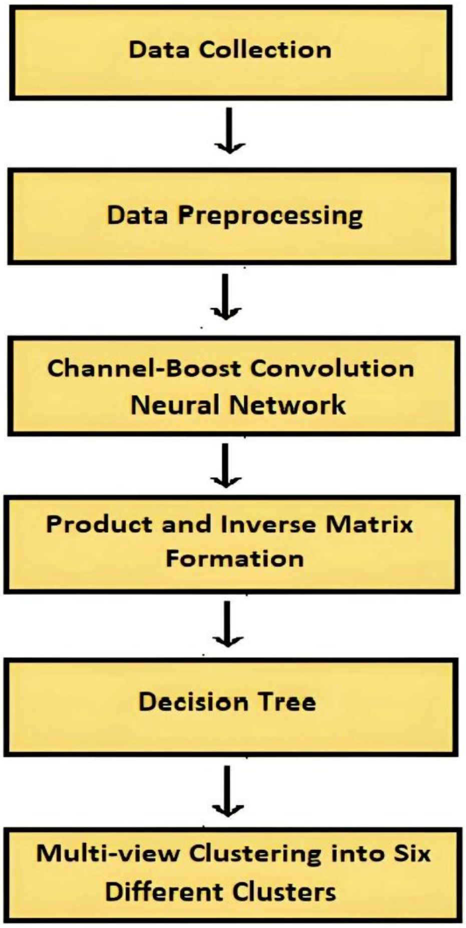

Figure 2. Flow diagram of Multi-View Clustering

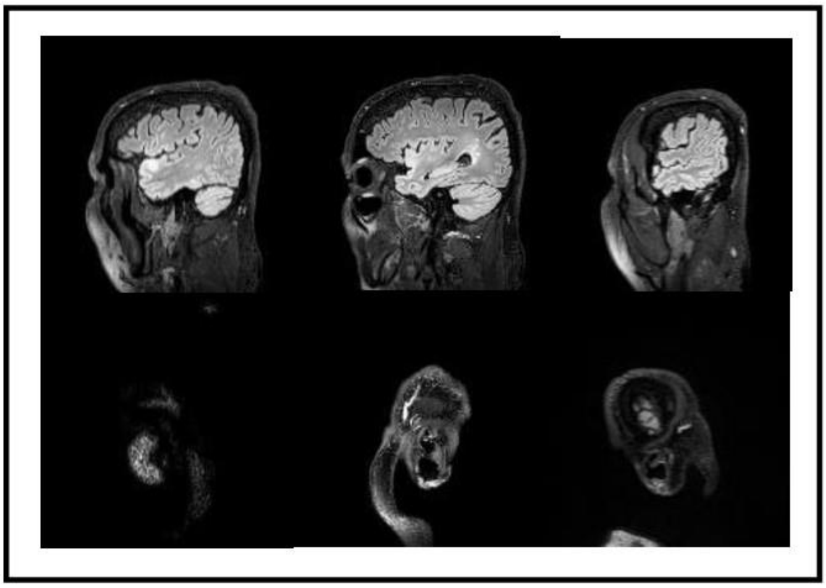

Figure 3. Alzheimer's dataset images

Three thousand nine hundred ninety-nine axial view images covering the six phases of Alzheimer's disease have been downloaded from the ADNI website. Conversely, 8737 sagittal view photos for the same six stages of Alzheimer's disease are retrieved from the ADNI website. From stage 1 to stage 6, these six stages of the disease are referred to as CN, SMC, EMCI, MCI, LMCI, and AD, in that order.

When images are fetched from the URL, they are saved with a .dcm extension. Here 8323 images are utilized for training and 4666 images are utilized for testing. However, these file extensions cannot be utilized for subsequent tasks. Therefore, it is necessary to convert these file format images into proper .jpg images using the Pydicom library in the Python programming language. The directory contains .dcm files that are processed by the model to convert them into .jpg format by recursively traversing the files. After the process is finished, all the files are saved in their designated directory as .jpg files, which will be utilized for future processes.

