



Diagnosis of Arthritis from Digital X-Ray Images Using Svm Classifier

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ABSTRACT

Arthritis is a kind of inflammation that occurs in the bone joints. Almost 80 percent of the world population is affected by this disease. This disease cannot be cured but can be controlled if it's diagnosed at an early stage. A number of diagnosing methods are followed for the diagnosis of the disease. Imaging of the joint under analysis is one of the conventional techniques followed for identifying the erosions caused by the disease and radiography is the technique followed for such studies. However such images are analyzed manually which can lead to the probability of faulty diagnosis. A computer aided analysis of such images can avoid the manual error in diagnosis. One such analyzing tool has been discussed in this paper. This method used Local Binary pattern for the extraction of features from the digital x-ray images and it uses Support Vector machines (SVM) for the classification of the disease. Totally fifty images were used to evaluate the developed algorithm. The specificity and sensitivity produced by the algorithm is satisfactory.

Keywords : arthritis, support vector machines classification, local binary pattern, kernel functions

I.INTRODUCTION

Cartilage is the protein substance that serves as the cushion between the bone joints. Arthritis starts with the breakdown of cartilage volume (1).A variety of diagnostic tools have been followed for the diagnosis of this disease. The coefficients of a polynomial expansion and the coefficients of wavelet decomposition are the two different features are investigated (1). A systematic computer aided image analysis method is used to analyze pairs of weight bearing knee x-rays(2).An automated method for the identification of bone lesions from Magnetic resonance images was developed. The algorithm uses two different methods for the quantification of changes in the bone volume and bone intensity (3).The Local binary pattern (LBP) features and Support vector machine (SVM) classification for the identification of facial paralysis has provided a quantitative method for the analysis of facial paralysis (4). Similarly the SVM classifier has produced satisfactory results for the classification of electrocardiogram signals. The algorithm developed to classify normal waveforms from five kinds of abnormal waveforms (5).However SVM classifier has produced unsatisfactory results as compared to other classifier when applied for the classification of imbalance data sheets of Eukaryotic genomes (6).This paper discusses a semi-automated method for the identification of arthritis from digital X-ray images. The paper is organized as follows. Section II Describes the data used in this system and the modification done on those data. The proposed system is discussed in Section III. The results obtained are discussed in Section IV.

II.DATA

Arthritis results in the reduction of the joint space width in the bone joints. The severity of the disease depends on the joint space width. Kell-Gren Lawrence grading given in Table (1) is used to grade the joint space width. The joint spacing which falls under grade the data used is the digital x-ray images of the Knee joints. The joint spacing which fall under grade -I and grade -II are considered as normal cases, grade-III and grade -IV are considered as medium cases and grade-V are considered as worst cases for the developed algorithm. The actual size of the image which is shown in figure (1.a) is around 1000 x 1000 and the region of interest is cropped

manually to a size of 200 x 200 from the actual image as shown in figure (1.b).These pre-processing is done on images used for both training set and for testing set.



Figure 1(a): Actual Image 2(b) ROI Image

TABLE-I
KELLGREN LAWRENCE GRADING FOR ARTHRITIS

Grade I	Unlikely narrowing of the joint space, possible Osteophytes
Grade II	Small Osteophytes, possible narrowing of the joint
Grade III	Multiple, moderately sized Osteophytes, definite joint space narrowing.
Grade IV:	Multiple large Osteophytes, severe joint space narrowing deformity.

III.PROPOSED SYSTEM

The block diagram of the proposed system is shown in figure (2).It consists of two stages. Initial stage classification and final stage classification. The brief explanation of each block is described in the following section.

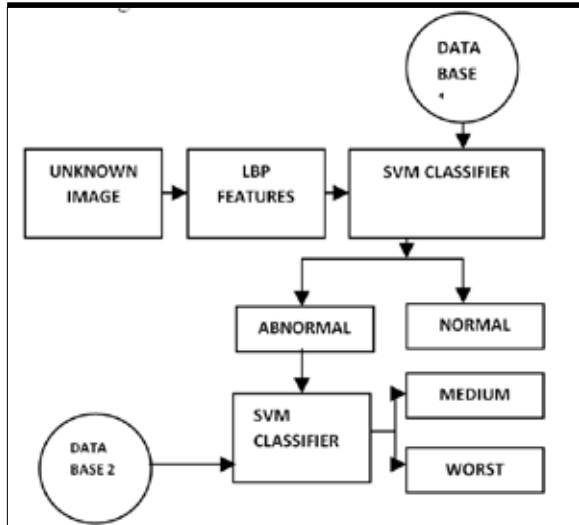


Figure 2: Block diagram of the proposed system.

LOCAL BINARY PATTERN (LBP)

The local binary pattern is an efficient texture operator. It labels the pixels of the image by thresholding the neighborhood of each pixel and considers the result as the binary number. This operator works in a 3X3 neighborhood and it consider the central pixel value as the threshold value. The LBP is produced by multiplying the threshold value with the weights by the corresponding pixels and summing up the result. As the neighborhood consists of 8 pixels a total of 28=256 labels can be obtained depending upon the grey value of the center and the pixels in the neighborhood. The illustration of LBP operator is described in figure (3).

