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Research Article

A Novel Pre-processing and Kernel Based Support Vector Machine Classifier with Discriminative Dictionary Learning for Bone Age Assessment

Ananthi Sheshasaayee and C. Jasmine
Department of Computer Science, Quaid-E-Millath Government College for Women, University of Madras, Chennai, Tamil Nadu, 600 002, India

Abstract: Aim of this study: Bone age assessment and X-ray assessment on hand radiographs is an expensive and time consuming process in radiology. This research work presents a powerful Graphical User Interface (GUI) for IRMA that gives exceptional medical image retrieval results. Methods: This study gives complete details regarding the execution of a novel Discriminative Dictionary Learning (DDL) for the purpose of matching query and input medical image samples. In order to further boost the quality of the medical images, Principal Component Analysis (PCA) based noise level estimation scheme is introduced. This helps to eliminate noises included in the medical images. Furthermore, to enhance the performance, a new relevance score scheme via Kernel Support Vector Machine (KSVM) is formulated, which efficiently make use of medical images features in order to discriminate the images accurately. This system initiated a new discriminative name called 'pairwise similarity measurement' for the discriminativeness of pairs of query and input medical database images and subsequently integrate it with the classification error for discriminativeness in classifier production to generate a unified objective function. Results: Experimentation results assessed the proposed DDL in IRMA framework on a numerous medical images like BAA images and X-Ray skull images and results confirm that DDL performs far better than the state-of the-art approaches significantly in terms of precision, recall, sensitivity, specificity and accuracy. Conclusion: The resulting DDL has a considerable impact on medical CBIR applications.

Keywords: Bone Age Assessment (BAA), Content Based Image Retrieval in Medical Applications (IRMA), Discriminative Dictionary Learning (DDL), Kernel Support Vector Machine (KSVM), Principal Component Analysis (PCA)

INTRODUCTION

At present, direct digital imaging methods are of growing significance in medical diagnosis. As a consequence of the Digital Imaging and Communications in Medicine (DICOM) protocol, currently huge archives hosting medical imagery are utilized consistently. On the other hand, purposeful utilization to the mounting amount of digital image data is even now based on alphanumeric attributes like patient name, study descriptors, imaging modality, or the recording date. As a result, content-based application to medical images has constructive impact on Computer Aided Diagnosis (CAD), evidence-based medicine, or case-based reasoning (Müller *et al*., 2004).

The complication of archiving those medical image sets have been handled with numerous solutions like Picture Archiving and Communication Systems (PACS) (Gutierrez *et al*., 2006) or modular and dedicated systems for the utilization image databases (Marcos *et al*., 2007). Efficiency of those systems may perhaps be crucial in medical practice, in view of the fact that they are accountable for accumulating medical images in a responsible manner. In addition, these systems have to permit users to resourcefully access this information.

Conventional medical image database systems accumulate images as a complementary data of textual information, affording the most fundamental and familiar operations on images: Transmit and visualization. Typically, these systems are constrained to query a database simply by means of keywords, however this type of queries restrict information access, in view of the fact that it does not make use of the intrinsic character of medical images. In contrast, a medical image database system is supposed to have a flexible structural design together with an extensive variety of functionalities supporting medical,

Corresponding Author: Ananthi Sheshasaayee, Department of Computer Science, Quaid-E-Millath Government College for Women, Chennai, Tamil Nadu, 600 002, India

educational and research operations (Doi, 2007). Medical users must count on a set of automated and efficient tools, which permits efficient access to relevant information.

This type of systems permit assessment of new clinical cases with the intention that when related cases are necessary, the system is capable of retrieving comparable data for supporting diagnoses in the process of decision making process. Numerous systems have been formulated following this approach like IRMA (Lehmann *et al*., 2003), FIRE (Deselaers *et al*., 2006) among others (Müller *et al*., 2007). The foremost concept of this type of systems is to accomplish sufficient support to physicians in reaching their medical objectives.

In the midst of them, the IRMA framework is better, in which the Bone Age Assessment (BAA) is a common and time consuming process for growth disturbances determination in the parts of human body. Typically, this process is done physically by radiologists, readily available radiographs, must possess domain knowledge and skill. Previous efforts on BAA (Harmsen *et al*., 2013) formulated initial approaches in automation of this process with CBIR techniques. Consider a radiologist is interpreting a chest X-ray, when he notices uneven nodules in the upper portion of the left and the lower portion of the right pulmonary lobes, he intends to check with other cases with comparable patterns in the radiograph.

With the availability of the entire schemes, there is still no well-organized approach for the relevance score computation and eliminating noise from medical images samples for additional clarity, effective extraction of the features becomes not adequately solved for IRMA framework, with the aim of surpassing these complications, in this study presented a novel Discriminative Dictionary Learning (DDL) for accurate matching of the query and input image samples for X-ray and BAA images. In order to effectively carry out this process, this study emphasizes advanced Graphical User Interface (GUI) concepts for the purpose of CBIR applications. In the beginning, the above stated two images are gathered from databases and the process of noise removal is done by means of Principal Component Analysis (PCA), subsequently five different categories of the global features are obtained and at the same time local features are also derived. Once the features are extracted Relevance Score (RS) techniques with Kernel Support Vector Machine (KSVM) is proposed to enhance the retrieval function of IRMA systems. With the assistance of continuous-valued RS, it refines the query until the returned pattern equals the request. The similar iteration is done for the remaining ROI. Subsequently, the two resulting sets of the query and medical input image samples are matched by using DDL. The DDL scheme unambiguously incorporates pair wise constraints for RS matching results and a linear predictive classifier into one objective function. The learned dictionary promotes RS based feature results for medicals images from the identical class and KSVM results from different classes. The result is shown to the physician, who picks the most excellent matching images and accesses the related patient records.

LITERATURE REVIEW

Presently several schemes are available for the purpose of capturing medical images and helps in taking clinical conclusions, however there exists modest work to build up clever management systems. The required systems have to support the medical workflow, which comprises medical, educational and research operations. In the list of all approaches, IRMA framework with BAA and X-ray skull happens to be more difficult task. Numerous amount of the works have been carried out to analysis these tasks. Some the approaches and its concerns are discussed below.

In spite of a huge amount of scientific research on BAA, there is a requirement of agreement concerning the accuracy of bone age techniques which is adequate for a clinical atmosphere (Zaproudina *et al*., 2007). In case of BAA, both clinical atmosphere and courts of justice, it is significant to provide the most precise result. A computerized bone age system possibly will eradicate the function of a human observer, which would diminish the subjectivity in evaluation as the main reason for the lack of accuracy.

Researchers disclose the consequence in automating the process for the assessment of bone age. These techniques employ certain intelligent schemes, like segmentation of the hand, at the same time few are only employed in the research atmosphere (Übeyli, 2007). It is found that the computerized schemes in BAA could considerably reduce the cost of estimation of bone age, also a reduction in the time that radiologists use in determining the bone age (Yildiz *et al*., 2011).

Mansourvara *et al*. (2012) established a novel scheme for BAA that makes use of a histogram based assessment scheme. This scheme is implemented as a web based system that employs an image repository and similarity measures depending on content-based image retrieval. This author intends to surpass the drawbacks of conventional schemes utilized to assess human age which were regularly inaccurate. The scheme offers age prediction for hand and wrist x-ray images up till age limit of 18 years. However in this scheme noises exist in the medical image samples are not eliminated, consequently diminishes the quality of the image and relevance feedback based learning is also not carried out for extracted feature vectors from medical image samples, furthermore constantly monitoring of the relevance feedback is significant to enhance the IRMA framework results.

