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Osteoporosis Analysis using Evolutionary Algorithm

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***Abstract*—Already, a greater number of techniques and algorithms are evolving. but the existing system was lacking somewhere and had limitations in its implementation. At present, existing studies or research are done only for local optima. Local optima were the main problem in our study. The objective of the system revolves around the combination of natural and fused evolutionary algorithms with clinical expertise data to result in global optimal early detection and better accuracy of osteoporosis to get the best fitness score for the improvement of patient. We are collecting the sample data and diagnosing the patient with X-ray techniques. The X-ray image will be in noisy form. To eliminate noise in the image, we are doing the denoising and deblurring processes. After that, enhance the image, and pixel-based segmentation is done in this x-ray image. From the sample data, we are extracting features. . So, we can obtain the result from the performance parameters, i.e., whether the patient has osteoporosis or not. Through this process, we get the 97.93 best accuracy compared to other studies.**

Keywords*— Bone Mass Density (BMD), feature extraction, evolutionary algorithm - genetic algorithm, Deep learning modules, Jaccard index

I. INTRODUCTION

Analysis of Osteoporosis using evolutionary algorithms" ,Osteoporosis is a chronic disease that generally refers to a decrease in bone density due to calcium deficiency. This disease is caused by many factors such as alcohol consumption, age, medications and sometimes genetics. Osteoporosis weakens bones, making them brittle, and even the slightest stress, such as coughing or bending over, can cause bones to break. Osteoporosis of the hip, wrist, and spine is the most common. Procedures have been developed to identify high- risk groups that are candidates for treatment in order to prevent harm. The most important consequence of osteoporosis is bone loss, especially in the spine or hip. Loss of the hip bone can cause disability and increase the risk of death within the first year after injury. Examine the various factors involved in defining the bone and its parameters to deal with it. This study aims to evaluate osteoporosis using the evolutionary algorithm. An optimization method called the evolutionary algorithm is inspired by natural selection. These algorithms use techniques such as rotation, permutation, and selection to refine answers to complex questions. They are used for research and good deeds in many different fields. The aim of this study is to evaluate osteoporosis using an evolutionary algorithm. Because the pain is severe and often asymptomatic in the early stages, patients are often diagnosed with osteoporosis when a bone is broken. In order to prevent osteoporosis, methods have been developed to identify high-risk grOoups suitable for treatment. Bone density can be determined using osteoporosis tests such as dual-energy X-ray absorptiometry (DXA). BMD measurement and determination of risk groups. However, this process may not fully reflect the complexity of the disease because other genetic and environmental factors also play an important role in the development of osteoporosis. To overcome this, we use many evolutionary algorithms and Deep learning techniques to optimize and identify bones condition i.e-Osteoporosis.

A .OSTEOPOROSIS ANALYSIS TECHNIQUES

As the previous paper speaks about the Analysis Osteoporosis using several algorithms and their techniques i.e. In the year of 2018 Jae-Seo Lee et al proposed for testing, validating and training they used 2 methods (SC-DCNN) and (MC-DCNN). This technique only used in some selection criteria of the panoramic radiographs, the patient have no pathological bone or surgery history on the mandible and the patient should not have systematic disease except osteoporosis. But these techniques has several limitation i.e. This technique only used in some selection criteria of the panoramic radiographs, the patient have no pathological bone or surgery history on the mandible and the patient should not have systematic disease except osteoporosis. Few proposed the observation extracted from x-ray and clinical symptoms of patients with osteoporosis by top radiologists and orthopaedists also with some biochemical parameters. These proposed techniques also has its own limitations were the Global optimization techniques and additional info like clinical information the general. With these reference we had proposed the Analysis of Osteoporosis Using Evolutionary Algorithms.

B. ANALYSIS OF OSTEOPOROSIS USING EAs

When discussing the analysis of osteoporosis utilizing EAs, there are numerous modules that make up the process. To start ,Complex optimization: Screening for osteoporosis often requires optimization of many variables, including determining which features to use for diagnosis, treatment options, or prognosis chance of fracture. Optimization problems are good for evolutionary algorithms because of the many variables, constraints and targets ,Feature Selection: Evolutionary algorithms can be used to find the best and most important features for bone diagnosis. By selecting a small number of features from a large pool, they can reduce the complexity of the data and potentially increase the accuracy of the diagnostic model, Fracture Risk Estimation: Fracture risk estimation is important for fracture management. The development of forecasting models that take into account various risks with the help of evolutionary algorithms can make the analysis of explosion risks more efficient and reliable, Adoptability: Osteoporosis is a disease that changes over time due to lifestyle, health, and other changes. Evolutionary algorithms can update treatment plans and predictions as new information emerges, Innovative Approaches: Fusion Evolutionary algorithms with Deep learning techniques offer a new way of solving problems. They may find new ways or ideas in bone analysis that have not been considered before.

C. SCOPE OF THE PROJECTS

The importance of this project is in the field of optimization and discovery. Locally optimal solutions lead to slower convergence and higher computational costs. Medical research results are open books because of good results, problem-solving models, data privacy and security, conventions and international solutions to improve the quality of life of people affected by osteoporosis, early accident prevention, such as the evolutionary algorithm for research. and power use is under control. A better combination of indicators and the best Fitness Score Prediction.

Data Attribution
Osteoporosis data may not be available or may be popular, so data attribution is required. EA can assist in assigning missing data to improve the accuracy of data used for analysis. While evolutionary algorithms allow for improvement, it is important to remember that the effectiveness of their implementation depends on the quality of the data and the characteristics of the selection. Collaboration between orthopedics, genetics, data science and computer modeling professionals is essential to ensure the effective and ethical use of these models. When analyzing osteoporosis with data attribution, one looks at a dataset that contains different properties (features) about people, both those who have the condition and those who don't, in order to ascertain how these features affect a person& risk of getting it.

Genetic Risk Assessment
Recent research has shown that GRS, which has a wide range of therapeutic applications in disease control, can predict illness risk more correctly than the uncommon single gene prediction of disease risk. I n the year (2016 Mitchell JA el at) has proposed that the 63 BMD-related loci utilized to generate the GRS were connected with changes in BMD, and since OP is diagnosed based on BMD, the GRS might be used to predict OP. Genetic risk score (GRS) is a useful tool in assessing complex genetic diseases by combining multiple genetic loci with small effects and has been widely used in disease risk prediction like Osteoporosis. The extent to which a healthy lifestyle can offset the incident risk of OP and fracture in people with high genetic risk has not been determined, and these studies are limited to genetic factors of disease. Environmental factors also play a significant role in the development of disease. .EA can be used to analyze an individual's genetic information to find a link between genetic markers associated with osteoporosis risk. This will help find the genetics of the disease and estimate the person's risk.

Imaging Analysis
In the year 2016 Keni Zheng has proposed Especially in the elderly, osteoporosis is a common bone disease that frequently causes impairment. Low bone mineral density and the microstructural degeneration of bone tissue are the
direct causes of this disease. Currently , one of the most significant trends for supporting doctors in making accurate decisions regarding the existence and progression of this disease, in addition to clinical examinations, is the detection of this disease using X-ray imaging, despite its restricted clinical use. Numerous researchers have created computer-assisted bone image analysis approaches in this context to help in the identification of this illness. Unfortunately, the biggest obstacle is that the images obtained from an osteoporosis patient are quite similar to those obtained from healthy participants, making categorization challenging[11]. Where this limitations can be overcome by using DL-Deep Learning techniques which holds large image data. EA along with Deep Learning Techniques can help analyse medical images such as dual-energy X-ray absorptiometry (DXA) scans to identify bones. They can help identify and identify bone loss or changes in bone density that are signs of osteoporosis[7].

