The Scientific Temper (2025) Vol. 16 (2): 3710-3721
Doi: 10.58414/SCIENTIFICTEMPER.2024.16.2.03
E-ISSN: 2231-6396, ISSN: 0976-8653
https://scientifictemper.com/

RESEARCH ARTICLE

Gaussian kernelized transformer learning model for brain tumor risk factor identification and disease diagnosis

P. S. Renjeni[1], B. Senthilkumaran[1], Ramalingam Sugumar[1], L. Jaya Singh Dhas[2]

Abstract

Brain tumor is an abnormal growth of cells in brain or central spinal canal. Tumors are benign (non-cancerous) or malignant (cancerous). They can be invented in the brain (primary tumors) or spread to other elements of the body. Early detection significantly improves survival rates and overall prognosis for patients by enabling intervention before tumors grow larger or spread, which can complicate treatment. Early intervention also preserves brain function and quality of life while minimizing severe neurological damage or symptoms. Epileptic seizures are a significant clinical symptom and a potential early indicator of brain tumors in patients. Conventional machine learning and deep learning face significant challenges in accurately detecting brain tumors with minimal time consumption. In this paper, a novel technique called multivariate relief matching gaussian kernelized transformer learning (MRMGKTL) model has been developed. The major intent of the MRMGKTL model is to enhance the accuracy of brain tumor detection through the recognition of epileptic seizures. MRMGKTL model comprises data acquisition, feature selection, and classification. In the data acquisition phase, electrical activity data from the brains of patients are collected from datasets for diagnosing brain tumors based on epileptic seizures. Following data acquisition, Sokal– Michener's multivariate relief matching technique is used to choose the most significant aspects of the dataset. The feature selection process in the proposed method aims to minimize the time required for tumor detection. Using the selected features, brain tumor disease diagnosis is performed using a Gaussian Kernelized transformer learning model to detect and diagnose brain tumors associated with epileptic seizure severity levels with higher accuracy. This approach ensures the accurate identification of brain tumors and associated risk factors with minimal time consumption. Experimental assessment evaluates various factors. Analyzed outcomes demonstrate that the proposed MRMGKTL model achieves superior performance in accuracy of brain tumor diagnosis and reduces time consumption compared to conventional deep learning methods.

Keywords: Brain tumor diagnosis, Epileptic seizures detection, Sokal–Michener's multivariate relief matching technique, Optimizer to minimize data dimensionality, Gaussian Kernelized Transformer Learning model, ROC curve analysis.

[1]Department of Computer Science, Christhu Raj College, (Affiliated to Bharathidasan University), Tiruchirappalli – 12, Tamilnadu, India.

[2]Department of Computer Science, Scott Christian College, (Affiliated to Manonmaniam Sundaranar University), Nagercoil-3, Tamilnadu, India.

***Corresponding Author:** Renjeni, P. S., Senthilkumaran, B., Sugumar, R., Dhas, L. J. S. Department of Computer Science, Christhu Raj College, (Affiliated to Bharathidasan University), Tiruchirappalli – 12, Tamilnadu, India, E-Mail: renjenips@gmail.com

How to cite this article: P. S. Renjeni, B. Senthilkumaran, Ramalingam Sugumar, L. Jaya Singh Dhas (2025). Gaussian kernelized transformer learning model for brain tumor risk factor identification and disease diagnosis. The Scientific Temper, 16(2):3710-3721.

Doi: 10.58414/SCIENTIFICTEMPER.2025.16.2.03

Source of support: Nil

Conflict of interest: None.

Introduction

Brain tumor disease diagnosis involves the identification and characterization of abnormal growths within the brain or central spinal canal. This process is crucial for determining the presence, type, location, and severity of Tumors which is essential for guiding treatment decisions as well as enhancing patient results. Seizure detection is essential to the comprehensive evaluation and management of brain tumor disease. Advances in machine learning technology and diagnostic methodologies continue to improve the ability to Detect and characterize seizures, leading to earlier diagnosis, more targeted treatments, and improved outcomes for patients with brain tumors. A Multi-dimensional CNN-BiLSTM framework (MD CNN- BiLSTM) was developed (Aravind Britto K.R *et al*.,2023) for identifying epileptic seizures using EEG signal analysis to identify abnormal brain activities. However, the framework faced

Received: 04/01/2025 **Accepted:** 16/02/2025 **Published** : 20/03/2025

a major challenge in requiring important sum of training information to accurately detect abnormal brain activities. A PS+Bi- LSTM+attention was developed (Yixuan Tang *et al*.,2024) for automatic epilepsy detection by extracting discriminative features. However, it did not provide better accuracy for multi-class classification. An integration of a CNN (Conv1D) through the LSTM network was designed (Ahmed Omar *et al*.,2024). However, the size as well as variability of the database employed were restricted, impacting the method's effectiveness. ML and DL methods, integrated with the Internet of Things framework, were developed (Sobhana Jahan *et al*.,2023) for epileptic seizure detection. However, this approach did not develop a more efficient and feasible method for improving the performance of epileptic seizure prediction. A new C-LSTM model was developed (Yuan Liu *et al*.,2020) for detecting seizures as well as tumors in the human brain. However, achieving higher accuracy remained a major challenge.

A relationship between the time of incidence of seizures and the progression of brain tumors was analyzed (Vibhangini S Wasade *et al*.,2020) to enable earlier detection and better management of brain tumors, aiming for longer survival of these patients. However, efficient ML and DL techniques were not employed to improve seizure detection. Investigation of the clinical features of BTRE and exploration of factors influencing the identification of EAT were presented (Xianwen Zhang *et al*.,2020). However, it failed to handle the large sample size in predicting brain tumor-related epilepsy.

An efficient bio-inspired machine learning technique was employed (Ahed Abugabah *et al*., 2021) to detect epilepsy seizures from EEG signals with elevated accuracy. However, the classifier's result was not improved. The diagnosis of seizures and status epilepticus (Sophie Von Brauchitsch *et al*., 2022) was established. However, the seizure diagnosis was complex. Brain lesion location detection was performed (Janne Nordberg *et al*., 2023), along with secondary generalization of epileptic seizures.

However, it failed to improve the identification of patients at risk in lesion location detection. It also instigated the diagnosis, treatment, and research of neuro-oncological conditions, including brain tumors and other central nervous system cancers (P Roth *et al*.,2021).

A machine learning method was developed (Gopal Nath *et al*., 2023). However, it failed to utilize the DM methods to design brain cancer prognosis methods through elevated accuracy. A logistic regression multivariate analysis was developed (Kenichiro Asano *et al*., 2021) to identify risk factors for brain tumor detection. However, efficient significant feature selection was not performed to enhance brain tumor detection. A new machine learning-based approach was designed (Ly V Tran *et al*., 2022) for detecting epileptic seizures. Significant statistical features were selected using a binary particle swarm optimizer to minimize data dimensionality and computational time. However, a deep learning model was not employed for epileptic seizure detection. GAM was developed (Kevin Akeret *et al*., 2020) to predict seizure risk for the diagnosis of brain tumors.

