Classification of Texture Parameters Between Normal And Tumor Portions of a CT Scan Image

A Thesis submitted in partial fulfilment of the

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Master of Engineering

in

Electronic Instrumentation and Control

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Declaration

I hereby declare that the report entitled "**Classification of Texture Parameters Between Normal And Tumor Portions of a CT Scan Image**" is an authentic record of my own work carried out as requirements for the award of degree of **Master Of Engineering** in **Electronics Instrumentation and Control** at **Thapar University**, Patiala, under the guidance of **Dr. Deepti Mittal** (Assistant Professor, EIED) January to June 2014.

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Abstract

Medical imaging has provided a non invasive way of extracting information from the internal organs of humans. Tumor diagnosis is one of the key factors for which medical imaging such as computer tomography CT scan are used. However medical images such as CT scan may not provide accurate information of the tumor or may be the information is based on human perception. Hence medical images have to be analysed in order to diagnose tumors accurately.

Texture analysis of a CT scan image may help in differentiating between normal and the tumor portions. In this thesis we have used abdominal CT scan with tumor region marked on them. Texture parameter were calculated using the statistical approach proposed by haralick[1] called grey-level co-occurrence matrix(GLCM). Further a comparison was carried out between normal and the tumor portion texture parameters using box-plots.

On the basis of the box-plot comparison further classification between normal and the tumor portion using values of texture parameters was performed .SVM classifier with different kernel functions was used for classification purpose.

Further more we used a image enhancement technique called the adaptive histogram equalization technique to enhance the contrast of the CT scan images. The texture parameters calculated from the normal and the tumor portion of the enhanced images were subjected to the same procedure as the original images.

This study investigates the texture features which are able to discriminate between normal and the tumor portions in a CT scan image both original and enhanced.

Organization of the Thesis

First chapter provides introduction to the CT scan imaging and why texture analysis is needed for diagnosis of tumor in a CT scan. In the end of this chapter we provide the review of the literature. Second chapter is based on various texture analysis methods and the method used in our thesis. The third chapter provides explanation for SVM classifiers. The fourth chapter is methodology. This chapter explains the procedure used in our investigation, this chapter also explains how texture parameter were calculated and used in SVM classifier. The fifth chapter is result and discussion. This chapter provides all the values of texture parameters calculated for the normal and the tumor portions of original and enhanced images. In the end this chapter also hold the results of classification using SVM classifier. The sixth chapter is conclusion and future scope of our work.

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List of abbreviation

CAD system – computer aided diagnostic system

CLAHE- contrast -limited adaptive histogram equalization

CT scan- computer tomography scan

GLCM- grey level co-occurrence matrix

Rbf – radial basis function

SVM- support vector machine

Chapter 1 Introduction

Tumor diagnosis is a vast field of study. In the last 3 decades many studies have been done on tumor diagnosis, still this field have a vast scope for improvement. Tumor if a cancer is a deadly diseases and only early diagnosis may help the patients in surviving. Diagnosis not only should be early but also should be accurate and reliable for better treatment. Medical imaging techniques such as computer tomography(CT) scan, Magnetic resonance imaging(MRI) have provided a non invasive way to diagnose tumors. CT scans due to their inexpensiveness and better availability have been widely used for tumor diagnosis.

However, CT scan alone cannot provide a conclusive diagnostic information, hence a computer aided diagnosis(CAD) system is needed. In this thesis we have studied algorithms that can help a CAD system to differentiate between normal and the tumor portions in a CT scan image. Texture variation between normal and the tumor portions have been taken into consideration.

1.1 Tumors

A tumour are existence of an abnormal mass of tissue with a ability of progressive growth. It is a term used to describe chaotic growth of body cell in an uncontrollable manner. These tissues effect the life span of the cells as well as formation of new cells. As a result, these diseased extra cells which consume oxygen and nutrients from the healthy cells would contribute to the formation of the tumour tissue.

cancerous tumors are the Cells which can invade other tissues travelling through the bloodstream and form new tumours in other body parts hence, causing death .The site at which cells initially spread from is the primary tumour and the nearby affected site is called the secondary or metastatic tumour. cancerous tumours are treated with surgery followed by radiation and chemotherapy. These are also called malignant tumors

non-cancerous tumors are the Cells do not travel to surrounding tissue or spread to other parts of the body. Often these can be completely removed without reoccurring. These are also called benign tumors.

1.2 Computer tomography

CT scans are the reconstruction of a cross-sectional image of the body part it is subjected to. It using virtual piles of X-ray photographs. A thin collimated beam of X-rays are passed through the body and the transmitted intensity is detected by a detector that measures the intensity transmitted it. Measurements are made on various points as the source and the detector are moved around the body together at various angles. The intensity measured at various points and at each angle is then sent to a computer for reconstruction of the image. In this thesis we have used abdominal CT scan images with tumor in the liver region.

1.2.1 Texture in a CT scan image

Visual diagnosis of a tumor in a CT scan is base on morphological information such as size and shape. Identifying relationship between patters and possible diagnosis depends on the knowledge and skills of a radiologists. However humans have difficulties in discriminating texture information such as coarseness and regularity. Hence more qualitative information from a image is necessary which is not possible through visual analysis. The answer to this problem can be texture analysis which is a vital component of computer-aided diagnosis(CAD) system.

Texture in medical imaging are of two types, cellular and tissue, each of which represent some properties of an organ of interest . Tissue images have a micro-scale structure due to the fine overall appearance of the texture. On the other hand, in cellular images the internal structure of small specimens such as blood samples is magnified to acquire there molecular properties. The cell nuclei is the main texture descriptor and the morphology of the cell nuclei, i.e. shape, colour, structure and pattern, and with their relatively large size adds the graininess to the image, hence this type of texture is defined as macro-scale structure.

` Texture analysis is very useful in describing homogeneous areas in a CT scan image. A set of texture parameters are calculated and used to describe the characteristics of the region of interest. The parameters are calculated using histogram based statics or more sophisticated co-occurrence matrix .

Texture analysis of a abdominal CT scan images face many challenges such as the similarity in the gray levels of different organs in the abdominal due to which thresholding is limited. Furthermore difficulties arise due lack of tissue homogeneity in texture, within and among different slices of CT scan.

1.3 Feature extraction

Feature extraction is the initial step for image analysis. Feature extraction refers to the gathering of information from an image at a particular level

1. Feature extraction at data level- consists of joint information from the pixels of an image. Hence all techniques effecting the whole image matrix at once come under data level feature extraction. Techniques such as Fourier transforms are the best examples for data level feature extraction.
2. Feature extraction at pixel level- depends on information gathered from individual pixel. Point operations such as histogram, provide information about each pixel intensity are the best examples of pixel level feature extraction.
3. Feature extraction at edge level- emphasizes on the difference between the intensities of adjacent pixels. Various high pass filters and edge detectors such as sobel, perwitt, and canny are the examples of edge level feature extraction.
4. Feature extraction at region level- emphasizes on object recognition and classification in a segmented region. Parameters such as localization descriptive and delineation descriptive are used to extract features. Localization descriptive measures the size, orientation and position and delineation descriptive measure shape, length of the boundary and convexity.
5. Feature extraction at texture level- emphasizes on homogeneity in a heterogeneous periodic structure image. Texture level feature extraction uses various approaches such as statistical, structural, model based and transform based to extract some qualitative information from a image. Haralik texture features are the best examples.

In this thesis we have used texture extraction and each texture parameter was calculated for each image. The enhanced version of the images were also used to calculate texture. Variation in the texture parameter values in the normal portions and the tumor portions are used to detect whether a texture parameter can differentiate between both the portions.

1.4 Literature review

Haralick et. al proposed a method to extract texture features from the blocks of[1] images. These features were statistical in nature and were calculated in spatial domain. Haralick made an assumption that the texture properties in an image are average or overall spatial relationships which the grey levels in a image have with each other. They computed a metrics called grey tone spatial dependence probability distribution metrics and suggested 14 texture features which can be calculated using this metrics. The number of operations required to compute these features depend upon the number of resolution cells in the image.

Davis et. al proposed a generalized co-occurrence (GCM)metrics for determining[2] texture feature. These metrics described the spatial arrangement of local image features such as edge and lines. The GCM metrics is based on image feature prototype, spatial predicate and prototype attributes. These prototypes were the structural definition of the features in an image. Spatial predicate is mapping of features into (true, false) category. They compared three prototypes i.e. edge pixels, pixel intensity, and extended edge and spatial predicates were defined for each of them.

Walker et. al proposed improvement in co-occurrence metrics features. The[6] classification of the haralick[1] was done between features which were weighted on metrics elements value (e.g. energy ,entropy) and features which were weighted on spatial location (e.g.correlation,variance). It this paper it was shown that it is best to suppress those elements of metrics that yield little discrimination. On the basis of Bhattacharya distance, we can find which element discrimination ability is more. A matrics containing these weights was multiplied to the original matrics , hence a better representation of the value with good discrimination ability was achieved. From this matrix we can compute features as weighted sum elements.

H. Mir. et. al used texture features for diagnostic information in a CT scan image. [7] They calculated number of texture features from the CT scan of liver. They investigated the texture features which can discriminate between various tissues without human perception. They concluded that texture features were useful for diagnosis purpose in the liver tissue. Entropy homogeneity and grey level distribution were found to be effective in detecting the early malignancy with a confidence level of above 99%.

E.liang.C. et. al proposed a CT liver diagnostic classification system which[9] automatically find and extract the liver boundary and classified the liver diseases. The system consisted of a detect before extract system which used feature descriptors to distinguish between the normal and two types of tumors, hepatoma and hemageoma. The detect before extract system applied the concept of normalized fractional Brownian motion model to find liver boundary and then used the deformable contour model to precisely delineate the liver boundary. A modified probabilistic neural network was used to classify liver tumors based on fractal features and GLCM features.

Gokturk, S.B et. al proposed a method for computer aided detection of polyps in a[12] CT colonography, in which the polyp is imaged along the wall of air-inflated, cleansed colon with X-ray CT. Authors proposed a statistical approach that used SVM to distinguish the differentiating properties of polyps and healthy normal tissue. They used this information for classifying new cases. Authors used a new 3-D pattern processing approach, called random orthogonal shape sections method. This method combined the information from the random images to generate reliable signatures of shape. The input to this system was the collection of volume data from the polyps.

Gletsos, M et. al designed a computer aided diagnostic system for classification of[15] heptic lesions from CT images. The regions of interest (ROIs) Were taken from nonenhanced CT images of normal liver, hepatic cysts, hemangiomas, and hepatocellular carcinomas were used as input to the system. The proposed system consisted of two modules, the feature extraction and the classification modules. The feature extraction module calculated the average gray level and 48 texture characteristics, which were derived from the spatial gray-level co-occurrence matrices, obtained from the ROIs. The classifier module consisted of three sequentially placed feed forward neural networks (NNs). The first NN classified normal or pathological liver regions. The pathological liver regions were characterized by the second NN as cyst or other disease .The third NN classified other disease into hemangioma or hepatocellular carcinoma. Three feature selection techniques were applied to each individual NN: the sequential forward selection, the sequential floating forward selection, and a genetic algorithm for feature selection.

Al.Kadi,O.S and D.Watson showed the potential for fractal analysis of time[16] sequence contrast-enhanced (CE) computed tomography (CT) images to differentiate between aggressive and nonaggressive malignant lung tumors (high and low metabolic tumors). The aim was to enhance CT tumor staging prediction accuracy by identifying malignant aggressiveness of lung tumors. The branching of blood vessels was considered a fractal process, they examined vascularized tumor regions that exhibited strong fractal characteristics. The analysis was performed after injecting 15 patients with a contrast agent and transforming at least 11 time sequence CE CT images from each patient to the fractal dimension and determined corresponding lacunarity. The fractal texture features were averaged over the tumor region and a quantitative classification was done. These results indicate that fractal analysis of time sequence CE CT images of malignant lung tumors could provide additional information about likely tumor aggression.

Huan Yu et. al identified textural features useful for distinguishing tumor from[17] normal tissue in head and neck via quantitative texture analysis of PET and CT images. Abnormal and typical normal tissues were manually segmented from PET/CT images. Texture features derived from spatial grey-level dependence matrices (SGLDM) and neighborhood gray-tone-difference matrices (NGTDM) were selected for characterization of these segmented regions of interest (ROIs). Both k-nearest neighbors (KNNs) and decision tree based KNN classifiers were employed to discriminate images of abnormal and normal tissues. The leave-one-out and bootstrap techniques were used to validate the results. NGTDM features such as PET Coarseness, PET Contrast, and CT Coarseness extracted from PETandCT images provided good discrimination performance.

Rahmath.S. Hameed and S.S. Kumar proposed a CAD system that diagnosed[18] malignant from begnignliver tumors. CT images of liver lesion were taken as input and then region of interests(ROI) were segmented. From these ROIs, texture fratures were extracted using GLCM. Features such as contrast, correlation, entropy, homogeneity, variance, were extracted from GLCM and fed to a probabilistic neural network(PNN) and pulsed coupled neural network(PCNN) for classification purpose. The authors found which one of the classifiers were more adaptable for diagnosis. The PCNN classifier showed better results than PNN.

Jinsa Kuruvilla and K. Gunavathi proposed a computer aided classification [19] method in computed tomography(CT) images of lungs developed using artificial neural network. The entire lung was segmented from the CT images and the parameters were calculated from the segmented image. The statistical parameters like mean, standard deviation, skewness, kurtosis, fifth central moment and sixth central moment were used for classification. The classification process was performed by feed forward and feed forward back propagation neural networks. Compared to feed for-ward networks the feed forward back propagation network gave better classification. The parameter skewness gave the maximum classification accuracy. Two new training functions were proposed. The results show that the proposed training function 1 gave an accuracy of 93.3%. The proposed training function 2 gave a accuracy of 93.3%.

W.Huang et. al proposed an approach for detection and segmentation of liver [20] tumors in a 3D computed tomography (CT) images. The automatic detection of tumor were formulized as novelty detection or two-class classification issue. The method could also be used for tumor segmentation, where each voxel was to be assigned with a correct label, either a tumor class or non-tumor class. A voxel was represented with a rich feature vector that distinguishes itself from voxels in different classes. A fast learning algorithm Extreme Learning Machine (ELM) was used and trained as a voxel classifier. In automatic liver tumor detection, it was proposed that ELM can be trained as a one-class classifier with only healthy liver samples in training. It resulted in a method of tumor detection based on novelty detection. The authors compared it with two-class ELM. To extract the boundary of a tumor, semi-automatic approach was used by randomly selecting samples in 3D space within a limited region of interest (ROI) for classifier training.

Selvathi, D et.al evaluated the role of the adaptive hybrid segmentation ,[21] algorithm Contourlet transform and the Extreme Learning Machine in the differential diagnosis of liver tumors in CT images . The liver was segmented from CT images using adaptive threshold method and morphological processing. Extraction of tumor was done by Fuzzy C Means (FCM) clustering from the segmented liver region. The statistical and textural information were obtained from the extracted tumor using Contourlet Transform.The features like mean, standard deviation and entropy of the obtained sub bands were calculated and stored in a feature vector. The extracted features were fed as input to Extreme Learning Machine classifier to classify the diseases such as hepatoma, hemangioma and cholangiocarcinoma.

Table 1.1 Summary of literature review in the area of classification of texture features using CT scan images

Reference	**Type of detection**	**Features extracted**	**Classifier**	**Results**
E.liang et .al (1998) [9]	Hapetoma and Hemageoma liver tumors	Fractal features and GLCM features such as Contrast, energy, entropy, homogeneity,sum entropy	Modified probabilistic neural network classifier(MPNN)	83% accuracy
Gokturk, S.B et .al (2001)[12]	Adenomatous polyps	Shape and intensity geometric features	Support vector machine(SVM) classifier	0.69 and 0.74 specificity
Gletsos, M et .al (2003)[15]	Hepatic cysts, hemangiomas and hepatocellular carcinomas liver tumors	Average Grey-level, Energy, contrast, correlation, variance, homogeneity, entropy, inverse difference moment, cluster tendency.	Feed forward neural network	100% accuracy
Al –Kadi.O.S & D. Watson (2008)[16]	High and low metabolic tumors	Average fractal texture dimensions, Lacunarity features	Quantitative classification	83.3% accuracy
Huan yu et. al (2009)[17]	Head and neck cancer	Coarseness, entropy, contrast, busyness, energy, mean, standard deviation	K-nearest neighbours(knn) and decision tree (DT)-based KNN	Sensitivity 89% and specificity 99%
Rahmath.S. Hameed.; S.S. Kumar(2012)[18]	Hepatoma, hemangiomas, liver tumors	Contrast, correlation, homogeneity, entropy and variance	Probabilistic neural network(PNN) and pulse coupled neural network (PCNN) classifiers	Accuracy of 84% in PNN and 87% in PCNN
Jinsa Kuruvillaa and K. Gunavathi (2013)[19]	Lung cancer	Mean, standard deviation, skewness, kurtosis, fifth central moment and sixth central moment	Feed forward back propagation network classifier	Training function 1 accuracy 93.3%, Training function 2 accuracy 93.3%
W.Huang et. al(2013)[20]	Tumor and Non tumor classes	Neighborhood mean variance, intensity, Intensity power, entropy, intensity co-occurrence, Law's Texture , and Sum and Difference Histogram	Extreme learning machine (ELM) classifier	Volume Overlapped =67.15%
Selvathi, D et.al (2013)[21]	Hepatoma, hemangioma and cholangiocarcinoma liver tumors	Mean, standard deviation and entropy using contourlet transform	Extreme Learning Machine(ELM) classifier	Accuracy=96.56% Sensitivity=94.33% Specificity=97.78%

Chapter 2 Texture Analysis

2.1 Introduction

In machine vision and image processing texture does not hold a rigid definition, still it is a rich source of visual information. We can say that texture is the spatial distribution of pixel intensities or gray levels in an image or It is the regular repetition of patterns in an image. Texture is a property which cannot be defined for a point. It depends on the resolution at which a image is observed. Let us take a example of a grid of tiles on a floor. If we observe the tiles from a distant place we can observe the texture due placement of tiles but not the texture within the tiles. If the same is observed from a closer distance the property of texture will change. Hence texture is the regular repletion of pattern at a observed resolution.

The main issues of texture analysis are-:

1. Feature extraction
2. Texture classification
3. Texture segmentation
4. Shape recovery

Texture feature extraction is to compute texture properties and numerically describe the characteristics of an image. We can use grey-level co-occurrence matrix(GLCM) to compute these properties which is a statistical approach for feature extraction.

In texture classification, the identification of a given texture region from various texture classes is the main problem. In an image each region may have different texture characteristics. Analysing texture and extracting features which distinguish between each region facilitates classification of such regions. Features such as entropy, energy homogeneity, and contrast which can be calculated from gray-level co-occurrence matrix(GLCM) can be used for classification. On the other hand some structural approaches are also present if the size of primitives is larger. Structural approaches determine the shape and properties of these primitives and then examine the rule which define the placement these primitives. In case of statistical approach the primitives should be micro textures and in the case of structural approaches the primitives are macro textures.

Texture segmentation determines the boundaries between different texture regions in the image. Texture features once determined using statistical approach, are useful for texture segmentation but statistical approaches are not accurate until subjected to a single texture region. Hence there is no general method for texture segmentation. Texture segmentation still is a active area of research and various methods have been proposed for some particular applications.

Shape recovery exploits variations in the texture properties such as orientation, size, and density of texture primitives. Texture gradient which is define as the magnitude and direction of the maximum change in primitive size, determines the orientation of the image plane. The main objective of the shape recovery is to construct 3D surface using texture properties.

2.2 Approaches for texture analysis

The four types of approaches are used for texture analysis. structural approach, statistical approach, model based approach, transform based approach.

2.2.1 Structural approach

Structural approach is used when the texture primitives are macro textures. The structural models of texture assume that textures are composed of texture primitives and the texture is produced by the placement of these primitives according to certain placement rules. These algorithms, in general, are limited unless one is dealing with very regular textures. Structural texture analysis consists of two major steps i.e. extraction of the texture elements, and defining the placement rule. Texture elements are referred to the regions in an image with uniformity in the gray levels.

While using structural approach on gray-scale images, we can define a property which satisfies all pixels within each blob corresponding to a primitive. Blob is referred to a region in an image where some properties are constant. A commonly used property is the gray-level homogeneity. The image is pre-processed using a laplacian of gaussian filter and primitive regions are identified by grouping pixels which are not nearer to the edge pixels. Properties such as size, elongation, and orientation are useful features for homogeneous blobs. Measures based on co-occurrence of these primitives obtained by analyzing their spatial relationship are then used to define the placement rule.

Structural approaches provide a good symbolic description of the image. However, these features are more useful for synthesis than analysis tasks. These descriptions are ill defined for natural textures because of the variability of both micro and macro-texture and no clear distinction between them.

2.2.2 Statistical approach

Instead of understanding the hierarchical structure of the texture, statistical approach represent the texture using non-deterministic properties that govern the distributions and relationships between the grey levels of an image. Let us define the first and the second order statics.

First-order statistics measure the likelihood of a gray value in an image. First-order statistics can be computed from the histogram of pixel intensities in the image. These depend only on individual pixel values and not grey level co-occurrence. The image gray intensity in an image is an example of the first-order statistic.

Second-order statistics measure the likelihood of observing a pair of gray values occurring at a random distance in the image at a random location and orientation. These are properties of pairs of pixel values. Statistical approach based on second-order statistics achieve higher discrimination rates as compared to structural approach.

The most common second-order statistical features for texture analysis are derived from the co-occurrence matrix.

2.2.3 Model based approach

Model based approach characterises texture by determining an analytical model of a textured image. These models have a set of parameters which determine the properties of the texture. Analysis using fractal and stochastic models, attempt to explain an image texture by using generative image model and stochastic model respectively. The parameters of the model are estimated and used for image analysis. While analyzing image texture using model based approach, the computational complexity in the estimation of stochastic model parameters is the primary problem. On the other hand fractal model has is useful for modelling some natural textures. It can be used also for texture analysis and discrimination but lacks orientation selectivity and is not suitable for describing local image structures.

2.2.4 Transform based approach

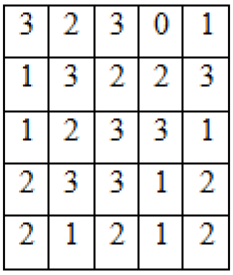
Transform based approaches such as Fourier, Gabor and wavelet transforms represent an image in a co-ordinate space that has an interpretation that is closely related to the characteristics of a texture such as frequency or size. They analyze the frequency content of the image. Fourier transforms have some limitations in a spatial localization so they do not perform well. On the other hand, Gabor filters provide means for better spatial localization but their use is limited in practice because there is no single filter resolution that can localize a spatial structure in natural textures. As compared to Gabor transform, the wavelet transforms have several advantages such as, by varying the spatial resolution allows it to represent textures at the most suitable scale and also there is a wide range of choices for the wavelet function. The problem with wavelet transform is that it is not translation-invariant.

2.3 Approach used : Texture analysis using gray-level co-occurrence matrix(GLCM)

The grey-level co-occurrence matrix first introduced by haralick in 1973 is a statistical approach for texture analysis. It is frequency matrix representing the second order histogram of an image. GLCM show how many times a pixel pair which are d distance apart, occur in a image.

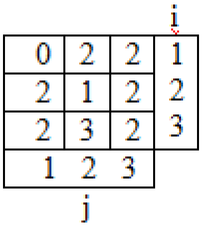
Let us consider a gray scale image I and G be the number of grey levels in the image. Then GLCM is a G x G square matrix P[i, j], where the $(i, j)^{th}$ entry of the matrix represents the number of times a pixel with intensity i is adjacent to a pixel with intensity j with a displacement vector d = (dx, dy) .

For example, consider the simple 5 x 5 image, having gray levels 1, 2, and 3 as shown in Figure 3.1(a). Since there are only three gray levels, P[i, j] is a 3 x 3 matrix. In a 5 x 5 image there are 16 pairs of pixels which satisfy the spatial separation of d(1, 1). We now count all pairs of pixels in which the first pixel has a value of i and its matching pair displaced from the first pixel by d has a value of j, and we enter this count in the i^{th} row and j^{th} column of the matrix P[i, j]. For example, there are three pairs of pixels having values [3,2] which are separated by the specified distance, and hence the entry P[3, 2] has a value of 3. The complete matrix P[i ,j] is shown in Figure 2.1(b).



3	2	3	0	1
1	3	2	2	3
1	2	3	3	1
2	3	3	1	2
2	1	2	1	2

Figure2.1(a)



			i
0	2	2	1
2	1	2	2
2	3	2	3
1	2	3	
	j		

Figure2.1(b) show the GLCM for the image in figure2.1(a)

P[i, j] is not symmetric since the number of pairs of pixels having gray levels [i,j] does not necessarily equal the number of pixel pairs having gray levels [j, i]. The elements of P[i,j] are normalized by dividing each entry by the total number of pixel pairs. In our example, each entry is divided by 16. This normalized P[i, j] is then treated as a probability mass function since the entries now add up to 1.

In addition to distance d between the pixels i and j we can also define direction of calculation of GLCM. The default being the horizontal direction($\theta = 0^o$) there are also co-occurrence matrices for vertical direction ($\theta = 90^o$) and both diagonal directions ($\theta = 45^o$, 135^0). If the direction from bottom to top and from left to right is considered, there will be eight directions (0^o, 45^o, 90^o, 135^o, 180^o, 225^o, 270^o, 315^o).Feature calculated using gray level co-occurrence matrix(GLCM) have been described in chapter 4.

In this chapter we analysed the texture with different approaches to extract it. Statistical texture analysis is a process in which using various grey level matrices we can calculate various texture properties. GLCM represents the second order histogram of a image. It represents the histogram for a pair of pixels which are a particle distance apart from each other. Parameters such as entropy, homogeneity etc are calculate on the basis of this matrix.

Other matrices used for texture parameter calculations are generalized co-occurance matrix(GCM), grey –level spatial dependency matrix(GLSDM).

Chapter 3 Support vector machine

3.1 Introduction

Support Vector Machine (SVM) is a classifier which was first introduced in 1992 by Boser, Guyon, and Vapnik. Support Vector Machine (SVM) uses machine learning theory for classification and regression prediction to maximize predictive accuracy. Classification in SVM is an example of Supervised Learning. Given a set of training data, each belonging to one of two categories or labels, an SVM training constructs a hyperplanes in a high-dimensional space assigning new samples called the testing data into one label or the other creating a SVM model. An SVM model is a representation of the training data as points in high-dimensional space, mapped so that the training data of the separate categories or label are divided by a hyperplane that is as wide as possible. Testing data are then mapped into that same high-dimensional space and are labelled based on which side of the hyperplane they fall on. A good separation is achieved by the hyperplane that has the largest distance to the nearest training data point of any class.

