Neuroscience Research xxx (xxxx) xxx

Contents lists available at ScienceDirect

Neuroscience Research

journal homepage: www.sciencedirect.com/journal/neuroscience-research

Determination of affected brain regions at various stages of Alzheimer's disease

Fayyaz Ahmad [a], Muqaddas Javed [a,*], Muhammad Athar [a,b], Samra Shahzadi [c]

[a] Departement of Statistics, University of Gujrat, Gujrat, Pakistan
[b] Govt. Zamindar Graduate College, Bhimber Road, Gujrat, Pakistan
[c] Department of Computer Science, University of Gujrat, Gujrat, Pakistan

ARTICLE INFO

Keywords:
Brain regions
Independent component analysis
Mild cognitive impairment
Alzheimer's disease
Deep learning algorithm
Binary classification

ABSTRACT

The objective of study was to explore those brain areas that were affected at each stage during the progression of Alzheimer's disease (AD). Six affected brain areas were explored at mild cognitive impairment, four at first stage and six at each of second and third stage of Alzheimer's disease. The common brain regions among these stages were cuneus, precuneus, calcarine cortex, middle frontal gyrus, superior frontal gyrus, and frontal superior medial gyrus. The fMRI data at the resting state of 18 AD patients who were converted from MCI to stage 3 of Alzheimer's were taken from ADNI public source database. Among these patients, there were ten males and eight females. Independent component analysis was used to explore affected brain regions and an algorithm based on deep learning convolutional neural network was proposed for binary classification among the stages of Alzheimer's disease. The proposed CNN model delivered 94.6 % accuracy for separating stage 1 of Alzheimer's disease from mild cognitive impairment. 96.7 % accuracy was acquired to distinguish stage 2 of Alzheimer's disease from mild cognitive impairment, and stage 3 of Alzheimer's disease was separated from mild cognitive impairment with an accuracy of 97.8 %.

1. Introduction

Alzheimer's is a disease (AD) that is considered to cause dementia. Most of Dementia cases are driven by Alzheimer's disease (Weiming et al., 2018). Dementia is not only a single disease but a general term used for various symptoms of memory loss, cognitive decline, trouble in communication, and many other related brains to perform routine tasks. Alzheimer's disease is said to be an irreversible disease that is caused by damage to the brain cells (Ahmad et al., 2019). This disease was named after Dr. Alois Alzheimer when he noticed a change in brain cells of a woman who died in 1906 due to an unusual mental illness and found that the women brain contained two proteins: beta-amyloid (plaques) and tangle (tau) (Hippius and Neundörfer, 2003). These plaques develop between neurons, and tangles grow inside neurons. The development of these proteins causes a loss in the connection between neurons and thus breaks the transmission of messages that travel from one region to other brain regions. Our brain consists of around a hundred billion neurons, and each neuron is connected with many others to form a communication network (Yadav et al., 2018). Each cluster of neurons has a specific task to perform. Some are responsible for thinking, remembering, vision, listening, smelling, and other charges. Each neuron group is associated with others, and these neurons communicate to execute a task. AD causes shrinkage of various brain regions and networks associated with thinking, memory, planning, and decision making (Sarrafa and Tofigh, 2016).

Scientists believe that AD prevents the communication between neurons, and consequently, their job is not performed as it could be. Blockage in communication happens due to damage in the brain cells (neurons), and as the damage spreads, the neurons in the whole cluster cannot function well, due to which the connected neurons become unable to receive information and execute the task. Hence the destruction of brain cells continues and cannot be reversed or repaired. Alzheimer's disease progresses in three stages where the pre-initial stage, when AD shows some symptoms of memory trouble, is known as mild cognitive impairment (MCI). In the next stage, the disease gets severe, and the patient suffers trouble in performing daily tasks. The studies given in Ahmad and Dar (2018), Ahmad et al. (2019), Davatzikos et al. (2011), Casanova et al. (2011) and Wang et al. (2006) identified some brain regions that are affected by AD. Despite all these studies, to the best of authors' knowledge, no study was designed to investigate the affected

* Corresponding author.
E-mail address: Muqaddas.Javed@uog.edu.pk (M. Javed).

https://doi.org/10.1016/j.neures.2023.01.010
Received 18 July 2022; Received in revised form 13 January 2023; Accepted 18 January 2023
Available online 20 January 2023

brain regions at each stage of AD.