Main contribution

The key contributions of the MRMGKTL model are listed as follows:

- To enhance brain tumor diagnosis, the MRMGKTL model is developed, incorporating feature selection and classification.
- To minimize brain tumor diagnosis time, Sokal–Michener's multivariate relief matching technique is developed to select significant aspects and remove irrelevant aspects from the dataset.
- To enhance the accuracy of brain tumor diagnosis, the Gaussian Kernelized Transformer Learning model analyzes the testing and training data with the selected significant features.
- Finally, an experimental evaluation is conducted to estimate the result of MRMGKTL using various parameters and comparing it to other existing approaches.

Paper organization

The manuscript is structured as outlined below: Section 2 appraises the literature review. Section 3 elaborates on the different processes of the MRMGKTL model with a clear diagram. Section 4 outlines the experimental setup and provides a dataset description. Section 5 presents comparative analyses of various metrics. Lastly, Section 6 gives a conclusion.

Literature review

A convolutional neural network was developed (Sadia Anjunm *et al*., 2022) using a transfer learning approach aimed at detecting brain tumors. However, the approach failed to incorporate other types of brain tumors, utilize a larger dataset, consider additional clinical variables, and explore alternative deep-learning algorithms. KNN and SVM were introduced for the classification of brain tumors (Saneesh Cleatus T *et al*., 2021). However, the accuracy of the classification did not improve. TAENN method developed (M. V. V. Prasad) determines whether seizures are present by selecting optimal features.

A deep learning model was developed (Anis Malekzadeh *et al*., 2021) for epileptic seizure recognition of EEG signals by non-linear feature extraction. However, it did not leverage advanced deep-learning models for epileptic seizure recognition. The Iterative Filtering Decomposition, as well as the Hidden Markov method, were developed (Deba Prasad Dash *et al*., 2020) for the automatic recognition of epileptic seizures with higher accuracy. However, the system was less robust to noise. A stacked bidirectional LSTM_GAPNN was developed (D.K.Thara *et al*., 2021) to identify epileptic seizure

events without noise. However, it failed to achieve effective modeling for outstanding performance. Efficient machine learning approaches were developed (Dinesh Kumar Atal *et al*., 2020) for detecting epileptic seizures by extracting statistical features. However, these approaches faced higher computational complexity in sustaining a definite level of classification accuracy. QKLMS adaptive filter was developed (Ahmed S Eltrass *et al*., 2021) for epileptic seizure detection. A cluster-based k- k-nearest neighbor algorithm was designed (S. Syed Rafiammal *et al*., 2021) to enhance the accuracy of seizure recognition as well as minimize complexity.

CNN was designed (Shota Yamamoto *et al*., 2021) to identify epileptic seizures based on electrophysiological features. However, the larger dataset was not utilized for clinical epilepsy detection. S-transform and BiLSTMNN were developed (Minxing Geng *et al*., 2020) for automatic seizure detection, aiming to achieve a minimal false positive rate. Various classification algorithms were developed (Khaled M. Alalayah *et al*., 2023) for premature recognition of epileptic seizures depending on significant aspects derived from t-SNE, as well as the K-Means algorithm. An integration of EMD with a general spatial pattern was developed (Chaosong Li *et al*., 2021) for seizure onset detection. The Convolutional Neural Network (CNN) developed (by Wenna Chen *et al*., 2023) effectively achieves elevated-precision automatic recognition as well as categorization of epilepsy. However, it did not reduce false detections of seizures. A deep convolutional autoencoder with bidirectional LSTM was developed (Waseem Ahmad Mir *et al*.,2023) for epileptic seizure detection.

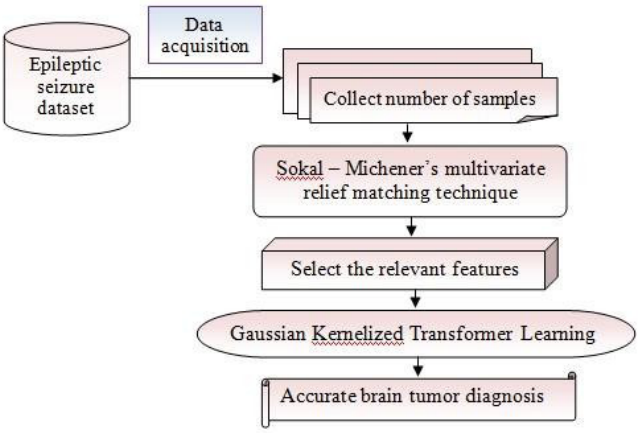

Figure 1: Architecture of proposed MRMGKTL model

Proposed Methodology

Brain tumor diseases (BTD) are a major health concern, affecting many people through abnormal cell growth. They are characterized by lesions that develop on the inside layer of the brain. Detecting tumor diseases at an early stage is crucial for effective management and treatment. In this manuscript, a new MRMGKTL model is developed for improving BTD detection using different patient data.

Figure 1, given above, depicts the architecture diagram of the proposed MRMGKTL model for accurate Brain tumor diagnosis. The proposed MRMGKTL model involves three important steps: data acquisition, feature selection, and classification. These three fundamental processes are explained in the following subsections.

Table 1: Identifiers and their descriptions

Sl. No	*Identifiers*	*Descriptions*
1.	eeg_id	A unique identifier for the entire EEG recording
2.	eeg_ sub_id	An ID for the specific 50 seconds subsample for the labels
3.	eeg_label_ offset_seco nds	The time between the beginning of the consolidated EEG and the subsample
4.	spectrogram_id	A unique identifier for the entire EEG recording
5.	spectrogram_sub.id	An ID for the specific 10 minutes subsample for the labels
6.	spectrogram_label_offs et_seconds	The time between the beginning of the consolidated spectrogram and the subsample
7.	label_id	An ID for the set of labels
8.	patient _id	An ID for the patient who donated the sample
9.	expert _ consensus	The consensus annotator label
10.	seizure _ vote	Indicates epileptic seizure activity
11.	lpd_vote	lateralized periodic discharges, highest seizure rates
12.	gpd_vote	generalized periodic discharges, Moderate seizure areas
13.	lrda_vote	Lateralized rhythmic delta activity (Intermediate seizure rates)
14.	grda_vote	Generalized rhythmic delta activity (lowest seizure rates)
15.	other_ vote	Includes annotations for brain activity that doesn't fit into the above categories.

Data acquisition

Data acquisition is the fundamental process of the proposed MRMGKTL model that involves gathering various types of data that are essential for accurately identifying seizure activity. The data is collected from the HMS - Harmful Brain Activity Classification dataset https://www.kaggle.com/competitions/hms- harmful- brain-activity-classification. The Major intent of the dataset is to detect and classify seizures and other types of harmful brain activity in electroencephalography (EEG) data. To train the data CSV files are used for classifying the seizures. The dataset includes 1,06,800 instances and 15 identifiers or attributes.

