Organ Origin Identification Based on Fine Feature Analysis using Support Vector Machines

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Abstract

With increased usage of digital imaging equipments, approaches that can automatically categorize histological images for patient diagnosis and management are urgently needed more than ever. Since histological images are visually varied and complicated, to automatically identify the organ origin poses difficulties not just for computer but for clinicians as well. In this paper, we propose a hierarchical classification approach: an analysed image is divided into small images that will be measured with predefined meaningful fine features, which are visually discriminated by their texture components. The output of such measurement, although with certain inaccuracy, will be used for organ classification. Multi-class support vector machines (SVMs) are used to implement the hierarchical classification. This two-level classification approach minimises the dependence on accuracy of fine feature detection and considers not only the similarity between fine features but also the relationship between the performance of fine feature classification and organ identification. An empirical research demonstrates good performance of such approach.

Keywords: Histological image, image classification, image recognition, support vector machines, Gabor filter, texture feature, organ classification

1. Introduction

For a century, histopathology has remained as one of the major tools of diagnosis in clinical practice. With increased demand on managing histopathological image archive for training, referencing and assisting making diagnostic decision, automatic analysing and classifying such images become very meaningful and challenging research issues. Unlike other types of medical images, e.g. computed tomography (CT), magnetic resonance image (MRI), histopathological images are of more complicated visual content that is difficult to identify even for a doctor. Visual features in images are understood by subtle details in visual appearance. This required image content identification is based on their inherent semantics. Current research on content-based image retrieval (CBIR),

focusing purely on image primitives (like colour, texture and shape), cannot achieve such task unless more high level association of image primitives is introduced. With such concepts, a number of comprehensive surveys (Arnold, 2000; Rui, 1999) pointed out the promising and urgent research direction in bridging the semantic gap between low-level visual features and high-level concepts for CBIR. A review of content-based image retrieval in medical domain is discussed by Tang et al (1999), addressing the necessity of recognizing built-in semantics in histological images.

Organ classification is one of the important high-level information within histological images. In practice, to tell where the image is taken from is sometimes a challenging task even for a pathologist. Most importantly, such information also plays as a key cue to performance further semantic analysis for automatic annotating histological images (Tang, 2003). Figure 1 shows sample images taken respectively, from left to right, large intestine, anus, appendix, small intestine. The visual appearance is greatly different between images from different organs. Figure 2 gives further evidence on the complexity of analysing such images: four images all are taken from stomach, at the same magnification, the visual appearance also varies due to the different cutting angle, different time of taking the picture, or different preparation methods. However, on the other hand, images from the same organ, although this is not always the case, tend to share some common features (fine features) in local regions regardless the difference at a global scale. This provides a basis of the proposed approach for organ classification.

This paper describes a hierarchical classification approach for organ origin identification. Meaningful fine features as basic processing units were first defined and identified and this followed by further analysis for organ classification. The system is able to be tolerant to the inaccuracy of fine feature detection and in fact it will makes use of such result for further organ classification through Multi-class support vector machines (SVMs). SVMs is an on-going research topic in classification and has just begun in the recent decade, state-of-the-art performances in different applications using SVMs such as text categorization, face detection have been reported. It can obtain a comparatively good performance in limited domains or small data set. In this paper we try to use this method for large volumes of complicated histological features based on texture features extracted by Gabor filters. To explore the capability of SVMs in large scale multi-classes pattern recognition will be meaningful.

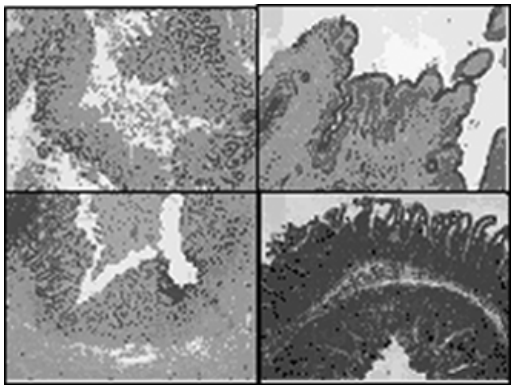

Figure1 images taken from respectively large intestine, anus, appendix, small intestine

The remaining of the paper is arranged as follows: Section 2 introduces the definition of fine features and image collection. The fine feature analysis and organ classification are proposed in Section 3 and 4 respectively. In the design of fine feature detection, we compare Gaussian Maximum Likelihood and Multi-class Support Vector Machines based on the same data set. In the organ classification level, an empirical comparison is also given between Maximum set algorithm and SVMs based on fine feature analysis. The experiment results

show that SVMs achieve a better accuracy in executing classification tasks of both levels. The conclusive remarks are given in section 5.