Haak *et al*. (2013) build up an automatic scheme integrating CBIR and Support Vector Machines (SVM). Here, execute Support Vector Regression (SVR) as a novel scheme, providing a gain in performance. The schemes are intended to handle the age limit 0-18 years as compared against the age limit 2-17 of the commercial product BoneXpert. On a benchmark data set from University of South Carolina, the schemes accomplish a root mean-square error of 0.95 and 0.80 years for SVM and SVR, correspondingly. However, here noises exist in the medical image samples are not eliminated, as a result reduces the quality of the image and relevance feedback based learning is also not carried out for extracted feature vectors.

Hsu *et al*. (2007) formulated a web-based retrieval system called SPIRS (Spine Pathology and Image Retrieval System) at the U. S. National Library of Medicine that reveals current growth in shape representation and retrieval from a large data-set of 17,000 digitized x-ray images of the spine and related text data. Users can look for these images by offering an outline of the vertebral sketch or choosing an example vertebral image and certain appropriate text constraints. Pertinent pathology on the image/outline can be interpreted and weighted to point out significance. This hybrid text-image query provides images containing related vertebrae together with appropriate fields from related text records, which permits users to inspect the pathologies of vertebral abnormalities. The most important element of this scheme is to assist in the following ways, retrieval excellence by learning using user feedback and user interaction and visualization not concentrated majorly.

Amaral *et al*. (2010) investigate the complication of hierarchical medical image annotation by constructing a CBIR system trying to discover the integration of three different schemes using SVMs: Initially united the global image descriptors with an interest points Bag-of-Words (BoW) to construct a feature vector; then, carry out an initial annotation of the data by means of two known schemes, ignoring the hierarchy of the IRMA code and a third that takes the hierarchy into account by categorizing consecutively its instances; at last, utilize pair wise majority voting among schemes by just summing strings with the aim of producing a final annotation. The results prove that even though almost all fusion schemes result in an enhancement over other, none evidently surpasses each other.

Numerous researches have been carried out on how to assess user feedback like semi-supervised learning in Hoi *et al*. (2008) to enhance the performance of image retrieval. Hoi *et al*. (2008) executed active learning scheme to enhance the retrieval performance of Laplacian SVM. On the other hand, these schemes typically necessitate many assumptions of unlabelled images, which possibly will not hold with unconstrained consumer photos. But, perfect GUI is not created these schemes. All of the above mentioned issues for IRMA framework based problems are solved in this research work.

MATERIALS AND METHODS

In the architecture of Content Based Image Retrieval (CBIR) system for the purpose of medical applications, initially Principal Component Analysis (PCA) based technique is employed to eliminate noise from medical images, in view of the fact that the noise exists in the medical images samples which considerably diminishes the clarity, excellence of the image. The retrieval results of the CBIR also diminished significantly as a consequence of the above mentioned setback, with the aim of surpassing these complications and lessen the noise from medical images samples, here, a novel PCA technique is employed, which eliminates noises from medical images samples during the preliminary stage of processing, consequently improves the quality of the input images. Subsequent to the removal of noise, then global and local features are extracted. Relevance Score (RS) has been commonly employed to assist in acquiring the search purpose from the user and further enhance the retrieval results. The proposed Kernel Support Vector Machine (KSVM) further enhance the medical image retrieval results with the assistance of the pre-learned KSVM classifier from a huge amount of labelled loosely medical images feature vectors and a lesser amount of accurately labelled medical image photos from user with RS. This is the first attempt that employs the KSVM learning for RS. Also, proposes a novel Discriminative Dictionary Learning (DDL) analysis scheme which learns a flexible nonlinear proximity function with local fisher discriminant to enhance visual similarity search in CBIR for the purpose of medical images is illustrated in Fig. 1.

Noise removal using Principal Component Analysis (PCA): This study carried out some pre-processing by resizing the entire images to the scale of 500×500 pixels at the same time maintaining the aspect ratio unaffected for medical images. With the intention of removing the noise, execute PCA scheme. Consider a noise free image as $\mathrm{mix_k}$ of size 500×500 pixels size with $S_1 \times S_2$ in which S_1 indicates the number of columns and S_2 indicates the number of rows, $\mathrm{miy} = \mathrm{mix} + \mathrm{n}$ represents an image corrupted with signal-independent additive white Gaussian noise n with zero mean. Noise variance σ^2 is indefinite and has to be estimated. Each of medical imagesmix, n, miy includes