Sokal–Michener's multivariate relief matching technique for feature selection

The next fundamental process of the MRMGKTL model is a feature selection for tumor disease diagnosis. Feature selection is fundamental in ML and data analysis, where a subset of relevant features or attributes is used in building predictive models. This process helps improve model performance, reduce time complexity, and enhance accuracy. Therefore, the proposed MRMGKTL model utilizes Sokal–Michener's multivariate relief matching technique for selecting the more significant features from the dataset and removing the other features. The input dataset 'DS' is formulated in the form of a matrix as given below.

$$M = \begin{bmatrix} A_1 & A_2 & \dots & A_m \\ D_{11} & D_{12} & \dots & D_{1n} \\ D_{21} & D_{22} & \dots & D_{2n} \\ \vdots & \vdots & \dots & \vdots \\ D_{m1} & D_{m2} & \dots & D_{mn} \end{bmatrix} \quad (1)$$

From the above input matrix 'M,' where 'm' denotes a column that represents the features A1, A2, … Am and the overall samples or instances or data or records represented as 'D' stored in the 'n' row respectively. Then, a multivariate relief matching method was applied to discover more relevant features of the database.

multivariate Relief matching algorithm is a feature selection technique employed to recognize mainly relevant aspects for classification tasks. It works by estimating the quality of features based on their values and distinguishing between instances that are near each other. The proposed multivariate Relief matching algorithm defines the number of iterations

t, typically equal to a number of instances in the database. Initialize weight vector 'W' for all features

A1, A2, … Am with zeros.

$$Q = W\,[A_m] \quad (2)$$

For each iteration, randomly selects feature vector of instances as of database. Find the nearest hit and nearest miss for the selected instances with the help of the Sokal–Michener's matching method. Sokal–Michener's matching is a statistical method used to compute similarity among two feature vectors of instances.

$$SM = 1 - \frac{|D_r - D_{ij}|}{n} \quad (3)$$

Where SM denotes a Sokal–Michener's matching score, D_r denotes a randomly selected feature vector of the instances, and D_{ij} denotes another feature vector of the instances in i^{th} row and j^{th} column of the input matrix, n denotes the number of feature vectors of the instances. The Sokal– Michener's matching score gives output ranges from 0 to 1. From analysis, the nearest hit-and-miss value is computed as follows:

$$SM = \begin{cases} 1, & NH \\ 0, & NM \end{cases} \quad (4)$$

The Sokal–Michener's matching score 'SM' provides the output as 1 represents the nearest hit, coefficient provides the output as 0 represents the nearest miss. After that, the weight vector gets updated as follows:

$$W_{new} = W_{old} - (A_j - NH_j)^2 + (A_j - NM_j)^2 \quad (5)$$

Where W_{new} indicates an updated weight vector, $Wold$ represents the old weight vector, and Aj denotes a j^{th} feature vector, NHj denotes the nearest hit rate of the j^{th} feature vector, and NMj denotes the nearest miss rate of the of the j^{th} feature vector. The above process gets repeated until it reaches the iteration. At

last, the features are ranked based on the final weights 'W_{final}'.

$$R_j = rank\,[A_j(W_{final})] \quad (6)$$

Where R_j denotes a rank of feature 'j' and $[A_j(W_{final})]$ denotes the position of feature 'A_j' when the final weights are sorted in descending order. The feature with the highest weight is ranked first. Finally, the features with top-ranked or top scoring are selected based on a predefined threshold as more relevant for tumor diagnosis than the other ranked features

$$Y = \begin{cases} R_j > T, & Selecled \\ R_j < T, & Removed \end{cases} \quad (7)$$

Where Y denotes an output of feature selection, T denotes a predefined threshold, and Rj denotes a rank of feature 'j.' Select the top-ranked features with a rank more significant than the predefined threshold and remove the lower-ranked features with a rank less than the predefined threshold. The algorithmic process of Sokal–Michener's multivariate relief matching technique is given below:

Algorithm 1

Sokal-Michener's multivariate relief matching technique based on feature selection

Input

Dataset 'DS', features A_1, A_2,…A_m, datapoints or samples or instances D_2, D_z, D_z…

Output

Select to ranked feature 'A_k'

Begin

Initialize maximum iteration 'tmax,' weight vector **'W=0'**

1. Collect the number of features A_2, Az,…Amand Instances D_2, Dz,…Dn
2. Formulate the matrix using (1)
3. While ($t=t_{max}$) do
4. For each feature Aj
5. Assign the weight vector 'W' using(2)
6. End for
7. Select the instance from dataset D_R corresponding feature vector 'Aj.'
8. For each D_R
9. For each Dij
10. Measure the matching core 'SM' using(3)
11. End for
12. End for
13. if (SM = 1) then
14. instance is said to be the nearest hit
15. else
16. instance is said to be the nearest miss
17. End if
18. Update weight (W_{new}) using (5)
19. t = t + 1
20. Go to step 3
21. End while
22. Sort the weights in descending order
23. Rank the features based on weights using (6)
24. if (Rj> T) then
25. Features are selected as relevant
26. else
27. Features are irrelevant and removed
28. end if End

Algorithm 1 illustrates a process for relevant feature selection using Sokal–Michener's multivariate relief matching technique-based feature selection, aimed at improving the accuracy of brain tumor diagnosis while minimizing time consumption. The dataset serves as input to the feature selection algorithm. For each feature in the dataset, a weight value is defined. The Sokal–Michener matching score between the instances for the corresponding feature vectors is measured. Based on the score value, the nearest miss and hit are determined. Subsequently, the weight is updated until it reaches the maximum number of iterations. Then, the features are ranked according to their weight values. Finally, the top-ranked features are selected for further processing, and the other features are removed from the dataset.

Gaussian kernelized Transformer learning model for tumor disease diagnosis.

After the feature selection process, tumor disease diagnosis and risk factors are analyzed using the Transformer learning model. A Gaussian kernelized Transformer learning model is a type of deep learning architecture. The main advantage of transformer learning model having no recurrent units, and it require less training time than other deep learning model on large datasets.

Figure 2 depicts the architecture of the transform learning model, a type of deep learning network used for classification and feature learning. The transform learning structure includes an input layer, position embedding, and transformer block and decoder (i.e., fully connected layer) as shown in the above Figure 2, let us consider that the training set $\{Di,\}$ where Di denotes a training data instances with selected features '$\{A1, A2, \ldots, Ak\}$' and a label or output 'Z' representing its category which belongs to the multiple classes of seizure activity in the brain.

First, the input embedding process begins with assigning tokens to each selected instance of training data. The embedding layer then transforms these input tokens (i.e., features) into dense vectors by mapping each token to a continuous-valued representation using a weight matrix. This transformation allows the model to process and learn from the data in a format that captures both semantic meaning and relationships between tokens. This initial step is crucial for effectively giving the input data instances into a form that the subsequent layers of the model.