The following stage in the suggested model involves resizing the photos to a dimension of 128 by 128 and converting them to grayscale by utilizing the opencv module as part of the Python programming language.

Step 2: Channel boost-Convolution Neural network - This is one of the important phases of the deployed system, where the obtained and preprocessed images are subjected to train the model. In this process, the dataset is classified into two types train and test, both train and test segments consist of 12 classes made of 6 phases of Alzheimer's disease with two views axially and sagittal.

To get ready for the commencement of the training phase, the convolutional neural network libraries from Keras and Tensorflow are imported and installed. To generate an object for the photos, we make use of an image data generator class for both the training data and the testing data. This allows us to provide an object for the images. This allows us to generate an object for the images. To learn the pixel in detail, a ratio of 1:255 is subsequently set. After that, the batch size for the images in the dataset is brought up to 64. "Grayscale" is the color mode that is selected for the "categorical class" mode of the form.

The further configuration of a sequential neural network model to generate its object occurs after all of the early steps have been finished. A convolution layer with 32 kernels of size 3 X 3 and the "Relu" activation function is introduced as the first layer of the neural network. This layer is the first layer that is applied. The initial layer of the convolution neural network has been finished, and it has a color channel of one and a dimension of 128 pixels by 128 pixels. Within the second layer of the convolution neural network, which is comprised of 64 kernels that are of a 3 x 3 type, the activation function known as "Relu" is applied. The Dropout function is enabled after the insertion of a max pooling 2D layer with a kernel size of 2 X 2, which causes a dropout rate of 0.25 to take place. This is the outcome of the dropout rate being active.

Following the addition of 128 kernels with a size of 3 x 3, the "Relu" activation function is then applied to the Third and Fourth Layers. Following each layer is the addition of a maxpooling two-dimensional layer with a kernel size of two by two. At last, a dropout layer with a proportion of 0.25 drop rate is added to the composition. Immediately following the flattening of the neural network, the tensors are gathered by applying an activation function of "Relu" and a size of 1024. To gather the trained data in twelve distinct categories, a dropout layer with a degree of fifty is applied at the very end of the model. Utilizing the "Softmax" activation function is how this objective is attained. Six of these twelve classes are derived from auxiliary views, and the remaining six are derived from sagittal views. These classes include phases such as CN, SMC, EMCI, MCI, LMCI, and AD.

After that, the "Adam" Optimizer is employed to optimize the neural network model that was constructed, and it is carried out for a total of one hundred epochs for the images that are included in the Alzheimer's dataset Figure 3 depicts the Alzheimer's dataset images. The information that has been acquired is saved in a file that has the extension ".h5" so that it can be utilized throughout the process of fusing the weights.

The Softmax and Relu activation functions that were utilized are represented in equations 1 and 2, respectively.

$$\sigma(Z) = \frac{e^{zi}}{\sum_{j=1}^{k} e^{zj}} \qquad (1)$$

$$\mathrm{Relu} = \max(0, x) \qquad (2)$$

Where

X = neuron value

σ = softmax

z = input vector

e^{zi} = A normal exponential function for the vector that is being entered

K = number of classes

e^{zj} = A normal exponential function for the vector that is being entered for the output

The CB-CNN architecture can be seen in the depicted in figure 4.

