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Analysis of the contour structural irregularity of skin lesions using wavelet decomposition

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Abstract

The boundary irregularity of skin lesions is of clinical significance for the early detection of malignant melanomas and to distinguish them from other lesions such as benign moles. The structural components of the contour are of particular importance. To extract the structure from the contour, wavelet decomposition was used as these components tend to locate in the lower frequency sub-bands. Lesion contours were modeled as signatures with scale normalization to give position and frequency resolution invariance. Energy distributions among different wavelet sub-bands were then analyzed to extract those with significant levels and differences to enable maximum discrimination.

Based on the coefficients in the significant sub-bands, structural components from the original contours were modeled, and a set of statistical and geometric irregularity descriptors researched that were applied at each of the significant sub-bands. The effectiveness of the descriptors was measured using the Hausdorff distance between sets of data from melanoma and mole contours. The best descriptor outputs were input to a back projection neural network to construct a combined classifier system. Experimental results showed that thirteen features from four sub-bands produced the best discrimination between sets of melanomas and moles, and that a small training set of nine melanomas and nine moles was optimum.

Keywords: melanoma detection, structural irregularity of contours, wavelet decomposition, multi-scale descriptors, significant wavelet sub-bands

1. Introduction

Melanomas are malignant tumors comprised of epidermal or mucosal cells and have a high possibility of lymphatic metastasis resulting in unfavorable prognosis. Early detection of melanomas in clinics depends on a well-known ABCD rule to determine the benign or malignant nature of skin lesions [1]. That is, Asymmetry of the lesion's boundaries, Boundary irregularity, Color distributions and lesion Diameters. Alternative classifications based on color texture appearance has been researched recently [2, 3], and by employing a biopsy and electron tomography, a classification from 3D cell images has been reported [4]. The technique of dermoscopy used polarized light or oil coverage to make more of a lesion's structure visible [5]. CAD systems have been researched to aide the clinician. These often comprise image acquisition, artifact detection, lesion segmentation, feature extraction and lesion classification stages [6].

In the previous decade, there have been many studies concerning the boundary irregularity of lesions using both geometric [7,8,9,10] and local fractal [11] measures. There are two types of irregularities found on boundaries: textual and structural, these correspond to fine changes and obvious convex and concave features respectively [7]. The structural irregularity has clinical importance for melanoma diagnosis. The first task of boundary irregularity analysis is to identify and extract the boundary as a 1D signal from the 2D image. The contours of skin lesions can be considered as a mixture of structural and textural irregularity as can be seen by following those in Fig.1. The benign mole is smooth with little variation on its contour, while that of the melanoma contains many indents and protrusions in its structure, and has an obvious visual roughness. However, for measurements of structural irregularity, multi-scale analysis of skin lesion boundaries is an important technique for correctly isolating the structural from the textural information. Wavelet transforms are useful multi-resolution analytical tools for revealing object information at a defined scale or to select particular frequency bands of interest [12]. A requirement for the design of structural irregularity descriptions is to explore ways of extracting features not only from structural variations along the original contour, but also to separate the scaled information in the significant sub-bands and thus with this extra information to improve the accuracy of the diagnosis.

Previously T. K. Lee proposed an irregularity measure based on a deduced scale level using a curvature model of multi-scaled boundaries [7]. However it involved heavy computation as the proposed irregularity index was evaluated from a hierarchical structure with its roots as global curve segments and leaves as local segments for each of the consecutive smoothed contours. The Gaussian smoothing-scale increases on the original lesion contour indicated the evolution of the curve's indented and protruding segments.

