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Deep learning convolutional neural network (CNN) With Gaussian mixture model for predicting pancreatic cancer

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Abstract
The tremendous research towards medical health systems are giving ample scope for the computing systems to emerge with the latest innovations. These innovations are leading to the efficient implementations of the medical systems which involve in automatic diagnosis of the health related problems. The most important health research is going on towards cancer prediction, which has different forms and can be affected on different portions of the body parts. One of the most affected cancer that predicted to be incurable are Pancreatic Cancer, which cannot be treated efficiently once identified, in most of the cases it found to be unpredictable as it lies in the abdomen region below the stomach. Therefore the advancements in the medical research is trending towards the implementations of an automated systems which identifies the stages of cancer if affected and provide the better diagnosis and treatment if identified. Deep learning is one such area which extended its research towards medical imaging, which automates the process of diagnosing the problems of the patients when appended with the set of machines like CT/PET Scan systems. In this paper, the deep learning strategy named Convolutional Neural network (CNN) model is used to predict the cancer images of the pancreas, which is embedded with the model of Gaussian Mixture model with EM algorithm to predict the essential features from the CT Scan and predicts the percentage of cancer spread in the pancreas with the threshold parameters taken as a markers. The experimentation is carried out on the CT Scan images dataset of pancreas collected from the Cancer Imaging Archive (TCIA) consists of approximately 19,000 images supported by the National Institutes of Health Clinical Center to analyze the performance of the model.

Keywords Convolutional neural network (CNN) · Gaussian mixture model (GMM) · Expectation-Maximization algorithm (EM) · TCIA

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1 Introduction

According to medical health information analysis, Cancer is one of the most problematic diseases that pretend to be incurable some times. It may be considered as a genetic disease as it can cause due to changes in genes that control the cells functionality of a human body. These genetic changes may be inherited from the successors of a family or due to the lifestyle of a human being or because of the damage happened to DNA due to environmental exposure which includes substances, such as smoking, ultra violet radiations etc. The effects of the genetic changes will happen on three types of genes, they are tumor suppressor genes, proto-oncogenes, and DNA repair genes which acts as a drivers for cancer. The spread of cancer from its initial/ starting place to other parts of the body is called as a metastatic cancer and the process of cancer cells spreading is referred to as a metastasis, according to the medical survey, some of the incurable cancers identified are: Breast Cancer, Lung Cancer, Pancreas cancer.

Now a days, the Pancreas cancer is the most typical cancer which develops in the tissues of the pancreas which aids in digestion, located behind the lower part of the stomach. It contains exocrine glands and endocrine glands which helps in digesting food as well as helps to maintain the blood sugar levels in the body. The sign and symptoms of the pancreatic cancer include jaundice, pain in the upper or middle abdomen and back, sudden weight loss for unknown reason, loss of appetite, and being tired always.

In general, there are two forms of pancreatic cancer, which is of endocrine gland and exocrine gland which is the most effected form of cancer obtained due to enzyme producing cell of the pancreas. The exocrine tumors are also referred as adnocarcinomas, formed in the pancreas ducts. The treatments of this tumor is based on stage of its growth, whereas the endocrine tumors are often obtained from a cancer stemming which affects the harmone producing cells, which are also referred as islet cell tumors or neurendocrine tumors.

The set of latest computing innovations towards health research are being adopted for the efficient and faster processing of information either by imaging analysis or using PHR data record analysis. The Artificial intelligence research techniques are being trending towards the research in various fields like cognitive computing, health care and pervasive computing technologies.

In our paper, an attempt is made to consider the deep learning strategy a branch of Artificial intelligence is considered for the automatic detection of problematic area form the given CT Scan image of pancreatic cancer, in order to predict the cancer the subset of the image or region of interest or a seed point from the image considered, segmented and features are extracted using Gaussian Mixture Model with Expectation Maximization algorithm for the efficient classification of the infected area. This classified area is further feeded to the deep learning framework with a decision layer in order to analyze the percentage of cancer affected area. The latest innovation in medical health research using deep learning [1, 16] includes “FISHMAN” a deep learning project used to take millions of images and presents the prediction of pancreas cancer [12] at the early stage of identification and helps patients for the better treatment for cure. (Figure 1)

2 Literature review

Hiba Asri et al. [2], discussed about the set of machine learning algorithm and suggested that the Support Vector Machine (SVM) is better classification algorithm for classifying the data with respect to the Wisconsin Breast Cancer (original) datasets with lower error rate. He provided the comparative results in terms of efficiency and effectiveness of the four different

Fig. 1 Different CT scan images of the pancreas demonstrating the tumor sections

data mining and machine learning algorithms like K-Nearest Neighbor, Naïve Bayes and C4.5 with the parameters like accuracy, precision, sensitivity and specificity and proved that SVM outperforms among the other algorithm by proving the efficiency of results up to 97.13% and predicts the breast cancer with lower error rate.