The present study aimed to explore those brain areas that are affected at each stage during the progression of AD, which has not been done so far. Moreover, recent advancements in deep learning that grabbed research scholars are image classification based on Convolutional Neural Networks (CNN). It is a powerful technique that involves convolutional layers to extract different features from data, and further classification and prediction are performed using those extracted features (Albawi et al., 2017). This study will add to the literature by proposing a novel CNN model based on the DL algorithm to perform classification among AD stages based on fMRI data.

2. Materials and methods

2.1. Data description

The present study used fMRI data at the resting state of 18 AD patients who converted from MCI to stage 3 Alzheimer's. The data was obtained from Alzheimer's Disease Neuroimaging Initiative ADNI dataset (adni.loni.usc.edu). Among these patients, there were ten males and eight females. Each patient was given a separate ID as 2036 F, 2045 M, 2055 M, 2073 F, 2123 F, 2130 M, 2133 F, 2155 F, 2180 F, 2191 F, 2195 M, 2208 M, 2225 M, 2264 M, 2274 M, 2301 M, 2304 M and 2373 F where F stands for female and M stands for male. The resting-state fMRI was taken using a Philips scanner; the number of scans per subject were 105; the volume dimensions were X = 64, Y = 64, and Z = 20; the voxel size is X = 4, Y = 4, and Z = 5, 3 T; and repetition time (TR) is 3400.0 ms. The fMRI data were preprocessed on a statistical parametric mapping tool (SPM), usually known as SPM12 in MATLAB. Four steps (reorientation, realignment, normalization, and smoothing) were performed to clean data from preprocessing. Conversion of the functional image according to temple image 'EPI.nii' so that each image can be transformed to a similar position was done with reorientation. Further noise was removed from reoriented data using realignment or generally called motion correction. Such a correction is needed due to the fact that a subject may move his head up or down or tilt from left to right. To remove both types of noise, 'translation' and 'rotation' realignment was mandatory.

Normalization is used to modify the functional images to a standard MNI template brain; this can help compare functional activation across individuals. When normalization was done, all the realigned and normalized images were smoothed. Smoothing averages data points with their neighbors. It blurs sharp edges so that high-frequency signals are suppressed, and low-frequency signals may be enhanced.

2.2. Methodology

The proposed architecture for data analysis consists of two phases. In the first phase, group ICA was applied to fMRI data to extract information from mixed data so that those specific brain areas affected at different AD stages may be located. In the second phase, the DL algorithm was proposed for separation between MCI and the three stages of AD. These phases are described in the following sections.

2.3. Application of ICA

Independent component analysis (ICA) also known as blind source separation (BSS) method is mostly used to find out those independent hidden sources/factors where the information originated (Stone, 2004). It has also been used for separating components from fMRI data. Chatterjee et al. (2019), Correa et al. (2007), Zhao et al. (2004) and Calhoun et al. (2004) used ICA in their studies with fMRI data.

Fig. 1 describes how ICA uses mixed information (observable) generated from different sources and then converts that information to original sources. Mathematically, we observe 'n' linear mixtures $(x_1, x_2, \ldots, x_n)$ of 'n' independent components $(s_1, s_2, \ldots, s_n)$ defined as:

