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ORIGINAL RESEARCH

Brain epilepsy seizure detection using bio-inspired krill herd and artificial alga optimized neural network approaches

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Abstract
Nowadays, Epilepsy is one of the chronic severe neurological diseases; it has been identified with the help of brain signal analysis. The brain signals are recorded with the help of electrocorticography (ECoG), Electroencephalogram (EEG). From the brain signal, the abnormal brain functions are a more challenging task. The traditional systems are consuming more time to predict unusual brain patterns. Therefore, in this paper, effective bio-inspired machine learning techniques are utilized to predict the epilepsy seizure from the EEG signal with maximum recognition accuracy. Initially, patient brain images are collected by placing the electrodes on their scalp. From the brain signal, different features are extracted that are analyzed with the help of the Krill Herd algorithm for selecting the best features. The selected features are processed using an artificial alga optimized general Adversarial Networks. The network recognizes the intricate and abnormal seizure patterns. Then the discussed state-of-art methods are examined simulation results.

Keywords Brain informatics · Epilepsy · Electroencephalogram (EEG) · Krill herd algorithm · Artificial alga optimized general adversarial networks

1 Introduction

Epilepsy (Yan et al. 2015) is one of the neurological disorders that have unique characteristics and founded in Babylonian medicine text. The epilepsy disorder not only identified in human beings; it also founded in all species like rats, cats, and dogs. Epilepsy is spread all over the world because of abnormal or disturbed electrical activities (Andrzejak et al. 2001) in the brain. The brain signal disturb happened due to the low blood sugar level, shortage of oxygen at the time of childbirth and malformations. Around 50 million peoples are affected by this disease, and 100 million peoples are changed at least once in their lifespan. Therefore, this disease is most dangerous, and burden and the prevalence rate is nearly 0.5–1% (Chaudhary et al. 2011). The seizure disease is identified by several symptoms such as momentary consciousness loss, patient behavior, and sensation. According to the symptoms, Epilepsy is divided into partial and generalized types (Fisher et al. 2017). The Partial seizure is named as a focal seizure that is occurred when the cerebral hemisphere is affected. It has been divided into simple and complex partial seizures. The complex epilepsy seizure patients are getting confused about recognizing the surrounding activities and behave abnormally. The uncomplicated partial seizure patients cannot communicate properly, but they do not lose their consciousness. The generalized seizure entire brain networks are affected very fast, which is classified into nonconvulsive and convulsive (Thurman et al. 2011).

From the analysis, epilepsy seizures are more crucial in the medical field to recognize in earlier stage for eliminating the unwanted complexity. So, different machine learning techniques (Siddiqui et al. 2020) are introduced by various researchers to examine the biological and health dataset. The researchers cover different domains like machine learning techniques, artificial intelligence, data mining techniques (Aljumah and Siddiqui 2016) to provide better solutions while predicting seizure (Devi and Gomathi 2020). During the analysis process, researchers use the various brain datasets for predicting the epilepsy lateralization, seizure detection, seizure localization, and seizure sates differentiating process (Gomathi et al. 2019). This process is achieved

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with the help of multiple methodologies like the random forest, decision forest, support vector machine, artificial neural networks, and decision tree approaches. The discussed method efficiency is evaluated using various researcher reviews (Shakeel et al. 2019); from that analysis, seizures are detected correctly, but the methods did not focus on the data difficulties. So, the discussions and literature review are extended to covering the deep learning techniques (Mahmud et al. 2018) for predicting the abnormal brain pattern by resolving the data complexity. The researchers are focused on EEG data to examine the brain function using different processing steps such as data pre-processing, feature extraction (Jiao et al. 2019), selection, and classification process. From the various stages, feature extraction played a crucial role because that used to derive the exact patterns from the EEG signal (Boonyakitanont et al. 2020). The extracted patterns are more useful in discovering the brain functions and location of the seizure.

Therefore, in this research work, the EEG dataset (Quintero-Rincón et al. 2019) is used to classify the Epilepsy by applying the different optimized machine learning techniques. During the analysis process, this work uses different datasets such as European Epilepsy Database (https://www.epilepsy-database.eu/)brainstorm epilepsy dataset (https://neuroimage.usc.edu/brainstorm/DatasetEpilepsy), and UCI repository dataset (Andrzejak et al. 2001). These datasets consist of a massive volume of brain data that helps to recognize the changes in the brain patterns effectively. From the collected information, features are derived and analyzed using applying Krill Herd (KH) feature selection algorithm. The selected characteristics are further examined with the help of an optimized general Adversarial Networks; this process helps to predict the seizure effectively. By considering these methodologies, the following contributions are achieved.

- The main intention of the work is to maximizing the seizure detection accuracy by using a massive amount of brain datasets (EEG).
- To reducing the seizure prediction time and reducing the miss-classification rate using optimized feature selection and classification techniques.
- Providing a detailed explanation of feature selection for improving the seizure detection process.
- This study helps to give a detailed explanation of the feature selection process to improve the overall seizure detection efficiency.
- This study used to get the idea of how effectively the introduced method works on the different epilepsy dataset.

The above-discussed contributions are achieved by applying the effective machine learning techniques that successfully classifies the brain epilepsy. Then the rest of the paper is arranged as follows; Sect. 2 discusses the various researcher's works and analyses of the brain epilepsy recognition process; Sect. 3 elaborates the detailed working process of introduced epilepsy detection. The efficiency of the system is evaluated in Sect. 4 and concludes in Sect. 5.

2 Related works

Ahmadi et al. (2020) creating the automatic Epilepsy and psychogenic non-epileptic seizures (PNES) detection system from EEG microstate and brain features. The authors utilize the short-term electroencephalogram data for analyzing the seizures. The EEG recordings are examined depending on the microstate features, network functions, and signal characteristics. During this process, signals are divided into different bands according to the frequency level, from the analysis beta group only provides effective results while classifying the seizures.

Mera-Gaona et al. (2020) detecting epileptic spikes from EEG signals using neural networks and matched filters. The EEG signal is collected from different subjects, changes present in the brain activities are detected using mentioned networks. The identified patterns are matched with a spiked template for recognizing the abnormal features effectively. Then the efficiency of the system is evaluated using simulation results in which the system ensures 99.26% accuracy compared to the existing methods.

