# Classification of Benign and Malignant bone lesions on CT ImagesUsing Support Vector Machine: A Comparison of Kernel Functions

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Abstract—Skeletal metastasis has tendency to develop from any kind of primary tumor. In the spine, the vertebral body is the most common site of metastasis which then extends to pedicle. About 2/3<sup>rd</sup> of the malignant tumor cases are found to develop metastasis. This work presents a Computer Aided Diagnosis (CAD) system that helps radiologists in differentiating malignant and benign bone lesions in the spine on Computed Tomography (CT) images usingSupport Vector Machines(SVM).The CT images are segmented using Snakes or Active Contour Model to retrieve the Region of Interest(ROI). From the segmented images, Haralick features are calculated. These features are then passed to the SVM classifier. With the help of SVM model generated, the data are classified into benign and malignant nodules. The performances of different kernel functions are compared.

Keywords—Bone metastases, Haralick Features, Snakes, Support Vector Machines, SVM Kernels.

#### I. INTRODUCTION

Cancer is a genetic disease that is mainly caused due to environmental factor. People get exposed to carcinogens present in water, food, air, sunlight, and chemicals. Cancer cells are basically the damaged Deoxyribose Nucleic Acid(DNA) cells. These cells neither get repaired nor undergonecrosis, instead, they undergo division and replication. Brain, bone, liver, and lungs are few different sites where cancers spread.

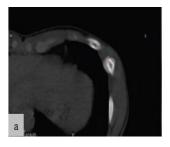
Bone metastasis or metastatic bone disease, is a class of cancer that results from primary tumor invasion to bone. Nearly all types of cancer can metastasize to the bones. But some types of cancer are particularly likely to spread to bone, including breast cancer and prostate cancer [1]. These are usually associated with severe bone pain. There are many other consequences namely Leucoerythroblastic anemia, bone deformity, hypercalcemia and nerve compression syndrome, etc.

Metastasis of cancer into spine is due to the rich availability of red bone marrow in the region that provides a supporting micro-environment for the growth and proliferation of cancer cells. In case of metastatic spine tumor, treatment of tumor should be focused on improving the quality of life rather than extension of survival.

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CT images are useful in evaluation of malignant and benign vertebral collapse [2]. Characteristics differentiating bone lesions into benign include: being well defined, homogenously and fully sclerotic, lytic with regular sclerotic margins, localization to the vertebral endplate or articular surface. Similarly, malignant tumors show the characteristics that include: being ill defined, irregularly or heterogeneously sclerotic, lytic with irregular sclerotic margins, associated with cortical destruction or extra osseous soft tissue component. These features can be seen in figure 1:



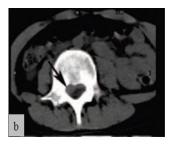


Fig. 1 (a) CT image showing the sclerotic margin, a feature of benign lesion.

(b) Involvement of spinal canal- a feature of malignant lesion [3].

The onset of bone metastasis is an important indicator of the worsening of morbidity and mortality of the cancer patients. The spreading of various types of malignant primary tumors to skeletal region may prove to be fatal as it is often seen that most of the patients die not because of the growth of primary cancer but because of its spread to secondary sites.

Furthermore, metastasis to the skeletal system is a frequent and serious complication of various cancer types with high incidence and prevalence. In many cases, it has been found that radiologists fail to identify bone lesions. These small tumor cells are capable of affecting the course of treatment if they go unnoticed. Accurate detection of bone lesions plays a key role in providing valuable clinical information and also helps determine the course of treatment (surgical intervention or radiation) making it an important part of a radiologist's work. Additionally, bone metastasis could be a prognostic factor and indicate if chemotherapy would help the patient.

#### II. METHODOLOGY

The CT image is first pre-processed using a Gaussian low pass filter. The processed image is segmented using Snake Algorithm [4]. The segmented image is masked and then multiplied by the original image to obtain the ROI. From the generated ROI, Haralick textural features are extracted of which 7 features namely autocorrelation, contrast, homogeneity,



entropy, energy and cluster values, are used to make the dataset for training and testing the SVM. Performance of different kernel functions is compared based on parameters such as sensitivity, specificity, and accuracy and Receiver Operating Characteristics(ROC) curve. The outline of this method has been depicted in Fig 2.

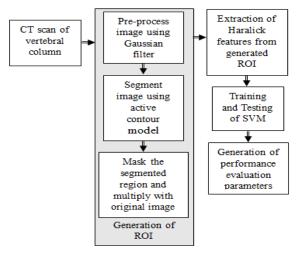


Fig 2. System block diagram of the proposed methodology

## A. Generating ROI using Snake Algorithm

We use active contour model (or snake), which isan energy minimizing spline to segment our CT images. There are three types of forces that affect the position of the snake: external constraint forces that pull the snake towards lines and edges, image forces that put the snake toward lines, edges and subjective contours, and external forces that put the snake near the desired local minimum.