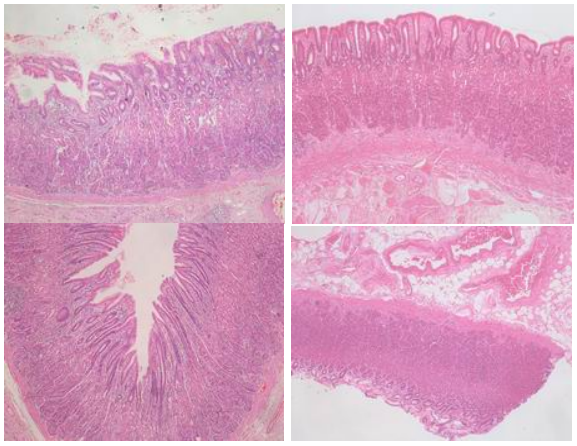

Figure2 images taken from stomach

2. The Definition of Fine Features and Image Collections

In order to define meaningful computable visual feature, the image is initially divided into a number of 64x64 sub-images as shown in figure 3 (visualised division by white lines). These sub-images form the basic feature units in this research, which need to be categorised and grouped and associated to certain histological meanings. For example, in figure 3, the sub-images within area A, B and C belong to different feature groups. When associating these features with their histological meanings, the sample sub-images are labelled by their histological names and the organ origin they belong to. Figure 4 gives some image feature samples and their corresponding histological labels including the organ origin. List 1 provides further examples or such in label set. In total there system tries to identify 63 meaningful visual features and classify images from 6 organs.

List 1 sample fine feature name and their organ origins.

lamina propria (all)
muscle: fine muscularis mucosae (all)
junctions: submucosa and fine muscularis mucosae (all)
oesophageal glands (OE)
stomach: cardia glands (ST)
small intestine: Brunner's glands (SI)
small intestine: intestinal glands (long) (SI)
large intestine: ovoid colon glands (LI)
appendix muscularis mucosae (AP)
anus: hair follicle (AN)

Where: all means the feature can appear in all the organs, SI means small intestine, LI, large intestine, ST stomach, OE, oesophagus, AP, appendix and AN, anus respectively.

All the feature detection and analysis processes are based on these feature units and we select training samples of sub-images deriving from different histological features to train the visual feature detectors. The relevant research issue at this stage are to determine the set of relevant visual features that are discriminating between different histological meanings.

3. Fine Feature Analysis

An image is partitioned into 64x64 pixels grids and texture features of each grid are extracted and then multi-class support vector machines are applied to classify each sub-image into correspondent fine features.

3.1. Texture features

The fine features are intrinsically made of various textured components which can be analyzed by many well-developed approaches such as wavelet transform (Wang, 2002; Kim, 2000; Manjunath, 2001), Gabor filter (Manjunath, 1996), cosine transform etc. Comprehensive surveys on texture analysis are given in (Ma, 1995; Randen,

1999). Among other methods, Gabor filter obtains a relatively good performance. An image is filtered using a bank of Gabor filters with different scales and orientations. The "post-Gabor" processing applies different operators to extract new feature vector for analysis, segmentation, or classification. Grigorescu, et. al. (2002) compared some operators based on Gabor filters: Gabor energy, complex moments, and grating cell operator features that gives the best discrimination and segmentation results. To simplify the research problem in this work, Gabor filters and "post-Gabor" operators in (Manjunath, 1996) are adopted.