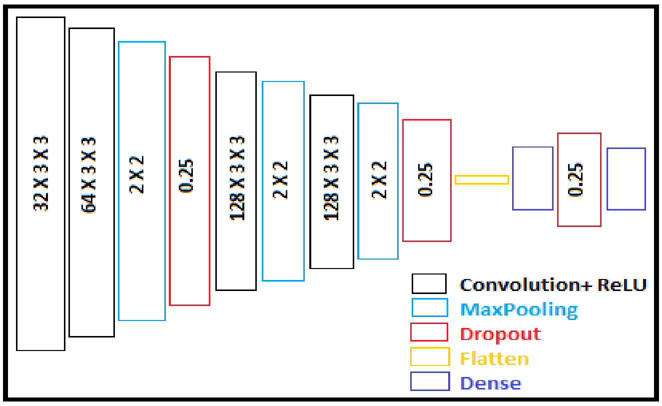

Figure 4. CB-CNN Architecture

Step 3: Product and Inverse matrix formation – The weights that have been learned for each picture are saved in .h5 files after the images have been trained for the channel boost-convolution neural network model. The user gave the suggested model a number of random images to work with, such as 200, 400, 600, 800, and 1000. Once these pictures are added to the system, they go through a total of N/2 iterations for a total of N pictures. Two random images are taken out at the end of each loop and then put through a process that includes clustering.

The first random pictures that show different points of view are put through the process of making their matrix based on the value of their first pixel, which is red. The first step in the process is now here. The pictures usually all have the same RGB value because they have already been turned into grayscale. In order to finish making the first matrix, the obtained R-value will be put into the right place in the matrix. One way to see this is in method 1, which is described below.

Algorithm 1: Image Matrix formation

```
// Input: Random Image $R_{IMG}$
//Output: $MatA_{ij}$
// function: imageMatrixFormation($R_{IMG}$)
Begin
    $R_{IMG} = \emptyset$
    for i = 0 -> W of $R_{IMG}$
        for j=0 0->H of $R_{IMG}$
            color[] = $R_{IMG [i, j]}$ RGB
            $mat_{A[i][j]}$= color[0]
        end Inner for
    end outer for
    return $MatA_{ij}$
stop
```

The second random image is also adjusted to get the optimized values of the pixels to form the fusion matrix. Since A is a matrix with the form $[a_{ij}]m \times n$ and k is a scalar, it follows that kA is another matrix that can be constructed by multiplying each element of A by the scalar k. This matrix may be created by multiplying each element of A by k. Therefore, it may be said that the equation $kA = k\ [a_{ij}]\ m \times n$ is identical to the equation $[k\ (a_{ij})]m \times n$. This indicates that the (i, j)th element of kA is ka_{ij} for every value of i and j that is theoretically possible. Based on the above-mentioned principle both the feature matrix and original matrix are multiplied to obtain the product matrix P. The product matrix P is used to estimate the inverse feature values as mentioned in equation 3.

$$A - 1 = 1/|A| * \boldsymbol{Adj\ A} \qquad (3)$$

In this context, the term "adj" refers to the adjoint of a matrix that holds the definition of a square matrix. A = $[a_{ij}]n \times n$ is a mathematical expression that represents the adjoint of the matrix $[A_{ij}]n \times n$, where A_{ij} represents the cofactor of the element a_{ij}. The transpose of the matrix is what is meant to be understood by the adjoint. To put it another way, the adjoint of the matrix is something that is referred to as the transpose of a cofactor matrix of the square matrix. adj A is the notation used to refer to the adjoint of the matrix A.

Step 4: Decision Tree - Once the inverse matrix process is complete, the two random images are enhanced and prepared for integration with the Channel boost-convolution neural network model. By utilizing these enhanced images, we can estimate the weights for each image and evaluate which cluster they belong to. The feature extraction is followed by a division into training weights and fusion modules. The trained weights and fused parameter estimations are then used to create a feature list, which is subsequently classified by the decision tree subsystem to produce multi-view clusters. The obtained indices are tracked within the range of 1 to 12 since 12 classes are trained during the Channel boost-convolution neural network. If the index falls within the range of 10 to 11, it is categorized as cognitively normal (CN) in stage 1 of Alzheimer's disease. An index value of 1 or 12 indicates subjective memory complaint (SMC), 2 to 3 represents early mild cognitive impairment (EMCI), 4 to 5 signifies mild cognitive impairment (MCI), 6 to 7 corresponds to late mild cognitive impairment (LMCI), and finally, an index value of 8 is associated with Alzheimer's disease (AD).

4. Results and Discussions

A Windows laptop with a core i5 CPU and 8 gigabytes of random access memory (RAM) is utilized in the construction of the designed approach for clustering the multi-view Alzheimer's image.