$$x_j = a_{j1}s_1 + a_{j2}s_2 + \ldots + a_{jn}s_n \quad (1)$$

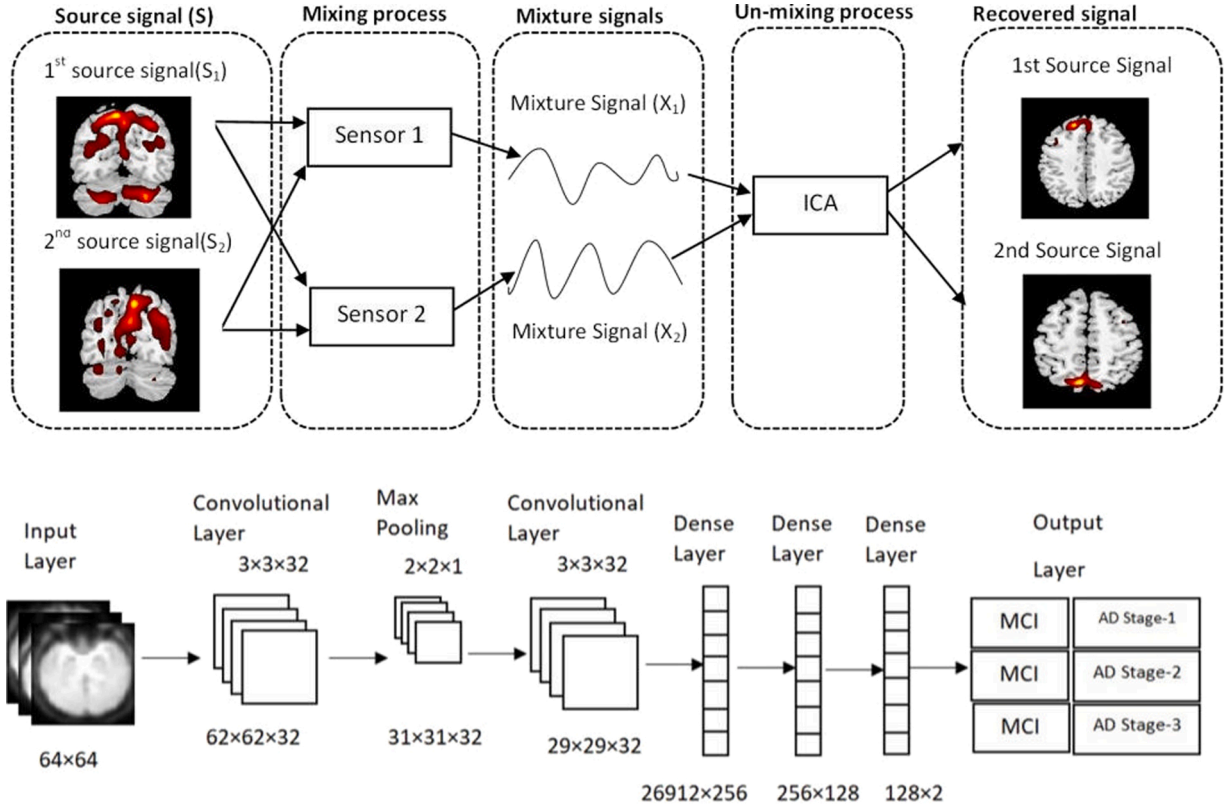

Fig. 1. Un-mixing mixed information using ICA and proposed CNN model.

Where $j = 1, 2, \ldots, n$. Now consider $x = (x_1, x_2, \ldots x_n)^T$, $s = (s_1, s_2, \ldots s_n)^T$ and weight matrix A with a_{ij} components, then the above mixing model can be written as:

$$x = As \tag{2}$$

The purpose of ICA is to determine component vectors, which can be found as:

$$s = A^{-1}x \tag{3}$$

The matrix 'A' is further determined by using singular value decomposition method (SVD) by the equation:

$$A = u\Sigma v^T \tag{4}$$

Where u is $m \times n$ matrix of the orthonormal eigenvectors of AA^T, v^T is the transpose of a $n \times n$ matrix containing the orthonormal eigenvectors of A^TA.

Thus the final model can be written as:

$$s = \left(u\Sigma v^T\right)^{-1}x \tag{5}$$

After preprocessing of data, independent component analysis was applied to extract the active brain regions. We do not know from the literature which part of the brain has a problem at each stage of AD. Using ICA, mixed signals generated from various parts of the brain were separated for each patient at each stage. This was done with the help of a toolbox called 'GIFT'. It divides the activations into various locations from which these were initially generated. GIFT only identifies the particular active region and provides its peak MNI coordinates but does not tell the name of that particular region. This is further done with MRICron using the aal.nii image given in it to identify the particular region using coordinates given by GIFT.

2.4. Application of convolutional neural network

After detecting the affected brain region by ICA at various stages of AD, a convolutional neural network based on a deep learning approach for making classification between stages of AD was applied. Basaia et al. (2019) used CNN for making binary classification between converted MCI, stable MCI, and healthy controls. They used pre-trained weights for classification purposes. This study proposed a novel CNN model with two convolutional layers and three flattened layers and trained the parameters using python programming. The structure of the proposed model is given in Fig. 1.