The mother Gabor filter and its bank of filters are (1) and (2) respectively.

$$g(x,y)=\left(\frac{1}{2\pi\sigma_x\sigma_y}\right)\exp\left[-\frac{1}{2}\left(\frac{x^2}{\sigma_x{}^2}+\frac{y^2}{\sigma_y{}^2}\right)+2\pi jwx\right] \quad (1)$$

$$g_{mn}(x,y)=a^{-m}g\left(x',y'\right) \quad (2)$$

$$x' = a^{-m}(x\cos\theta + y\sin\theta),$$

where $y' = a^{-m}(-x\sin\theta + y\cos\theta),$

$$\theta = \frac{n\pi}{k}$$

m = 0,1,…,*s*-1 and n = 0,1,…,*k*-1. *s* is the number of orientations and *k* is the number of scales.

Figure3 an image example divided into sub-images

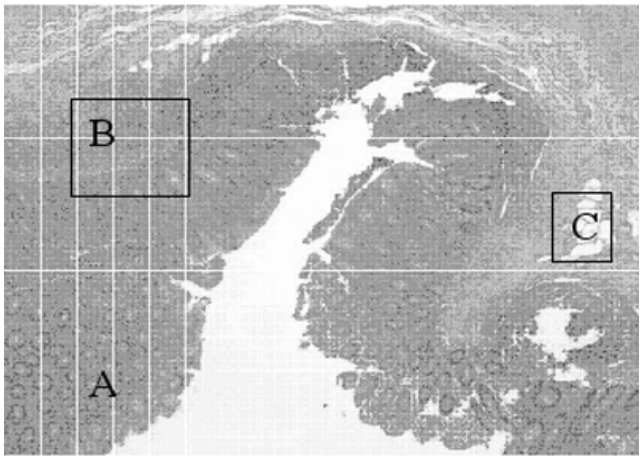

Figure4 sub-image feature samples

The following formulas are used to calculated parameters used in (2):

$a = \left(\frac{u_h}{u_l}\right)^{\frac{1}{s-1}}$, u_h and u_l denote the lower and upper centre frequencies of Gabor filters,

$\sigma_x = \frac{\sqrt{2}(a-1)u_h}{\sqrt{\ln 2}(a+1)\pi}$ and

$$\sigma_y = \tan\left(\frac{\pi}{2k}\right)\left[u_h - 2\ln\left(\frac{2\sigma_u^{\,2}}{u_h}\right)\right]\left[2\ln 2 - \frac{(2\ln 2)^2\sigma_u^{\,2}}{u_h^{\,2}}\right]^{-\frac{1}{2}}\left(\frac{2}{\pi}\right)$$

Given an image I(x, y) with $R \times C$ pixels, its Gabor wavelet transform is then defined as (3)

$$W_{mn} = \sum_{x_r=1}^{R}\sum_{y_c=1}^{C} I(x_r, y_c) g_{mn} * (x - x_r, y - y_c) \qquad (3)$$

* is the complex conjugate. The mean μ_{mn} and deviation δ_{mn} of W_{mn} are used in texture feature space. Since some fine features have the dominant colour compared with the other features under the same dyeing method such as lumen is grey and blood is red in the current image collections, the mean and deviation of R, G, B and grey intensity are added into texture feature space. In this paper, scales = 4 and orientation = 6, thus the feature vector for classification is

$$f = < \mu_{00}, \delta_{00}, \mu_{01}, \delta_{01}, ..., \mu_{35}, \delta_{35}, \mu_r, \delta_r, \mu_g, \delta_g, \mu_g, \delta_g, \mu_b, \delta_b, \mu_{grey}, \delta_{grey} >$$

3.2 Multi-Class Support Vector Machines

Support vector machines (SVMs) (Vapnik, 1998; Hearst, 1998; Burges, 1998) are initially designed for solving binary problems of pattern recognition. Its simplest linear form: $y = sign(w \bullet x - b)$, where $b \in R, w, x \in R^N, y \in \{1, -1\}$-see figure 5. An SVM is a hyperplane that separates positive examples from negative examples with maximum margin. The margin γ is defined as the distance of the nearest positive and negative examples, which equals to $\frac{2}{\|w\|^2}$. Maximizing margin becomes to the following optimization problem:

$$\min_{w,b} \frac{1}{2}\|w\|^2, \text{ subject to } y_i(w \bullet x_i - b) \geq 1, \forall i \qquad (4)$$

where x_i is the *i*th training example and y_i is the correct output of x_i.