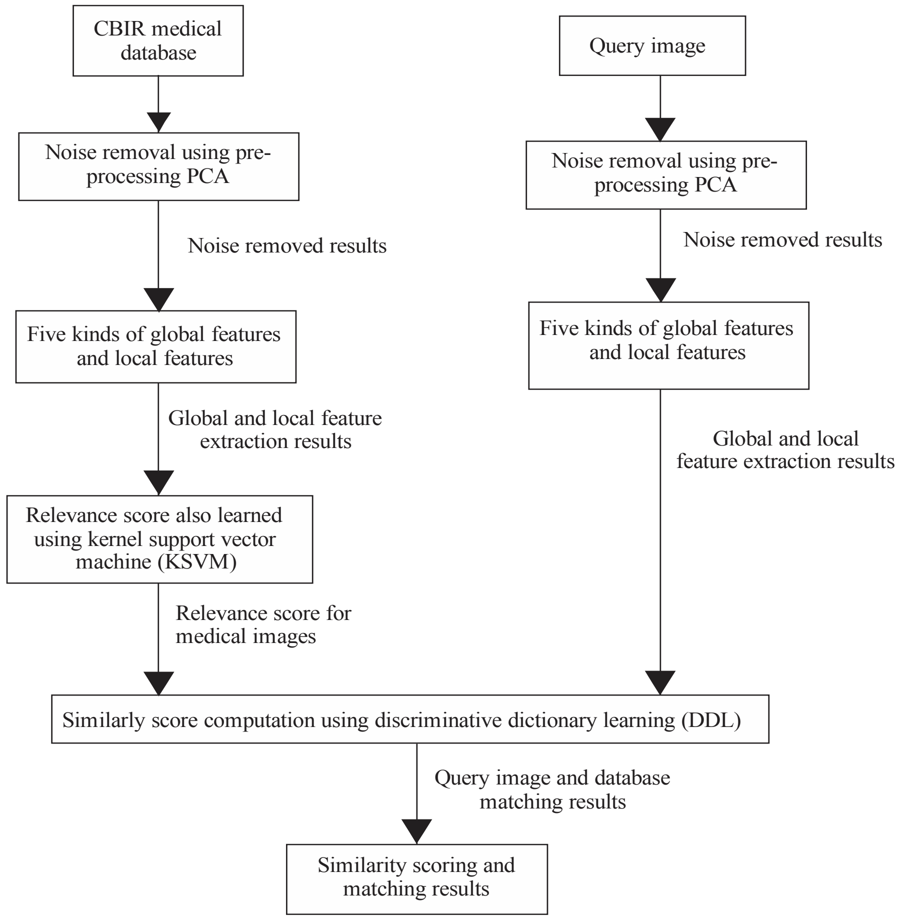


Fig. 1: Proposed methodology architecture

$N = (S_1 - M_1 + 1)(S_2 + M_2 + 1)$ blocks of size $M_1 \times M_2 = 500 \times 500$, pixel size whose left top corner spots are taken from set $\{1,..,S_1 + M_1 + 1\} \times \{1,\dots,S_2 \times M_2 + 1\}$. These blocks can be reorganized into vectors with $M = M_1M_2$ constituents and taken as realizations $mx_i, n_i, my_i,\ i = 1,\dots,N$ of random vectors MX, N and MY correspondingly. At the same time as n is signal-independent additive white Gaussian noise, $N \sim NM(0, \sigma^2 I)$ and $\text{cov}(X; N) = 0$. Consider m represents a predetermined positive integer number. The data in noise-free medical image mx is superfluous, in the manner that the entire mx_i lies in subspace$V_{M-m} \subset \mathbb{R}^M$, whose dimension $M - m$ is lower than the amount of coordinates M. The noise variance estimate results for medical images are presented in the main function noise variance evaluation, which calls Upper Bound and Get Next Noise variance Estimate. With these functions, $Q(p)$ indicates the p −quantile of $\{s^2(my_i), i = 1,\dots,N\}$ and $B(p)$ indicates the subset of blocks of medical image my whose sample variance is not bigger than:

$$B(P) = \{Y_i | s^2(my_i) \leq Q(p), i = 1,\dots,N\} \tag{1}$$

Function noise variance estimate takes the outcome of function Upper Bound as the preliminary estimate and iteratively calls function. Get Next variance Estimate until convergence is accomplished. Parameter i_{max} indicates the highest number of iterations to entire noise variance estimation. Function Upper Bound calculates a noise variance upper bound value. This function doesn't depend on any image block. Related to several other noise estimation approaches, it depends on the analysis of the image block based noise variance distribution for resized medical images, specifically, this function returns $C_0Q(p_0)$.

Function 1: Noise variance estimation
Input: Medical image with noise miy
Output: Noise variance estimation results from PCA σ^2_{est}.

1. $\sigma^2_{ub} \leftarrow get\ upper\ bound(miy)$
2. $\sigma^2_{est} \leftarrow \sigma^2_{ub}$
3. For i = 1 to i_{max}
4. $\sigma^2_{next} \leftarrow$ $get\ next\ variance\ estimate(miy, \sigma^2_{est}, \sigma^2_{ub})$
5. If $\sigma^2_{est} = \sigma^2_{next}$ then
6. Return σ^2_{est}

Table 1: Algorithm parameters

Parameter	Value
M_1	5
M_1	5
M_1	3.1
M_1	0.0005
M	7
T	49
Δp	0.05
p_{min}	0.06
i_{max}	10

7. End if
8. $\sigma_{est}^2 \leftarrow \sigma_{next}^2$
9. End for
10. Return σ_{est}^2

Maximum possible p is equal to 1, which related to the complete set of medical image blocks. Subsequently, it rejects blocks with the maximum variance by diminishing p to $1-\Delta p, 1-2\Delta p$ and so on, until p is lower than p_{min}. The values of p_{min}, Δp and T are given in Table 1. Upper bound $\sigma_{ub}^2$is employed as an extra test of the accuracy of the computed estimate. Function Apply PCA calculates $\tilde{\lambda}_{MIY,i}, i = 1, \ldots, M$.

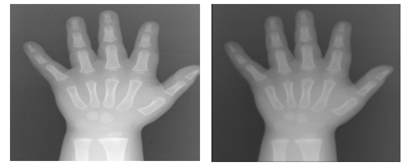
Function 2: Get next variance estimate
Input: Medical image with noise miy, Noise variance estimation outcome from PCA σ_{est}^2, upper bound σ_{ub}^2.
Output: Next variance estimate σ_{next}^2.

1. $p \leftarrow 1$
2. $\sigma_{next}^2 \leftarrow 0$
3. While $p \geq p_{min}$ do
4. $\tilde{\lambda}_{MIY,1}, , , , \tilde{\lambda}_{MIY,M} \leftarrow Apply\ PCA(B(p))$
5. $\sigma_{next}^2 \leftarrow \tilde{\lambda}_{MIY,M}$
6. If $\tilde{\lambda}_{MIY,M} - m + 1 - \tilde{\lambda}_{MIY,M} < T\sigma_{est}^2 / |\sqrt{|B(p)|}$ and
7. $\sigma_{next}^2 \leq \sigma_{ub}^2$ then
8. Return σ_{next}^2
9. End if
10. $p \leftarrow p - \Delta p$
11. End while
12. Return σ_{next}^2

While taking the execution time of the program into account, have to focus on function Apply PCA, since it is called inside two loops: the initial loop is from lines 3-9 of function Noise variance estimation; and the subsequent loop is from lines 3-10 of function Get Next noise variance Estimate. Function Apply PCA includes two elements:

- Calculation of the sample covariance matrix:

$$\frac{1}{|B(p)|-1}\left(\sum_{miy_i \in B(p)} MIY_i MIY_i^T - \frac{1}{|B(p)|}\sum_{miy_i \in B(p)} MIY_i \sum_{miy_i \in B(p)} MIY_i^T\right) \quad (2)$$



(a) (b)

Fig. 2: Preprocessed and query image results; (a): Query image; (b): Preprocessed image

The amount of the operations is relative to $|B(p)|M^2$.

- Calculation of the Eigen values of the samples covariance matrix.

In view of the fact that, $|B(p)| \gg M$, the calculation of the sample covariance matrix is the most vital element of the function Apply PCA. Consider $C_{MIX} = \sum_{MIY_i \in MIX} MIY_i MIY_i^T$ and $c_{MIX} = \sum_{MIY_i \in MIX} MIY_i$. It is to be observed that for disjoint sets MIX_1 and MIX_2, $C_{MIX_1 \cup MIX_2}$ and $c_{MIX_1 \cup MIX_2} = C_{MIX_1 + MIX_2}$. At that moment (2) can be rewritten as:

$$\frac{1}{|B(p)|-1}\left(C_{B(p)} - \frac{1}{|B(p)|} C_{B(p)} c_{B(p)}^T\right) \quad (3)$$

Function Apply PCA is called only with arguments:

$$B(1) \supset B(1-\Delta p) \supset .. \supset B(1-n\Delta p) \quad (4)$$

where, $n = [1 - p_{min})/\Delta p]$ and $= [mix]$ is the highest integer not above mix. For $j = 0, \ldots n-1$, consider:

$$MIY_j = \left\{miy_i \middle| \begin{matrix} Q(1-(j+1)\Delta p) < s^2(miy_i) \leq \\ Q(1-j\Delta p) \end{matrix}\right\} \quad (5)$$

Subsequently:

$$B(1-j\Delta p) = B(1-(j+1)\Delta p \cup MIY_j \quad (6)$$

During the start of the PCA techniques for noise variance estimation, pre-computes the covariance matrices $C_{B(1-j\Delta p)}$ and vectors $c_{B(1-j\Delta p)}, j = 0, \ldots n$. Matrices $C_{B(1-n\Delta p)}$, $C_{MIY_0, \ldots\ldots} C_{MIY_{n-1}}$ and vectors $c_{B(1-n\Delta p)}, c_{MIY_0, \ldots\ldots} c_{MIY_{n-1}}$,:

$$C_{B(1-j\Delta p)} = C_{B(1-(j+1)\Delta p)} + C_{MIY_j} \quad (7)$$

$$c_{B(1-j\Delta p)} = c_{B(1-(j+1)\Delta p)} + c_{MIY_j} \quad (8)$$

Consider an input hand bone image. Figure 2 shows the input noise image and preprocessed image.