3.2 Linear SVM classifier

Support vector machines(SVM) is a linear two-class classifier. Let us consider a two class problem in which the population of a data set is labelled with positive samples(1) and negative samples(-1). Let K denotes a vector with components x_i and K_i be the ith vector in the population $\{(K_i, Y_i)\}_{i=1}^{n}$ where Y_i is the label(positive samples or negative samples) for K_i.

Dot product between two vectors is the key concept for linear classifier. Dot product of two vectors also called scalar product is defined as $W^t K$=$\sum_i w_i \, x_i$. A linear classifier is defined by a linear discriminant function $f(x)$ of the form

$$f(K) = W^T K + b \qquad (1)$$

Where W is a vector called the weight vector and b is bias. Consider if b=0 the set of points K are the points that perpendicular to W and go through the origin such that such that $W^T K = 0$. these are called hyperplane. The bias b is responsible for the translation of hyperplane away from the origin. A hyperplane $f(K) = W^T K + b = 0$ divides the space into two and the sign of the function $f(K)$ will determine the side of the hyperplane a point will belong.

A decision boundary is a boundary defined by the hyperplane between regions classified. A decision boundary is linear if it is linear in the input samples(eq 1). A classifier with a linear decision boundary is a linear classifier. Figure3.1

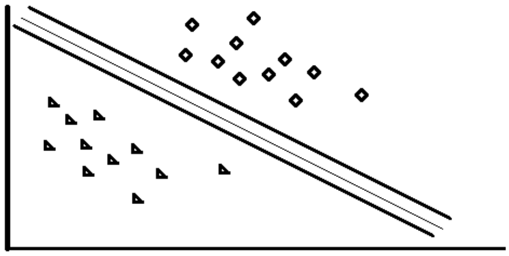


Figure3.1 show the linear classification of the data points of two labels.

3.3 Non linear SVM classifier (kernel trick)

If the data is linearly separable, hyperplane may be used to divide the samples. However it is often that the data is not linear and the samples are inseparable. For non linear data, kernels are used to map the input data to a high-dimensional space. The new mapping is then linearly separable.

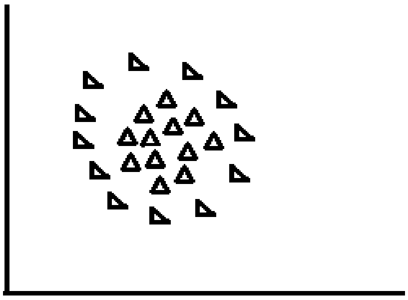


Figure 3.2 show the non linear data which cannot be separated by a hyperplane

A non-linear classifier can be made out of a linear classifier by mapping of data from the input space to a feature space. Mapping the data into feature space defines a similarity measure on the basis of the dot product. A non-linear function Φ is used to map the data into feature space. The discriminant function for the feature space will be

$$f(x) = W^T \Phi(K) + b \qquad (2)$$

Consider mapping of data to a 3D space using

$$\Phi(K) = (x_1^2, \sqrt{2}x_1x_2, x_2^2)^T \qquad (3)$$

and if we linearly separate the mapped data, the result will be a decision boundary for the classifier in the form $f(x) = W^TK + b = 0$ which is a ellipse (Eq (4)).

$$W^T\Phi(K) = w_1x_1^2 + \sqrt{2}w_2x_1x_2 + w_3x_2^2 \qquad (4)$$

Explicit mapping of data in a high dimensional feature space does not do well when the dimension of the data used is high. While mapping the data in the feature space using above expression(eq.4), the dimensions of the feature space is quadratic in the original space. This results in increase in memory usage and time required to calculate the discriminant function.

Kernel method solves this problem by avoiding explicit mapping of data in the feature space. Some examples of Kernel Functions $K(\mathbf{x}_i,\mathbf{x}_j)$ used with SVM classifier are-:

1. Linear: $K(\mathbf{x}_i,\mathbf{x}_j)= \mathbf{x}_i^T\mathbf{x}_j$
2. Polynomial of power p: $K(\mathbf{x}_i,\mathbf{x}_j)= (1+ \mathbf{x}_i^T\mathbf{x}_j)^p$
3. Gaussian (radial-basis function network): $K(\mathbf{x}_i, \mathbf{x}_j) = \exp(-\frac{\|\mathbf{x}_i - \mathbf{x}_j\|^2}{2\sigma^2})$
4. Sigmoid: $K(\mathbf{x}_i,\mathbf{x}_j)= \tanh(\beta_0\mathbf{x}_i^T\mathbf{x}_j + \beta_1)$

3.4 Margins

The points closest to the hyperplane are denoted by K_+ for the positive samples and K_- for the negative samples. The length of the weight vector W is denoted by $||W|| = \sqrt{W^TW}$. Hence the margin of a hyperplane with respect to a data set J is

$$M_J(f(K) = \frac{1}{2}\widehat{W}^T(K_+ - K_-) \qquad (5)$$

Where $\widehat{W}$ is a unit vector in the direction of W and is given as $\widehat{W} = \frac{W}{||W||}$

We assume that the closest points K_{+} and K_{-} are equidistant from to the decision boundary. Hence

$$f(K_{+}) = W^{T}K_{+} + b = a \tag{6}$$

$$f(K_{-}) = W^{T}K_{-} + b = -a \tag{7}$$

Where constant $a > 0$

To make the concept of margins meaningful let us set the decision boundary at the closest points to the hyperplane for $a = 1$. Adding the above two expressions(Eq(6) &(7)) and dividing by $||W||$ we get

$$(f(K) = \frac{1}{2}\widehat{W}^{T}(K_{+} - K_{-}) = \frac{1}{||W||} \tag{8}$$

Now let us assume that data is linear. To get maximum margin we maximize the margin $\frac{1}{||W||}$ or minimize $||W||^2$. This ensures that maximum margin with high accuracy since we assumed the data to be linear. Conversely if the data is not linear the maximum margin can be achieved by allowing some misclassification. This introduces a slack variable or margin error(ξ). A sample is misclassified if the value of margin error ξ>1. Hence minimization of $||W||^2$ is argued by a term $C\sum_{i}\xi_{i}$ to penalize margin error. Our objective of maximizing the margin and minimizing the margin error depends on the constant C also called the soft margin constant. The optimization problem finally formulated is

$$minimize_{W,b} \qquad \frac{1}{2}||W||^2 + C\sum_{i=1}^{n}\xi_{i}$$

$$\text{Subjected to} \qquad Y_{i}(W^{T}K_{i} + b) \geq 1 - \xi_{i} \qquad \xi_{i} \geq 0 \tag{9}$$

Which is a soft margin SVM classifier.

3.5 Application of SVM

SVM has a wide application domain such as text identification, digital image analysis, character recognition and bioinformatics.

1. Face Detection- The face detection algorithm scans input images with a 19x19 window and a SVM with a polynomial kernel is trained. SVM is used on different feature of the segmented regions of the skin to avoid extensive scanning for face detection.
2. Object Detection- This algorithm is used for detection of moving people or traffic for surveillance purpose. Two types of muti-class SVM, bottom-up and top-down were used. Both the SVMs gave similar performance.
3. Handwritten Character or Digit Recognition- Handwritten character have high variability and distortions of patterns. Hence hidden markov model(HMM) is used which discard variability and distortions. But HMM works on local characteristics only. To work on global characteristics SVM is used after HMM has been used locally and is normalized. For digit recognition structural and statistical features were used in the SVM classifier. Testing was performed on both the features as one set using single SVM classifier and also two feature sets were tested on two different SVM classifiers. The results obtained were combined together using rule based reasoning
4. Information and Image Retrieval- A metric called distance-from-boundary is used to retrieve the texture image. The boundaries between classes are obtained by SVM. To retrieve more images relevant to the query image, SVM classifier was used to classify relevant images and irrelevant images.
5. Prediction- C-ascending SVMs are used predict the next point by increasing the value of C. This SVM works on a assumption that it is better to give weight to recent data then to distant data. C-ascending SVM gave better performance than classic SVM classifier.

Chapter 4 Methodology

4.1 Introduction

In this study , an attempt has been made to extract the best texture feature, which can be used to differentiate between the tumor portion and the normal portion of the CT scan image. Further we have also used some image enhancement technique to improve the texture features for better differentiability. The features extracted are fed to a SVM classifier for classification purpose. To achieve this objective following procedure have been used.

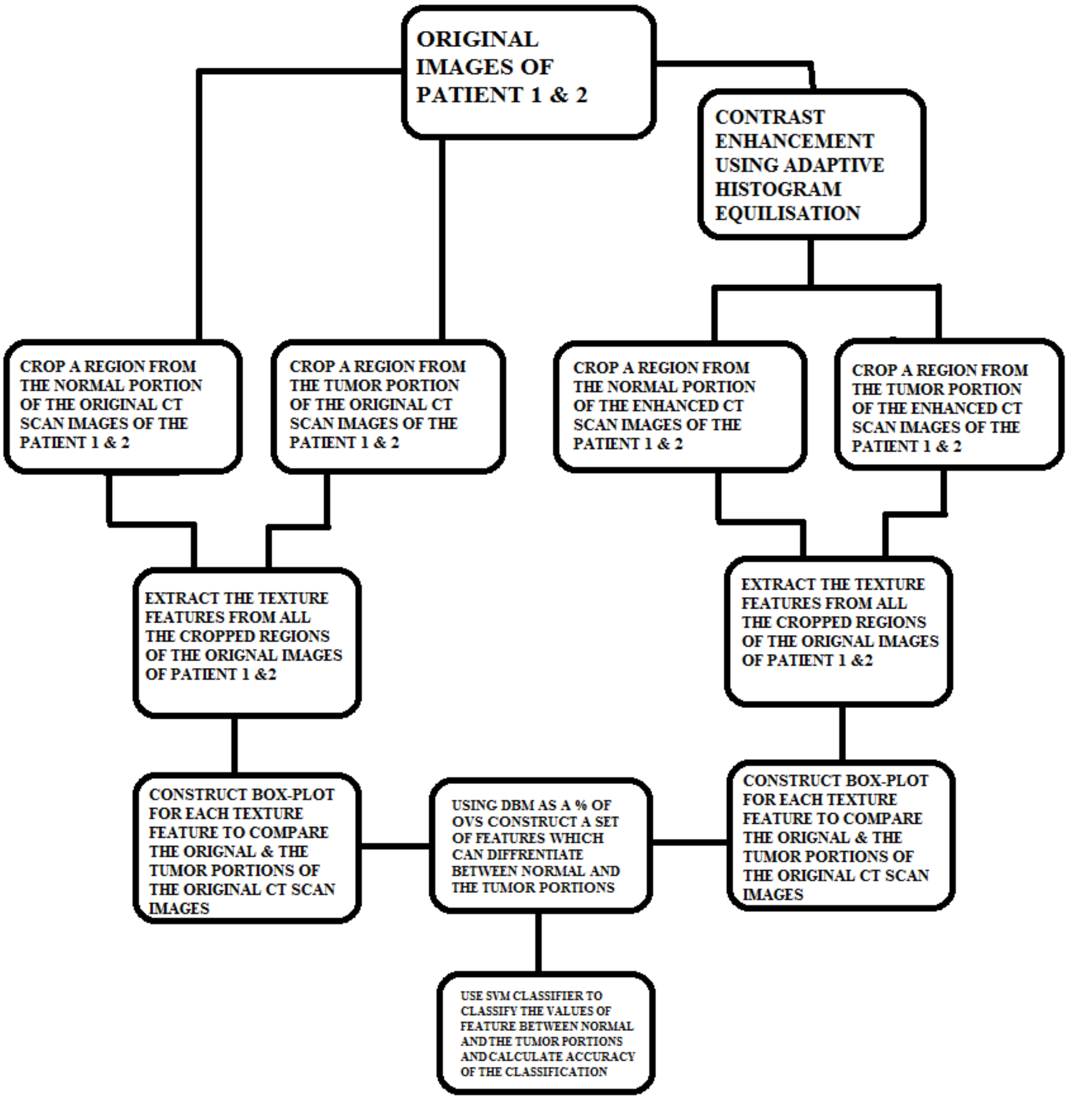


Figure 4.1 Block diagram of the methodology

4.2 Matlab Software

Matlab or matrix laboratory is a software from Mathworks which helps in evaluating matrices. It allows matrix manipulation, algorithm implementation, creating graphical user interfaces. It consists various tool boxes for users to work with them. In our study we have used image processing tool box for image analysis, and statistical tool box for SVM classifier. Other than using its own language, it can use other high level programming languages such as C/C++ and java by integrating with external software’s.

4.3 Image Enhancement

Image enhancement was achieved by adaptive histogram equalisation. This technique enhances the contrast of the image. This technique was used to improve differentiability in terms of texture features between normal and tumor portion.

A matlab function called adapthisteq( ) was used to equalize histogram of the image. J = adapthisteq(I) enhances the contrast of the greyscale image I by transforming the values using contrast-limited adaptive histogram equalization (CLAHE). This technique operates on small regions in the image, rather than the entire image.

For each region histogram is equalized, so that the histogram of the whole image approximately matches the histogram specified by the distribution' parameter. All the regions are then combined using bilinear interpolation to eliminate artificial boundaries.

The distribution parameter can be specified as uniform, bell shaped, and curved shaped using strings i.e uniform, Rayleigh, exponential respectively.

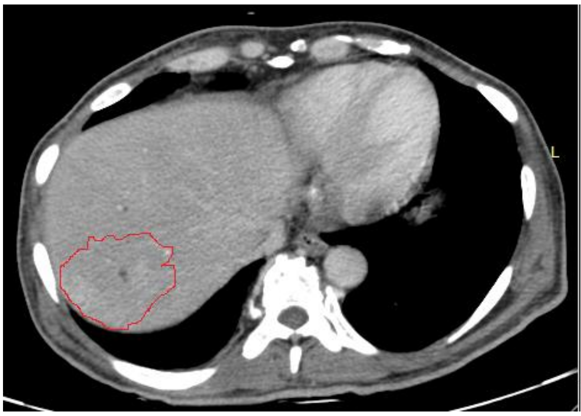


Figure4.3(a) original image

Figure4.3 (b)enhanced image

4.4 Extracting Regions

Regions have been extracted from the normal as well as tumor portions both before and after the image enhancement. The size of the region extracted was 24x25 because the smallest region of interest in the CT scan images of both the patients 1 & 2 which can be extracted from the tumor region was 24x25. A simple matlab function called imcrop ( ) was used to crop the regions from the images. The reason for using imcrop() function was that, it does not allow any change in the pixel intensities of the region as it was in the original image.

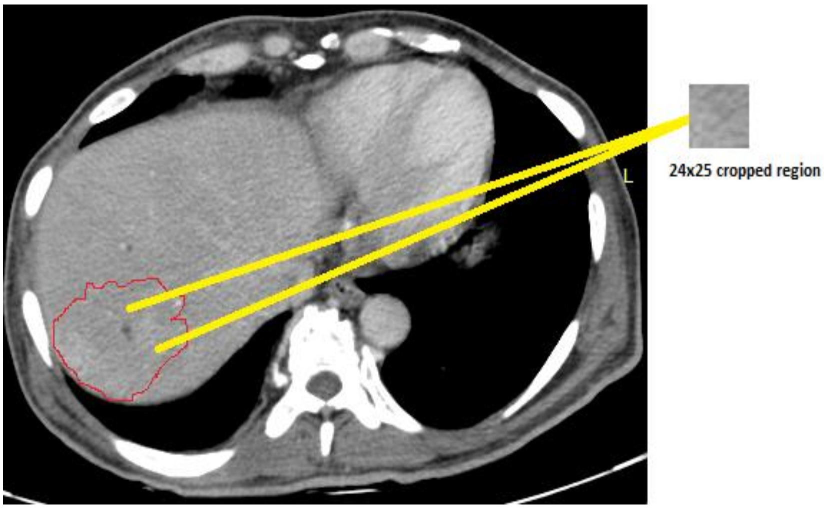


Figure4.4 show the extracted region from the tumor portion

4.5 Texture feature extraction using GLCM

For extracting texture feature from GLCM following two steps are performed

1. Creating a grey level co-occurrence matrix
2. Extracting texture features using their formule.

4.5.1 Creating a grey-level co-occurrence matrix(GLCM)

Matlab image processing toolbox was used to create a grey-level co-occurrence matrix for each extracted region from the original as well as enhanced images. Matlab function glcm = graycomatrix(I) creates a gray-level co-occurrence matrix (GLCM) from image I.

Graycomatrix creates the GLCM by calculating how many times a pixel with some gray-level value occurs horizontally adjacent to some other pixel. Each element in a GLCM specifies the number of times these pixels occurred horizontally adjacent. Suppose I is a binary image, graycomatrix scales the image to two gray-levels. and if I is an intensity image, graycomatrix scales the image to eight gray-levels.

4.5.2 Calculating texture parameters

Table 4.5.2 Features calculated using GLCM

Parameter	**Description**	**Formula**
Autocorrelation	It is a is a measure of similarity between the pixels and a translated copy of the pixels. It characterises similarity patterns in an image	$\sum_i \sum_j (ij)\, p(i,j)$
Contrast	It is a measure of local intensity variations of the pixels in there neigbourhood .	$\lvert i-j \rvert^2 \left\{ \sum_i \sum_j p(i,j) \right\}$
Correlation	It is a measure of gray level linear dependence between the pixels at the specified positions relative to each other.	$\frac{\sum_i \sum_j (ij) p(i,j) - u_x u_y}{\sigma_x \sigma_y}$ where u_x , u_y σ_x and σ_y are the mean and standard deviation of p_x and p_y.
Cluster prominence	It is a measure of the grouping of the pixels that have similar gray-level values.	$\sum_i \sum_j \{i+j-u_x-u_y\}^4 p(i,j)$ Where u_x and u_y are the mean of p_x and p_y.
Dissimilarity	It is a measure that quantifies the dependency (independency) between the pixel and its neighbourhood pixels.	$\sum_i \sum_j \lvert i-j \rvert p(i,j)$
Energy	It is also called angular second moment. It measures the number of repeated pairs or uniformity of an image.	$\sum_i \sum_j p(i,j)^2$

Entropy	It is a measure of randomness of intensity distribution in a image.	$-\sum_i \sum_j p(i,j) \log(p(i,j))$
Homogeneity	It is a measures of the closeness of the distribution of elements in the GLCM to the GLCM diagonal.	$\sum_i \sum_j \frac{p(i,j)}{1+\lvert i-j \rvert}$
Maximum probability	It is a measure of the largest p(i,j) value in the matrix in the centre pixel of the window. High MAX values occur if one pixel pair dominate the other pixel pairs in the window.	$\max_{i,j} p(i,j)$
Sum of squares: variance	It is a measure of the dispersion of the values around the mean of combinations of reference and neighborhood pixels.	$\sum_i \sum_j (i-u)^2 p(i,j)$
Sum averages	Sum and difference histogram features-: Sum histogram is simply the histogram of the sums of all the pixels x and y apart. The number of possible values of sum histogram is 2G-1. Feature such as sum entropy sum average and sum variance are derived from sum histogram. Difference histogram is simply the histogram of the difference of all the pixels x and y apart. The number of	$\sum_i^k i p_{x+y}(i,j)$ k= 2G-2 where G is number of grey level used.
Sum entropy		$-\sum_i^k p_{x+y}(i) \log\{p_{x+y}(i)\}$ k=2G-2 where G is number of gray level used.
Sum variance		$\sum_i^k \lvert i-f_8 \rvert^2 p_{x+y}(i)$ k=2G-2 where G is number of gray level used and f_8 is the sum of entropy.

Difference entropy	possible value for difference histogram is G-1. Features such as difference variance and difference entropy are derived from difference histogram.	$-\sum_{i=0}^{k} p_{x-y}(i) log\{p_{x-y}(i)\}$ k=G-1 where G is number of gray level used.

4.6 Constructing Box Plot for Each Parameter

A box plot is a graphical representation of statistical data that show the minimum value, maximum value, median and the size of first and third quartile of a data set. In this study box-plots for each parameter of all the extracted regions have been constructed to compare the values of a parameters in the tumor portion with the normal portion. By using box-plots we can observe the parameters which can be used to differentiate between both the portions.

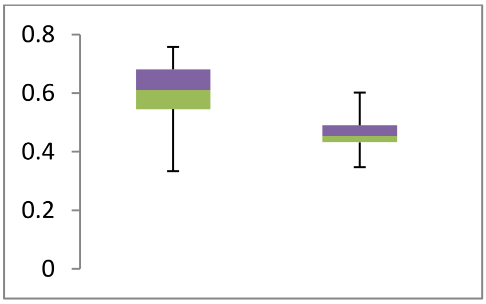


Figure 4.4(a)Box-plot

4.6.1 Procedure to construct a box-plot

To construct a box plot we have used Microsoft office excel 2012. Following are the procedural steps-:

1. The values are first placed in ascending order to calculate the median for the box-plot. This value is the second quartile(Q2) of the box-plot.
2. The next step is to calculate first and the third quartile. Taking the median as the centre the medians of the two half's are calculated. The median of the first half is the first quartile(Q1) of the box-plot. The median of the second half is the third quartile (Q3)of the box-plot.

3. The whiskers of the box-plot are specify the maximum and the minimum values in the data. The upper adjacent limit or the upper whisker is the maximum value of the data and the lower adjacent limit or the lower whisker is the minimum value of the data.
4. First quartile(Q1) represents the 25th percentile of the data. The median(Q2) represents the 50th percentile and the third quartile represents the 75th percentile of the data.

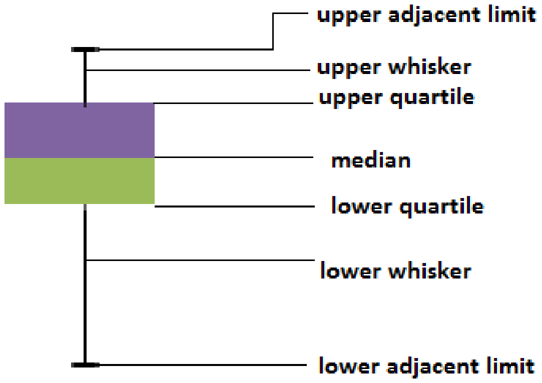


Figure 4.6(b) the median, upper and lower quartiles and upper and lower adjacent limits

4.6.2 Comparing Two Sets Of Data Using Box-Plot

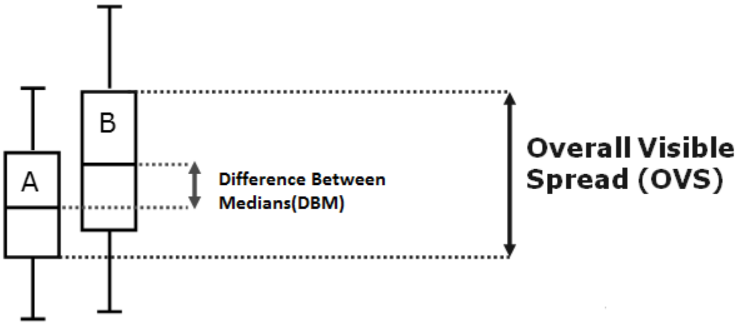
Comparison of two sets of data in box-plots can be done by using a parameter called Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS). In our case two sets of data are the parameters for tumor portion and the parameters for the normal portion.

Figure 4.5(c) show Distance Between Medians (DBM) and Overall Visible Spread (OVS)in a box-plot.

OVS=Max(Q3 of the tumor and the normal sets) – Min(Q1 of the tumor and the normal sets)

DBM=ABS(Median of tumor set – Median of normal set)

Higher the Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) higher is the differentiability between the two sets. In our case-:



$$\frac{DBM}{OVS}X100$$

Figure 4.6(c) Distance between medians and overall visible spread

1. If the Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) is greater than or equal to 65% then the two sets of data are highly differentiable.
1. If the Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) is less than 65% but greater than to 40% then the two sets of data are slightly differentiable.
2. If the Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) is less than or equal to 40% then the two sets of data are not differentiable at all.

4.7 Using support vector machine classifier to classify the features

Support vector machine(SVM) classifier classifies the given statistical data on the basis of the knowledge gained by the SVM from the training data, test samples are assigned the classes or labels. SVM maps the training data into higher dimensional space . Hyperplane also called the decision surface are constructed in this higher dimensional space that differentiates the two categories and maximises the distance between itself and the support vectors which are the points lying nearest to the hyperplane. This hyperplane is then used as a basis for classifying vectors of unknown classification.

Matlab statistical tool box was used to train and classify the data with labels i.e. normal and the tumor portions.

Matlab function SVMStruct = svmtrain(Training,Group) trains the SVM classifer using the data provided and returns a structure, SVMStruct, containing information about the trained SVM classifier. The data given to the svmtrain function is called the training data. Training a SVM classifier effectively will give better classification of the test data. Training parameter in the svmtrain function is a vector containing the training data. The group parameter contains the groups or labels into which data is to be classified. Group parameter can be a numerical or logical vector or a vector of strings or characters. In our case the two groups or labels were the normal and the tumor portion.

In svmtrain function we can also specify the kernel function being used to classify data. Kernel function such as linear, polynomial, quadratic, gaussian radial basis function and multilayer perceptron can be used to classify the data.

After training the data using svmtrain function the next step is to classify the test data. Matlab function output = svmclassify(SVMStruct,test)classifies test data on the basis of the knowledge gained by SVMStruct from the training data. Here the test is a vector containing test data, which is to be classified between the two labels, in our case normal and the tumor portion.

Various kernels were used with svmtrain function. A kernel function can be defined using a sting called ‘kernel_function’, we can define various kernel with their string such as linear for linear kernel, which is by default, quadratic for order 2 polynomial. Polynomial for order 3. Mlp for multilayer perceptron, rbf kernel using rbf string. Rbf _sigma can be used to change the value of sigma in the rbf kernel. Order of the polynomial kernel can also be changed by using polyorder function.

These kernel are used to map the data which is non linear most of the times, into higher or infinite dimensional space. Then this non linear data can be linearly classified.

Chapter 5 Results and discussion

5.1 Introduction

In this study various texture parameters have been calculated for the cropped regions from the normal and the tumor portions of the original and the enhanced CT scan images of two patients i.e. patient1 and patient2. We have used 12 CT scan images of patient1 i.e.patient1_1 to patient1_12 and 17 CT scan images of patient2 i.e. patient2_1 to patient2_17 with the region of tumor marked on them. Total 14 Texture parameters like autocorrelation, contrast, correlation, cluster prominence, dissimilarity, energy, entropy, homogeneity, maximum probability, variance, sum average, sum variance, sum entropy, and difference entropy have been calculated. Further box-plots have been constructed for each parameter comparing normal and the tumor portions. Comparison in the box-plot have been done on the basis of a parameter called Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS). In the end classification of the parameters have been preformed between normal and the tumor portions using support vector machine (SVM) classifier.

