

# Multi-Trend Structure Descriptor At Micro-Level For Histological Image Retrieval

M.Natarajan, S.Sathiamoorthy



**Abstract:** Since hospitals are generating and using image data extensively, medical image databases and its size are rising rapidly. This led to difficulties in browsing and managing the huge databases. Therefore, the necessity for the development of efficient content-based medical image retrieval (CBMIR) system arises and is more challenging problem for researchers. In this paper, to alleviate the unbalanced distribution of image representation using multi-trend structure descriptor (MTSD), MTSD is computed at micro level i.e., image is divided into number of sub-images and for each sub-image MTSD is exploited. In similarity measurement, we compared the MTSDs of corresponding sub-images in query and target images than the linear ordered collection of smallest similarity values between the sub-images are considered for retrieval. Experiments reveal that computation of proposed feature at micro level retains the localized representation and considering the linear ordered collection of smallest similarity values between the sub-images provides consistency under illumination changes and noise and thus proposed CBMIR achieves better results.

**Keywords:** Multi-Trend Structure descriptor, Micro-level, Manhattan measure, Local structure, Trends.

## I. INTRODUCTION

Comprehensively to ease the disease diagnosis in medical domain. Therefore, effective searching and management of medical image data received more attention of researchers. Over the decade, several medical image retrieval systems are provided by the researchers and are specific to organ or modality or dealing with all categories of medical images, and uses either DICOM format or low-level visual information or high-level information. Since DICOM attributes are in text format and fallouts in error prone [1] and the problem of semantic gap in the mapping of low-level visual information into high level information, researchers still interested in enhancement of CBMIR using low level visual information. Several research interests associated with CBMIR have been suggested in the past.

Gray level co-occurrence matrix (GLCM) exploited along various directions and distances are reported for CBMIR in [2]. IRMA presented in [3, 4] is a web-based retrieval system for X ray images and it performs analysis of X-ray images

using raw and registered data, object, feature, scheme and knowledge that is IRMA is based on six layers model. Spatial weighted entropy is used in fuzzy c-means for CBMIR [5]. He et al. analyzed the facial paralysis using local binary patterns (LBP) [6]. Sorensen et al. performed pulmonary emphysema disease analysis using LBP [7]. In [8], regularity of structure and brightness is captured for CT images of chest using rotation invariant LBP and the variances in gradient orientations. Unay et al. performed retrieval of MR images of brain using structures exploited from local level [9]. Signatures computed from wavelet transform is described in [10] for CBMIR system. Local patterns computed from the mesh of neighbor pixels are used for indexing and retrieving medical images [11]. Murala et al. presented peak valley edge pattern for medical image retrieving [12]. Indexing and retrieving CT and MR images is performed by integrating local mesh and peak valley edge patterns in [13].

Qayyum et al., [14] presented deep learning framework for CBMIR using deep convolutional neural network. In [15], the topics of clustered SIFT features is encoded by Latent Dirichlet Allocation (LDA) and performed early and late fusion for integrating text and visual features for the retrieval of medical images. In [16], for CBMIR, mean, standard deviation and skewness of H, S and V channels, higher order features of GLCM and histogram of edge direction are computed than feature dimensionality is decreased by applying principal component analysis than fusion of supervised support vector machine (SVM) and unsupervised fuzzy c means (FCM) is used for reducing the search space and image matching is performed using Bhattacharyya distance. In [17], histogram of edge direction, color layout descriptor computed from the DCT coefficients of YCbCr color model, GLCM computed from five overlapping sub images are classified using multi-class SVM and represented in probabilistic feature space. In [18], Rahman et al., advances CBMIR by combining visual and semantic features and is further enhanced in [19] and [20]. In [21], Self-organizing map is utilized for codebook generation from key points which are derived using SIFT from edge cooperative maps exploited from  $L^*a^*b^*$  color model. Seetharaman and Sathiamoorthy [22] introduced CBMIR for diverse medical image collection in the context of full range autoregressive model with Bayesian approach. In [23], retrieval of pathological images of breast cancer is reported and it performs supervised hashing for complementary features by combining several kernel functions. Later on, several CBMIR systems for histological images are reported [24-30]. Wide-ranging review for CBMIR is presented on [1, 31 - 37]. Recently, MTSD, which exploits rich texture, shape and color information in the form of trends from local level structure, have shown considerable performance in image retrieval task [38].