Feature extraction: Then most significant five categories of features are extracted in this phase. The five features are:

- Color histogram and color moments (81 dimensions)
- Gabor wavelets transform (120 dimensions)
- Edge direction histogram (37 dimensions)
- GIST features (512 dimensions)
- Local binary pattern (59 dimensions)

For input images of X-ray skull and hand bone image, color histogram and color moments (81 dimensions) results is shown in Fig. 3. Color histogram and color moments for pre-processed hand bone image results are shown in Fig. 4.

Edge histogram outcome of the feature extraction for the entire input image samples results are illustrated in Fig. 5. Edge histogram results of the feature extraction for pre-processed input image samples results are illustrated in Fig. 6.

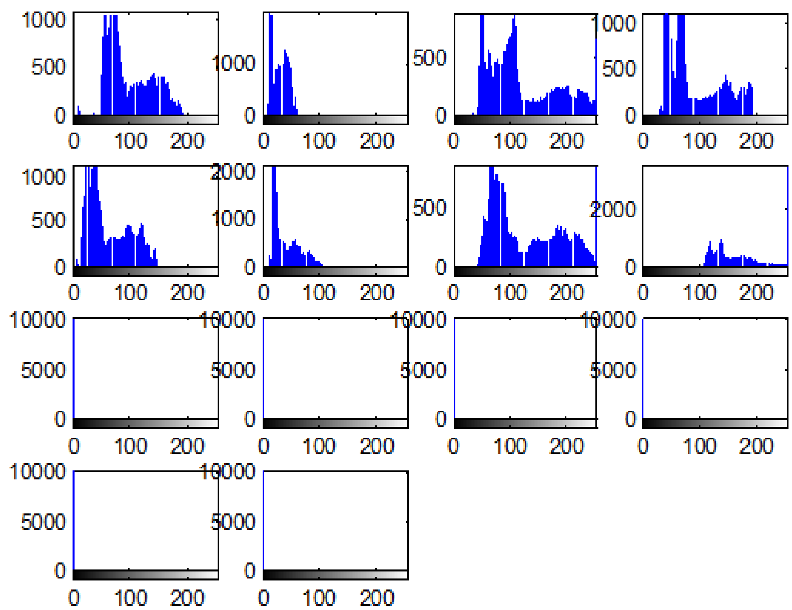


Fig. 3: Color histogram and color moments feature extraction results for all images

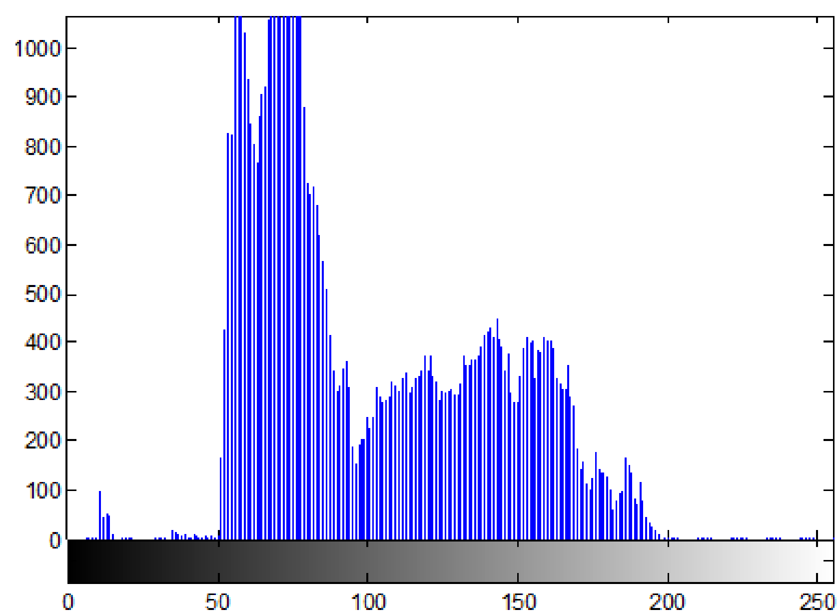


Fig. 4: Color histogram and color moments feature extraction results for pre-processed images

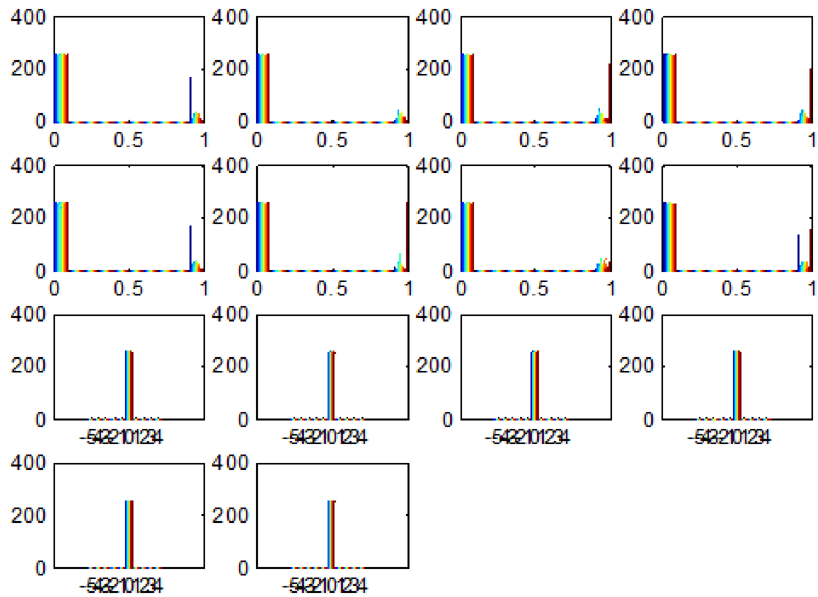


Fig. 5: Edge direction histogram feature extraction results for all images

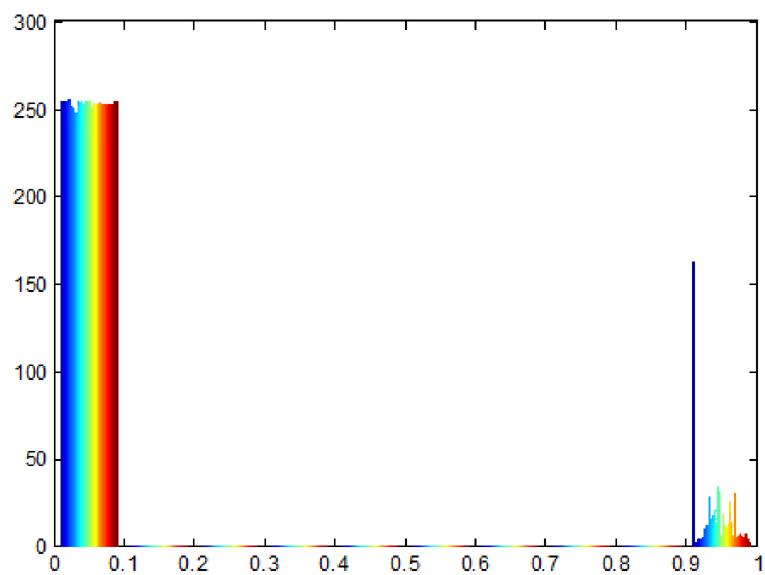


Fig. 6: Edge direction histogram feature extraction results for pre-processed image

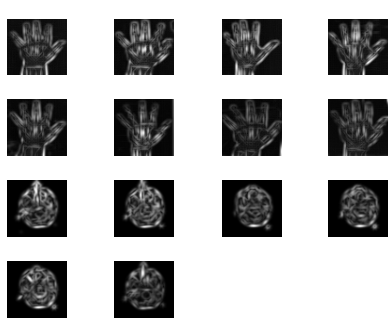


Fig. 7: Gabor wavelet transform feature extraction results for input images

Figure 7 shows the Gabor wavelets transform based feature extraction results for complete input images and the same for pre-processed input image samples is illustrated in Fig. 8.

