

DNA Sequence Analysis for Brain Disorder Using Deep Learning and Secure Storage

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Abstract: Analysis of brain disorder in the neuroimaging of Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), and Computed Tomography (CT) needs to understand the functionalities of the brain and it has been performed using traditional methods. Deep learning algorithms have also been applied in genomics data processing. The brain disorder diseases of Alzheimer, Schizophrenia, and Parkinson are analyzed in this work. The main issue in the traditional algorithm is the improper detection of disorders in the neuroimaging data. This paper presents a deep learning algorithm for the classification of brain disorder using Deep Belief Network (DBN) and securely storing the image using a Deoxyribonucleic Acid (DNA) Sequence-based Joint Photographic Experts Group (JPEG) Zig Zag Encryption Algorithm (DBNJZZ). In this work, DBNJZZ implements an efficient and effective prediction model for disorders using the open-access datasets of Alzheimer's Disease Neuroimaging Initiative (Adni), the Center for Biomedical Research Excellence (Cobre), the Open Access Series of Imaging Studies (Oasis), the Function Biomedical Informatics Research Network (Fbirn), a Parkinson's dataset of 55 patients and 23 subjects with Parkinson's syndromes (Ntua), and the Parkinson's Progression Markers Initiative (Ppmi). This algorithm is implemented and tested using performance metric measures of accuracy, Root Mean Square Error (RMSE), Mean Absolute Error (MAE), and Mean Absolute Percentage Error (MAPE). DBNJZZ gives better performance with an accuracy of 99.21% and also surpasses previous methods on other measures.

Keywords: DBN; Zig zag; deep learning; MAPE; RMSE; DNA; genomics

1 Introduction

Genomics is an associative field of biology that concentrates on the genomes structure, genomes function, genomes evolution, and genomes mapping, and editing. A complete DNA set is called the genome of an organism and includes all its genes. Deep learning algorithms have been applied within the areas of genetics and genomics. When any specific gene is damaged or affected and prone to some disorder it results in what is known as a genetic disorder. The genetic disorder diseases of



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Alzheimer, Schizophrenia and Parkinson are affecting humans by disrupting normal brain functions [1–3]. Medical imaging has become the foremost and effective tool to represent various modalities of an image like X-ray, MRI, CT, mammography, and PET [4]. Storing sensitive information of medical images securely and privately also plays a vital role in the medical field. Traditional approaches of DNA-based molecular cryptography design and DNA writing techniques to store images securely became very interesting in the field of research. The main issue with these traditional techniques is that they cannot resist brute force attacks. Therefore, this paper implements a DNA Sequence-based JPEG Zig Zag Encryption Algorithm (DBNJZZ).

For detecting the above mentioned brain disorders, many traditional algorithms are implemented. The drawbacks of the traditional algorithm are pre-processing and feature extraction which are not clearly defined and are inefficient in handling complicated genomic data. To overcome these drawbacks, the proposed work, DBNJZZ, presents exploring pre-processing methods and feature extractors with the open access datasets of Adni, Cobre, Oasis, Fbirn, Ntua, Ppmi [5–10].

This proposed work consists of image registration, image enhancement, normalized filtering and smoothening for pre-processing, and implements an unsupervised feature extractor of Deep Belief Network (DBN). This approach of extraction maps the input values with multiple hidden layers. The features extracted in DBN will improve the prediction performance of the image. For performance evaluation, accuracy, Root Mean Square Error (RMSE), Mean Absolute Error (MAE), and Mean Absolute Percentage Error (MAPE) were calculated. To summarize, the main contributions of this work are:

1. Implementing the analysis of brain disorder diseases using a deep learning algorithm and showing how to store sensitive information securely in image format using DNA based encryption algorithm.
2. Evaluating the accuracy of the pre-processed image in terms of image registration, image enhancement, normalized filtering, and smoothening.

The paper has been organized as follows: Section 2 includes the literature review, Section 3 introduces the proposed algorithm, Section 4 discusses the experiment results, and Section 5 concludes the paper with future directions.