The CNN model in Fig. 1 was applied to separate MCI from stage 1, stage 2, and stage 3 of AD. The first layer of the CNN model is the input layer. Very next to the input layer, we have a convolutional layer derived from the input layer. The goal of the convolution layer is to apply filters, also referred to as kernels, to the input layer to extract different features of the input image. Each filter is designed to extract different features such as line, curve, edge, or color. The interesting thing is that there is no hard and fast rule to fix the number of filters and size of each filter to be used in each convolutional layer. Next to the convolutional layer, non-linearity was introduced by using a function called the activation function because for classification a clear image is required. The activation functions are used to increase the non-linearity because images are naturally non-linear. ReLu (Rectified linear units) and sigmoid are the most well-known activation functions for this purpose. The ReLu function returns zero value to negative value; for the positive value, it returns the same value. Mathematically, it can be shown in Eq. (6), where x is the input value;

$$f(x) = \max(o, x) \tag{6}$$

A pooling layer was introduced after applying the activation function. The purpose of pooling is to reduce the output neurons by combining them. The average pooling or max-pooling method is used for this purpose. Fully connected layers are introduced after the pooling layer. These fully connected layers are similar to multilayer neural networks.

3. Analysis results

After preprocessing of data, we investigated the brain regions that were active during the resting state at MCI, stage 1, stage 2, and stage 3 of AD. These regions were extracted with independent component analysis (ICA) by using the group independent component analysis toolbox (GIFT). Fifteen ICs were run for each subject, and those ICs that showed some pattern in variation were chosen. GIFT only identifies the active brain regions but fails to identify the particular region name. It only gives the peak MNI coordinate of that particular region. To identify the name of a particular region, MRICron was used by using automated anatomical labeling (aal.nii) and MNI coordinates provided by the GIFT toolbox. By using MRICron and inserting peak coordinates in the MNI field, we located the specific region corresponding to each component, such as in the slice view given in the Fig. 2 (left side), IC shows activation in the superior frontal gyrus region. A multi-slice view of the area 'precuneus' corresponding to another IC of the same subject is given in Fig. 2 (right side). Similarly, using the MNI coordinates in mricron32, specific regions of other components were identified.

The Fig. 3 (left side) shows the slice and composite view of 5 independent components of a single subject. On the left top of the figure, signals recorded are drawn to show up and down variations. The element with red color represents the variation from the 3rd IC, which corresponds to the region of the middle frontal gyrus; the blue color shows the variation of the 8th IC, which is against the region of precuneus. Similarly, the green color represents the variation from the area of the cuneus, the pink-colored area is for the superior frontal gyrus, and the area marked with yellow color represents the variation of 15th IC, which has peak activation in the region of the putamen. The connectogram in Fig. 3 (right side) shows different components were plotted in a circle, the correlation between different components is shown with different colors according to the color map given at the right bottom. Each of the components is also represented by a different color. Outside the circle, each component's sagittal view is also mapped.

3.1. Voxel data extraction

We combined the data of each patient by calculating the mean image. That is, all the 105 images of each patient were combined. The first-level analysis was performed, and voxel data of specified regions were extracted using the labels given in SPM12. When the brain regions were specified using ICA, the voxel data for the corresponding brain regions were extracted at each stage by using SPM12.

3.2. Identification of affected brain regions of Alzheimer's disease

After preprocessing data, we investigated the brain regions that were active during the resting state at MCI, stage 1, stage 2, and stage 3 of AD. These regions were extracted with independent component analysis (ICA) by using the group independent component analysis toolbox (GIFT). Result summary of the GIFT toolbox not only extracted ICs but also provided peak coordinates against each component; these coordinates were further used to label corresponding brain regions that were active during the resting state experiment. A template file "Anatomical Automated Labeling" (AAL.nii) from the MRICron toolbox was used to label the corresponding region at each peak coordinate of each component. We selected only those identified regions that were most common. For example precuneus was observed as an affected region in 5 patients out of 18 at MCI and stage 2 of AD. It was also observed in 3 patients at stage-3 but was observed in only 2 patients at stage 1 of AD. That is why this particular region was not selected as an affected region at stage 2. After identifying the affected brain regions, the voxel

