

Modelling Selective Perception for Knowledge from Image Database

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Abstract: Designing a mathematical model for understanding the properties of the images components is a complex task which embodies in it the process of visualizing image for the discrimination features.

In present work since we are considering a medical image the components or stages like preprocessing will in itself be a tough job.

The process of cognition of images has to be done at a first step for the machine intelligence to create a scale for set of particular images, which in turn will be used to characterize or classify the test image which in a process involved in Recognition phase.

I. INTRODUCTION

Human vision seems to recognize fractured part in X-ray image with relative ease, when compared to machine recognition which is much more daunting task. In addition to cognitive aspects, understanding X-ray is important, since the same underlying mechanism could be used to build a system for the machine identification of fractured part in X-ray image [1]. The machine recognition of fractured X-ray image is emerging as an active research broader area spreading among several disciplines such as Image Processing, Pattern Recognition, Computer Vision and Neural Networks.

We feel, Computers can now out perform human in X-ray identification tasks, particularly those in which large database of X-ray images must be searched. A system with the ability to detect and recognize fractured part in X-ray has many potential applications in medicine. Specially to understand progression of calcification system. But one need to address several related issues such as:

- i. X-ray image must be clear noise free, so that we can detect or identify the fractured part.
- ii. Search the given X-ray image in data base.
- iii. Identification and verification of fractured part in an X-ray using appropriate algorithms.

Identifying fractured part in an X-ray image is a difficult task mostly because of the inherent variability of the image formation in terms of image quality, photometry, geometry, occlusion [2]. While solutions to the task of identifying fractured part in an X-ray image have been

presented, recognition performance of many systems are heavily dependent upon a strictly constraint environment. The problem of identifying fractured part in an X-ray image remains largely unsolved.

II. LITERATURE REVIEW

Pattern Recognition

The existence of an uncomfortable situation is very often experienced in almost all the domains man encounters, and it becomes imperative (essential) to apply necessary recovery or corrective operations on the system to reestablish the health of the system.

Cases of such disorders, requiring multi-disciplinary support are to be found in plenty in many fields and in particular, in the medical field. Although, in general, a medical expert is proficient in diagnosing or recognizing the fracture in an X-ray image, it could become difficult to assess and accurately quantify the depth of fracture, which is a very important stage in deciding the course of the treatment to be administered to a patient.

This entire research is due to the inspiration provided by the burgeoning discipline of Pattern Cognition and Recognition (DH-90;FK-99). Pattern Recognition and classification covers a wide spectrum of disciplines (DH-73;DHS-01). The field of Pattern Recognition has attained considerable importance. Pattern Recognition is considered a major field in the wider realm (domain) of Artificial Intelligence (Don-98).

Classification

Classification of an n-dimensional data set or cluster analysis is one of the Pattern Recognition techniques and should be appreciated as such (DH-73; JD-88; DHS-01). The Pattern Recognition field has developed several classification techniques (DK-73; JRD-00). The classification can be of two types: Unsupervised and Supervised (JD-88).

The Unsupervised type of classification is broadly referred to as Cluster analysis. It deals with the problem of finding natural partitions in the n-dimensional data space of m samples, where each partition represents a class of

homogeneous samples (DJ-76;JD-88). However this type of cluster analysis cannot be considered suitable for the type of case-study that we have chosen for this research work. The type of model required has to assign a sample into a pre-defined class. This type of classification is known as supervised classification (JD-88; Rip-96).

The Training phase ends in creating a comprehensive knowledge base (FPS-91) of classes, which is a repository (Place where things are stored or may be found) of necessary information about each class and is used for making subsequent decisions along with an improved performance, when unknown samples are presented for proper recognition. Designing a knowledge base and a classifier will be a more complex task when the input data objects[3].

Matching Problem

In Present work, involving a case study from the medical field, the type of classifier to be designed has to be based essentially on the principle of supervised classification, requiring the design of a proper knowledge scale with apriori known samples.

Primarily an individual (a patient) has to be accurately diagnosed and then placed in one of the two classes-

- (i) Un-Affected class and
- (ii) Affected class.

Viewed from a position of close proximity it can be observed that the classifier need not identify the existence of two distinct classes, on the contrary characterizing one class will imply that the other class is automatically characterized as having a reference to a particular disorder/disease. Hence the problem can be more appropriately called the problem of recognizing a class and its complimentary class, where a class refers to a set of unaffected samples and a complimentary class refers to the dual set of affected samples with reference to a specific problem.

