UtilitasMathematica

ISSN0315-3681Volume122,2025

Preliminary analysis of deep learning models for predicting Alzheimer’s disease progression

Naga Padmaja Indeti*
Sri Padmavati Mahila Visvavidyalayam. Department of Computer Science, Research scholar, Tirupati, A.P, India.

K.Usha Rani
Sri Padmavati Mahila Visvavidyalayam, Department of Computer Science, Professor & HoD, Tirupati, A.P, India.

Corresponding author:nagapadmaja.indeti@gmail.com

Abstract

Correct diagnosis of Alzheimer's disease (AD) is crucial to patient care, particularly in the early stages of the illness, as risk knowledge enables patients to take preventative actions before irreversible brain damage develops. The majority of machine detection techniques are restricted by congenital observations, despite the fact that numerous recent research have employed computers to diagnose AD. Early diagnosis of AD is possible , however it cannot be predicted because prediction is only useful up until the point at which the disease starts to show symptoms. Deep Learning (DL) has emerged as a popular method for AD early diagnosis. Recurrent neural networks, of which Convalutional Bidirectional long short-term memory (Conv-BiLSTM) is a particular variety, may be able to relate prior knowledge to the current task. We suggest a prediction model based on Convalutional Bidirectional long short-term memory (Conv-BiLSTM after observing that a patient's temporal data may be useful for forecasting the course of their illness. In order to representthe temporal relationship between characteristics and thesubsequent stage of Alzheimer's disease, an Convalutional Bidirectional long short-term memory (Conv-BiLSTM) network with fully linked layer and activation layers is constructed.The Results indicate that our model performs better than the majority of the current models.

Keywords: Conv-BiLSTM, Alzheimer's, Deep Learning

1Introduction

These objectives align with improving early detection, diagnosis, and treatment planning for Alzheimer's disease Accurate Prediction of Alzheimer's Progression: The primary objective is to forecast the development of Alzheimer's disease (AD) by leveraging a unique multi-view model that processes varied medical data sources to ensure early intervention and treatment. Integrationof Multiple Modalities: The model aims to combine diverse data types, such as MRI scans, PET images, and clinical data, to provide a comprehensive understanding of disease patterns, enhancing the accuracy and depth of the predictions.

Alzheimer's disease is a major problem in the healthcare faced by elderly people. This disease is classified into Non- demented, Mild-Demented, Moderate-demented, and very mild-demented.

Alzheimer's disease progression prediction algorithms have traditionally depended on single-view data, restricting their capacity to capture the complexities of the disease's stages. Multi-view data provides a more complete depiction, but integrating and exploiting it efficiently is not remain easy. The research presents a Consensus Multi-View Clustering (CMC) model based on nonnegative matrix factorization (NMF), which is intended to incorporate different perspectives of medical data, such as MRI scans, to improve AD progression prediction. This methodology enhances prediction accuracy by automatically constructing a consensus representation across perspectives, eliminating the need for manual parameter settings [1].Traditional cancer subtype identification methods frequently rely on single-view clustering methods that analyse only one type of data, which can overlook the intricate correlations found in multi-omic datasets. As cancer data are increasingly obtained from a variety of biological sources, combining different perspectives can lead to a more sophisticated knowledge of patient subgroups.This study introduces Parea, a multi-view hierarchical ensemble clustering method intended to improve cancer subtype detection. Parea achieves higher performance in detecting cancer subtypes across distinct datasets by employing several clustering algorithms suited to the specific characteristics of each data view. This improves patient stratification and guides precision medicine activities [2]. Traditional breast cancer detection technologies, such as thermography and mammography, frequently use single-view images (frontal, left, and right). These technologies are expensive, expose patients to radiation, and require clinicians to interpret results manually. Deep transfer learning models, such as VGG16, have shown the capacity to automate this procedure. This work presents a novel approach for concatenating multi-view thermal breast pictures (left, frontal, and right) into a more comprehensive image. This enhances detection accuracy by capturing global breast patterns and increasing the model's capacity to recognize cancer-related asymmetries. Compared to other deep learning models (e.g., ResNet50V2, InceptionV3), the VGG16 model in this study achieved the highest testing accuracy of 99%, significantly improving breast cancer detection from thermal images[3].Traditional breast cancer diagnosis methods, such as single-view deep learning models, process mammograms individually, frequently missing connections between distinct views (craniocaudal and mediolateral oblique). This results in inferior cancer detection accuracy, as radiologists rely on numerous views to make more precise diagnoses. There search offers a multi-view hyper complex learning model that uses hyper complex algebra to capture global and local connections across several mammography views, similar to how radiologists analyse pictures. This strategy enhances breast cancer classification accuracy over real-valued neural networks while reducing model parameters [4].Alzheimer's disease (AD) is difficult to diagnose, especially in its early stages. Traditional machine learning algorithms have helped diagnose Alzheimer's disease using neuro imaging, but they frequently require human feature extraction, which limits their scalability and accuracy. The research examines deep learning techniques for automated feature extraction, specifically convolutional neural networks (CNNs), and their capacity to recognise subtle patterns in MRI data. The review discusses how deep learning has improved the early identification of Alzheimer's disease, leading to better treatment planning[5].Cancer subtypes are required for personalized treatment, however, they are difficult to detect due to the complexity and variety of cancer data. Traditional clustering approaches focus on single data modalities while ignoring linkages between various viewpoints (e.g., genomes, transcriptomics). The research introduces Deep Multi-view Contrastive Learning (DMCL), which combines reconstruction, contrastive, and clustering losses into a single model to integrate multi-omics data better and identify cancer subtypes. This methodology outperforms previous algorithms on numerous datasets and provides therapeutic insights for certain tumours,