The positional embedding is used to incorporate positional information and assign a unique vector to each embedding output within a sequence before transmitted into the transformer layers. It also provides the model with information about the relative or absolute position information within a sequence. An absolute positional embedding method is employed for assigning a unique position vector to each data instance within a sequence. The embedding process is carried out as follows:

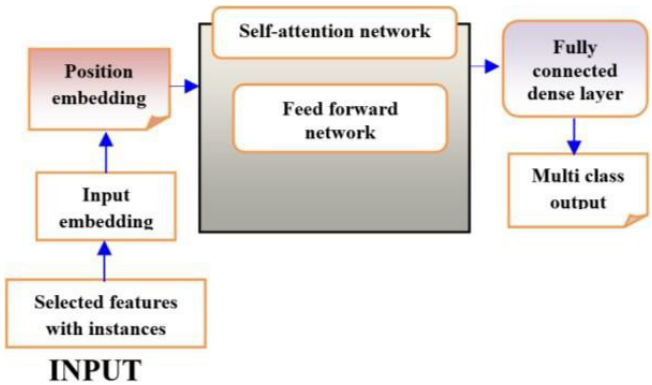

Figure 2: Architecture of Gaussian Kernelized deep transformer learning model

$$P_E(K, 2_s) = \sin\left(\frac{K}{M^{\left(\frac{2s}{d}\right)}}\right) \quad (8)$$

$$P_E(K, 2_{s+1}) = \cos\left(\frac{K}{M^{\left(\frac{2s}{d}\right)}}\right) \quad (9)$$

Where P_E denotes a position embedding, K denotes a length of sequence starti n g from 1 and going up to $n-1$, where n is sum number of instances in sequence, s represents dimension of the positional embedding vector ranges from 0 to $d-1$ where d represents the embedding size, $P_E(K, 2_s)$ represents the s^{th} dimension of the embedding for the position 'K' with a sine function, $P_E(K, 2_{s+1})$ represents the s^{th} dimension of the positional embedding for the position 'K' with a cosine function, M denotes user-defined scalar term used to scale the position index (i.e. 10,000). Based on the above equation (8) (9), the position matrix is formulated as given below:

Where $PE(D)$ denotes a position embedding matrix. These data instance position embedding matrix are transferred into the Transformer encoder layers. It involves two main layers, such as self-attention and feed-forward layers.

$$P_E(D) = \begin{bmatrix} P_{00} & P_{01} & \cdots & P_{0d} \\ P_{10} & P_{11} & \cdots & P_{1d} \\ \cdots & \cdots & \cdots & \cdots \\ P_{s0} & P_{00} & \cdots & P_{sd} \end{bmatrix} (10)$$

Self-attention method permits the method to consider the significance of dissimilar elements of the input sequence (i.e., selected features with data instances) dynamically. For each attention layer, the transformer model learns three weights such as query weights, key weights, and value weights. For each data instance, the input 'D_i' is multiplied with each of the three weight matrices as given below:

$$\left.\begin{aligned} \alpha &= D_i * w_\alpha \\ \vartheta &= D_i * w_\vartheta \\ \gamma &= D_i * w_\gamma \end{aligned}\right\} \quad (11)$$

Where, $\alpha, \vartheta, \gamma$ denotes a query, key, and value vector, $w_\alpha, w_\vartheta, w_\gamma$ learned weight matrices for queries, keys, values. The scaled dot product attention score is computed as the sum of 'ω' and the values vector 'γ.'

$$AS = \sum \omega \gamma \quad (12)$$

$$\omega = Softmax\left(\frac{\alpha_i . \vartheta_i^{\,t}}{\sqrt{d_\vartheta}}\right) (13)$$

Where AS denotes an attention score, $d\vartheta$ denotes a dimension of the Key vectors ( ), $\vartheta^{\,t}$ denotes a key vector transpose. Each component of the resulting vector 'ω' provides the output range (0, 1), and the sum of all components is 1. $Softmax$ denotes a softmax activation Function used to convert a vector of values into a probability distribution.

Feed-forward layer typically contains two linear transformations divided through a non-linear activation function like ReLU.

$$FF(D_i) = ReLU\left[D_i w_1 + b_1\right] w_2 + b_2 (14)$$

Where $FF(D_i)$ denotes a feed-forward layer with particular data instance 'D_i,' $w1$, $b1$ denotes a weight matrix, bias vector of a first linear transformation, w_2,

b_2 denotes a weight matrix as well as a bias vector of the second linear transformation.

Feed-forward layer output typically passes through additional layers, including fully connected dense layers, to perform classification. The fully connected layers combine information from the Transformer encoder's outputs and learn higher-level representations that are suitable for making brain tumor disease predictions. In that layer, the testing and training data instances are analyzed by applying the Gaussian kernel function as follows:

Where $GK(D_t, D_r)$ denotes a Gaussian kernel function, D_t represents testing data instances, and D_r represents training data instances, σ denotes a deviation, $|D_t - D_r|^2$ indicates the difference between the two data instances.

$$GK(D_t, D_r) = \exp\left[-\frac{|D_t - D_r|^2}{2\sigma^2}\right] \quad (15)$$

$$Z = \varphi_s\left[GK(D_t, D_r)\right] \quad (16)$$

$$\varphi_s = \frac{exp^{[GK(D_t D_r)_c]}}{\sum_{v=1}^{C} exp[GK(D_t, D_r)_c]} \quad (17)$$

Where, Z denotes the output of the transformer learning model, φ_s denotes the softmax activation function, which outputs probability distribution above multi-class classification results such as seizure, lpd, gpd, lrda, grda, and others based on the Gaussian kernel function output, $GK(D_t, D_r)_c$ denotes a kernel output for the c^{th} class. Through the output of the transformer learning model, patient's brain tumor severity risk levels was effectively classified. Therefore, the proposed Transformer learning approach enhances the performance of brain tumor disease diagnosis while minimizing time consumption.

//Algorithm 2: Gaussian kernelized deep transformer learning

Input: *Dataset 'Ds', selected features '{A , A ,....., A}',*

Data instances '{D1, D2, ..., Dn}'

Output: Increased brain tumor disease diagnosis accuracy

Begin:

1. Collect a number of selected features Aj € {A1,A2,…Ak} and Data instances Di € {D1,D2,…Dn}
2. For each feature Ak with data instance Di

3. Perform position embedding using (8) and(9)
4. Obtain the position embedding matrix using (10)
5. End for
6. For each data instance Di^{φ} transformer encoder
7. Measure self-attention score using (12)
8. Obtain a feed-forward neural network using(14)
9. End for
10. Measure kernel between the instances
11. 'GK(Dt, Dr)' using (15) fully connected dense layer Apply softmax activation function ' $^{\varphi}s$'
12. If $^{\varphi}s = 1$ then
13. Diagnosis of the seizure disease severity level
14. End if
15. Obtain final results → (output layer) End

Algorithm 2 outlines the process of brain tumor disease diagnosis using a Gaussian kernelized deep transformer learning model. Initially, selected relevant features are provided as input to the Transformer learning network. Each input feature undergoes a position embedding process to arrange its sequential order in the input sequence. The resulting position embedding matrix is then transferred into the transformer layer. In the transformer layer, Attention scores are computed to identify which features of the input sequence are most influential for making disease predictions. These feature vectors are subsequently fed into a feed-forward network, where ReLU activation functions in each hidden layer enable effective modeling of complex relationships within the data instances. The fully connected dense layer following the feed-forward network often reduces the dimensionality of the aggregated representation from the transformer encoder. This reduction helps in managing computational complexity and focusing on the most relevant features. A Gaussian kernel and softmax activation function serves as the final layer producing disease diagnosis outputs for classification tasks. This method aims to enhance the accuracy of brain tumor disease diagnosis.