Further inspection shows that learning phase need not and cannot be exclusively designed to formulate the knowledge scale for the two classes. It is quite sufficient if the characteristic parameters of the unaffected class are learnt properly. The feature set of an unknown Test Image (individual) is contrasted with the knowledge scale of healthy samples. The most important decision is then taken as to whether the individual is unaffected or affected.

Distance Measure

In the field of Pattern Recognition many distance measures are defined. Distance measures are equally important for solving the *Matching Problem* which involves making a proper choice of the distance measure.

There are many distance measures defined in Pattern Recognition. Each of them exhibits different properties and are meant to be used for different application domains. In fact,

for data mining in a particular domain, it is necessary to devise a useful and relevant distance measure that would respond properly and effectively [4].

In the present context of solving a Matching problem, the essential properties to be satisfied by a distance measure are as follows:

- i. It should clearly project whenever a Test Image is a normal or unaffected sample.
- ii. It should clearly discriminate an affected sample, by categorically refuting to put such a Test Image even in the slightest close proximity to the Knowledge scale.
- iii. In case the Test Image is Un-Affected, it should quantify the strength of such Test Image. With the Knowledge scale.
- iv. In case the Test Image is an affected one, it should quantify the level of the Test Image, such that the assessment of the disorder is error-free.

From the pattern recognition and algorithm-design view point, it is necessary to keep the dimensionality of the feature space to a lower level so that the complexities of time and memory could be kept under control. However, the performance quality cannot be sacrificed. Hence, exploratory investigation may be required to reduce the number of features and to arrive at an optimal set of features.

Drawbacks of Traditional Approaches

Strict algorithmic approaches to decision support in the field of medicine have not yet been successful because, in most instances complete models that describe biological system functioning are not known (GMR-01). The lack of deterministic models was recognized quite early leading to the development of Pattern Recognition approaches to address classification problems, such as differential diagnosis. These models allowed the computer to search for patterns in the data. Approaches based solely on accumulated data present a number of drawbacks. The most obvious problem is that not only is the model dependent on the accuracy of the data, but is also limited by the applicability of the data to other populations **Problem Definition**

The advantages of the X-ray technique are common availability and low cost; however, interpretation of radiograms is not an easy task. It is estimated that by means of traditional X-ray analysis, changes related to calcium decrease can be noticed at 30-60% loss of the bone mass, which corresponds to an already advanced phase of the disease (Czekalski 1993; Southard 1996). There is a need for an inexpensive and simple diagnostic technique that would allow detection of early changes in the structure and mass density of the bone. Such a method would be very useful for prevention of the skeletal system diseases as well as for their treatment in a non-developed phase. It is postulated in paper that texture analysis of digitized X-ray images can be considered as an alternative to standard techniques of skeletal system

diagnosis.

A general statement of the problem can be formulated as follows: Given still images of X-ray's, recognize the fractured part using a stored database of X-ray images. And compare a given Test image with the images present in the Database. And display the image which has the highest similarity component, also next to that.

Principal Component Analysis

TECHNICAL ORIENTATION

Principal Components Analysis (PCA) is a multivariate procedure which rotates the data such that maximum variability is projected onto the axes. Essentially, a set of correlated variables are transformed into a set of uncorrelated variables which are ordered by reducing variability. The uncorrelated variables are linear combinations of the original variables, and the last of these variables can be removed with minimum loss of real data [5].

The first Principal Component is the combination of variables that explains the greatest amount of variation. The second principal component defines the next largest amount of variation and is independent to the first principal component. The number of PC are proportional to number of variables.

The main use of PCA is to reduce the dimensionality of a data set while retaining as much information as is possible. It computes a compact and optimal description of the data set .

It can also be viewed as a rotation of the existing axes to new positions in the space defined by the original variables. In this new rotation, there will be no correlation between the new variables defined by the rotation. The first new variable contains the maximum amount of variation; the second new variable contains the maximum amount of variation unexplained by the first and orthogonal to the first, etc...

There are several algorithms for calculating the Principal Components. Given the same starting data they will produce the same results with the one exception. This exception is that, if at some point, there are two or more possible rotations that contain the same "maximum" variation, and then which one is used is indeterminate. In two dimensions the data cloud would look like a circle, instead of an ellipse. In a circle, any rotation would be equivalent. In an elliptical data cloud, the first component would be parallel to the major axis of the ellipse.

It can be viewed as finding a projection of the observations onto orthogonal axes contained in the space defined by the original variables. The criteria being that the first axis "contains" the maximum amount of variation, or "accounts" for the maximum amount of variation. The second axis contains the maximum amount of variation orthogonal to

the first. The third axis contains the maximum amount of variation orthogonal to the first and second axis and so on until one has the last new axis which is the last amount of variation left. As you can see these are really two slightly different ways of saying the same thing!