Introducing Lagrangian multipliers, (4) is converted into the dual form (5), which is a QP problem.

$$\min_{\alpha} \frac{1}{2}\sum_{i=1}^{l}\sum_{j=1}^{l} y_i y_j \alpha_i \alpha_j x_i \bullet x_j - \sum_{i=1}^{l}\alpha_i, \text{ subject to}$$

$$\sum_{i=1}^{l} y_i \alpha_i = 0, \ \alpha_i \geq 0 \quad i = 1, ..., l \qquad (5)$$

where *l* is the number of training data.

After calculating α, $w = \sum_{i=1}^{l} y_i \alpha_i x_i$ and $b = w \bullet x_j - y_j$ for some $\alpha_j > 0$.

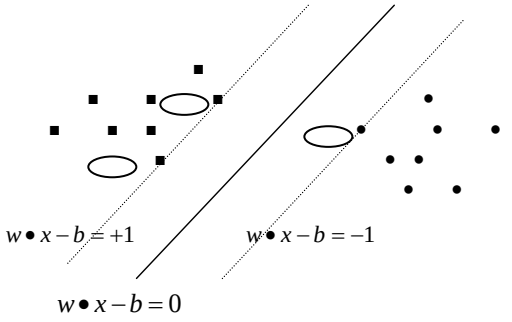

Figure5. Linear Support Vector Machines

However not all problems in reality are linear. Kernel functions for non-linear SVMs are proposed to nonlinearly map input space into other high dimension space: $\phi : R^N \to R^{N'}$ subject to $N << N'$ (see figure 6).

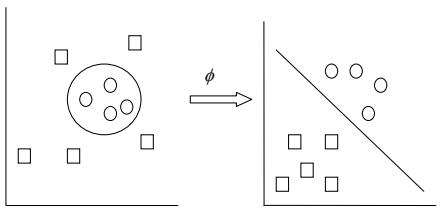

Figure6. Non-linear mapping

The formula (4) is added by penalty:

$\min_{w,b} \frac{1}{2}\|w\|^2 + C\sum_{i=1}^{l}\zeta_i$, subject to

$y_i(w \bullet \phi(x_i) - b) \geq 1 - \zeta_i, \forall i$ (6)

Its Lagrangian form is

$$\min_{\alpha} \frac{1}{2}\sum_{i=1}^{l}\sum_{j=1}^{l} y_i y_j \alpha_i \alpha_j \phi(x_i) \bullet \phi(x_j) - \sum_{i=1}^{l}\alpha_i$$

$$= \min_{\alpha} \frac{1}{2}\sum_{i=1}^{l}\sum_{j=1}^{l} y_i y_j \alpha_i \alpha_j K(x_i \bullet x_j)$$

subject to $0 \leq \alpha_i \leq C, \forall i$ (7)

The decision function $y = sign(w \bullet x - b)$ is converted into the following forms:

$$y = sign(w \bullet \phi(x) - b)$$

$$= sign(\sum_i y_i \alpha_i \phi(x_i) \bullet \phi(x) - b)$$

$$= sign(\sum_i y_i \alpha_i K(x_i \bullet x) - b)$$

Training an SVM requires the solution of a very large quadratic programming (QP) problem. Any optimisation approaches can be used to learn weights on training data. Platt (1999) proposed a new and fast algorithm for training SVMs: *Sequential Minimal Optimisation* (SMO), which breaks the large QP problem into a series of possible smallest QP problems. SMO are widely applied in solving (7) in practice because of its fast and simple performance.

