Intelligent Diagnosis System for Breast Cancer Thermal Image Using Optimized GA-SVM and Ann

Vaghani Rushikumar L., Prof. Srivani A

M.Tech. Computer Science and Engineering, Vellore Institute of Technology, Vellore, India

Assistant Professor, Department of Computer Science and Engineering, Vellore Institute of Technology, Vellore, India

ABSTRACT: Breast cancers can begin in any tissue inside the breast. Be that as it may, most breast tumors begin in the pipes, where littler rate happen in the lobules, less cases begin in other breast's tissues. Breast malignancy mortality among ladies is expanding all inclusive. The routine technique in medication screening instrument (mammogram) for picture order and tumor location is by clinician investigation; these strategies are frequently unrealistic for a lot of information included and are likewise not reproducible. This is particularly so for pictures from ladies with thick breasts, these would prompt to genuine errors grouping. In this manner, there is a requirement for more compelling strategies with high affectability and specificity for recognizing of Breast cancer. Consequently, warm imaging [thermography] is a non-obtrusive imaging system used to record the warm examples utilizing Infrared (IR) camera. The point of this venture is to assess the likelihood of utilizing warm imaging as a potential device for identifying Breast cancer. To enhance the recognition exactness we utilize the manmade brainpower machine adapting, for example, SVM and Neural Network. Alongside these strategies we utilize Genetic Algorithm for the Selection components of picture which decrease the dimensionality of database. Our Simulation results are demonstrates that identification of Breast tumor from warm
picture with high precision and limited intricacy.

KEYWORDS: Neural network, Support Vector Machine, SVM, Classifier, Benign, Malignant.

I. INTRODUCTION

Breast cancer is positioned first among the main sources of tumor influencing female. Measurements have demonstrated that one among ten ladies is influenced by breast growth in their life time. Recognition and determination of the illness at a prior stage can guarantee a long survival of lives. The manifestations of breast tumor incorporate mass, changes fit as a fiddle and measurement of breast. Different demonstrative tests and methodology are accessible for recognizing the nearness of breast malignancy.

One of these is investigation of a biopsy taken from the breast to distinguish the breast malignancy. A few techniques for a breast biopsy exist like Fine needle goal, Core needle biopsy, Vacuum helped biopsy, Open surgical biopsy, and so on to distinguish the breast growth.

The Fine Needle Aspiration [FNA] is a percutaneous system that uses a fine needle and a syringe to test liquid from a breast blister or expel Clusters of cells from a strong mass. The specimens of breast tissue are broke down utilizing magnifying instrument and the outcome might be favorable [non-carcinogenic cells] or Malignant [Cancerous cells]. Breast thermal image is a highly specialized form of medical imaging; it can't be done with an ordinary camera. All objects with a temperature above absolute zero [−273 K] emit infrared radiation from their surface.

The Stefan-Boltzmann Law defines the relation between radiated energy and temperature by stating that "The total radiation emitted by an object is directly proportional to the object's area and emissivity and the fourth power of its absolute temperature". Since the emissivity of human skin is extremely high [within1% of that of a black body], measurements of infrared radiation emitted by the skin can be converted directly into accurate temperature values. This makes infrared imaging an ideal procedure to evaluate surface temperatures of the body. Clinical infrared imaging is a

procedure that detects, records, and produces an image of a patient's skin surface temperatures and thermal patterns. The image produced resembles the likeness of the anatomic area under study.

The procedure uses equipment that can provide both qualitative and quantitative representations of these temperature patterns. Infrared imaging does not entail the use of ionizing radiation, venous access, or other invasive procedures; therefore, the examination poses no harm to the patient. Classified as a functional imaging technology, infrared imaging of the breast provides information on the normal and abnormal physiologic functioning of the sensory and sympathetic nervous systems, vascular system, and local inflammatory processes.
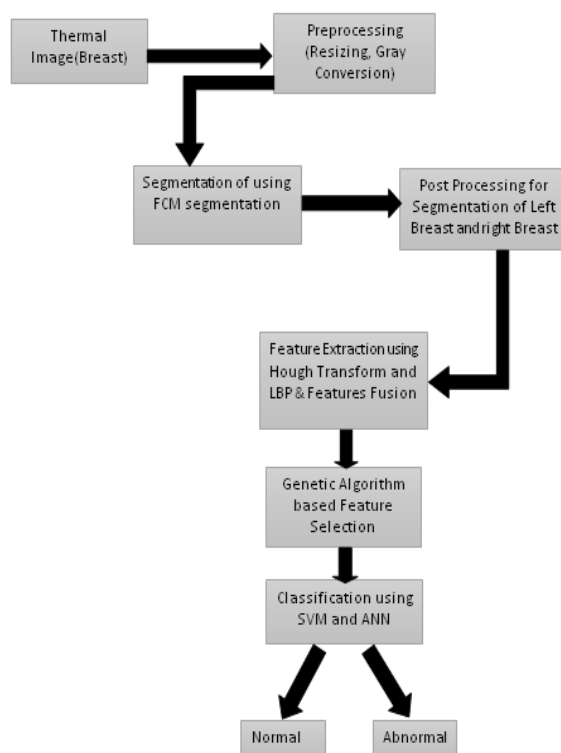