MEDICAL ORIENTATION

Using all of the available information with an X-ray image seems a reasonable goal, despite the problems associated with the approach. Dimensionality Reduction can be used to emphasize statistically important features of an X-ray image whilst reducing the high storage requirements often associated with holistic or template matching approaches. The aim is to reduce the dimensionality of the input X-ray image whilst maximizing the information which is retained.

Principal Component Analysis (PCA) also known as the Karhunen-Loeve transform is a statistical technique used to provide a linear mapping of the input data to a new orthogonal coordinate frame. Each axis in the new coordinate frame represents a different mode of variation in the original input data. The input data's dimensionality can be reduced while maximizing the data's variance retained in the new space by discarding the least significant dimensions of the new space. This linear transform is reversible, so the original data, or an approximation of it, can be reconstructed. In practice, PCA is done by calculating an estimate for the mean and then the covariance matrix from sample data. An eigenvector decomposition method (of which there are many) is then applied to the symmetric covariance matrix. This gives both eigenvectors and eigenvalues. A weighted sum of the eigenvectors can be used to reconstruct any simple within the original data set. A truncated set of the best eigenvectors (those with the highest eigenvalues) can then be used to project mean-centered sample data into the new lower-dimensional space.

Principal Component Analysis is a statistical tool used in a widely range of areas (economy, biology, engineering, etc.) for statistical analysis of multivariate phenomena. It is concerned with explaining the variance-covariance structure through a few linear combinations of the original variables.

Principal Component Analysis (PCA) is a very popular technique for dimensionality reduction. It is well-known fact that PCA is optimal in terms of the reconstruction error but not for the separation and recognition of the classes. Nevertheless, PCA is often used directly for pattern and object recognition tasks. In the computer vision community for example it has been used for recognition of faces (Turk and Pentland, 1991) and 3D objects (Measure and Nayar, 1995) as well as dealing with partial conclusion by using robust estimation techniques (Black and Jepson, 1998).

Recently, Lee and Seung (1999) proposed a new technique, called Non-Negative matrix factorization (NMF), of obtain a reduced representation of data only using positive

restrictions. NMF differs from other methods by its use of non-negativity constraints. They demonstrated with a set of faces images (Lee and seung 1999) that NMF can be used to obtain a set of bases of localized features correspond to the intuitive notion of the face parts such as eyes and mouth. Guillamet et al. (2001) presented a study of a weighed version of the original NMF (weighted non –negative matrix factorization, WNMf) where they demonstrated that for local data representations NMF can generate redundant basis when the dimensionality of the feature space is high and they presented a modification of the original technique that minimizes this behaviour. WNMf is also based on the same principles as NMF but with a new weighed matrix that is able to weigh each training feature vector minimizing the presence of possible repeated bases.

A recent study (Guillamet et al . 2002) compares both PCA and NMF techniques in an image patch classification framework where the main claim is that both techniques can be merged in a common classifier. Since both PCA and NMF techniques are of different nature, they can not be compared in a direct way (Buchsbaum and Bloch, 2002). The final classifier that merges PCA and NMF is based on the L norm of the reconstruction error but it remains unclear whether this is the best way to merge both techniques.

This paper presents a comparative study of PCA, NMF and WNMf techniques in the same color classification scheme used in (Guillamet et al.2002). one of the main goals is to validate that WNMf can also be introduced in a classification framework as an improvement of the original NMF, additionally, since L-norm seems not to be an appropriate metric to use in conjunction with NMF (Guillamet and Vitria, 2002), we introduce a reliable probabilistic framework to compare all techniques, for each method, we define a probabilistic density function that is used to merge all techniques in a simple and unique classifier that out performs each of them and the L-norm based results.

Eigenimage Approach

The X-ray image recognition module is based on the eigenimage approach. In this approach, there are two separate phases depending on the task to be performed – the training phase and the recognition phase. In the training phase, the PCA algorithm reads in a set of images and from these forms a data matrix. Specifically, each image is unwrapped to form a column vector, and these column vectors are merged to form the data matrix. The data matrix is then used to create a sample covariance matrix, and the eigenvalues and eigenvectors of this covariance matrix are then determined. These eigenvectors can be thought of as a set of features that together characterize the variation between X-ray images.

When used to perform recognition in recognition phase, a test image can be classified as X-ray image or non-X-ray image by measuring the Euclidean distance between the original and projected images and using a threshold to reject non-X-rays, thus avoiding further processing of non-X-ray

images. The eigen_images can be linearly combined to reconstruct any image in the training set exactly. In addition, if we use a subset of the eigen_images which have the highest corresponding eigenvalue (which accounts for the most Variance in the set of training images), we can reconstruct (approximately) any training image with a great deal of accuracy. This idea leads not only to computational efficiency (by reducing the number of eigen_images we have to work with), but it also makes the recognition more general and robust. A mathematical derivation of the eigenimage approach, based on the work of Turk and Pentland has been explored.