II OBJECTIVE AND METHODOLOGY

To find and modify appropriate evolutionary algorithms to tackle certain problems in osteoporosis analysis, including as feature selection, parameter optimization, or data-driven modelling. Selection of a particular and suitable Algorithm is a key step for the analysis of osteoporosis using Evolutionary algorithms. As Evolutionary Algorithms are used there are such popular EAs i.e. Genetic Algorithm In genetic algorithms there are subset of the algorithms that is HTGA

A. HYBRID TAGUCHI-GENETIC ALGORITHM

this algorithm is used because it is proposed to solve global numeric optimization problems with continuous variables.
The IMPROVED CATASTROPHIC GENETIC ALGORITHM (ICGA), is used to optimize reactive power[].. First, a novel catastrophic operator is suggested to improve the convergence stability of genetic algorithms.

B. DEEP LEARNING MODE

- *CNN* For the investigation of osteoporosis, combining a Convolutional Neural Network (CNN) deep learning model with evolutionary algorithms can provide a potent method for removing characteristics from bone scans and perfecting the model's architecture and hyperparameters.

- *Saimese Networks* A Pair-wise comparisons and picture similarity tasks both use Saimese networks. They can be used in osteoporosis analysis to analyse the similarity of bone structures in various photographs, which may assist detect patterns related to osteoporosis progression.

C. DATA AND FEATURE EXTRACTION

In osteoporosis the feature extraction is the specific area, where it plays a major role in order to get a precise output and identify relevant information characteristics or attributes from raw data . The goal is to improve accuracy and to attain a desire output in a precise way with efficiency in detection and diagnosis There some major feature extraction contributions ,score calculation in the Analysis of Osteoporosis Using Evolutionary Algorithms.

Bone Mineral Density Test is done by dual x-ray absorptiometry which measure how much calcium and other types of mineral are in the area of our bone .is a painless scan used in diagnosis bone loss and osteoporosis , how well medicine is working ,predict the risk fracture the result of the test are usually reported as :

- T-Score – is a comparison of patient bone density with healthy, young individual of same sex . a negative T-score of -2.5 or less at the bone defines osteoporosis .
- Z-Score- is a comparison with bone density of people of same age and sex as the patient . a negative z score of -2.5 or less should raise suspicion of a secondary cause of osteoporosis.
- Dataset- We selected a standard data set with clinical history of the patients with some feature extracted value from the x-ray images.
- Gray Level Co-occurrence Matrix (GLCM -texture analysis) is used to describe the texture properties of images , it qualifies the relationship between pairs of pixels intensities in image distance and directions among entropy, energy, contrast, homogeneity and correlation options that come with GLCM the contrast feature values accurate results.
- Principal component analysis (dimensionality reduction) is a mathematical procedure that uses linear transformation to map from high dimensional space to low dimensional ,is a dimensionality reduction that identifies important relationship of our data ,transforms the existing data based on that relationship this is achieved by covariance matrix.minimize the squared reconstruction error maximize the variance of projected input vectors.and optimal reconstruction is defined as their key property .
- Active appearance model(AAM) forms the texture, shape of the object to (shape analysis) produce a set of immediate and realistic photos .it is generative ,nonlinear, parametric model .Is originated from ASM active shape model which is more accurate and robust than ASM .In the training set calculated correlation coefficient matrix related to shape and texture the AAM connects shape and texture of PCA parameter for one group of vector and a weight vector.

D. SOFTWARE AND RESULT ANALYSIS

At first the input images are retrieved for the performance of Data-Preprocessing. After that the code for the respective Data-Preprocessing modules are fed to the software i.e. MATLAB. Once the code is fed the fusing of the segmented images to the selected features. Further fusion of the images interface with Algorithms that were choses before and with the Deep Learning techniques where the data from algorithms are Pre-trained data and the data from Deep learning are acting as Trained . At last the Performance matrix is build for the overall analysis i.e. Result analysis.

*Data Source :*We are collecting the standard data with clinical history of the patients for the analysis of osteoporosis, these data can be in several formats and in several environments which includes gender, age, height, menopause, weight, smoker, alcoholic, diabetics, no. of. pregnancies, seizer disorder, estrogens, occupation, history of fracture, etc.. The Data are in our project is in the format of images from X-Ray scan with T-score, Z-score ,BMD so that Data-pre processing can done in a precise method.

Data Pre Processing: We collected n numbers of radiographs of various bones of the body and categorized them as normal, osteoporosis, and osteopenia by concluding the results of below processes.

Denoising: The obtained noisy x-ray image is undergone a preprocessing method in two phases by utilizing the adaptive algorithm based on an algorithm 2D LPA RICI . local polynomial approximation intersection of confidence intervals have smoothed the noise locally near the thought about pixels and abstained from obscuring ancient rarities in the subsequent denoised pictures . it utilize the assessment of the commotion free picture pixel, rely upon the content and changes from one pixel to another with quadrilateral, octagonal, and hex decagonal locales, a bigger number of polynomial points expands the technique's computational weight. two, four, and eight lines crossing in the considered pixel shaping quadrilateral, octagonal and hex decagonal districts. They denoised by octagonal due their higher accuracy (peak signal-to-noise ratio of 10.50 db) instead of using different nonlinear frequency domain spatial approaches we opted 2D LPA RICI measured capabilities using MATLAB.

E. MATHEMATICAL NOTATION

ICI(intersection of confidence intervals) RULE:

The LPA-ICI method used the local polynomial approximation for design estimators. Prevents original one-dimensional ICI rule and extended to denoising 2D images[9].

We introduce original 1D signal filter procedure:

ICI algorithm introduce the range of K estimators with increasing widths h_i:

H= $\{h_1 < h_2 < \ldots < h_K\}$, ,

Holding the same probability p . it shows that exists an optimal h_k, denoted as h* , providing an optimal estimation clearly as $h_k \leq h*$

$\widehat{y_{h_k}}(n) - \Gamma \cdot \sigma_{h_k}(n) \leq y(n) \leq \widehat{y_{h_k}}(n) + \Gamma \cdot \sigma_{h_k}(n)$

RICI (relative intersection of confidence intervals) algorithm:

The ICI algorithm is highly affected by the selected value of the Γ parameter. Too large Γ value result in over smoothing and too small Γ value result in undersmoothing. so, we proposed a modification of the ICI rule to extend with 2D medical image denoising by tracking the value of the ratio the overlapping the confidence intervals and the length of the current confidence interval,[9]

$$R_{h_k}(n) = \frac{\underline{U}_{h_k}(n) - \overline{L}_{h_k}(n)}{U_{h_k}(n) - L_{h_k}(n)}$$

The $R_{h_k}(n)$ used as an additional criterion for selecting the adaptive filter width.

$R_{h_k}(n) \geq R_c$

Where R_c stands for the data driven threshold value.

Here, RICI algorithm smoothes De noise and preserves object contours and edges in the denoised image.

Deblurring: Image deblurring uses a point spread function (PSF) to deconvolve the blurred image . we uses non-blind deconvolution method which has less complex and less time consuming than other . our algorithm used in this paper is iterative Landweber algorithm. This algorithm is more stable , attain more reliable result when performing additional number of iteration.

the mathematical formula of this algorithm is ;

$$f^{n+1} = f^n + \beta H(g - Hf^n)$$

Where

f^{n+1} - new approximation from the previous f^n.