Fig.1. Block Diagram

On January 29, 1982, the Food and Drug Administration published its approval and classification of thermography as an adjunctive diagnostic screening procedure for the detection of breast cancer. Since then, numerous medical centers and independent clinics have used thermography for a variety of diagnostic purposes.

As mentioned breast thermal image can't be done with an ordinary camera and there are many important technical aspects to consider when choosing an appropriate clinical infrared imaging system, and in order to produce diagnostic quality infrared images, certain laboratory and patient preparation protocols must be strictly adhered to.

II. LITERATURE SURVEY

In the year of 2010 the authors "Sarvestan Soltani A, Safavi A A, Parandeh M N and Salehi M" issued a paper titled "Predicting Breast Cancer Survivability using Data Mining Techniques", they described such as the prediction of breast cancer survivability has been a challenging research problem for many researchers. Since the early dates of the related research, much advancement has been recorded in several related fields. For instance, thanks to innovative biomedical technologies, better explanatory prognostic factors are being measured and recorded; thanks to low cost computer hardware and software technologies, high volume better quality data is being collected and stored

automatically; and finally thanks to better analytical methods, those voluminous data is being processed effectively and efficiently.

Therefore, the main objective of this manuscript is to report on a research project where we took advantage of those available technological advancements to develop prediction models for breast cancer survivability. We used two popular data mining algorithms (artificial neural networks and decision trees) along with a most commonly used statistical method (logistic regression) to develop the prediction models using a large dataset (more than 200,000 cases).

We also used 10-fold cross-validation methods to measure the unbiased estimate of the three prediction models for performance comparison purposes. The results indicated that the decision tree (C5) is the best predictor with 93.6% accuracy on the holdout sample (this prediction accuracy is better than any reported in the literature), artificial neural networks came out to be the second with 91.2% accuracy and the logistic regression models came out to be the worst of the three with 89.2% accuracy. The comparative study of multiple prediction models for breast cancer survivability using a large dataset along with a 10-fold cross-validation provided us with an insight into the relative prediction ability of different data mining methods. Using sensitivity analysis on neural network models provided us with the prioritized importance of the prognostic factors used in the study.

In the year of 2001, the authors "Werner J C and Fogarty T C" proposed a paper titled "Genetic Programming Applied to Severe Diseases Diagnosis", in that they described such as This paper addresses the problem of how to obtain a mathematical discriminate function to quantify the severity of a disease with genetic programming (GP). It was applied to thrombosis testing because it is important to develop a fast, reliable and accurate test to identify the mechanism of thrombosis occurrence.

Artificial intelligence can help with information extraction from databases facilitating better decision making in complex systems. One possible approach is the building of a mathematical model to allow the simulation of future events based on past records. The method consists of applying an algorithm that has data as input and a model as output satisfying some optimisation criteria such as minimum error.

In the year of 2001, the authors "Iranpour M, Almassi S and Analoui M" described into the paper titled "Breast Cancer Detection from fna using SVM and RBF Classifier" such as we consider the benefits of applying support vector machines (SVMs), radial basis function (RBF) networks, and self-organizing maps (SOMs) for breast cancer detection. The Wisconsin diagnosis breast cancer (WDBC) dataset is used in the classification experiments; the dataset was generated from fine needle aspiration (FNA) samples through image processing. The 1-norm C -SVM (L1-SVM), 2-norm C -SVM (L2-SVM), and υ-SVM classifiers are applied, for which the grid search based on span error estimate (GSSEE), gradient descent based on validation error estimate (GDVEE), and gradient descent based on span error estimate (GDSEE) are developed to improve the detection accuracy.

The gradient descent (GD) tuning method based on the span error estimate (SEE) is employed for the L2-SVM classifier because of its reachable smooth nonlinearity. Such a GDSEE tuning system also has the advantage of saving available samples for the training procedure. The SOM–RBF classifier is developed to improve the performance of only the SOM learning procedure based on distance comparison, in which the RBF network is employed to process the clustering result obtained by the SOM. Experimental results demonstrate that SVM classifiers with the proposed automatic parameter tuning systems and the SOM–RBF classifier can be efficient tools for breast cancer detection, with the detection accuracy up to 98%.