Riccardo Miotto et al. [11], presented a novel application on the medical health system which predicts the future disease of a patient by considering the Electronic health records and the set of parameters set for each disease to predict the diseases correctly. The data about the prediction of diseases is obtained by training the system or application with the set of data about several diseases, types of diseases and the threshold parameter to identify or diagnose the disease. The set of health records they used and maintained are about liver cancer, heart failure, diabetes.

Benjamin S. Glicksberg et al. [7] suggested the electronic phenotyping algorithms from the data available in the form of electronic health records for cohort selection and to supervise the features of the disease basing on the data available in order to provide diagnosis of disease basing on the query typing about the disease and rank the patients by their proximity. They used word2vec to provide the unsupervised embeddings of the phenotype space within an EHR System.

Xin Zhen et al. [18] has developed an application based on convolutional neural network (CNN) model to analyze the rectum dose distribution and predict rectum toxicity in cervical cancer patients by having the combinational data of beam radiotherapy (EBRT) and brachytherapy (BT). They adopted a transfer learning strategy to extend the patient data. The adaptive synthetic sampling technique is being used for the data augmentation to address the data imbalance challenge and scarcity factors. The gradient-weighted classes of activation maps (Grad-CAM) are generated for highlighting the discriminative regions, on the RSDM with the prediction model. The CNN-based rectum dose-toxicity prediction model with transfer learning for cervical cancer radiotherapy has been analyzed with the set of experimental results.

Chris Pearce [13], investigated the tumor classification mechanism by applying the set of deep learning mechanisms using the tumor data set and found the reasonable performance with respect to the dataset of the mid-age patients, he attempted to identify whether the subsamples contain mitoses with respect to the set of tumors. He attempted to develop the adversarial network with a fully connected network to identify the proportion of tumor present in the scan image provided.

H.Zhong et al. [10] presented survival prediction based on image features with the traditional clinical information for the tumor segmentation using deep learning techniques to hypothesize the survival risks of cancer patients basing on the imaging data. To analyze better,

the Cox proportional hazards model (CPH) is used for the better regression analysis. The Gross tumor volume is used to define a bounding box for the extraction of imaging feature from the PET Scans. The survey is made by considering the CPH model based on the radiomic features from the PET Scans, The methods like Gray level co-occurrence matrix, Local Binary Patterns were used to identify the features. The reduction of radiomic feature dimensionality is done using Principal Component analysis before the CPH model analysis.

Christopher P. Bridge et al. [3], specified in his research paper about the correlation among body composition of muscles and cancer risks, cancer survival and cardiovascular risk. They suggested a two step process for fully automating the analysis process of CT body composition using DenseNet for selecting the CT Slice and for segmentation, they proposed the U-Net model which performed experimentation of training and testing datasets on independent cohorts. They presented the results of correlation coefficients of $R = 0.99$ on the each dice (0.95–0.98) which are favorable to human readers and comfortable for both clinical use and for the study on large-population datasets.

Sarfaraz Hussein et al. [8], suggested that the characterization of tumors from radiology images can be more accurate and much faster with Computer Aided Design (CAD) Tools. The Characterization of the tumor using these may also enable non-invasive cancer, staging, foster personalized treatment planning as a part of precision medicine. Therefore they proposed an unsupervised and supervised machine learning strategies for the characterization of tumor. They used Deep learing algorithms using 3D Convolutional Neural Network and Transfer Learning. They developed a MultiTask Learning (MTL) framework for generating the graph-regularized sparse representation via CAD System. They adapted Unsupervised learning algorithm to address the availability of the Labeled Training data, which is a common problem in medical diagnosis. They use proportion-SVM for characterizing the tumors. They experimented their model on Tumor Diagnosis [9] using 1018 CT and 171 MRI scans of the Lumg and Pancreas images.