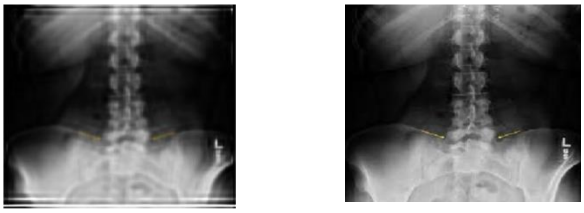
g - captured blurred image

n – number of the iteration

H – blurred function called point spread function

β – constant that controls the sharpening quantity

f^n – the first iteration same as blurred image g.



a) De-Noising ***b) De Blurring***

Fig 1. De-noise and Deblur

TABLE I-DEBLURRING

PSF	**Deblurring**			
	Algorithm	***Mathematical operation***	***PSNR***	***Execution Time (s)***
Gausian (3*3)	*Blur*	-	34.6665	-
	Iterative landweber	-	42.2980	0.1190

Enhancement: The above procedure result undergo as a input to image enhancement process which works on contrast-limited Adaptive Histogram Equalization (CLAHE) []. The purpose is to measure the characteristics and structure of the picture, sharpen image details and to result better quality image. we employed by converting each pixel with a derived function from a neighboring region, CLAHE differs from conventional equalization. An x-ray picture typically has the following gray color space, high noise , low intensity , poor contrast , weak boundaries which impact on the content. The information about the pixel's intensities is represented via gray scale picture. The range of pixel intensity is 0 (black) to 255 (white). (0-255) Through modification and adjustment of the gray-level intensity, CLAHE may give a strong contrast. This is possible with the use of the histogram equalization approach. Adaptive histogram equalization is used by CLAHE to improve the contrast in a limited area of the picture (tiles) [].

c)Enhancement

Fig 2. Enhancement

TABLE I-DEBLURRING

CLAHE			
TP	***FP***	***FN***	***TN***
32.20%	34.10%	32.40%	33.30%
CLAHE			
Image	***Accuracy***	***Sensitivity***	***Specificity***
X-RAY	0.9754	0.10224	0.9959

TP-True Positive

FP-False Positive

FN-False Negative

TN-True Negative

Segmentation: Obtained clear image being segmented using K-means cluster technique , K- means clusters are used to separate groups of people with similar qualities and place them in groups. The k-means algorithm locates groups in data, with the variable 'k' representing the number of groups. The digital images are divided into various group of pixels or object via image segmentation, making it simpler to describe and analyse the images. K-means clustering, an unsupervised learning approach, is used to discover several classes or clusters in the provided data based on how similar the data is. K must be a positive integer. Clustering is a pixel-based segmentation method and is usually used for large-sized images. Since it is pixel-based, clustering involves relatively simple algorithms, and its complexity is generally lower than that of region- or edge-based segmentation methods. Automatic segmentation of the trabecular bone area in periapical radiographs for osteoporosis detection. But isn't guaranteed to bring about improved precision value so we are going with intersection over union (IOU) for high accuracy.

Consider a picture that has to be clustered into k number of clusters and has a resolution of x*y. Let ck be the cluster centers and let p(x, y) be an input pixel to be clustered. The k-means clustering algorithm is as follows:

1.Initialize the cluster k and center numbers.

2. Using the connection shown below, get the Euclidean distance d between the center and each pixel of a picture.

$$d = \| p(x\,,y) - c_k \|$$

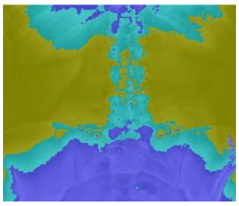
3. Based on the distance d, assign each pixel to its nearest center.

4. Once every pixel has been assigned, use the relation below to recalculate the center's position.

$$c_k = \frac{1}{k} \sum_{y \in c_k}^{\infty} * \sum_{x \in c_k}^{\infty} p(\,x\,,y)$$

5. Continue the process until the tolerance or error value is met.

6. Resize the pixels in the picture cluster.



d)Segmentation

Fig 3. Segmentation

Feature Extraction: Feature extraction in osteoporosis analysis using evolutionary algorithms refers to the process of selecting or generating a subset of relevant and informative features from a larger set of potential features obtained from medical imaging or other data sources[]. Osteoporosis analysis often involves the use of medical images and clinical data to diagnose and assess the condition of bones.

Gray Level Co-Occurrence Matrix: GLCM is a feature detector that looks for the intensity relation in image captures spatial relations of pixel intensities, image data is used to create matrix co-occurrence[]. This method is a way of extracting second order statistical texture features. The GLCM functions characterize the texture of an image by calculating how frequently dyads of pixels with specific values and in a specified spatial relationship do in an image, creating a GLCM, and also rooting statistical measures from this matrix.A GLCM is a matrix where the number of rows and columns equal to the number of gray level ,G , in the image[]. the four important features are ,

Angular second moment (energy) is a uniformity energy . It is the sum of squares of entries that measures image homogeneity .ASM is high when pixels are similar .

$$\text{ASM}= \sum_{i=0}^{Ng-1} \sum_{j=0}^{Ng-1} P_{i^2 j}$$

where i,j are sapital coordinates of function p(i,j), Ng is gray tone .

Inverse Difference Moment (IDM) is local homogeneity .It is high when local gray level is uniform and inverse GLCM is high[10] .IDM weight value is the inverse of contrast weight.

$$\text{IDM} = \frac{\sum_{i=0}^{Ng-1} * \sum_{j=0}^{Ng-1} * P_{IJ}}{1+(i-j)^2}$$

Entropy shows the amount of information of the image that is needed for image compression. measures the loss of information in a transmitted signal and also measures the image information.

$$ENTROPY = \sum_{i=0}^{Ng-1} * \sum_{j=0}^{Ng-1} * - P_{ij} * log P_{ij}$$

Correlation measures linear dependency of grey levels of neighbour pixels[7,10].

$$Correlation = \frac{\sum_{i=0}^{Ng-1} * \sum_{j=0}^{Ng-1} * (i,j) p(i,j) - \mu_x \mu_y}{\sigma_x \sigma_y}$$

The formulation and extraction of the four given image features are extraction using matlab for calculating GLCM as images cannot be directly given as input to implement.[]

All the texture features are real numbers which show only bits as outputs .By extracting the features of an image by GLCM approach ,the image compression time can be greatly reduced in the process of converting RGB to gray level image when compared to other DWT techniques.

Principal Component Analysis **:**Is beneficial in reducing the computational burden and removing multicollinearity among features which can lead to more efficient and effective feature .this is unsupervised algorithm, therefore doesn't care about data labels but only about variations, our original data is projected into a set of orthogonal axes and each of the axes gets ranked in order of importance . We take as input our original data and try to find a combination of the input features which can best summarize the original data distribution so as to reduce its original dimensions. Is a dimensionality reduction that identifies an important relationship of our data, transforms the existing data based on that relationship this is achieved by covariance matrix. It puts all features along the axes where the variance of the first principal component is highest when compared to other principal components. the linear transformation defined as

$$y = Wx$$

The stationary transforming stochastic data $x \subset R^N$ into vector $y \subset R^K$ using the matrix $W \subset R^{KxN}$ dimension reduction by K<N in output space y but most important information compact in the input space x

$$R_{xx} = E[xx^T]$$

where x be random vector of zero mean R_{xx} in correlation matrix all vector X_i.the eigen values can be sort from highest value $\lambda_I$to lowest value λ_N and in similar way eigenvector W_i associated with them. according to eigendecomposition principal equation can be

$$R_{xx} = \sum_{k=1}^{N} * \lambda_i w_i w_i^{T^1}$$

If the eigenvalues' magnitudes are of the least magnitude, the association of eigenvectors will be ignored. K is therefore more significant than N eigenvalues, . You can rewrite W in the PCA transformation matrix as W=[w1, w2,...,wk] T.Here, x stands for the reconstruction's original vector and is defined by equation.

$$\underline{x} = W^T y$$

Here the axes correspond to the largest Eigenvalues of the data. PCA maximizes variance of extracted features which are uncorrelated. also evaluated using (accuracy, sensitivity , specificity , AUC-ROC).

$$Variance\ of\ PC1\ and\ PC2 = \left(\frac{\lambda_1 + \lambda_2}{\sum_{i=1}^{P} * \lambda_i}\right)$$

Compute the feature vector by multiplying the image vector with selected components .