2 Literature Review

The rapid development of advanced technology has contributed various tools to diagnose brain disorder diseases, effectively. Deep learning techniques have helped in many ways to tackle the complicated problems of genomic data and analysis the diseases. Neurological diseases such as Alzheimer's, Schizophrenia, and Parkinson's are related to the disruption of brain functions. Traditional methods are employed in handling genomic data for brain disorder diseases. The main drawback of these methods is they are still inefficient to handle complicated genomic data for the brain image with disorder.

This paper presents DBN feature extraction for images of Alzheimer's, Schizophrenia, and Parkinson's to improve the quality of performance. For Alzheimer's disease, data collected in the ADNI dataset, which are derived from MRI, CT, and PET images, was validated and processed. Genetics and biomarkers were used for prediction of disorder disease [11]. A deep learning algorithm is designed to diagnose Parkinson's disease using Single-photon Emission Computed Tomography (SPECT) image dataset. Features of Sparse filtering, a new framework for automated diagnosis of Parkinson's disease, is designed [12]. Using MRI images to diagnose schizophrenia patients, a novel

DBN architecture was designed that can explore statistical values from observed data and easily detect the affected region [13].

DNA sequencing is used to improve the speed of processing genomic data [14]. The classification of DNA sequence is performed using a machine learning algorithm for extracting features that will be stored in a vector format. The classification mentioned here is a supervised learning process. Its drawback is that it cannot read by machine and also it has a high dimensionality of data. The genome sequences extracted from images as features using deep learning algorithms are used in various fields of genomic medicine, bioinformatics application, and medical imaging analysis [15]. Tab. 1 shows the survey summary of brain disorder analysis using a deep learning algorithm.

Table 1: Survey Summary of brain disorder analysis

Author name	Algorithm name	Application
Mahmud et al. [14]	Deep learning	Biological data mining
Fabiatti et al. [15]	Neural network	Artifact detection in neural probes
Islam et al. [16]	Deep learning	Generative adversarial network (GAN)-based synthetic brain PET image generation.
Rabby et al. [17]	Deep learning	The tree-based unsupervised key phrase extraction technique
Baiying et al. [18]	Deep learning	Neurodegenerative disease diagnosis using adaptive sparse learning.
Chand et al. [19]	Machine learning	Neuroanatomical of schizophrenia
Ali et al. [20]	Neural network	Segmentation of MRI image
Noor et al. [21]	Deep learning	Neurodegenerative disease in MRI
Basaia et al. [22]	Convolutional neural network (CNN)	Classification of Alzheimer's disease using MRI
Li et al. [23]	Deep learning	Prediction of Alzheimer's disease using MRI

3 Proposed DNA Sequence-based JPEG Zig Zag Encryption Algorithm (DBNJZZ)

Medical imaging is an effective tool to diagnose a disease. For analyzing brain disorders, this paper implements a deep learning algorithm of DBN. This workflow (DBNJZZ) consists of two modules:

Module 1: Pre-processing

Module 2: Feature extraction of image with disorder and DNA Sequence-based privacy storage of brain image DBN-JPEG Zig Zag encryption algorithm (DBNJZZ). (Proposed) Fig. 1 shows the workflow of the DBNJZZ.