Python and the Spyder integrated development environment (IDE) are utilized in the development of the proposed model. As was mentioned before, the auxiliary and sagittal Alzheimer's images are obtained for the experiment by registering for an account on the Alzheimer's Disease Neuroimaging Initiative (ADNI) website [24].

We utilized the ADNI dataset [24] for the proposed model. There are a total of 13319 images of two views of disease. A total of 3199 images were retrieved from the Alzheimer's Disease National Institute website to obtain the axial view images for each of the six stages of Alzheimer's disease.

Alternatively, 8737 images for the sagittal view of the same six phases of Alzheimer's disease were downloaded from the ADNI website. These images were taken from both sides of the disease. There are six phases of the sickness, which are referred to as CN, SMC, EMCI, MCI, LMCI, and AD.

Stage 1 is the first stage, and stage 6 is the sixth stage. After being downloaded in the .dcm format, each of the photos is subsequently converted to the.jpg format. To obtain the final 62.52% training images and 37.50% for the testing phase images, the majority of the undesired and mediocre images are manually deleted. These images are utilized for training the model with the Channel boost - Convolution neural network. The accuracy and loss of the deployed model for 100 epochs can be seen in Figures 5 and 6 correspondingly.

The accuracy and loss of the deployed model for 50 epochs can be seen in Figures 7 and 8 correspondingly.