*featureVector= imageVector *selectedComponents;*

Reduce the dimensionality without losing information from any featuresReduce the storage needed to store data,Speed up the learning algorithm ,Address the multicollinearity issue (all principal components are orthogonal to each other)

Acitve Appearance Model: AAM forms the texture, shape of the object to (shape analysis) produce a set of immediate and realistic photos .it is generative ,nonlinear, parametric ,deformable model[] .Is originated from ASM active shape model which is more accurate and robust than ASM and require more computation time . AAM can be used to capture and model the variability in bone shape and texture across different subjects and reduce sensitivity . the typical workflow involves,[]

- Training the model on dataset with point of interest
- Learning a shape model and texture model their variations
- Aligning the model to a new image to locate landmarks

The correlation coefficient matrix is analyzed using PCA .the eigen vectors P of C are a hybrid parameter required for the form and texture of an AAM.***Ci=C+A.(P.b)*** can be proposed for each pattern in the training program ,here the diagonal matrix and diametrical contrast correspondents to ith coefficient are pointed out as C [12]. the extracted image feature can be found a h^{AAM} , which is used to extract image in a single method as $A^{A}AM$.

III - EVOLUTIONARY ALGORITHM

Evolutionary algorithm have been applied to study osteoporosis by optimizing treatment strategies identifying genetic factors and predicting bone density changes .these algorithm simulate natural selection processes to find optimal solutions ,aiding in the development of personalized interventions and better understanding of osteoporosis progression . Inserted all these collected results into a minimum of four evolutionary algorithms classified as genetic algorithm from the genetic algorithm chose a hybrid Taguchi-genetic algorithm (HTGA) and Catastrophic Genetic Algorithm ,differential algorithm , metaheuristic algorithm .

A. ALGORITHM SELECTION:

An algorithm may become caught in the local optima of the objective function in global optimization problems when the dimension is large and there are many local optima.

we used *HTGA- HYBRID TAGUCHI(HTGA)-GENETIC ALGORITHM* and *CATASTROPHIC GENETIC ALGORITHM* where both are genetic algorithm where a hybrid Taguchi-genetic algorithm (HTGA) is proposed to solve global numerical optimization problems with continuous variables. The HTGA combines the traditional genetic algorithm (TGA), which has a powerful global exploration capability, with the Taguchi method, which can exploit the optimumoffspring[2,8]. The Taguchi method is inserted between crossover and mutation operations of a TGA and for optimal reactive power optimization we used ICGA to enhance the genetic algorithm Convergence stability is proposed is solve the main conflict of convergent speed with global astringency[2]. in the presence of multiple genetic algorithms like non-dominated sorting GA, and contextual GA, we used ICGA and HTGA.

B. GENETIC ALGORITHMS:

The primary distinctive characteristic of the GA as an optimization approach is its latent parallelism, which results from the process of evolution and hereditary behavior[2,5]. First, GA improvements have been attempted in the ideal ratio and adaptation of the key parameters, namely population size, crossover operator, likelihood of mutation, and probability of crossover.

C.HYBRID TAGUCHI-GENETIC ALGORITHM

The HTGA combines the Taguchi techniques which may take advantage of the ideal offspring with the classic genetic algorithm, which has a strong potential for global exploration[6,11]. The HTGA can then be more trustworthy, statistically sound, and quickly convergent. The proposed HTGA is effectively applied to solve 15 benchmark global optimization problems in the range of 30 to 100 dimensions and a large number of local minima. The outcomes of these computer tests demonstrate that the suggested HTGA strategy is more dependable and efficient than a method that has been published in the literature when it comes to locating optimal or nearly optimal solutions[12]. Hybrid approaches occasionally combine two or more distinct optimization or analytical techniques in order to maximize each technique's strengths and reduce its weaknesses. In order to optimize a process connected to osteoporosis, a hybrid Taguchi genetic algorithm technique would combine Taguchi methodology with genetic algorithm principles.[]

Taguchi Technique: The parameter design technique proposed by Taguchi is a crucial tool for robust design. A robust design strategy is an approach to engineering that focuses on minimizing sensitivity to variation-causing factors while producing high-quality products at cheap development and manufacturing costs. Two essential tools in the Taguchi method are the orthogonal array and the SNR[]. Standard orthogonal arrays with two levels use the following generic symbol:

$$L_n(2^{n-1})$$

The SNR combines multiple repeats into a single value that depicts both the degree of variation and the mean response.

The SNR has been utilized as the preferred quality characteristic in the field of communication engineering. This idea was included in the design of experiments by Taguchi, a communication and electrical engineering graduate. The SNR has been utilized as the preferred quality characteristic in the field of communication engineering[]. This idea was included in the design of experiments by Taguchi, a communication and electrical engineering graduate. Assume we have a collection of qualities in the instance of the smaller-the-better feature[]. The natural estimate is thus

$$S = \frac{1}{n}\sum_{t=1}^{n} y_t^2$$

$$\eta = -10log\left(\frac{1}{n}\sum_{t=1}^{n}\frac{1}{y_t^2}\right)$$

The books provided by Phadke contain more information as well as comprehensive description arrays.

D.IMPROVED CATASTROPHIC GENETIC ALGORITHM

The ICGA (Improved Catastrophic Genetic Algorithm) is used to optimize reactive power. First, a novel catastrophic operator is suggested to improve the convergence stability of genetic algorithms[]. The major tension between the convergent speed and the global astringency is then resolved by a new probability algorithm of crossover depending on the number of generations and new probability algorithm of mutation depending on the fitness value. The ICGA can prevent genetic-catastrophic algorithms (GCA) from convergent too soon and becoming unstable in this method. Giving a suitable value for N0 and choosing how to create new people are the two main components of a catastrophic operation. In a conventional catastrophic operation, N0 has a constant value.In terms of the catastrophic operator, Nc, or the number of newly generated individuals, is the source of exploration. By keeping Nc low, the algorithm is able to take advantage of the more capable individuals[]. The algorithm can explore multiple solution spaces by increasing Nc.

The study shown above suggests that by varying Nc in accordance with the number of generations, the convergence features of GA can be enhanced. Nc is therefore given as:

$$\boldsymbol{N_C} = \text{Integer}\left[\boldsymbol{exp}\left(\frac{-a \times t}{T_{Gen}}\right) \times N_0\right]$$

Where N0 is the maximum number of newly generated individuals, TGen is the maximum generation, Integer is a rounding sign, and t is the current generation.