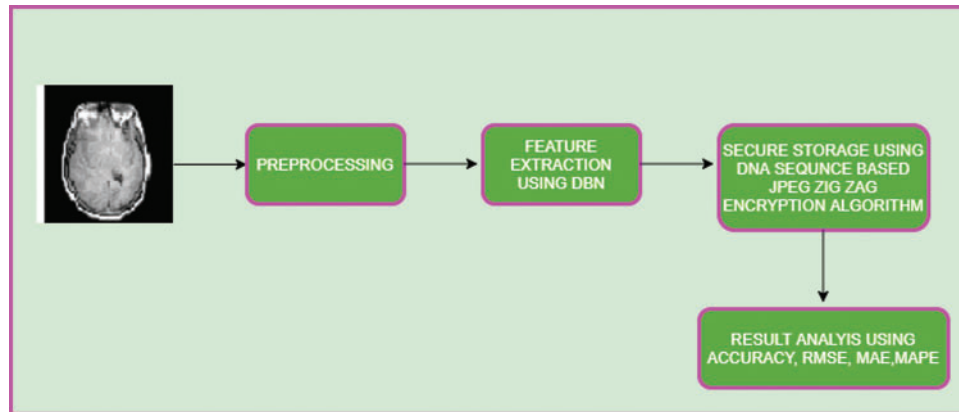


Figure 1: Workflow of DBNJZZ

3.1 Pre-processing (Module 1)

Neuroimaging modalities of brain images are CT, MRI, and PET. To improve the quality of an image, it is adjusted in a pre-processing stage. The steps involved in the pre-processing phase are given in Fig. 2.

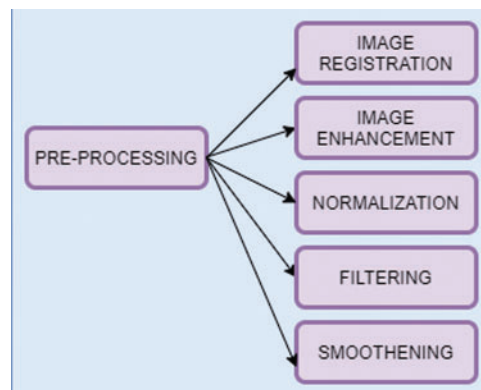


Figure 2: Pre-processing steps

3.1.1 Image Registration

Image registration acquires two or more of same image features with different time frame variations into a single informative image. Linear regression algorithm is used for image registration which includes the functions of rotation, translation, and scaling for an image on the axes of x, y, z. At all angles, the algorithm will align the spatial correlation of the image. In general, image registration is given by:

$$I_b = R(I_b'), \{\beta\} \quad (1)$$

where, I_b' is the coordinate value of the image b, β is the set of parametric values of transformation.

3.1.2 Image Enhancement

It improves the quality of the image by filtering with contrast Contrast-limited Adaptive Histogram Equalization (CLAHE). This approach will enhance the image brightness with its background to improve visibility.

3.1.3 Normalization

It is the process of aligning the image in terms of size and shape to interpret them into common features of the image. This process maps the data point acquired from discrete space value to the reference space value.

3.1.4 Filtering

Using Weiner filtering, unwanted features will be removed from the image which consequently will minimize the image noise.

$$R(u) = \frac{H(u)^*}{|H(u)|^2 + k} \quad (2)$$

where k is the low-frequency value of the Wiener filter; the high pass filter value is used to blurred the image.

3.1.5 Smoothing

It is the process of reducing the noise of the image. Spatial smoothing is applied which calculates the average value of pixels from the adjacent pixel elements. With smoothing, the Signal-to-noise ratio (SNR) value is enhanced and spatial resolution value is reduced.

3.2 Feature Extraction of Image with Disorder and DNA Sequence-Based Privacy Storage of Brain Image DBN-JPEG Zig Zag Encryption Algorithm (DBNJZZ).

In this work, Deep Belief Network (DBN) is used to extract features type from biomarkers of the image. Biomarker acts as a tool for the diagnostic purpose and it is used to identify the abnormal condition of the image. DBN here is based on Restricted Boltzman Machines (RBM) architecture [16–18]. DBN is unsupervised feature extractor that extracts the features from the image for performance improvement. In this context, it will extract the normal structure features from the brain image to identify brain-related disorders. Fig. 3 shows the workflow of recommended biomarkers.

DBN architecture is composed of RBM stacks which contain one visible layer and multiple hidden layers. Each layer consists of nodes. The connection between the input layer and hidden layers is established by assigning a weight value. During the process of training the network, the weight vector value will be adjusted. The structure of DBN is given in Fig. 4. The architecture of RBM is given in Fig. 5.