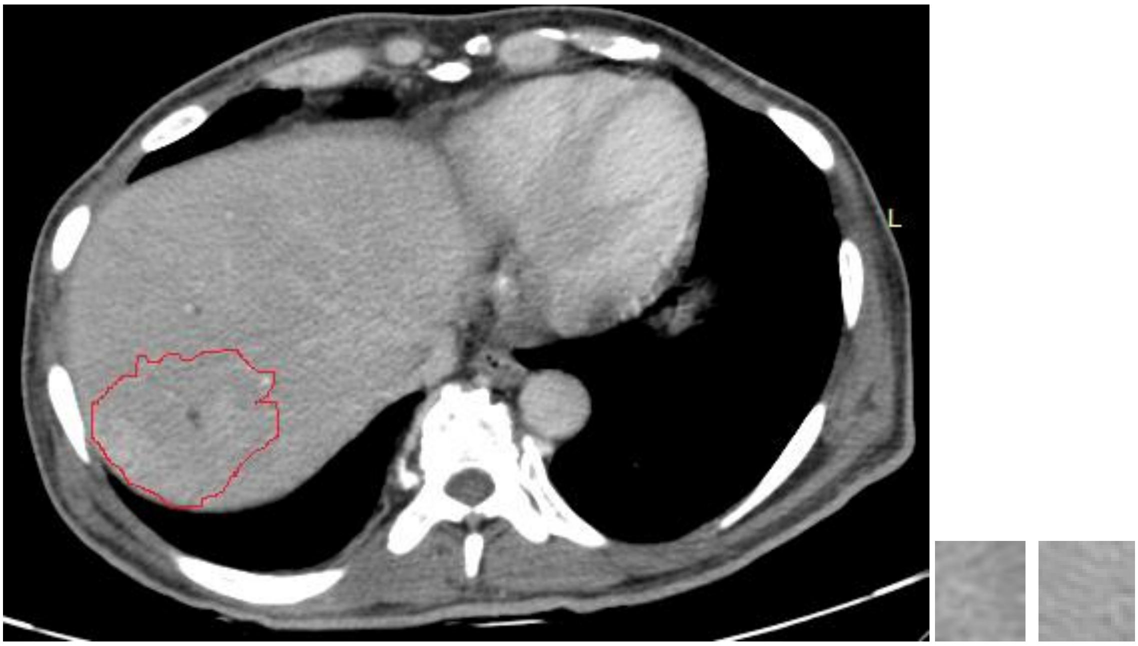


Figure5.1(a) 5.1(b) 5.1(c)

Figure 5.1(a) shows the type of CT scan images used in the analysis, Figure 5.1(b) show the cropped region from the tumor portion marked in the image, Figure 5.1(c) shows the cropped region from the normal portion.

5.2 Autocorrelation

Table5.2.1 show the values of autocorrelation for the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1 1	32.5913	29.3339	36.6944	34.4844
Patient1 2	32.1635	28.5965	36.1215	31.6059
Patient1 3	28.8539	29.6504	35.1372	36.3767
Patient1 4	32.3426	30.2435	38.066	36.6059
Patient1 5	31.3583	34.1009	34.2465	45.7309
Patient1 6	31.9391	33.2817	35.8038	42.4601
Patient1 7	30.9026	31.3426	37.217	43.5382
Patient1 8	30.6052	29.953	35.2014	31.026
Patient1 9	32.4035	29.6765	31.6962	34.2135
Patient1 10	31.433	31.8904	35.0625	43.191
Patient1 11	32.033	31.2609	36.7309	39.3861
Patient1 12	32.8348	33.5791	36.8281	41.7795
Mean	31.6217	31.0757	35.7337	38.3665
Variance	1.2201	3.2888	2.7739	24.7880
Min	28.8539	28.5965	31.6962	31.026
Max	32.8348	34.1009	38.066	45.7309

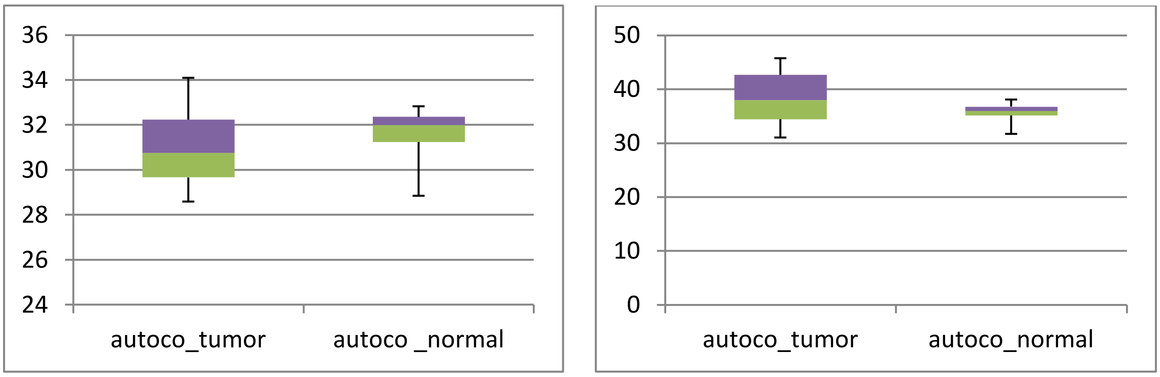


Figure5.2(a) Figure5.2(b)

Above box-plot compares autocorrelation for the tumor and the normal portion of the original images Figure5.2(a)) & enhanced images Figure 5.2(b) of patient1

5.2.1 Autocorrelation comparison for Patient1

The mean of autocorrelation for the normal and the tumor portions in the original images of patient1 is 31.6217 and 31.0757 with a variance of 1.2201 and 3.2888 respectively. Hence the data clearly suggest more variations of autocorrelation in tumor portions as compared to the normal portions. But the means of the two portions do not show significant difference.

On the other hand mean of autocorrelation of the normal and the tumor portions in enhanced images is 35.7337 and 38.3665. with a variance of 2.7739 and 24.7880 respectively. Hence the data clearly suggest high variation of autocorrelation in the tumor portions as compared to normal portion after enhancement of image. The means of the two portions also show slight difference .

For more conclusive comparison of data we study the box-plot comparison of both the portions. Figure 5.2(a) and 5.2(b) show the box-plot comparison of the autocorrelation between tumor and normal portions of the original and enhanced images respectively of patient1.

The Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.2(a)) is 46%. Hence autocorrelation slightly differentiate the two portions in the original images of patient1.

On the other hand the Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.2(b)) is 25%. Hence the autocorrelation, individually is not able to differentiate between the two portions in the enhanced images of patient1

Table5.2.2 show the values of autocorrelation for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	22.3478	24.6452	34.5868	38.1094
Patient2_2	22.9809	25.76	34.1319	37.7431
Patient2_3	21.9409	26.0035	34.2188	41.3183
Patient2_4	22.1652	27.5496	36.6875	42.9531
Patient2_5	21.5843	29.2174	34.8681	45.3073
Patient2_6	21.7426	30.3663	36.5052	46.0104
Patient2_7	21.6261	30.5113	36.1615	45.1007
Patient2_8	21.7252	30.6285	36.2847	45.5513
Patient2_9	21.6504	31.6574	35.9184	47.184
Patient2_10	21.6887	30.4348	35.3611	46.0747
Patient2_11	22.8243	32.807	34.849	47.4601
Patient2_12	21.5478	35.3078	35.0642	47.7361
Patient2_13	22.2209	34.3635	36.2083	48.1597
Patient2_14	22.0435	34.9983	36.1372	48.9687
Patient2_15	22.0574	35.233	37.9809	48.1215
Patient2_16	22.4087	34.9583	37.6319	46.9583
Patient2_17	23.0835	35.233	36.9236	47.7014
Mean	22.0963	31.1573	35.8540	45.3210
Variance	0.2442	13.1015	1.2832	11.4774
Min	21.5478	24.6452	34.1319	37.7431
Max	23.0835	35.3078	37.9809	48.9687

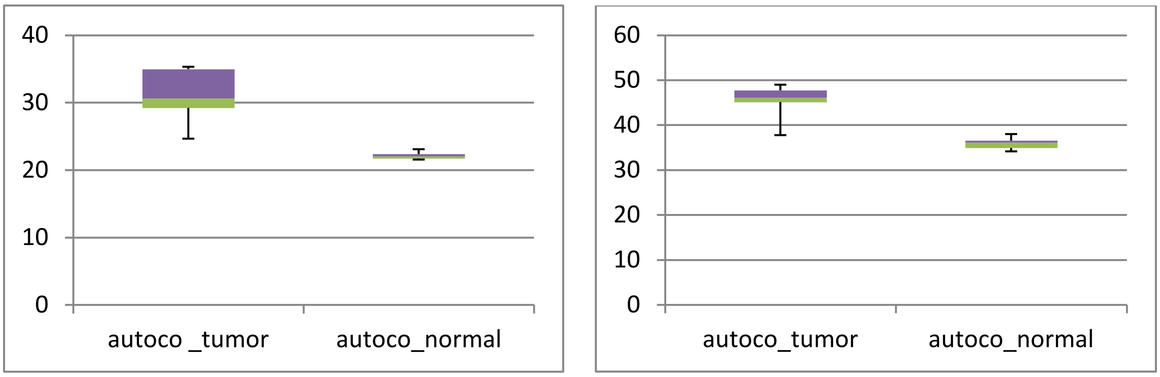


Figure5.2(c) Figure 5.2(d)

Above box-plot compares autocorrelation for the tumor and the normal portions of the original Figure5.2(c) and the enhanced images Figure5.2(d) of patient2

5.2.2 Autocorrelation comparison for Patient2

The mean of autocorrelation for the normal and the tumor portions in the original images of patient2 is 22.0963. and 31.1573 with a variance of 0.2442 and 13.1015 respectively. Hence the data clearly suggest high variation of autocorrelation in tumor portions as compared to normal portions. Also the means of the two portions have significant difference.

On the other hand mean of autocorrelation for the normal and the tumor portions in enhanced images is 35.8540 and 45.321. with a variance of 1.2832 and 11.4774 respectively. Hence the data clearly suggest high variations in autocorrelation in the tumor portions after enhancement of image. Also the means of the two portions have significant difference.

For more conclusive comparison of we study the box-plots comparing both the portions. Figure 5.2(c) and 5.2(d) show the box-plot comparison of the autocorrelation between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.2(c)) is 65%. Hence the autocorrelation is able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.2(d)) is 77%. Hence the autocorrelation is able to differentiate between the two portions in the enhanced images of patient2.

5.2.3 Overall comparison of autocorrelation

Table5.2.3 show the mean, variance minimum and the maximum values of the combined values of autocorrelation of patient1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	26.0378	31.1235	35.8042	42.4433
Variance	23.4138	8.7803	1.8266	28.4476
Min	21.5478	24.6452	31.6962	31.026
Max	32.8348	35.3078	38.066	48.9687

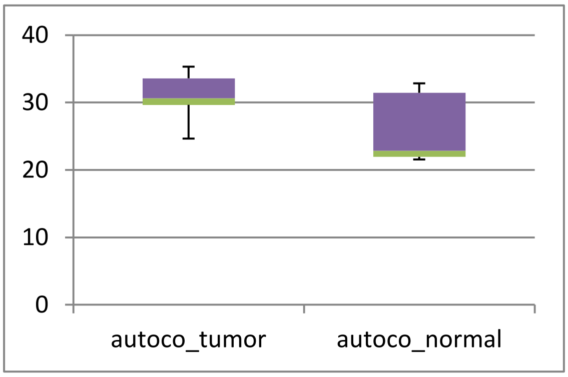


Figure5.2(e)

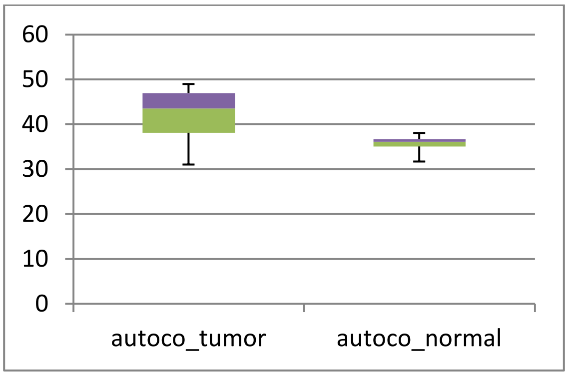


Figure5.2(f)

Above box-plots compares the overall autocorrelation for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.2(e) and enhanced images Figure5.2(f)

In original images

The mean of autocorrelation for the normal portions and the tumor portions of the original images is 26.0378 and 31.1235 with a variance of 23.4138 and 8.7803 respectively. Hence the data clearly suggests high variations of autocorrelation in the normal portions of the original images as compared to tumor portion. Also the means of the two portions have significant difference.

For more conclusive comparison of data we study the box-plot comparing both the portions Figure 5.2(e) show the box-plot comparison of the autocorrelation between tumor and normal portions of the original images of patient1 and 2 combined together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.2(e)) is 67%. Hence autocorrelation is able to differentiate between the two portions in the original images of patient1 and 2 combined together .

In enhanced images

The mean of autocorrelation for the normal portions and the tumor portions of the enhanced images is 35.8042 and 42.4433 with a variance of 1.8266 and 28.4476 respectively. Hence the data clearly suggests high variation of autocorrelation in tumor portion as compared to normal portions in enhanced images. Also the means of the two portion have significant difference.

For more conclusive comparison of data, we study box-plots comparing both the portions. Figure 5.2(f) show the box-plot comparison of the autocorrelation between tumor and normal portions of the enhanced images of patient1 and 2 combined together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.2(f)) is 62%. Hence autocorrelation slightly differentiate the two portions in the enhanced images of patient1 and 2 combined together.

5.3 Contrast

Table5.3.1 show the values of contrast for the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1_1	0.1983	0.1704	0.5017	0.533
Patient1_2	0.2122	0.0957	0.5139	0.4948
Patient1_3	0.193	0.1496	0.533	0.5313
Patient1_4	0.1791	0.1878	0.4861	0.4774
Patient1_5	0.1774	0.1217	0.5122	0.4566
Patient1_6	0.1826	0.16	0.4149	0.5139
Patient1_7	0.2278	0.2278	0.5208	0.4583
Patient1_8	0.2104	0.1826	0.7031	0.7552
Patient1_9	0.1722	0.1809	1.0243	0.7969
Patient1_10	0.2383	0.1617	0.6788	0.7465
Patient1_11	0.2243	0.1878	0.5	0.6017
Patient1_12	0.1896	0.1617	0.4653	0.5312
mean	0.2004	0.1656	0.5711	0.5747

variance	0.0004	0.0011	0.0270	0.0149
min	0.1722	0.0957	0.4149	0.4566
max	0.2383	0.2278	1.0243	0.7969

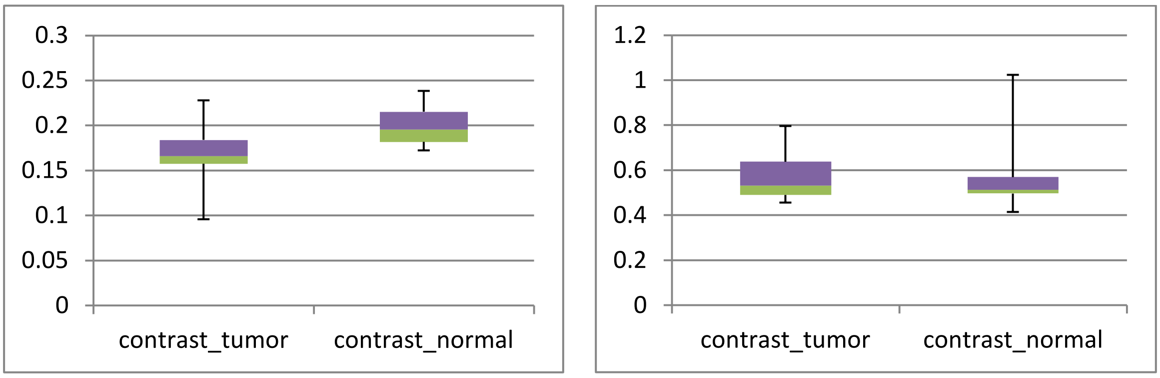


Figure 5.3(a)

Figure 5.3(b)

Above box-plot compares contrast for the tumor and the normal portion of the original images Figure5.3(a) and enhanced images Figure5.3(b) of patient1

5.3.1 Contrast comparison for Patient1

The mean of contrast for the normal and the tumor portions in the original images of patient1 is 0.2004 and and 0.1656 with a variance of 0.0004 and 0.0011 respectively. Hence there is not much variations of contrast in the tumor portion or the normal portions of the original images of patient1. But the means of the two portions have slight difference.

The mean of contrast for the normal and the tumor portions in the enhanced images of patient1 is 0.5711 and 0.5747 with a variance of 0.027 and 0.0149 respectively. Hence there is not much variations of contrast in tumor portion or normal portion in the enhanced images of patient1. Also the means of the two portions do not have significant difference.

For more conclusive comparison we study the box-plots comparing both the portions. Figure 5.3(a) and 5.3(b) show the box-plot comparison of the contrast between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.3(a)) is 51%. Hence contrast slightly differentiates the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.3(b)) is 12%. Hence the contrast individually is not able to differentiate between the two portions in the enhanced images of patient1.

Table5.3.2 show the values of contrast for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	0.3409	0.2226	0.9323	1.0191
Patient2_2	0.28	0.2278	1.0399	1.3872
Patient2_3	0.3426	0.4139	1.0243	0.7826
Patient2_4	0.353	0.3096	0.8455	0.7031
Patient2_5	0.3583	0.2852	1.0052	0.5382
Patient2_6	0.3861	0.3351	0.8281	0.5069
Patient2_7	0.4052	0.3165	0.8785	0.5799
Patient2_8	0.367	0.375	0.908	0.7635
Patient2_9	0.3287	0.367	0.8212	0.4549
Patient2_10	0.3878	0.3322	0.9097	0.5885
Patient2_11	0.2957	0.3652	0.8628	0.4288
Patient2_12	0.3496	0.3583	1.0295	0.5642
Patient2_13	0.3913	0.3461	0.7153	0.4306
Patient2_14	0.3322	0.4365	0.9653	0.4045
Patient2_15	0.3583	0.3896	0.8038	0.4444
Patient2_16	0.3757	0.4696	0.809	0.5747
Patient2_17	0.2852	0.6278	0.8906	0.717
mean	0.3492	0.3634	0.8981	0.6404
variance	0.0013	0.0088	0.0085	0.0630
min	0.28	0.2226	0.7153	0.4045
max	0.4052	0.6278	1.0399	1.3872

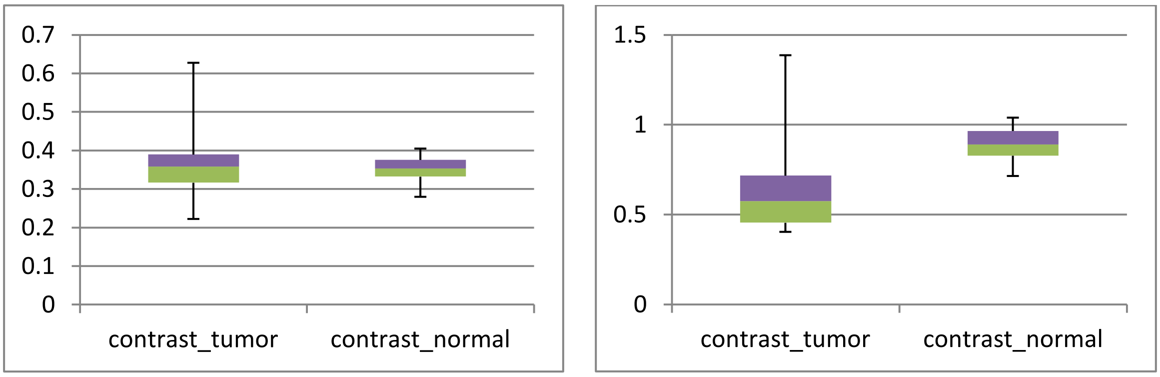


Figure5.3(c) Figure5.3(d)

Above box-plot compares contrast for the tumor and the normal portion of the original Figure5.3(c) and enhanced images Figure5.3(d) patient2

5.3.2 Contrast comparison for Patient2

The mean of contrast for the normal and the tumor portions in the original images of patient2 is 0.3492 and 0.3634 with a variance of 0.0013 and 0.0088 respectively. Hence there is not much variations of contrast in the tumor portions or the normal portions of the original images of patient2. Also the means of the two portions do not have significant difference.

The mean of contrast for the normal and the tumor portions in the enhanced images of patient2 is 0.8981 and 0.6404 with a variance of 0.0085 and 0.0630 respectively. Hence there is not much variations of contrast in the tumor or the normal portion. But the means of the two portions have slight difference.

For more conclusive comparison we study the box plots comparing the two potions. Figure 5.3(c) and 5.3(d) show the box-plot comparison of the contrast between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.3(c)) is 7%. Hence the contrast individually is not able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.3(d)) is 62%. Hence contrast slightly differentiate the two portions in the enhanced images of patient2.

5.3.3 Overall comparison of Contrast

Table5.3.3 show the mean, variance minimum and the maximum values of the combined values of contrast of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.2876	0.2815	0.7628	0.6132
Variance	0.0065	0.0153	0.0423	0.0429
Min	0.1722	0.0957	0.4149	0.4045
Max	0.4052	0.6278	1.0399	1.3872

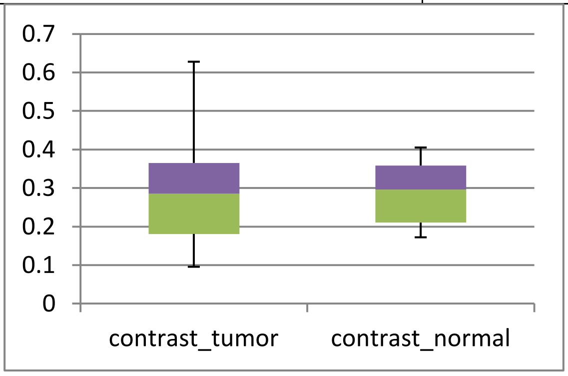


Figure5.3(e)

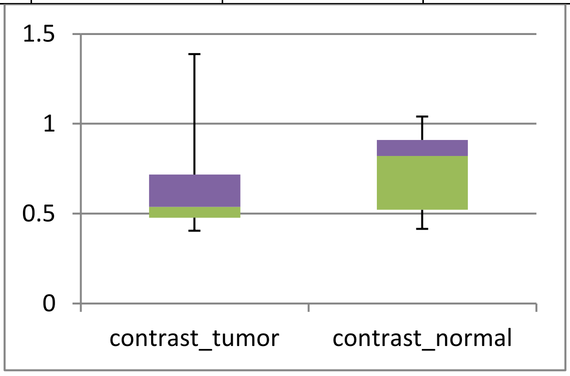


Figure5.3(f)

Above box-plots compares the overall contrast for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.3(e) and enhanced images Figure5.3(f).

In original images

The mean of contrast for the normal portions and the tumor portions of the original images is 0.2876 and 0.2815 with a variance of 0.0065 and 0.0153 respectively. Hence the data clearly suggests not much variations of contrast in the normal portions or the tumor portion of the original images of patient1 and patient2. Also the means of the two portion do not have significant difference.

For more conclusive comparison of data we study the box-plot comparing both the portions**.** Figure 5.3(e) show the box-plot comparison of the contrast between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 (Figure5.3(e)) is 6%. Hence the contrast individually is not able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of contrast for the normal portions and the tumor portions of the original images is 0.7628 and 0.6132 with a variance of 0.0423 and 0.0429 respectively. Hence the data clearly suggests not much variations of contrast in the normal portions or the tumor portion of the original images of patient1 and patient2. But the mean of the two portions have slight difference.

For more conclusive comparison of data we study the box-plot comparing both the portions Figure 5.3(f) show the box-plot comparison of the contrast between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.3(f)) is 65%. Hence contrast is able differentiate between the two portions in the enhanced images of patient1 and 2.

5.4 Correlation

Table5.4.1 and show the values of correlation for the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1_1	0.5288	0.6458	0.421	0.6811
Patient1_2	0.527	0.7856	0.4897	0.7174
Patient1_3	0.5806	0.6953	0.4773	0.672
Patient1_4	0.5914	0.6243	0.4361	0.6439
Patient1_5	0.6344	0.6938	0.5475	0.6581
Patient1_6	0.6048	0.6082	0.6017	0.736
Patient1_7	0.5404	0.5303	0.5322	0.6741
Patient1_8	0.5786	0.6375	0.4828	0.5696
Patient1_9	0.604	0.6368	0.4538	0.601
Patient1_10	0.5056	0.7543	0.51	0.6576
Patient1_11	0.5073	0.6206	0.4544	0.6106
Patient1_12	0.529	0.5285	0.6002	0.5765
mean	0.5609	0.6467	0.5005	0.6498
variance	0.0018	0.0059	0.0035	0.0027
min	0.5056	0.5285	0.421	0.5696
max	0.6344	0.7856	0.6017	0.736

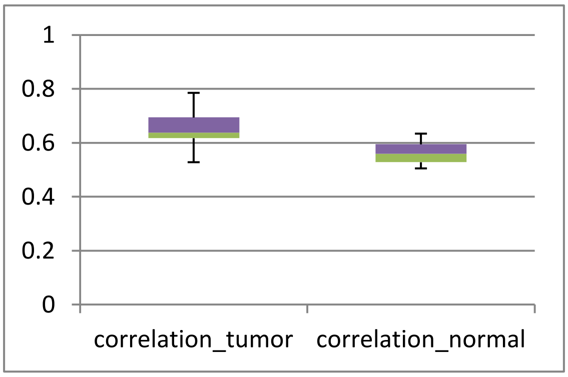


Figure 5.4(a)

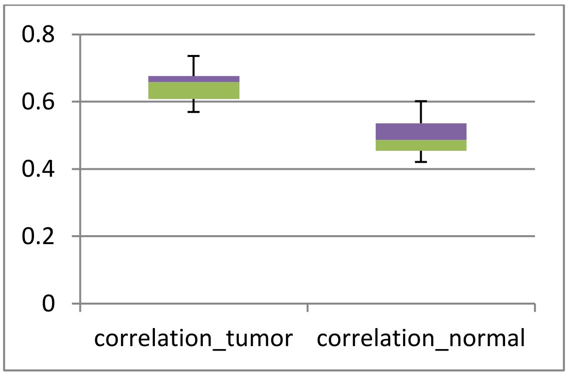


Figure 5.4(b)

Above box-plot compares correlation for the tumor and the normal portion of the original images Figure5.4(a) and the enhanced images patient1 Figure5.4(b).