How to expand binary SVMs to multi-class problems is still on-going. Normally there are two types of approaches: one is to combine several binary SVMs and the other is to solve it in one optimization formulation ("all-together"). In general, "all-together" is computationally expensive than combining binary SVMs on the same data set. There are normally three methods in combining binary SVMs: one-vs.-the rest, one-vs.-one and directed acyclic graph (DAG). "One-vs.-the rest" constructs *m* binary SVMs for *m* classes. All the examples in the *i*th class are labelled as positive labels and the rest of examples are labelled as negative labels in the *i*th SVM. After solving (7) for each class, when *x* is inputted, it belongs to the class with the largest value of the decision functions: $class(x) = \max_{i=1,2,...,m}(w_i \bullet \phi(x) - b_i)$. "One-vs.-one" calculates binary SVM between the *i*th and the *j*th class, thus totally $\frac{m(m-1)}{2}$ binary SVMs are constructed.

There are different methods for selecting the class based on results from these binary SVMs. A normal and simple decision method is "Max-Wins" voting strategy: if $sign(w_{ij} \bullet \phi(x) - b_{ij})$ says *x* belongs to the *i*th class, the vote for the *i*th class increased by one, otherwise the *j*th class increased by one. A small problem of this method is to deal with more than two classes with same voting value. Directed acyclic graph SVMs (Platt 2000) also construct $\frac{m(m-1)}{2}$ binary SVMs, but these SVMs are internal nodes and classes are leaves in DAG. SVMs start from single boot node and go through *m*-1 decision nodes when *x* is inputted. Hsu and Lin (2002) gave a comparison of methods for multi-class SVMs. Their experiments indicate that "one-against-one" and DAGSVM are more suitable for practical usage than the other methods. "One-against-one" is applied in this paper and the kernel function is radial basis function (RBF):

$k(x_i, x_j) = \exp(-\gamma\|x_i - x_j\|^2), \gamma > 0$.

Table1. Confusion matrix of 63 classes classification

labels	1	2	3	…	33	…	38	39	40	41	…	63	No.	Accuracy (%)
1.A_ tissue	**29**	0	0	…	0	…	0	0	0	0	…	0	44	65.91
2.An_epithelium	0	**30**	0	…	0	…	0	0	0	0	…	0	33	90.91
3.An-hair_ follicle	0	0	**3**	…	0	…	0	0	1	0	…	1	13	23.08
…				…										
33.lumen	2	0	0	…	**44**	…	0	0	0	0	…	0	48	91.67
…				…										
38.oe-epithelium	0	0	0	…	0	…	**112**	0	2	2	…	0	135	82.96
39. oe-glands	0	0	0	…	0	…	0	**13**	0	0	…	0	21	61.91
40. oe-j-epithelium.l_propria	0	0	0	…	0	…	1	0	**30**	0	…	0	45	66.67
41.oe-j-epithelium.m_ mucosae	0	0	0	…	0		2	0	0	**20**	…	0	22	90.91
…														
63.st-j-lumen. foveolae	1	0	0	…	0	…	0	0	0		…	30	**53**	56.60

No. = the totally number of testing samples for class *i*.
The total accuracy for 2755 testing data
=the number of the labels classified into accurate classes / the total number of testing data
= 64.21%.

3.3 Experiment Results

In the experiment, we segment thousands of large images into 64x64 sub-images. We randomly select 5509 as data set and then divide them into training data (2754 samples) and testing data (2755 samples). There is no overlapping between these two sets. The confusion matrix of 63 class classification is shown in table 1. In table 1, the rows represent the true classes and the columns represent the predicted classes; for example, the line 1 denotes 44 testing samples which belong to the fine feature 1: a_tissue (adipose tissue). 29 are classified into the fine feature 1, none are classified into 2, and so on, and none are classified into the feature 63. The accuracy is 65.91%.

From table 1, it is obvious that which features are similar and how similar they are. Such information will be used for the later organ classification.

3.4 Discussion

Compared with multi-class SVMs, the experiments in (Platt, 1999) used Gaussian Maximum Likelihood to classify the same data set. Table 2 compares these two classifiers. In our experiment, test set1 and test set2 are put together as testing data set. In general, multi-class SVMs achieve much better results in these complicated and large-scale image collections.