Image Acquisition and Pre-Processing

An aggregate of 5 phases required in the proposed display that starts from the information contribution to yield. The principal stage is the picture pre-preparing framework. In this work a sum of 60 bosom thermograms were acquired from General Hospital utilizing noncontact bosom thermography, 30 of the patients are determined to have bosom growth and the rest are ordinary (favorable). The proposed display requires changing over the picture into an arrangement that is appropriate of start control by the PC. The bosom thermogram pictures are resized and changed over from RGB to greyscale shape by utilizing MATLAB.

FCM Division

Clustering is an unsupervised strategy and a mechanized procedure in which tests are separated into classifications that contain comparable individuals, named groups. The group is a gathering of items that are like each

other and unique with different protests in different Clusters. The variouscriteria for similitude can be considered. For instance, separate measure can be utilized for the Clustering and the articles that are nearer to each other are considered as one group.

This is called remove based Clustering. In the information tests on the left side are isolated into four groups on the correct side. In this illustration, every info test has a place with one of the Clusters and there is no example that has a place with more than one group. In most grouping calculations, a progression of the essential agents for information tests are gathered and afterward from the closeness of these info tests, the delegates can figure out which test has a place with which bunch. After this stage, new delegates are ascertained for every bunch and again the illustrations are contrasted with these agents with figure out which tests have a place with which group. This assignment is rehashed until specialist groups don't change.

Fuzzy C-Means (FCM) grouping calculation like the great C-Means calculation, in this calculation the quantity of groups (c) have been already decided. The target work for this calculation is characterized as takes after

$$J = \sum_{i=1}^{c}\sum_{k=1}^{n} u_{ik}^{m} d_{ik}^{2} = \sum_{i=1}^{c}\sum_{k=1}^{n} u_{ik}^{m}||x_k - v_i||^2$$

In the above equation, m is a genuine number more noteworthy than 1. Much of the time, 2 will be chosen for m. $X_k$is the kth sample and $V_i$is the agent or center of ith group. U_{ik}, demonstrates the participation estimation of ith test in the kth cluster. $\| * \|$ is the similitude (remove) file of the specimen from the group focus which can be any capacity that communicates the comparability of the example with the cluster'scenter.

By U_{ik}, a grid can be characterized by with c lines and n sections and its parts can embrace any an incentive between 0 to 1. On the off chance that every one of the parts of the U framework are 0 or 1, then the calculation will be like the exemplary C-Means. In spite of the fact that the parts of the U framework can embrace any an incentive between 0 to 1, the total of the segments in every section must be equivalent to 1, 34 and we have

$$\sum_{i=1}^{c} u_{ik} = 1, \quad \forall k = 1, \dots, n$$

The meaning of this condition is that the total membership of each sample to c clusters should be equal to 1. Using the above requirement and according to the minimum objective function, we have:

$$v_i = \frac{\sum_{k=1}^{n} u_{ik}^{m} x_k}{\sum_{k=1}^{n} u_{ik}^{m}}$$

$$u_{ik} = \frac{1}{\sum_{j=1}^{c}(\frac{d_{ik}}{d_{jk}})^{2/(m-1)}}$$

Algorithm 1: FCM

1. Initialized c, m and U0. Initial clusters guessed.
2. Cluster centers are calculated (vi are calculated).
3. Calculate the membership matrix from given clusters in step 2.
4. If $\|U^{l+1} - U^{l}\| \le \varepsilon$, the algorithm ends. Otherwise, again go to step 2
5. If the classic C-means algorithm is used, data will be divided into two separate clusters where each cluster will only belong to one cluster. In other words, membership function of each sample will have a value of 0 or 1.
6. Classic clustering results are shown in figure 7.
7. This figure shows the membership function of cluster A. It is visible that input samples only belong to one of the clusters. In other words, matrix U is in binary form.
8. In this figure, the membership function is smoother and the boundary between the clusters is not specified with certainty. For example, a sample which is marked with arrows belongs to cluster A with the membership value of 0.2 and to cluster B with a value of 0.8.

Hough Transform

The Hough transform is a technique which can be used to isolate features of a particular shape within an image. Because it requires that the desired features be specified in some parametric form, the *classical* Hough

transform is most commonly used for the detection of regular curves such as lines, circles, ellipses, *etc*. A *generalized* Hough transform can be employed in applications where a simple analytic description of a feature(s) is not possible. Due to the computational complexity of the generalized Hough algorithm, we restrict the main focus of this discussion to the classical Hough transform. Despite its domain restrictions, the classical Hough transform (hereafter referred to without the *classical* prefix) retains many applications, as most manufactured parts (and many anatomical parts investigated in medical imagery) contain feature boundaries which can be described by regular curves. The main advantage of the Hough transform technique is that it is tolerant of gaps in feature boundary descriptions and is relatively unaffected by image noise.