5.4.1 Correlation comparison for Patient1

The mean of correlation for the normal and the tumor portions in the original images of patient1 is 0.5609 and and 0.6467 with a variance of 0.0018 and 0.0059 respectively. Hence there is not much variations of correlation in the tumor portion or the normal portions of the original images of patient1. But the means of the two portions have slight difference.

The mean of correlation for the normal and the tumor portions in the enhanced images of patient1 is 0.5005 and 0.6498 with a variance of 0.027 and 0.0149 respectively. Hence there is not much variations of correlation in the tumor portion or the normal portion in the enhanced images of patient1. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plots comparing both the portions. Figure 5.4(a) and 5.4(b) show the box-plot comparison of the correlation between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.4(a)) is 47%. Hence correlation slightly differentiate the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.4(b)) is 77%. Hence correlation able to differentiate between the two portions in the enhanced images of patient1.

Table5.4.2 and show the values of correlation for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal portion	**Tumor portion**	**Normal portion**	**Tumor portion**
Patient2_1	0.1768	0.4125	0.454	0.3754
Patient2_2	0.1889	0.375	0.4208	0.3332
Patient2_3	0.2139	0.38	0.3468	0.521
Patient2_4	0.1941	0.5669	0.416	0.5448
Patient2_5	0.2341	0.5443	0.433	0.5131
Patient2_6	0.1539	0.5696	0.4718	0.5282
Patient2_7	0.1648	0.5515	0.457	0.5942
Patient2_8	0.1865	0.443	0.4409	0.4509
Patient2_9	0.2813	0.5755	0.4975	0.5689
Patient2_10	0.1637	0.5267	0.3742	0.5152
Patient2_11	0.1874	0.5953	0.3957	0.6054
Patient2_12	0.251	0.7316	0.3786	0.7193
Patient2_13	0.0769	0.786	0.4975	0.7038
Patient2_14	0.2368	0.7955	0.4316	0.7091
Patient2_15	0.1859	0.7008	0.4644	0.6914
Patient2_16	0.075	0.7348	0.4483	0.6183
Patient2_17	0.1581	0.7175	0.4391	0.7577
mean	0.1840	0.5886	0.4333	0.5735
variance	0.0028	0.0188	0.0017	0.0145
min	0.075	0.375	0.3468	0.3332
max	0.2813	0.7955	0.4975	0.7577

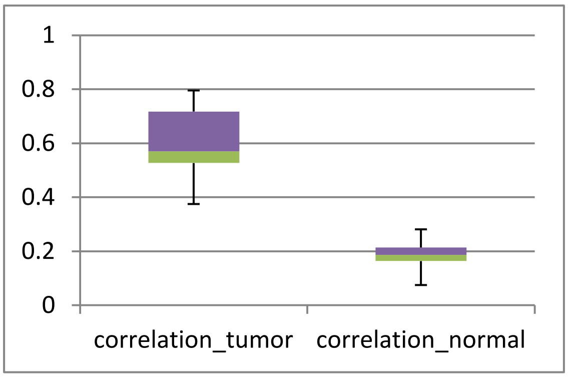


Figure 5.4(c)

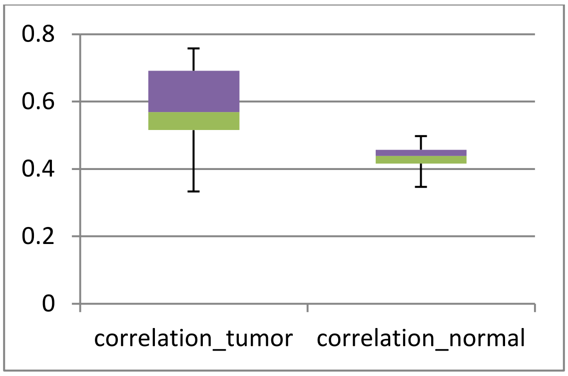


Figure 5.4(d)

Above box-plot compares correlation for the tumor and the normal portion of the original Figure5.4(c) and enhanced images Figure5.4(d) of patient2 .

5.4.2 Correlation comparison for Patient2

The mean of correlation for the normal and the tumor portions in the original images of patient2 is 0.1840 and 0.5886 with a variance of 0.0028 and 0.0188 respectively. Hence there is not much variations of correlation in the tumor portions or the normal portions of the original images of patient2. However the means of the two portions have significant difference.

The mean of contrast for the normal and the tumor portions in the enhanced images of patient2 is 0.4333 and 0.5735 with a variance of 0.0017 and 0.0145 respectively. Hence there is not much variations of correlation in the tumor or the normal portion. But the means of the two portions have slight difference.For more conclusive comparison we study the box-plots comparing the two portions. Figure 5.4(b) and 5.4(d) show the box-plot comparison of the correlation between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.4(c)) is 69%. Hence the correlation is able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.4(d)) is 47%. Hence correlation slightly differentiate the two portions in the enhanced images of patient2.

5.4.3 Overall comparison of correlation

Table5.4.3 show the mean, variance minimum and the maximum values of the combined values of correlation of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.3400	0.6126	0.4611	0.6050
Variance	0.0380	0.0139	0.0035	0.0108
Min	0.075	0.375	0.3468	0.3332
Max	0.6344	0.7955	0.6017	0.7577

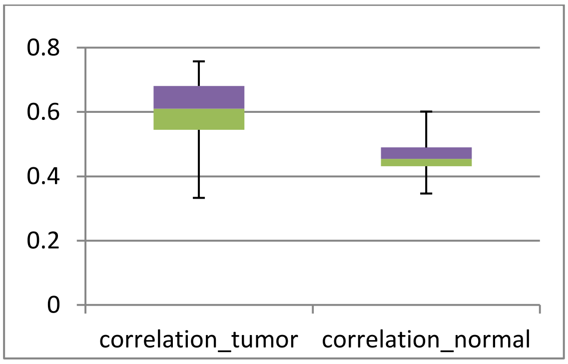


Figure 5.4(e)

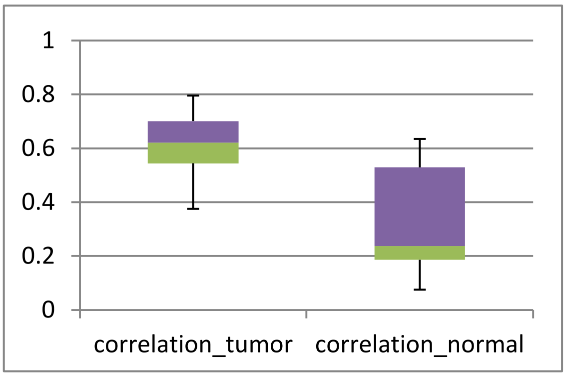


Figure 5.4(f)

Above box-plots compares the overall correlation for the tumor and normal portions of patient1 and patient2 combined together from the original Figure5.4(e) and the enhanced images Figure5.4(f).

In original images

The mean of correlation for the normal portions and the tumor portions of the original images is 0.34 and 0.6126 with a variance of 0.038 and 0.0139 respectively. Hence the data clearly suggests not much variations of correlation in the normal portions or the tumor portion of the original images of patient1 and patient2. However the mean of the two portion show significant difference.For more conclusive comparison we study the box-plots comparing the two portions. Figure 5.4(e) show the box-plot comparison of the correlation between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.4(e)) is 75%. Hence the correlation is able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of correlation for the normal portions and the tumor portions of the original images is 0.4611 and 0.6050 with a variance of 0.0035 and 0.0108 respectively. Hence the data clearly suggests not much variations of correlation in the normal portions or the tumor portion of the enhanced images of patient1 and patient2. However the means of the two portion show significant difference.For more conclusive comparison we study the box-plots for the two portions. Figure 5.4(f) show the box-plot comparison of the correlation between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.4(f)) is 63%. Hence the correlation slightly differentiate the two portions in the enhanced images of patient1 and 2.

5.5 Cluster prominence

Table5.5.1 show the values of cluster prominence of the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1 1	0.8548	0.8628	5.6543	16.4998
Patient1 2	0.8309	1.0278	6.0603	18.8793
Patient1 3	0.8549	0.8711	5.7206	17.3416
Patient1 4	0.8894	0.8129	4.0839	12.9806
Patient1 5	0.8477	1.6885	8.3165	19.7938
Patient1 6	0.8694	1.1531	9.0289	32.1687
Patient1 7	0.7775	0.7886	7.4772	21.5557
Patient1 8	0.7906	0.8868	11.0371	22.412
Patient1 9	0.903	0.8805	19.0383	22.2518
Patient1 10	0.7786	3.2229	10.4074	47.3838
Patient1 11	0.8101	0.9019	4.8062	16.357
Patient1 12	0.8645	0.8871	16.7423	15.2757
mean	0.8392	1.16533	9.0310	21.9083
variance	0.0017	0.4796	21.9965	88.4579
min	0.7775	0.7886	4.0839	12.9806
max	0.903	3.2229	19.0383	47.3838

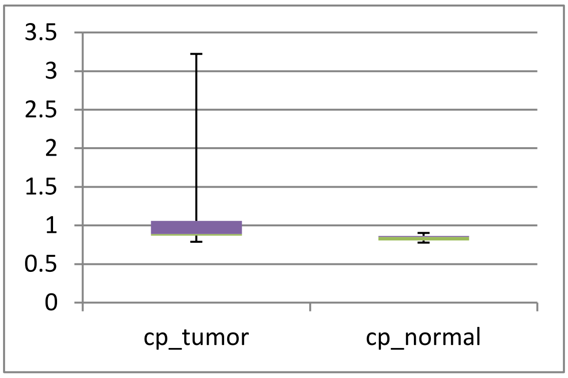


Figure5.5(a)

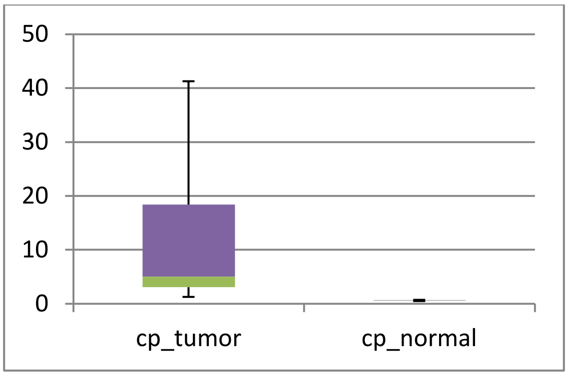


Figure 5.5(b)

Above box-plot compares cluster prominence(cp) for the tumor and the normal portion of the original Figure5.5(a) and enhanced images Figure5.5(b) of patient1.

5.5.1 Cluster prominence comparison for patient1

The mean of cluster prominence for the normal and the tumor portions in the original images of patient1 is 0.8392 and and 1.1653 with a variance of 0.0017 and 0.4796 respectively. Hence the data clearly suggest high variations of cluster prominence in the tumor portion as compared to the normal portions of the original images of patient1. The means of the two portions also show significant difference .

The mean of cluster prominence for the normal and the tumor portions in the enhanced images of patient1 is 9.031 and 21.9083 with a variance of 21.9965 and 88.4579 respectively. Hence both the portions show high variations of cluster prominence but the cluster prominence in the tumor portions as compared to the normal portions show huge variations in the enhanced images of patient1. The means of the two portions also show significant difference.

For more conclusive comparison we study the box-plots comparing the two portions. Figure 5.5(a) and 5.5(b) show the box-plot comparison of the cluster prominence between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.5(a)) is 14%. Hence the cluster prominence individually is not able to differentiate between the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.5(b)) is 69%. Hence the cluster prominence is able to differentiate between the two portions in the enhanced images of patient1.

Table5.5.2 and show the values of correlation for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	0.6004	2.3506	15.2415	23.5162
Patient2_2	0.5571	1.2751	16.0279	28.0692
Patient2_3	0.6008	4.1839	11.3936	45.0903
Patient2_4	0.6477	4.3514	10.7103	26.3375
Patient2_5	0.6504	2.6091	16.5209	10.3768
Patient2_6	0.5886	5.3423	12.626	11.325
Patient2_7	0.7298	4.3357	12.8461	41.6712
Patient2_8	0.5845	2.2115	13.4733	26.0078
Patient2_9	0.6518	6.1768	13.5041	20.169
Patient2_10	0.6121	3.0748	10.6325	13.2901
Patient2_11	0.5719	5.0728	9.7245	10.9276
Patient2_12	0.637	12.4908	12.6854	42.5612
Patient2_13	0.5161	25.3796	11.6104	38.8453
Patient2_14	0.6428	39.2565	14.8666	39.0343
Patient2_15	0.626	18.3979	12.5333	24.0183
Patient2_16	0.4999	32.1438	13.0132	19.1343
Patient2_17	0.5665	41.2692	13.2524	100.204
mean	0.6049	12.3483	12.9801	30.6222
variance	0.0030	187.4907	3.5735	456.6256
min	0.4999	1.2751	9.7245	10.3768
max	0.7298	41.2692	16.5209	100.204

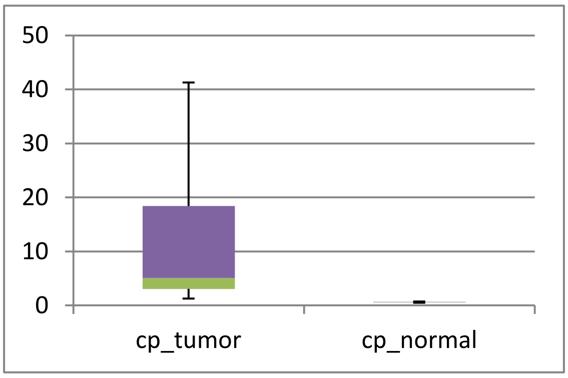


Figure5.5(c)

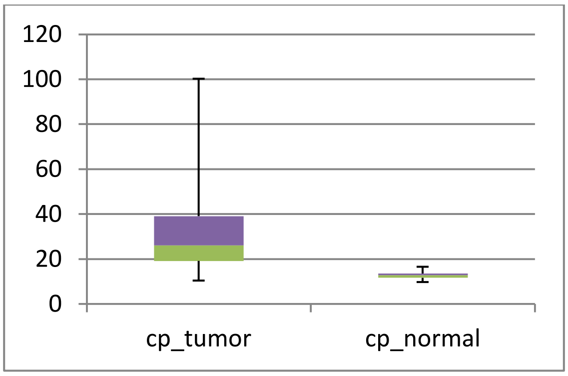


Figure 5.5(d)

Above box-plot compares cluster prominence(cp) for the tumor and the normal portion of the original Figure5.5(c) and the enhanced images Figure5.5(d) of patient2

5.5.2 Cluster prominence comparison for Patient2

The mean of cluster prominence for the normal and the tumor portions in the original images of patient1 is 0.6049 and and 12.3483 with a variance of 0.003 and 187.4907 respectively. Hence there is huge variations of cluster prominence in the tumor portion as compared to the normal portions of the original images of patient2. The means of the two portions also have significant difference .

The mean of cluster prominence for the normal and the tumor portions in the enhanced images of patient1 is 12.9801 and 30.6222 with a variance of 3.5735 and 456.6256 respectively. Hence tumor portions as compared to the normal portions show high variations of cluster prominence in the enhanced images of patient1. The means of the two portions also have significant difference.

For more conclusive comparison we study the box-plots comparing the two portions. Figure 5.5(c) and 5.5(d) show the box-plot comparison of the cluster prominence between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.5(c)) is 25%. Hence cluster prominence individually is not able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.5(d)) is 48%. Hence cluster prominence slightly differentiate the two portions in the enhanced images of patient2.

The cluster prominence even though show a huge amount of variations in the tumor portions but do not show much differentiability factor. This parameter show even more variation in tumor portion after enhancement. The box- plot also suggest that the same. The maximum value of cluster prominence is 100.204 in tumor portions as compared to 16.5209 in the normal portions of the enhanced images. This shows the amount of variations. The box-plot suggests that the values of the two portions overlap too much even though variations are high.

5.5.3 Overall box-plot comparison of cluster prominence

Table5.5.3 show the mean, variance minimum and the maximum values of the combined values of cluster prominence of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.7018	7.7208	11.3460	27.0164
Variance	0.0162	138.7449	14.6014	314.7569
Min	0.4999	0.7886	4.0839	10.3768
Max	0.903	41.2692	19.0383	100.204

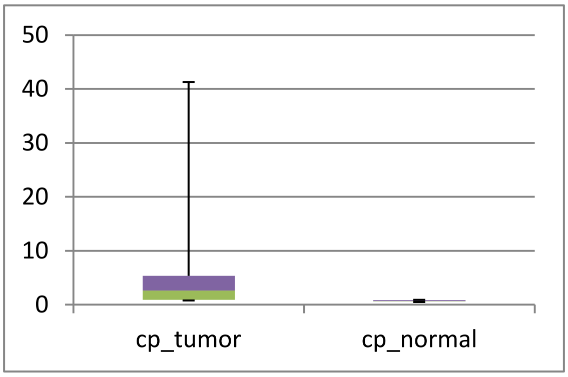


Figure5.5(e)

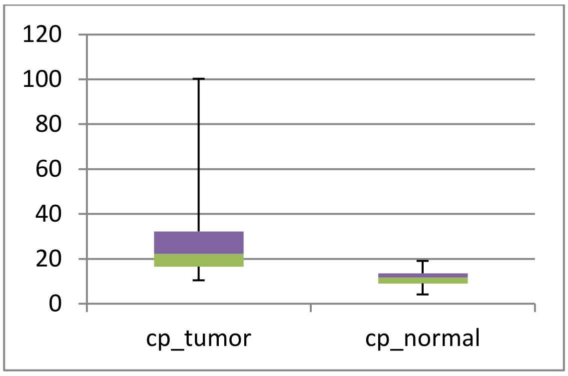


Figure 5.5(f)

Above box-plots compares the overall cluster prominence for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.5(e) and enhanced images Figure5.5(f).

In original images

The mean of cluster prominence for the normal portions and the tumor portions of the original images is 0.7018 and 7.7208 with a variance of 0.0162 and 138.7449 respectively. Hence the data clearly suggests huge variations of cluster prominence in the tumor portions as compared to the normal portion of the original images of patient1 and patient2. The means of the two portion also show significantly high difference.

For more conclusive comparision we study the box-plot comparison between the two portions. Figure 5.5(e) show the box-plot comparison of the cluster prominence between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.5(e)) is 41%. Hence cluster prominence slightly differentiate the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of cluster prominence for the normal portions and the tumor portions of the enhanced images is 11.3460 and 27.0164 with a variance of 14.6014 and 314.7569 respectively. Hence the data clearly suggests huge variations of cluster prominence in the tumor portions as compared to the normal portion of the enhanced images of patient1 and patient2. The means of the two portion also show significantly high difference.

For more conclusive comparision we study the box-plot comparison between the two portions. Figure 5.5(f) show the box-plot comparison of the cluster prominence between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.5(f)) is 46%. Hence cluster prominence slightly differentiate the two portions in the enhanced images of patient1 and 2 .

5.6 Dissimilarity

Table5.6.1 show the values of dissimilarity of the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1 1	0.1983	0.1704	0.4531	0.474
Patient1 2	0.2122	0.0957	0.4618	0.4635
Patient1 3	0.193	0.1496	0.4844	0.4722
Patient1 4	0.1791	0.1878	0.4479	0.4253
Patient1 5	0.1774	0.1217	0.467	0.4323
Patient1 6	0.1826	0.16	0.401	0.4618
Patient1 7	0.2278	0.2278	0.4653	0.4028
Patient1 8	0.2104	0.1826	0.5851	0.6024
Patient1 9	0.1722	0.1809	0.75	0.6476
Patient1 10	0.2383	0.1617	0.5747	0.5625
Patient1 11	0.2243	0.1878	0.4653	0.5357
Patient1 12	0.1896	0.1617	0.4271	0.4861
mean	0.2004	0.1656	0.4985	0.4971
variance	0.0004	0.0011	0.0091	0.0055
min	0.1722	0.0957	0.401	0.4028
max	0.2383	0.2278	0.75	0.6476

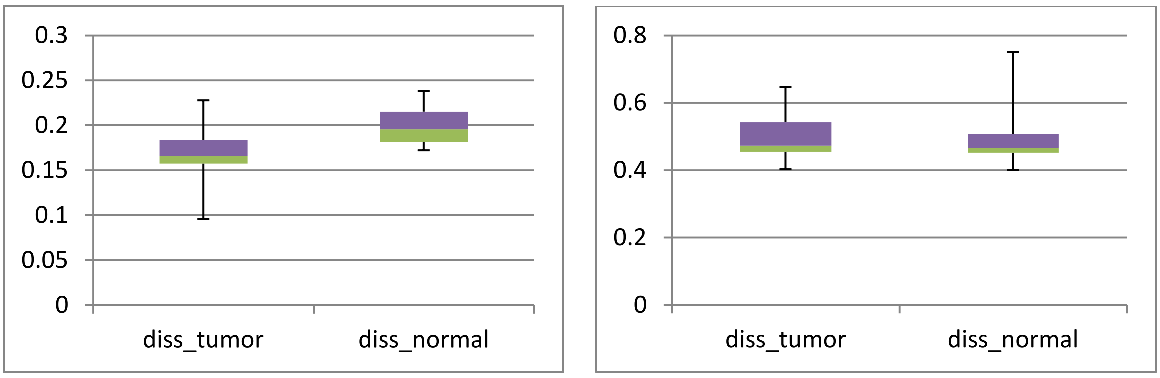


Figure 5.6(a) Figure5.6(b)

Above box-plot compares dissimilarity(diss) for the tumor and the normal portion of the original images Figure5.6(a) and the enhanced images Figure5.6(b) of patient1.

5.6.1 Dissimilarity comparison for Patient1

The mean of dissimilarity for the normal and the tumor portions in the original images of patient1 is 0.2004 and and 0.1656 with a variance of 0.0004 and 0.0011 respectively. Hence there is not much variations of dissimilarity in the tumor portion or the normal portions of the original images of patient1. Also The means of the two portions do not have significant difference.

The mean of dissimilarity for the normal and the tumor portions in the enhanced images of patient1 is 0.4985 and 0.4971 with a variance of 0.0091 and 0.0055 respectively. Hence there is not much variations of dissimilarity in the tumor portion or the normal portion in the enhanced images of patient1. The means of the two portions also do not have significant difference.

For more conclusive comparison we study the box-plots comparing the two portions Figure 5.6(a) and 5.6(b) show the box-plot comparison of the dissimilarity between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.6(a)) is 51%. Hence dissimilarity slightly differentiate the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.6(b)) is 9%. Hence the dissimilarity individually is not able to differentiate between the two portions in the enhanced images of patient1.

Hence we can observe that after enhancement of the images the dissimilarity in both the portions decrease in terms of their differentiability factor. More over, less variance in both the portions show that dissimilarity remains constant most of the times. We can observe the that the values of dissimilarity increases as we enhance the images. But the increase in the dissimilarity is almost same in both the portions. Dissimilarity is not able to differentiate between tumor and normal portions of patient1. Now for patient 2 let us calculate the dissimilarity parameter for each of the 17 images.

Table5.6.2 show the values of dissimilarity for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	0.3409	0.1983	0.6858	0.7031
Patient2_2	0.28	0.2139	0.7344	0.7517
Patient2_3	0.3426	0.3165	0.7396	0.5078
Patient2_4	0.3496	0.2957	0.658	0.5122
Patient2_5	0.3583	0.2852	0.724	0.4618
Patient2_6	0.3861	0.3316	0.651	0.4375
Patient2_7	0.4017	0.3061	0.6771	0.4549
Patient2_8	0.367	0.3646	0.6858	0.4539
Patient2_9	0.3287	0.353	0.6302	0.3889
Patient2_10	0.3878	0.3252	0.6806	0.4705
Patient2_11	0.2957	0.3548	0.6719	0.3976
Patient2_12	0.3461	0.3513	0.7344	0.4566
Patient2_13	0.3878	0.3426	0.5937	0.3681
Patient2_14	0.3322	0.3983	0.7014	0.3733
Patient2_15	0.3583	0.3617	0.6337	0.3889
Patient2_16	0.3757	0.3722	0.6319	0.4705
Patient2_17	0.2817	0.4678	0.658	0.4462
mean	0.3482	0.3316	0.6759	0.4731
variance	0.0013	0.0040	0.0017	0.0110
min	0.28	0.1983	0.5937	0.3681
max	0.4017	0.4678	0.7396	0.7517

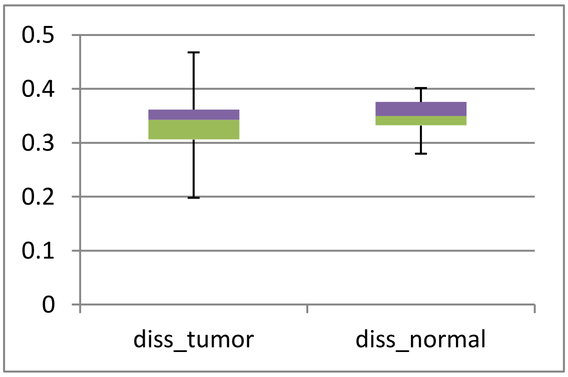


Figure 5.6(c)

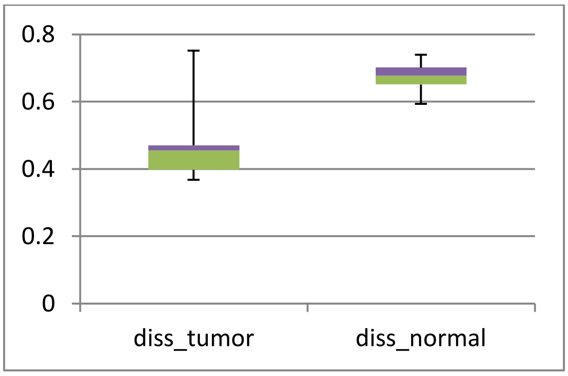


Figure5.6(d)

Above box-plot compares dissimilarity(diss) for the tumor and the normal portion of the original Figure5.6(c) and the enhanced images Figure5.6(d) of patient2

5.6.2 Dissimilarity comparison for Patient2

The mean of dissimilarity for the normal and the tumor portions in the original images of patient2 is 0.3482 and and 0.3316 with a variance of 0.0013 and 0.004 respectively. Hence there is not much variations of dissimilarity in the tumor portion or the normal portions of the original images of patient2. The means of the two portions also do not have significant difference.

The mean of dissimilarity for the normal and the tumor portions in the enhanced images of patient2 is 0.6759 and 0.4731 with a variance of 0.0017 and 0.0110 respectively. Hence there is not much variations of dissimilarity in the tumor portion or the normal portion in the enhanced images of patient2. But the means of the two portions show slight difference. For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.6(c) and 5.6(d) show the box-plot comparison of the dissimilarity between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.6(c)) is 10%. Hence the dissimilarity individually is not able to differentiate between the two portions in the original images of patient2.On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.6(d)) is 73%. Hence the dissimilarity is able to differentiate between the two portions in the enhanced images of patient2.