The motivation for this study is to show that the filtered information in the sub-bands can be used by structural irregularity descriptors to provide a good separation between melanomas and benign moles. We show that multi-scale wavelet decomposition of the extracted contour

followed by the selection of significant sub-bands can be an appropriate approach for the evaluation of structural irregularity. The novelty of the proposed structural irregularity features is:- (1) The extracted structural components of the contours are reconstructed by the summation of the approximate wavelet coefficients at the selected maximum scale and only those detail coefficients that are from structurally significant sub-bands; (2) Two classes of statistical and geometric irregularity descriptors are defined and used. These were evaluated in each of the significant sub-band to determine firstly that they were independent and did not correlate with other features, and secondly their effectiveness in distinguishing between melanomas and moles was measured. Features were discarded if they did not separate sets of moles and melanomas sufficiently in order to maintain a compact feature space.

The steps in the procedure to reconstruct just the structural components of the contours are:- Perform a 1D wavelet decomposition to produce a series of detailed contour signals for all the lesion contours in the data set; Calculate energy measures for each of the detail, that is high frequency, sub-bands; Perform a Hausdorff Distance (HD) [13,14] analysis based on energy values in each sub-band to determine which detail coefficients are significant for distinguishing the two sets; Select the significant sub-bands; Label the sub-bands with scales below these as containing the textural component of the contour and rejected them from further consideration; Sum the approximation coefficients and the remaining detail coefficients to generate the connected structural component of the contour. This procedure approximately isolates the structural portion of the original contour, and then the irregularity descriptors are used to refine this and partition the lesions appropriately.

(a)   **(b)**
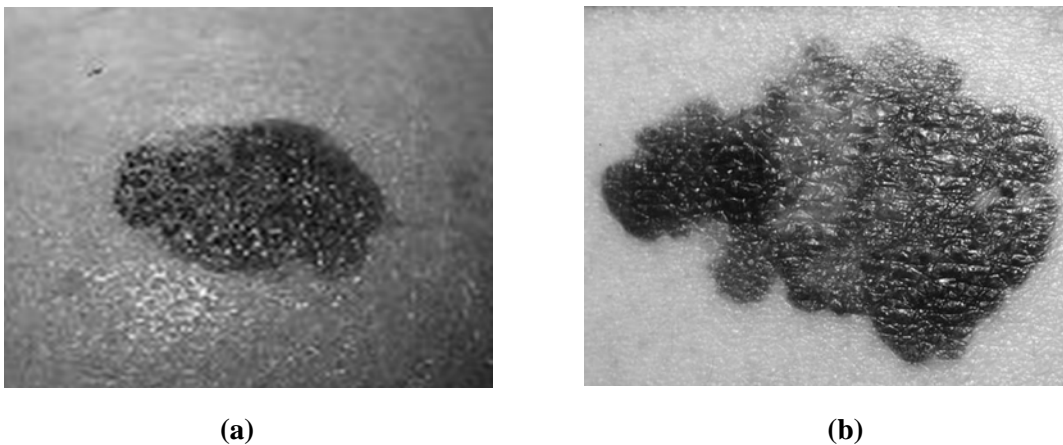
Fig.1 Images of skin lesions (a) mole (b) melanoma

Section 2 describes the procedure to extract the structural components of the lesion contours including the wavelet decomposition, the scale normalization necessary to process contours of different length, and the selection of the significant sub-bands. Section 3 discusses the design of the statistical and geometric descriptors of contour irregularity that are applied at multi-scales. Section 4 concerns the selection techniques that ensure features are independent and that the

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feature vector is compact. Section 5 provides the experimental results for the significant structural component extraction and feature evaluation. A combined classifier using a back projection neural network is described together with issues concerning training and the evaluation of the structure of the feature vector. Finally Section 6 provides conclusions.

2. Extraction of the structural components of the skin lesion contours

2.1 Wavelet decomposition of a lesion contour

The contour of a skin lesion in an image is described by the points. $C=\{x_1,y_1,x_2,y_2,...,x_N,y_N\}$. There are two ways of to represent this 2D data as a 1D signal: 1) The contour is split into two 1D sub-vectors $C_x=\{x_1,x_2,...,x_N\}$ and $C_y=\{y_1,y_2,...,y_N\}$; or 2) The contour is modeled as a signature $C_r=\{r_1,r_2,...,r_N\}$ where the radial distance from the geometric center,

$$r_i = \sqrt{(x_i - x^{'})^2 + (y_i - y^{'})^2}$$, $i=1,2,...n$ and (x',y') is the coordinate of the geometric center of

the closed contour. The signature representation was adopted in the paper as it provided the advantage of position invariance.