3 Architecture

The schematic architecture for the proposed work is shown in Fig. 2, where the input for the work ranges with the set of images taken for the period of time or at the stages of the treatment, and the set of features like tumor specific area in the blood vessels or the specific tissues of the pancreas head or is tail considered for the study of diagnosis. The features selected with the region of interest is given to the deep learning networks, like alexanet or convolutional neural networks with the set of threshold parameter values to identify / recognize the affected area of tumor.

4 Methodology

The Dataset used for experimenting this model are The Cancer Imaging Archive (TCIA) which is used for the Public Access supported by National Institutes of Health Clinical Center, the dataset consists of approximately 19,000 images with a size of 10.2 GB. The dataset is constructed by performing a study on 82 abdominal CT Scan images at the rate of 70 s after the contrast injection in portal- venous on 53 male and 27 female patients, the age range of these patients are from 18 to 76 years among which some acted as a kidney donors and some are selected by a radiologists who neither has a abdominal pathologies

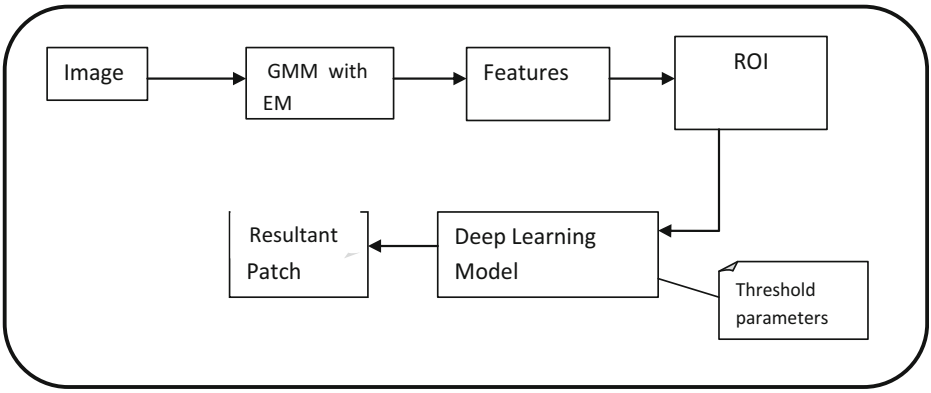

Fig. 2 Architecture for the prediction using Deep Learning with the advent of GMM

nor pancreatic cancer lesion. The CT scans collected are of 512 × 512 pixels resultions with variations in slice thickness between 1.5–2.5 mm which were collected using Philips and Siemens MDCT Scanners.

The methods we adapt to model are Gaussian Mixture model with EM Algorithm and Deep Learning Convolution Neural Network (CNN) [4] to design an algorithm is explained in the preceding sections.

4.1 Gaussian mixture model with EM algorithm

4.1.1 Gaussian mixture models

For $x \epsilon R^d$ a Gaussian mixture model can be defined by considering each of the K components as a Gaussian density with μk and Σk parameters where each component is a multivariate Gaussian density

$$pk(x|\theta k) = \frac{1}{(2\pi)^{d/2}|\Sigma k|^{1/2}}\, e^{-1/2(x-\mu k)\ \Sigma\ (x-\mu k)} \quad where\ \theta k = \{\mu k, \Sigma k\}.$$

4.1.2 The EM algorithm for Gaussian mixture models

The EM (Expectation-Maximization) algorithm for the Gaussian mixtures is given as follows. It is an iterative algorithm starts from initial estimate of Θ (e.g., random), and proceeds to iteratively with the update Θ until convergence is detected.

Each iteration consists of an E-step and an M-step.

- **E-Step:** The parameter values are denoted as Θ. Compute w_{ik} (using the equation above for membership weights) for all data points xi, $1 \le i \le N$ and all mixture components $1 \le k \le K$.

for each data point xi, the membership weights are calculated as

$$\sum_{K=1}^{K} w_{ik} = 1.$$

Which yields an N × K matrix of membership weights, where the sum of the rows leads to 1.

- **M-Step:** Now use the membership weights and the data to calculate new parameter values.