5.6.3 Overall comparison of dissimilarity

Table5.6.3 show the mean, variance minimum and the maximum values of the combined values of dissimilarity of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.2870	0.2629	0.6025	0.4830
Variance	0.0064	0.0096	0.0124	0.0086
Min	0.1722	0.0957	0.401	0.3681
Max	0.4017	0.4678	0.75	0.7517

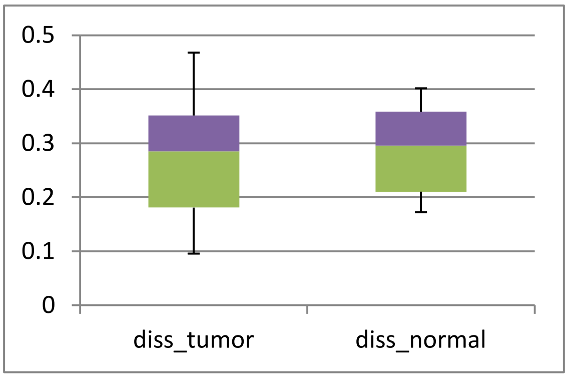


Figure 5.6(e)

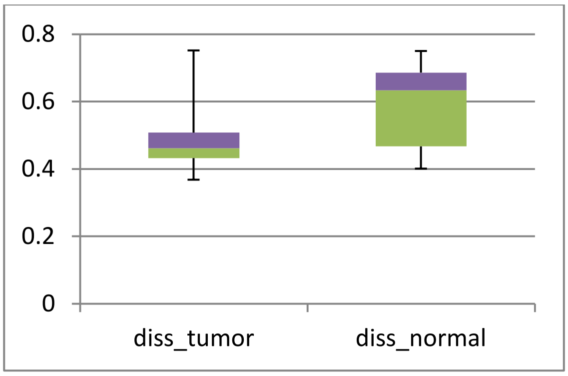


Figure5.6(f)

Above box-plots compares the overall dissimilarity for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.6(e) and enhanced images Figure5.6(f).

In original images

The mean of dissimilarity for the normal portions and the tumor portions of the original images is 0.2870 and 0.2629 with a variance of 0.0064 and 0.0096 respectively. Hence the data clearly suggests not much variations of dissimilarity in the normal portions or the tumor portion of the original images of patient1 and patient2. The means of the two portion also do not have significant difference.

For more conclusive comparison we study the box-plot comparison of the two portions. Figure 5.6(e) show the box-plot comparison of the dissimilarity between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.6(e)) is 6%. Hence the dissimilarity individually is not able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of dissimilarity for the normal portions and the tumor portions of the enhanced images is 0.6025 and 0.4830 with a variance of 0.0124 and 0.0086 respectively. Hence the data clearly suggests not much variations of dissimilarity in the normal portions or the tumor portion of the enhanced images of patient1 and patient2. But the means of the two portion have slight difference.

For more conclusive comparision we study the box-plot comparion of the two portions. Figure 5.6(f) show the box-plot comparison of the dissimilarity between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.6(f)) is 68%. Hence dissimilarity is able to differentiate between the two portions in the enhanced images of patient1 and 2 .

5.7 Energy

Table5.7.1 show the values of energy in the normal and the tumor portions of patient1

Patient1	Original images		Enhanced images	
	Normal	Tumor	Normal	Tumor
Patient1_1	0.4204	0.378	0.2266	0.1259
Patient1_2	0.3847	0.4708	0.1772	0.1242
Patient1_3	0.3839	0.3829	0.1709	0.1347
Patient1_4	0.4147	0.348	0.1993	0.1656
Patient1_5	0.3689	0.5345	0.163	0.1949
Patient1_6	0.3896	0.4752	0.1921	0.1553
Patient1_7	0.3285	0.3392	0.1614	0.2172
Patient1_8	0.3346	0.3543	0.1302	0.111
Patient1_9	0.4229	0.3593	0.0896	0.0937
Patient1_10	0.3369	0.355	0.1243	0.1143
Patient1_11	0.3707	0.3599	0.1895	0.1323
Patient1_12	0.444	0.5248	0.1812	0.1765
mean	0.3833	0.4068	0.1671	0.1454
variance	0.0014	0.0053	0.0013	0.0013
min	0.3285	0.3392	0.0896	0.0937
max	0.444	0.5345	0.2266	0.2172

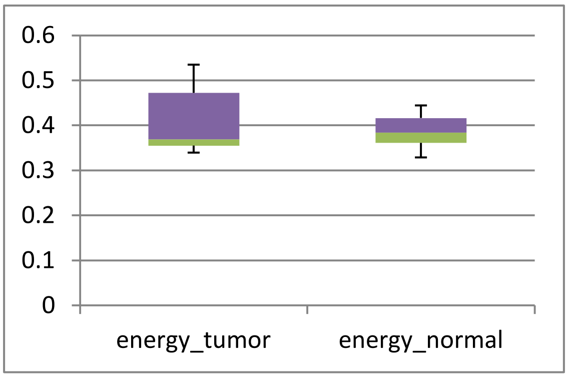


Figure5.7(a)

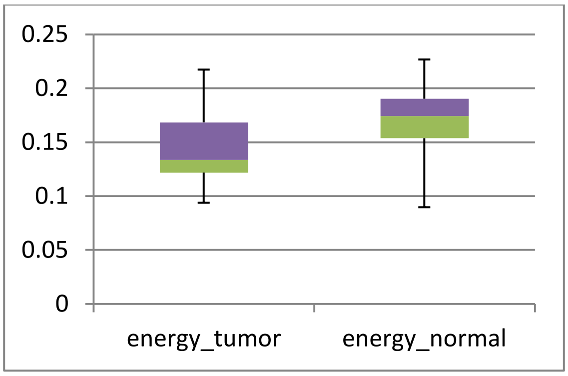


Figure 5.7(b)

Above box-plot compares energy for the tumor and the normal portion of the original images Figure5.7(a) and the enhanced images Figure5.7(b) of patient1.

5.7.1 Energy comparison for Patient1

The mean of energy for the normal and the tumor portions in the original images of patient1 is 0.3833 and and 0.4068 with a variance of 0.0014 and 0.0053 respectively. Hence there is not much variations of energy in the tumor portion or the normal portions of the original images of patient1. The means of the two portions also do not have significant difference.

The mean of energy for the normal and the tumor portions in the enhanced images of patient1 is 0.1671 and 0.1454 with a variance of 0.00136 and 0.00138 respectively. Hence there is not much variations of energy in the tumor portion or the normal portion in the enhanced images of patient1. The means of the two portions also do not have significant difference.

For more conclusive comparison we study the box-plot comparison of the two portions. Figure 5.7(a) and 5.7(b) show the box-plot comparison of the energy between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.7(a)) is 13%. Hence the energy individually is not able to differentiate between two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.7(b)) is 59%. Hence energy slightly differentiate the two portions in the enhanced images of patient1.

Table5.7.2 show the values of energy of the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	0.3668	0.5739	0.1016	0.1316
Patient2 2	0.4572	0.5262	0.0928	0.1302
Patient2 3	0.339	0.4038	0.1027	0.2193
Patient2 4	0.3448	0.3185	0.1157	0.2099
Patient2 5	0.3061	0.2977	0.0954	0.2281
Patient2 6	0.3101	0.2496	0.1141	0.2435
Patient2 7	0.2938	0.266	0.1064	0.2688
Patient2 8	0.3167	0.2444	0.1043	0.2789
Patient2 9	0.322	0.2282	0.1084	0.2998
Patient2 10	0.3044	0.2543	0.1113	0.2042
Patient2 11	0.4323	0.2138	0.1142	0.2195
Patient2 12	0.31	0.168	0.0988	0.1519
Patient2 13	0.3453	0.1716	0.1205	0.2485
Patient2 14	0.3464	0.1308	0.0991	0.2241
Patient2 15	0.3363	0.2126	0.1162	0.2193

Patient2_16	0.3643	0.1666	0.1178	0.1558
Patient2_17	0.467	0.1285	0.1103	0.1563
mean	0.3507	0.2679	0.10762353	0.2111
variance	0.0028	0.0161	0.00006	0.0025
min	0.2938	0.1285	0.0928	0.1302
max	0.467	0.5739	0.1205	0.2998

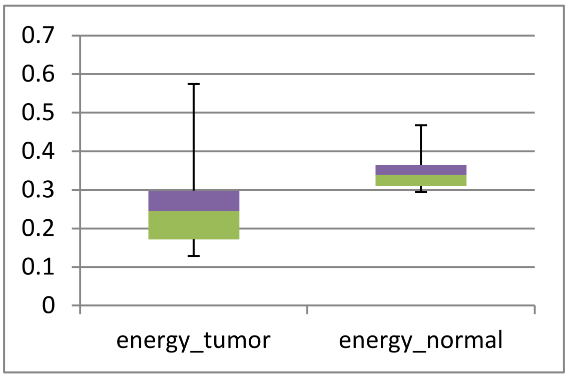


Figure5.7(c)

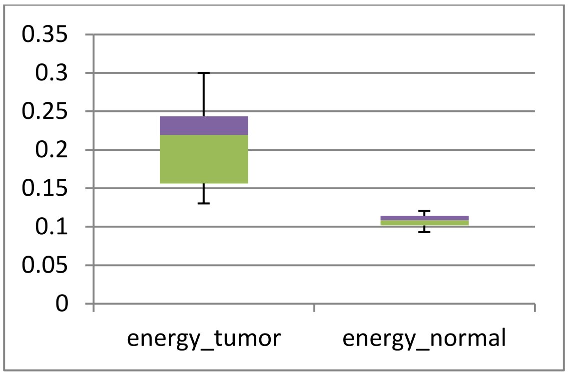


Figure 5.7(d)

Above box-plot compares energy for the tumor and the normal portions of the original Figure5.7(c) and enhanced images Figure5.7(d) of patient2.

5.7.2 Energy comparison for Patient2

The mean of energy for the normal and the tumor portions in the original images of patient2 is 0.3507 and and 0.2679 with a variance of 0.0028 and 0.0161 respectively. Hence there is not much variations of energy in the tumor portion or the normal portions of the original images of patient2. The means of the two portions also do not have significant difference.

The mean of energy for the normal and the tumor portions in the enhanced images of patient1 is 0.1076 and 0.2111 with a variance of 0.00006 and 0.0025 respectively. Hence there is not much variations of energy in the tumor portion or the normal portion in the enhanced images of patient1. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.7(c) and 5.7(d) show the box-plot comparison of the energy between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.7(c)) of patient2 is 49%. Hence the energy slightly differentiate the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.7(d)) is 78%. Hence energy is able to differentiate between the two portions in the enhanced images of patient2.

5.7.3 Overall comparison of energy

Table5.7.3 show the mean, variance minimum and the maximum values of the combined values of energy of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.3642	0.3253	0.1322	0.1839
Variance	0.0024	0.0161	0.0014	0.0030
Min	0.2938	0.1285	0.0896	0.0937
Max	0.467	0.5739	0.2266	0.2998

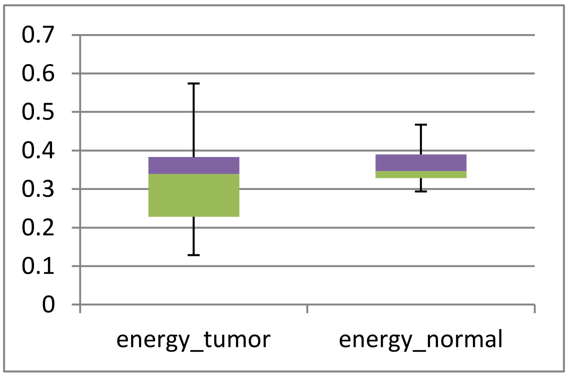


Figure5.7(e)

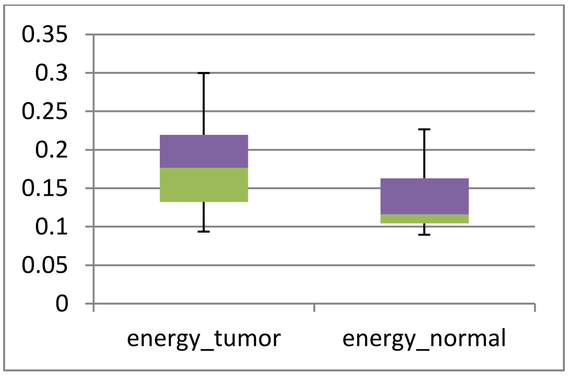


Figure 5.7(f)

Above box-plots compares the overall energy for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.7(e) and enhanced images Figure5.7(f).

In original images

The mean of dissimilarity for the normal portions and the tumor portions of the original images is 0.3642 and 0.3253 with a variance of 0.0024 and 0.0161 respectively. Hence the data clearly suggests not much variations of energy in the normal portions or the tumor portion of the original images of patient1 and patient2. The means of the two portion also do not have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.7(e) show the box-plot comparison of the energy between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.7(e)) is 4%. Hence the energy individually is not able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of energy for the normal portions and the tumor portions of the enhanced images is 0.1322 and 0.1849 with a variance of 0.0014 and 0.0030 respectively. Hence the data clearly suggests not much variations of energy in the normal portions or the tumor portion of the enhanced images of patient1 and patient2. But the means of the two portion have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.7(f) show the box-plot comparison of the energy between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.7(f)) is 53%. Hence the energy slightly differentiate the two portions in the enhanced images of patient1 and 2 .

5.8 Entropy

Table5.8.1 show the values of entropy of the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1 1	1.0876	1.1257	1.861	2.2488
Patient1 2	1.1419	0.9405	1.9777	2.2555
Patient1 3	1.1335	1.1024	2.0101	2.224
Patient1 4	1.0855	1.1751	1.8513	2.0722
Patient1 5	1.1424	0.9936	2.0589	2.0538
Patient1 6	1.1191	1.0552	1.9163	2.2833
Patient1 7	1.2239	1.2099	2.0294	2.0428
Patient1 8	1.2067	1.1803	2.248	2.4712
Patient1 9	1.0705	1.1731	2.6232	2.5293
Patient1 10	1.2176	1.3432	2.2506	2.5186
Patient1 11	1.1662	1.1773	1.9132	2.2857
Patient1 12	1.0515	0.9414	1.9827	2.077

mean	1.1372	1.1181	2.0602	2.2551
variance	0.0033	0.0141	0.0482	0.0313
min	1.0515	0.9405	1.8513	2.0428
max	1.2239	1.3432	2.6232	2.5293

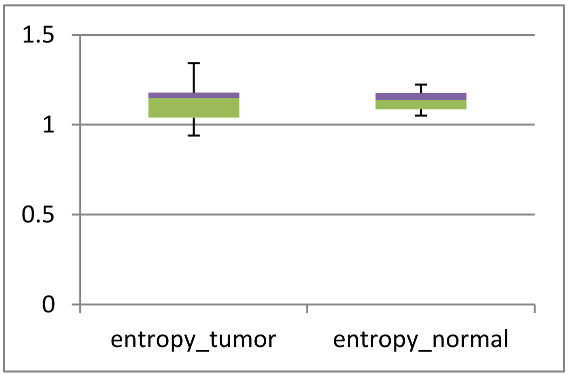


Figure5.8(a)

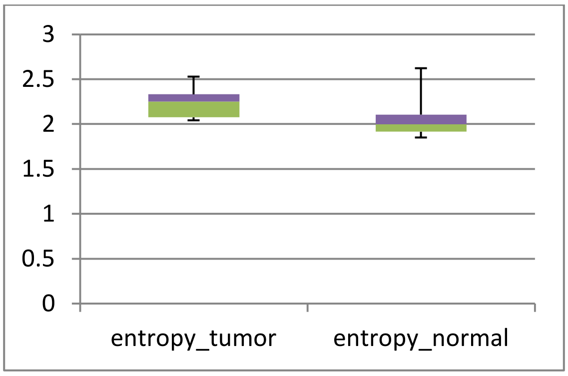


Figure 5.8(b)

Above box-plot compares entropy for the tumor and the normal portion of the original Figure5.8(a) and the enhanced images figur5.8(b) of patient1 .

5.8.1 Entropy comparison for Patient1

The mean of entropy for the normal and the tumor portions in the original images of patient1 is 1.1372 and 1.118 with a variance of 0.0033 and 0.0141 respectively. Hence there is not much variations of entropy in the tumor portion or the normal portions of the original images of patient1. The means of the two portions also do not have significant difference.

The mean of entropy for the normal and the tumor portions in the enhanced images of patient1 is 2.0602 and 2.2551 with a variance of 0.0482 and 0.0313 respectively. Hence there is not much variations of entropy in the tumor portion or the normal portion in the enhanced images of patient1. But the means of the two portions have slight difference.

For more conclusive comparision we study the box-plots comparison for both the portions. Figure 5.8(a) and 5.8(b) show the box-plot comparison of the entropy between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.8(a)) is 8%. Hence the entropy individually is not able to differentiate between the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.8(b)) is 61%. Hence the entropy slightly differentiate the two portions in the enhanced images of patient1.

Table5.8.2 show the values of entropy of the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	1.2138	1.0602	2.4723	2.3039
Patient2_2	1.0634	1.0975	2.5606	2.4249
Patient2_3	1.2327	1.3928	2.4608	2.0097
Patient2_4	1.2661	1.5665	2.331	2.1524
Patient2_5	1.3052	1.4849	2.5127	1.9642
Patient2_6	1.2972	1.6612	2.3662	1.9213
Patient2_7	1.3697	1.5512	2.4428	1.9357
Patient2_8	1.2694	1.6101	2.4704	1.8966
Patient2_9	1.2606	1.7756	2.4141	1.7757
Patient2_10	1.3136	1.6145	2.3693	2.0532
Patient2_11	1.1048	1.7841	2.341	1.9306
Patient2_12	1.2895	1.9914	2.5192	2.2682
Patient2_13	1.2461	2.121	2.3261	1.9354
Patient2_14	1.2381	2.3434	2.5277	1.9303
Patient2_15	1.266	1.9769	2.3945	2.0044
Patient2_16	1.2089	2.1506	2.3879	2.1827
Patient2_17	1.0549	2.3613	2.4398	2.3143
mean	1.2352	1.7378	2.4315	2.0590
variance	0.0074	0.1469	0.0053	0.0331
min	1.0549	1.0602	2.3261	1.7757
max	1.3697	2.3613	2.5606	2.4249

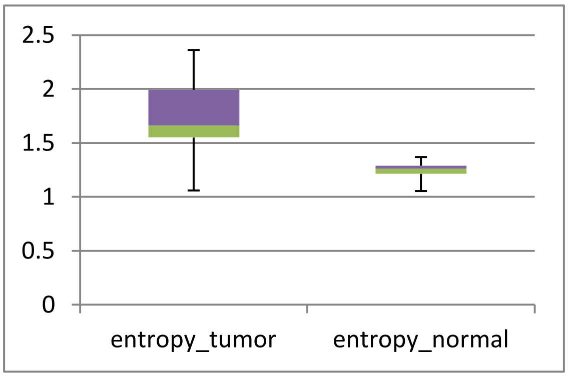


Figure5.8(c)

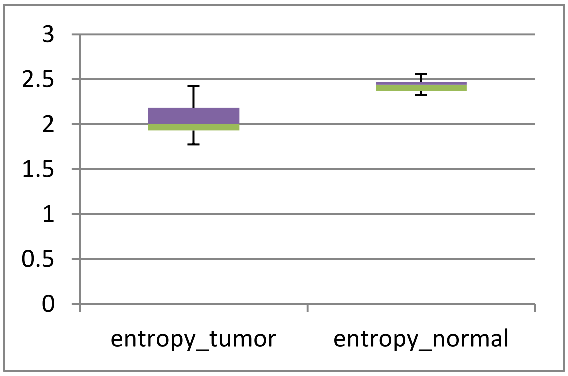


Figure 5.8(d)

Above box-plot compares entropy for the tumor and the normal portion of the original Figure5.8(c) and enhanced images Figure5.8(d) of patient2

5.8.2 Entropy comparison for Patient2

The mean of entropy for the normal and the tumor portions in the original images of patient2 is 1.2352 and and 1.7378 with a variance of 0.0074 and 0.1469 respectively. Hence there is more variations of entropy in the tumor portion as compared to the normal portions of the original images of patient2. Also the means of the two portions have slight difference.

The mean of entropy for the normal and the tumor portions in the enhanced images of patient2 is 2.4315 and 2.0590 with a variance of 0.0053 and 0.0331 respectively. Hence there is not much variations of entropy in the tumor portion or the normal portion in the enhanced images of patient2. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.8(c) and 5.8(d) show the box-plot comparison of the entropy between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.8(c)) is 52%. Hence the entropy slightly differentiate the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.8(d)) is 80%. Hence the entropy is able to differentiate between the two portions in the enhanced images of patient2.

5.8.3 Overall comparison of entropy

Table5.8.3 show the mean, variance minimum and the maximum values of the combined values of entropy of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	1.1947	1.4814	2.2778	2.1401
Variance	0.0080	0.1860	0.0566	0.0409
Min	1.0515	0.9405	1.8513	1.7757
Max	1.3697	2.3613	2.6232	2.5293

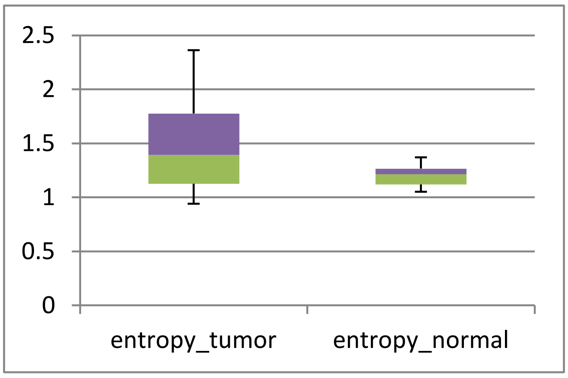


Figure5.8(e)

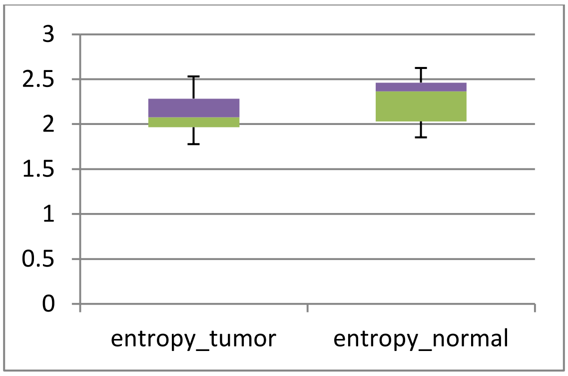


Figure 5.8(f)

Above box-plots compares the overall entropy for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.8(e) and enhanced images Figure5.8(f).

In original images

The mean of entropy for the normal portions and the tumor portions of the original images is 1.1947 and 1.4814 with a variance of 0.0080 and 0.1860 respectively. Hence the data clearly suggests much variations of entropy in the tumor portions as compared to the normal portions of the original images of patient1 and patient2. Also the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.8(e) show the box-plot comparison of the entropy between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.8(e)) is 27%. Hence the energy individually is not able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of energy for the normal portions and the tumor portions of the enhanced images is 2.2778 and 2.1401 with a variance of 0.0566 and 0.0409 respectively. Hence the data clearly suggests not much variations of entropy in the normal portions or the tumor portion of the enhanced images of patient1 and patient2. Also the means of the two portions do not have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.8(f) show the box-plot comparison of the energy between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.8(f)) is 58%. Hence the energy slightly differentiate the two portions in the enhanced images of patient1 and 2 .

5.9 Homogeneity

Table5.9.1 show the values of homogeneity for the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1 1	0.9009	0.9148	0.7815	0.7729
Patient1 2	0.8939	0.9522	0.7778	0.7734
Patient1 3	0.9035	0.9252	0.7659	0.7737
Patient1 4	0.9104	0.9061	0.7824	0.796
Patient1 5	0.9113	0.9391	0.774	0.7879
Patient1 6	0.9087	0.92	0.8018	0.7778
Patient1 7	0.8861	0.8861	0.7762	0.8074
Patient1 8	0.8948	0.9087	0.7271	0.7225
Patient1 9	0.9139	0.9096	0.6681	0.7007
Patient1 10	0.8809	0.9191	0.73	0.7455
Patient1 11	0.8878	0.9061	0.7731	0.7432
Patient1 12	0.9052	0.9191	0.7928	0.7645
mean	0.8997	0.9171	0.7625	0.7637
variance	0.0001	0.0002	0.0013	0.0009
min	0.8809	0.8861	0.6681	0.7007
max	0.9139	0.9522	0.8018	0.8074

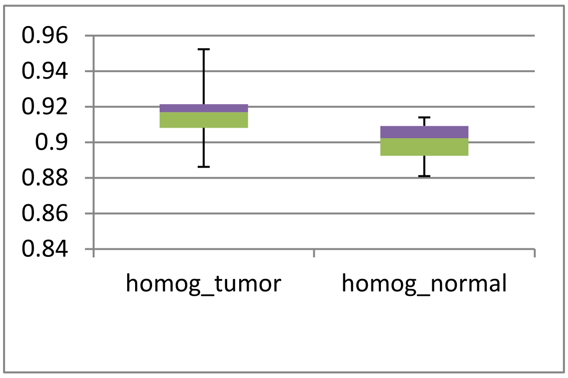


Figure5.9(a)

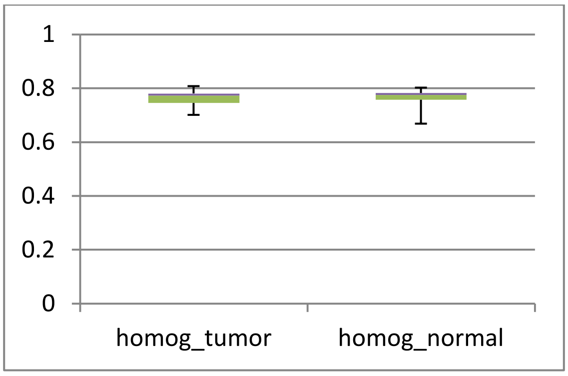


Figure5.9(b)

Above box-plot compares homogeneity for the tumor and the normal portion of the original images Figure5.9(a) and the enhanced images Figure5.9(b)of patient1.

5.9.1 Homogeneity comparison for Patient1

The mean of homogeneity for the normal and the tumor portions in the original images of patient1 is 0.8997 and 0.9171 with a variance of 0.0001 and 0.0002 respectively. Hence there is not much variations of homogeneity in the tumor portion or the normal portions of the original images of patient1. The means of the two portions also do not have significant difference.

The mean of homogeneity for the normal and the tumor portions in the enhanced images of patient1 is 0.7625 and 0.7637 with a variance of 0.0013 and 0.0009 respectively.