2.1.1 Scale normalization

It was noted that many moles have a shorter contour for a given nominal area than do melanomas. Together with size variability between the samples in the database, this can lead to variations in estimated frequency and resolution in the frequency domain. Scale normalization is required to enable a comparison between moles and melanomas in this domain. The proposed normalization was modified from [15] to give radius:

$$r_i' = \begin{cases} r(\lceil i\dfrac{n}{N} \rceil) + \mu_1 - \mu_2 & r(i) < T \\ \\ r(\lceil i\dfrac{n}{N} \rceil) & otherwise \end{cases} \qquad i=1,2,...,N \qquad (1)$$

Where i is an integer used to resample the contour points with a spacing distance of (n/N) and the ceiling function $\lceil \ \rceil$ is used to produce an integer index to r. The values μ_1 and μ_2 are the averaged radial distances of all the melanomas and benign moles respectively in the data base. Their inclusion provides a mean value platform on to which the lowest level approximation coefficients will be superimposed. T is a threshold used to determine if a mole has a small value of r. If so, r is increased to reach a similar size to that of a melanoma. For melanomas and large moles, the value of r is never increased. r_i' is the radial distance of the ith point of a contour after this normalization. The lesions were sometimes small with $r(i) < T$, and sometimes not circular with sections where $r(i) < T$. In these cases normalizing the individual $r(i)$ was performed to improve the discrimination of the classifiers described in the later sections.

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2.1.2 Wavelet decomposition

Wavelet decomposition is a powerful tool for multi-scale signal analysis. By using a pair of low-pass and high-pass filters, an original signal is decomposed into approximation and detail coefficients with the approximations feeding into the next level of decomposition, and thus creating a decomposition tree [16]. The tree structure of such a 1D wavelet decomposition is shown in fig 2.
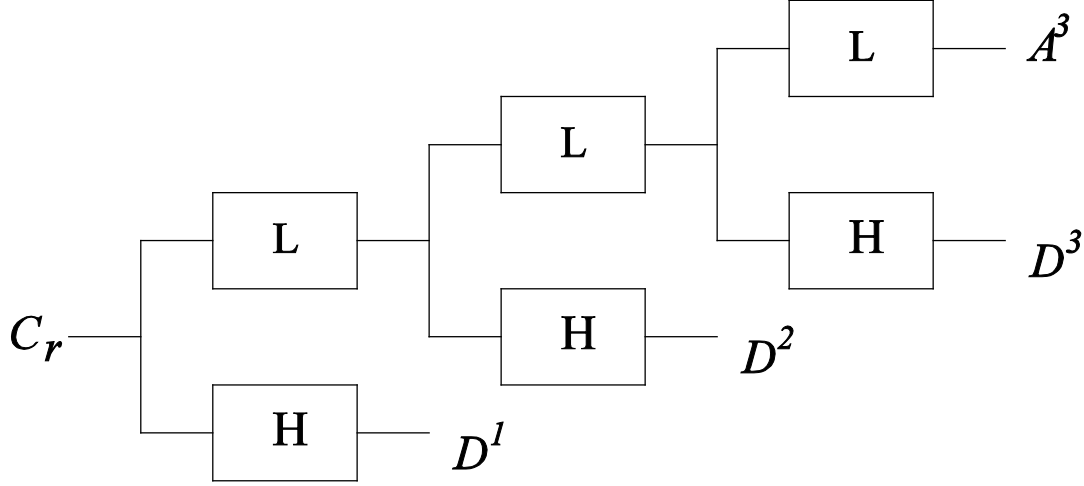
Fig.2 Tree structure of wavelet decomposition