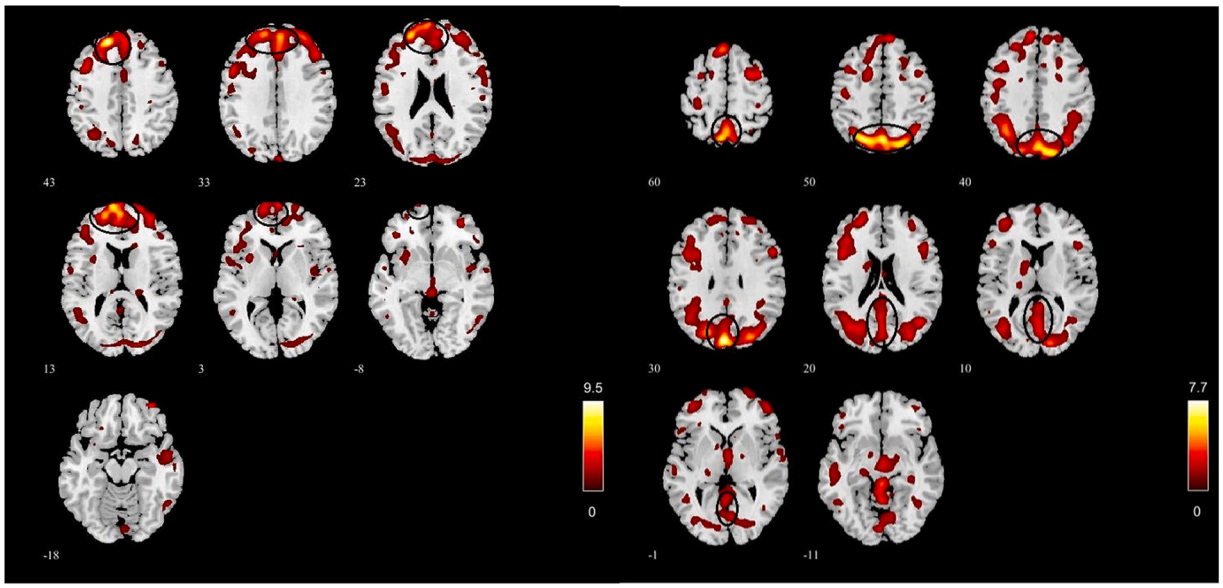

Fig. 2. Multi-slice view of frontal superior gyrus and precuneus.

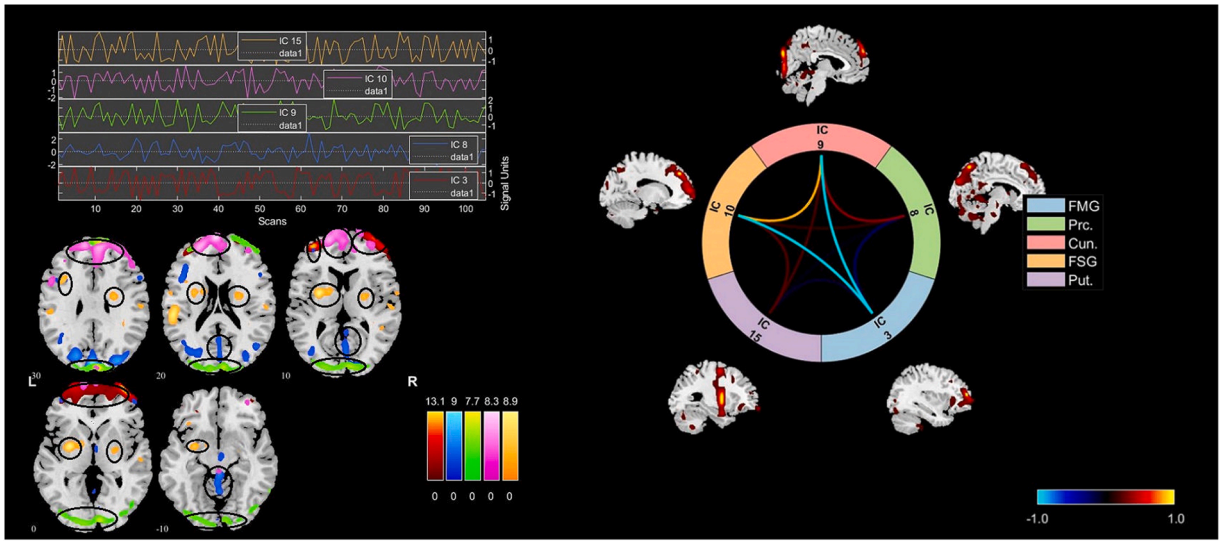

Fig. 3. Multi-slice composite view along with connectogram between components.