Hence there is not much variations of homogeneity in the tumor portion or the normal portion in the enhanced images of patient1. Also the means of the two portions do not have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.9(a) and 5.9(b) show the box-plot comparison of the homogeneity between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.9(a)) is 51%. Hence the homogeneity slightly differentiate the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.9(b)) is 5%. Hence the homogeneity individually is not able to differentiate between the two portions in the enhanced images of patient1.

Table5.9.2 show the values of homogeneity of the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2 1	0.8296	0.9049	0.6969	0.6925
Patient2 2	0.86	0.8949	0.6811	0.7005
Patient2 3	0.8287	0.858	0.6759	0.7813
Patient2 4	0.8258	0.8545	0.701	0.7727
Patient2 5	0.8209	0.8574	0.684	0.7814
Patient2 6	0.807	0.8348	0.7031	0.7928
Patient2 7	0.7997	0.8487	0.6937	0.7907
Patient2 8	0.8165	0.819	0.6933	0.8081
Patient2 9	0.8357	0.8258	0.7159	0.8166
Patient2 10	0.8061	0.8386	0.697	0.7831
Patient2 11	0.8522	0.8243	0.6955	0.8064
Patient2 12	0.8275	0.8255	0.679	0.7888
Patient2 13	0.8067	0.8293	0.7225	0.8255
Patient2 14	0.8339	0.8072	0.6907	0.8186
Patient2 15	0.8209	0.8238	0.7111	0.8144
Patient2 16	0.8122	0.8265	0.7127	0.7804
Patient2 17	0.8597	0.7852	0.708	0.8103
mean	0.8260	0.8387	0.6977	0.7861
variance	0.0003	0.0008	0.0001	0.0013
min	0.7997	0.7852	0.6759	0.6925
max	0.86	0.9049	0.7225	0.8255

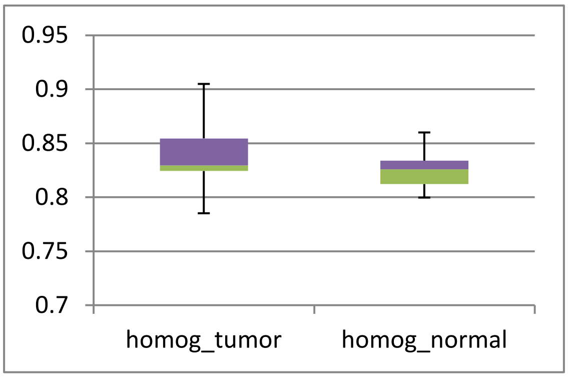


Figure5.9(c)

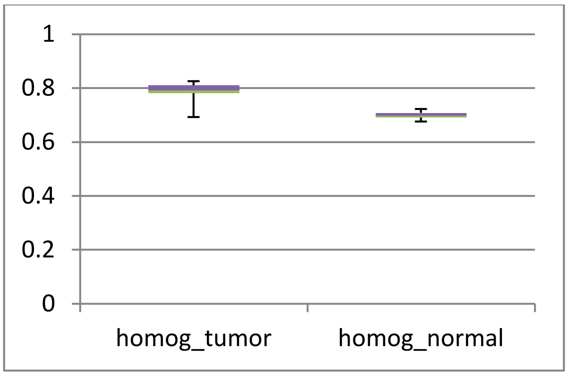


Figure5.9(d)

Above box-plot compares homogeneity for the tumor and the normal portion of the enhanced images of patient1 Figure5.9(c) and patient2 Figure5.9(d).

5.9.2 Homogeneity comparison for Patient2

The mean of homogeneity for the normal and the tumor portions in the original images of patient2 is 0.8260 and 0.8387 with a variance of 0.0003 and 0.0008 respectively. Hence there is not much variations of homogeneity in the tumor portion or the normal portions of the original images of patien2. The means of the two portions also do not have significant difference.

The mean of homogeneity for the normal and the tumor portions in the enhanced images of patient2 is 0.6977 and 0.7861 with a variance of 0.0001 and 0.0013 respectively. Hence there is not much variations of homogeneity in the tumor portion or the normal portion in the enhanced images of patient2. But the means of the two portions have slight difference

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.9(c) and 5.9(d) show the box-plot comparison of the homogeneity between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.9(c)) is 8%. Hence the homogeneity individually is not able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.9(d)) is 78%. Hence the homogeneity is able to differentiate between the two portions in the enhanced images of patient2.

5.9.3 Overall comparison of Homogeneity

Table5.8.3 show the mean, variance minimum and the maximum values of the combined values of homogeneity of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.8565	0.8711	0.7245	0.7768
Variance	0.0016	0.0021	0.0016	0.0012
Min	0.7997	0.7852	0.6681	0.6925
Max	0.9139	0.9522	0.8018	0.8255

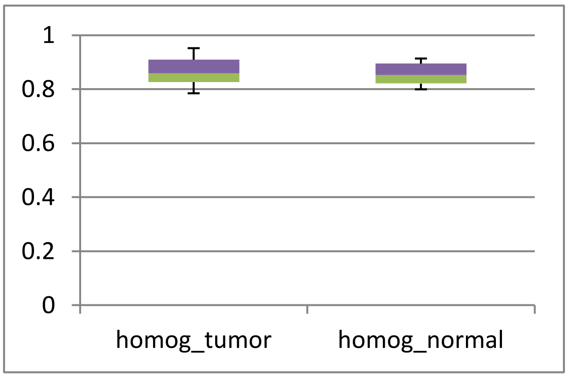


Figure5.9(e)

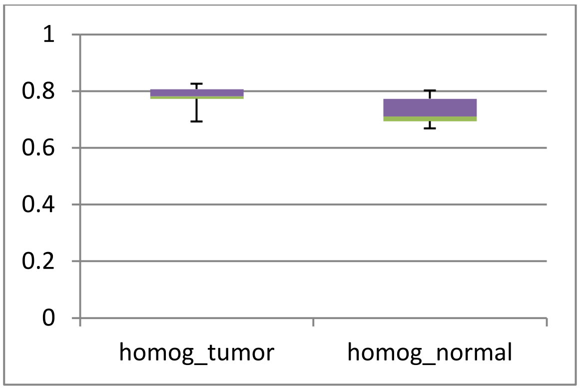


Figure5.9(f)

Above box-plots compares the overall homogeneity for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.9(e) and enhanced images Figure5.9(f).

In original images

The mean of homogeneity for the normal portions and the tumor portions of the original images is 0.8565 and 0.8711 with a variance of 0.0016 and 0.0021 respectively. Hence the data clearly suggests not much variations of homogeneity in the tumor portions or the normal portions of the original images of patient1 and patient2. Also the means of the two portions do not have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.9(e) show the box-plot comparison of the homogeneity between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.9(e)) is 7%. Hence the homogeneity individually is not able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of homogeneity for the normal portions and the tumor portions of the enhanced images is 0.7245 and 0.7768 with a variance of 0.0016 and 0.0012 respectively. Hence the data clearly suggests not much variations of homogeneity in the tumor portions or the normal portions of the enhanced images of patient1 and patient2. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.9(f) show the box-plot comparison of the homogeneity between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.9(f)) is 62%. Hence the homogeneity slightly differentiate the two portions in the enhanced images of patient1 and 2 .

5.10 Maximum probability

Table5.10.1 show the values of maximum probability for the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1_1	0.6	0.513	0.4184	0.1927
Patient1_2	0.5548	0.6209	0.3316	0.2222
Patient1_3	0.5443	0.4957	0.3229	0.2135
Patient1_4	0.5861	0.4209	0.3542	0.2934
Patient1_5	0.4974	0.7113	0.3073	0.3854
Patient1_6	0.5478	0.6574	0.3611	0.3351
Patient1_7	0.433	0.473	0.283	0.4184
Patient1_8	0.4139	0.4539	0.2483	0.2014
Patient1_9	0.5948	0.473	0.1493	0.1406
Patient1_10	0.4765	0.4957	0.2066	0.2396
Patient1_11	0.5374	0.487	0.3507	0.24
Patient1_12	0.6261	0.7026	0.3368	0.3212
mean	0.5343	0.5420	0.3058	0.2669
variance	0.0044	0.0103	0.0054	0.0070
min	0.4139	0.4209	0.1493	0.1406
max	0.6261	0.7113	0.4184	0.4184

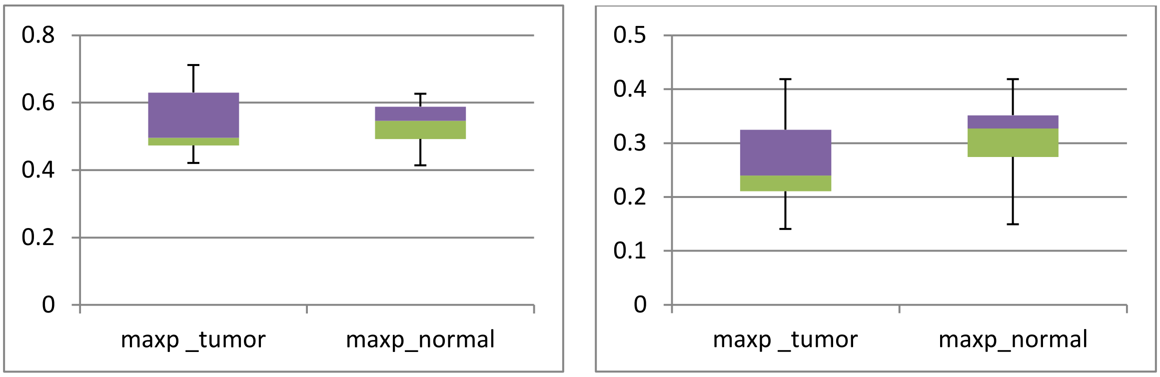


Figure5.10(a) Figure5.10(b)

Above box-plot compares maximum probability for the tumor and the normal portion of the original images Figure 5.10(a) and the enhanced images Figure5.10(b) of patient1

5.10.1 Maximum probability comparison for Patient1

The mean of maximum probability for the normal and the tumor portions in the original images of patient1 is 0.5343 and 0.5420 with a variance of 0.0044 and 0.0103 respectively. Hence there is not much variations of maximum probability in the tumor portion or the normal portions of the original images of patient1. Also the means of the two portions do not have significant difference.

The mean of maximum probability for the normal and the tumor portions in the enhanced images of patient1 is 0.3058 and 0.2669 with a variance of 0.0054 and 0.0070 respectively. Hence there is not much variations of maximum probability in the tumor portion or the normal portion in the enhanced images of patient1. Also the means of the two portions do not have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.10(a) and 5.10(b) show the box-plot comparison of the maximum probability between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.10(a)) is 32%. Hence the maximum probability individually is not able to differentiate between the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.10(b)) is 62%. Hence the maximum probability individually slightly differentiate the two portions in the enhanced images of patient1.

Table5.10.2 show the values of maximum probability of the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	0.5461	0.7513	0.1771	0.2292
Patient2_2	0.6435	0.7148	0.1441	0.2465
Patient2_3	0.5078	0.6139	0.1927	0.4122
Patient2_4	0.52	0.5165	0.1719	0.4132
Patient2_5	0.4574	0.4574	0.1458	0.4306
Patient2_6	0.4626	0.375	0.1806	0.4531
Patient2_7	0.44	0.3774	0.1632	0.4878
Patient2_8	0.473	0.3368	0.1736	0.4991
Patient2_9	0.4817	0.3304	0.1597	0.5191
Patient2_10	0.4539	0.3617	0.1875	0.3976
Patient2_11	0.6191	0.3183	0.2049	0.4149
Patient2_12	0.4626	0.2435	0.1545	0.2865
Patient2_13	0.513	0.3374	0.2049	0.4583
Patient2_14	0.52	0.2643	0.1632	0.4132
Patient2_15	0.5061	0.393	0.184	0.4184
Patient2_16	0.5374	0.2783	0.2066	0.3003
Patient2_17	0.6522	0.2313	0.1736	0.2691
mean	0.5174	0.4059	0.1757	0.3911
variance	0.0042	0.0245	0.0003	0.0082
min	0.44	0.2313	0.1441	0.2292
max	0.6522	0.7513	0.2066	0.5191

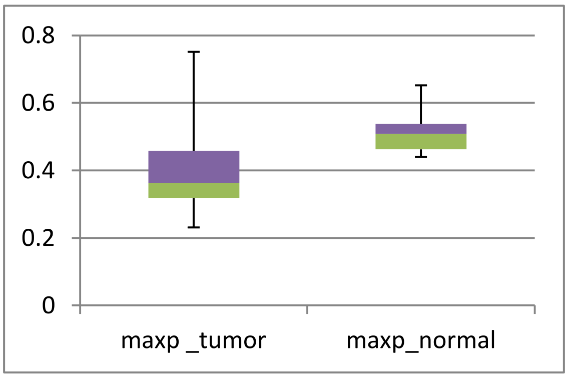


Figure5.10(c)

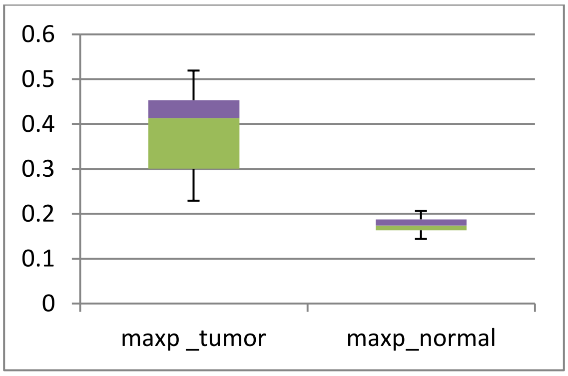


Figure5.10(d)

Above box-plot compares maximum probability for the tumor and the normal portions of the original Figure 5.10(c) and enhanced images Figure5.10(d). of patient2.

5.10.2 Maximum probability comparison for Patient2

The mean of maximum probability for the normal and the tumor portions in the original images of patient2 is 0.5174 and 0.4059 with a variance of 0.0042 and 0.0245 respectively. Hence there is not much variations of maximum probability in the tumor portion or the normal portions of the original images of patient2. But the means of the two portions have slight difference.

The mean of maximum probability for the normal and the tumor portions in the enhanced images of patient2 is 0.1757 and 0.3911 with a variance of 0.0003 and 0.0082 respectively. Hence there is not much variations of maximum probability in the tumor portion or the normal portion in the enhanced images of patient2. But the means of the two portions have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.10(c) and 5.10(d) show the box-plot comparison of the maximum probability between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.10(c)) is 67%. Hence the maximum probability is able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.10(d)) is 83%. Hence the maximum probability is able to differentiate between the two portions in the enhanced images of patient2.

Maximum probability in patient2 images show a better differentiability factor in both the original and enhanced images. We can observe increase in differentiability factor as we enhance the images. The value of 83% difference in the median as percentage of overall visible spread suggest that maximum probability can be used in enhanced images of patient2 to differentiate between normal and the tumor portion. A 67% of difference between medians as percentage of overall visible spread is also satisfactory.

5.10.3 Overall comparison of maximum probability

Table5.10.3 show the mean, variance minimum and the maximum values of the combined values of maximum probability of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.5244	0.4622	0.2295	0.3397
Variance	0.0042	0.0227	0.0066	0.0113
Min	0.4139	0.2313	0.1441	0.1406
Max	0.6522	0.7513	0.4184	0.5191

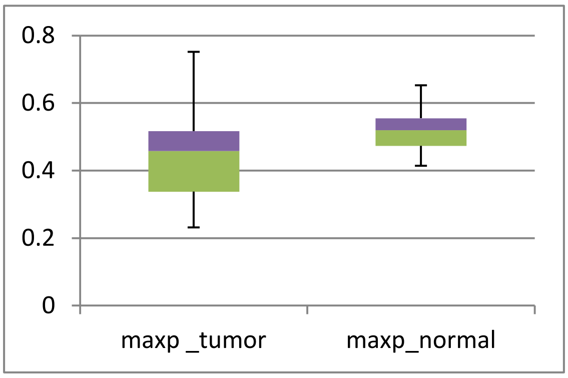


Figure5.10(e)

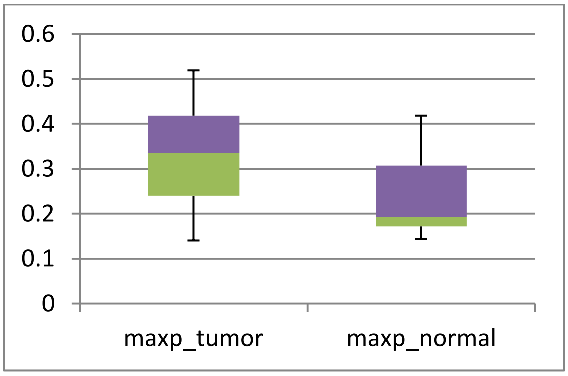


Figure5.10(f)

Above box-plots compares the overall maximum probability for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.10(e) and enhanced images Figure5.10(f).

In original images

The mean of maximum probability for the normal portions and the tumor portions of the original images is 0.5244 and 0.4622 with a variance of 0.0042 and 0.0227 respectively. Hence the data clearly suggests not much variations of maximum probability in the tumor portions or the normal portions of the original images of patient1 and patient2. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.10(e) show the box-plot comparison of the maximum probability between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.10(e)) is 29%. Hence the maximum probability individually is not able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of maximum probability for the normal portions and the tumor portions of the enhanced images is 0.2295 and 0.3397 with a variance of 0.0066 and 0.0113 respectively. Hence the data clearly suggests not much variations of maximum probability in the tumor portions or the normal portions of the enhanced images of patient1 and patient2. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.10(f) show the box-plot comparison of the maximum probability between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.10(f)) is 58%. Hence the maximum probability slightly differentiate the two portions in the enhanced images of patient1 and 2 .

5.10 Sum of square: variance

Table5.11.1 show the values of variance for the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1_1	32.4744	29.3269	36.8476	34.461
Patient1_2	32.0166	28.6211	36.2747	31.2304
Patient1_3	28.7737	29.6512	35.3292	36.3257
Patient1_4	32.2837	30.2425	38.0962	36.4466
Patient1_5	31.2917	34.0752	34.287	45.5491
Patient1_6	31.9594	33.2011	35.7085	42.2228
Patient1_7	30.8911	31.3299	37.0801	43.8327
Patient1_8	30.5096	29.9408	35.2899	31.4157
Patient1_9	32.36	29.6165	32.0096	34.4233
Patient1_10	31.4443	31.9198	35.3505	43.5634
Patient1_11	31.9403	31.1998	36.7888	39.7212
Patient1_12	32.7796	33.5843	36.6853	42.0642
mean	31.5603	31.0590	35.8122	38.4380
variance	1.2181	3.2564	2.4856	25.1531
min	28.7737	28.6211	32.0096	31.2304
max	32.7796	34.0752	38.0962	45.5491

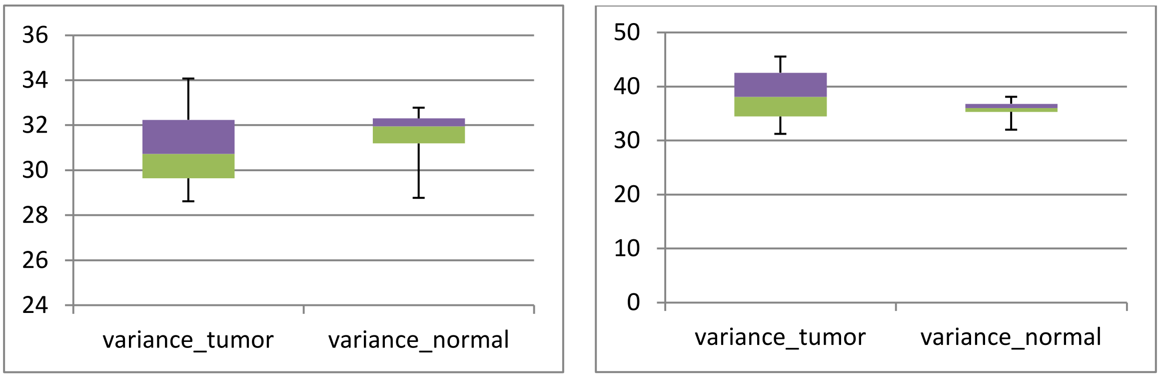


Figure5.11(a) Figure5.11(b)

Above box-plot compares variance for the tumor and the normal portion of the original Figure5.11(a) and enhanced images Figure5.11(b)o f patient1

5.11.1 Variance comparison for Patient1

The mean of Variance for the normal and the tumor portions in the original images of patient1 is 31.5603 and 31.0590 with a variance of 1.2181 and 3.2564 respectively. Hence there are much variations of Variance in the tumor portion as compared to the normal portions of the original images of patient1. But the means of the two portions do not have significant difference.

The mean of Variance for the normal and the tumor portions in the enhanced images of patient1 is 35.8122 and 38.4380 with a variance of 2.485 and 25.1531 respectively. Hence there is huge variations of Variance in the tumor portions as compared to the normal portions in the enhanced images of patient1. Also the means of the two portions have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.11(a) and 5.11(b) show the box-plot comparison of the Variance between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.11(a)) is 46%. Hence the Variance slightly differentiate the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.11(b)) is 26%. Hence Variance individually is not able to differentiate between the two portions in the enhanced images of patient1.

Table5.11.2 show the values of variance for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	22.4021	24.6227	35.0825	38.4382
Patient2_2	22.9636	25.7444	34.6515	37.9489
Patient2_3	21.9428	26.1835	34.5889	41.5498
Patient2_4	22.1872	27.7354	36.9626	43.0865
Patient2_5	21.6187	29.3011	35.3943	45.1245
Patient2_6	21.7747	30.4828	36.8243	46.0026
Patient2_7	21.7071	30.5654	36.4971	45.1698
Patient2_8	21.8024	30.732	36.672	45.6061
Patient2_9	21.6776	31.7189	36.2287	47.3016
Patient2_10	21.6655	30.4769	35.6882	46.1015
Patient2_11	22.8232	33.011	35.1791	47.1077
Patient2_12	21.5996	35.3947	35.4132	47.599
Patient2_13	22.2929	34.481	36.3289	48.0955
Patient2_14	22.0087	35.3628	36.2738	48.7537
Patient2_15	22.0901	35.4571	38.0883	47.9915
Patient2_16	22.4489	35.1698	37.8476	46.954
Patient2_17	23.0607	35.7046	37.2174	47.5239
mean	22.1215	31.3025	36.1728	45.3149
variance	0.2295	13.6681	1.0889	10.5367
min	21.5996	24.6227	34.5889	37.9489
max	23.0607	35.7046	38.0883	48.7537

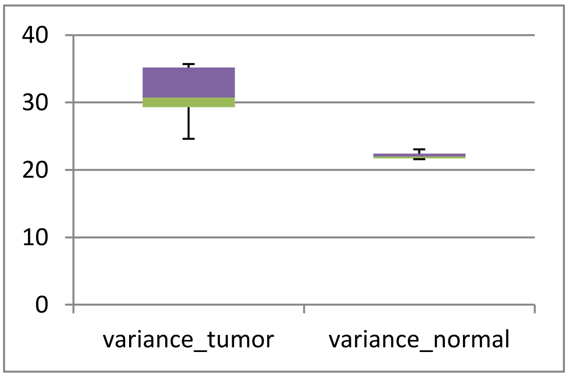


Figure5.11(c)

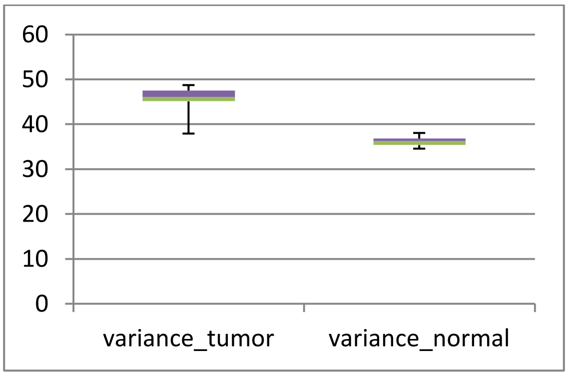


Figure5.11(d)

Above box-plot compares variance for the tumor and the normal portion of the original Figure 5.11(c) and enhanced images Figure5.11(d)of patient2 .

5.11.2 Variance comparison for Patient2

The mean of Variance for the normal and the tumor portions in the original images of patient2 is 22.1215 and 31.3025 with a variance of 0.2295 and 13.6681 respectively. Hence there are high variations of Variance in the tumor portion as compared to the normal portions of the original images of patient2. Also the means of the two portions have significantly high difference.

The mean of Variance for the normal and the tumor portions in the enhanced images of patient2 is 36.1728 and 45.3149 with a variance of 1.0889 and 10.5367 respectively. Hence there is huge variations of Variance in the tumor portions as compared to the normal portions in the enhanced images of patient2. Also the means of the two portions have significantly high difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.11(c) and 5.11(d) show the box-plot comparison of the Variance between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.11(c)) is 65%. Hence the Variance is able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.11(d)) is 81%. Hence the Variance is able to differentiate between the two portions in the enhanced images of patient2.

5.11.3 Overall comparison of variance

Table5.11.3 show the mean, variance minimum and the maximum values of the combined values of Variance of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	26.0272	31.2018	36.0236	42.4693
Variance	22.9924	9.1045	1.6314	27.7840
Min	21.5996	24.6227	32.0096	31.2304
Max	32.7796	35.7046	38.0962	48.7537

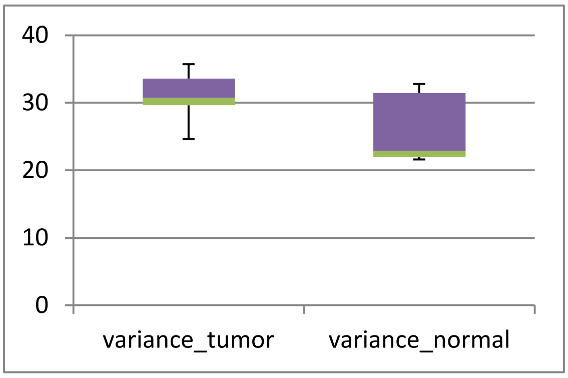


Figure5.11(e)

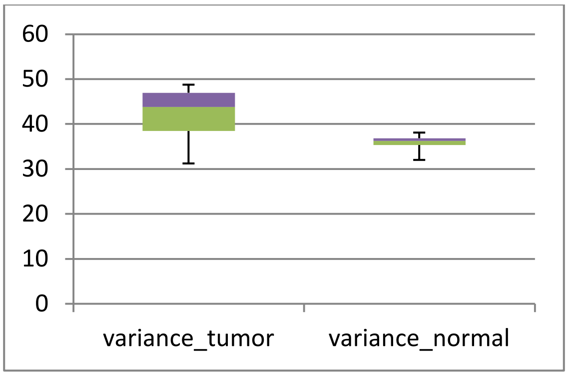


Figure5.11(f)

Above box-plots compares the overall variance for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.11(e) and enhanced images Figure5.11(f).