The choice of pc and pm is believed to have a substantial impact on how well the GA performs. The pc determines how quickly solutions are subjected to crossover; the greater the value of pc, the faster new individuals are added to the population, and vice versa[12]. When a population converges to a global optimal solution (or even a local optimal solution), pc and pm increase and may cause the disruption of the near-optimal solutions, therefore, it is hoped that pc is given a high value to create more individuals at the early stage of evolution and maintaining a relatively low value for the purpose of protecting superior individuals and algorithm’s stability at the late stage of evolution process, in this paper, pc is gradually decreased depending on the number of generation in sigmoid function form:

$$P_c(t) = \frac{(P_{cmax} - P_{cmin})}{1 + exp\left(\frac{-A \times (T_{Gen} - 2t)}{T_{Gen}}\right)} + P_{cmin}$$

where pc(t) is crossover probability generation in t generation, Pcmax is maximum crossover probability, Pcmax is minimum crossover probability.PM is adjusted according to each individual's fitness value and number generation.

$$\mathrm{P_{mt}} = \left(\frac{f_{max} - f(X_i)}{f_{max}}\right) \times \frac{(\mathrm{P_{m\,max}} - \mathrm{p_{m\,min}})}{\left(\frac{-A \times (\mathrm{T_{Gen}} - 2t)}{\mathrm{T_{Gen}}}\right)} + \mathrm{P_{mmin}}$$

Example1.1

TGen is provided with 100, and the population size for all functions is 64. Pcmax = 0.9, Pcmin = 0.5, Pmmax = 0.1, Pmmin = 0.01 for the SGA, Pc = 0.9, Pm = 0.1, and k1 = k3 = 1 for the AGA. Pcmax = 0.9, Pcmin = 0.5, Pmmax = 0.1, Pmmin = 0.01, a = 10 and N0 = 59 are the values for the ICGA. When each GA achieves a solution with an objective functional value of f1 (f2) equal to the threshold 0.0001, the algorithm will stop.[12]

E. METAHEURISTIC ALGORITHM

Hybrid metaheuristic optimization algorithm is developed on fusing two nature inspired metaheuristic optimization algorithm namely *Artificial Algae Algorithm* (AAA_{ML})with multi light source and *Hybrid Monarch Butterfly Optimization Algorithm* (HMBA), to increase the accuracy of diagnosis of ELM is optimized with HMBA they resulted in terms of sensitivity, specificity accuracy and precision. Even though ANN yield good performance but ELM always proved to be efficient because ofits tunning free nature and less computation time and increase the number of hidden nodes for better performance as there are directly proportional which leads to network complexity overcome by ELM optimized with meta heuristic efficient even with less number of hidden neurons.[2,8]

Related Work for Above Algorithms:

From 3426 data, osteoporosis was found using 20 different machine learning (ML) algorithms. Tenfold cross validation was used to evaluate the classifiers, and the results show that the classifiers' highest accuracy is less than 75%. When used to categorize data on osteoporosis with 141 records, the ANN improved using the monarch butterfly optimization algorithm has obtained 99.3% accuracy. Osteoporotic categorization is where ELM optimized with such effective meta-heuristics is first used. The HMBA-ELM classifier is presented system framework for osteoporosis dataset classification.

In 2015, S. A. Uymaz et al. created AAAML based on the living behavior of microalgae. This algorithm is based on how microalgae behave while they are alive . It is known that the algae are photosynthetic organisms. As a result, they are always dependent on light to complete the process of photosynthesis and obtain enough food. In order to survive, they adapt to their surroundings; otherwise, they perish. They divide during mitosis to reproduce. Algal population is made up of a collection of colonies of algae.[]

Artificial Algae Algorithm: The AAAML goes through three phases: helical movement, reproduction or evolution, and adaptability.

Helical movement phase: Each algal colony makes an effort to get closer to the water's surface in order to get enough sunlight to survive. They move in three separate dimensions in helical patterns. In other words, they move in three separate directions—one direction in each direction—in a helical motion toward three different light sources (multi-light source). A number of variables, including energy (g), friction surface (), and shear force (), have an impact on this movement[].When moving on a surface with less friction and more energy, algae can go farther. This increases the scope of searches without limiting them to local minimums. Utilizing, the friction surface is computed using

$$\tau(A_i) = 2\pi\left(3\sqrt{\frac{3G_i}{4\pi}}\right)^2$$

The other three alternative light sources (j, r, and v) are chosen using the Tournament selection method to carry out the helical movement by algal colony I. As a light source, other algae colonies are maintained. Due to the fact that this method requires multiple parent recombination, it is referred to as multi-light source movement[]. These light sources randomly choose m, k, and l, three separate algal cells. Consequently, three equations are used to express the helical movement using several sources.

$$a_{i,m}^{t+1} = a_{j,m}^{t} + \left(a_{r,m}^{t} - a_{v,m}^{t}\right)\left(\Delta - \tau^{t}\left(a_j\right)\right)\rho, \rho\epsilon[-1,1]$$

$$a_{i,k}^{t+1} = a_{r,k}^{t} + \left(a_{v,k}^{t} - a_{j,k}^{t}\right)\left(\Delta - \tau^{t}(a_r)\right)cos\gamma, \gamma\epsilon[0,2\pi]$$

$$a_{i,l}^{t+1} = a_{v,l}^{t} + \left(a_{j,l}^{t} - a_{r,l}^{t}\right)\left(\Delta - \tau^{t}(a_v)\right)sin\beta, \beta\epsilon[0,2\pi]$$

Where, $a_{i,m}^{t+1}, a_{i,k}^{t+1}, a_{i,l}^{t+1}$ and represent the ith algal colony's x, y, and z coordinates at time t+1; i = 1, 2,... NP; i = j = r = v; ijrv; and m, k, l = 1, 2,...Dm, m≠k≠l. The shear force is. The friction surface area of the ith algal cell is t(a,j,r,v). During the helical movement process, only three algal cells from each algal colony are present[]. This new algal colony's fitness has been calculated

Evolutionary phase: An algal colony that receives enough nutrients (and is in adequate physical condition) expands in size and divides through mitosis. In the alternative, the smaller algal colony, which lacks adequate nutrients, perishes[]. Algal cells from the largest algal colony are substituted for those from the smallest algal colony, which is dying. The largest and smallest algal colonies are located for this. A randomly selected algal cell is used. The smallest colony's mth algal cell dies and is replaced by the largest colony's mth cell. That is when the biggest colony's mth cell replicates. The following equations are used to express this replication process.

$$biggest^{t} = maxG_i^{t}, i = 1,2, \dots NP$$

$$smallest^{t} = mixG_i^{t}, i = 1,2, \dots NP$$

$$smallest^{t}{}_{m} = biggest_m^{t}, m = 1,2, \dots NP$$

Adaptation phase: The execution of the adaptation process is determined by the adaptation parameter (AP). The starving colony (colony with a high starvation value) is chosen for this[]. The adaption parameter is compared to a random value. If it falls short of AP, the process of adaptation begins. Eq is employed to express it.

$$Starv^{t} = max\left(STARVE_i^{t}\right), i = 1,2, \dots NP$$

$$Starv^{t+1} = Starv^{t} + (biggest^{t} - smallest^{t}) * rand$$

Where $STARVE_i^t$ is the starvation value of the ith algal colony in time t. Starvt is the colony with maximum starvation value at time t. AP Є [0,1]. The best colony is chosen as biggest colony for this phase. These three phases are repeated for required number of generations or till the best solution is achieved. The pseudocode of AAAML is given below. The helical movement phase which helps in the modification of algal colonies, provides the balance between exploration and exploitation[]. The exploitation is further helped by adaptation phase and evolutionary phase.

typically AAAML follows three phase Based on their optimization fusion ,

- Evolutionary phase
- Adaptation phase
- Helical Moment Phase

Evolution migrated AAA_{ML} technique is the upgraded evolutionary phase of HMBA algorithm .to distinguish osteoporosis data from normal ones , the ELM is optimized using HMBA[11].