In an image analysis context, the coordinates of the point(s) of edge segments (*i.e.* (x_i, y_i)) in the image are known and therefore serve as constants in the parametric line equation, while r and θ are the unknown variables we seek. If we plot the possible (r, θ) values defined by each (x_i, y_i), points in cartesian image space map to curves (*i.e.* sinusoids) in the polar Hough parameter space. This *point-to-curve* trans formation is the Hough transformation for straight lines. When viewed in Hough parameter space, points which are collinear in the cartesian image space become readily apparent as they yield curves which intersect at a common (r, θ) point.
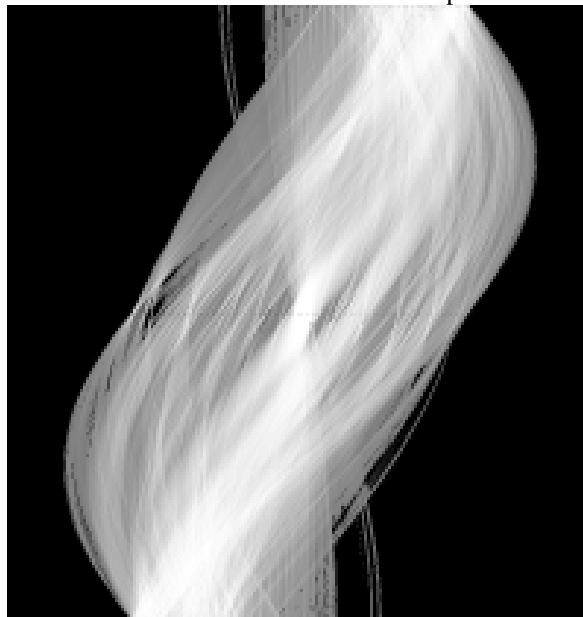

Fig.2. Hough Transform

The transform is implemented by quantizing the Hough parameter space into finite intervals or *accumulator cells*. As the algorithm runs, each (x_i, y_i) is transformed into a discretized (r, θ) curve and the accumulator cells which lie along this curve are incremented. Resulting peaks in the accumulator array represent strong evidence that a corresponding straight line exists in the image. We can use this same procedure to detect other features with analytical descriptions. For instance, in the case of *circles*, the parametric equation is

$$(x - a)^2 + (y - b)^2 = r^2$$

where a and b are the coordinates of the center of the circle and r is the radius. In this case, the computational complexity of the algorithm begins to increase as we now have three coordinates in the parameter space and a 3-D accumulator.