Such as liver cancer[6]. Traditional methods for predicting overall survival(OS) in cancer struggle to handle multi view clinical data, resulting in overfitting and poor prediction accuracy. These data frequently come from a variety of sources, including pathology diagnoses and patient health indicators, necessitating the use of models to identify both useful and duplicate information. To overcome these issues, the authors offer a multiview deep forest (MVDF) model that combines several kernels and integrated learning algorithms. This method enables better processing of complicated, high-dimensional clinical data. The model also incorporates a pruning method to minimise noise and outliers, therefore boosting there liability of OS predictions[7].Breast cancer classification has generally relied on single- omics data and traditional machine learning methods, which do not account for the intricate biological interactions between several types of omics data, such as gene expression, DNA methylation, and copy number variation. To address this restriction, there search introduces a multi-view graph neural network (MVGNN) that combines multi-omics data to improve breast cancer differentiation and subtype classification. Using graph convolutional networks (GCN) and attention processes, the model efficiently preserves biological semantics and geometric structures, resulting in higher cancer classification performance compared to conventional methods [8].With developments in high-throughput technology, the capacity to collect massive multi-omic datasets has opened up new paths for cancer research. However, present clustering approaches frequently fail to integrate these disparate datasets, making it difficult to identify meaningful connections. This paper summarises several multi-omic clustering techniques and presents a systematic benchmarking methodology based on cancer data from The Cancer Genome Atlas (TCGA). The results emphasise the strengths and disadvantages of single-omic versus multi-omic clustering methodologies and provide insights into the selection of clustering strategies that might maximise the information acquired from complicated datasets, hence boosting our understanding of cancer kinds[9].Detecting lung cancer with a single imaging modality (e.g., CT scans) is frequently insufficient to capture both the morphological and functional elements of lung disease. Traditional single-view models have issues with false positives and sensitivity, particularly in small nodules. In this idea, multi view image registration and fusion are used to combine several CT scans for better detection. This method uses deep learning techniques, specifically a ResNet-18 convolutional neural network classifier, to increase the accuracy of diagnosing and staging lung cancer. Using multi view pictures and advanced registration algorithms, this system achieves 98.2% detection accuracy and 96.4% sensitivity, greatly surpassing existing methods. The model demonstrates the potential for practical applications, minimising false positives and supporting early-stage lung cancer identification. [10].Breast cancer diagnosis has previously relied on single-view mammograms, which limit the detection of abnormalities due to a lack of cross-view correlation. The suggested Multi-View Feature Fusion (MVFF) model uses four mammography images (CC and MLO for each breast), which mimics how doctors analyse numerous perspectives to detect malignancy. The approach incorporates information retrieved using convolutional neural networks (CNNs) across all views and considerably increases classification accuracy, with an AUC of 0.932 for mass detection and calcification, outperforming single-view methods[11].Alzheimer's disease (AD) develops over time, and early detection is critical for mitigating its symptoms. Most current models focus on categorising the disease's current stage rather than predicting its progression. This research presents a long short-term memory (LSTM) model for predicting the progression of Alzheimer's disease using longitudinal time series data, such as MRI scans. The model contains temporal correlations between clinical variables and future illness stages, delivering a considerable boostin prediction accuracy over existing techniques [12].

In retinoblastoma, precise segmentation of ocular structures and tumour tissues is essential for personalised therapy planning. Traditional segmentation approaches, while successful, either require time-consuming human delineation or are constrained by their reliance on sequential processing pipelines. This paper introduces a unique multi-view convolutional neural network (MV-CNN) or automating the segmentation of ocular structures and tumours from MRI data.The MV-CNN achieves great volumetric and spatial accuracy by combining information from several image sequences into a single framework, exceeding traditional segmentation algorithms. This breakthrough not only accelerates the segmentation procedure but also has the potential for improved diagnostic capabilities in retinoblastoma treatment [13].Alzheimer's disease (AD) diagnosis entails analysing complicated data such as MRI, PET, CSF, and SNPs to identify biomarkers and make preliminary judgments. Current single-modality approaches are limited in their capacity to successfully combine these many data kinds. The study describes Tensor Kernel Learning (TKL), which combines several modalities using CP/PARAFAC tensor decomposition and kernel learning. TKL combines information from several modalities to improve AD classification, achieving greater accuracy(91.31%forCNvs.AD) than individual data modalities [14].

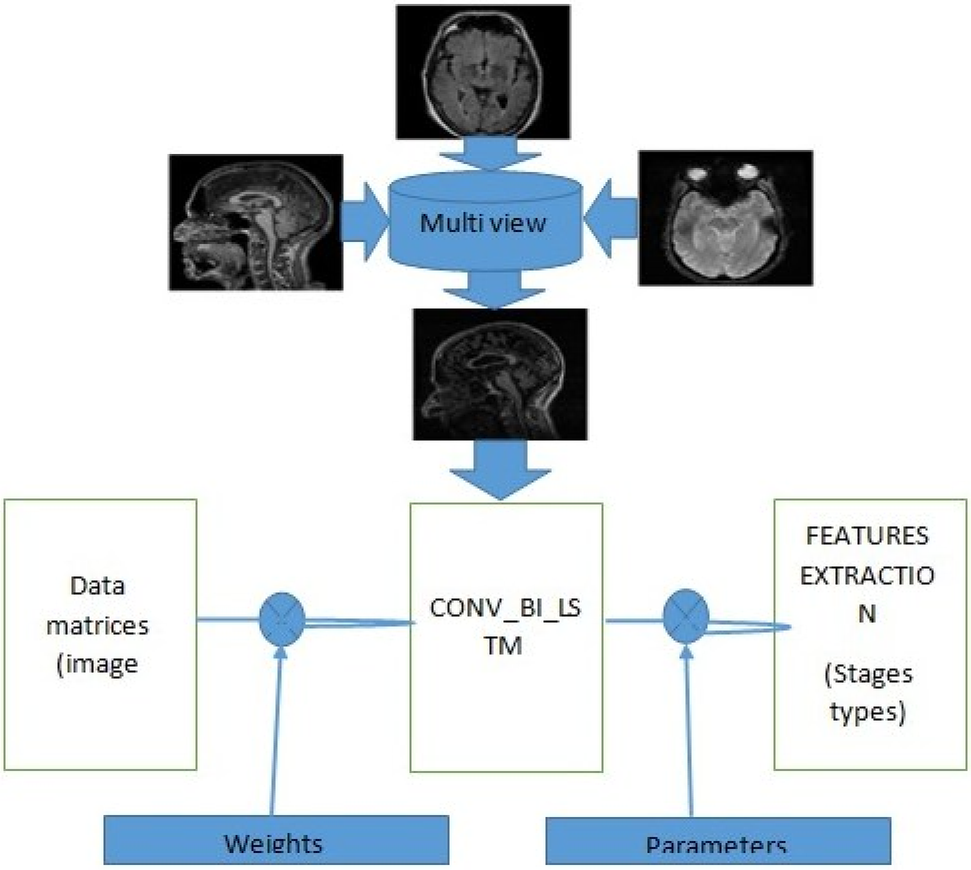


Fig.1. General framework for our proposed model Conv-BiLSTM

With multi-view data, we propose an CNN-based model called ConV_Bi_LSTM that can integrate Bi_LSTM features in multiple views and automatically learn a singular matrix to help with clustering. This model can capture important information among multiple views and learn the neighborhood relationship between samples. Fig. 1 illustrates the ConV_Bi_LSTM framework, which can fuse more features from various perspectives, particularly for multi-view MRI datasets that have small quantity and small difference characteristics. This allows for significantly better clustering results than those obtained from a single view.