Figure 9 shows the local binary pattern based feature extraction results for the entire input images results and the same for pre-processed input image samples is given in Fig. 10.

These global features have been extensively employed in the previous CBIR researches.

In case of local features, obtain the bag-of-visual-words features by means of two categories of descriptors:

Fig. 8: Gabor wavelet transform feature extraction results for pre-processed images

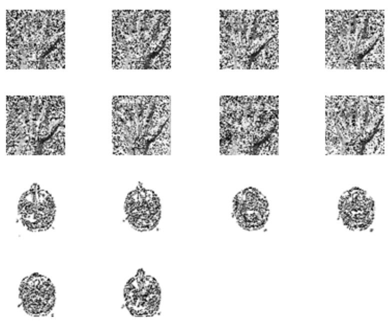


Fig. 9: Local binary pattern feature extraction results for all input images

Fig. 10: Local binary pattern feature extraction results for pre-processed images

- The SIFT descriptor-adopt the Hessian-Affine interest area detector with threshold 500
- The SURF descriptor-implement the SURF detector with threshold 500. In case of the clustering phase, implement a forest of 16 kd-trees and look for 2,048 neighbours to accelerate the clustering process. In the end, implement the TF-IDF weighing scheme to produce the concluding bag of-visual-words representation. By means of selecting different descriptors (SIFT/SURF) and vocabulary sizes (200/1,000), completely extracted four kinds of local features: SIFT200, SIFT1000, SURF200 and SURF1000.

Relevance score calculation using Kernel Support Vector Machine (KSVM): Through the assistance of Relevance Score (RS), it is easy to obtain a limited amount of appropriate and unrelated medical image photos or their characteristics from the query image phase to additionally refine the retrieval results. On the other hand, the feature distributions of medical image from several domains might vary significantly and as a result have extremely diverse statistical properties. In order to distinguish the medical images from these two domains, characterize the labelled and unlabeled feature vector from last step $\mathrm{fvD}_{\mathrm{l}}^{\mathrm{T}} = (\mathrm{fv}_{\mathrm{l}}^{\mathrm{T}}, \mathrm{fvy}_{\mathrm{l}}^{\mathrm{T}})_{\mathrm{i}=1}^{\mathrm{n_l}}$ and $\mathrm{fvD}_{\mathrm{u}}^{\mathrm{T}} = \mathrm{fv}_{\mathrm{l}}^{\mathrm{T}}|_{\mathrm{i}=\mathrm{n_l}+1}^{\mathrm{n_l}+\mathrm{n_u}}$, correspondingly, in which $\mathrm{fvy}_{\mathrm{l}}^{\mathrm{T}} \in \{\pm 1\}$ indicates the label of $\mathrm{fv}_{\mathrm{l}}^{\mathrm{T}}$. Then FV^{W} is indicated as the data set feature vector from the medical image database and $\mathrm{FV}^{\mathrm{T}} = \mathrm{FVD}_{\mathrm{l}}^{\mathrm{T}} \cup \mathrm{FVD}_{\mathrm{u}}^{\mathrm{T}}$ as the feature vector medical image samples data set from the input image with the size $\mathrm{n_T} = \mathrm{n_l} + \mathrm{n_u}$. In order to learn RS using the Kernel based Support Vector Machine (KSVM) in this process, Fuzzy sigmoid kernel function is employed as kernel function. A KSVM technique efficiently recognizes relevant and irrelevant features vectors by the process of maximization of margin size between feature vectors. Simplify the process of RS learning for medical image database with feature extracted results, it computes the similarity between variables, it makes use of inner product as metric. In this process, let $\mathrm{fvD}_{\mathrm{l}}^{\mathrm{T}} = (\mathrm{fv}_{\mathrm{l}}^{\mathrm{T}}, \mathrm{fvy}_{\mathrm{l}}^{\mathrm{T}})_{\mathrm{i}=1}^{\mathrm{n_l}}$ distinguish the medical images from these two domains; characterize the labelled and unlabeled feature vector. $\mathrm{fvy}_{\mathrm{l}}^{\mathrm{T}} \in \{\pm 1\}$ indicates the RS learning, where C represents the number of classes, for $\mathrm{c} = 1, \ldots, \mathrm{C}$ and $\sum_{\mathrm{c}} \mathrm{fvy}_{\mathrm{ic}}^{\mathrm{T}} = 1\, \phi(.)$ is indicated as nonlinear mapping function of gradient function, it is done in accordance with the Cover's theorem (Samuelson and Brown, 2011) which promises high classification accuracy rate for linearly separated medical image feature vector samples and it is commonly higher dimensional feature space s:

$$\min_{W,\xi_i,b}\left\{\frac{1}{2}||w||^2 + r\sum_i \xi_i\right\} \tag{9}$$

Constrained to the:

$$\mathrm{fvy}_{\mathrm{l}}^{\mathrm{T}}\left(\phi^{\mathrm{T}}\left(\mathrm{fv}_{\mathrm{l}}^{\mathrm{T}}\right)\mathrm{W} + \mathrm{b}\right) \geq 1 - \xi_{\mathrm{i}} \forall \mathrm{i} = 1, \ldots.\mathrm{n}, \\ \xi_{\mathrm{i}} \geq 0\ \forall \mathrm{i} = 1, \ldots.\mathrm{n} \tag{10}$$

Where $\mathrm{W}\&b$ indicates a linear classifier for medical image data samples. RS, KSVM processes are managed by regularisation parameter r and it is automatically selected by the user, the error values of medical image with feature extracted vectors are represented using the parameter ξ_i. With the aim of increasing the classification accuracy, a kernel function K is employed:

$$\mathrm{K}\left(\mathrm{fvy}_{\mathrm{il}}^{\mathrm{T}}, \mathrm{fvy}_{\mathrm{jl}}^{\mathrm{T}}\right) = \phi\left(\mathrm{fvy}_{\mathrm{il}}^{\mathrm{T}}\right).\phi\left(\mathrm{fvy}_{\mathrm{jl}}^{\mathrm{T}}\right) \tag{11}$$

This kernel function effect does not enhance the medical information retrieval results, in order to surpass these complication, here kernel function are estimated in accordance with fuzzy sigmiod function and is defined as follows:

$$f(fvy_l^T) = \mathrm{sgn} \sum_{i,j=1}^{n} fvy_{il}^T fvy_{jl}^T \alpha_i \alpha_j K(fv_{il}^T, fv_{il}^T) + b \quad (12)$$