In original images

The mean of Variance for the normal portions and the tumor portions of the original images is 26.0272 and 31.2018 with a variance of 22.9924 and 9.1045 respectively. Hence the data clearly suggests huge variations of Variance in the normal portions as compared to the tumor portions of the original images of patient1 and patient2. Also the means of the two portions have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.11(e) show the box-plot comparison of the Variance between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.11(e)) is 68%. Hence the Variance is able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of Variance for the normal portions and the tumor portions of the enhanced images is 36.0236 and 42.4693 with a variance of 1.6314 and 27.7840 respectively. Hence the data clearly suggests high variations of Variance in the tumor portions as compared to the normal portions of the enhanced images of patient1 and patient2. Also the means of the two portions have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.11(f) show the box-plot comparison of the Variance between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.11(f)) is 65%. Hence the Variance is able to differentiate between the two portions in the enhanced images of patient1 and 2 .

5.12 Sum average

Table5.12.1 show the values of sum average of the normal and the tumor portions of patient1

Patient1	Original images		Enhanced images	
	Normal	Tumor	Normal	Tumor
Patient1_1	11.3983	10.8035	12.0851	11.6476
Patient1_2	11.3217	10.6626	11.9792	11.1337
Patient1_3	10.7183	10.8591	11.8142	11.9722
Patient1_4	11.3513	10.9704	12.309	12.0295
Patient1_5	11.1722	11.6557	11.651	13.4601
Patient1_6	11.2783	11.5165	11.9149	12.9236
Patient1_7	11.0939	11.1739	12.1528	13.125
Patient1_8	11.0383	10.9165	11.8108	11.0503
Patient1_9	11.3617	10.8661	11.184	11.5955
Patient1_10	11.1913	11.2504	11.783	13.0347
Patient1_11	11.2991	11.1548	12.0868	12.4765
Patient1_12	11.4417	11.5739	12.0799	12.8715
mean	11.2221	11.1169	11.9042	12.2766
variance	0.0401	0.1069	0.0856	0.6664
min	10.7183	10.6626	11.184	11.0503
max	11.4417	11.6557	12.309	13.4601

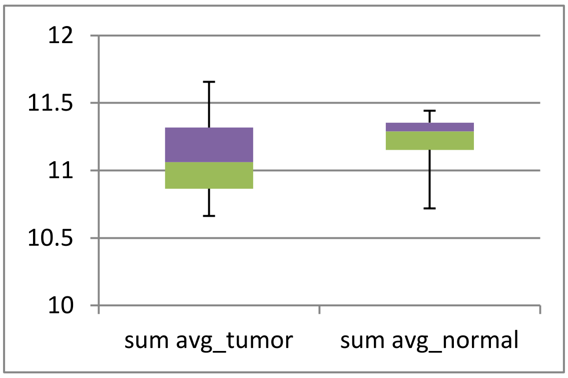


Figure5.12(a)

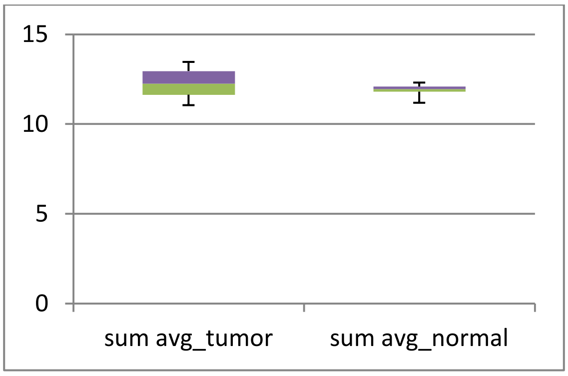


Figure5.12(b)

Above box-plot compares sum average for the tumor and the normal portion of the original Figure5.12(a) and enhanced images Figure5.12(b) of patient1.

5.12.1 Sum average comparison for Patient1

The mean of sum average for the normal and the tumor portions in the original images of patient1 is 11.2221 and 11.1169 with a variance of 0.0401 and 0.1069 respectively. Hence there are not much variations of sum average in the tumor portion or the normal portions of the original images of patient1. But the means of the two portions do not have significant difference.

The mean of sum average for the normal and the tumor portions in the enhanced images of patient1 is 11.9042 and 12.2766 with a variance of 0.0856 and 0.6664 respectively. Hence there is much variations of sum average in the tumor portions as compared to the normal portions in the enhanced images of patient1. Also the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.12(a) and 5.12(b) show the box-plot comparison of the sum average between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.12(a)) is 46%. Hence the sum average slightly differentiate the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.12(b)) is 23%. Hence the sum average individually is not able to differentiate between the two portions in the enhanced images of patient1.

Sum average in patient1 images do not have a good differentiability factor in both the original and the enhanced version of the images. We observe that the differentiability factor decreases as we enhance the images but the variations in the tumor portions increase. Further more the difference in the means also increases as compared to the difference in the original images which was very less. Hence we observe improvement in sum average after enhancement of images.

Table5.12.2 show the values of sum average for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	9.447	9.913	11.6962	12.2969
Patient2_2	9.5809	10.1374	11.6198	12.2309
Patient2_3	9.3583	10.1739	11.6528	12.7896
Patient2_4	9.407	10.4591	12.0642	13.0434
Patient2_5	9.28	10.7791	11.7448	13.4201
Patient2_6	9.3183	10.9809	12.0226	13.5243
Patient2_7	9.2922	11.0122	11.9653	13.3681
Patient2_8	9.313	11.0417	11.9878	13.4522
Patient2_9	9.2922	11.2087	11.9184	13.6944
Patient2_10	9.3061	11	11.8472	13.5295
Patient2_11	9.5478	11.4087	11.7587	13.7309
Patient2_12	9.2713	11.8017	11.7899	13.7135
Patient2_13	9.4243	11.6157	11.9757	13.8056
Patient2_14	9.3791	11.6887	11.9618	13.9253
Patient2_15	9.3843	11.7948	12.2691	13.8021
Patient2_16	9.4643	11.7148	12.2153	13.6372
Patient2_17	9.6035	11.7374	12.0955	13.651
mean	9.3923	11.0863	11.9167	13.3891
variance	0.0113	0.3886	0.0358	0.2583
min	9.2713	9.913	11.6198	12.2309
max	9.6035	11.8017	12.2691	13.9253

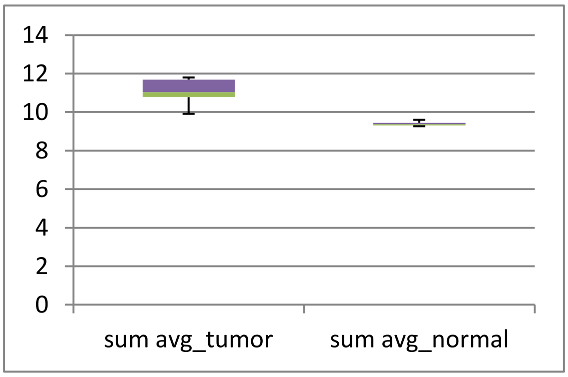


Figure5.12(c)

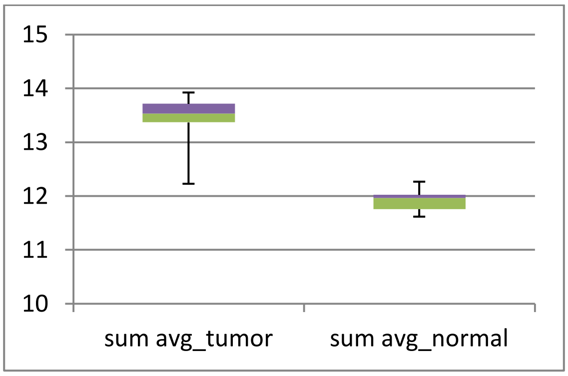


Figure5.12(d)

Above box-plot compares sum average for the tumor and the normal portion of the original Figure 5.12(c) and the enhanced images Figure5.12(d) of patient2

5.12.2 Sum average comparison for Patient2

The mean of sum average for the normal and the tumor portions in the original images of patient2 is 9.3923 and 11.0863 with a variance of 0.0113 and 0.3886 respectively. Hence there are high variations of sum average in the tumor portions as compared to the normal portions of the original images of patient2. Also the means of the two portions have slight difference.

The mean of sum average for the normal and the tumor portions in the enhanced images of patient2 is 11.9167 and 13.3891 with a variance of 0.0358 and 0.2583 respectively. Hence there is high variations of sum average in the tumor portions as compared to the normal portions in the enhanced images of patient2. Also the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.12(c) and 5.12(d) show the box-plot comparison of the sum average between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.12(c)) is 70%. Hence the sum average is able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.12(d)) is 80%. Hence the sum average is able to differentiate between the two portions in the enhanced images of patient2.

5.12.3 Overall comparison of sum average

Table5.12.3 show the mean, variance minimum and the maximum values of the combined values of sum average of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	10.1495	11.0990	11.9115	12.9288
Variance	0.8634	0.2643	0.0541	0.7203
Min	9.2713	9.913	11.184	11.0503
Max	11.4417	11.8017	12.309	13.9253

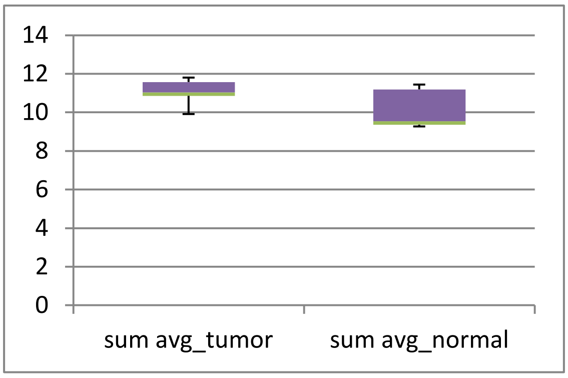


Figure5.12(e)

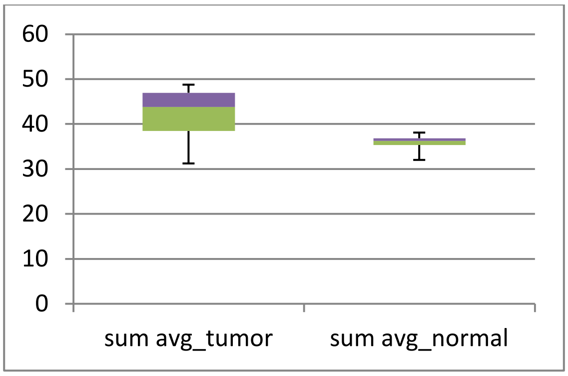


Figure5.12(f)

Above box-plots compares the overall sum average for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.12(e) and enhanced images Figure5.12(f).

In original images

The mean of sum average for the normal portions and the tumor portions of the original images is 10.1495 and 11.0990 with a variance of 0.8634 and 0.2643 respectively. Hence the data clearly suggests high variations of sum average in the normal portions as compared to the tumor portions of the original images of patient1 and patient2. Also the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.12(e) show the box-plot comparison of the sum average between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.12(e)) is 67%. Hence the sum average is able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of sum average for the normal portions and the tumor portions of the enhanced images is 11.9115 and 12.9288 with a variance of 0.0541 and 0.7203 respectively. Hence the data clearly suggests high variations of sum average in the tumor portions as compared to the normal portions of the enhanced images of patient1 and patient2. Also the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.12(f) show the box-plot comparison of the sum average between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.12(f)) is 74%. Hence the sum average is able to differentiate between the two portions in the enhanced images of patient1 and 2.

5.13 Sum variance

Table5.13.1 show the values of sum variance for the normal and the tumor portions of patient1

Patient1	Original images		Enhanced images	
	Normal	Tumor	Normal	Tumor
Patient1_1	109.8039	96.7407	113.737	98.8826
Patient1_2	107.3208	96.5333	109.6789	88.4141
Patient1_3	95.1778	98.0388	105.8921	105.7125
Patient1_4	108.6475	99.3162	118.4208	108.7255
Patient1_5	103.8707	116.1215	101.364	140.0479
Patient1_6	106.5147	112.4283	107.7894	124.8062
Patient1_7	101.3196	103.1928	112.4015	132.8464
Patient1_8	100.336	98.0916	103.7341	86.3649
Patient1_9	109.073	97.2139	88.7372	96.102
Patient1_10	103.5148	101.4937	102.9414	125.6317
Patient1_11	106.536	102.967	112.7034	115.7325
Patient1_12	111.3192	115.9454	111.0361	127.2402
mean	105.2861	103.1736	107.3696	112.5422
variance	21.5650	55.2134	59.4215	318.3879
min	95.1778	96.5333	88.7372	86.3649
max	111.3192	116.1215	118.4208	140.0479

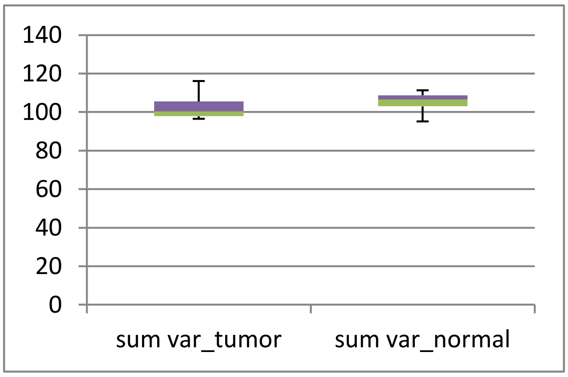


Figure5.13(a)

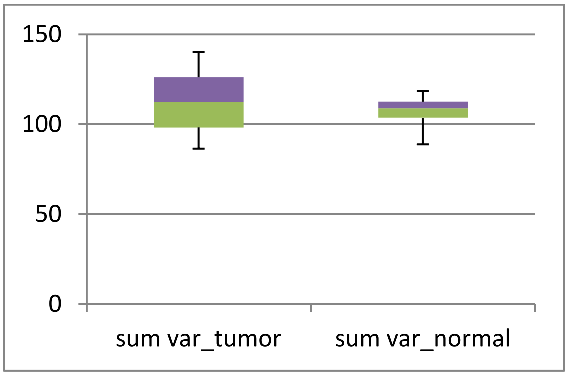


Figure5.13(b)

Above box-plot compares sum variance for the tumor and the normal portion of the original Figure5.13(a) and enhanced images Figure5.13(b) of patient1.

5.13.1 Sum variance comparison for Patient1

The mean of sum variance for the normal and the tumor portions in the original images of patient1 is 105.2861 and 103.1736 with a variance of 21.5650 and 55.2134 respectively. Hence there are high variations of sum variance in the tumor portion as compared to the normal portions of the original images of patient1. Also the means of the two portions have slight difference.

The mean of sum variance for the normal and the tumor portions in the enhanced images of patient1 is 107.3696 and 112.5422 with a variance of 59.4215 and 318.3879 respectively. Hence there are high variations of sum variance in the tumor portions as compared to the normal portions in the enhanced images of patient1. Also the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.13(a) and 5.13(b) show the box-plot comparison of the sum variance between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.13(a)) is 56%. Hence the sum variance slightly differentiate the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.13(b)) is 13%. Hence the sum variance individually is not able to differentiate between the two portions in the enhanced images of patient1.

The sum variance in the patient1 images show huge amount of variation especially in the tumor portion. We observe that after enhancement these variation increase even more. But the differentiability factor decreases. We also observe that the means of sum variance is more in normal portions in the original images. But after enhancement the increase in mean and is less in normal portion and more in tumor portion. This is due to huge amount of variation created by enhancement. Also the maximum and the minimum values in the table suggest the same.

Table5.13.2 show the values of sum variance for the normal and the tumor portions of patient2

Patient2	Original images		Enhanced images	
	Normal	Tumor	Normal	Tumor
Patient2_1	72.2168	81.6571	99.8546	114.7539
Patient2_2	76.3007	85.0519	97.783	111.4069
Patient2_3	70.4685	81.6055	99.8061	128.331
Patient2_4	70.9522	84.0048	108.6141	131.1518
Patient2_5	68.1977	91.0406	100.5264	141.7608
Patient2_6	69.228	92.5481	107.1964	144.4924
Patient2_7	67.9635	94.7859	105.4379	141.2944
Patient2_8	69.3893	94.8187	105.628	143.3406
Patient2_9	68.8031	95.5768	104.2273	150.776
Patient2_10	68.7801	93.7632	104.336	142.9287
Patient2_11	75.2184	99.281	102.692	148.4649
Patient2_12	68.3262	103.6724	102.0357	143.6249
Patient2_13	71.9605	97.6532	105.9969	150.2958
Patient2_14	70.613	97.4875	104.68	153.1147
Patient2_15	70.5224	104.4757	112.0252	148.937
Patient2_16	72.9553	100.0913	110.9277	142.9872
Patient2_17	77.0117	98.3059	108.2099	141.8151
mean	71.1122	93.8717	104.7045	139.9691
variance	8.0261	50.7936	15.8487	142.8168
min	67.9635	81.6055	97.783	111.4069
max	77.0117	104.4757	112.0252	153.1147

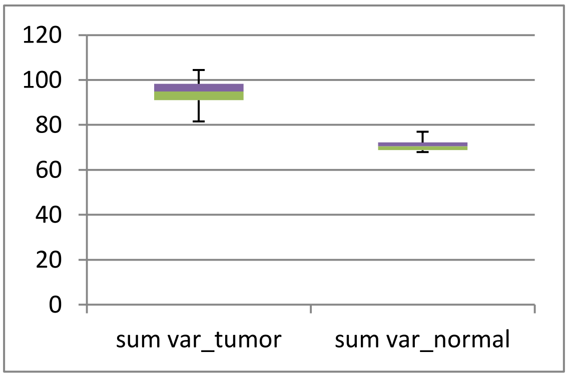


Figure5.13(c)

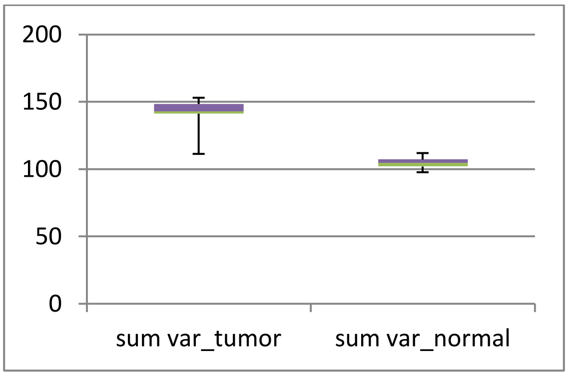


Figure5.13(d)

Above box-plot compares sum variance for the tumor and the normal portion of the original Figure5.13(c) and enhanced images Figure5.13(d) of patient2

5.13.2 Sum variance comparison for Patient2

The mean of sum variance for the normal and the tumor portions in the original images of patient2 is 71.1122 and 93.8717 with a variance of 8.0261 and 50.7936 respectively. Hence there are high variations of sum variance in the tumor portions as compared to the normal portions of the original images of patient2. Also the means of the two portions have significantly high difference.

The mean of sum variance for the normal and the tumor portions in the enhanced images of patient2 is 104.7045 and 139.9691 with a variance of 15.84870 and 142.8168 respectively. Hence there are high variations of sum variance in the tumor portions as compared to the normal portions in the enhanced images of patient2. Also the means of the two portions have significantly high difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.13(c) and 5.13(d) show the box-plot comparison of the sum variance between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.13(c)) is 82%. Hence the sum variance is able to differentiate between the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.13(d)) is 83%. Hence the sum variance is able to differentiate between the two portions in the enhanced images of patient2.

5.13.3 Overall comparison of sum variance

Table5.13.3 show the mean, variance minimum and the maximum values of the combined values of sum variance of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	85.2531	97.7207	105.8073	128.6200
Variance	306.4616	72.4536	34.1850	395.6766
Min	67.9635	81.6055	88.7372	86.3649
Max	111.3192	116.1215	118.4208	153.1147

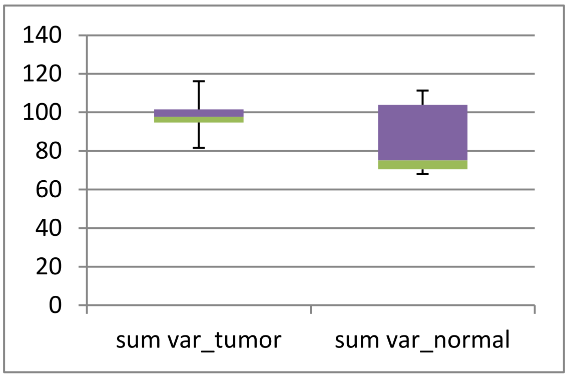


Figure5.13(e)

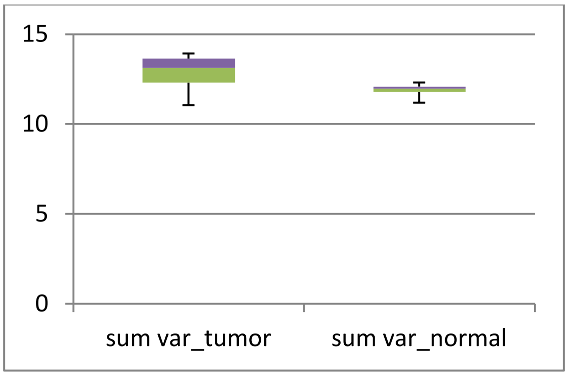


Figure5.13(f)

Above box-plots compares the overall sum variance for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.13(e) and enhanced images Figure5.13(f).

In original images

The mean of sum variance for the normal portions and the tumor portions of the original images is 85.2531 and 97.7207 with a variance of 306.4616 and 72.4536 respectively. Hence the data clearly suggests high variations of sum variance in the normal portions as compared to the tumor portions of the original images of patient1 and patient2. Also the means of the two portions have significantly high difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.13(e) show the box-plot comparison of the sum variance between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.13(e)) is 67%. Hence the sum average is able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of sum variance for the normal portions and the tumor portions of the enhanced images is 105.8073 and 128.62 with a variance of 34.1850 and 395.6766 respectively. Hence the data clearly suggests high variations of sum variance in the tumor portions as compared to the normal portions of the enhanced images of patient1 and patient2. Also the means of the two portions have significantly high difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.13(f) show the box-plot comparison of the sum variance between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.13(f)) is 67%. Hence the sum average is able to differentiate between the two portions in the enhanced images of patient1 and 2 .

5.14 Sum entropy

Table5.14.1 show the values of sum entropy of the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1 1	0.9503	1.0081	1.4782	1.8456
Patient1 2	0.9952	0.8778	1.5782	1.8895
Patient1 3	0.9997	0.9997	1.5973	1.8229
Patient1 4	0.9614	1.0455	1.4839	1.708
Patient1 5	1.0195	0.9109	1.6704	1.7195
Patient1 6	0.9936	0.9443	1.6132	1.9022
Patient1 7	1.0661	1.0521	1.6312	1.7013
Patient1 8	1.0609	1.0541	1.7252	1.9062
Patient1 9	0.9514	1.0478	1.9098	1.9567
Patient1 10	1.0528	1.2333	1.7405	1.9882
Patient1 11	1.0108	1.0471	1.5336	1.8346
Patient1 12	0.9201	0.8304	1.6309	1.6792
mean	0.9984	1.0042	1.6327	1.8294
variance	0.0021	0.0110	0.0144	0.0111
min	0.9201	0.8304	1.4782	1.6792
max	1.0661	1.2333	1.9098	1.9882

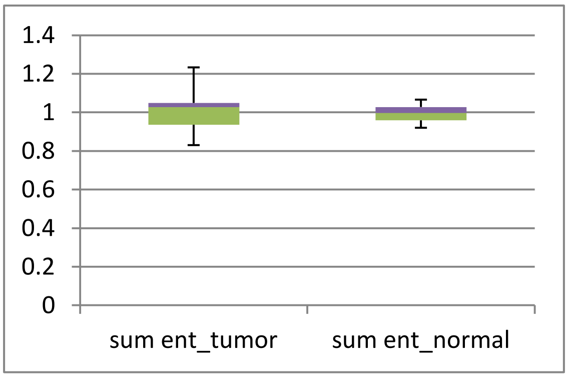


Figure5.14(a)

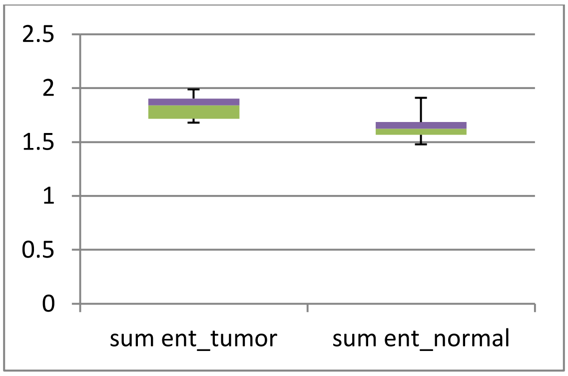


Figure5.14(b)

Above box-plot compares sum entropy for the tumor and the normal portion of the original Figure5.14(a) and the enhanced images Figure5.14(b) of patient1.

5.14.1 Sum entropy comparison for Patient1

The mean of sum entropy for the normal and the tumor portions in the original images of patient1 is 0.9984 and 1.0042 with a variance of 0.0021 and 0.011 respectively. Hence the data clearly suggests not much variation of sum entropy in the tumor portion or the normal portions of the original images of patient1. Also the means of the two portions do not have significant difference.

The mean of sum entropy for the normal and the tumor portions in the enhanced images of patient1 is 1.6327 and 1.8284 with a variance of 0.0144 and 0.0111 respectively. Hence the data clearly suggests not much variations of sum entropy in the tumor portion or the normal portions in the enhanced images of patient1. Also the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.14(a) and 5.14(b) show the box-plot comparison of the sum entropy between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.14(a)) is 26%. Hence the sum entropy individually is not able to differentiate the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.14(b)) is 65%. Hence the sum entropy is able to differentiate between the two portions in the enhanced images of patient1.

The sum entropy in patient 1 show a significant amount of improvement in terms of differentiability after enhancement. The difference in the means of the two portions in the original images is not significant but after enhancement it show improvement and also the difference between them also slightly increases. This leads to increase in differentiability factor from 26% to 65 %. Hence sum entropy can be used in original images but can be used in enhanced images to differentiate between both the portions.