Yan et al. (2019) creating an emotion recognition system using memory neural networks. This system used to recognize the people's emotions from the EEG signal by creating the rhythmic characteristics and EEG temporal memory characteristics. The identified EEG features are analyzed using a defined network that classifies the people emotions according to the arousal and valence. The created system proficiency is determined in various time scales, and the introduced rhythm characteristics model ensures the effective results.

Paul et al. (2018) analyzing different seizure detection techniques for improving the seizure prediction rate. During this process, brain activities are continuously recorded because the seizure-affected ratio is increased drastically in 65 above-aged people. Therefore different seizure detection techniques are examined according to the time–frequency, time, empirical mode, frequency, and rational function. By considering these techniques, the paper discusses the methods working process that helps to improve the seizure detection process in the future.

Rahman et al. (2020) developing the effective multiclass EEG signal classification process using the Renyi min-entropy and wavelet packet transformation approach. Here, the BCI competition IV EEG dataset is used to classify the

EEG signal. The collected EEG signal is processed by applying the wavelet packet transformation process that derives the useful features. The extracted features are handled by mutual information, Shannon entropy and renyi min-entropy approach to select the best features. The selected EEG signals are examined using various machine-learning techniques that classify the EEG signal successfully. According to different research author opinions, epilepsy detection played an important role. Therefore, in this work, the epilepsy detection system is created using optimized machine learning techniques. As discussed above, several machine-learning methods are used to process the extracted EEG features without organizing any difficulties. From the various researcher opinions, in this work, bio-inspired optimization techniques are integrated with deep learning networks to recognize Epilepsy effectively.

3 Materials and methods

3.1 Dataset description

The Epilepsy is detected using bio-inspired machine learning techniques. During the implementation process system, use the three different datasets that are discussed as follows.

3.1.1 European Epilepsy Database

The European Epilepsy dataset (https://www.epilepsy-database.eu/) is created from Freiburg, Paris, and Coimbra, which is one of the largest collections of EEG recordings. Around 250 patients are analyzed, 2500 seizure-related information is gathered. The collected EEG signal has metadata information that used to examine the various subclinical seizures, clinical manifest, and interictal events. The EEG has been recorded up to 150 h with a sample rate. Based on the discussion, the collected EEG signal characteristics are depicted in Table 1.

3.1.2 Brainstorm EEG dataset

The dataset (https://neuroimage.usc.edu/brainstorm/DatasetEpilepsy) (Fig. 1) collects from the person who affected by Epilepsy with dyscognitive, secondarily seizures, and sensory seizure around eight years. The brain functions are captured with the help of an MRI image, PET image, but pathological changes are challenging to identify. Therefore, the brain's electrical activities are recognized using the EEG signal from left-frontocentral sharp waves. During the recording process 256 Hz, the sampling rate is used along with 128 channels and 16 bit A/D converter. The recorded EEG signal is pre-processed by using a high-pass filter (0.16 Hz-cut off frequency) and a low pass filter (344 Hz-cut off rate).

3.1.3 UCI- Epileptic Seizure Recognition Data Set

This dataset (https://neuroimage.usc.edu/brainstorm/DatasetEpilepsy) is generally used to recognize the epileptic seizure; it is pre-processed and re-structured version. The dataset is multi-variant; time-series characteristics around 11,500 instances are presented. Totally 179 attributes are offered, which are used to classify the seizure without creating any difficulties. The EEG recordings are captured 23.6seconds brain activities and 4097 data points in time series. The data was collected from five different activities such as seizure activities, tumor located area EEG, healthy brain area activities, eye closed EEG recordings, and eye open related brain activities are recorded. This collected EEG information is processed by applying the bio-inspired

Table 1 European epilepsy database characteristics

Patients	Sex	Age	Type of Seizure	H/NC	Origin	Electrodes	Analyzed Seizure	Interictal duration (h)
1	M	38	SP, CP, GTC	H	Temporal		3	24
2	F	15	SP, CP	NC	Frontal	G, s	5	24
3	F	26	SP, CP, GT	H	Temporal	D, g, s	5	24
4	M	14	SP, CP	NC	Frontal	G, s	5	24
5	F	16	SP, CP, GTC	NC	Frontal	G, s	3	24
6	M	13	SP, CP	NC	Temporal	G, s	5	24
7	F	31	CP, GTC	H	Temporo–occipital	D, g, s	3	24
8	M	33	SP, CP, GTC	NC	Temporo–partiental	D, g, s	5	24
9	M	44	CP, GTC	NC	Temporo–occipital	G, s	5	24
10	M	31	SP, CP, GTC	H and NC	Temporal	G, s	4	24

[a] Type of seizure: *SP* simple partial, *CP* complex partial, *GTC* generalized tonic–clonic seizure, *NC* neocortical, *H* Hippocampal, *g* electrodes grid, *d* depth, and *s* strip