Let N represent the membership weights count such that, $\Sigma_{i=1}^{k=N}$ w_{ik}, is the sum of the membership weights for the kth component—this is the effective number of data points assigned to component k.

Specifically,

$$\alpha_k^{new} = \frac{N_k}{N}, 1 \leq k \leq K.$$

the new mixture weights are represented as

$$\alpha_k^{new} = \left(\frac{1}{N_k}\right) \sum_{K=1}^{K} w_{ik} x_i \quad 1 \leq k \leq K$$

The updated mean is calculated in a manner similar to how we could compute a standard empirical average, except that the ith data vector xi has a fractional weight wik and μ new k and xi are d-dimensional vectors.

$$\alpha_k^{new} = \left(\frac{1}{N_k}\right) \sum_{K=1}^{K} w_{ik} \left(x_i - \mu_k^{new}\right) \left(x_i - \mu_k^{new}\right)^t \; 1 \leq k \leq K$$

Again we get an equation that is similar in form to how we would normally compute an empirical covariance matrix, except that the contribution of each data point is weighted by wik. Note that this is a matrix equation of dimensionality d × d on each side.

After the computation all of the new parameters, the M-step is complete and we can now the membership weights in the E-step are recomputed so that the parameters are updated. Each pair of E and M steps is considered to be one iteration.

4.1.3 Deep learning strategies

The study of deep learning [17] involves the number of hidden layers up to 150 layers in the neural network rather than the traditional neural networks that can contain only 2–3 layers, which are trained using the large set of labeled data and the neural architectures learn the data directly from these data without the requirement of manual feature extraction (Fig. 3).

The most important type of deep learning network is Convolutional Neural Network or ConvNet [5, 6, 15]. It convolves the learned features with input data and uses two dimensional convolutional layers for the best support of 2D Data like images. The CNNs generally does not require the manual feature extraction process as it can classify the images directly by extracting from the images. The network trains relevant features from the collection of images for achieving the better accuracy of object classification (Fig. 4).

The hidden layers in the network increases the complexity of the learned image features with the set of tasks like detection of edges, complex shapes and the specific classification of shapes we are trying to identify or predict.

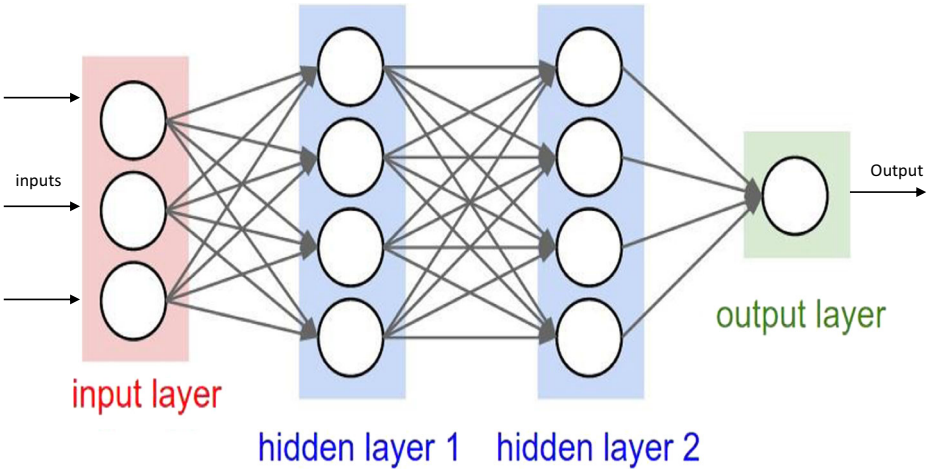

Fig. 3 The neural network organized with hundreds of hidden layers

5 Algorithm

5.1 Proposed algorithm: lump feature extraction (LFE)

"Lump Feature Extraction" (LFE) [15] emphasize on extracting features from the specified region of interest, from the CT scan image provided as an input. This algorithm is intended to optimize the spatial redundancy allowing to select the specified region of interest for the process of lump identification thus reduces the time complexity. The algorithm is illustrated as follows:

- ***Input:*** *Image Database ID* $= \{I_1, I_2 \ldots I_n\} \; \forall \, I_i \; \{i = 1, 2 \ldots n\}$
- ***Output:*** *Feature Database FD* $= \{F_1, F_2 \ldots F_n\} \forall \, F_i \; \{i = 1, 2 \ldots n\}$

  Attributes $\{A_1, A_2 \ldots A_n\}, \; \forall \, A_i \; \{i = 1, 2 \ldots n\}$.
  Represent set of attributes namely depth, width, length, size and shape of the lump in PRD.