Table5.14.2 show the values of sum entropy for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	0.9776	0.9063	1.8283	1.6898
Patient2_2	0.8694	0.9422	1.861	1.8077
Patient2_3	0.9953	1.1914	1.7688	1.5713
Patient2_4	1.0147	1.3547	1.7412	1.6959
Patient2_5	1.0568	1.2883	1.8458	1.584
Patient2_6	1.0296	1.4243	1.781	1.5723
Patient2_7	1.0825	1.3327	1.8124	1.5775
Patient2_8	1.0152	1.3541	1.8247	1.5638
Patient2_9	1.0328	1.5022	1.8298	1.4829
Patient2_10	1.0453	1.3723	1.731	1.6514
Patient2_11	0.8999	1.517	1.7237	1.6175
Patient2_12	1.0407	1.7338	1.8024	1.8739
Patient2_13	0.9683	1.8803	1.7842	1.6474
Patient2_14	1.008	2.0097	1.8499	1.6473
Patient2_15	1.0177	1.6819	1.7892	1.6982
Patient2_16	0.9486	1.8647	1.7844	1.7817
Patient2_17	0.8502	2.0156	1.8035	1.9616
mean	0.9913	1.4924	1.7977	1.6720
variance	0.0043	0.1116	0.0016	0.0153
min	0.8502	0.9063	1.7237	1.4829
max	1.0825	2.0156	1.861	1.9616

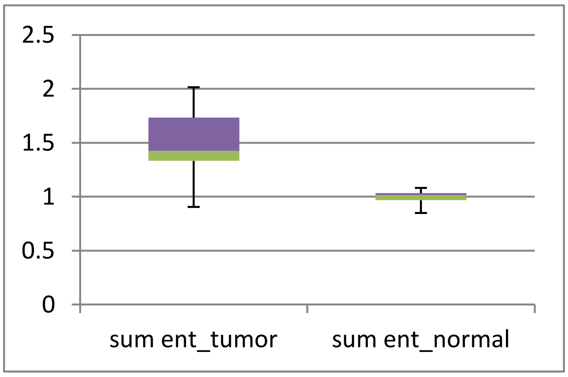


Figure5.14(c)

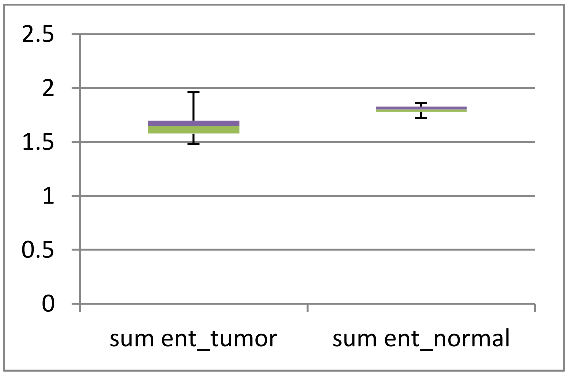


Figure5.14(d)

Above box-plot compares sum entropy for the tumor and the normal portion of the original Figure5.14(c) and enhanced images Figure5.14(d) of patient2.

5.14.2 Sum entropy comparison for Patient2

The mean of sum entropy for the normal and the tumor portions in the original images of patient2 is 0.9913 and 1.4924 with a variance of 0.0043 and 0.1116 respectively. Hence there are high variations of sum entropy in the tumor portions as compared to the normal portions of the original images of patient2. Also the means of the two portions have slight difference.

The mean of sum entropy for the normal and the tumor portions in the enhanced images of patient2 is 1.7977 and 1.6720 with a variance of 0.0016 and 0.0153 respectively. Hence the data clearly suggests not much variation of sum entropy in the tumor portion or the normal portions in the enhanced images of patient2. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.14(c) and 5.14(d) show the box-plot comparison of the sum entropy between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.14(c)) is 54%. Hence the sum entropy slightly differentiate the two portions in the original images of patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.14(d)) is 62%. Hence the sum entropy slightly differentiate the two portions in the enhanced images of patient2.

5.14.3 Overall comparison of sum entropy

Table5.14.3 show the mean, variance minimum and the maximum values of the combined values of sum entropy of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.9942	1.2904	1.7294	1.7371
Variance	0.0033	0.1280	0.0134	0.0193
Min	0.8502	0.8304	1.4782	1.4829
Max	1.0825	2.0156	1.9098	1.9882

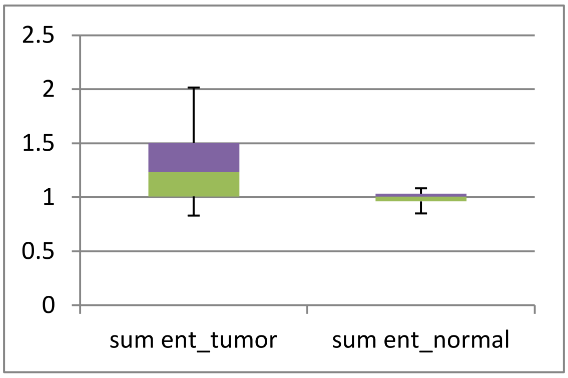


Figure5.14(e)

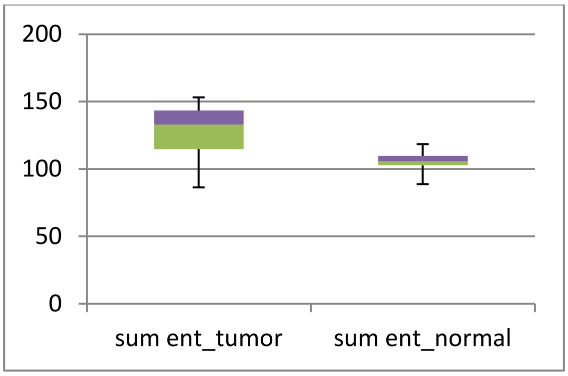


Figure5.14(f)

Above box-plots compares the overall sum entropy for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.14(e) and enhanced images Figure5.14(f).

In original images

The mean of sum entropy for the normal portions and the tumor portions of the original images is 0.9942 and 1.2904 with a variance of 0.0033 and 0.1280 respectively. Hence the data clearly suggests more variations of sum entropy in the tumor portions as compared to the normal portions of the original images of patient1 and patient2. Also the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.14(e) show the box-plot comparison of the sum entropy between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.14(e)) is 42%. Hence the sum entropy slightly differentiate the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of sum entropy for the normal portions and the tumor portions of the enhanced images is 1.7294 and 1.7371 with a variance of 0.0134 and 0.0193 respectively. Hence the data clearly suggests not much variations of sum entropy in the tumor portions or the normal portions of the enhanced images of patient1 and patient2. Also the means of the two portions do not have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.14(f) show the box-plot comparison of the sum entropy between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.14(f)) is 31%. Hence the sum entropy individually is not able to differentiate between the two portions in the enhanced images of patient1 and 2 .

5.15 Difference entropy

Table5.15.1 show the values of difference entropy for the normal and the tumor portions of patient1

Patient1	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient1_1	0.498	0.4566	0.7763	0.7955
Patient1_2	0.5168	0.3154	0.7835	0.7555
Patient1_3	0.4906	0.422	0.7851	0.795
Patient1_4	0.4701	0.4831	0.7611	0.769
Patient1_5	0.4674	0.3704	0.7762	0.7354
Patient1_6	0.4753	0.4397	0.7055	0.7835
Patient1_7	0.5366	0.5366	0.786	0.7588
Patient1_8	0.5145	0.4753	0.8765	0.9054
Patient1_9	0.4593	0.4727	0.9975	0.9054
Patient1_10	0.5491	0.4425	0.8616	0.9106
Patient1_11	0.5324	0.4831	0.7612	0.815
Patient1_12	0.4856	0.4425	0.7532	0.7807
mean	0.4996	0.4449	0.8019	0.8091
variance	0.0008	0.0032	0.0058	0.0039
min	0.4593	0.3154	0.7055	0.7354
max	0.5491	0.5366	0.9975	0.9106

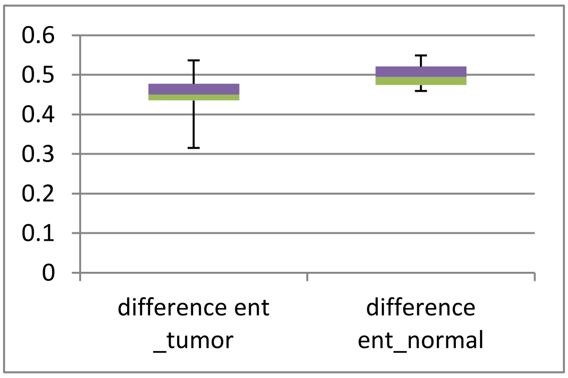


Figure5.15(a)

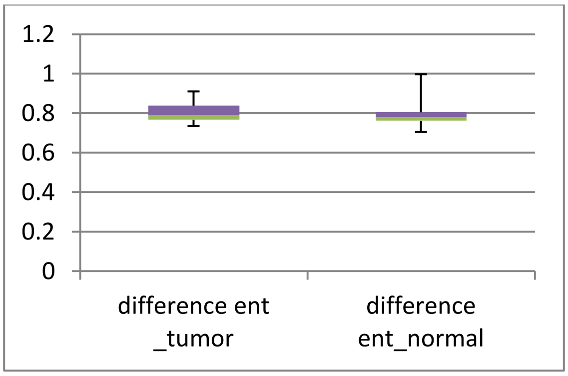


Figure5.15(b)

Above box-plot compares difference entropy for the tumor and the normal portion of the original Figure5.15(a) and the enhanced images Figure5.15(b) of patient1.

5.15.1 Difference entropy comparison for Patient1

The mean of difference entropy for the normal and the tumor portions in the original images of patient1 is 0.4996 and 0.4449 with a variance of 0.0008 and 0.0032 respectively. Hence the data clearly suggests not much variation of difference entropy in the tumor portion or the normal portions of the original images of patient1. Also the means of the two portions do not have significant difference.

The mean of difference entropy for the normal and the tumor portions in the enhanced images of patient1 is 0.8019 and 0.8091 with a variance of 0.0058 and 0.0039 respectively. Hence the data clearly suggests not much variations of difference entropy in the tumor portion or the normal portions in the enhanced images of patient1. Also the means of the two portions do not have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.15(a) and 5.15(b) show the box-plot comparison of the difference entropy between tumor and normal portions of the original and enhanced images of patient1 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.15(a)) is 52%. Hence the difference entropy slightly differentiate the two portions in the original images of patient1.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.15(b)) is 12%. Hence the difference entropy individually is not able to differentiate between the two portions in the enhanced images of patient1.

Difference entropy show a decreases in differentiability factor as we enhance the images. The mean of the two portions in original images is almost same also we can observe almost same amount of increase in mean in both the portions after enhancement. Also the variation in both the portions of original and enhanced images is very less. Hence difference entropy show very slight differentiability factor in the original images and a decrease in differentiability factor after enhancement of the image.

Table5.15.2 show the values of difference entropy for the normal and the tumor portions of patient2

Patient2	**Original images**		**Enhanced images**	
	Normal	**Tumor**	**Normal**	**Tumor**
Patient2_1	0.6416	0.5255	0.9882	1.0066
Patient2_2	0.593	0.5323	1.0266	1.1202
Patient2_3	0.6428	0.7081	1.0109	0.9092
Patient2_4	0.657	0.6338	0.94	0.9083
Patient2_5	0.6524	0.5978	1.009	0.8091
Patient2_6	0.667	0.6449	0.9322	0.7924
Patient2_7	0.6842	0.6379	0.9507	0.8348
Patient2_8	0.6573	0.6651	0.9688	0.8442
Patient2_9	0.6333	0.6791	0.9455	0.7609
Patient2_10	0.6678	0.6474	0.9749	0.8458
Patient2_11	0.6071	0.6743	0.9429	0.7303
Patient2_12	0.6548	0.6656	1.0176	0.8331
Patient2_13	0.6781	0.6525	0.8781	0.7387
Patient2_14	0.6357	0.7394	0.9982	0.7162
Patient2_15	0.6524	0.7045	0.9274	0.7505
Patient2_16	0.6619	0.7461	0.9335	0.8286
Patient2_17	0.6035	0.8263	0.9779	0.8567
mean	0.6464	0.6635	0.9660	0.8403
variance	0.0006	0.0053	0.0015	0.0107
min	0.593	0.5255	0.8781	0.7162
max	0.6842	0.8263	1.0266	1.1202

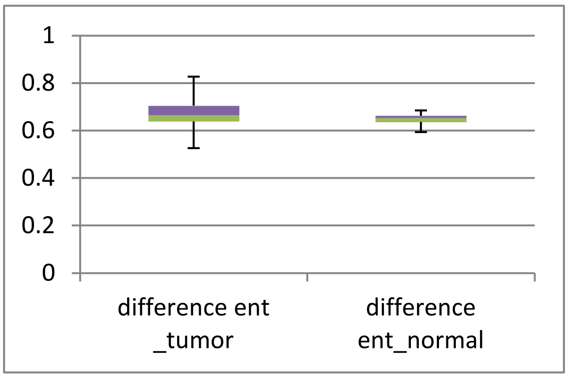


Figure5.15(c)

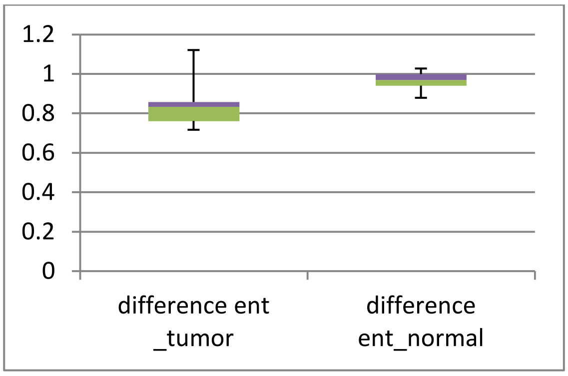


Figure5.15(d)

Above box-plot compares difference entropy for the tumor and the normal portion of the original Figure5.15(c) and enhanced images Figure5.15(d) of patient2 .

5.16.2 Difference entropy comparison for Patient2

The mean of diffrence entropy for the normal and the tumor portions in the original images of patient2 is 0.6464 and 0.6635 with a variance of 0.0006 and 0.0053 respectively. Hence the data clearly suggests not much variations of difference entropy in the tumor portion or the normal portions of the original images of patient2. Also the means of the two portions do not have significant difference.

The mean of difference entropy for the normal and the tumor portions in the enhanced images of patient2 is 0.9660 and 0.8403 with a variance of 0.0015 and 0.0107 respectively. Hence the data clearly suggests not much variations of difference entropy in the tumor portion or the normal portions in the enhanced images of patient2. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.15(c) and 5.15(d) show the box-plot comparison of the difference entropy between tumor and normal portions of the original and enhanced images of patient2 respectively.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images(Figure5.15(c)) is 18%. Hence the difference entropy individually is not able to differentiate between the two portions in the original images patient2.

On the other hand Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images (Figure5.15(d)) is 57%. Hence the difference entropy slightly differentiate the two portions in the enhanced images patient2.

5.15.3 Overall comparison of difference entropy

Table5.14.3 show the mean, variance minimum and the maximum values of the combined values of difference entropy of patent1 and patient2

Combined data of patient1 and patient2	Original image		Enhanced images	
	Normal portion	Tumor portion	Normal portion	Tumor portion
Mean	0.5857	0.5731	0.8981	0.8274
Variance	0.0061	0.0163	0.0099	0.0079
Min	0.4593	0.3154	0.7055	0.7162
Max	0.6842	0.8263	1.0266	1.1202

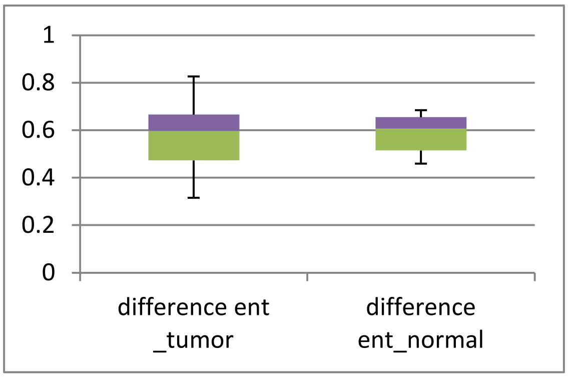


Figure5.15(e)

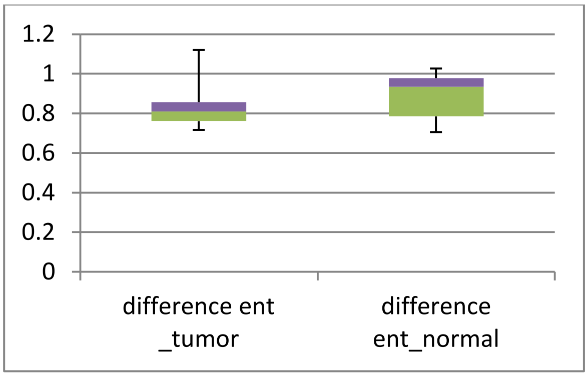


Figure5.15(f)

Above box-plots compares the overall difference entropy for the tumor and normal portions of patient1 and patient2 combined together from the original images Figure5.15(e) and enhanced images Figure5.15(f).

In original images

The mean of difference entropy for the normal portions and the tumor portions of the original images is 0.5857 and 0.5731 with a variance of 0.0061 and 0.0163 respectively. Hence the data clearly suggests not much variations of difference entropy in the tumor portions or the normal portions of the original images of patient1 and patient2. Also the means of the two portions do not have significant difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.16(e) show the box-plot comparison of the difference entropy between tumor and normal portions of the original images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the original images of patient1 and 2 together (Figure5.16(e)) is 5%. Hence the difference entropy individually is not able to differentiate between the two portions in the original images of patient1 and 2 .

In enhanced images

The mean of difference entropy for the normal portions and the tumor portions of the enhanced images is 0.8981 and 0.8274 with a variance of 0.0099 and 0.0079 respectively. Hence the data clearly suggests not much variations of difference entropy in the tumor portions or the normal portions of the enhanced images of patient1 and patient2. But the means of the two portions have slight difference.

For more conclusive comparison we study the box-plot comparison of both the portions. Figure 5.16(f) show the box-plot comparison of the difference entropy between tumor and normal portions of the enhanced images of patient1 and 2 together.

Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) for the box-plot of the enhanced images of patient1 and 2 together (Figure5.16(f)) is 57%. Hence the difference entropy slightly differentiate the two portions in the enhanced images of patient1 and 2.

5.16 Summary of all the parameters for patient1 and patient2

Table 5.16.1 show Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) of all the parameters for patient1 and 2

Parameter	**Patient1**		**Patient2**	
	Original images	**Enhanced images**	**Original images**	**Enhanced images**
Autocorrelation	46%	25%	65%	77%
Contrast	51%	12%	7%	62%
Correlation	47%	77%	69%	47%
Cluster prominence	14%	69%	25%	48%
Dissimilarity	51%	9%	10%	73%
Energy	13%	59%	49%	78%
Entropy	8%	61%	52%	80%
Homogeneity	51%	5%	8%	78%
Maximum probability	32%	62%	67%	83%
Variance	46%	26%	65%	81%
Sum average	46%	23%	70%	80%
Sum variance	56%	13%	82%	83%
Sum entropy	26%	65%	54%	62%
Difference entropy	52%	12%	18%	57%

Table 5.16.2 show Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) parameter for original and enhanced images

Parameters	**Original images**	**Enhanced images**
Autocorrelation	67%	62%
Contrast	6%	65%
Correlation	75%	63%
Cluster prominence	41%	46%
Dissimilarity	6%	68%
Energy	4%	53%
Entropy	27%	58%
Homogeneity	7%	62%
Maximum probability	29%	58%

Variance	68%	65%
Sum average	67%	74%
Sum variance	67%	67%
Sum entropy	42%	31%
Difference entropy	5%	57%

5.17 Classification of the parameters using SVM classifier

Let us define classes to the parameters according to their Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS).

1 Let Class A be the parameters which have Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) less than 40%..
2 Class B be the parameters which have Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) greater than 40% but less than 65%.
3 Class C be the parameters which have Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) greater than equal to 65%.

Hence the parameters which will be in Class C are the parameters which are able to differentiate between normal and the tumor portion. Class B parameters are those parameters which slightly differentiate between the two portion. Class A parameters are those which individually are not able to differentiate between both the portions.

Table 5.17.1 show the classes defined on the basis of Distance Between Medians (DBM) as a percentage of Overall Visible Spread (OVS) parameter.

Classes	Original images	Enhanced images
Class A	Contrast, dissimilarity, energy, entropy, homogeneity, maximum probability, difference entropy	Sum entropy
Class B	Cluster prominence, sum entropy	Autocorrelation, correlation, Cluster prominence, energy, entropy, homogeneity, maximum probability, difference entropy
Class C	Autocorrelation, correlation, variance, sum average, sum variance	Contrast, dissimilarity, variance, sum average, sum variance

5.18 Classification results using SVM classifier

The classification was performed on all the classes defined in sec 5.17. The two categories or labels in which the data was classified were the tumor and the normal portions. approximately 40% of the feature value were given for training of the SVM classifier in which 50 % of the values were of patien1 and rest 50% of patient2. This was done to generalize the results. Giving proper data for training tends to give better accuracy to the classifier, hence better classification of the test data is the result.

Table 5.18.1 show the overall results obtained from the SVM classifier.

Classes	**Training data**	**Testing data**	**Number of features**	**linear**	**quadratic**	**Polynomial (order=3)**	**Rbf σ=1**	**Rbf σ=0.1**
Class A	192	306	8	88.23%	88.23%	88.23%	88.23%	50%
Class B	240	340	10	97.05%	88.23%	88.23%	100%	52.94%
Class C	240	340	10	94.11%	97.05%	82.35%	94.11%	61.76%
Class A + Class B	432	612	18	97.05%	91.17%	97.05%	85.29%	50%
Class B + Class C	480	680	20	94.11%	82.35%	85.29%	91.17%	50%
Class A + Class C	432	612	18	55.88%	76.47%	91.17%	50%	50%
Class A + Class B+ Class C	672	952	28	100%	97.05%	100%	82.35%	50%

5.18.1 Overall discussion for the results obtained from SVM classifier

In table 5.18.1 results for the classification of different classes defined in the sec5.17 are shown. Different kernels were used for the classifications. The results with polynomial kernel were also evaluated with order greater than 3 but the accuracy of the classifier decreased significantly for all the classes and after order 9 the classifier showed no convergence. The results with rbf kernel were also evaluated for σ=0.01 and lower but the accuracy of the classifier decreases.

Let us discuss the results for class C value first. For class C parameter values the best results were obtained by SVM classifier with polynomial order=2 kernel or the quadratic kernel. The accuracy of classification classification was 97.05%. On the hand The rbf kernel with σ=0.1 produced a accuracy of just 61.76% which was lowest for this class. According to box-plot study the class C parameters were able to differentiate between the two portions(normal and the tumor portions). Hence the results are satisfactory.

Class B parameter value were best classified by rbf kernel with σ =1. The accuracy of the classification was 100%. Other kernels such as linear, quadratic, and polynomial produced satisfactory results but Rbf kernel with σ=0.1 produced the worst results of just

52.94% accuracy. According to box-plot study the class B parameters slightly differentiated between both the portions(normal and the tumor portions). Conversely SVM classifies these parameters with 100% accuracy which is even better than class C . Hence SVM classifier with rbf kernel(σ =1) was able to find a decision boundary in higher infinite dimensional space which was able divide these values into normal and tumor portions. here we say infinite dimension space because at σ =1 the feature space of rbf kernel has infinite number of dimensions.

Class A parameters were classified with a accuracy of 88.23% by all the kernels except for rbf kernel with σ =0.1 which produced a classification with a accuracy of just 50 %. According to box-plot study class A parameters were the parameters which individually were not able to differentiate between the two portions(normal and tumor portion). Due to this class A show the lowest classification accuracy between all the classes.

When we fed the whole set of data i.e. class A + class B + class C we observe 100% accuracy of classification using SVM linear and polynomial order=3 kernels. This shows that the data in the whole set can be classified between normal and the tumor portions without any error. These results show that SVM was able to find a decision boundary for the whole data in the sample space as well as high dimensional feature space.

Further more we have used the combination of two classes to be fed to the SVM classifier. The accuracy for class A + class B was best in all of the two class combinations. This set of data was best classified by linear and polynomial order=3 kernel with a 97.05% accuracy. It is to be noted that the accuracy of the classifier does not depends on the individual accuracy of the classes. The accuracy of the SVM classifier depends on the how well training data helps in training the classifier. Class B + class C data was best classified by linear kernel with a accuracy of 94.11% and class A + class C data was best classified by polynomial kernel of order=3. further we observe that the worst results were produced by rbf kernel with σ =0.1 and as we decrease the value of rbf sigma(σ) the accuracy decreases further for all the classes and combination of classes.

Chapter 6 Conclusion And Future Scope

6.1 Conclusion

In this study we have calculated the texture parameters for the tumor and the normal portions of both the original and the enhanced versions of CT scan images. On the basis of the values of texture parameters, box-plots comparing the normal and the tumor portions were constructed. A comparison was made on the basis of difference between medians as a percentage of overall visible spread which was calculated for all the box-plots. Further the whole data of texture parameter values of both the portions in original and enhanced images was divided into three classes which were defined on the basis of distance between medians as a percentage of overall visible spread of the box-plots. These classes were fed to a SVM classifier individually, in combination of two and the overall data. the results were obtained using various kernel functions.

We can conclude that by better training of a SVM classifier we can classify the data into normal and tumor portions even if the data is not much distinguishing in the sample space. The box-plot comparison showed us that the data in class A was not able to differentiate between the tumor and the normal portions, still SVM classifier with the help of different kernel functions produced a distinguishing hyperplane which classified the data with high accuracy. The problem here is the selection of kernel function. Lots of research is going on this problem but a generalized kernel function for a particular task is not know yet.

Further on the basis of our study we can say that a computer aided diagnostic(CAD) system can diagnose a tumor using statistical texture parameters and SVM classifier. Parameters in class B, such as Cluster prominence and sum entropy for the original image and Autocorrelation, correlation, Cluster prominence, energy, entropy, homogeneity, maximum probability, and difference entropy in the enhanced images had the best feature values that were classified by SVM and hence can be used to diagnose tumors in a CAD system.

6.2 Future scope

In this thesis we used texture parameters to discriminate between the tumor and the normal portions of a CT scan image. Features of class A produced lesser accuracy in classification as compared to features in class B and class C. Further enhancement of the CT images may improve the discrimination factor in these features.

Further the number of images and the number of patient used in our study were lesser. To get more accurate discrimination factor and better classification more number of images from several patients must be used. This will help in providing better training to classifier because larger is the training vector better will be classification.

Only tumor portions from the abdominal CT scan were used in this study. Images from other body parts such as lungs can also be investigated. Further more medical images other than CT scan can also be subjected to this analysis.

In this thesis we have divided the data into three classes on the basis of a discrimination factor called the distance between median of the box-plots as a percentage of overall visible spread. More classes can be produced from the data by reducing the boundaries of the classes which were defined by this discrimination factor.

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