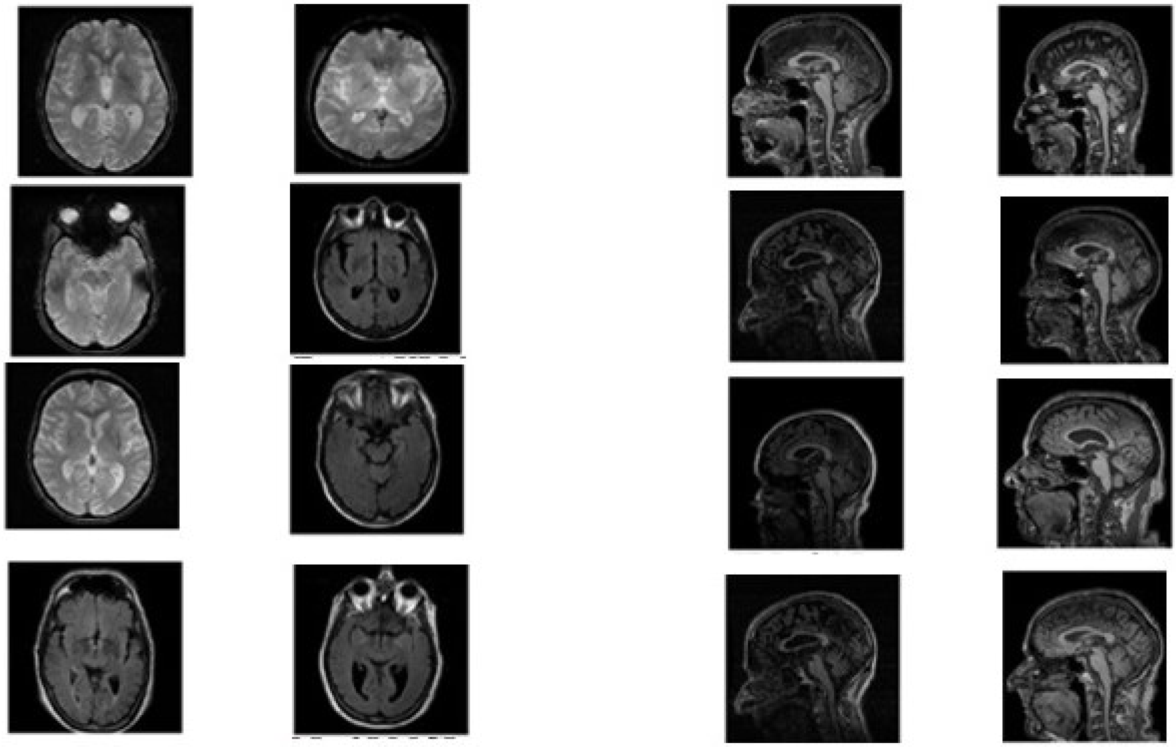


Fig.2(a) Four images of the two subjects for AXI MRI view. Fig.2(b) Four images of the two subjects with SAG MRI view.

Dataset Description

The total number of samples is 40 and 50 respectively ,the total MRI number in MRI2 and MRI3 for each view1 and view2. AD samples is represented with two views (AXI view and SAG view). Some examples of the AXI and SAG MRI data of the two subjects from MRI2 and MRI3 database are shown in Fig.2(a) and Fig.2(b) .

Methodology: The suggested Conv-Bi-LSTM model is presented in this section, along with an explanation of each component's specifics. The objective function and the parameter learning technique are finally presented.

CONv-Bi-LSTM Model

Convolutional neural network

It was Le Cunetal, that first proposed CNN. It is able to extract spatial data relationships. CNNs are extensively employed across diverse domains and exhibit exceptional efficacy in assignments including image identification, facial recognition, and handwritten digit identification. Convolutional and pooling layers make up the majority of CNN.CNNs are primarily distinguished by pooling, weight sharing, and local vision sharing. The traffic speed-based congestion indicator developed in this work can accurately reflect the condition of the road over time, and the CNN is highly good at handling spatial difficulties. Additionally, the congestion indicator's properties align with weight sharing and local vision sharing. Only the surrounding data needs to be analyzed by each neuron; this makes employing a CNN to extract spatial information efficient.

Bidirectional long short-term memory

Two unidirectional LSTMs placed on top of one another make up the construction of a bidirectional LSTM (Fig. 3). This structure states that the time series prior to and following the prediction time are included in the BiLSTM input. Two LSTMs with opposing directions receive the input sequence at each time slot t, and they jointly determine the output.