A 1D wavelet decomposition is performed on a contour signature C_r. The approximate and detail coefficients at scale i are given by $A^i = \{a_1^i, a_2^i, \cdots a_M^i\}$ and $D^i = \{d_1^i, d_2^i, \cdots d_M^i\}$ respectively where $M = N/2^i$. As the scale increases, the approximate coefficients are further decomposed into low and high frequency components at the next higher scale. Generally the textural components of a contour occupy the lower scale, higher frequency bands, with the energy distributed evenly between bands to give a relatively small total energy within each. However the structural components generally have a larger energy and occupy the lower frequency bands. By using wavelet decomposition to level s, an original contour signature C_r is transformed to a series of sub-band signals $A^s, D^s, D^{s-1}, \cdots D^1$ covering the whole signal frequency space at $[0, 1/2^s f_{\max}]$, $[1/2^i f_{\max}, 1/2^{i-1} f_{\max}], i = s, s-1, \cdots, 2, 1$ and f_{max} is half the sampling frequency. This represents a concatenation of the frequency bands from the lowest to the highest. The task is to identify at which decomposition levels the structural components of a lesion contour can be extracted and which sub-bands in the frequency domain are significant for distinguishing moles and melanomas.

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2.2 Sub-band descriptions of contour structural components

For a 1D contour signal, the FFT provides the magnitude and phase against frequency. The weakness of the FFT is that the spectral profiles are unrelated to the position of an event in the boundary and the resolution is fixed throughout the frequency band. On the other hand the discrete wavelet transform (DWT) presents the capability of confining signal components to dyadically increasing width frequency bands with different resolutions. The left two columns of Fig.3 present mole, and the right two melanoma data. The plot in the first row of the first column is the FFT spectrum of a mole where the zero frequency component has been translated to the center. The plot on the right indicates the sub-band division in the frequency domain when two levels of wavelet decomposition are implemented. A^1, A^2, D^1, D^2, refer to approximate and detail signals. The plots in the rows below show the signals in each band. Similarly the two columns on the right are for a melanoma. Differences can be seen between the mole and the melanoma signals in the D^1 and D^2 bands. We continue to describe the selection of the bands which enable the best discrimination between moles and melanomas.
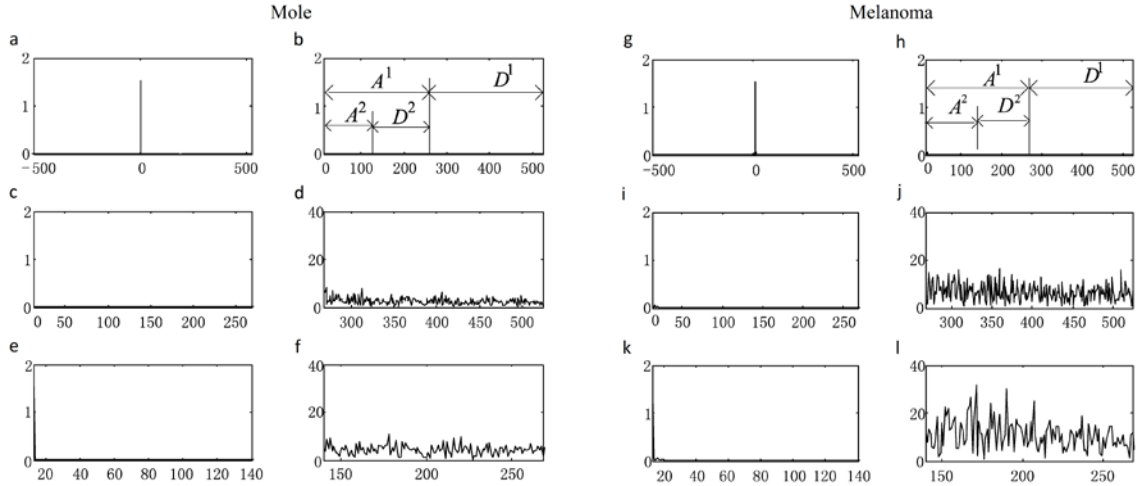
Fig.3 Spectral and wavelet comparisons between a mole and a melanoma. Mole: (a) FFT, (b) A^1, A^2, D^1, D^2 wavelet coefficient frequency map, (c) A^1, (d) D^1, (e) A^2, (f) D^2; Melanoma: (g) FFT, (h) A^1, A^2, D^1, D^2 wavelet coefficient frequency map, (i) A^1, (j) D^1, (k) A^2, (l) D^2;