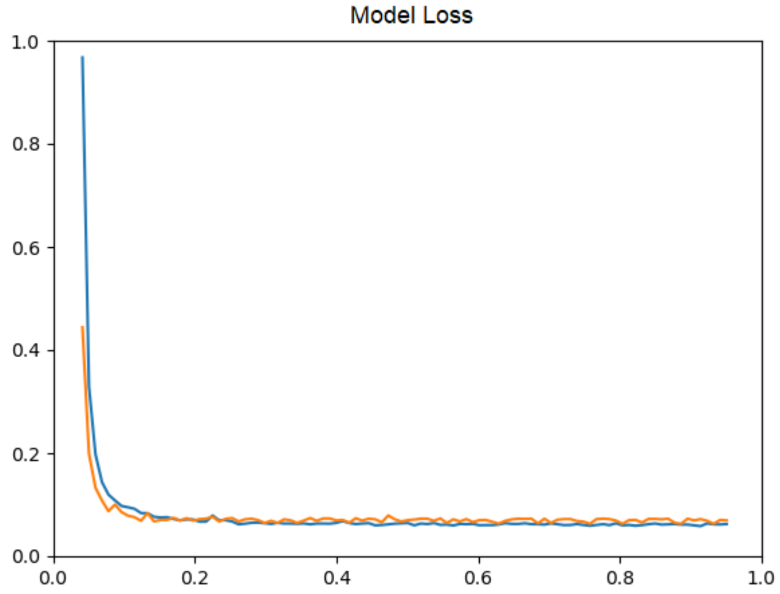

Figure 5. CB-CNN model Accuracy for 100 epochs

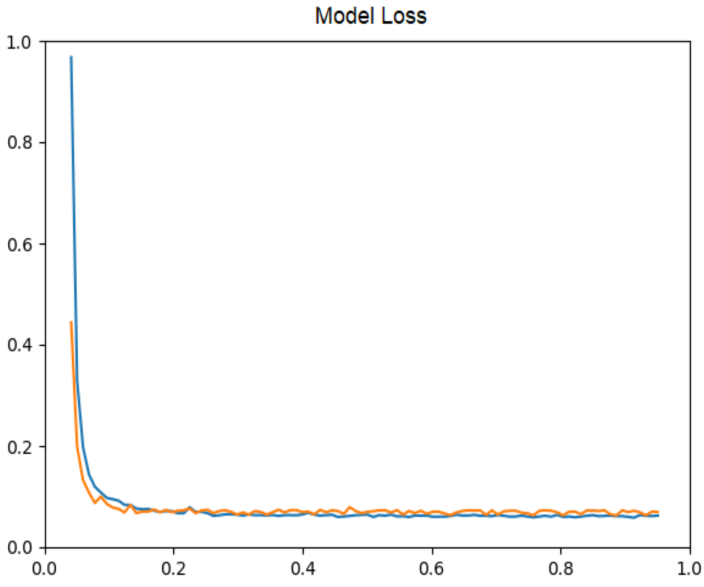

Figure 6. CB-CNN model Loss for 100 epochs

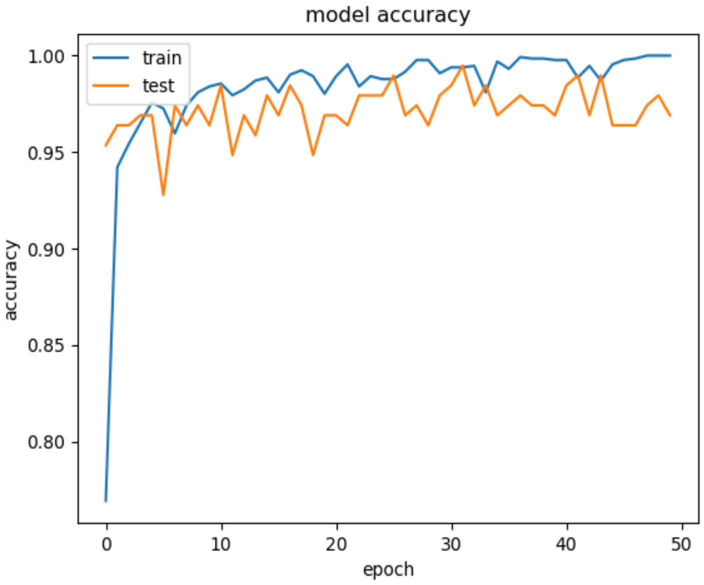

Figure 7. CB-CNN model Accuracy for 50 epochs

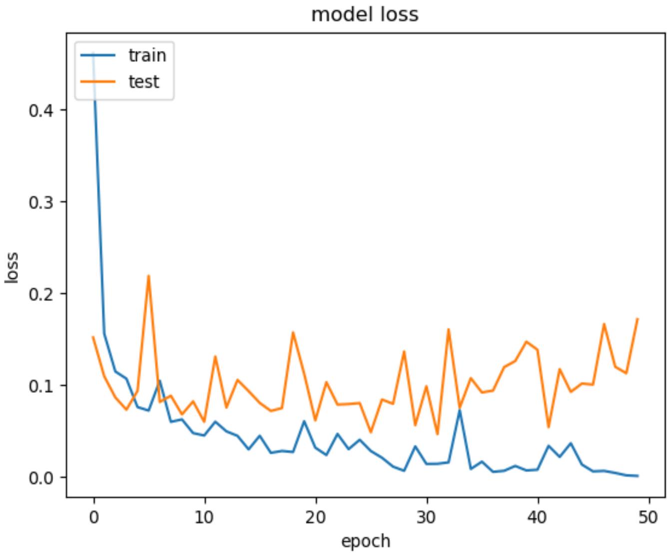

Figure 8. CB-CNN model Loss for 50 epochs

10 experiments were conducted where 100, 200, and 300. Like this the multiple of 100 images are given as input for the clustering. It is possible to determine the error that the model being given accomplishes by using the Root Mean Square Error, or RMSE. When evaluating the error between two continuously connected metrics, the RMSE method makes it easier. What the models examine are the accuracy and inaccuracy levels of face identification. Equation 4 is used to determine the inaccuracy after these data have been assessed.

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n}\left(x_{1,i} - x_{2,i}\right)^2}{n}} \qquad (4)$$

Where,

∑ - Summary

(x1 – x2)2 – Disparities Squared for the total of the differences

N - The Count of Trails

The obtained RMSE for the recorded experiment is shown in below table 1 and the respective graph is shown in Figure 9 and 10. The average MAE is obtained for the conducted experiment and RMSE of 2.32.