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Later, inspired by the efficacy of MTSD, we combined the efficiency of MTSD with fuzzy k nearest neighborhood [39] and fuzzy SVM [40] respectively for CBMIR. In [41], we computed MTSD from pyramid structure multiresolution domain for the retrieval of stock photos and the approach is considerably less overhead in computation and retains the performance of MTSD. Even so, MTSD is rich in information and is computed from local level, representation of image using MTSD is at global level. But such a global level representation is not appropriate for medical images because the information in medical images is very minute and location based. Therefore, the motivation of this paper is introducing a novel CBMIR system using MTSD. In this respect, we decomposed the medical image into pyramid structure using discrete Haar wavelet than the whole image at optimum level decomposition is divided into number of sub-images and for each sub-image we computed MTSD. In the matching stage, we compared the corresponding patches of query and target images than the linear ordered collection of smallest similarity values are considered for retrieval. That is instead of global and unbalanced distribution of information provided by MTSD, we propose the computation and matching of MTSD at micro-level and it significantly enhances the retrieval rate of CBMIR system and also deals with illumination changes and noise. As well, the computation of MTSD for CBMIR is significantly reduced than the existing MTSD based CBMIR systems [39, 40] because of incorporation of wavelet-based decomposition approach. Consequently, the proposed CBMIR balances between retrieval rate and time cost.

The rest of the paper is organized as: the proposed methodology for CBMIR is discussed in Section 2, Section 3 illustrates similarity measure employed, and Section 4 illustrates experiments and results and Section 4 deals conclusion.

## II. PROPOSED FEATURE EXTRACTION

First, we transformed RGB images to HSV than pyramid structure decomposition is done using discrete Haar wavelet transformation as illustrated in [41]. The decomposition of HSV image is done up to the level of 3, which is found to be more optimum in [41]. The image at level 3 significantly reduces the computation cost as well preserves the accuracy of MTSD as in [38].

Later, HSV image at level 3 on multiresolution domain is divided into equal and non-overlapping sub-images which are in rectangular shape and size of each sub-image is  $M \times N$ , and the sub-images are numbered as  $1, 2, 3, \dots, S$ . Later on, we computed MTSD as follows. Uniform quantization is performed for each sub-image as illustrated in [38]. The quantization process produces 12, 3 and 3 levels for color, 20 and 9 levels for texture and shape respectively [38]. Both texture and shape information are exploited from V channel. In [38], Sobel operator is applied on V channel to compute the edges which is performed before uniform quantization. Afterwards, MTSD computes trends on quantized color, edge and texture information of the image. In [38],  $3 \times 3$  non-overlapping blocks are considered for computing the MTSD. Accordingly, for each  $3 \times 3$  blocks of  $M \times N$  sub-image, from left to right or bottom to top directions in  $0^\circ$  or  $45^\circ$  or  $90^\circ$  or  $135^\circ$  orientations, the values of pixels from large to small, small to large and same are coined as small, large and equal trends [38] and these trends are computed for

all the sub-images of quantized color, edge and texture images. The computed MTSDs for color, edge and texture information for each sub-image is expressed as follows

$$FV_C = (N_E^{Q_c}, N_S^{Q_c}, N_L^{Q_c}) \quad (1)$$

$$FV_t = (N_E^{Q_t}, N_S^{Q_t}, N_L^{Q_t}) \quad (2)$$

$$FV_E = (N_E^{Q_e}, N_S^{Q_e}, N_L^{Q_e}) \quad (3)$$

where  $FV_C, FV_t, FV_E, N, Q_c / Q_t / Q_e, E, S$  and  $L$  symbolizes color feature vector, texture feature vector, edge feature vector, number of trends, quantized color, quantized texture, quantized edge, equal trend, small trend and large trend respectively. For sample, MTSD for color information is given in Fig.1. Fig.2 illustrates various trends at various orientations. The fusion of MTSDs for color, edge and texture information for each sub-image is expressed as

$$FV_S = \{FV_C, FV_t, FV_E\} \quad (4)$$

Where  $FV_S$  symbolizes the MTSD of sub-image  $i$ . Therefore, the MTSD of whole image is ordered collection of  $S$  number of MTSD's, i.e.,

$$FV_I = \{FV_{i_1}, FV_{i_2}, \dots, FV_{i_S}\} \quad (5)$$

Accordingly, computing MTSD at micro-level, the proposed approach alleviates the global distribution of feature representation.

## III. SIMILARITY MEASURE

Let  $I$  and  $G$  be the two images and represented using the collections of MTSDs of sub-images say  $\{FV_{i_1}\}_{i=1}^S$  and  $\{FV_{g_i}\}_{i=1}^S$ . The normalized Manhattan measure [41] is incorporated as the measure between the corresponding local sub-images of images  $I$  and  $G$  and is expressed as

$$D_i(I, G) = \left\| \frac{FV_{i_1}}{\|FV_{i_1}\|_1} - \frac{FV_{g_i}}{\|FV_{g_i}\|_1} \right\|_1 \quad (6)$$