Table 1
Identification of affected brain regions at AD.

MCI	**Brain Region**	Cuneus	Precuneus	Parahippocampal	Putamen	Superior Frontal Gyrus	Middle Frontal Gyrus
	N (%)	4 (22.2)	4 (22.2)	5 (27.7)	3 (16.6)	5 (27.7)	4 (22.2)
	Mean Correlation	0.6657	0.5918	0.5899	0.7153	0.6686	0.5623
Stage 1	**Brain Region**	Cuneus	Calcarine Cortex	Superior Frontal Medial Gyrus	Middle Frontal Gyrus		
	N (%)	4 (22.2)	3 (16.6)	6 (33.3)	6 (33.3)		
	Mean Correlation	0.6045	0.5997	0.6813	0.583		
Stage 2	**Brain Region**	Calcarine Cortex	Precuneus	Insula	Superior Frontal Gyrus	Superior Frontal Medial Gyrus	Middle Frontal Gyrus
	N (%)	4 (22.2)	5 (27.7)	4 (22.2)	4 (22.2)	4 (22.2)	7 (38.8)
	Mean Correlation	0.5554	0.7247	0.7112	0.6429	0.646	0.6774
Stage 3	**Brain Region**	Calcarine Cortex	Precuneus	Parahippocampal	Superior Frontal Gyrus	Superior Frontal Medial Gyrus	Middle Temporal Gyrus
	N (%)	6 (33.3)	3 (16.6)	4 (22.2)	5 (27.7)	3 (16.6)	3 (16.6)
	Mean Correlation	0.6847	0.707	0.8446	0.6955	0.6238	0.615

data of these particular areas were extracted using the SPM atlas, and the mean voxel was calculated using MATLAB.

The voxel's values are then mapped with the TC of ICA using correlation analysis. Here we considered the absolute value of the correlation coefficient. All the regions given in Table 1 were found to have a high positive correlation with their corresponding TC, which confirmed the activation of these brain regions of AD patients at MCI, stage 1, stage 2 and stage 3 of AD patients. Supplemental Figure *1* shows the orthogonal view of active brain areas during the resting state at MCI (A), stage 1 (B), stage 2 (C), and stage 3 (D) where all regions are mapped with different colors. Legends at the right bottom show names of corresponding brain regions.

The proposed deep learning algorithm achieved 94.7 % accuracy for classifying MCI and stage 1 of AD, 96.7 % for classifying MCI and stage 2 of AD, and 97.8 % for separating MCI from stage 3 of AD. Table 2 presents the results attained by the deep learning algorithm CNN that was considered for classification, the results of the diagnostic tests are also given in the Table 2. Supplemental Figure *2* presents the train and test accuracy during each epoch. The blue line represents the accuracy attained by training data, while the red line represents the accuracy achieved by test data, left to right are the three stages respectively. The trend of both lines advocates a gradual increase in accuracy after every epoch.

Table 2
CNN results for classification.

Class	Accuracy	sensitivity	Specificity	PPV	NPV	LR+	LR-
MCI and AD Stage-1	0.947	0.92	0.94	0.94	0.92	17.5	0.07
MCI and AD Stage-2	0.967	1.00	0.93	0.93	1.0	15.1	0.0
MCI and AD Stage-3	0.978	1.00	0.96	0.96	1.0	26.1	0.0

4. Discussion and conclusion

Alzheimer's disease damages various brain regions that are related to memory and cognition. Many researches have been carried out to investigate and validate these regions. Ahmad and Dar (2018) considered hippocampus as an affected area of the brain during AD. Davatzikos et al. (2011) stated that deterioration occurs in temporal lobe gray matter and white matter, posterior cingulate/precuneus, and insula among individuals who are converted from MCI to AD. Casanova et al. (2011) stated that neurodegeneration occurs in the entorhinal cortex and hippocampus and then spreads in some temporal, frontal, and parietal regions as they affect brain areas in AD. Wang et al. (2006) found a decline in functional connectivity between the hippocampus and other brain regions; medial frontal cortex, anterior cingulate cortex, inferior temporal cortex, cuneus, precuneus, superior temporal gyrus, middle temporal gyrus, and posterior cingulate gyrus, whereas growth in functional connectivity was observed between left hippocampus and lateral prefrontal cortex.