Hybrid Monarch Butterfly Optimization Algorithm (HMBA)

We examine the experimental details of the proposed HMBA classifier, such as GA (Genetic algorithm)-ELM, DE (Differential evolution)-ELM, AAAML-ELM.

The HMBA-ELM approach Following are the instructions for classifying an osteoporosis dataset using HMBA-ELM[].

1. Load the training data for osteoporosis, then initialize all the parameters.

2. The training data was normalized.

3. Set the algal population's initial value at random.

4.Determine the fitness of each algal colony.

Use the below to calculate the H hidden neuron output matrix.

$$H=\begin{bmatrix} h(X_1)\\ \vdots \\ h(X_N)\end{bmatrix} = \begin{bmatrix} g(\omega_1.x_1+b_1) & \dots & g(\omega_L.x_1+b_L)\\ \vdots & \ddots & \vdots\\ g(\omega_1.x_N+b_1) & \dots & g(\omega_L.x_N+b_L)\end{bmatrix}_{NXL}$$

Use $\beta = H^{\dagger}T = \begin{bmatrix}\beta_1\\ \vdots \\ \beta_L\end{bmatrix}_{NXL}$ to compute the output weight.

Use $y = f_L(X) = \sum_{i=1}^{L} \beta_i h_i(X) = h(X) = h(X)\beta = H\beta$ calculate the output of the training data.

Determine fitness for the training date or RMSE

Formulation of fitness functions

Between the goal output and network output, the RMSE is determined. The fitness function of

6. Determine the size of the algal colonies

7.Calculate the energy and surface friction of algal colonies.

F. DEEP LEARNING CLASSIFIER

Our algorithm's evaluated generation results are feed to deep learning classifier models -CNN, SAIMESE NETWORKS.

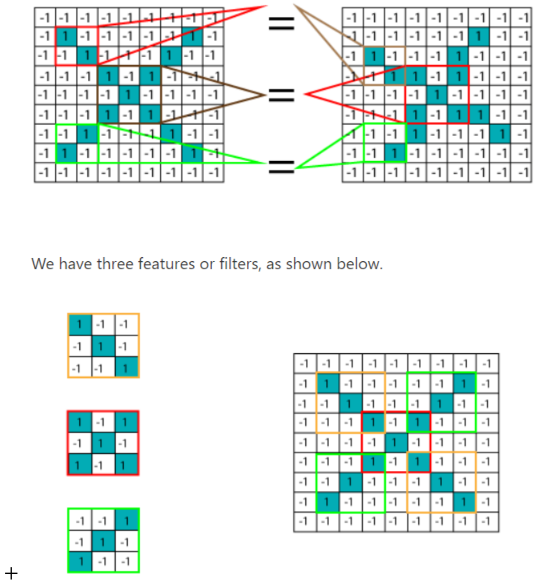
Convolutional Neural Network:

Convolution is a mathematical operation on two functions that produces a third function that expresses how the shape of one is modified by other. But we don't really need to go behind the mathematical part to understand what a CNN is or how it works.[1].

Matplotlib can used to import an image into memory from file ,the computer doesn't see the image all it sees is an array of numbers .there are three layers convolution[only a small region of input layer neurons connected to neuron hidden layer] , pooling[reduce the dimensionality of feature], fully connected layer [form the last few layer in the network, The input to the fully connected layer is the output from the final Pooling or Convolutional Layer, which is flattened and then fed into the fully connected layer.] it performs series of mathematical operation on image to extract the relevant feature during training weights are adjusted to minimize the output differences once trained CNN can classify new image . Make a CNN architecture specifically suited for bone image analysis. The CNN can detect patterns and structures linked to bone health by automatically learning pertinent information from the photos.

Working :

An RGB is a image nothing but a matrix of pixel values having three planes whereas grayscale image is the same but it has a single plane. The first layer usually extract basic feature such as horizontal or diagonal edges . this output is passed on to the next layer which detects more complex feature such as corner or combinational edges.The Convolved Feature's spatial size is condensed by the Pooling layer[]. By lowering the dimensions, this will lower the amount of CPU power needed to process the data. Average pooling (returns average of all the values from the portion of the image covered performs dimensionality reduction as noise suppressing mechanism) and maximum pooling (performs Noise suppressant) are the two types of pooling. [] By comparing sections of photos, CNN is far better at identifying similarities than entire image matching systems. This is accomplished by locating rough matches in roughly the same location in two images. []



We have three features or filters, as shown below.

Fig 4.CNN

Optimization of Architecture Using Evolutionary Algorithm Investigate several CNN architectures using an evolutionary method, such as a genetic algorithm [1,5]. In order to identify the ideal configuration, the algorithm can evolve the architecture by modifying variables like the number of layers, filter sizes, ad activation functions that are retrieved from the proposed Dataset

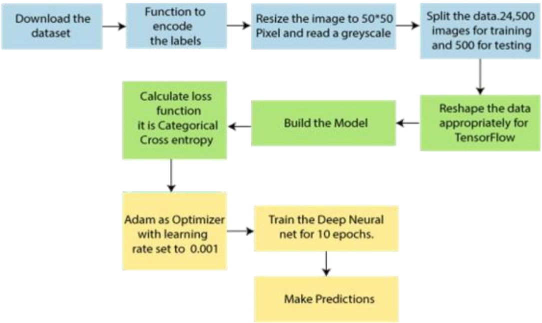


Fig 5. Flow Diagram for Deep learning Classifier

Saimese Network: Is a class of neural network architecture that contains two or more identical subnetworks. By contrasting its feature vectors with the inputs, it determines how similar the inputs[4,8]. Pairwise comparisons and picture similarity tasks both use siamese networks. They can be used in osteoporosis analysis to analyze the similarity of bone structures in various photographs, which may assist detect patterns related to osteoporosis progression. they are effective in few shot learning, where model can be generalize from small number of labels and they are seamlessly integrated with evolutionary algorithm. here Using Siamese networks in conjunction with an evolutionary algorithm allows for the development of a tailored deep learning model for osteoporosis analysis, even when data is limited and the optimal network configuration is not known beforehand.

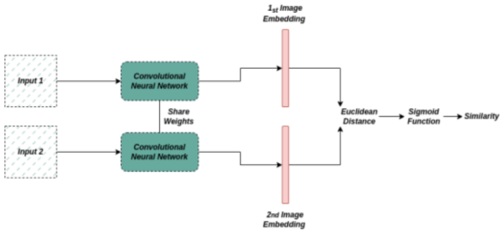


Fig 6. Saimese Network

SNN involve pairwise learning we cannot use cross entropy loss cannot be used .there are two functions we typically use to tain siamese networks triplet loss where in we compare baseline input to positive and negative.

$$\mathcal{L}(A,P,N)=\max(\|f(A)-f(P)\|^2-\|f(A)-f(N)\|^2+\alpha,0)$$

contrastive loss is an increasingly popular loss function.used to learn embedding in which two similar points have a low euclidean distance and two dissimilar points have a large euclidean distance.

$$(1-Y)\frac{1}{2}(Dw)^2+(Y)\frac{1}{z}(max(0,m-Dw))^2$$

siamese network have more robust to class imbalance , nice to pair with the best classifier , SNN focuses on learning embeddings that place same classes close together[]. SNN needs more training time than normal networks , don't output probabilities.Diagnosis based on similarity: Saimese networks may be taught to contrast bone density scans of people with and without osteoporosis. This might make it easier to spot osteoporosis-related patterns of bone density reduction. As we are taking the images from Hip, Lumbar Spine, Femoral Neck, Femure, Knee, Shoulder, which are in the cluster and clumsy order so it's difficult to the differentiate in a precise manner to overcome this effect we are going for the network named Saimese. Diagnostic Feature^{2}E^1 extraction: The most important, elements for differentiating between osteoporotic and healthy bone states can be extracted from bone scans using Siamese networks. Inputs for diagnostic models might then be created using these properties. This differentiation is undergone through the analyzing the features.