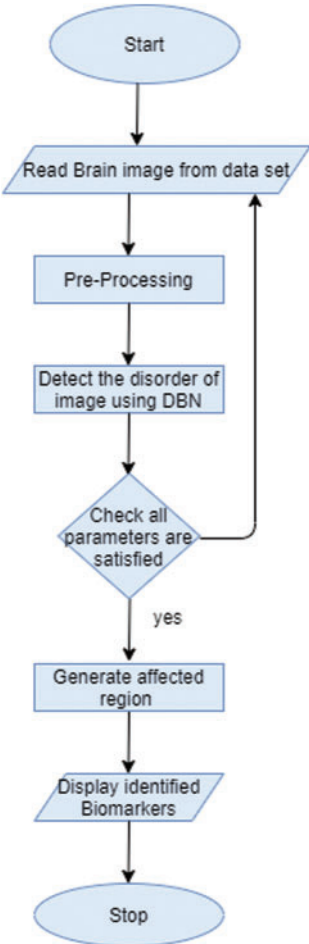


Figure 3: Workflow of generating biomarker

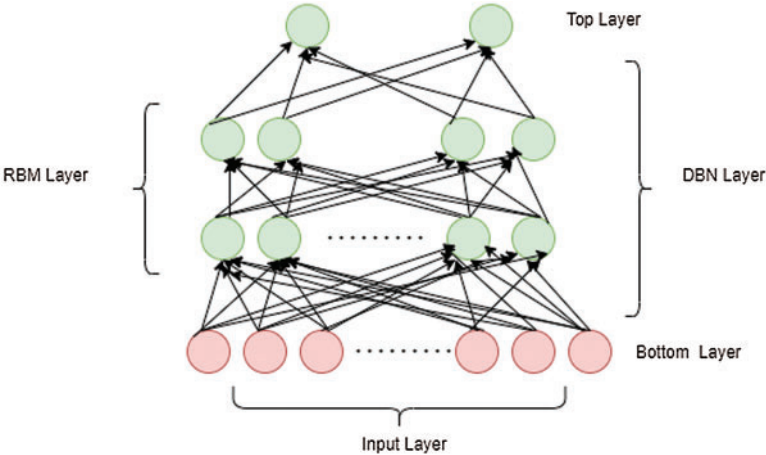


Figure 4: DBN layer

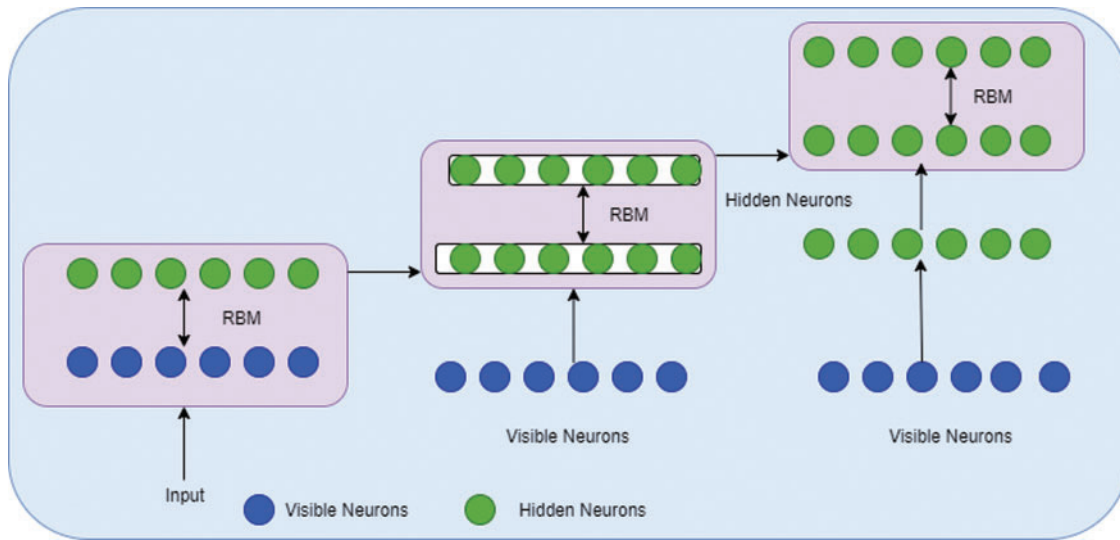


Figure 5: RBM architecture

The algorithm for training the DBN is given below:

Algorithm 1: Training DBN

Step 1: Let I_i ; $0 \leq i \leq N$ is input neuron that contains binary values and N is the total number of input neurons.