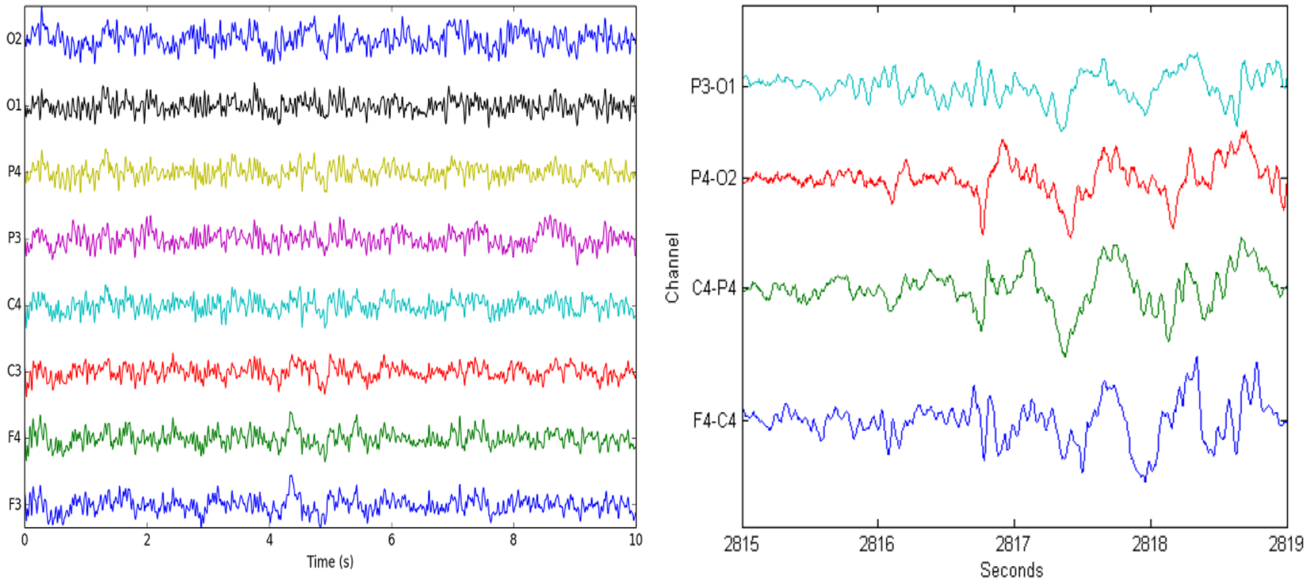


Fig. 1 Sample brainstorm EEG database

deep learning network; the detailed working process framework is depicted in Fig. 2.

Figure 2 illustrated that a seizure detection framework that has several steps, such as data collection, noise removal, seizure feature extraction, feature selection, and seizure detection. Among these steps, the EEG data collection process is explained in Sect. 3.1. The collected data is processed by the data preparation process that helps to make the system easier to predict the changes in brain activities. Here already noise removed EEG signal has been used to remove the unwanted information. From the data, different features (Islam 2019) are extracted. Here the extracted features are listed in Table 2.

Based on Table 2, the features are extracted from the collected EEG signal that is the representation of brain activities and seizure activities. The gathered EEG signal massive in dimension when it comes to the entire dataset. Therefore, the dimensionality of the dataset must be reduced by applying an optimized feature selection process. The detailed feature selection process is explained as follows.

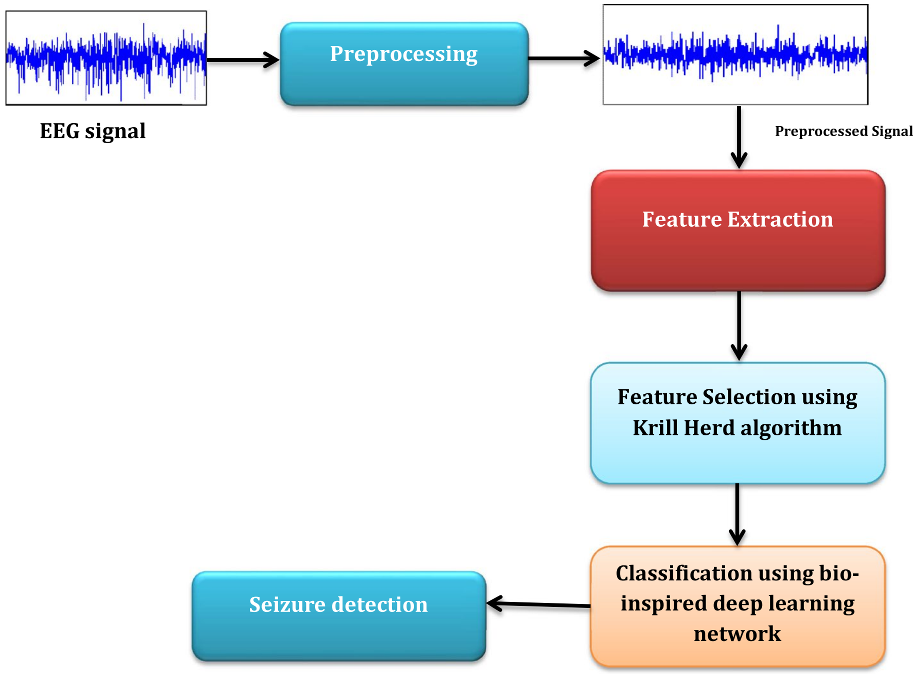


Fig. 2 Seizure detection framework

Table 2 Feature extraction

Features	Extraction formula
Mean	$\sum_{i=0}^{2(n-1)} i.p_{x+y}(i)$
Variance	$\sum_{i=0}^{n-1} \sum_{j=0}^{n-1} (i-\mu)^2.p(i,j)$
Mode	Frequent value in the EEG recordings
Median	Center value in the EEG recording
Skewness	$\frac{1}{n}\sum_{i=1}^{n}\left(\frac{x_i-\bar{x}}{\text{std dev}(x)}\right)^3$
Kurtosis	$\frac{1}{n}\sum_{i=1}^{n}\left(\frac{x_i-\bar{x}}{\text{std dev}(x)}\right)^4$
Maximum	Min (electrodes info or frequency level)
Minimum	Max (electrodes info or frequency level)
Zero-crossing	$x_j < 0\text{and}x_{j+1} > 0$ or $x_j > 0\text{and}x_{j+1} < 0$, $\left\lvert x_j - x_{j+1} \right\rvert \geq \varepsilon, \varepsilon$is threshold value
Energy	$\sum_{i,j=0}^{n-1} \left(P_{ij}\right)^2$
Shannon entropy	$\frac{1}{1-\alpha}\log\left(\sum_{i=1}^{n} p_i^{\alpha}\right)$
Sample entropy	$-log\frac{A_\delta}{B_\delta}$
Approximate entropy	$\Phi^m(r) - \Phi^{m+1}(r)$
Entropy	$\sum_{i,j=0}^{n-1} -\ln\left(P_{ij}\right)P_{ij}$
Standard deviation	$\sqrt{\left(\sum_{i=0}^{2(n-1)} i.p_{x+y}(i)\right)^2}$
Spectral entropy	$-\sum_{k=1}^{P} a_k x_{i-k} + y_i$