- ***Parameters:*** *RID* $= \{R_1, R_2 \ldots R_n\}, \; \forall \, R_i \; \{i = 1, 2 \ldots n\}$

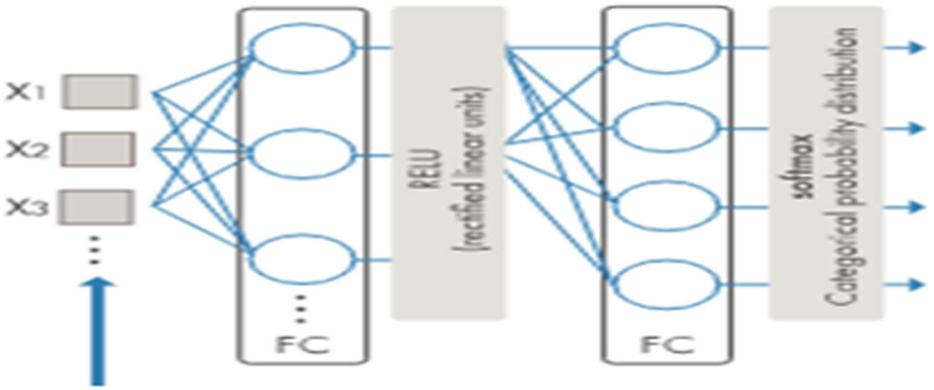

Fig. 4 The Training process for the fully connected (FC) network using the Rectified linear units (RELU)

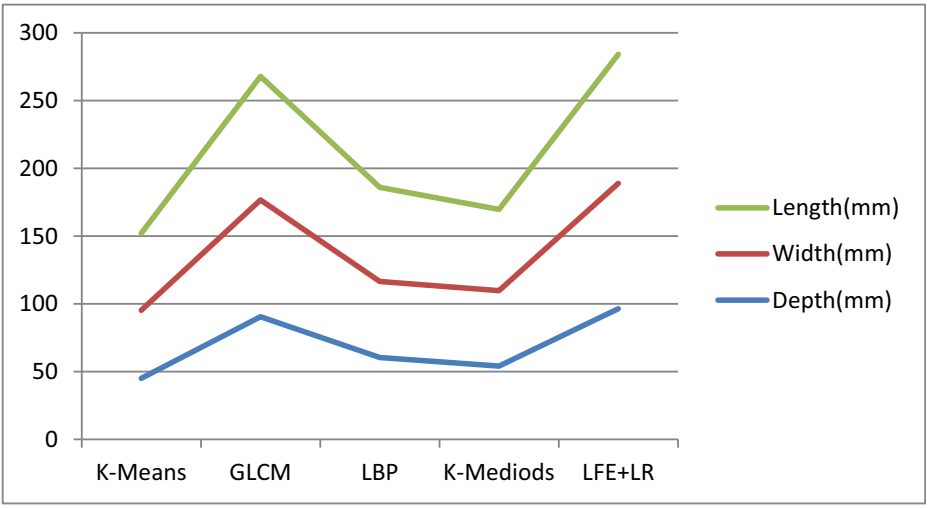

Fig. 5 Performance analysis of various algorithms for identifying the Lumps

A = Set of attributes for lump specification.
T = Set of Tuples with respect to user details.

6 Method

1. Consider the Image Database I as a collection of CT scan images.
2. Specify the Region of interest window for the analysis of lump with respect to size, width, depth and shape parameters, and the ROI range specified is maintained as a database named Region of Interest Database (RID).