Step 2: Let h_i ; $0 \leq i \leq K$ is a hidden neuron that contains binary values and K is the total number hidden neurons.

Step 3: Calculate the energy function $Er(i, j)$ between input neurons and hidden neurons by using:

$$Er(I, h_i) = \sum_i b_i I_i - \sum_i a_j h_j - \sum_i \sum_j I_i W_{ij} h_j \quad (3)$$

Step 4: Train the RBM's first layer (visible layer) by applying input values to all neurons.

Step 5: The output of Step 4 will be used as input of the next layer (hidden layer).

Step 6:

$$D(I, h_i) = \frac{1}{F} e^{-Er(I, h_i)} \quad (4)$$

The pair values of visible and hidden values are summed up and produce F as a function.

Step 7: Evaluate the unbiased value between visible neurons and hidden neuron

$$D \left(h_j = \frac{1}{F} = \sigma \left(b_j + \sum_i I_i W_{ij} \right) \right) \sigma \text{ is a sigmoid function.}$$

Step 8: Repeat steps 6, 7 until all layers are evaluated.

Step 9: Output Binary Values B_{ij}

In algorithm 1, the image was trained to detect the disorder in the image. The resulted output will be stored in a secure way using DBNJZZ Encryption Algorithm. DNA is made up of monomers in a polymer structure which are called Deoxyribonucleotides. The basic components of nucleotide

are phosphate, deoxyribose sugar, and nitrogenous [19,20]. The bases of nitrogenous are Adenine (A), Cytosine (C), Thymine (T), and Guanine (G). After implementation of algorithm 1, the output values are plotted in a matrix format corresponding to the four base variables of DNA: A, C, T, and G nucleotides. The encoded value of A is [0,0,0,1], C's encoded value is [0,0,0,1], T's encoded value is [0,0,0,1] and G's encoded value is [0,0,0,1]. Therefore, the disorder image value can be represented as an equivalent DNA sequence of code. The encryption key of DNA in DBNJZZ is defined by Fig. 6.

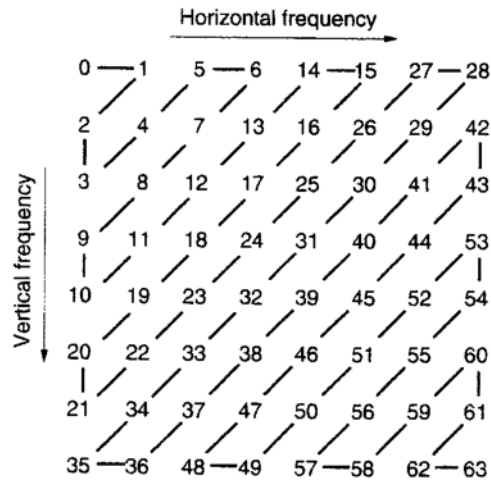


Figure 6: JPEG Zig Zag format

By substituting DNA sequence nucleotides quadruple values by one and translating brain image to one value from randomly selected nucleotides quadruple sequences, a security component is achieved. Specifically, the gene binary sequence value is considered as an encrypted image and is stored securely. The encryption DBNJZZ algorithm is given below:

Algorithm 2: DNA sequence JPEG Zig Zag Encryption

Step 1: Call Algorithm 1

Step 2: Translate B_{ij} to its corresponding DNA Sequence value.

Step 3: $A \leftarrow DNA(B_{ij})$ // Convert the image into DNA image

Step 4: $Z_A \leftarrow A$ // Translate the DNA image according to JPEG Zig Zag as in Fig. 5

Step 5: Encrypted Image

Algorithm 3: DNA sequence JPEG Zig Zag Decryption

Step 1: $B \leftarrow DNA$ sequence of binary file F

Step 2: $B \leftarrow Reverse\ function\ of\ JPEG\ ZIG\ ZAG(B)$

Step 3: Convert B into its binary value and produce a decrypted image as an output.