3.2 Feature selection

The most crucial process of this work is feature selection that is performed by applying the krill herd algorithm (KH) (Zolghadr-Asli et al. 2018). It is one of the effective bio-inspired swarm intelligent techniques that work according to the krill individuals' herding behavior. The krill individuals are poignant in the multi-dimensional search space to identify the close foods. The main reason for choosing the KH algorithm is it is select the feature similarities also resolve the multi-objective problem effectively. In addition to this, the algorithm selects the best closest food (features) from the high-density elements (groups). Here feature density is one of the critical factors because it chose the best solution from features. Suppose the KH individuals are close to the food, then the density is high, that is, if the feature is close to the seizure detection process, then the group density is high vice versa. In general, the KH algorithm searches each features for selecting the best solution based on herd with high frequency (similar group) and select closest centroid (closest food). During the feature selection process, the similarity between a feature or total distance measure (Mukherjee and Mukherjee, 2015; Hofmann et al. 2004) is used as the fitness value. The general working process of the krill herd optimization algorithm is described in Fig. 3.

The KH algorithm uses three steps to select the best features; first, the krill individual's movement is induced

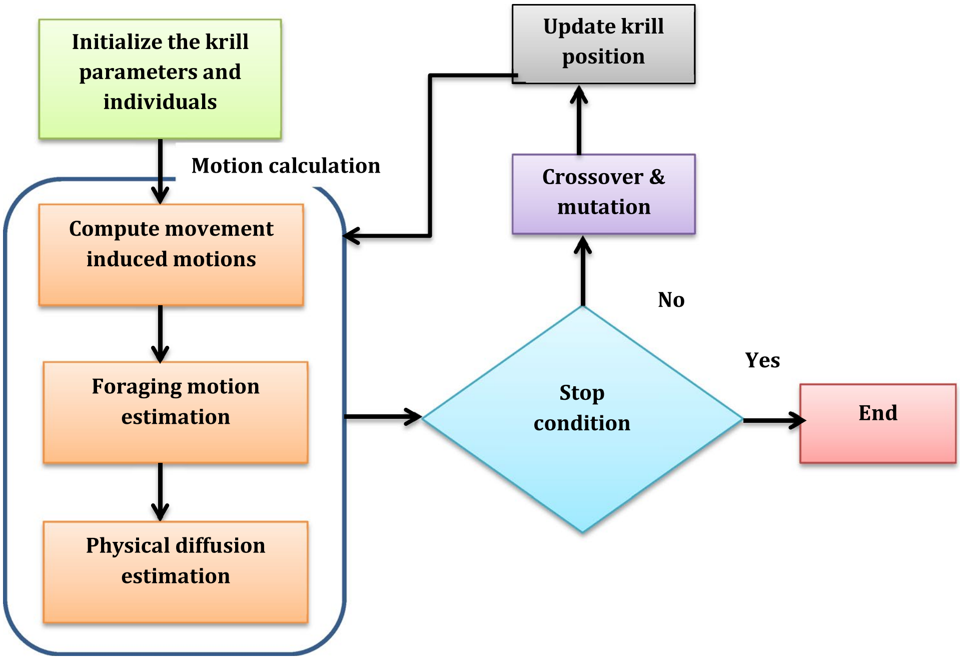


Fig. 3 Krill Herd algorithm working process

only other krill individuals (neighboring individuals may affect), foraging activity (searching for food resources) and random diffusion (net movement of individuals according to the feature density region). Initially, the i^{th} krill position is updated using the Lagrangian model defined in Eq. (1)

$$\frac{dx_i}{dt} = M_i + Fo_i + Dp_i \tag{1}$$

In Eq. (1), i denoted as krill individuals

i^{th} krill motion is represented as M_i- which is computed from local swarm density, repulsive density, and target swarm density.

Fo_i Is foraging motion of i^{th} krill individuals that is calculated from food location, food attractiveness, last individual movement, best fitness value, and foraging speed.

Dp_i Is mentioned as physical diffusion of i^{th} krill individuals. Then the individual krill values are obtained from individual random direction and maximum diffusion speed. After that, krill's first characteristics, such as movement induced by other krill, should be computed.

3.2.1 Krill movement inducement

Krill movement inducement is nothing but finding the closest food and helps to increase the density. The movement inducement direction is defined as follows

$$M_i^{\text{new}} = M^{\max}\alpha_i + w_n M_i^{\text{old}} \tag{2}$$

$$\alpha_i = \alpha_i^{\text{local}} + \alpha_i^{\text{target}} \tag{3}$$

In Eq. (2) $M^{\max}$ is tuning parameter in movement inducement

Local swarm density is represented as α_i, α_i^{local} is ith individual neighboring movement, target direction is denoted as α_i^{target}

The inertia weight value is w_n

Last updated tuning parameter is M_i^{old}

During this movement inducement, individuals are repulsive tendency, and the local neighboring movement is estimated as follows.

$$\alpha_i^{\text{local}} = \sum_{j=1}^{n} \hat{k}_{ij}\hat{x}_{ij} \tag{4}$$

$$\hat{k}_{ij} = \frac{K_i - K_j}{K^{\text{worst}} - K^{\text{best}}} \tag{5}$$

Objective function normalized value is defined as $\widehat{k}_{ij}$, K_i is the ith objective function of I neighbor and K_j is the j the neighbor objective function. The worst and best objective functions of ith krill individual is represented as K^{worst}andK^{best}. I^{th} individual related position normalized value is $\widehat{x}_{ij}$ that is estimated as follows,

$$\hat{x}_{ij} = \frac{\|x_j - x_i\|}{x_j - x_i + \varepsilon} \tag{6}$$

Individual krill current position is x_i and jth neighbor krill position is denoted as x_j

Vector normalization is $\|x_j - x_i\|$ And the singularities are avoided by small positive values such as ε. After finding the movement direction, sensing distance is estimated as follows.

$$de_i = \frac{1}{5n}\sum_{j=1}^{n} x_i - x_j \tag{7}$$

I^{th} krill individuals sensing distance is defined as de_i. The individuals are treated as neighbors if the two individual de_i values are minimal when compared to the current value. From the computation, the best fitness value is computed from Eq. (8), and the solutions are moved towards the best fitness value.

$$\alpha_i^{\text{target}} = c^{\text{best}}\hat{k}_{i,\text{best}}\hat{x}_{i,\text{best}} \tag{8}$$

$$c^{\text{best}} = 2\left(\text{rand} + \frac{I}{I_{\max}}\right) \tag{9}$$

Individual's coefficients are represented as c^{best}, $\widehat{k}_{i,best}$ i^{th} krill individual's best objective function, ith krill best position is $\widehat{x}_{i,best}$, I is the iteration number (current), and the maximum iteration number is $I_{\max}$. Once the movement induced is identified, then the respective foraging motion should be computed.