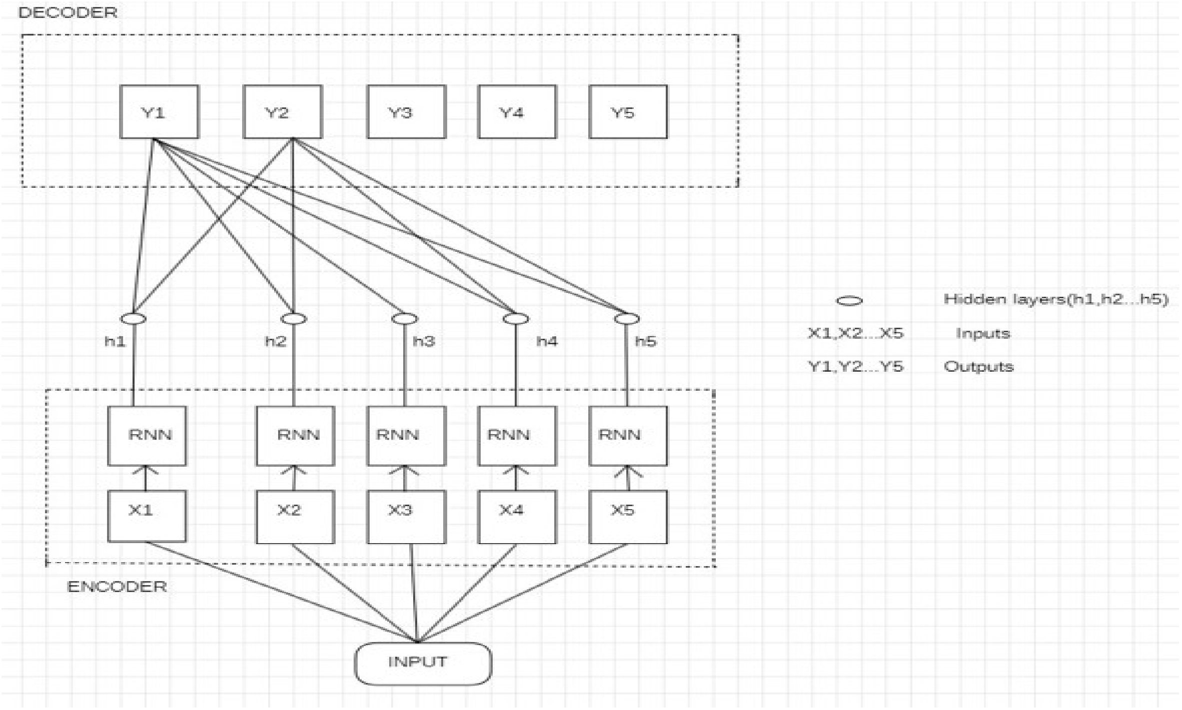


Fig.3(a)Structure of Basic RNN algorithm

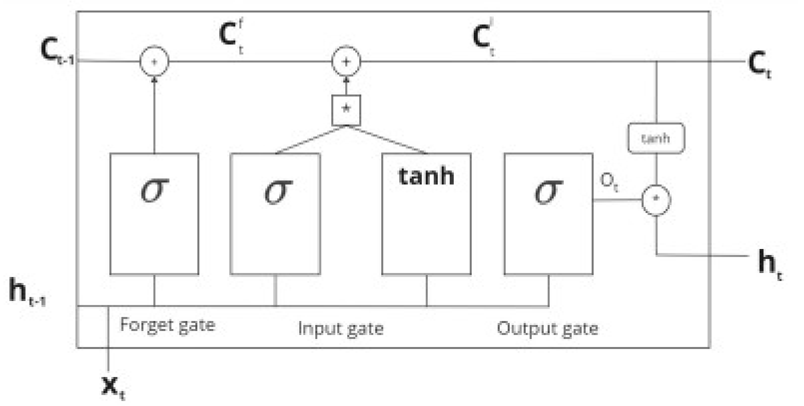


Fig.3(b)Structure of Conv–Bi-LSTM algorithm

Convolutional neural network–Bidirectional long short term memory

This is because the CNN was originally used to process pictures. To extract spatial features more accurately, we folded the data into a more efficient form. After that, the data are unfolded as the input of the BiLSTM network, because its input form is a time series. Finally AD features and periodicity features are concentrated to predict traffic congestion. The structure of the proposed Conv-BiLSTM network is shown in Fig. 3

$\delta_t = \sigma\left[(w_{fh} * h_{t-1}) + (w_{fx} * x_t) + b_f\right]$

$$C_t = C_{t-1} * f_t \rightarrow 1$$

$$i_t = \sigma\left[(w_{ih} * h_{t-1}) + (w_{ix} * x_t) + b_i\right]$$

$$g_t = \text{tanhtanh}\left[(w_{gh} * h_{t-1}) + (w_{gx} * x_t) + b_g\right]$$

$$C_t = i_t * g_t \rightarrow 2$$

$$o_t = \sigma\left[(w_{oh} * h_{t-1}) + (w_{ox} * x_t) + b_o\right]$$

$$h_t = \text{tanhtanh}(C_t) * o_t \rightarrow 3$$

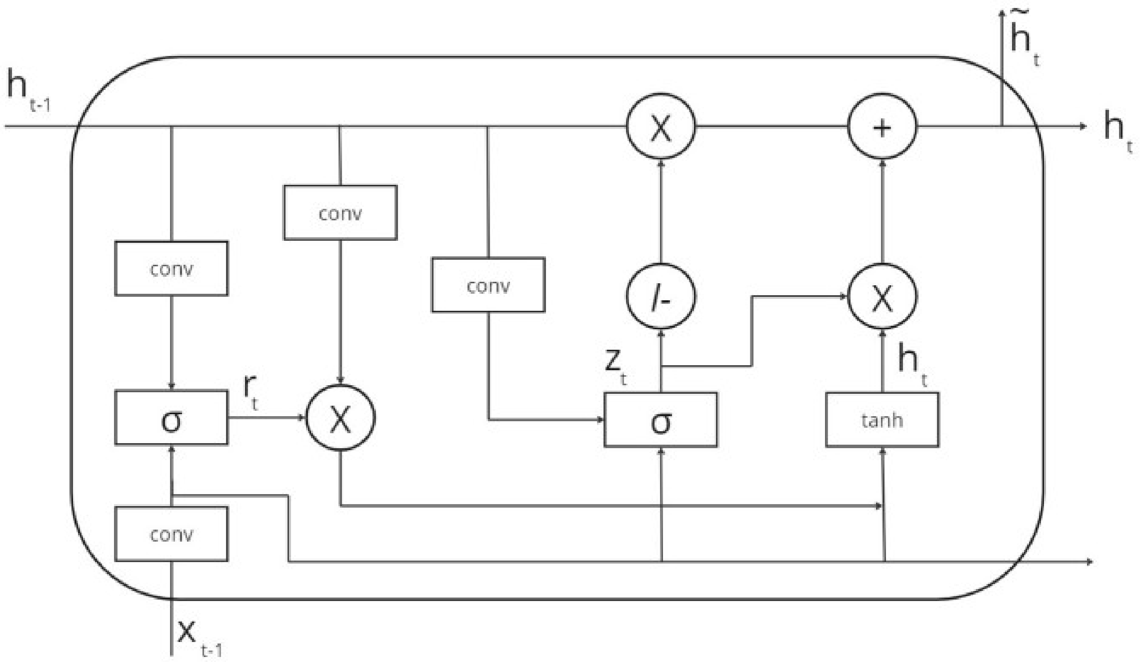


Fig.3(c)Structure of GRU algorithm

$$r_t = \sum_{\square}^{\square} \square \left(Conv(X_{t-1}) + Conv(h_{t-1}) \right)$$