Integration Of Eas And Deep Learning Classifier:

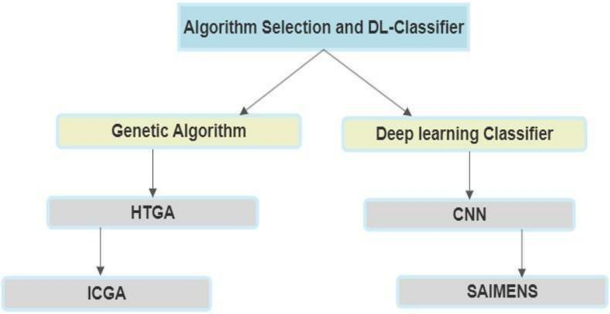


Fig 7. Algorithm selection

Hybridization Approach: Used HTGA and ICGA to optimize hyperparameter and architecture of deep learning models and implemented CNN for image classifications and Siamese network for similarity comparison, let our evolutionary algorithm fine tune deep learning models, improving their performance []. train and evaluate hybridized models using preprocessed data. assess model performance with standard metrics they are kappa, Jaccard index, MCC, F1-score ,accuracy . then integrate models into healthcare system for osteoporosis diagnosis.

G. SOFTWARE(MATLAB)

Software Tools – MATLAB: MATLAB provides a wide range of built in functions and toolboxes for image preprocessing and deep learning , making it$_2$a$_2$ versatile platform for handling both images and algorithm . it has a robust image processing libraries , allowing for tasks like image resizing , noise reduction, contrast enhancement and feature extraction which are crucial ,it simplifies the implementation of deep learning including CNN and Siamese networks .is a powerful visualization capabilities aiding in th analysis and interpretation of data and model result . MATLAB scripting environment is well suited for rapid algorithm prototyping and experimentation, making it ideal with deep learning models .allow seamless data exchange and collaboration with external system[].supports parallel computing and advantageous for large scale image processing and algorithm hybridization . It more practical to continue using

MATLAB for consistency and compatibility.

Experimental Setup Evolution Metrics: In preprocessing technique we evaluated the best method by their accuracy [measure the proportion of correctly classified instance out of total instance) then with their specificity, sensitivity , precision .In feature extraction evaluated their Contrast Correlation Energy Homogeneity Entropy., t score [comparison of patient bone density with healthy, young individual of same sex] , Z score [comparison with bone density of people of same age and sex as the patient] , BMD [Test is done by dual x-ray absorptiometry]Finally we obtained and concluded with accuracy , F1 score [harmonic mean of precision and recall,balance between false positive and false negative strike] Matthews correlation coefficient MCC [comprehensive assessment of the overall performance of algorithm and accounts true positive /negative, false positive/negative],Jaccard index [similarities between two sets by comparing their intersection to their union],kappa statistic.

IV PROPOSED WORK MODULE

- *Osteoporosis:* In the realm of osteoporosis analysis harnessing the power of evolutionary algorithm presents a promising avenue.by integrating evolutionary algorithms, we aim to optimize feature selection process ultimately enhancing the accuracy and efficiency of osteoporosis diagnosis and risk assessment
- *Objective:* Optimized feature selection to employ evolutionary algorithms for the selection of the most relevant and discriminative features, improved diagnostic performance and reliability, enhanced clinical decision support to provide healthcare professionals with an advance tool for assessment aiding early detection nad personalized care.
- *Input Data*

  Collection Of Patients Detail: Work Proposed For The Analysis Of Osteoporosis Is Carried Out In Several Steps, To Start With, Data Collection proposed in excel sheet which included clinical data, environmental data, physical activity data, **fracture** history etc.
- *Processing The Data:* The images that are retrieved from the data collection module contains noise on it so to overcome this we need to process the images once again by data pre-processing as denoising and deblurring added CLAHE process module and k means cluster modules, steps include noise reduction, image resizing, contrast and quality adjustment for better performance.
- *Feature-Extraction:* Feature extraction begins with the acquisition of medical images which serve as the primary input data for osteoporosis analysis these images could include X-ray here. raw medical images are preprocessed. the genetic algorithm chosen its ability to optimize feature selection is employed to extract relevant information from preprocessed images. this purpose include technique as GLCM for texture analysis, PCA for dimensionality reduction and AAM is a powerful tool for modelling deformable objects as well as some scores.

A. COMBINING EAs AND DEEP LEARNING

Evolutionary Algorithm: The genetic algorithm's ability to explore vast search space of features combination makes it a powerful tool and adapt themselves then evolve features subsets overtime, making them well suited for addressing the complexity in imaging data. The work module for osteoporosis analysis including HTGS, ICGA, HMBA-ELM, differential Algorithm its aims to revolutionize diagnostic precision . the inter disciplinarily approaches promises to significantly advance the field of medical imaging and osteoporosis diagnosis. works under deep learning classifiers.

- *Deep Learning Classifier:* In this paper we are fusing the Evolutionary algorithms and some Deep learning models so we are classifying the deep learning modules. Using deep learning with the CNN model demonstrated that osteoporosis can be classified with relatively higher accuracy from dental panoramic radiographs[1,6]. In addition, an ensemble model that included patient covariates demonstrated more accurate classification of osteoporosis.

TABLE II- CNN combined with EAs

DL	*Evolutionary Algorithm*	*Accuracy*	*Auc*	*Kappa*	*Mcc*	*Jaccard & F-Score*
CNN	***HTGAs***	87.06%	0.91	65.5%	0.95	0.93 & 79.70%
	ICGAs	96.49%	0.97	55%	0.9	0.89 & 96.50%
	Metaheuristic Algorithm	96.65%	0.94	71%	0.94	0.97 & 88.55%
	Differential EAs	97.93%	0.96	70%	0.87	0.92 & 82.84%

- Siamese Networks: Pair-wise comparisons[19]and picture similarity tasks both use siamese networks. They can be used in osteoporosis analysis to analyze the similarity of bone structures in various photographs, which may assist detect patterns related to osteoporosis progression.

TABLE III- SAIMESE combined with EAs

DL	*Evolutionary Algorithm*	*Accuracy*	*Auc*	*Kappa*	*Mcc*	*Jaccard & F-Score*
Saimese	***HTGAs***	89.88%	0.94	71.1%	0.93	0.92 & 83.60%
	ICGAs	94.87%	0.89	62.9%	0.87	0.84 & 71.46%

	Metaheuristic Algorithm	97.40%	0.92	76.4%	0.91	0.97 & 93.30%
	Differential EAs	86.12%	0.9	75%	0.84	0.91 & 52.10%

By this we have clearly, identify who have been affected by osteoporosis and who are all normal. Then, the application of evolutionary algorithms and deep learning methods to the study of osteoporosis are a potent and novel strategy that has considerable promise for improving our comprehension and treatment of this crippling disease.