2.2.1 Significant sub-band selection

To obtain just the contour's structural components, several lower frequency sub-bands need to be identified from which to reconstruct that portion of the original contour using both multi-scale approximate and detail coefficients. The evaluation of the significant sub-band range was performed between each of the sample sets by HD distribution analysis at each level of wavelet decomposition [17]. When analyzing the decomposition of a contour signal, the total energy at any decomposition level indicates the significance of that sub-band frequency to the original signal. The energy of a wavelet sub-band D^j is defined as

$$E_j = \sum_i (D_i^j)^2 \quad j=1,2,\ldots n \qquad\qquad (2)$$

2.2.2 Procedure for investigating significant sub-band selection

An algorithm was developed to identify those sub-bands which enabled the largest discrimination between moles and melanomas. Given a set of p benign mole contours,

$\Omega^b = \{x_1^b, x_2^b, \cdots, x_p^b\}$ where x_k^b was the kth contour, and a set of q melanoma contours,

$\Omega^m = \{x_1^m, x_2^m, \cdots, x_q^m\}$ where x_k^m was the kth contour.

Step1. For a preset maximum level of wavelet decomposition n, calculate the wavelet energy for every contour x_k^b and x_k^m within each set Ω^b and Ω^m. First perform wavelet decomposition to obtain the detail sub-band signals, D^n, D^{n-1}, ... D^1, for each lesion contour, and then calculate the energy for either x_k^b or x_k^m in each band, E_{lk}^b and E_{lk}^m, where sub-band $l = 1,2,\cdots,n$ using Eq.(2).

Step2. Form energy sets $\text{E}^b = \{E_{l1}^b, \ E_{l2}^b, \cdots, E_{lp}^b\}$ and $\text{E}^m = \{E_{l1}^m, \ E_{l2}^m, \cdots, E_{lq}^m\}$ from the individual energies calculated for each transformed benign and melanoma contour at each sub-band $l = 1,2,\cdots,n$.

Step3. Compute the HD^l value between energy sets of moles E^b and melanomas E^m for each band $l, l = 1,2,\cdots,n$. This measures the discrimination between the two classes for each sub-band.

Step4. Plot the distribution of HD^l with respect to sub-band number l. The sub-bands with the highest HD are considered as the most significant and used in the final classification.

Step5. The sub-bands with the higher HDs are considered as significant bands for use in classification.

2.2.3 Extraction of the structural component of a lesion contour

Based on the theory of wavelet reconstruction, the structural component of a lesion contour is given by combining the significant coefficient groups from $A^s, D^s, D^{s-1}, \cdots D^1$ where the original decomposition was stopped at level s. The decomposed detail sub-bands need to be divided into high-scale (low-frequency) and low-scale (high-frequency) groups using a

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threshold s_t so that:

$$C_s = A^s + D^s + D^{s-1} + \cdots + D^{s_t} \qquad (3)$$

$$C_t = D^{s_t-1} + D^{s_t-2} + \cdots + D^1 \qquad (4)$$

Where C_s contains lower-frequency information and represents the structural component of the contour, and C_t contains higher-frequency information and represents the textural component. Choosing both s and s_t are difficult tasks, as a large s generates many narrow sub-bands close to zero frequency. Although these will contain structural information that will be relatively free of textural irregularity, there is an extra cost in increased computational complexity. A small s can lead to structural contours contaminated with textural irregularity. The value of s_t chosen is crucial to obtain useful structural and textural contour information. The significant sub-band selection process described in Section 2.2.2 was run on the test data and in practice the HD distribution (Fig. 4) produced had a single peak that lead to the straightforward selection of a single, general value for s_t as described in Section 5.1.