The generation of ROI includes the following steps:

- 1. A predefined filter using the MATLAB function *fspecial()* is created that returns a rotationally symmetric Gaussian low pass filter of size three times the standard deviation. Then using the function *filter2()* a filtered image is obtained that uses 2D correlation.
- 2. To generate the snake, the seed points are initiated which then interpolates with a spline curve and finer spacing.
- Based on parameters like tension, rigidity, step size, energy term, weights for line, edge and terminal energy components and number of iterations, the new position of the snake is generated.
- 4. Using the function roipoly(), a binary image is created which is used as a mask for masked filtering and is then multiplied with the original image to get the required ROI. Then all zero columns and rows are removed from the ROI.

# B. Extraction of Haralick Features from the Generated ROI

Texture is a surface property, characterized by the spatial distribution of gray level in the neighborhood. Gray Level Cooccurrence Matrix (GLCM) are used for calculation of Haralick features [5].A GLCM is a square matrix with dimension  $N_l$ , where  $N_l$  is the number of gray levels in the image. Elements [i,j] of the matrix are generated by counting the number of occurrences of pixel with value i which is a neighbor to a pixel with value j. The matrix is then normalized by the total number of such comparisons made. For eg: (0,0) represents the number of times pixels have been neighbor which have the value 0. This is the reason why we removed all rows and column with value 0 to get the ROI, as a large number of elements with value 0 will give absurd GLCM matrix and thus wrong feature values. The GLCM matrix can be calculated for different orientations and displacement.

The generated ROI is fed to a GLCM function which calculates the GLCM matrix to generate Haralick features. The GLCMs are stored in i x j matrix. The parameter n is number of GLCMs used to generate the feature set in different orientations and different displacement.

The second order statistics obtained from the GLCM matrix are then used for calculation of Haralick features. Of the fourteenHaralick features, seven features: Autocorrelation, contrasts, Homogeneity, Energy, Entropy, Cluster Shade, Cluster Prominence were considered.

#### III. SUPPORT VECTOR MACHINE

The SVMis a supervised learning model. It classifies data by finding an optimal separating hyperplane that separates all data points which belongs to either of the two class. By optimal, we assume a surface such that the distance from the nearest data point to the hyperplane is as large as possible. The closest point from the either class is at the same distance away from the hyperplane. The data points which lie on the margin are called as support vectors.SVM can be used for linearly and non-linearly separable data.

It is possible that the data might not be linearly separable, but in a transformed dimension it becomes easily separable. Thus, for constructing an efficient support vector machine, a suitable kernel function should be selected. A kernel function is similar to taking an inner product in a higher dimension. The following are the kernel functions:

i. Linear kernel function

$$G(x, x') = \langle \emptyset(x), \emptyset(x') \rangle \tag{1}$$

ii. Polynomial kernel function

$$G(x, x') = (1 + \langle x, x' \rangle)^{\wedge} d$$
 (2)

where d is the order of polynomial kernel function

iii. Radial Basis function (RBF)

$$G(x, x') = e^{-||x - x'||/2\sigma^2}$$
(3)

Radial Basis kernel or Gaussian kernel function are the most useful amongst the three as it has localized and finite response across the entire range of real x-axis.

#### A. Traning an SVM Classifier

Feature extraction is performed on 100 bone lesions, 50 each of benign and malignant. These features are divided into two sets 50 each for training and testing the classifier. Using MATLAB function *fitcsvm()*, a SVM model is obtained. Following are the inputs:

• Matrix of training data

- A column array of class label, 1 representing benign and 0 represents malignant.
- Standardize, 'true': This parameter finds the standard deviation of each column and normalizes all the elements in the column thereby giving a uniform set of data
- Kernel Function: This parameter is used to select the kernel function. A comparative study of the three kernel function is mentioned in the result.

Once we obtain the SVM model, *predict()* function is used to find the classes of test data set. The result of classification on test set is stored in vector *label*, which is a new observation.

#### B. Cross-Validation

A 10-fold cross-validation is performed on the training data set. In situations where the goal is prediction and accuracy of the system, cross-validation is a useful tool. The original sample is partitioned into two complementary set, a training set to train the model and a test set to evaluate the performance of classifier.

The original sample is partitioned randomly into 10 subsamples of equal size. Out of these 10 subsamples, 9 subsamples are used for training the classifier and the remaining subsample is used as a validation set for testing the performance of classifier. This entire process of partitioning, training and testing is repeated 10 times with each subsample considered as test case only once. The result obtained from these folds are then averaged and to find a single estimation. Since all observations are used for training and testing the classifier, it is a better parameter for assessing the performance of SVM

A 10-fold cross-validation is performed using *kfoldloss()* function, which returns the loss obtained.