This study focused on the extraction of those specific regions that are affected by AD at each stage which was ignored in previous literature. This objective was achieved by ICA, which was run on GIFT Toolbox v4.0 in MATLAB. Chatterjee et al. (2019) used GIFT to run ICA on fMRI data to identify the affected brain regions that are associated with working memory in case of schizophrenia. They considered 13 ICs of each subject/patient. After identification of ICs, they used Automated Anatomical Labeling (AAL) atlas to mark the corresponding brain region. In their conclusion, the most repeated ICs were reported as affected brain regions during Schizophrenia problems. The present study was headed in a similar way but with four stages. The same process was repeated on fMRI data on AD for each patient/subject at the initial stage (MCI), stage 1, stage 2, and stage 3. 15 ICs of each patient were considered, and the signal pattern of each IC was observed. Those ICs that were not showing any pattern were ignored, and for the remaining ICs, the corresponding brain regions from where the signals were generated was evacuated using Automated Anatomical Labeling (AAL) atlas in the mricron32 tool. The correlation method confirmed the ICs that were taken out. The voxel data of identified regions against each component were extracted using SPM12, and correlation between IC and voxel data was observed using correlation coefficient. The regions for which the correlations between components and corresponding voxels data found greater/equal to 0.5 were considered to be confirmed affected regions/areas. The regions that were repeated among subjects at a particular stage were taken out, Table 1 provides those repeated regions that were observed at the initial stage MCI, Stage 1, Stage 2 and Stage 3. It may be noted that some of the regions that we identified here have also been discussed in previous studies, but those studies did not identify the particular stage. Secondly, our study affirmed some new regions that have not been reported to date in the literature related to working with brain regions during AD. Thus this work may open a new path for the researchers and may be a significant part of new studies in this area.

Along with detecting various brain regions that are affected in case of AD, a deep learning-based model was also introduced for binary classification known as convolutional neural network (CNN). Binary classification was done between MCI and stage 1, MCI and stage 2, MCI and stage 3 with the proposed model. CNN is also designed to deal with big data with more efficiency and accuracy. In our study, CNN was used to make classification between various stages of AD using fMRI data. The algorithm of CNN was developed using Python language and executed on Google Co-lab so that heavy and huge data can be handled successfully. Maqsood et al. (2019) applied CNN to make classification between the stages of AD. They only considered OASIS data containing only 382 images and used a pre-trained CNN model (Alex-Net). In their study three stages of AD, very mild, mild, and moderate, were taken into account along with no AD. Another study by Basaia et al. (2019) collected data on three phases from ADNI-1, ADNI-Go, and ADNI-2 and named these stages as healthy control, MCI, and Probable AD and performed binary classification using pre-trained CNN model. In our study, we considered four stages of AD as MCI, stage 1, stage 2, and stage 3 for binary classification with the CNN algorithm, and for each algorithm, 1860 images were used, which means a large number of images were taken for this classification purpose. Moreover, we trained our model with the data in hand rather than using pre-trained weights. Our model provided 94.6 % accuracy for classifying MCI and stage 1 of AD, 96.7 % for separating MCI from stage 2 of AD, and 97.8 % for distinguishing between MCI and stage 3 of AD.

Funding statement

This research did not receive any funding.

Conflict of Interest

Authors have no conflicts of interest to disclose.

Data Availability

Data will be made available on request.

