Tumor Identification from X-Ray Images Using SVM Kernels

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Abstract -Image Processing has become one of the most emerging domains in the medical field. There are many different types of imaging methods like CT scans, X-Ray and MRI. X-Ray is a low-priced imaging technique when compared with other imaging techniques. These techniques allow us to identify the tumor in human body. The sole aim of this project is to extract useful information from the X-Ray images obtained from the patient using feature extraction by Single Value Decomposition (SVD) and classify it using GURLs (Grand Unified Regularized Least Squares) and Lib-SVM (Library for Support Vector Machine). The process of detecting tumor from X-Ray can be classified into four different categories: Pre-Segmentation, Feature Extraction Processing, and *Classification. The primary goal of this paper is to detect the* presence of tumors and improve the efficiency using different kernels.

Key Words: Feature Extraction, SVD, GURLS, Lib-SVM, Classification.

1. INTRODUCTION

Tumor is a swelling which occurs in any part of the body, caused by an abnormal growth of tissue. Tumor is generally without inflammation which may be benign or malignant. It has a slow growth rate. Cancerous tumors are malignant and is life threatening. They are difficult to identify because it is time consuming and incurs high cost for other imaging techniques. X-Ray image is obtained by passing a beam of X-Rays onto the body parts of the person and a shadow image is obtained. As bones do not allow X-rays to pass through them, a clear image of the bones are obtained in white shades whereas the body tissues appear in different shades of grey. Based on the grey taints, tumors are identified. So, X-Ray is one among the many medical imaging techniques which involve less time and cost.

1.1 GURLS

GURLs is a new algorithm for recursive RLS. It is a least square, software library which is used for the processing of multiple output problems. It uses the RLS method for classification and regression. GURLS is available in C++ and MATLAB. It has an advantage of memory mapped storage and distribution task architecture. The main advantages of GURLs when dealing with large datasets include:

- Increase in system performance
- Low computation cost

These advantages play a vital role in the classification, as it meets the primary goal for which it was developed.

- Speed
- Memory
- Performance
- Usability

1.2 Lib-SVM

Lib-SVM is an open source library used in machine learning. It uses Sequential Minimal Optimization algorithm. It is used for training support vector machines. It solves the quadratic problem that arises during the process of training the support vector machines. Lib-SVM works well with high dimensional svm spaces.

1.3 SVD

SVD is the abbreviated form of Singular Value Decomposition. It is a mathematical concept mainly used for matrix decomposition. It decomposes the given matrix into simpler matrices in order to make the calculations easier. The diagonal elements of the Σ matrix are the singular elements of the original matrix. The columns of the U matrix and V are left and right singular vectors of original matrix respectively.



A=U∑V^T

A Real m*n matrix **U** m^{*}m matrix Σ m^{*}n diagonal matrix V^T transpose of n*n matrix.

2. METHODOLOGIES

2.1 PRE-PROCESSING

Pre-processing is the initial stage. It involves processing the input image in such a way that all the unwanted information's are removed. It improves the image clarity by suppressing all the distortions that are found useless. There are many different types of image pre-processing methods which are used to extract only desirable features for further processing. The pre-processing involves converting the original image into a grey scale image. Grey scale consists of many different shades of grey with white as the light shade and black as the dark shade. All the shades of grey has an intensity associated with that pixel. This helps enhance the image for further processing. Then the images are re-sized to a standard size.



2.2 FEATURE EXTRACTION

After the input image has been pre-processed, the decomposition phase takes place. Maximum information of the image is extracted using Singular Value Decomposition. It is a matrix factorization method. The features of the image will be present in the U matrix. The diagonal elements of the U matrix forms the feature set for the classification.



2.3 CLASSIFICATION

The feature set of the image is fed to the SVM kernels for classification on it. Support Vector Machine is a supervised algorithm used in machine learning. It is used for both classification and regression. It uses different SVM Kernels to transform the given data and using the transformations it finds an optimal boundary solution and outputs and optimal hyper plane. The tumors are classified according to the most differentiated cells with the exception of carcinomas where a few tumor cells show differentiation. The classification is done with two different libraries:

- GURLS (Grand Unified Recursive Least Square)
- Lib-SVM (Library Support Vector Machine)



3. EXISTING FRAMEWORK

Current systems use MRI (Magnetic Resonance Imaging) images to identify tumors in brain with algorithms like Kmeans and Fuzzy Clustering algorithms. CT scans are used to identify liver cancers using local binary patterns. Segmentation techniques are used to identify tumors in mammograms.

4. PROPOSED FRAMEWORK

Our approach aims to identify the presence of tumor in the legs from X-Ray image. The X-Ray image is obtained by performing pre-processing techniques. The useful features are extracted using Singular Value Decomposition (SVD). Based on the features extracted from the X-Ray image, the classifications are carried out. Classification is processed with different kernels using GURLs and Lib-SVM libraries in order to increase the efficiency and accuracy of the result. The accuracy of classification is determined by "Confusion Matrix", which allows us to visualize the performance. It includes parameters such as Actual NO, Actual YES, Predicted NO, Predicted YES and a F score which is an average of true positive rate and precision(P), where p is the number of correct positive results divided by the number of all positive results.



c) With Tumor d) Without Tumor



Fig -1: X-Ray images of legs with and without tumor

5. RESULTS

The experimental analysis of tumor identification from X-Ray images using different SVM kernels and libraries incurs that best efficiency can be achieved using RBF kernel in the implementation of GURLS. In Lib-SVM, we get 90% efficiency using RBF kernel whereas we get only 85% in normal SVM implementation. Thus we can conclude that efficiency is highest in RBF kernel in GURLS.

 Table -1: Efficiency table for SVM implementation using default Matlab library

Kernel	SVM Efficiency		
Linear	75%		
Polynomial	90%		
Gaussian/Rbf	85%		

 Table -2: Efficiency table for SVM implementation using

 Lib-SVM library

Kernel	Lib-SVM Efficiency		
Linear	80%		
Polynomial	85%		
Gaussian/Rbf	90%		

 Table -3: Efficiency table for SVM implementation using GURLS library

Kernel	GURLS Efficiency		
Linear	70%		
Polynomial	85%		
Gaussian/Rbf	95%		

Table -4: Comaprison between different libraries

Kernels	Efficiency Comparison			
	SVM	Lib-SVM	GURLS	
Linear	75%	80%	70%	
Gaussian/Rbf	85%	90%	95%	

6. CONCLUSION

The proposed framework explores the GURLS and Lib-SVM libraries to efficiently infer the presence of tumor in legs using X-Rays. The developed system analyses the grey shades present in the X-Ray and classifies them using different kernels and libraries. Among different kernels and libraries the above framework yields 95% efficiency using RBF-GURLS library.

The usage of GURLS simplifies and provides a wide range of methods for enhancing the classification. In future, the parameters can be fine-tuned to achieve greater efficiency.

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