Advantages of Eigen_images

- Systems speed and efficiency.
- In eigenimage recognition method, no knowledge of geometry and reflectance of image are required.
- Recognition is simple and efficient compared to other matching approaches and data compression is achieved by low-dimensional subspace representation.

Computing Eigen_images

Consider an X-ray images of size N x N, these images can be thought of as a vector of dimension N² or a point in N² dimensional space. A set of images therefore corresponds to a set of points in this high dimensional space. Since facial images are similar in structure, these points will not be randomly distributed, and therefore can be described by a lower dimensional subspace. Principal component analysis gives the basis vectors for this subspace. Each basis vector is of length N² and is the eigenvector of the covariance matrix corresponding to the original X-ray images.

Let **T**₁, **T**₂, ..., **T**_M be the training set of images. The *Average X-ray image* is defined by

$$A = [\Phi_1, \Phi_2, \dots, \Phi_M]$$

Each X-ray image differs from the average X-ray image by the vector

All the differences are converted into vector format

$$\Phi_i = T_i - \psi$$

And column wise concatenated as follows

The *Covariance matrix* of the data is defined as

$$C = \frac{1}{M} \sum_{i=1}^M \Phi_i, \Phi_i^T$$

The matrix has a dimension of N² by N².

Determining the eigenvectors of C for typical sizes of N is intractable. We need a computationally feasible method to find these eigenvectors. If the number of data points in the image space is less than the dimension of the space ($M < N^2$), there will be only M-1, rather than N^2 , meaningful eigenvector

$$L = A^T A$$

(The remaining eigenvectors will have associated eigenvalue of zero). The eigenvectors are determined by solving a M by M matrix using

where $L_{mn} = \Phi_m^T \Phi_n$ and find the M eigenvectors, V_i of L then

$$U_f = \sum_{k=1}^M V_{ik} \Phi_k \quad i = 1, \dots, M$$

Where U_f is the Eigen X-ray images.

$$\psi = \frac{1}{M} \sum_{i=1}^M T_i$$

Classification

In practice, a smaller M^1 is sufficient for X-ray image identification. The eigen_images span an M^1 dimensional subspace of the original N^2 image space. The M^1 significant eigenvectors of the L matrix are chosen as those with the largest corresponding eigenvalues.

A test X-ray image Γ is projected into image space by the following operation

Where U_i are the eigenvectors for C.

The weights ω_i form a vector $\Omega^T = [\omega_1, \omega_2, \dots, \omega_{M^1}]$ which describes the contribution of each eigen_images in representing the input X-ray image. This vector can then be used in a standard pattern recognition algorithm to fit the test image to a predefined image class.

A simple technique is to use the *Euclidian distance*

$$C_i = \| (\Omega - \Omega_i) \|^2 \text{ where } \Omega_i \text{ describes the } i^{\text{th}} \text{ image class.}$$

The simple method for determining which X-ray image class provides the best description of an input X-ray image is to find the image class that minimizes the Euclidian distance describing the image class. A test image is in class i when the minimum distance is below some chosen threshold i.e. $C_i < \theta_i$, otherwise the X-ray image is classified as “unknown or image not found in database”.

III. PROPOSED METHODOLOGY

Recognition of component features of image is a complex solution to any researcher the problem further increases its complexity when the image is made-up of

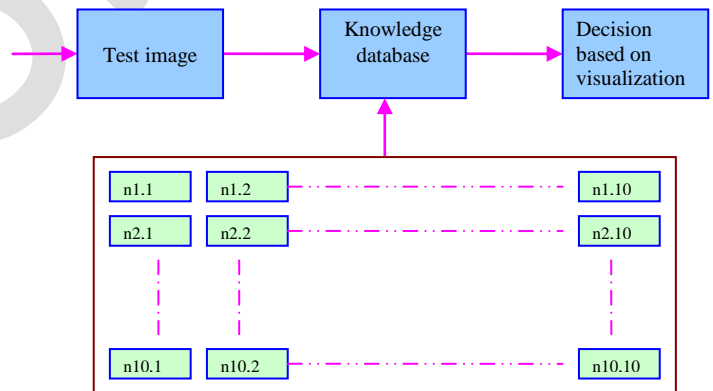
different features which invariably increases the noise component and reduces the recognition efficiency in context when the input image is medical image understanding the components is highly error prone.