Experimental setup

Experiments assessment of MRMGKTL model and conventional MD CNN-BiLSTM (Aravind Britto K.R *et al.*,2023) and PS+Bi-LSTM+attention (Yixuan Tang *et al.*,2024) are implemented in Python high-level language. In order to perform the experiments, HMS - Harmful Brain Activity Classification dataset is taken from https://www.kaggle.com/competitions/hms-harmful-brain-activity-classification. Main aim of this dataset is to identify as well as categorize seizures and other kinds of harmful brain activity in EEG data. The train.CSV files are used for classifying the seizures and their severity risk factors. The dataset includes a 1,06, 800 instances and 15 identifiers or attributes listed in Table 1.

Performance comparison analysis

The result analysis of the MRMGKTL model and conventional MD CNN-BiLSTM (Aravind Britto K.R *et al.*,2023), PS+Bi-LSTM+attention (Yixuan Tang *et al.*, 2024), with different parameters, is discussed.

The BTD time: it is the amount of time taken for categorizing patient information or data instances as of medical database according to total number of patient data.

$$TDT = D_n * Time(SPD) \quad (18)$$

Where TDT denotes tumor diagnosis time, D_n indicates a number of data instances, $Time(SPD)$ represents a time to classify single patient data or data instances. It is calculated in milliseconds (ms) (Table 2).

Brain tumor diagnosis accuracy

It is referred as number of patient data or data instances are classified as Brain tumor from total amount of data instances considered from dataset. It is mathematically formulated as follows.

$$Brain\ tumor\ diagnosis\ accuracy = \left[\frac{N_{CC}}{D_n}\right] * 100 \quad (19)$$

Where 'D_n' denotes the number of input patient data or data instances, and 'N_{CC}' denotes the number of patient data which properly classified. Overall accuracy is measured in percentage (%).

Precision

Precision in the multi-class classification of brain tumors refers to the capability of the method to properly recognize pertinent instances out of every instance it forecasts as positive in each class. It is calculated as the ratio of true positive forecasts to a total number of predicted positives for a given class. Mathematically, precision is calculated as follows:

$$PR = \frac{TP}{TP+FP} \quad (20)$$

Where 'PR denotes a precision, TP denotes a true positive rate (i.e., correctly classified instances), and false positive rate 'FP' (i.e., Instances that are incorrectly classified). It is measured in percentage (%).

Recall

it is also known as sensitivity used in multi-class classification of brain tumors. It calculates the proportion of actual positive samples, which are properly recognized through the method. Recall is computed as follows,

$$RL = \frac{TP}{TP+FN} \quad (21)$$

Where 'RL' denotes a recall, true positive rate 'TP' (i.e., correctly classified instances), and the false negative rate 'FN'. It is measured in percentage (%).

Specificity

It refers to a method's capability to properly recognize true negative instances for each class as the sum of true negatives and false positives.

$$SPE = \frac{TN}{TN+FP} \quad (22)$$

Where, 'SPE' denotes a specificity,'TN' indicates true negative rate and false positive rate

'FP'. It is measured in percentage (%).

F1-score

it is computed of the accuracy of a method at classification tasks, balancing both precision and recall in multi-class classification tasks.

$$F1 - score = 2 * \left(\frac{PR*RL}{PR+RL}\right) \quad (23)$$

Where, PR represents the precision, RL represents the recall. It is measured in percentage (%).

Figure 3 (a) (b) shows the performance outcomes of brain tumor diagnosis time with and without using three different classification methods: the MRMGKTL model and the existing MD CNN-BiLSTM (Aravind Britto K.R *et al.*,2023) and PS+Bi-LSTM+attention (Yixuan Tang *et al.*,2024).

When the number of instances increases (10,000, 20,000, 30,000 … 100,000), the overall brain tumor diagnosis time for all three methods increases linearly. In an experiment conducted with 10,000 data instances, the brain tumor diagnosis time with feature selection using the MRMGKTL model was found to be 65 ms. The time consumption of (Aravind Britto K.R *et al.*,2023) and (Yixuan Tang *et al.*,2024) was found to be 82ms and 74ms, respectively. From the observed results, the proposed MRMGKTL model minimizes the brain tumor diagnosis time by 19% and 10% compared to (Aravind Britto K.R *et al.*,2023) and (Yixuan Tang *et al.*, 2024), respectively. This is accomplished by applying Sokal–Michener's multivariate relief matching technique to find the significant features from the dataset weight value. Therefore, the high-ranked features are chosen as final for accurate brain tumor diagnosis, and the remaining features and their columns are removed from the dataset. This process reduces the time required for tumor diagnosis. From the observed results, the proposed MRMGKTL model reduces brain tumor diagnosis time without feature selection by 19 and 9% compared to [5] and (Yixuan Tang *et al.*,2024), respectively.

Figure 4 depicts performance outcomes of different metric comparisons, including accuracy, precision, sensitivity, *SPE*, and F1-score, for three dissimilar methods: the MRMGKTL model and the existing MD CNN-BiLSTM (Aravind Britto K.R *et al.*,2023) and PS+Bi- LSTM+attention (Yixuan Tang *et al.*,2024) (Table 3). Among the three methods, the MRMGKTL model outperforms the others in achieving higher accuracy, precision, sensitivity, *SPE*, and F1-score. This is because of applying a Gaussian kernelized transformer learning model to accurately diagnose the brain tumors associated with epileptic seizure severity levels.

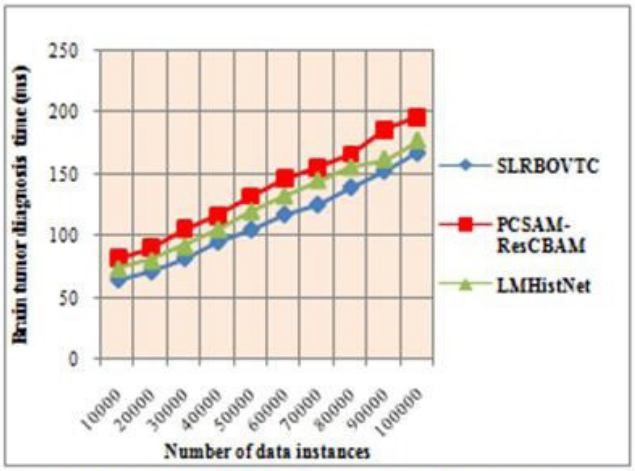

Figure 3 (a): Graphical results of brain tumor diagnosis time feature selection

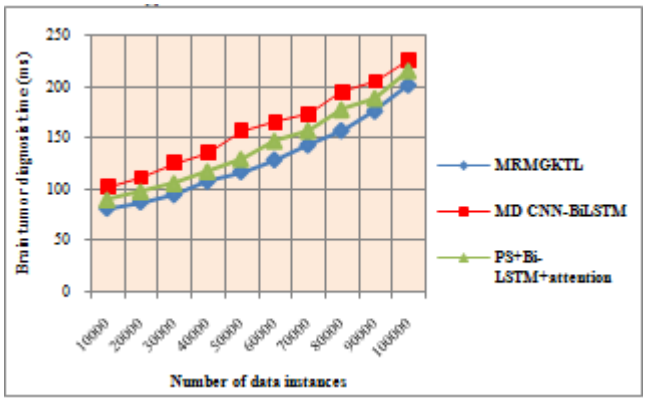

Figure 3 (a): Graphical results of brain tumor diagnosis time without feature selection