The mean absolute error (MAE) is a statistical metric that is used to determine the amount of error that exists between paired observations that reflect the same phenomena. Examples of Y against X include comparisons of predicted versus observed and subsequent time versus initial time, as well as comparisons of one technique of measurement versus an alternate approach of measurement.

The obtained RMSE is compared with that of [25] A complete integrated system for multi-view AD progression prediction using cognitive score prediction and 3D MRI prediction was proposed in this research. Thus, an individual's disease severity can be anticipated and the future informative MRI shown voxel-wise.

Table 1. RMSE data

Experiment Sr. No.	No of Images	Observed Properly Clustered	MAE
1	100	92	8
2	200	198	2
3	300	296	4
4	400	400	0
5	500	496	4
6	600	598	2
7	700	690	10
8	800	798	2
9	900	888	12
10	1000	990	10

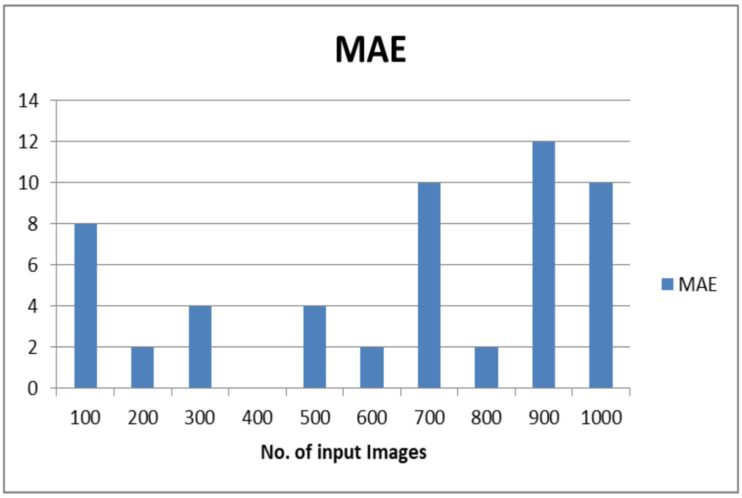

Figure 9. MAE for different trails

Table 2. The developed methodology was compared to other studies for predicting RMSE score

Method	**RMSE**
GAN [25]	2.804
CSL [26]	3.0705
cFSGL [27]	3.184
APANN [28]	3.0125
SMTL [29]	2.48
CB-CNN (Proposed Approach)	2.32

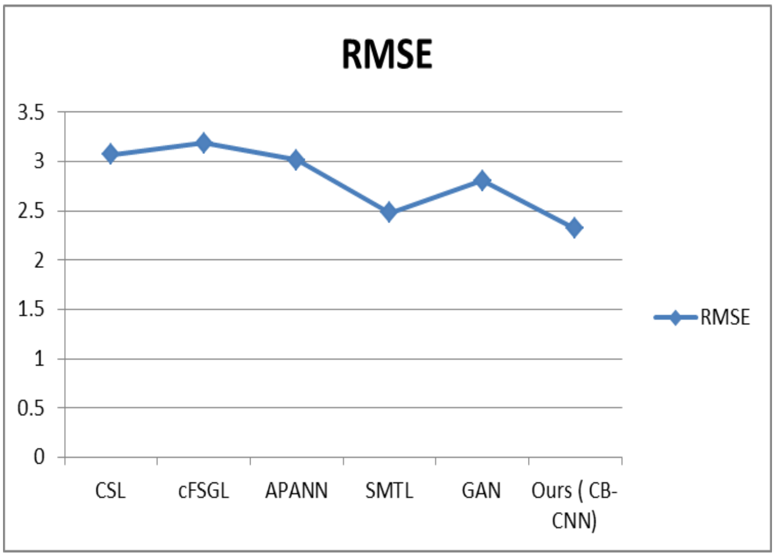

Figure 10. RMSE Comparison of CB-CNN ensemble approach with others

The regression and GAN models were combined and trained concurrently. The integrated framework also included the 3D ROI mask and ROI loss to harness expert disease progression knowledge. The model's ADNI dataset trials showed that the predicted MRI may greatly improve cognitive score prediction, while ROI removal can improve both MRI prediction and cognitive score prediction.