4. Organ Classification

As disused above, even trained histologists need to distinguish such complicated histological images based on subtle visual differences. For high resolution histological images as in this experiment they are sampled to 1123x870 pixels, general pattern recognition methods cannot categorize them well enough only based on global features. Detailed information such as the fine features in local region is needed for

organ classification. As introduced in previous sections, Gabor filter will be used to extract the texture features and then a multi-class SVM will categorize each unit into correspondent fine features. Figure 7 demonstrates the results of fine feature analysis for one unknown image. Based on the composition of fine features, organ information will be further analysed.

Figure7. The results from fine feature

Table2. Comparison of multi-class SVMs and Gaussian Maximum Likelihood

Total Accuracy (%)	Training set	Test set 1	Test set 2
Multi-class SVMs	**97.06**	**64.21**	
Gaussian Maximum Likelihood	48.5	42.8	21.5

Table3. Summary of organ classification using multi-class SVMs

organ	1	2	3	4	5	6	No.	Accuracy (%)
1. anus	17	0	0	4	0	0	21	80.95
2. appendix	0	33	3	0	1	2	39	84.61
3.large intestine	0	1	37	0	2	3	43	86.05
4.oesophagus	0	1	1	32	0	0	34	94.12
5.small intestine	0	0	7	0	24	1	32	75.00
6.stomach	0	0	0	3	1	37	41	90.24

The total accuracy for 210 test images

= the number of the images labelled accurate organs/the total number of test data

= 85.71%.

Table4. The performance of organ classification without fine feature detection

Accuracy (%)	anus	appendix	large intestine	oesophagus	small intestine	stomach
Training data	81.82	68.42	81.82	82.35	81.25	100
Testing data	90.00	75.00	57.14	82.35	56.25	80.95

The total accuracy of testing data = 72.38 %

4.1 Multi-Class SVM for Organ Classification

A multi-class SVM is used again to classify images into correspondent organs based on the output from the fine feature diction which may contains numerous errors. After fine feature analysis, an image is divided into 13x17 fine feature regions. An image is expressed in the format of $< label_1, label_2, ..., label_{63} >$. Table 3 summarizes the classification performance.

4.2 Discussion

The multi-class SVM uses the output from fine feature analysis as its input, and considers possibilities of the correlations of fine features including the wrong detection with the organ origins. The similarity between certain labels causes erroneous detection, however these errors tends to be concurrently related to certain organ origin. The method minimises the dependence on fine feature detection. The learned classifiers appear to be intuitively reasonable which shows the relationship between some features and organs no matter whether these features are detected correctly or not.

In order to demonstrate the goodness of this hierarchical architecture for categorizing histological images, we also test some data selected from the same data set based on the global texture features and multi-class SVMs described in Section 3 without fine feature detection. Table 4 shows the performance of the experiments without the fine feature detection on the same training and testing data. The experiments addresses that the complicated varied visual content in the histological images poses difficulties of such classification and the two-level classification approach increases the accuracy from 72.38% to 85.71%

5. Conclusion and Future Work

This paper presents an effective approach to analyse histological tissue images and automatically identify their organ origins. Through our experiment we also found that Gaussian Maximum Likelihood (GML) obtain better accuracy in detecting some features such as feature 25 (blood vessel) with 44.12% accuracy using GML but 28.57% using SVMs. It means some features are sensitive to some classifiers, i.e. only one classifier cannot achieve good performance for each feature. Currently we are researching how to combine different complementary classifiers to achieve a best possible performance (Kittler, 1998; Grim, 2002; Buxton, 2001).

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References

Arnold W.M. Smeulders, Marcel Worring, Simone Santini, Amarnath Gupta, Ramesh Jain (2000) “Content-Based Image Retrieval at the End of the Early Years”, *IEEE Transaction on Pattern Analysis and Machine Intelligence*, 22(12), pp. 1349-1380.

Brodley C. E., Kak A., Dy J., Shyu C. R., Aisen A., and Broderick L (1999) “Content-based Retrieval from Medical Image Databases: A Synergy of Human Interaction, Machine Learning and Computer Vision”, *Proceedings of The Sixteenth National Conference on Artificial Intelligence*, Orlando, FL, pp. 760-767.