$$Z_{t=¿\sum_{\square}^{\square} \square (Conv(X_{t-1})+Conv(h_{t-1}))¿}$$

$\tilde{h}_t = tanh(Conv(X_{t\ -1}) + r_t * Conv(h_{t-1}\ )$

$h_t = (1 - Z)_{t} * \ \tilde{h}_t + ¿ z_t * h_{t1\,-}$

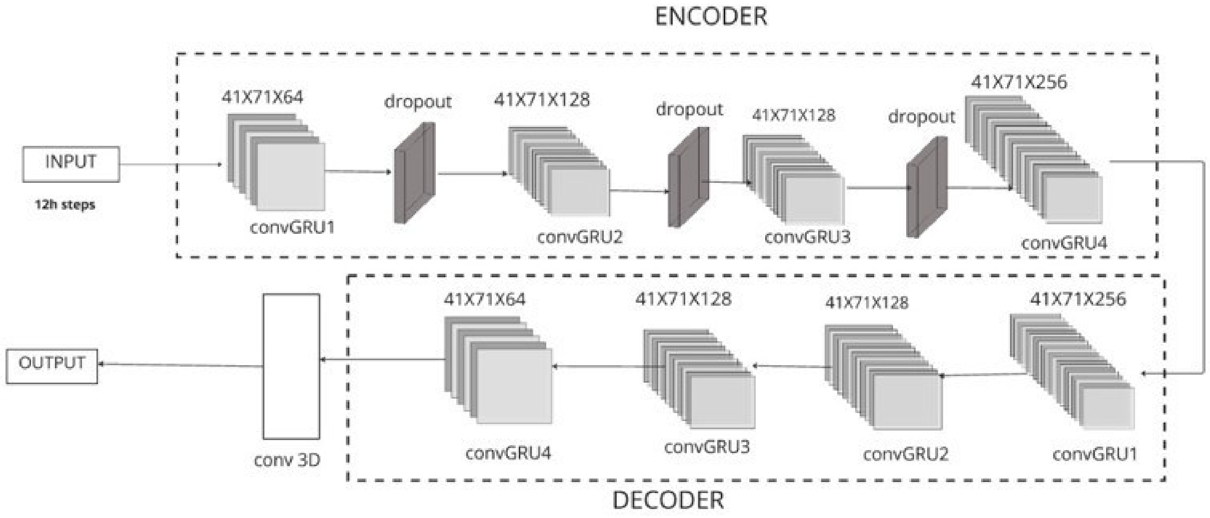
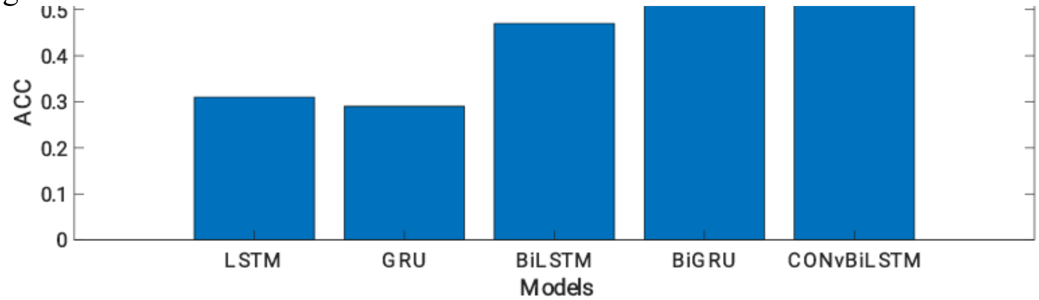


Fig.3(d) Structure of Conv–GRU algorithm

Results and Discussions

Table1and Table2 displays the individual performance results of each approach for the MRI2 and MRI3 datasets in terms of ACC, NMI, and F1. With the TWO brain MRI images, our Conv-BiLSTM gets the best ACC and NMI values for predicting the progression of AD in the MRI2 data set. The best ACC value of Conv-BiLSTM in terms of ACC performance is 44.17%, which is greater than the other superior approach. The performance of Conv-BiLSTM in terms of F1 and ARI is not particularly remarkable, according to the ADN3 dataset. Conv-BiLSTM's F1value is 28.25%, which is less than the optimal F1value.Utilization of Conv-BiLSTM The study seeks to enhance feature extraction by utilizing Conv-BiLSTM, which focuses on the most relevant portions of the medical data. This results in more precise identification of significant patterns in the progression of Alzheimer's.



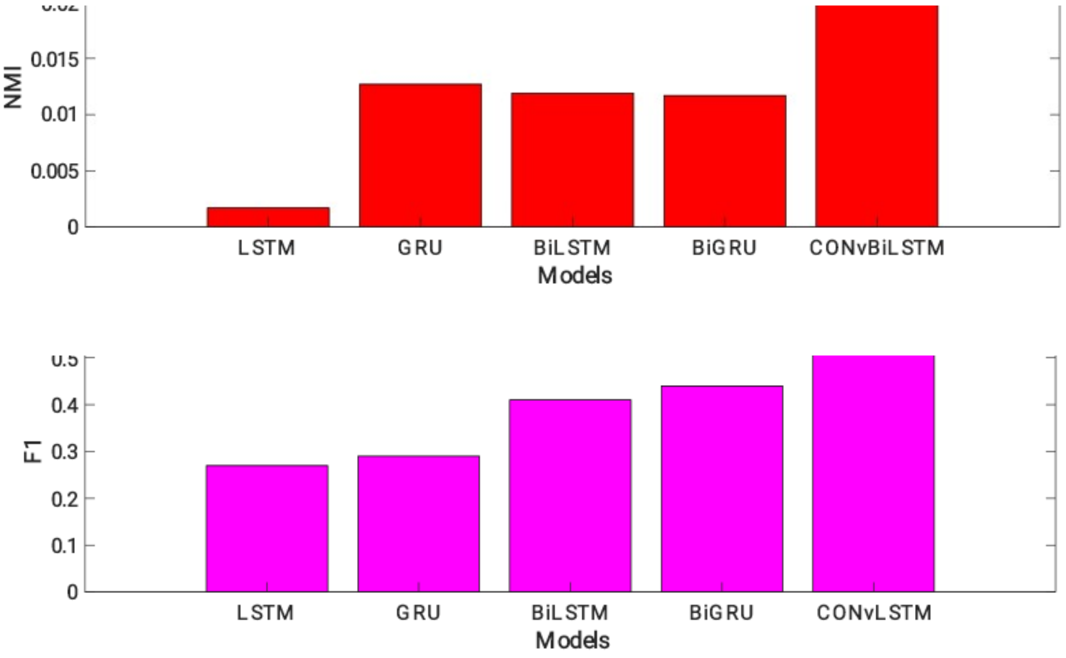


Fig.4.Each model performance's comparative findings using the top views on the MRI dataset