Both sender and receiver must have the same gene sequence value and store it in a binary format. For each DNA nucleotide sequence in B quadruple value, a binary format file is selected randomly and replaced by an image. Fig. 7 shows the result of storing an image using a JPEG Zig Zag pattern.

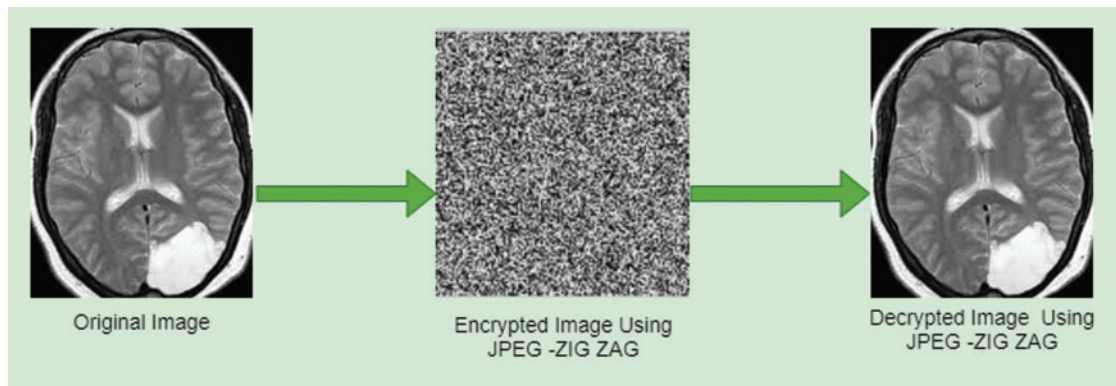


Figure 7: Applying JPEG Zig Zag encryption algorithm

4 Result Analysis

The four metrics for measuring performance are reported here to evaluate the analysis of DBNJZZ in detecting disorder image. The metrics are: Root Mean Square Error (RMSE), Mean Absolute Error (MAE), accuracy and Mean Absolute Percentage Error (MAPE).

$$RSME = \sqrt{\frac{1}{N} \sum_{i=1}^N (O_i - P_i)^2} \quad (5)$$

$$MAE = \frac{1}{N} \sum_{i=1}^N |O_i - P_i| \quad (6)$$

$$MAPE = \frac{100}{N} \sum_{i=1}^N \left| \frac{O_i - P_i}{O_i} \right| \quad (7)$$

$$Accuracy = 1 - \frac{\sum_{i=1}^N |O_i - P_i|}{\sum_{i=1}^N O_i} \quad (8)$$

where, O_i is the observation value of a variable, P_i is the prediction value of the variable and N is the number of observations. Eq. (5) is calculated as the square root of the mean of the squared differences between actual outcomes and predictions. Eq. (6) is the absolute difference between the actual or true values and the values that are predicted. The negative sign in the absolute difference result is ignored. Eq. (7) is defined as the error rate of the actual value or observed value minus the forecasted value. Accuracy classification was achieved by 10-fold cross-validation. Tab. 2 shows the different disorder diseases and their datasets.

Table 2: Various disorder diseases and theirs datasets [21]

Detection of disorder disease	Datasets
Alzheimer's disease	ADNI, OASIS
Schizophrenia	COBRE, FBIRN
Parkinson's disease	NTUA, PPMI

In the neurological disorder of Alzheimer's, the disease is affecting older age people by degrading them mentally and attack the brain function in a specific region. Using Eq. (8) accuracy metric measures for pre-processing activities of Alzheimer's disease are given in Tab. 3 using Tab. 2 datasets.