In [25], the root mean square error (RMSE) of a GAN-based model is compared with a wide variety of alternative approaches, which are detailed in Table 2 below, in addition to our way of assembling a CB-CNN model. By the information presented in [25], the graph in Figure 6 and Table 2 both demonstrate that our model of ensemble method produces the lowest RMSE of 2.32, making it the best of the others. For multi-view image clustering of Alzheimer's disease, this demonstrates that the findings produced indicate the efficiency of combining a deep learning model with the Inverse matrix factorization procedure.

To accurately forecast patients' cognitive scores at different time points and find the most predictive biomarkers, the CSL technique in [26] suggested a new multi-task learning formulation that takes into account a correlation-aware sparse and low-rank limited regularization. The suggested non-smooth convex objective formulation is further optimized using an effective iterative technique. [27] The cFSGL approach is used to choose biomarkers that are indicative of the course of Alzheimer's disease based on cognitive scores. By seeing the prediction at each time point as a separate task, authors can reframe the prediction problem as a multi-task regression problem. Additionally, the author presents two new multi-task learning formulations. In [28], APANN used a new model of anatomically partitioned artificial neural networks (APANN) to forecast clinical scores on an individual basis. Hippocampal segmentations and cortical thickness, two structural MRI variables associated with neurodegeneration processes in Alzheimer's disease, were inputted into the model. Using ADNI1 and ADNI2 cohorts as well as ADNI1 + 2, the author conducted three trials to assess the APANN model's performance using ten rounds of 10-fold cross-validation. To forecast patients' clinical scores at different future time points, SMTL in [29] suggests a combined learning approach that makes use of numerous longitudinal prediction models. In this study, the author investigates three significant connections between training sets, characteristics, and clinical ratings.

5. Conclusion and Future Scope

The research paper thoroughly explains the techniques used to achieve multi-view cluster formation for Alzheimer's patients. This research uses a vast collection of Alzheimer's images as input to generate the data for the multi-view clustering mechanism. With a deep understanding of network architecture, the collected dataset with a wide range of images can greatly enhance the clustering process, leading to improved diagnostic capabilities for this disorder and ultimately enhancing the lifestyle of individuals. The Alzheimer's image dataset is fed to the system at the beginning of the process of the methodology, and the image pair selection is performed. Once the image pairs are selected, they are used to generate the data matrices for the feature estimation module. The features are then efficiently divided into the following two modules: training weights and fusion. After the trained weights and fusion of the parameter estimations, they are passed on to the next component to create a feature list. The feature list is classified using the decision tree subsystem, which effectively provides the user with multi-view clusters as the output. This methodology has undergone extensive testing, which has a very important contribution in determining the performance metrics of the proposed multi-view clustering approach. The proposed model achieved an impressive RMSE of 2.32 which stands out as one of the good results among CSL method which is 3.0705, cFSGL having RMSE of 3.184, APANN with RMSE of 3.0125, SMTL with RMSE of 2.48 and with GAN mentioned in with RMSE of 2.804.

Designed model is having some limitations such as model is unable to learn transformed images during the run time without augmentation. The number of samples for training purposes should be more like more than 8 to 10 thousand. Lack of generating adversial neural network also a prominent factor to achieve more accuracy.

In future versions of our work, we will explore the advantages of using different kernel functions to better combine multimodal data. This model can be enhanced by exploring the integration of various imaging techniques to expand the range of our diagnostic capabilities. In addition, incorporating other advanced deep learning architectures and utilizing transfer learning techniques can significantly enhance the model's performance metrics.

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Authors Contribution Statement

Sneha Nimbre: Conceptualization, Original draft preparation. Priyanka Paygude: Conceptualization, Original draft preparation. Amol Dhumane: Methodology, Software. Snehal Rathi: Visualization, Investigation, Supervision. Vijaykumar Bidve: Visualization, Investigation, Supervision. All authors have read and approved the final manuscript

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Yes

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