III. EXPERIMENTAL RESULTS
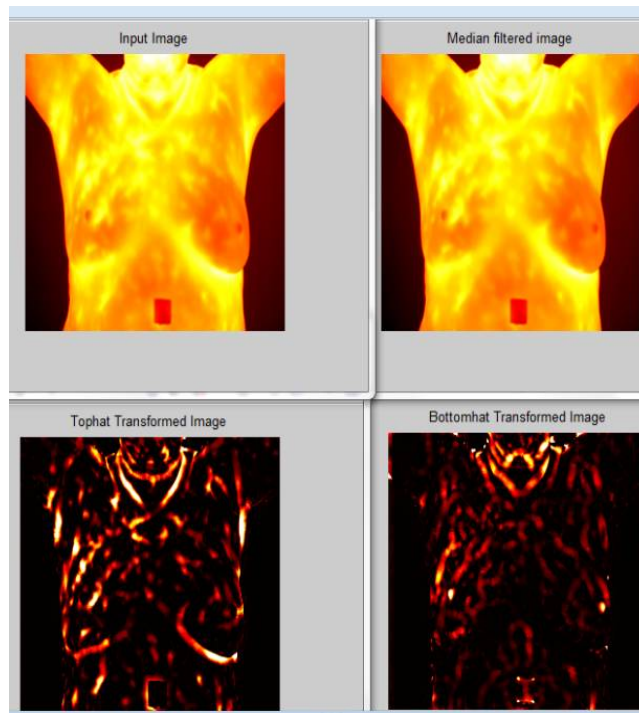
Fig.3. Image Preprocessing
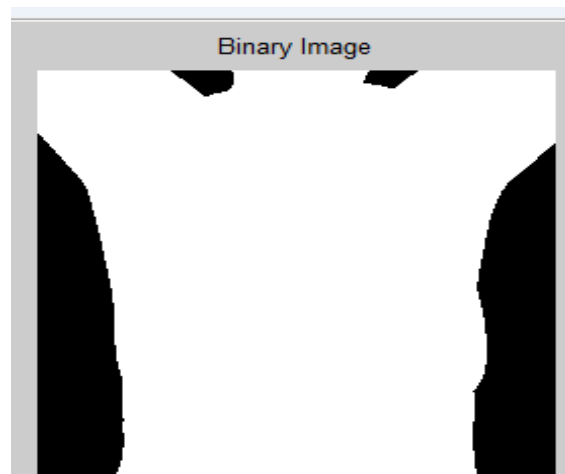
Fig.4. Image Binarization
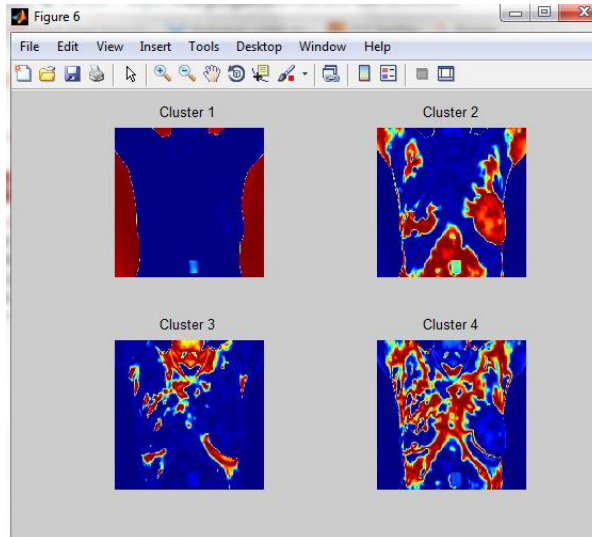
Fig.5. Image Clustering
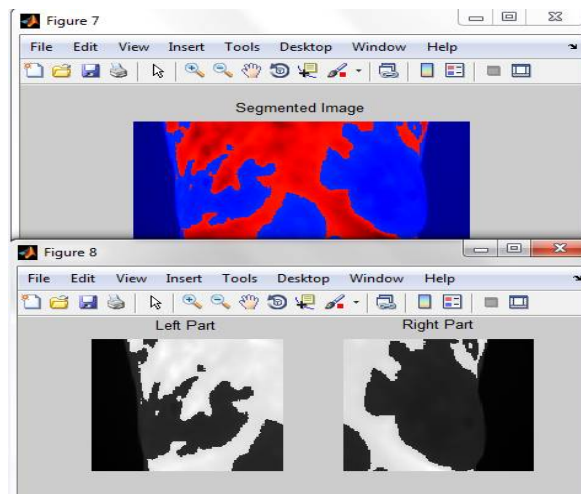
Fig.6. Segmentation
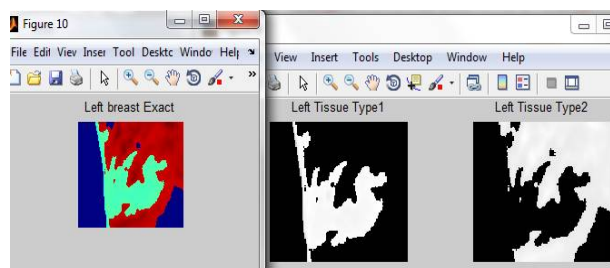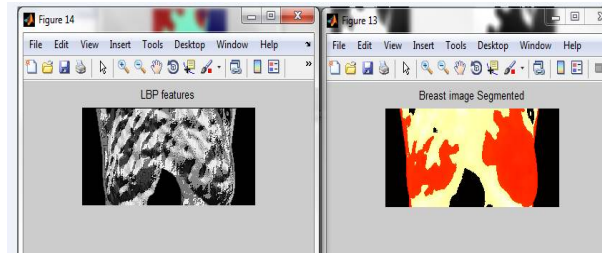

Fig.7. Image Extraction

Fig.8. LBP Feature Extraction

IV. CONCLUSION

This work demonstrates the modelling of breast cancer as classification task and describes the implementation of Support Vector Machine and Genetic programming approach for classifying breast cancer. Discipulus have been applied for generating LGP based classification models. It is observed that classification implemented by Genetic Programming in this paper is more efficient than other machine learning algorithms because the commercial GP software Discipulus uses automatic induction of binary machine code to achieve better performance. Effective models generated using linear genetic programming can be used by medical experts to classify the fine needle aspiration samples of breast tissue as benign or malignant and provide timely treatment.

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