Burges C. J. C. (1998) “A Tutorial on Support Vector Machines for Pattern Recognition”, *Data Mining and Knowledge Discovery*, 2(2), pp. 955-974.

Buxton B. F., Langdon W. B., Barrett S. J. (2001) “Data Fusion by Intelligent Classifier Combination”, *Measurement and Control*, 34(8), pp. 229-234.

Grigorescu S. E., Petkov N., Kruizinga P. (2002), “Comparison of Texture Features Based on Gabor Filters”, *IEEE Transactions on Image*

Processing, 10(10), pp. 1160-1167.

Grim J., Kittler J., Pudil P., Somol P. (2002) "Multiple Classifier Fusion in Probabilistic Neural Networks", *Pattern Analysis & Applications*, pp. 221-233.

Hearst M. A., Dumais S. T., Osman E., Platt J., Scholkopf B. (1998) "Support Vector Machines", 13(4), pp. 18-28.

Hsu C. W., Lin C. J. (2002) "A Comparison of Methods for Multi-class Support Vector Machines", *IEEE Transactions on Neural Networks*, 13 (2), pp. 415-425.

Kim S. D., Udpa S. (2000) "Texture Classification Using Rotated Wavelet Filters", *IEEE Transactions on Systems, Man and Cybernetics*, 30(6), pp. 847-852.

Kittler J., Hatef M., Duin R., Matas J. (1998) "On Combining Classifiers", *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 20(3), pp. 226-239.

Ma W. Y. and Manjunath B. S. (1995), "A Comparison of Wavelet Transform Features for Texture Image Annotation", *Proceedings of IEEE Intelligence Conference on Image Processing*, Washington D.C. USA, Vol. 2, pp. 2256-2260.

Manjunath B. S., Ma W. Y. (1996) "Texture Features for Browsing and Retrieval of Image Data", *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 18(8), pp. 837-842.

Manjunath B. S., Ohm J. R., Vasudevan V. V., Yamada A. (2001) "Color and Texture Descriptors", *IEEE Transactions on Circuits and Systems for Video Technology*, 11(6), pp. 703-715.

Platt J. C. (1999) "Fast Training of Support Vector Machines Using Sequential Minimal Optimisation", In B. Scholkopf, C. J. C. Burges, and A. J. Smola, editors, *Advances in Kernel Methods - Support Vector Learning*, Cambridge, MA, MIT Press. pp. 185-208.

Platt J. C., Cristianini N., Shawe-Taylor J. (2000) "Large Margin DAGs for Multiclass Classification", *Advances in Neural Information Processing Systems*, Vol. 12, pp. 547-553.

Randen T., Husøy J. H. (1999) "Filtering for Texture Classification: a Comparative Study", *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 21(4), pp. 291-310.

Ringo W. K. L., Ip H. H. S., Cheung K. K. T., Tang H. L., Hanka R. (2000) "A Multi-Window Approach to Classify Histological Features", *Proceedings of International Conference on Pattern Recognition*, Barcelona, Spain, Vol. 2, pp. 259-262.

Rui Y., Huang T. S., and Chang S. F. (1999) "Image Retrieval: Current Techniques, Promising Directions, and Open Issues", *Journal of Visual Communication and Image Representation*, Vol. 10, pp. 39-62.

Tang H. L., Hanka R., Ip H. H. S. (1999) "A Review of Intelligent Content-Based Indexing and Browsing of Medical Images", *Health Informatics Journal*, 5(1), pp. 40-49.

Tang H. L., Hanka R., Ip H. H. S. (2003) "Histological Image Retrieval Based on Semantic Content Analysis", *IEEE Transaction on Information Technology in BioMedicine*, 7(1), pp. 26-36.

Vapnik V. (1998), *Statistical Learning Theory*, New York, Wiley.

Wang J. W. (2002) "Multiwavelet Packet Transforms with Application to Texture Segmentation", *Electronics Letters*, 38(18), pp. 1021-1023.

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