Table 3: Accuracy of neurological disorder of Alzheimer's disease

Deep learning technique	Image registration	Contrast enhancement	Normalization	Wiener filter	Smoothing
CNN + JPEG ZIG-ZAG	92.74%	80%	89.47%	85%	93.84%
DNN + JPEG ZIG-ZAG	85%	78.12%	88.30%	80.25%	90.21%
DBN + JPEG ZIG-ZAG (proposed)	97.52%	89.56%	92.67%	88.89%	98.56%

Tab. 3 shows how the proposed work (DBN) has produced a better performance. Using Eq. (8), Tab. 4 shows accuracy for a neurological disorder of Schizophrenia disease. Schizophrenia is a psychiatric disorder and it changes a patient's behavior like emotion and cognition.

Table 4: Accuracy of neurological disorder analysis of Schizophrenia

Deep learning technique	Image registration	Contrast enhancement	Normalization	Wiener filter	Smoothing
CNN + JPEG ZIG-ZAG	89.47%	82.34%	85.74%,	81.20%	90.84%
DNN + JPEG ZIG-ZAG	87.45%	84.12%	86.67%	84.53%	91.45%
DBN + JPEG ZIG-ZAG (proposed)	96.25%	91.56%	94.76%	90.45%	99.21%

The experiment results in Tab. 5 show the accuracy metric measures for Parkinson's disease in the proposed work DBN. By using Eqs. (5) and (6) RMSE and MAE are plotted in Figs. 8–10. Eq. (5) is calculated as the square root of the mean of the squared differences between actual outcomes and predictions. Eq. (6) is the absolute difference between the actual or true values and the values that are predicted. The absolute difference result has a negative sign which is ignored.

Table 5: Accuracy of neurological disorder analysis of Parkinson disease

Deep learning technique	Image registration	Contrast enhancement	Normalization	Wiener filter	Smoothing
CNN + JPEG ZIG-ZAG	87.89%	86.43%	88.78%,	84.20%	89.48%
DNN + JPEG ZIG-ZAG	88.54%	87.21%	88.67%	86.36%	90.54%
DBN + JPEG ZIG-ZAG (proposed)	98.25%	92.67%	95.89%	92.65%	98.90%