- 1) Create a database of 10 sets and each set should contain the Images of different sizes
n1, n2, n3, n4.....n10.
- 2) **Image retrieval:** Take an image which is already present in database and compare.
t1=n11
t1-----> test image
- 3) Take an image which is not present in image [hair line fracture] database and compare test images with all the image present in the database, and indicate the similarity component of test image with all the images in database.
- 4) Take an image which is more changed or exact cut and compare with the temporal database.
Week1, week2, week3.....week8.

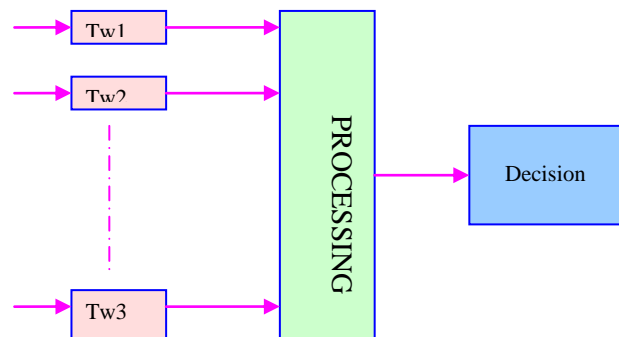
This helps in finding progression of disorders.

Expected outcome

Out come 1:



Out come 2:



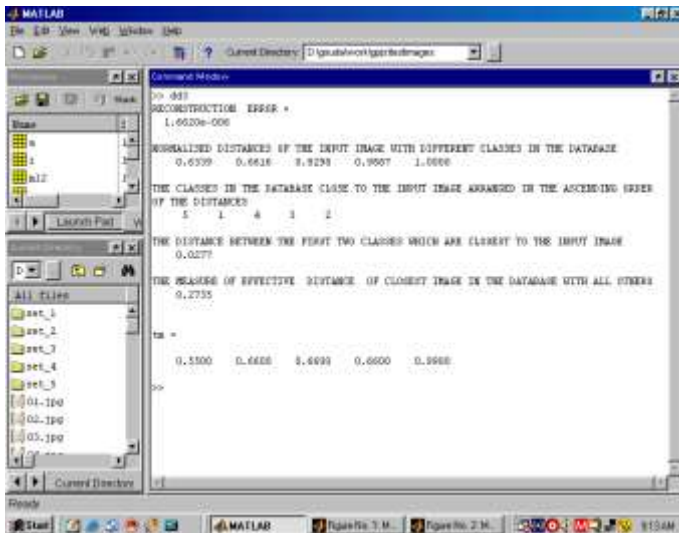


Figure shows the Results of effective distance of the closest image in the database.

IV. CONCLUSION

One can conclude that by measuring changes in statistical texture parameters and fractal dimensions of X-ray images it is possible to monitor changes in calcium contents and internal structure of the bone. Texture analysis shows potential usefulness as an aid to the diagnosis of skeletal diseases. This initial research was carried out using first-order texture features only. Further work is needed to select

optimum texture parameters from a variety of known approaches, including wavelet analysis and mathematical morphology derived features. It has been demonstrated also that there exist a degrading effect of image blur and noise, typical to X-ray images, on texture parameters.

There is a need to elaborate techniques to reduce these effects, which is the subject of the current study. Also, high-resolution flat bed transparency scanner is being used at present for image digitization with an increased accuracy compared to the CCD camera. First experiments show that fractal dimensions computed for scanned radiographic films demonstrate significantly higher correlation to BMD compared with CCD-recorded images.

REFERENCES

- [1]. Andrzej Materka, Piotr Cichy Institute of Electronics, Technical University of Lodz Stefanowskiego 18, 90-924 Lodz, Poland materka@ck-sg.p.lodz.pl Jerzy Tuliszkiewicz Polish Mother Memorial Hospital Institute Rzgowska 281, 93-338 Lodz, Poland
- [2]. K. L. Chan, "Quantitative Characterization of Electron Micrograph Image Using Fractal Feature", *IEEE Transactions on Biomedical Engineering* **42**, 10 (1995) 1033-1037.
- [3]. M. P. Dubuisson, R. C. Dubes, „Efficacy of fractal features in segmentation images of natural textures”, *Pattern Recognition Letters* **15** (1994) 419-431.
- [4]. C. Fortin, K. Kumaresan, W. Ohley, R. Hoefler, „Fractal Dimension in the Analysis of Medical Images”, *IEEE Engineering in Medicine and Biology* (June 1992) 65-71.
- [5]. E.Helomas and B.K.Low.Face detection: A survey. *Computer Vision and Image Understanding*, 83:236 –274, 2001.