Table 2: Comparison of the brain TDT

Number of data instances	*Brain tumor diagnosis time (ms) with feature selection time*			*Brain tumor diagnosis time (ms) without feature selection*		
	MRMKTL	*MD CNN–BiLSTM*	*PS+Bi-LSTM+ attention*	*MRMGKTL*	*MD CNN–BiLSTM*	*Ps+Bi-LSTM+ attention*
10000	65	82	74	82.5	103	90.6
20000	71.5	90.5	80.6	88.6	112.3	98.5
30000	82.2	105.4	92	95.6	126.3	106.6
40000	95.4	116.5	105.6	108.7	136.4	118
50000	105.3	132	120	118	157.6	130
60000	117.5	146	132.4	129.5	166	147.6
70000	125.4	155	145	144	174	157.6
80000	139.4	165.8	155.5	158	195	178
90000	152.6	185.5	162	177	205.6	189
100000	167	195.6	176.8	202.3	226.6	215.6

Table 3: Performance parameter comparison of proposed and different conventional methods

Parameters	*MRM GKTL*	*MD CNN-BiLSTM*	*PS+Bi-LSTM + attention*
Brain tumor diagnosis accuracy (%)	96.5	88.96	93.22
Precision (%)	97.45	86.42	92.56
Sensitivity (%)	98.07	87.55	93.74
Specificity (%)	90.90	86.45	88.45
F1-score (%)	97.75	86.98	93.14

The average brain tumor diagnosis accuracy was observed as 96.5% for the MRMGKTL model, 88.96% for the existing MD CNN-BiLSTM (Aravind Britto K.R *et al*.,2023), and 93.22% for PS+Bi-LSTM+attention (Yixuan Tang *et al*., 2024). Therefore, the observed results of the MRMGKTL model are compared to the outcomes of conventional (Aravind Britto K.R *et al*.,2023) and (Yixuan Tang *et al*.,2024). Overall comparison denotes which MRMGKTL model significantly improves accuracy by 8% and 4% compared to (Aravind Britto K.R *et al*.,2023) and(Yixuan Tang *et al*.,2024), respectively.

The precision scores were found to be 97.45%, 86.42%, and 92.56% for the MRMGKTL model and the existing MD CNN-BiLSTM (Aravind Britto K.R *et al*., 2023) and PS+Bi-LSTM+attention (Yixuan Tang *et al*.,2024), respectively. From the analysis, the overall precision result of the MRMGKTL method is improved by 13 and 5% than the existing classification techniques.

Performance of recall, or sensitivity, is measured using 100,000 data instances. The results were observed to be 98.07, 82.55, and 93.74% for the MRMGKTL model, MD CNN-BiLSTM (Aravind Britto K.R *et al*., 2023), and PS+Bi-LSTM+attention (Yixuan Tang *et al*., 2024), respectively. The overall comparison outcomes show performance of sensitivity for MRMGKTL model is enhanced by 12 and 5% compared to the conventional methods.

The performance of specificity is measured by applying 100,000 data instances. The results were observed to be 98.07, 82.55, and 93.74% using the MRMGKTL model, MD CNN-BiLSTM (Aravind Britto K.R *et al*.,2023), and PS+Bi-LSTM+attention (Yixuan Tang *et al*., 2024), respectively. The overall comparison outcomes show the result of sensitivity for the MRMGKTL model is improved by 12 and 5% compared to the conventional methods.

The performance of specificity was measured, and the outcomes were 90.90, 86.45, and 88.45% using the MRMGKTL model, MD CNN-BiLSTM (Aravind Britto K.R *et al*.,2023), and PS+Bi-LSTM+attention (Yixuan Tang *et al*.,2024), respectively. The overall comparison outcomes suggest that the specificity result of the MRMGKTL model is enhanced by 5% and 3% compared to the conventional methods.

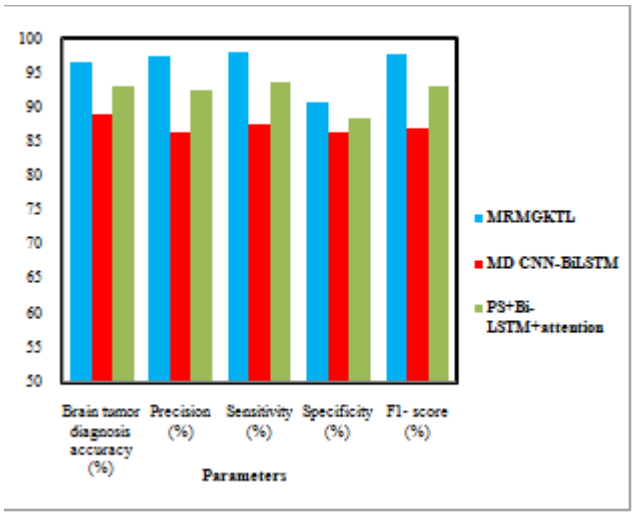

Figure 4: Overall performance results of different metric comparisons

The performance results of the F1-score for three methods, namely MRMGKTL, MD CNN-BiLSTM (Aravind Britto K.R *et al*., 2023), and PS+Bi- LSTM+attention (Yixuan Tang *et al*.,2024), were observed based on both precision and recall. The overall observed performance results show that the F1-score is 97.75% using MRMGKTL, 86.98% using (Aravind Britto K.R *et al*., 2023), and 93.14% using (Yixuan Tang *et al*., 2024). From these outcomes, it is evident which F1-score result using the MRMGKTL method is improved by 12 and 5% (Aravind Britto K.R *et al*., 2023), (Yixuan Tang *et al*., 2024), respectively.

Performance of ROC curve

It estimates a result of a classifier for positive class prediction. It plots TPR against the FPR.

Figure 5 illustrates the graphical representation of ROC curve analysis comparing the proposed MRMGKTL model with two existing methods (Aravind Britto K.R *et al*.,2023) and (Yixuan Tang *et al*.,2024). In this graphical representation,

Table 4: Tabulation for ROC curve

	TPR		
	MRMGKTL	*MD CNN-BiLSTM*	*PS+ Bi- LSTM+ attention*
1.	0.11	0.06	0.09
2.	0.33	0.15	0.21
3.	0.48	0.24	0.32
4.	0.6	0.36	0.47
5.	0.68	0.48	0.6
6.	0.78	0.6	0.68
7.	0.85	0.68	0.74
8.	0.9	0.75	0.8
9.	0.94	0.8	0.88
10.	0.99	0.86	0.92

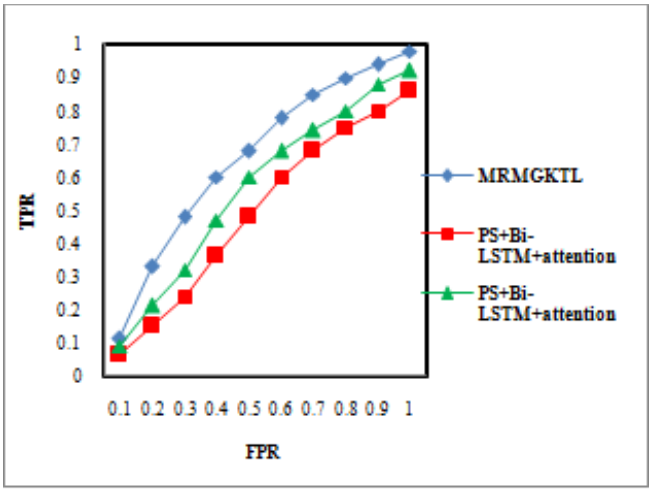

Figure 5: Performance results of ROC curve

Table 5: Confusion matrix using MRMGKTL model

	Total Instances 1,00,000	*Actual Value*		
		Positive	*Negative*	
Prescribed Value	Positive	TP = 76500	FP = 2000	78500
	Negative	FN =1500	TN= 20000	21500
		78000	22000	

the x-axis represents FPR, and the y-axis represents TPR. ROC curve analyzes brain tumor disease diagnosis based on these rates. From the Figure, it is evident that the ROC curve of the MRMGKTL model demonstrates superior performance in brain tumor diagnosis compared to the two existing methods as shown in Table 4.