Where  $FV_{i_1}$  and  $FV_{g_i}$  represents  $i$ -th sub-image in  $I$  and  $G$  images. We only the measure the similarity between corresponding local sub-images between image  $I$  and  $G$ . In the proposed approach, instead of summing up the similarity measurements of all sub-images of image  $I$  and  $G$ , we pool the  $p$  ( $p < S$ ) smallest measurements and neglected the large measurements between sub-images of image  $I$  and  $G$  [42]. First, we computed  $\{D_i(I, G)\}_{i=1}^S$  than the results of similarity measures of corresponding sub-images of  $I$  and  $J$  are sorted in ascending manner such that

$$\{D_1(I, G)\} \leq \{D_2(I, G)\} \leq \dots \leq \{D_S(I, G)\} \quad (7)$$

Finally, similarity measurement between image  $I$  and  $G$  is the sum of  $p$  smallest order statistics and expressed as in [42]

$$D_p(I, G) = \sum_{i=1}^p D_i(I, G) \quad (8)$$

When  $p$  increases from 1 to  $S$ , the efficacy of proposed system increases first than decreases when weaker measurements i.e., larger the similarity values are included. Experimentally, we determined that  $1 < p < S$  provides better results. The computation cost for the matching process in the proposed work is  $O(LS)$  where  $L$  and  $S$  symbolizes dimension of MTSD and number of sub-images. The approach requires additional computation cost on sorting of similarity measures of corresponding sub-images of  $I$  and  $G$  and is  $O(S^2)$ . In general, linear combination of order statistics is expressed as in [42]

$$\sum_{i=1}^S w_i D_i(I, G) \quad (9)$$

Where  $w_i$  symbolizes weight and is either 0 or 1. The weight is assigned active i.e., 1 for smallest  $D_i(I, G)$  because smaller  $D_i(I, G)$  are stronger so that  $p$  smallest order statistics are added as in Eq. (8) for better matching output.

	E	S	L
0	21	20	1
1	36	12	9
.	.	.	.
.	.	.	.
108	23	10	0

Fig.1. MTSD for color feature

68	80	55	60	43	55	80	70	80	80	43	36
70	68	55	70	36	80	55	70	55	55	80	0
36	80	9	10	43	8	0	70	70	70	60	80

(a) (b) (c) (d)

Fig.2. (a). Small trends along 0° (b). Large trend along 45° (c). Equal trends along 90° (d). Equal trend along 135°

#### IV. EXPERIMENTAL RESULTS

We conducted extensive experiments to evaluate the proposed approach. The benchmark dataset used in [22] is employed in our experiments. The dataset contains diverse collections of medical images of various body parts, modalities and diseases. The dataset includes the images of modalities like Microscopy, Endoscopy, X-ray, CT, Ultrasound, MRI and Mammogram. The dataset has 6400 images of 83 classes with ground truth details. In the proposed work, we considered microscopy images only and the number of microscopy images in the database is 1708.

The MTSD is exploited as explained in Section II for all the histological images in the dataset and kept separately. The query image is randomly selected from image dataset and is fed to proposed CBMIR which computes MTSD for query image as explained in Section II. In the proposed matching operation as in Eq. (8), experimentally, we fixed  $p=70\%$  of  $S$  for similarity measurement. In the proposed CBMIR, the number of sub-images is determined on basis of trial and error and is fixed to 20 which give better output for the proposed CBMIR. Therefore, 70% of  $S$  is nothing but 14 and thus we added 14 smallest similarity measurements between corresponding sub-images of  $I$  and  $G$ . The remaining 30% of  $S$  having higher values in similarity measures and it is because of severe noise or lightening conditions [35].

The computation cost of proposed approach in matching process is reduced when we use Eq. (8) instead of using Manhattan measure [32]. Fig.3 shown clearly that recall increases first and start to decreases when  $p$  increases. Specifically, the similarity measure with 14 smallest similarity measurements over the 20 is significant and is obviously visible in Fig.3. Therefore, it very clear from Fig.3 that the new matching operation is more effective than [32]. We tested it for all the histological images in the dataset. In specific the proposed combination of MTSD at micro-level and matching method based on linear ordered collection of

smallest similarity values is well effective for images involving noise and illumination changes.