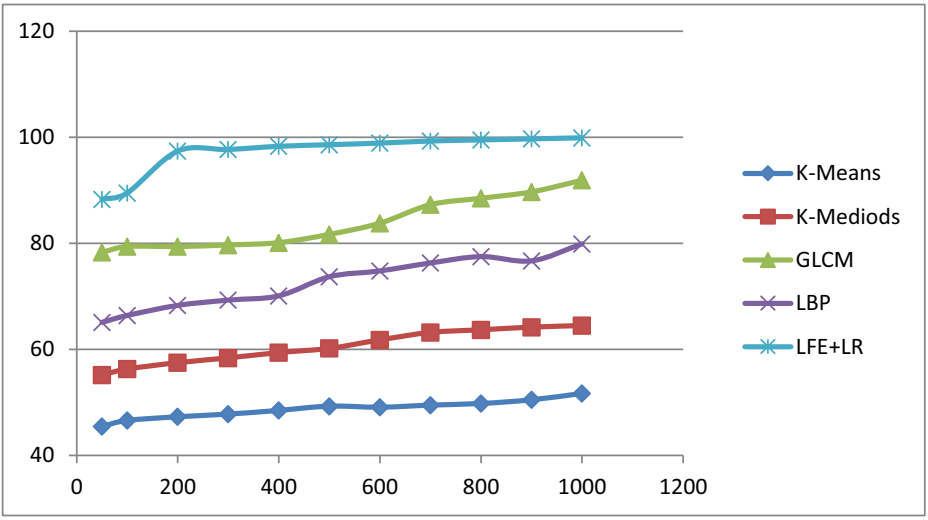

Fig. 6 Recognition ratio Vs number of images in the training dataset

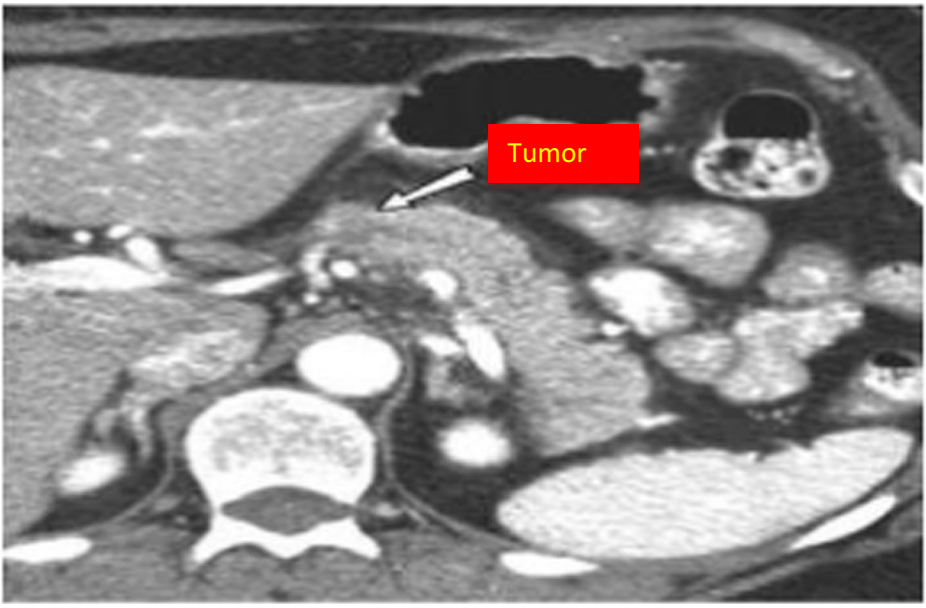

Fig. 7 CT Scan image of pancreas cancer recognizing the tumor portion

3. The analysis of shape of lump is performed with the help of Gaussian Mixture model as follows:

$$g\left(x|\mu,\sigma^2\right)=\frac{1}{\sqrt{2\pi\sigma_i}}ecp\left\{-\frac{(x-\mu_i)^2}{2\sigma_i^2}\right\}\mathrm{i}=1,2,\ldots\mathrm{N}$$