Confusion matrix

It is a table employed to estimate the result of the classification method. It summarizes forecasts made through the MRMGKTL method on 100,000 data instances for which the true values are known.

- *True Positive (TP)*

Instances that are properly classified to a particular class

- *True negative (TN)*

Instances that are properly forecasted as not belonging to a particular class

- *False Positive (FP)*

Instances that are wrongly classified as belonging to a particular class

- *False Negative (FN)*

Instances that are wrongly classified into their true class.

The provided Table 5 presents the confusion matrix of the MRMGKTL method based on a dataset of 100,000 patient records. The MRMGKTL model achieved 76,500 true positives (TP) and 20,000 true negatives (TN), with 2,000 false positives (FP) and 1,500 false negatives (FN).

Conclusion

Brain tumor disease diagnosis not only enhances diagnostic accuracy but also supports healthcare providers in delivering personalized and timely care to patients, thereby improving overall healthcare outcomes in neurology and oncology. We have introduced a novel MRMGKTL method for brain tumor disease diagnosis based on seizure classification. Initially, significant features are selected from the dataset to minimize its dimensionality and reduce processing time. Subsequently, accurate classification results are achieved by applying a transformer learning model based on the Gaussian kernel function with minimal error. A comprehensive experimental assessment is conducted, incorporating different parameters. Quantitatively analyzed outcomes reveal which MRMGKTL model outperforms existing classification methods through attaining superior accuracy, PR, RL, SPE, and F1-score. Moreover, MRMGKTL method proves to be efficient in reducing the time required for brain tumor recognition compared to existing classification techniques.

Acknowledgments

The completion of this research paper would not have been possible without the support and guidance of Dr. B. Senthilkumaran, Assistant Professor, Christhu Raj College of Arts & Science. His dedication and overwhelming attitude towards helping his students is solely responsible for completing my research paper. The encouragement and insightful feedback were instrumental in accomplishing this task.

References

Ahed Abugabah, Ahmad Ali AlZubi, Mohammed Al Maitah, Abdulaziz Alarif,(2021). Brain epilepsy seizure detection using bio-inspired krill herd and artificial alga optimized neural network approaches, Journal of Ambient Intelligence and Humanized Computing, Springer, 12, 3317- 3328. https://doi.org/10.1007/s12652-020-02520-y

Ahmed Omar, Tarek Abd El-Hafeez, (2024). Optimizing epileptic seizure recognition performance with feature scaling and dropout layers, Neural Computing and Applications, Springer,36,2835– 2852. https://doi.org/10.1007/s00521-023-09204-6

Ahmed S. Eltrass, Mazhar B. Tayel, Ahmed F. EL-qady, (2021). Automatic epileptic seizure detection approach based on multi-stage Quantized Kernel Least Mean Square filters, Biomedical Signal Processing and Control, Elsevier,70,1-12. https://doi.org/10.1016/j.bspc.2021.103031

Anis Malekzadeh, Assef Zare, Mahdi Yaghoobi and Roohallah Alizadehsani, (2021). Automatic Diagnosis of Epileptic Seizures in EEG Signals Using Fractal Dimension Features and Convolutional Autoencoder Method, Big data and cognitive computing, 5(4), 1-31. https://doi.org/10.3390/bdcc5040078

Aravind Britto K.R, Saravanan Srinivasan, Sandeep Kumar Mathivanan, Muthukumaran Venkatesan, Benjula Anbu Malar M.B, Saurav Mallik, Hong Qin, (2023). A multi-dimensional hybrid CNN- BiLSTM framework for epileptic seizure detection using electroencephalogram signal scrutiny, Systems and Soft Computing, Elsevier, 5, 1-14. https://doi.org/10.1016/j.sasc.2023.200062

Chaosong Li, Weidong Zhou, Guoyang Liu, Yanli Zhang, Minxing Geng, Zhen Liu, Shang Wang, and Wei Shang, (2021). Seizure Onset Detection Using Empirical Mode Decomposition and Common Spatial Pattern, IEEE Transactions on Neural Systems and Rehabilitation Engineering, 29, 458 – 467. DOI: 10.1109/TNSRE.2021.3055276

Deba Prasad Dash, Maheshkumar H. Kolekar, Kamlesh Jha, (2020). Multi-channel EEG based automatic epileptic seizure detection using iterative filtering decomposition and Hidden Markov Mode, Computers in Biology and Medicine, Elsevier, 116, 1-14. https://doi.org/10.1016/j.compbiomed.2019.103571

Dinesh Kumar Atal and Mukhtiar Singh, (2020). A hybrid feature extraction and machine learning approaches for epileptic seizure detection, Multi-dimensional Systems and SignalProcessing, Springer, 31, 503-525.https://doi.org/10.1007/s11045-019-00673-4

Gopal Nath, Austin Coursey, Yang Li, Srikanth Prabhu, Harish Garg, Shaymal C. Halder, Saptarshi Sengupta, (2023). An interactive web-based tool for predicting and exploring brain cancer survivability, Healthcare Analytics Elsevier,3,1-11.https://doi.org/10.1016/j.health.2022.100132

Janne Nordberg, Frederic L. W. V. J. Schaper, Marco Bucci, Lauri Nummenmaa, Juho Joutsa, (2023). Brain lesion locations associated with secondary seizure generalizationin tumors and strokes, Human brain mapping, 44(8), 3136- 3146.https://doi.org/10.1002/hbm.26268

Kenichiro Asano, Seiko Hasegawa, Masashi Matsuzaka, and Hiroki Ohkuma, (2021). Brain tumor–related epilepsy and risk factors for metastatic brain tumors: analysis of 601 consecutive cases providing real-world data, Journal of neurosurgery,136(1), 76-87.https://doi.org/10.3171/2020 11.JNS202873

Kevin Akeret, Vittorio Stumpo, Victor E. Staartjes, Flavio Vasella, Julia Velz, Federica Marinoni, Jean-Philippe Dufour, Lukas L. Imbach, Luca Regli, Carlo Serra, Niklaus Krayenbühl, (2020). Topographic brain tumor anatomy drives seizure risk and enables machine learning based prediction, Neuro Image: Clinical, Elsevier, 28, 1-16. https://doi.org/10.1016/j.nicl.2020.102506