Our CONV-Bi-LSTM model's NMI metric performance is not particularly optimistic for the MRI2 and MRI3 datasets. The explanation could be that there are two states of AD, and that most of the time there is little difference or separation between them. Thus, it could be necessary to refine our approach by illustrating and specifying more particular characteristics for every AD state. Furthermore, Table 1's NMI and ACC scores for the two data sets are indeed quite low. The primary cause is that machine learning techniques face certain challenges due to the extremely sparse characteristics of medical MRI image data and the slight differences between several classes of original sample MRI data.

Table1.Performances of each method on the two sets of view1(MRI1)

Method	ACC	NMI	F1
LSTM	0.31	0.0017	0.27
GRU	0.29	0.0127	0.29
BI-LSTM	0.47	0.0119	0.41
BI-GRU	0.51	0.0117	0.44
CONV-BI-LSTM	0.54	0.0217	0.57

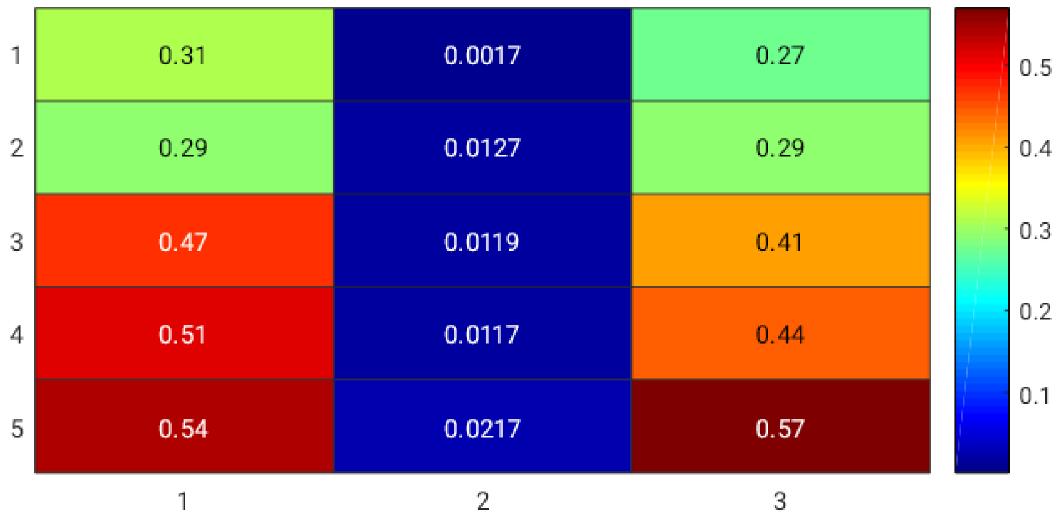


Fig.5(a)Visualization results of the all models effect with the two views on MRI2 datasets

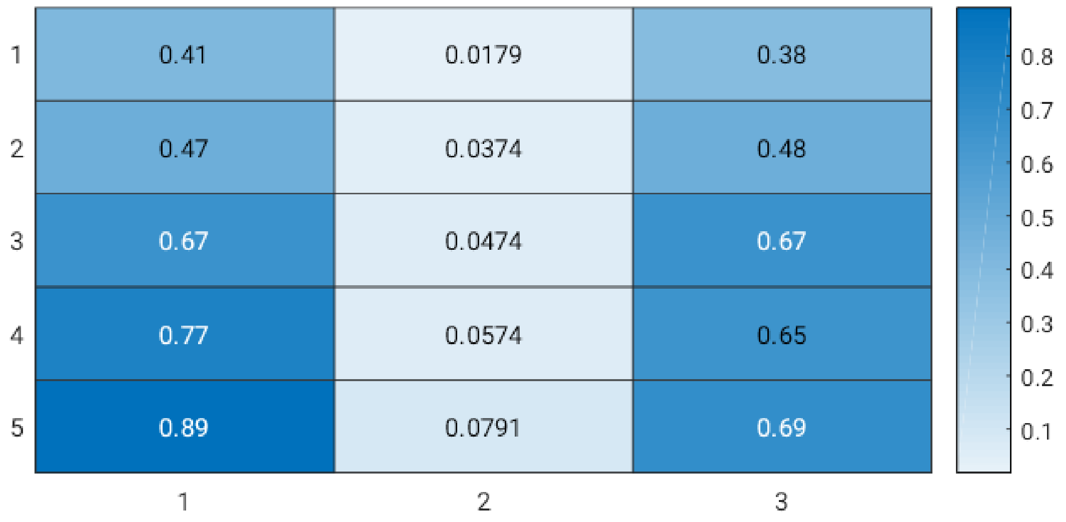


Fig.5(b)Visualization results of the all models effect with the two views on MRI datasets