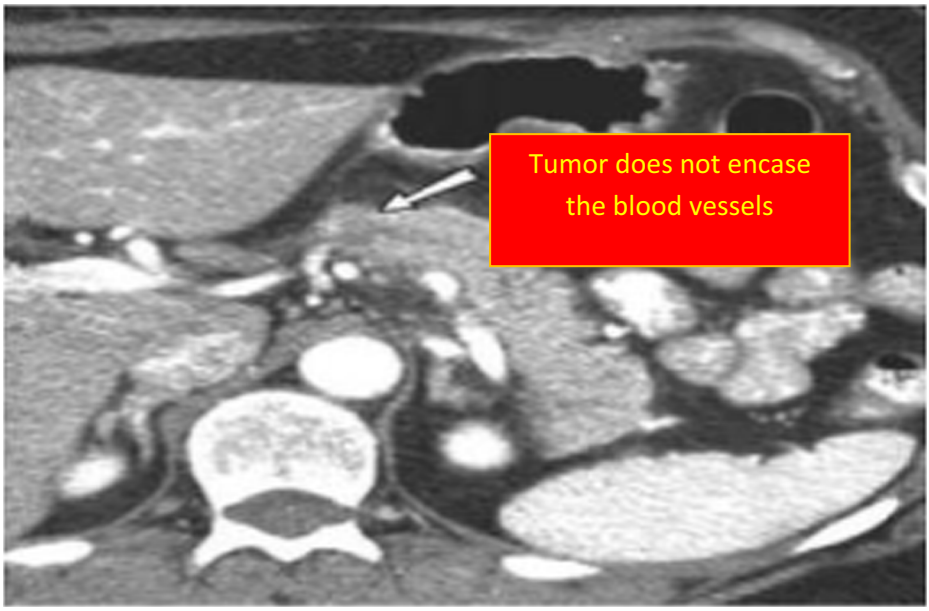

Fig. 8 CT Scan image predicting the spread of tumor with respect to blood vessels

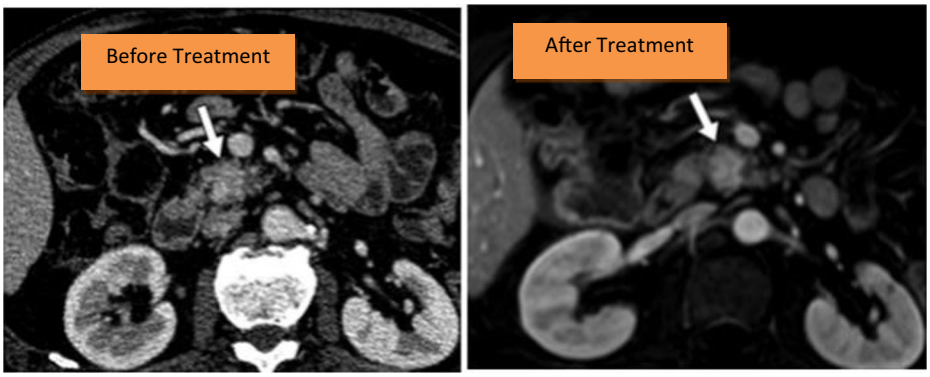

Fig. 9 CT Scan image shows the tumor before and after treatment

4. The shape identified by the previous step is given to the EM algorithm as input for maximum likelihood analysis of the shape of a lump.
5. Construct Feature database (FD) with a set of tuples and attributes T_i and A_i

$$T = \cup T_i \forall i = 1, 2 \ldots n.$$

$$A = \cup A_i \forall i = 1, 2 \ldots n.$$

$$FD = \sum A.T$$

6.1 Lump recognition algorithm

"Lump Recognition algorithm" (LR) concentrates on identifying the growth of a lump in the specified region of interest, provided as an input from the ROI Database for the specified scan image. The algorithm is intended to identify the lump from the set features extracted using LFE algorithm (considered as a training set) and set of threshold parameters considered for the specification of lump growth in the specified region of interest which helps to identify lump automatically and helps doctors for the early diagnosis. The algorithm is illustrated as follows:

- ***Input:*** *Image Database ID* = $\{I_1, I_2 \ldots I_n\}$ $\forall I_i$ $\{i = 1, 2 \ldots n\}$

  ROI Database RID = $\{R_1, R_2 \ldots R_n\}$, $\forall R_i$ $\{i = 1, 2 \ldots n\}$.
  Feature Database FD = $\{F_1, F_2 \ldots F_n\} \forall F_i$ $\{i = 1, 2 \ldots n\}$

- ***Output:*** *network with set of images as input and classifications of lump growth.*

  Lump image Database LID = $\{L_1, L_2 \ldots L_n\}$, $\forall L_i$ $\{i = 1, 2 \ldots n\}$.
  Represent lump images with a specifications like size, shape, weight.

- ***Parameters:*** *FD = Feature Database.*

RID = Region of Interest Database.
A = Set of attributes for lump specification.
T = Set of Tuples with respect to user details.