Acknowledgments

The authors acknowledge Alzheimer's Disease Neuroimaging Initiative (ADNI), National Institutes of Health Grant U01 AG024904

and DOD ADNI (Department of Defense Award Number W81XWH-12–2-0012) for providing access to Alzheimer's disease data. ADNI clinical sites in Canada are also funded by the Canadian Institutes of Health Research. Private sector contributions are facilitated by the Foundation for the National Institutes of Health (www.fnih.org). There is also a role of National Research Program for Universities (NRPU), Higher Education Commission, Pakistan, No. 20–16716/NRPU/R&D/HEC/2021 2021 in development and conducting this research work.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.neures.2023.01.010.

References

Ahmad, F., Dar, W.M., 2018. Classification of Alzheimer's disease stages: an approach using PCA-Based algorithm. Am. J. Alzheimer'S. Dis. Other Dementias® 33, 433–439.

Ahmad, F., Zulifqar, H., Malik, T., 2019. Classification of Alzheimer disease among susceptible brain regions. Int J. Imaging Syst. Technol. 1–12.

Albawi, S., Mohammed, T.A., Al-Zawi, S., 2017. Understanding of a convolutional neural network. 2017 International Conference on Engineering and Technology (ICET). Ieee,, pp. 1–6.

Basaia, S., Agosta, F., Wagner, L., Canu, E., Magnani, G., Santangelo, R., Filippi, M., Initiative, A.S.D.N., 2019. Automated classification of Alzheimer's disease and mild cognitive impairment using a single MRI and deep neural networks. NeuroImage: Clin. 21, 101645.

Calhoun, V., Pearlson, G., Adali, T., 2004. Independent component analysis applied to fMRI data: a generative model for validating results. J. VLSI Signal Process. Syst. Signal, Image Video Technol. 37, 281–291.

Casanova, R., Wagner, B., Whitlow, C.T., Williamson, J.D., Shumaker, S.A., Maldjian, J. A., Espeland, M.A., 2011. High dimensional classification of structural MRI Alzheimer's disease data based on large scale regularization. Front. Neuroinform. 5, 22.

Chatterjee, I., Kumar, V., Sharma, S., Dhingra, D., Rana, B., Agarwal, M., Kumar, N., 2019. Identification of brain regions associated with working memory deficit in schizophrenia. F1000Research 8.

Correa, N., Adalı, T., Calhoun, V.D., 2007. Performance of blind source separation algorithms for fMRI analysis using a group ICA method. Magn. Reson. Imaging 25, 684–694.

Davatzikos, C., Bhatt, P., Shaw, L.M., Batmanghelich, K.N., Trojanowski, J.Q., 2011. Prediction of MCI to AD conversion, via MRI, CSF biomarkers, and pattern classification. Neurobiol. Aging 32 (2322), e19–2322 e27.

Hippius, H., Neundörfer, G., 2003. The discovery of Alzheimer's disease. Dialog. Clin. Neurosci.

Maqsood, M., Nazir, F., Khan, U., Aadil, F., Jamal, H., Mehmood, I., Song, O.-Y., 2019. Transfer learning assisted classification and detection of Alzheimer's disease stages using 3D MRI scans. Sensors 19, 2645.

Sarrafa, S., Tofigh, H., 2016. DeepAD: Alzheimer's disease classification via deep convolutional neural networks using MRI and fMRI. bioRxiv 1–15.

Stone, J.V., 2004. Independent Component Analysis. A Bradford Book.

Wang, L., Zang, Y., He, Y., Liang, M., Zhang, X., Tian, L., Wu, T., Jiang, T., Li, K., 2006. Changes in hippocampal connectivity in the early stages of Alzheimer's disease: Evidence from resting state fMRI. NeuroImage 31, 496–504.

Weiming, Tong, T., Qinquan, Guo, D., Du, X., Yang, Y., Guo, G., Xiao, M., Du, M., Qu, X., 2018. Convolutional neural networks-based MRI image analysis for the Alzheimer's disease prediction from mild cognitive impairment. Front. Neurosci. 12, 1–13.

Yadav, R., Gautam, A., Mishra, R.B., 2018. Classification of Alzheimer using fMRI data and brain network. Comput. Sci. Inf. Technol. 109–119.

Zhao, X., Glahn, D., Tan, L.H., Li, N., Xiong, J., Gao, J.H., 2004. Comparison of TCA and ICA techniques in fMRI data processing. J. Magn. Reson. Imaging. 19, 397–402.