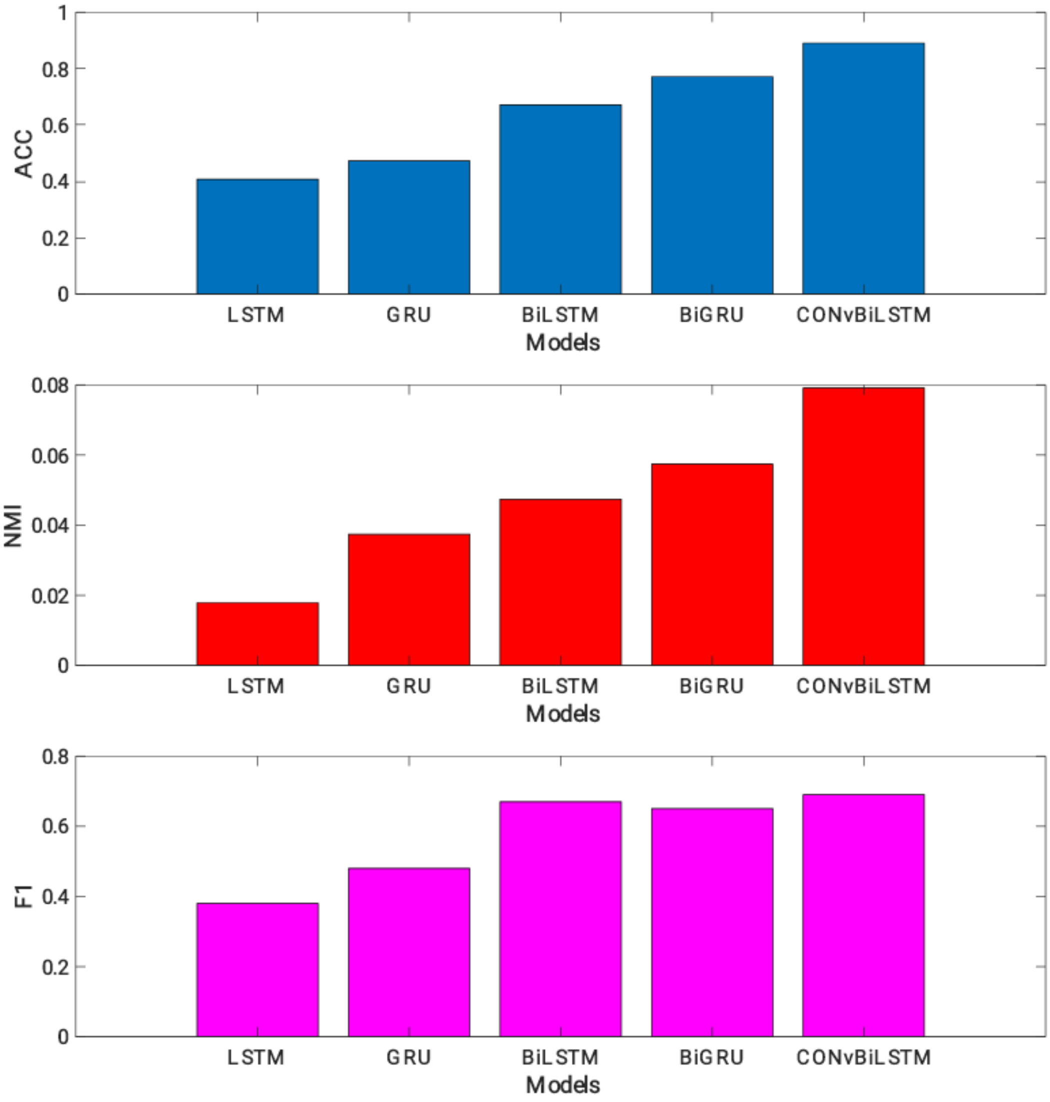


Fig.6.Each model performance's comparative findings using the top views on the MRI3 dataset

Table 2. Performances of each method on the two sets ofview2 (MRI3)

Method	ACC	NMI	F1
LSTM	0.41	0.0179	0.38
GRU	0.47	0.0374	0.48
BI-LSTM	0.67	0.0474	0.65
BI-GRU	0.77	0.0574	0.67
CONV-BI-LSTM	0.89	0.0791	0.69