3.2.2 Foraging motion

Next, KH characteristics are foraging motion, which utilizes two processes, namely food location, and current food. The food location is identified according to the attractiveness of krill individuals. Therefore, the i^{th} krill individual foraging motion is defined as follows.

$$F_i = V_f\beta_i + \omega_f F_i^{\text{old}} \tag{10}$$

$$\beta_i = \beta_i^{\text{food}} + \beta_i^{\text{best}} \tag{11}$$

$$\beta_i^{\text{food}} = c^{\text{food}}\widehat{K_{i,\text{food}}}\hat{x}_{i,\text{food}} \tag{12}$$

$$c^{\text{food}} = 2\left(1 - \frac{I}{I_{\max}}\right) \tag{13}$$

$$x^{\text{food}} = \frac{\sum_{i=1}^{n} \frac{1}{k_i} x_i}{\sum_{j=1}^{n} \frac{1}{K_j}} \tag{14}$$

where foraging speed tuning parameter is V_f, i$^{\text{th}}$ individual food location is β_i, foraging speed inertia weight value is ω_f, food attractiveness is β_i^{food}, ith krill individuals best objective function defined as β_i^{best}. I$^{\text{th}}$ centroid normalized objective function is $\widehat{K_{i,\text{food}}}$, N is the number of krill individuals of ith position. From the analysis, best-foraging motion best value is computed as follows.****

$$\beta_i^{best} = \hat{K}_{i,best}\hat{x}_{i,best} \tag{15}$$

$\hat{x}_{i,best}$ is denoted as last visited food position and the previous best objective function is represented as $\hat{K}_{i,\text{best}}$. The computed movement induced and foraging motion minimize the iteration time.

3.2.3 Physical diffusion

Along with these two characteristics, physical diffusion must be computed to get the best solution. During this computation, the searching process is moved from high density to low-density vice versa. As discussed earlier, feature physical diffusion is computed from δ(random directional vector) and D_m (maximum diffusion speed). So, the krill individual's physical diffusion is estimated as follows.

$$D_i = D^{\max}\left(1 - \frac{I}{I_{\max}}\right)\delta \tag{16}$$

Diffusion speed tuning parameter is $D^{\max}$, the random directional vector value is $\{-1,1\}$, and the maximum iteration is denoted as $I_{\max}$. By considering these three characteristics, the optimal solutions are selected from the high-density feature set. After choosing the solution, individuals are updated for further feature selection process. The feature selection process is done as follows.

$$x_i(I+1) = x_i(I) + \Delta t \frac{dx_i}{dt} \tag{17}$$

$$\Delta t = C_t \sum_{j=1}^{n} \left(UB_j - LB_j\right) \tag{18}$$

In Eq. (18), the sensitive constant value is Δt, n is the entire amount of individuals, upper and lower bound is represented as UB_j, LB_j. The constant value is belonging to [0,2].

During the individual position updating process, the coverage problem is resolved with the help of genetic operators such as crossover and mutation. First, the crossover operator is applied to the individuals to getting the global solution that is defined as follows,

$$x_{i,m} = \begin{cases} x_{p,m} & \text{if rand} < cr \\ x_{q,m} & \text{else} \end{cases} \tag{19}$$

$$cr = 0.2\hat{K}_{i,\text{best}} \tag{20}$$

$$\hat{K}_{i,\text{best}} = K_i - K^{\text{best}} \tag{21}$$

Here p and q values are belongs to {1,2,….i − 1,i + 1,….n}. The cr value is belonging to [0,1] and the values are increased when the fitness function value is decreases. After performing the cross over process, mutation should be performed as follows.

$$x_{i,m} = \begin{cases} x_{\text{gbest},m} + \mu\left(x_{p,m} - x_{q,m}\right) & \text{if rand} < \text{Mu} \\ x_{i,m} & \text{else} \end{cases} \tag{22}$$

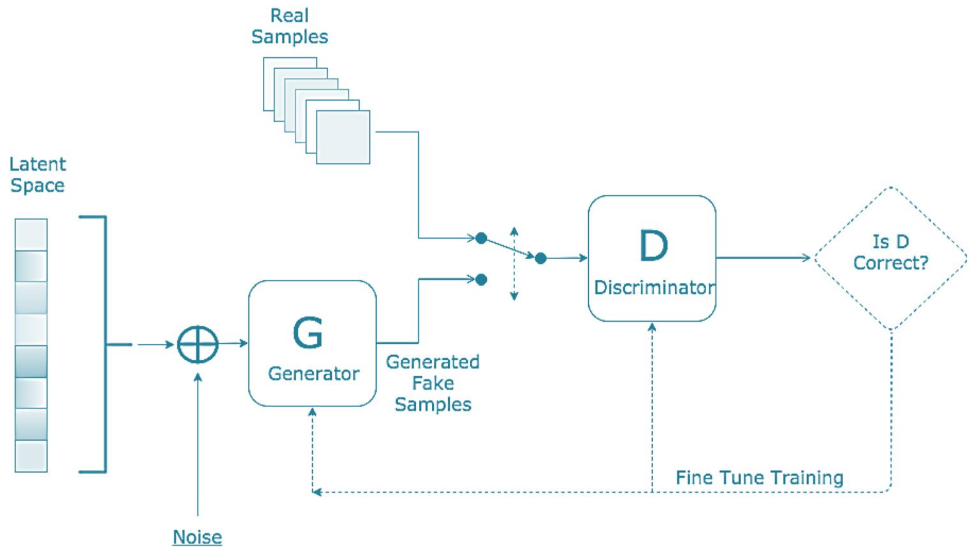
$$\text{Mu} = 0.05/\hat{K}_{i,best} \tag{23}$$

In Eq. (23) mutation probability value is computed using Eq. (23) and the p, q value is {1,2,…i − 1,i + 1…S}. The Mu value is [0, 1], which is increases with decreasing fitness. Based on the above criteria, the best features are selected to perform the classification process. In this work, around 4–8 features are selected for further research purposes. The detailed working process of classification is discussed in the following subsection.