Where the biases value (b) of fuzzy kernel can be effortlessly computed from the α_i, it happens to be neither 0 nor C. This study broadens the fundamental conceptions of hyperbolic tangent function from Müller *et al*. (2001) and it is given as follows:

$$K(fv_{il}^T, fv_{jl}^T) = \begin{cases} -1 & fv_{il}^T . fv_{jl}^T is low \\ +1 & fv_{il}^T . fv_{jl}^T is high \\ m. fvy_{il}^T . fvy_{jl}^T, fv_{il}^T . fv_{jl}^T & is medium \end{cases} \quad (13)$$

where m indicates a stable value denoting the effectiveness of the sigmoid tract. In the report of fuzzy logic theory, the sigmoid kernel function is characterized as collection of fuzzy membership functions. Several fuzzy membership functions presents; however in this study only concentrated on three triangular functions, as a consequence of their simplicity. Subsequent to fuzzy sigmoid kernel function be continuous, thus the Eq. (14) can be readily re-written as a function of a and γ, as given below:

$$K(fv_{il}^T, fv_{jl}^T) = \begin{cases} -1 & fv_{il}^T . fv_{jl}^T \le \gamma - \left(\frac{1}{a}\right) \\ +1 & fv_{il}^T . fv_{jl}^T \ge \gamma + \left(\frac{1}{a}\right) \\ 2\left(fvy_{il}^T . fvy_{jl}^T - \gamma\right) - & \\ a^2 \left(fvy_{il}^T, fvy_{jl}^T - \gamma\right) . \left|fv_{il}^T . fv_{jl}^T - \gamma\right) \right| & \end{cases} \quad (14)$$

which is the concluding form of the proposed fuzzy sigmoid function (fuzzy tanh) kernel. The foremost benefits of this function are:

- It executes more rapidly, for the reason that the final results of classification potential are expressed in a succession of saturated samples (Eq. (14))
- It allows to pick different levels of non-linearity by making a decision on the quantity and superiority of the membership functions.

Discriminative Dictionary Learning (DDL) for similarity matching: The majority of existing approaches make use of a distance metric learning for the purpose of similarity matching of the query and input image, restricts their capability of determining similarity of complex patterns in real-time applications. With the aim of overcoming this complication, Discriminative Dictionary Learning (DDL) is formulated which learns a flexible nonlinear proximity function in order to enhance visual similarity search in CBIR. In addition, DDL incorporates the pair wise constraints for feature vector values results from RS learning and a linear predictive classifier into the objective function for the purpose of dictionary learning, which takes care of the desirable features of discriminativeness in the feature vectors of query and input image. Consider $Y = [y_1, y_2, \dots, y_N] \in \mathbb{R}^{n\times N}$ indicates the feature vector RS learning results of query image and input medical image database, in which $y_i \in \mathbb{R}^n$ indicates the i-th input query in addition to input medical image database with n-dimensional feature description. Provided a dictionary $A = [a_1, a_2, \dots, a_N] \in \mathbb{R}^{n\times k}$, in which a_i indicates the i-th dictionary atom with l_1 regularization calculates the similarity score for input RS feature vector and it is given as $[x_1, x_2, \dots, x_N] \in \mathbb{R}^{k\times n}$, of the feature vector from RS, through solving the following l_1 minimization complication:

$$X^* = \arg\min_X \sum_{i=1}^{N} (\left|\left|y_i - Ax_i\right|\right|_2^2 + \gamma\left|\left|x_i\right|\right|_1) \quad (15)$$

where, γ constant indicates a sparsity constraint factor and the term $\left|\left|y_i - Ax_i\right|\right|_2^2$ indicates the reconstruction error for matching results. Every input feature vector from RS y_i can be indicated as a linear combination of a certain dictionary atoms. The objective of dictionary learning is to discover optimized dictionaries that offer a concise representation for most statistically representative feature vector values results from RS learning. The formulation (2) dictionary learning simply concentrates on reducing the reconstruction error and does not take the discriminative power of a dictionary into account for learning tasks. With the aim of overcoming these complications DDL is formulated in this study with pairwise constraints. Constraints algorithm which considers the associations of each pair of the feature vectors (x_i, x_j). The proposed DDL consequently concentrate on the consequences of accumulating a discriminative term and a classification error. In order to get hold of discriminative feature vector x by means of the pairwise constrained dictionary A, the objective function for dictionary creation is given as follows:

$$< A^*, X^* > = \arg\min_{A,X} \sum_{i=1}^{N} (\left|\left|y_i - Ax_i\right|\right|_2^2 + \gamma\left|\left|x_i\right|\right|_1) + \frac{\beta}{2}\sum_{i,j=1}^{N} ||x_i - x_j||_2^2 M_{ij} \quad (16)$$

$$\arg\min_{A,X} \sum_{i=1}^{N} (\left|\left|y_i - Ax_i\right|\right|_2^2 + \gamma\left|\left|x_i\right|\right|_1) + \beta(Tr(X^T XD) - Tr(X^T XM)) \quad (17)$$

$$\arg\min_{A,X} \sum_{i=1}^{N} (\left|\left|y_i - Ax_i\right|\right|_2^2 + \gamma\left|\left|x_i\right|\right|_1) + \beta(Tr(X^T XL) \quad (18)$$

where, the constants γ and β manage the virtual contribution of the resultant terms. The first term $\left|\left|y_i - Ax_i\right|\right|_2^2$ indicates the reconstruction error term, which assesses the reconstruction error of the approximation to the query and input image matching results for RS feature vector. The second term $||x_i||_1$ indicates the regularization term. The last term, which is fresh and proposed at this point, indicates the discrimination term called ‘pair-wise error feature vector’ in accordance with the pairwise constraints which are encoded in matrix M. $D = diag\{d_1, \ldots, d_N\}$ indicates a diagonal matrix where diagonal elements are the summations of the row elements of M:

$$d_i = \sum_{j=1}^{N} M_{ij} \, . \, L = D - M \tag{19}$$

Is the Laplacian matrix. Matrix M has various forms in accordance with the setbacks being taken into account. For instance, in face verification, the association of a pair (y_i, y_j) is provided as same/different. As a result, provided the sets of ‘similar feature vectors from RS learning’ and ‘diverse feature vectors from RS learning’ pairs S and D, characterize matrix M to encode the (dis) similarity information as given below:

$$M_{ij} = \begin{cases} +1 \text{ if } (y_i, y_j) \in S \\ -1 \text{if } (y_i, y_j) \in D \\ \quad 0 \text{ else} \end{cases} \tag{20}$$

Even though (18) can already be employed for the purpose of classification by defining M in accordance with the pairwise similarity constraints with category labels, the matching error can be additionally incorporated as an additional term in the objective functionin (18). At this point, employ a linear predictive classifier for the purpose of matching query and input matching results $f(x, W) = Wx$. The objective function for learning a pairwise constrained dictionary A for query and input image feature vectors from KSVM with both reconstructive and discriminative power can be given as:

$$< A^*, X^*, W^* > = \arg\min_{A,X,W} \sum_{i=1}^{N} (||y_i - Ax_i||_2^2 + \gamma||x_i||_1) + \frac{\beta}{2} \sum_{i,j=1}^{N} ||x_i - x_j||_2^2 M_{ij} + \alpha \sum_{i,j=1}^{N} ||h_i - Wx_i||_2^2 + \lambda||W||_2^2 \tag{21}$$

$||h_i - Wx_i||_2^2 + \lambda||W||_2^2$, $||h_i - Wx_i||_2^2$ indicates the classification query matching error, $||W||_2^2$ indicates the regularization penalty term, assists in learning an optimal linear predictive classifier $h_i = [0,0,..,1,..,0,0]^T \in \mathbb{R}^m$, (m indicates the number of classes) is a label vector related to a feature vectors results from KSVM learning, where non-zero position represents the class label of y_i.