#### C. Confusion Matrix, ROC curve and AUC

A confusion matrix shown in Table 1 provides the number of correct and incorrect predictions made by the classification model compared to the actual classes.

TABLE I. CONFUSION MATRIX

	PREDICTED: NO	Predicted: Yes	
Benign	True Negative(TN)	FALSE POSITIVE(FP)	
MALIGNANT	FALSE NEGATIVE(FN)	TRUE POSITIVE(TP)	

It is a N\*N matrix where N is the number of classes. The elements of the primary diagonal represent the number of correctly classified elements and off the diagonal represent the misclassified elements.

A False Positive(FP) is an error in which test result improperly indicates the presence of disease(tumor), while in reality it is not present. False Negative(FN) is an error in some evaluation process in which a condition tested for is mistakenly found to be absent. True Negative(TN) is the number of correct predictions given that an instance is negative. True Positive

(TP) is the number of correct predictions given that an instance is positive.

The confusion matrix is calculated using *confusionmat()* function. The *loss()* function returns the classification error, a scalar representing how well the trained SVM classifier SVM model classifies the predictor data.

$$Sensitivity = TP/(TP + FN) \tag{4}$$

$$Accuracy = (TN + TP)/(TN + FN + TP + FP)$$
 (5)

$$Specificity = TN/(TN + FP) \tag{6}$$

Receiver Operating Characteristics(ROC) is a graphical plot illustrating the performance of a binary classifier. The curve is created by plotting the true positive rate against the false positive rate. The Area Under Curve(AUC) is the accuracy of the system. The *perfcurve()* function returns the X and Y coordinates of an ROC curve for a vector of classifier predictions, given the true class label and the positive class label. Performance can be visualized by *plot(X,Y)*. It also returns the AUC.

#### IV. RESULTS AND DISCUSSION

The extracted Haralick features are then passed to the SVM Classifier with three different kernels namely, Linear, Polynomial and Radial Basis Function. The classifier's performance is measured based on parameters such as sensitivity and specificity, accuracy, ROC and AUC. The objective of this paper is to classify or identify the malignant and benign lesions in the spine. The results are tabulated below:

TABLE II. PERFORMANCE OF SVM CLASSIFIER

Kernel Function	Loss in cross- validation (%)	Loss in test set (%)	Sensitivity (%)	Specificity (%)	AUC
RBF	8	14	84.6	87.5	0.86
Polynomi al (deg=3)	8	16	79.3	90	0.84
Linear	28	22	75	81	0.78

As observed in Table 2, using RBF the sensitivity of detection is found to be 84.6% which is better compared to the sensitivity of detection using Polynomial (79.3%) and linear (75%) kernel function. Meanwhile, it is also observed that the polynomial function has better specificity of detection (90%) compared to RBF (87.5%) and Linear kernel function (81%). From the AUC value of 86% we conclude that RBF has better accuracy from that of polynomial and linear kernel function.

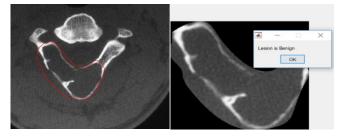


Fig 3: Spine affected by Hemangioma correctly classified as benign

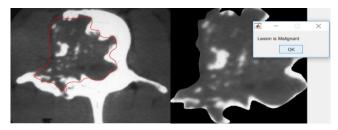


Fig 4: Osteogenic Sarcoma correctly classified as malignant

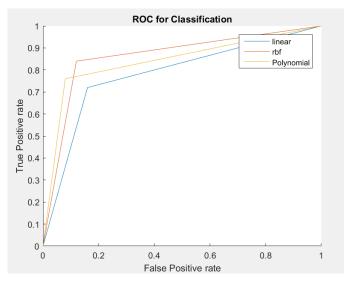


Fig.5: ROC Curve for comparison of the three kernel function

### V. CONCLUSION

This paper discusses a technique for the classification of benign and malignant lesions from CT images using SVM.Haralick texture features are extracted from ROI. Of the 14 features extracted, 7 features were considered for classification. From the results, it can be concluded that SVM with RBF gives the best results for classification. Although it is difficult to classify the bone lesions because in some malignant cases the osteoblastic activity is similar to that in benign lesions, the accuracy of RBF is 86% for the testset.

Future work can include Gradient Vector Flow(GVF) for segmenting the image. Gradient Vector flow provides better segmentation because of its ability to move into boundary concavities [6], [7]. This feature of GVF will provide us with better feature values and make classification more efficient. Due to increased rate of glucose metabolism in tumor cell, the sensitivity of Positron Emission Tomography(PET) image is high. Thus PET-CT images can potentially increase the performance of this method.

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