3.3 Seizure classification using optimized general adversarial networks

The last step of this work is seizure classification that is done by applying artificial alga optimized general Adversarial Networks. The collected EEG signals are processed by multiple layers of a deep learning network that has a self-learning process that used to derive the features from the previous layer (previously programmed instruction). The extracted features are processed, and the seizure and non-seizure related features are classified and labeled for testing purposes. Once the new patient's EEG information has arrived in the system, several elements are extracted, and optimized features are selected. The selected characteristics are examined using optimized general Adversarial Networks (Goodfellow et al. 2014). The defined network is one of the deep learning networks that recognize the seizure features using two models, such as discriminative model (D) and

Fig. 4 Generalized adversarial neural network structure



generative model (G). The G model analyzes the distribution of EEG data, and the D is used to compute the probability value of incoming data using training data. These G and D model sequences trained with the help of an adversarial process. Based on the discussion, the respective neural network structure is depicted in Fig. 4. Consider the G is (z, θ_x) which represented using multi-layer perceptron is with θ_g parameter. The defined parameters are mapped with the data space, and the learning process is performed in the G distribution ρ_g with prior random input noise variable z. Then D is defined as (x, θ_d) that receives the input from G, and the output is estimated using a mini-max game function that is defined as mentioned in Eq. (24).

$$\min_G \max_D V(D, G) = E_{x\sim\rho_{\text{data}(x)}}\left[\log D(x)\right] + E_{z\sim\rho_{\text{data}(z)}}[\log(1 - D(z))] \tag{24}$$

In Eq. (24), real testing data is x, input with random noise is z, real data and input noise is represented as ρ_{data} and ρ_z. The probability of the input data is represented as D(x), which is mapped with the G(x) (Ledig et al. 2017).

During the output estimation, process the network weight value is updated by applying the artificial alga optimization approach (Korkmaz et al. 2018). The network works according to microalgae living behavior. The alga lifestyle depends on adaptation, reproduction, and algal tendency. With the help of the simulation, alga includes several processes such as evolutionary process, helical movement, and adaptation. The algal colony consists of several algal cells, and the size of the algal colony is large. Most of the time, the algal colonies are difficult to grow up due to insufficient light. In the helical movement, the algal moves to the best algal colony. The algal population is represented as follows

$$\text{Algalcolony population} = \begin{pmatrix} x_{11} & \cdots & x_{1\alpha} \\ \vdots & \ddots & \vdots \\ x_{n1} & \cdots & x_{n\alpha} \end{pmatrix} \tag{25}$$

The algal colony size is $S_i, i = 1{,}2 \ldots .n$. Objective function $f(x_i)$, and the colony size is updated continuously as follows.

$$S_i = \text{size}\left(x_i\right) \tag{26}$$

$$\mu_i = \frac{S_i + 4f\left(x_i\right)}{S_i + 2f\left(x_i\right)} \tag{27}$$

$$S_i^{t+1} = \mu_i S_i^t, i = 1, 2 \ldots ..n \tag{28}$$

Algal colony updated coefficient is denoted as μ_i.

t is represented as the current generation. As discussed earlier, the algal moves in search space, which is denoted as the helical movement phase. The movement of algal is represented as follows.

$$X_{ih}^{t+1} = X_{ih}^t + \left(X_{jh}^t - X_{ih}^t\right)\left(sf - \sigma_i\right)p \tag{29}$$

$$X_{ik}^{t+1} = X_{ik}^t + \left(X_{jk}^t - X_{ik}^t\right)\left(sf - \sigma_i\right)\cos\alpha \tag{30}$$

$$X_{il}^{t+1} = X_{il}^t + \left(X_{jl}^t - X_{il}^t\right)\left(sf - \sigma_i\right)\sin\beta \tag{31}$$

Random integers are y, z, h, k and l, algal colony coordinates are X_{ih}^t,X_{ik}^t and X_{il}^t, an independent random number is p(− 1,1), an arbitrary degree is α and β (0–2). As discussed earlier, the searching process is increased in the more significant move; then, the simulation process is performed as the most significant and smallest function of Xi and Xj. After that, the adaptation probability value is computed using Eq. (32).

$$X_s = \operatorname{argmax}\left\{\text{starvation}\left(X_i\right)\right\}, i = 1, 2, \ldots .n \tag{32}$$

It has been further elaborated as,

$$X_{sj}^{t+1} = \begin{cases} X_{sj}^{t} + \left(\text{Biggest}_j - X_{sj}^{t}\right).\text{Rand1}, & \text{if rand2} < Ap, j = 1, 2 \ldots .d \\ X_{sj}^{t} & \text{otherwise} \end{cases} \tag{33}$$

Algal colony index value is s (high starvation value, rand 1 and rand 2 is a random number having the value between 0 and 1. *Ap* is the adaptation probability value is 0.3 and 0.7. Based on the above process, the network function is optimized while predicting seizure detection. The computed output is matched with the trained features; if the matching is similar, then the network returns the output as one else zero. Thus, the introduced system classifies brain seizure with maximum recognition accuracy.