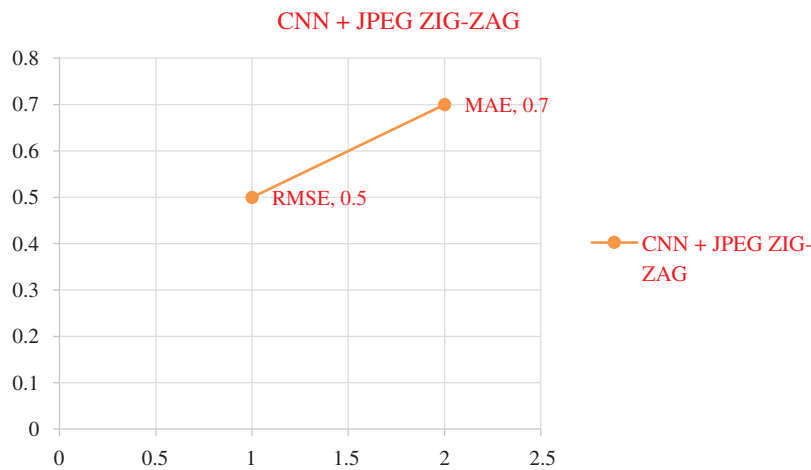


Figure 8: Error Rate using CNN+ JPEG ZIG-ZAG

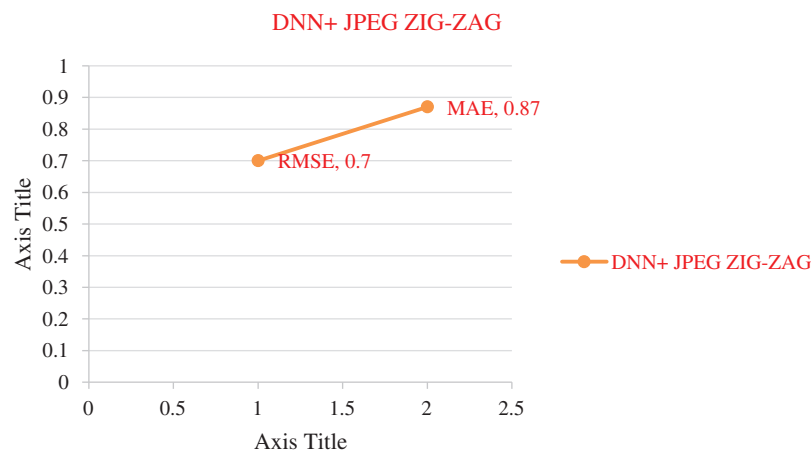


Figure 9: Error rate using DNN+ JPEG ZIG-ZAG

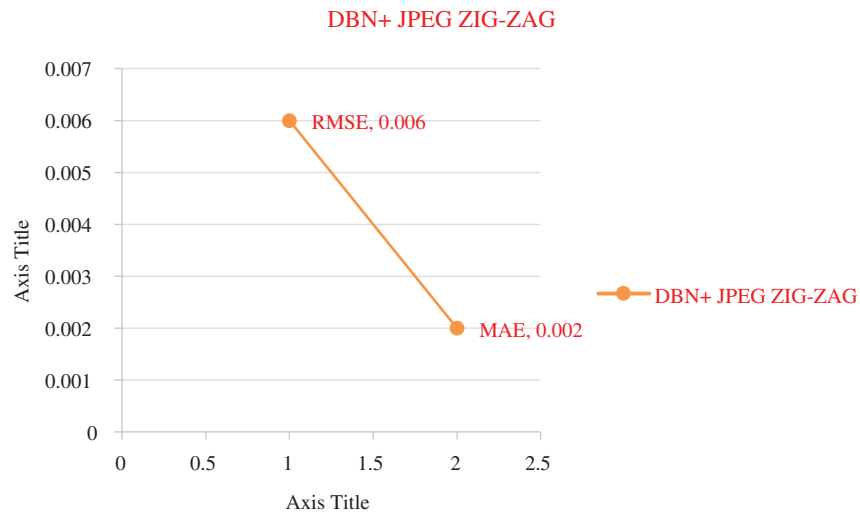


Figure 10: Error rate using DBN+ JPEG ZIG-ZAG

The experiment results in Figs. 8–11 show the superiority of the proposed work, DBN+JPEG ZIG-ZAG. Results prove the better prediction performance of DBN+JPEG ZIG-ZAG compared with existing algorithms in deep learning. In the above analysis, the accuracy metric is used for evaluating deep learning classification algorithms of brain disorder diseases: Alzheimer, Schizophrenia, and Parkinson. Proposed work reveals better performance in the accuracy metric. Visualizing the performance of algorithms in terms of error rate in Fig. 11 illustrates the lower error rate of the DBN algorithm and accordingly indicates the correct prediction of the result.

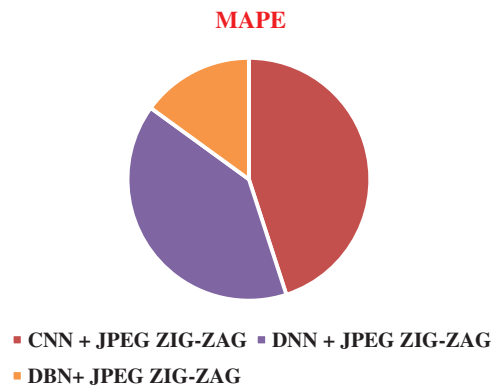


Figure 11: Result of MAPE in different algorithms DBN+ JPEG ZIG-ZAG

5 Conclusion

In this research, deep learning algorithms with CNN, DNN, and DBN are evaluated using secure storage of images in the JPEG Zig Zag encryption scheme. The DBN is proposed as an unsupervised feature extractor to extract biomarkers of the image and predict brain disorder diseases of Alzheimer, Schizophrenia, and Parkinson. The proposed work of the DBNJZZ system can process all features of the image and share this image securely. It can also provide a prompt prediction of the disorder using

the image. This work has only focused on three diseases. In the future, this work can be extended to cover different case studies with diverse DNA sequences.

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