Khaled M. Alalayah, Ebrahim Mohammed Senan, Hany F. Atlam, Ibrahim Abdulrab Ahmed and Hamzeh Salameh Ahmad Shatnawi, (2023). Effective Early Detection of Epileptic Seizures through EEG Signals Using Classification Algorithms Based on t- Distributed Stochastic Neighbor Embedding and K-Means,Diagnostics, 13(11),1- 24.https://doi.org/10.3390/diagnostics13111957

Ly V. Tran, Hieu M. Tran, Tuan M. Le, Tri T. M. Huynh, Hung T. Tran and Son V. T. Dao, (2022). Application of Machine Learning in Epileptic Seizure Detection, Diagnostics, 12(11),1-26.https://doi.org/10.3390/diagnostics12112879

Minxing Geng, Weidong Zhou, Guoyang Liu, Chaosong Li, and Yanli Zhang, (2020). Epileptic Seizure Detection Based on Stockwell Transform and Bidirectional Long Short-Term Memory, IEEE Transactions on Neural Systems and Rehabilitation Engineering, 28(3), 573–580.DOI: 10.1109/TNSRE.2020.2966290 Reports,14,1-22. https://doi.org/10.1038/s41598-024-51337-8

P. Roth, A. Pace, E. Le Rhun, M. Weller, C. Ay, E. Cohen-Jonathan Moyal, M.Coomans, R. Giusti, K. Jordan, R. Nishikawa, F. Winkler, J. T. Hong, R. Ruda, S. Villà, M. J.B. Taphoorn, W. Wick & M. Preusser, (2021). Neurological and vascular complications of primary and secondary brain tumours: EANO-ESMO Clinical Practice Guidelines for prophylaxis, diagnosis, treatment and follow- up, Annals of Oncology, 32(2), 171-182. https://doi.org/10.1016/j.annonc.2020.11.003

Sadia Anjum, Lal Hussain, Mushtaq Ali, Monagi H. Alkinani, Wajid Aziz, Sabrina Gheller, Adeel Ahmed Abbasi, Ali Raza Marchal, Harshini Suresh, Tim Q. Duong, (2022). Detecting brain tumors using deeplearning convolutional neural network with transfer learning approach, International system of imaging system and technology, Wiley, 32(1), 307-323.https://doi.org/10.1002/ima.22641

Saneesh Cleatus T, Thungamani M, (2021). Classification of EEG Signals using Non-linear Features and Preprocessing Techniques, International Journal of Engineering and Advanced Technology (IJEAT), 10(5), 297-301. DOI:10.35940/ijeat.E2789.0610521

Shota Yamamoto, Takufumi Yanagisawa, Ryohei Fukuma, Satoru Oshino, Naoki Tani, Hui Ming Khoo, Kohtaroh Edakawa, Maki Kobayashi, Masataka Tanaka, Yuya Fujita and Haruhiko Kishima, (2021). Data-driven electrophysiological feature based on deep learning to detect epileptic seizures, Journal of Neural Engineering, 18(5), 1-15.**DOI:** 10.1088/1741-2552/ac23bf

Sobhana Jahan, Farhana Nowsheen, Mahathir Mahmud Antik, Md. Sazzadur Rahman, M. Shamim Kaiser, A. S. M. Sanwar Hosen, and In-Ho Ra, (2023). AI- Based Epileptic Seizure Detection and Prediction inInternet of Healthcare Things: A Systematic Review, IEEE Access, 11, 30690 – 30725. **DOI:** 10.1109/ACCESS.2023.3251105

M. V. V. Prasad Kantipudi, N. S. Pradeep Kumar, Rajanikanth Aluvalu, Shitharth Selvarajan & K Kotecha, (2024). An improved GBSO-TAENN- based EEG signal classification model for epileptic seizure detection, Scientific Reports,14,1-22. https://doi.org/10.1038/s41598-024-51337-8

Sophie von Brauchitsch, Adam Strzelczyk, Felix Rosenow, Elisabeth Neuhaus, Daniel Dubinski, Joachim P. Steinbach & Martin Voss, (2022). High end-of-life incidence of seizures and status epilepticus in patients with primary and secondary brain tumors, Journal of Neuro- Oncology, Springer, 160, 277– 284. https://doi.org/10.1007/s11060-022-04133-1

S. Syed Rafiammal, D. Najumnissa Jamal & S. Kaja Mohideen, (2021). Detection of Epilepsy Seizure in Adults Using Discrete Wavelet Transform and Cluster Nearest Neighborhood Classifier, Iranian Journal of Science and Technology, Transactions of Electrical Engineering, Springer, 45, 1103–1115. https://doi.org/10.1007/s40998-021-00437-6

D. K. Thara, B. G. Premasudha,Ramesh Sunder Nayak,T. V. Murthy, G. Ananth Prabhu, Naeem Hanoon, (2021).

Electroencephalogram for epileptic seizure detection using stacked bidirectional LSTM_GAP neural network, Evolutionary Intelligence, 14, 823–833.https://doi.org/10.1007/s12065-020- 00459-9

Vibhangini S. Wasade, Tanuwong Viarasilpa, Indranil Balki, Gamaleldin Osman, Arya Gaddam, Devanshi Dharaiya, Napolon Pellumbi, James Snyder, Tobias Walbert, Marianna Spanaki, Lonni Schultz, (2020). Effect of seizure timing on long-term survival in patients with brain tumor, Epilepsy & Behavior, Elsevier,111,1-8. https://doi.org/10.1016/j.yebeh.2020.107307

waseem Ahmad Mir, Mohd Anjum, Izharuddin and Sana Shahab, (2023). Deep- EEG: An Optimized and Robust Framework and Method for EEG- Based Diagnosis of Epileptic Seizure, Diagnostics, 13(4), 1-17.https://doi.org/10.3390/diagnostics13040773

Wenna Chen, Yixing Wang, Yuhao Ren,Hongwei Jiang, Ganqin Du, Jincan Zhang & Jinghua Li, (2023). An automated detection of epileptic seizures EEG using CNN classifier based on feature fusion with high accuracy, BMC Medical Informatics and Decision Making, Springer,23,1-17. https://doi.org/10.1186/s12911-023-02180-w

Xianwen Zhang, Liaoyuan Zheng, Jingfeng Duan, Zongping Li and Yufeng Tang, (2020). Clinical characteristics of brain tumorrelated epilepsy and factors influencing the identification of epilepsy-associated tumors,Acta Epileptologica, Springer,2,1-6. https://doi.org/10.1186/s42494-020-00034-w

Yixuan Tang, Qianyi Wu, Haifeng Mao,(2024). Epileptic Seizure Detection Based on Path Signature and Bi-LSTM Network With Attention Mechanism, IEEE Transactions on Neural Systems and Rehabilitation Engineering, 32, 304–313 DOI:10.1109/TNSRE.2024.3350074

Yuan Liu, Yu-Xuan Huang, Xuexi Zhang, Wen Qi, Jing Guo, Yingbai Hu, Longbin Zhang, And Hang Su,(2020). Deep C-LSTM Neural Network for Epileptic Seizure and Tumor Detection Using High-Dimension EEG Signals, IEEE Access, 8, 37495 – 37504. DOI: 10.1109/ACCESS.2020.2976156