V RESULTS AND DISCUSSION

In this study, we have processed the patient's bone image by data pre-processing. the data preprocessing contains the flow as denoising, deblurring, enhancement and segmentation. In denoising we have to pre-processes the noisy image to denoise in MATLAB software by denoising algorithm. when denoise was finished the image become blurred. to deblurred this blurred image we have used deblurring algorithm and procced the image in the software. after that, enhancement was done, due to poor pixel after the deblurred. to view clear image of the bone segmentation were done with its algorithm. after that the segmented image was sent to feature extraction. then, the feature extraction image was given to the classifier (classifier = fusion of evolutionary algorithm and deep learning). then this classifier image result has to be evaluated by the confusion matrix (true positive, true negative, false positive, false negative). By taking the value from the confusion matrix we evaluate the performance metrics. we have calculated the performance metrics as (accuracy, AUC, MCC, Jaccard index, nuclear factor kappa, F-score). By this metrics we can identify whether the person have osteoporosis or normal person.

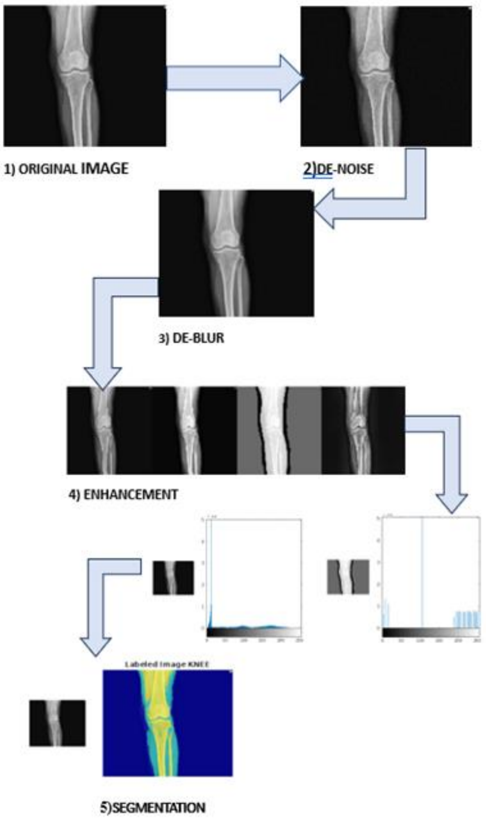


Fig 8. Flow diagram of Data pre-processing

A. Results

II. ACCURACY:

III. $accuracy = \frac{Correct\ prediction}{Total\ cases} * 100\%$

IV. $accuracy = \frac{(TP+TN)}{(TP+TN+FP+FN)} * 100\%$

V. MCC (MATTHEWS CORRELATION COEFFICIENT):

$$MCC = \frac{TN * TP - FN * FP}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}}$$

VI. JACCARD INDEX:

VII. NUCLEAR FACTOR KAPPA:

VIII. $kappa(k) = \frac{P_o - P_e}{1 - P_e}$

IX. F1- SCORE:

$$F1\ score = \frac{TP}{TP + \frac{1}{2}(FP + FN)}$$

Collecting the data from the patients as image in X-Ray techniques. we are going to pre-processing it with several methods

Overall Results from the trained data from the entire methodology as shown in below, HTGA-Hybrid Taguhi genetic algorithm under CNN classifier we obtained 87.06%accuracy, 0.91 area under curve , 65.50% nuclear factor kappa with F1-score as 79.70% , MCC (Matthews correlation coefficient) as 0.95 , Jaccard index =0.93.similarly for improved catastrophic genetic algorithm obtained 96.49% accuracy ,0.97 area under curve ,55%kappa, 96.50%fscore along with 0.9 of MCC and 0.89 of Jaccard index here under CNN classifier we worked and evaluated four evolutionary algorithm the other two are metaheuristic algorithm with 98.65%accuracy,0.94%AUC , 71%of kappa with 88.55%Fscore , 0.94 MCC and 0.97 Jaccard index ; differential evolutionary algorithm accuracy as 97.93%,0.96%AUC , 0.701 (70%) of kappa with 82.84% F-score , (Matthews correlation coefficient) (=1)as 0.87% and Jaccard as 0.92 now under Siamese network classifier these four Htga-Hybrid Taguhi-Genetic Algorithm shows 89.88% accuracy , 0.94 AUC, 71.13%kappa ,83.60%F-score ,with 0.94 MCC and 0.92 Jaccard index . Differential Evolution Algorithm 0.91 Jaccard index ,0.84 MCC 52.10% F-score, 75%kappa and 0.9 AUC, 86.12%Accuracy, Catastrophic Genetic Algorithm 94.87% accuracy, 0.89 AUC, 62.90% kappa ,71.46%F-score with 0.87 MCC, 0.84 Jaccard index.

Metaheuristic Algorithm gives 0.94 Jaccard ,0.91 MCC, 93.30 F-score percentage, 76.40% Kappa, 0.92 AUC and 97.87% accuracy. Jae-Seo Lee et al..[1], 2018, in this paper they have discussed about the panoramic radiographs using a deep convolution neural network for diagnosing the osteoporosis. Their overall, SC-DCNN accuracy is 92.5%. by comparing their accuracy with our paper accuracy, the fusion of deep learning with metaheuristic algorithm we have the accuracy percent as 98.65%. F1 score of their method SC-DCNN have 0.922. our metaheuristic algorithm gives F1 score give as 0.933 value. by comparing both the performance metric our method shows more advantages than this paper.

B. Results of The Proposed Work

Significance Of the Proposed Work: Combining an evolutionary algorithm with deep learning method have more accurate predictions of osteoporosis risks. Evolutionary algorithm identifies the most features associated with osteoporosis which reduces the dimensionality of the database and improve the model performance and it also reduces the overfitting by finding the best optimal model complexity parameters. By fusing this two evolutionary algorithm and deep learning have the transfer of knowledge and models from database and enabling better generalization and adaptation of osteoporosis techniques.

C. Strengths of The Proposed Work

Now a days, 30 years age group people have also detected as osteoporosis diseases. If we not treating as early as possible there were severely affected by the fractures in their bones in turns early disability and mortality also will happen. our method has the pre diagnosing process which can help the people to avoid the sever fractures in their bones because we were diagnosing in early stage of the osteoporosis condition.

D. Limitations of The Proposed Work

Our major concern, in our project is limited amount of time and we haven't collected the real time data from the patients. As we are using MATLAB software, though the MATLAB software is an interpreted language our code executing time is slow compared to some other existing software. By these issues our time consumption of getting the result might slow down.

VI CONCLUSION & SUGGESTIONS FOR FUTURE WORK

A. Conclusion

In conclusion, our proposed work is depending upon the fusion of evolutionary algorithm and deep learning which has the high accuracy with (86.12 % - 98.65%) and have the best area under curve (AUC) which has to be (0 to 1). in our method we have the range between (0.89 - 0.97) and we experienced the best fitness score as 96.50%. we have concluded that, we attained the best fitness score and also it will surely obtain in global optima. By this we have clearly, identify who have been affected by osteoporosis and who are all normal. Then, the application of evolutionary algorithms and deep learning methods to the study of osteoporosis are a potent and novel strategy that has considerable promise for improving our comprehension and treatment of this crippling disease. An important step forward in the global fight against osteoporosis is the integration of deep learning methods capable of reaching global optimums with evolutionary algorithms for the analysis of this condition. This strategy has the potential to enhance the lives of those affected by osteoporosis around the world by offering highly accurate, tailored, and internationally efficient remedies.

B. Suggestion For Future Work:

In future suggestion work As, we haven't taken the real time data from the patients due to time insufficiency. So, you can proceed with real time data if time premises. And also, we have used X-Ray image only. we haven't used advanced technology for the diagnosing the patients. So, you can go through with the deep analysation and diagnosis with latest techniques which shows high accuracy. We have used some old evolutionary algorithm. So, you can opt for advanced or hybrid evolutionary algorithm. If you did these changes, you can get high accuracy than ours.

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