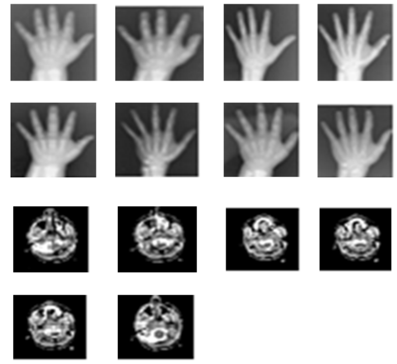


Fig. 11: IRMA for content-based image retrieval

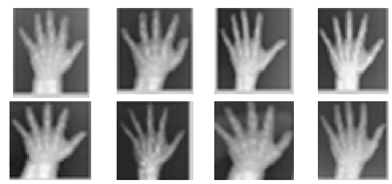


Fig. 12: IRMA for image retrieval results in content-based image retrieval after

RESULTS AND DISCUSSION

The assessment for extended query based image retrieval system was realized within the content based Image Retrieval with Medical Image (IRMA) framework. An online presentation for medical image retrieval in accordance with the IRMA framework is implemented using MATLAB environment. Medical CBIR can be done in a demonstration mode by means of the images within the IRMA system. A snapshot of the input image with X-ray skull and hand bone image is illustrated in Fig. 11. The image retrieval results are illustrated in Fig. 12. It was traced with the assistance of Google image search for “X-ray skull” and hand images and obtained from the University of Illinois at Chicago, College of Medicine, Department of Radiology, available online at (http://www.uic.edu/com/uhrd/images/Simpson_head Xray.jpg).

With its fundamental flexible construction of image processing and image retrieval approaches, the IRMA framework was fine-tuned to enhance CAD in the perspective of Bone Age Assessment (BAA). In view of the fact that the IRMA system incorporation into clinical information systems can be realized by Digital Imaging and Communications in Medicine (DICOM) Hosted Applications and DICOM Structured Reporting.

Sensitivity and specificity: Experimentation results of the proposed DDL methods for IRMA framework for two medical images shown in the Fig. 13 and 14 results are assessed with the help of the following metrics. In medical statics commonly exploited measurements are sensitivity and specificity defined as follows:

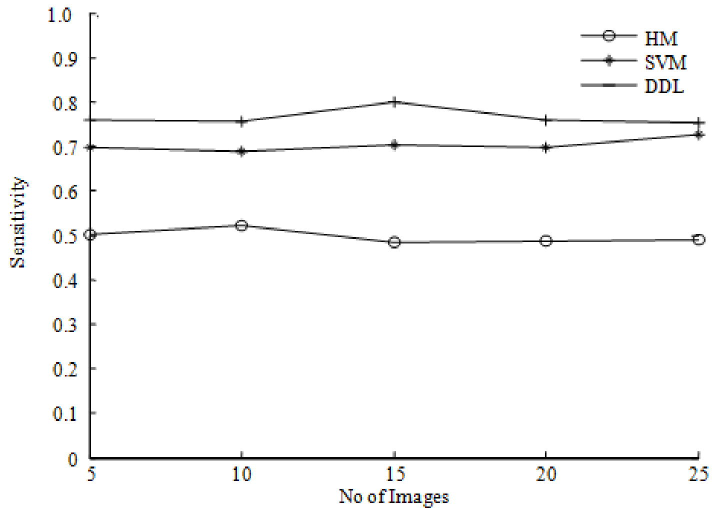


Fig. 13: Sensitivity results comparison for X rays images in IRMA

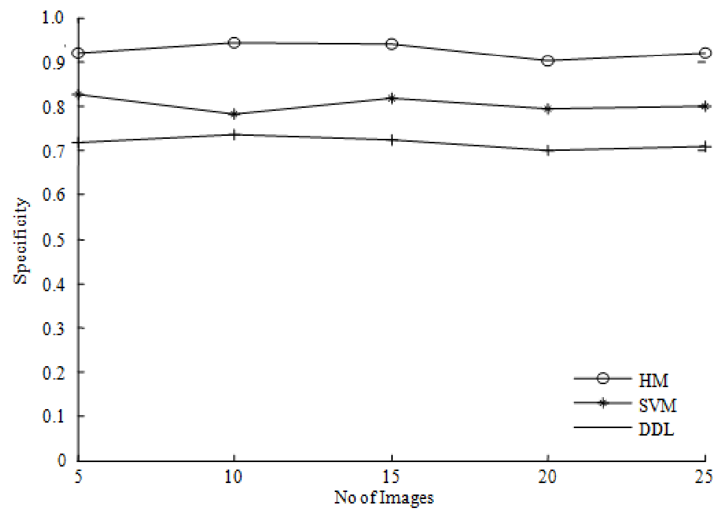


Fig. 14: Specificity results comparison for X rays images in IRMA

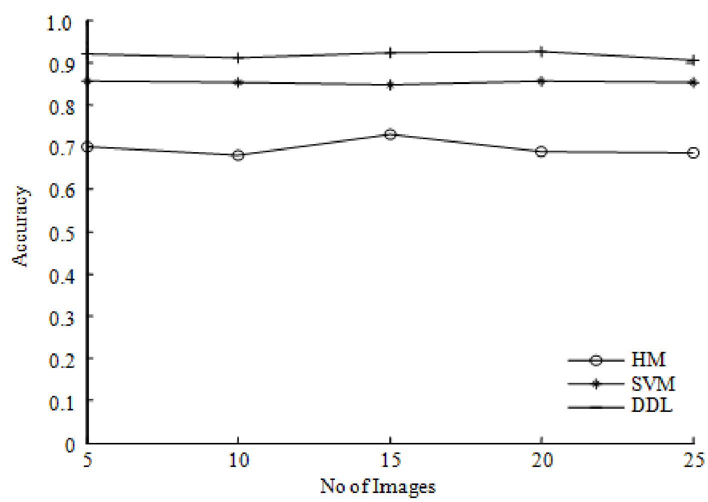


Fig. 15: Classification results comparison for X rays images in IRMA

$$\text{Sensitivity} = \frac{\text{positive items classified as positive}}{\text{all positive items}} \quad (22)$$

$$\text{Specificity} = \frac{\text{negative items classified as negative}}{\text{all negative items}} \quad (23)$$

The experimentation results of the proposed DDL with IRMA framework for Spine Pathology and Image Retrieval System (SPIRS) (Müller *et al*., 2001) was constructed at the U. S. National Library of Medicine to retrieve x-ray image and radiographs from clinical routine image is determined with SVM (Samuelson and Brown, 2011). It demonstrates that the sensitivity results of the proposed DDL for x-ray skull images have better sensitivity than the existing approaches, in view of the fact that it eliminates noise from x ray image samples at first prior to carrying out similarity matching, RS learning also done in the proposed work. The results are illustrated in Fig. 13. The experimentation specificity results of the proposed and existing methods for clinical routine image are represented in Fig. 14. It shows that the performance results of the proposed system is less since it falsely retrieve results are less.