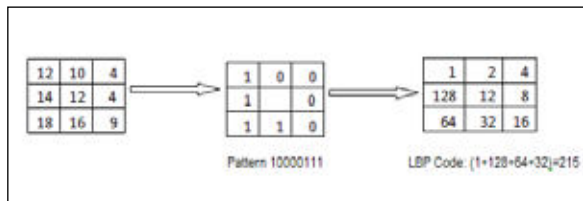


Figure 3: Illustration of LBP operator

SUPPORT VECTOR MACHINE (SVM) CLASSIFIER

Support vector machine performs classification by constructing hyper planes in a multi –dimensional space that is used to classify data of different type of classes. Support vector machine can be used for classification as well as for regression. This classifier doesn't need the prior knowledge for classification. SVM classifier can be used to classify both linearly separable and non-linearly separable data. The linearly separable data can be classified easily in the two dimensional space whereas the non-linearly separable data are classified by transforming them to the higher dimensional space. The Vectors that form near the boundary of the hyper planes form the support vectors. For better classification results the number of support vector has to be kept as minimum as possible. The support vector machines need an optimum input. The optimum input for the classification is decided by the Kernel Functions. Four kernel functions are used in this algorithm which has been discussed in the following sections.

KERNEL FUNCTIONS

A function is said to be kernel function if it satisfy the condition

$$\iint K(x,y)g(x)g(y)dxdy \geq 0(1)$$

The above condition is called as Mercers condition. These kernel functions forms the heart of SVM classification. The choice of Kernel function depends on the level of non-separable data of the data. The various kernel functions used this algorithm are discussed below.

LINEAR KERNEL FUNCTION

The linear Kernel function is given by

$$D = \{x_i, y_i | x_i \in R^p, y_i \in (-1, 1)\}_{i=1}^n (2)$$

Where D is the training data. is either 1 or -1 indicating the class to which the input belongs..Each has a p dimensional real vector. The hyper plane that divides the points having from those having is given by

$$W \cdot X - b = 0. (3)$$

Where

= weights used for training

= Input

=bias used in training.

POLYNOMIAL KERNEL FUNCTION

The polynomial kernel function is given by

$$K(x, y) = (x^T y + c)^n (4)$$

Where n is the degree of the polynomial and are the vectors in the input space. The polynomial kernel function is the most commonly used kernel function that is used to find the similarity of vector in feature space. By varying the value of n in equation (4) the function is moved from a lower dimension to the higher dimension. The problem with polynomial kernel function is that this kernel function suffers from numerical instability.

RADIAL BASIS KERNEL FUNCTION

RBF functions are used to approximate multivariable functions by using linear combinations. These functions can be applied for more than one dimension. They are used to approximate data which are only known at finite number of points. The radial basis kernel function is given by

$$K(X, Y) = \left(\frac{\|X-Y\|^2}{\sigma^2} \right) (5)$$

Where and are the feature vector in the input space. The function can be considered as the squared Euclidean distance between the feature vectors. σ can be considered as the independent parameter.

IV.RESULTS AND DISCUSSION

To evaluate the performance of the developed algorithm the algorithm was tested using 50 digital x- ray images of the knee joint. The 50 x -ray images contain 15 cases of normal joint and 35 cases of abnormal joint cases. The 35 abnormal joint in turn contains 17 medium cases and 18 worst cased bone joints. The results obtained are given below.

TABLE-II SPECIFICITY AND SENSITIVITY TABLE

Kernel Function	Specificity	Sensitivity
Linear	86.66	94.20
Radial Basis Function	86.66	94.20
Polynomial	86.66	94.20

From Table II it is observed that SVM classifier has produced satisfactory classification rate for all the kernel functions used for classifying arthritis from digital X-rays. However the classification rate has varied with the choice of kernel function in other applications. So proper choice of kernel functions and its relevant values should be done when support vector classifier is used.

REFERENCES

[1] Firestein GS, Zvaifler NJ: "Rheumatoid Arthritis, A Disease of Disordered Immunity". New York: Raven Press; 1992. | [2] Alexander K.Scheel and et.al "Assessment of proximal finger joint inflammation in patients with Rheumatoid arthritis using a novel laser based imaging technique": Arthritis and Rheumatism vol. 46, No.5 May 2002, 1177-1184. | [3] Kelvin K.Leung and et.al.(2006), "Automatic quantification of changes in bone in serial MR images of joints" IEEE TRANSACTIONS ON MEDICAL IMAGING, 25, 1617-1626. | [4] John J.Soraghan, Brian F.O'Reilly and Dongshan Xing.(2009), "Quantitative analysis of facial paralysis using local binary patterns in biomedicine videos", IEEE TRANSACTIONS ON BIOMEDICAL ENGINEERING, 56, 1864-1870. | [5] Farid Melgani, 2008, "Classification of Electrocardiogram with support vector machines and particle swarm optimization" IEEE TRANSACTIONS ON INFORMATION TECHNOLOGY IN BIOMEDICINE, 12, 667-677. | [6] Mohd.Faheem Khan, Gaurav Chauhan and A.K.Jaitly, (2011), "An approach to overcome datasets of eukaryotic genomes during the analysis by machine learning technique" INDIAN JOURNAL OF SCIENCE AND TECHNOLOGY, 4, 520-524. |