7 Method

1. Consider the Region of Interest Database (RID) for the set of scanned images.
2. Consider the Feature Database for the RID collected and mark it as a training set for the purpose of network training.
3. The number of input and hidden layers is generalized by means of set of features collected from the feature database. i.e., the training of the images is performed in such a way that each layer in the network represent one feature extracted from the feature database, which can be either shape specification, depth specification etc.
4. The Final output layer performs identification of a growth of the lump with respect to the threshold parameters provided as an input for perfectly diagnosing the lump.
5. The set of data images retrieved will be the lump images database LID with respect to the specifications like size, shape, weight factors, which can written as a set of tuple as:

$$\mathrm{LID} = < \mathrm{I}, \mathrm{R}, \mathrm{A}, \mathrm{L} >$$

Where.

I Image,
R Region of Interest Image
A Attributes/ features
L Lump Image

The algorithm specified in the above sections are performing the extraction and Identification process of Lump in the pancreas. The Set of Features collected using GMM model from the CT Scan images are size, weight, length and shape of a lump which is obtained from the slice images with a thickness of nearly 1.5–2.5 mm collected from the scanners and used in the CNN to train the system for the effective identification of the lump.

8 Comparative study

There are several methods in imaging analysis, to perform cancer recognition, the set of methods we use for the comparative study are K-Means, Gray Level Co-occurrence Matrix (GLCM), Local Binary Patterns(LBP),Fuzzy Logic and Convolutional Neural

Table 1 Techniques adapted for identification of lumps

Techniques	Parameters Obtained	Depth (mm)	Width (mm)	Length (mm)
K-Means	Mean (μ)	45.23	50.12	56.87
GLCM	Entropy, Angular Second Moment, correlation	90.5	86.2	91.15
LBP	Binary Codes	60.5	56.2	69.34
K-Mediods	Mean, mediods	54.13	55.64	59.9
LFE + LR with GMM + CNN	PDF, E-Step and M-Step	96.54	92.4	95.2

GLCM Gray level co-occurrence matrix, *LBP* Local binary patterns, *CNN* Convolutional neural network, *GMM* Gaussian mixture model, *LFE* Lump feature extraction, *LR* Lump recognition

Table 2 Recognition rate of images Vs Number of images, in the training dataset

Images	K-Means	K-Mediods	GLCM	LBP	LFE + LR with GMM + CNN
50 images	45.5	55.2	78.3	65.1	88.3
100	46.6	56.3	79.4	66.4	89.5
200	47.3	57.5	79.4	68.3	97.4
300	47.8	58.4	79.7	69.3	97.7
400	48.5	59.4	80.13	70.1	98.3
500	49.3	60.2	81.7	73.7	98.6
600	49.1	61.8	83.8	74.8	98.9
700	49.5	63.2	87.3	76.3	99.3
800	49.8	63.7	88.5	77.5	99.5
900	50.5	64.2	89.7	76.7	99.7
1000	51.7	64.5	91.9	79.9	99.9

Network with Gaussian Mixture Model (CNN + GMM). Table 1 presents the values of few dimension used with set of various techniques adapted for identification purpose per image.

The Fig. 5 presents the performance analysis of different algorithms with respect to three parameters of identification namely depth, width and length.

Table 2 shows the recognition rate of images with respect to the number of images present in the training dataset.

The Fig. 6 depicts the recognition ratio with respect to the number of images in the training database.

9 Results

The Results of the prediction of cancer with respect to the threshold parameters fed to the Deep learning is presented by identifying the tumor [14] rate of spread in the head section of the pancreas, after diagnosing and treatment, the spread of tumor size has been decreased, which helped patient to get cured than the traditional process of diagnosing Fig.(7, 8 and 9)

10 Conclusion

The research towards medical health includes latest innovations in computing for the effective and efficient analysis and diagnosis of the medical issues, the several innovations towards this research area includes machine learning, artificial intelligence and the latest technology included is deep learning, the project named FISHMAN, implemented with deep learning technology play the key role in diagnosing the abdomen cancer like pancreatic cancer or tumors in an early stage by considering multiple sets of images and diagnosing them with respect to the threshold parameters and features obtained using GMM with EM Algorithm stage at training phase. The experimental results presents the recovery from the tumor stage to less weightage of tumor stage after the period of treatment.

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