We used recall ( $\#$ ) and precision ( $\beta$ ) for measuring performance of proposed CBMIR and are explained as

$$\text{Precision } (\beta) = \frac{\text{No.of relevant images retrieved}}{\text{Total No. of images retrieved}} \quad (10)$$

$$\text{Recall } (\#) = \frac{\text{No.of relevant images retrieved}}{\text{Total No.of relevant images in dataset}} \quad (11)$$

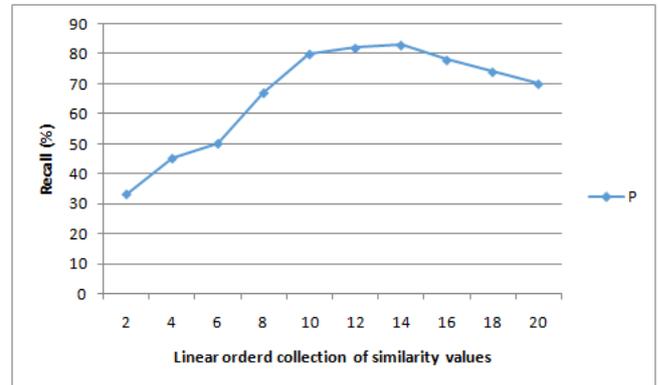


Fig.3. Recall ( $\#$ ) Vs linear order statistics for similarity values

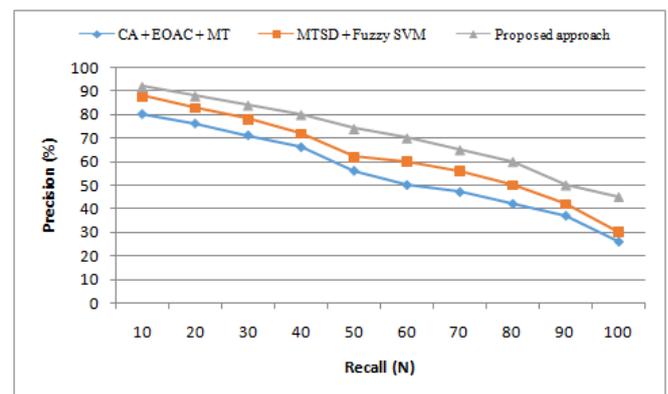


Fig.4. precision ( $\beta$ ) for proposed and existing approaches for histological dataset

We compared the output of proposed approach with the existing approaches [23, 40, 41]. In the proposed CBMIR, we considered both 14 and 20 sub-images in matching process. Compared with 20 sub-images, 14 improve the precision significantly as well maintains consistency against illumination changes and noise. The plot for recall ( $\#$ ) and precision ( $\beta$ ) is illustrated in Fig.4 and 5 for 14 sub-images. It is obviously seen from Fig.4 and 5 that proposed approach achieves significantly better than existing approach. Sample images from benchmark dataset are shown in Fig.6.

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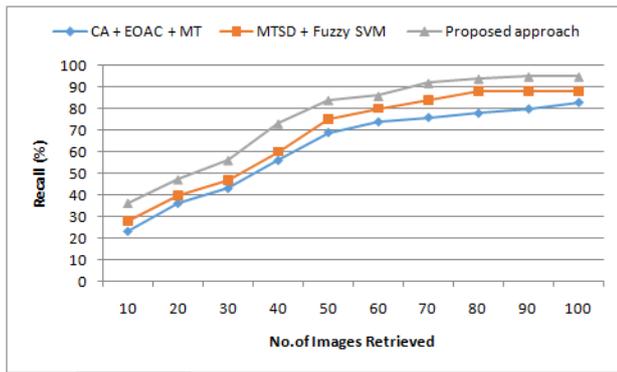


Fig.5. Recall ( $\bar{x}$ ) for proposed and existing approaches for histological dataset

Table 1. Retrieval rate for top 10 images retrieved by proposed and existing approaches on histological image data

Methods	Accuracy
Color Autocorrelogram (CA) + Micro-textures (MT) + Enhanced Edge Orientation Autocorrelogram (EOAC)	66.10
MTSD + Fuzzy SVM	60.91
Proposed approach	57.21

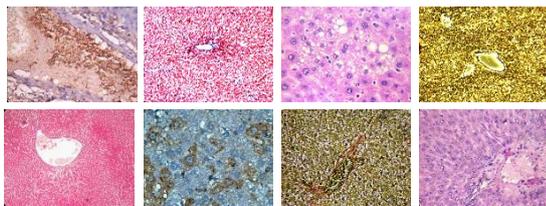


Fig.6. Sample images from the experimental datasets

## V. CONCLUSION

The aim of proposed CBMIR is improving the retrieval rate of histological images which are severely affected by noise or illumination changes. The proposed CBMIR employed MTSD feature which is computed from the local level structure of color, edge and texture image in the form of trends. To reduce the computational cost, pyramid structure wavelet is incorporated and the level of decomposition is set to 3. The image in multiresolution domain is divided into number of sub-images and MTSD is computed for each sub-image in order to alleviate the global distribution of MTSD representation. In the matching phase, only small similarity measurements between the sub-images are taken into consideration and the similarity measurements in larger values are caused by noise or illumination changes and so they are neglected in proposed CBMIR. Therefore, computation of MTSD at micro-level with the matching process in linear combination of order statistics provides better outputs. In future, we intend to increase the retrieval rate as well reduce the time cost by incorporating machine learning algorithms.

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