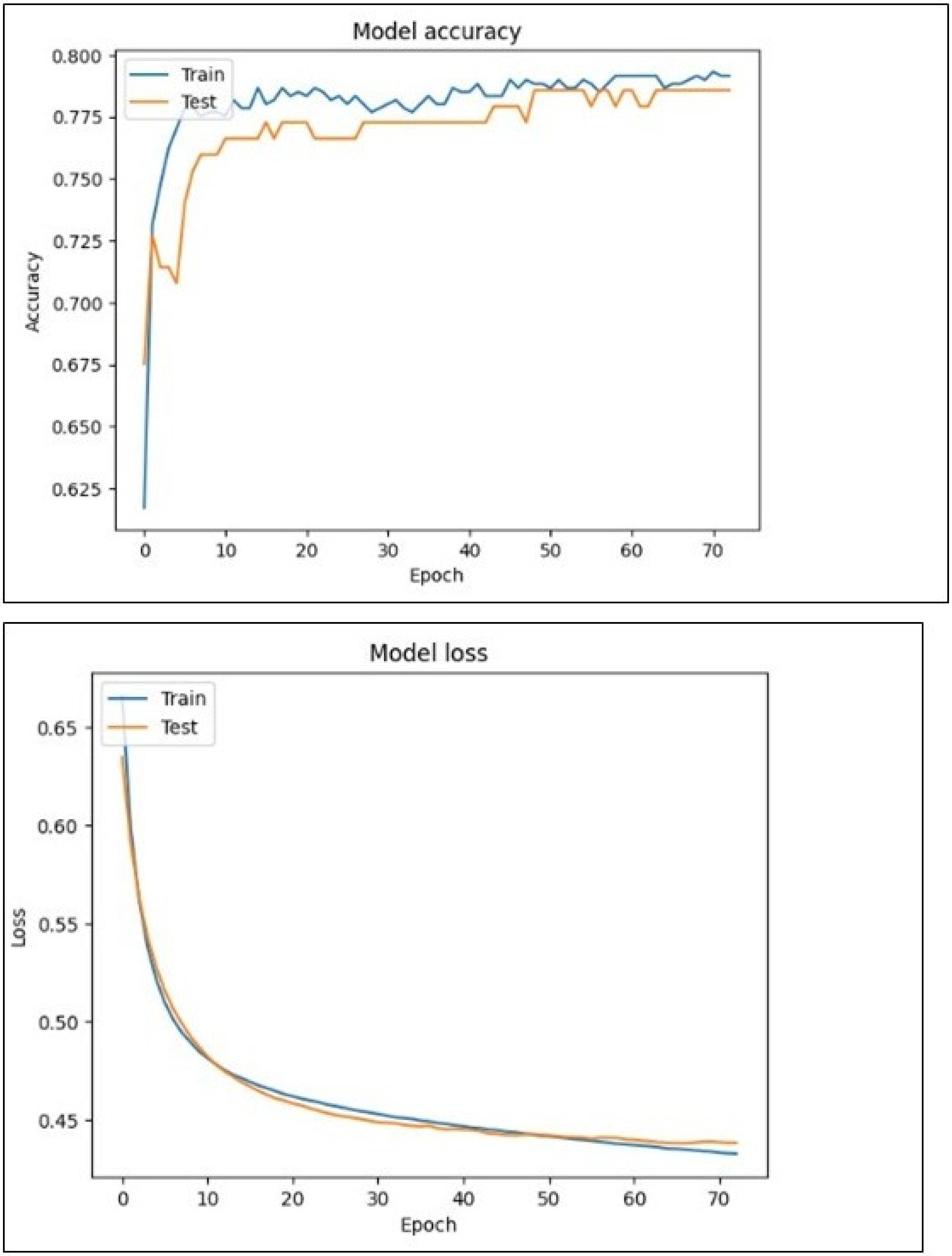


Fig 7. (a) The latent representation visualization on the MRI2 and MRI3 dataset.

Table 1 and 2 represents the ACC, NMI and F1 of deep learning models with model scaling and without model scaling. Each model showed different level of scores. An important observation is that, with model scaling, every model showed improvedF1 score when compared with the different model without exploiting model scaling. The NMI of BI-GRU is 0.0574 and with CONV-BI-LSTM model is 0.0791 respectively. The ACC of LSTM is 0.41and within Conv-BI-LSTM model scaling is 0.89 respectively. There is an increase in the accuracy when the number of epochs is increased in each model. Similarly, there is a decrease in loss when the number of epochs is increased in each model. These two observations and the final accuracy and loss at the last epoch reveal that the deep learning models show acceptable performance in AD progression.

Conclusions

In order to classify the various developmental stages of AD, we presented a Conv-BiLSTM Multi-View model in this study, which is based on CNN. In this work, we experimented using MRI data. The experimental results show that our suggested Conv-BiLSTM model performs better than the most advanced Bi-LSTM and Bi-GRU techniques. The experimental results demonstrated that our proposed Conv-BiLSTM model outperforms the state-of-the-art deep learning models LSTM, GRU, BI-LSTM and BI-GRU methods. The proposed model outer performance than the LSTM,GRU,BI-LSTM and BI-GRU methods

References

[1] Xiaobo Zhang, YanYang, TianruiLi, YilingZhang, HaoWang, HamidoFujita, CMC:A consensus multi-view clustering model for predicting Alzheimer’s disease progression, Computer Methods and Programs in Biomedicine, Volume 199, 2021, 105895, ISSN 0169-2607.

[2] Bastian Pfeifer, Marcus D. Bloice, Michael G. Schimek, Parea: Multi-view ensemble clustering for cancer subtype discovery, Journal of Biomedical Informatics, Volume 143, 2023, 104406, ISSN 1532-0464.

[3] Tiwari, D., Dixit, M., Gupta, K. (2021). Deep multi-view breast cancer detection: A multi-view concatenated infrared thermal images based breast cancer detection system using deep transfer learning. Traitementdu Signal, Vol. 38, No. 6, pp. 1699-1711.

[4] Eleonora Lopez, Eleonora Grassucci, Martina Valleriani, Danilo Comminiello, Multi-View Hypercomplex Learning for Breast Cancer Screening, Computer Vision and Pattern Recognition(cs.CV),Submitted on12Apr 2022 (v1), last revised 4 Mar 2024 (this version, v3)

[5] S. Al-Shoukry, T. H. Rassem and N. M. Makbol, "Alzheimer’s Diseases Detection by Using Deep Learning Algorithms: A Mini-Review," in IEEE Access, vol. 8, pp. 77131-77141, 2020.

[6] WenlanChen, HongWang, ChengLiang, Deep multi-view contrastive learning for cancer subtype identification, Briefings in Bioinformatics, Volume 24, Issue 5, September 2023, bbad282.

[7] Li, Qiucen, Du, Zedong, Chen, Zhikui, Huang, Xiaodi, Li, Qiu, Multiview Deep Forest for Overall Survival Prediction in Cancer, Computational and Mathematical Methods in Medicine, 2023, 7931321, 12 pages, 2023.

[8] Ren Yanjiao , Gao Yimeng , Du Wei , Qiao Weibo , Li Wei , Yang Qianqian , Liang Yanchun , Li Gaoyang, Classifying breast cancer using multi-view graph neural network based on multi-omics data, Frontiers in Genetics, Volume 15, 2024.

[9] Nimrod Rappoport, Ron Shamir, Multi-omic and multi-view clustering algorithms: review and cancer benchmark, Nucleic Acids Research, Volume 46, Issue 20, 16 November 2018, Pages 10546–10562.

[10] Nazir, Imran, Haq, Ihsan ul, AlQahtani, Salman A., Jadoon, Muhammad Mohsin, Dahshan, Mostafa, Machine Learning-Based Lung Cancer Detection Using Multiview Image Registration and Fusion, Journal of Sensors, 2023, 6683438, 19 pages, 2023.

[11] H. Nasir Khan, A. R. Shahid, B. Raza, A. H. Dar and H. Alquhayz, "Multi-View Feature Fusion Based Four Views Model for Mammogram Classification Using Convolutional Neural Network,"inIEEEAccess,vol.7,pp. 165724-165733, 2019, doi: 10.1109/ACCESS.2019.2953318.

[12] X.Hongetal.,"Predicting Alzheimer's Disease Using LSTM," in IEEE Access, vol.7,pp.80893-80901,2019, doi: 10.1109/ACCESS.2019.2919385.

[13] Strijbis, V.I.J., de Bloeme, C.M., Jansen, R.W. et al. Multi-view convolutional neural networks for automated ocular structure and tumour segmentation in retinoblastoma. Sci Rep 11, 14590 (2021).

[14] VuDuyThanh, ThanhTrungLe,P hamMinhTuan, NguyenLinhTrung, KarimAbed-Meraim, MouloudAdel, Nguyen Viet Dung, Nguyen Thanh Trung, Dinh Doan Long, Oliver Y. Chén, Tensor Kernel Learning for Classification of Alzheimer's Conditions using Multimodal Data, July 22, 2024.