4 Results and discussion

This section discusses the efficiency of bio-inspired optimized deep learning network based epilepsy seizure detection process. The introduced system uses the different seizure datasets such as European Epilepsy Database, brainstorm epilepsy dataset, and UCI- Epileptic Seizure Recognition Data Set for evaluating the proposed method. The detailed dataset description is explained in Sect. 3.1. The collected dataset is already noise removed; there is no need to remove eliminates the unwanted information. After that, several time and frequency domain features are extracted from the EEG signal. The extracted features are more relevant to the seizure detection process. The derived details are processed by the Krill Herd optimization algorithm that recognizes the best solution according to the discussion in Sect. 3.2. The selected EEG features are prepared with the help of optimized generalized adversarial networks to acknowledge the seizure features adequately. Then the excellence of seizure detection process is evaluated using following metrics precision, specificity, recall, accuracy, and F1-score. These metrics are estimated as follows.

$$\text{Accuracy} = (TP + TN)/(TP + TN + FP + FN) \times 100\% \tag{34}$$

$$\text{Specificity} = TN/(TN + FN) \times 100\% \tag{35}$$

$$\text{Precision} = \frac{TP}{TP + FP} \tag{36}$$

$$\text{Recall} = \frac{TP}{TP + FN} \tag{37}$$

$$F1\ \text{score} = 2 \cdot \frac{\text{precision} \cdot \text{recall}}{\text{precision} + \text{recall}} \tag{38}$$

During the seizure detection process, the overall feature selection efficiency is evaluated in Table 3.

The Table 3 depicted that the Krill herd based feature selection efficiency that is compared with the several feature selection algorithms. The KHA (accuracy-98.9%, specificity-99.2%, precision -99%, recall-99% and F1-score-99.7%) which is higher than collated with remaining feature selection methods such as Genetic Algorithm (GA) (accuracy-89.9%, specificity-90.6%, precision-92.4%, recall-90.1% and F1-score-90.4%), Particle swarm optimization (PSO) (accuracy-93%, specificity-96.4%, precision-90.7%, recall-91.8% and F1-score-93.5%), Artificial bee colony (ABC) (accuracy-93.4%, specificity-94.6%, precision – 96.4%, recall-92.4% and F1-score-95.2%), fireflies algorithm (FA) (accuracy-96.4%, specificity-97.5%, precision-93.1%, recall-95.2% and F1-score-96.4%), Butterflies optimization algorithm (BOA) (accuracy-94.7%, specificity-96%, precision-94.8%, recall-96.7% and F1-score-94.2%), greedy search algorithm (GSA)

Table 3 Feature selection efficiency

Techniques	A	S	P	R	F1
Genetic algorithm (GA)	0.899	0.906	0.924	0.901	0.904
Particle swarm optimization (PSO)	0.93	0.964	0.907	0.918	0.935
Artificial bee colony (ABC)	0.934	0.946	0.964	0.924	0.952
Fireflies algorithm (FA)	0.964	0.975	0.931	0.952	0.964
Butterflies optimization algorithm (BOA)	0.947	0.96	0.948	0.967	0.942
Greedy search algorithm (GSA)	0.952	0.96	0.937	0.98	0.955
Krill herd algorithm (KHA)	0.989	0.992	0.99	0.99	0.997

[a] *A* accuracy, *S* sensitivity, *P* precision, *R* recall and *F1* f1-score

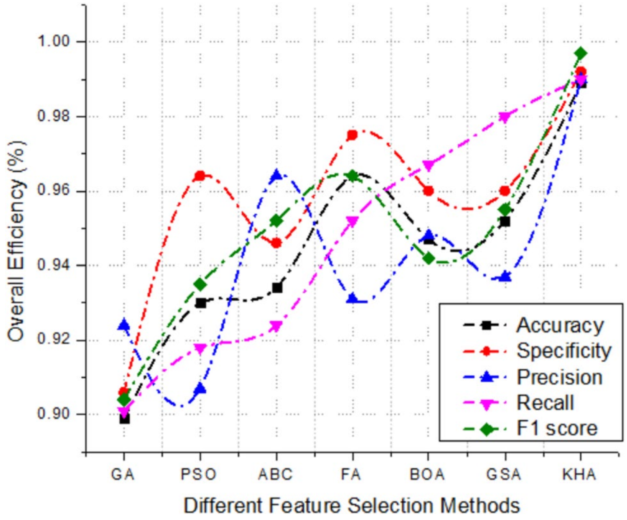


Fig. 5 Feature selection efficiency

Table 4 Selected features list

Methods	Number of features	Total no. of selected features
Genetic algorithm (GA)	50	38
Particle swarm optimization (PSO)	50	31
Artificial bee colony (ABC)	50	27
Fireflies algorithm (FA)	50	26
Butterflies optimization algorithm (BOA)	50	18
Greedy search algorithm (GSA)	50	15
Krill Herd algorithm (KHA)	50	8

(accuracy-95.2%, specificity-96%, precision-93.7%, recall-98% and F1-score-95.5%). According to above discussion respective graphical analysis is shown in Fig. 5.

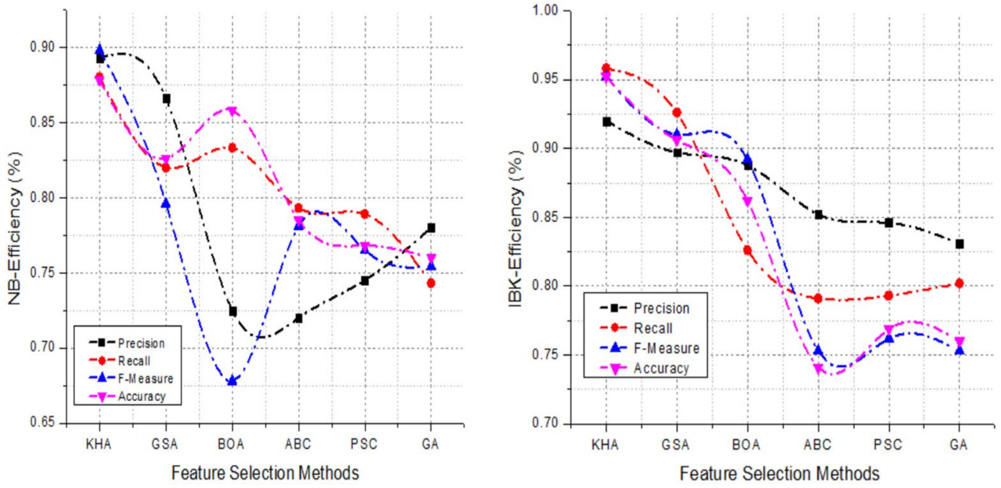
According to the above research analysis, the Krill Herd algorithm (KHA) selects the best solution or features from the overall extracted features. The algorithm uses the movement induction, foraging motion, and physical diffusion process while examining the feature characteristics. These characteristics help to choose the best solution because the searching is performed in the high-density feature set. From the analysis, the respective sample selected features are described in Table 4.