As many of the presented systems use classifications of images, accuracy is fundamentally employed to evaluate the system:

$$\text{Accuracy} = \frac{\text{items classified correctly}}{\text{all items classified}} \quad (24)$$

The experimentation classification results of the proposed DDL with IRMA framework for Spine Pathology and Image Retrieval System (SPIRS) was constructed at the U. S. National Library of Medicine to retrieve x-ray image and radiographs from clinical routine image is determined with SVM. It shows that the classification results of the proposed DDL for x-ray skull images are better than the existing approaches, as it eliminates noise from x ray image samples at first prior to carrying out performing similarity matching and then accurately performed matching for the entire image samples are illustrated in Fig. 15.

Precision and recall: It is to be noted that CBIR are not primarily being utilized for classification purpose, however for discovery of similar images or cases. This is habitually more supportive as the consultant must still judge the retrieved cases and the reasons for retrieving the images are often clearer whereas classification results are sometimes hard to detail and need to be explained. In order to evaluate CBIR, the precision P and the recall R, defined as follows:

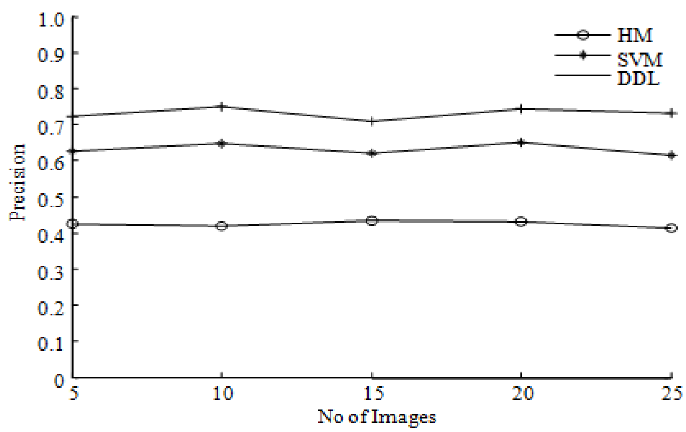


Fig. 16: Precision results comparison for X rays images in IRMA

Table 2: Performance comparison of methods in terms of sensitivity, specificity and accuracy for BAA

	Sensitivity (%)			Specificity (%)			Accuracy (%)		
No of images	HM	SVM	DDL	HM	SVM	DDL	HM	SVM	DDL
5	0.52	0.698	0.758	0.912	0.8245	0.724	0.714	0.874	0.926
10	0.53	0.712	0.765	0.9368	0.802	0.737	0.698	0.856	0.924
15	0.498	0.721	0.798	0.9218	0.834	0.7314	0.7412	0.864	0.9356
20	0.523	0.7458	0.7514	0.901	0.827	0.7213	0.7314	0.8641	0.925
25	0.598	0.7125	0.758	0.918	0.814	0.708	0.6941	0.851	0.901

Table 3: Performance comparison of methods in terms of precision and recall for BAA

	Precision (%)			Recall (%)		
No of images	HM	SVM	DDL	HM	SVM	DDL
5	0.420	0.624	0.718	75.46	81.56	87.97
10	0.4347	0.6348	0.754	75.98	81.90	87.99
15	0.4418	0.6278	0.7158	76.23	82.34	88.94
20	0.4517	0.6841	0.7537	77.57	82.94	89.46
25	0.4178	0.6218	0.7214	77.98	83.67	90.12

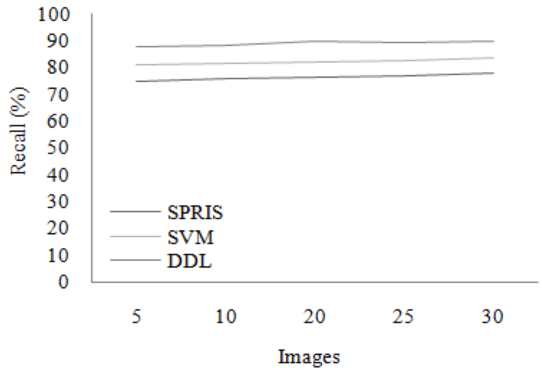


Fig. 17: Recall results comparison for X rays images in IRMA

$$\text{Precision} = \frac{\text{no.relevant items retrieved}}{\text{no.items retrieved}} \tag{25}$$

$$\text{Recall} = \frac{\text{no.relevant items retrieved}}{\text{no.relevant items}} \tag{26}$$

The experimentation results precision and recall parameters of the proposed DDL with IRMA framework for Spine Pathology and Image Retrieval System (SPIRS) (Hsu *et al*., 2007) was constructed at the U. S. National Library of Medicine to retrieve x-ray image and radiographs from clinical routine image is measured with SVM (Amaral *et al*., 2010). It shows that the precision and recall results of the proposed DDL for x-ray skull images have higher than the existing methods, since it removes noise from x ray image samples initially before performing similarity matching, results of the precision values are illustrated in Fig. 16. The experimentation recall results of the proposed and existing methods for clinical routine image are represented in Fig. 17. It shows that the performance results of the proposed system is less since it falsely retrieve results are less.

BAA on hand radiographs is an expensive and time consuming process in radiology. Mansourvara *et al.* (2012) formulated a Histogram based Matching (HM) to carry out CBIR for IRMA framework. In recent times, an automatic scheme combining CBIR and SVM regression has been formulated by Haak *et al.* (2013). The performance comparison results of the proposed DDL for DDL with IRMA framework context of BAA measured based on the classification parameters like sensitivity, specificity, accuracy results are tabulated in Table 2. The performance comparison results of the methods in terms of precision and recall values are tabulated in Table 3.

CONCLUSION AND RECOMMENDATION

In current scenario, image management and pathologically sensitive CBIR systems are ever more necessary to cooperate with the mounting volume of biomedical imaging data. Regardless of their acknowledged significance, limitations in current approaches have prevented their pervasive acceptance into medical research, practice. In recent times, BAA has drawn substantial academic attention. But, BAA image sets including noisy images from every day routine can effect in additional information. It is also complicated for individual x ray images systems to support unique requirements of different biomedical images. In order to overcome these complications, in this study presented learning methods with image pre-processing scheme to remove noise from medical images. The noises exists in the fields of BAA and X ray skull images noise are eliminated by using Principal Component Analysis (PCA). It is observed that higher noise level estimation accuracy paves way for higher denoising quality in most scenarios. To enhance the retrieval results for medical images, proposed RS methods, namely KSVM by utilizing the feature vectors of input medical database images and the score results images to efficiently enhance the retrieval performance at better response time. To precise matching of the images DDL based IRMA framework is potential enough to interact with and retrieving relevant information from huge medical images databases and user query image. By exploring the power of discriminative pairwise similarity measurement in combining medical data, DDL learns a much more flexible to enhance medical image retrieval results in IRMA for BAA and X ray Skull images. Besides, complete evaluation of hand radiograph data has shown that BAA prediction in CAD offers potential results for additional investigations. In future, it is essential to explore more applications and address both theoretical and practical confronts of the proposed DDL framework for extensive applications, like the multimedia images, video retrieval and other categories of medical images.

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