Table 4 illustrated that the number of selected features while classifying the brain epilepsy seizure detection process. Considered, this research work extracts the around 50 highlights from the EEG signal, in which introduced KHA algorithm selects the eight essential and best elements. During the selection process, different characteristics are used that helps to choose the most relevant features. These selected features are shallow compared to other feature selection methods listed in Table 3. Due to the excellent selected features, the seizure recognition accuracy is increased, and the obtained classification accuracy with different feature selection process is depicted in Fig. 6.

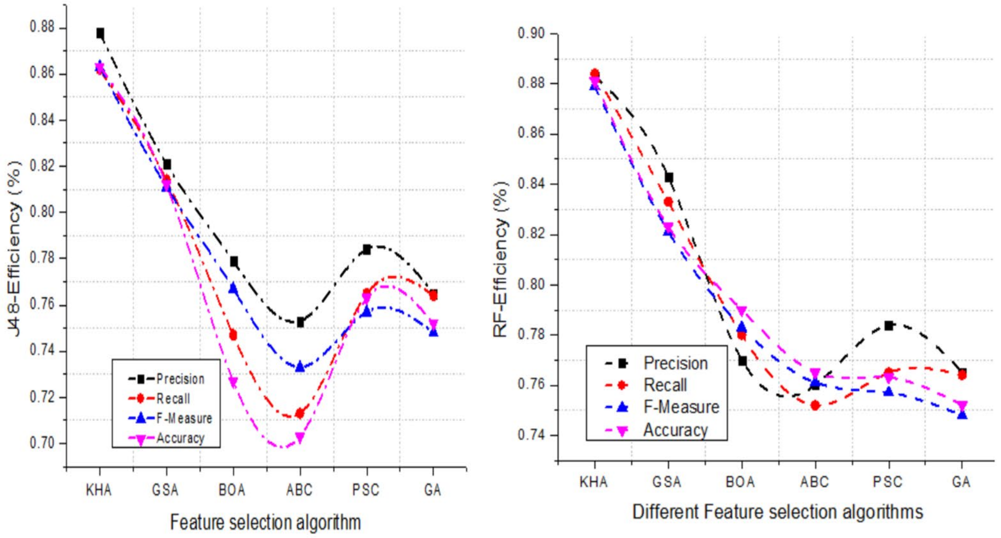
Figure 6a–f shows that the introduced Krill herd and bio-inspired optimized deep learning classification algorithms successfully identify the epilepsy seizure with maximum accuracy. Then the efficiency of the introduced Krill herd and bio-inspired optimized deep learning classification algorithm is evaluated using recall, precision, accuracy, and F-measure in which system ensures maximum accuracy (99.25%) compared to other methods. Thus the KHA and OGAN approach recognize the seizure by solving the discussed problem statement.

5 Conclusion

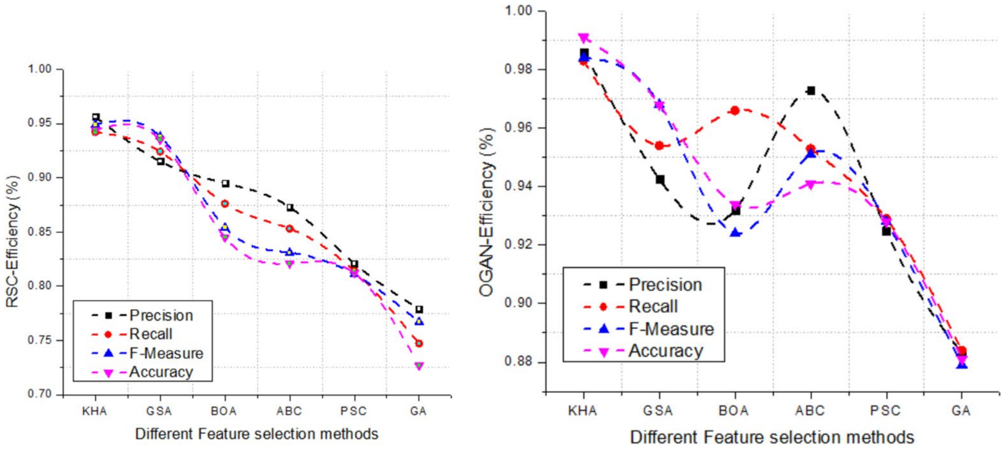
Thus the manuscript examines the EEG recordings for recognizing Epilepsy using bio-inspired deep learning networks. Initially, EEG is gathered from three different datasets such as European Epilepsy Database, brainstorm epilepsy dataset, and UCI- Epileptic Seizure Recognition Data Set. The collected information is processed by the time and frequency domain feature extraction process. From the extracted information, best and optimal features are chosen based on the Krill individual's movement induction, foraging motion, and physical diffusion characteristics. The selected features are processed according to the generator and discriminator model to recognize the testing features output. During the output estimation process, the network process is updated using the artificial algae method. Due to the effective feature selection process, the system recognizes



(a) Naïve Bayes (NB) classifier **(b)** IBK-efficiency



(c) J48 Efficiency **(d)** Random forest (RF) Efficiency



(e) RSC efficiency **(f)** OGAN Efficiency

Fig. 6 Efficiency of optimized generalized adversarial network-based seizure detection efficiency the seizure with 99.25% accuracy collated with the baseline approach. In the future, the classifier performance is improved using a meta-heuristic method.

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