3. Descriptors of contour irregularity at multiple scales

Irregularity measures of object boundaries are key components for shape related classifications. They are used after the contour structural components have been extracted. There are two categories of irregularity descriptors, with one based on statistical measures, and the other on geometry. The descriptors are only extracted at the previously determined significant levels j, $j \in \Omega$, where Ω is a significant level set formed by the sub-band selection procedure of Section 2.2.2.

3.1 Statistical measures

Together with the mean and variance of the energy of D^j at each significant level [9], the following features related to contour irregularity were defined:-

1) Entropy of wavelet energy, $\quad w_j = -\sum_{i=1}^{N} p_i^j \log\!\left(p_i^j\right) \qquad (5)$

where $\quad p_i^j = E_i^j \big/ E^j$ is the energy probability of the ith component of D^j, E^j is the total energy of the coefficients in band j as calculated by eqn (2), and $E_i^j = \left|D_i^j\right|^2$. The energy entropy measures the magnitude of signal fluctuations.

2) Ultimate width. For any signal $X = \{x_1, x_2, \ldots x_N\}$, the ultimate width is defined as

$$width = \frac{2 \times \sigma}{\mu} \qquad (6)$$

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Where μ and σ are the mean and variance of signal X. A large width indicates sharp variations.

3.2 Geometric based irregularity measures

At each significant level j, a supposed structural component C_j, $s \geq j \geq s_t$ of a contour is reconstructed from the wavelet coefficients, $C_j = A^s + D^s + D^{s-1} + ... + D^j$. In addition to a simple variance measure [11], the other irregularity measures of the reconstructed contours are evaluated as:-

$$\text{Radial Deviation,} \quad RD = \frac{1}{N} \sum_{i=1}^{N} |(r_i - \bar{r})| \tag{7}$$

where $\bar{r}$ is the mean radius of the contour signature.

$$\text{Contour Roughness [8],} \quad Ro = \frac{1}{N} \sum_{i=1}^{N} |r_i - r_{i+1}| \tag{8}$$

$$\text{Irregularity Measure,} \quad IM = \frac{Area(C_j \oplus S_s)}{Area(S_s)} \tag{9}$$

where S_s is reconstructed from the approximate data, A^s, at the significant level s, and $\oplus$ is the exclusive-or operator.

4. Feature selection

Feature selection was performed to remove some measures that were too similar to others and to identify those that were most independent for inclusion in an efficient feature vector. Initially 25 features were identified from six irregularity descriptors at four scales plus *IM* at the threshold scale s_t. Then a correlation analysis followed by a performance based feature selection was performed as detailed below.

4.1 Correlation analysis

Correlation analysis is a popular tool for removing those redundant features that have a strong relationship to others within a feature vector [18]. Given a feature vector $F\{t_1, t_2, \cdots, t_n\}$ and a sample set $S = \{x_1, x_2, \cdots, x_m\}$, the correlation coefficient ρ_{ij} of any pair of features t_i, t_j is calculated as follows:

$$\rho_{ij} = \frac{\sum\limits_{p=1}^{m}\left(t_{pi} - z_i\right)\left(t_{pj} - z_i\right)}{\sqrt{\sum\limits_{p=1}^{m}\left(t_{pi} - z_i\right)^2 \sum\limits_{p=1}^{m}\left(t_{pj} - z_j\right)^2}} \qquad (10)$$

where z_i is the mean value of feature t_i in the sample set and t_{pi} is the value of t_i for the sample x_p. The absolute value of ρ_{ij} indicates the correlation between t_i and t_j, so a redundant feature will have a large ρ_{ij}.

The following is the procedure for removing redundant features using correlation analysis:-

Step 1. Given an original feature vector F and a sample set S, Calculate a matrix of correlation coefficients, $\rho_{ij}, i \neq j, 1 \leq i, j \leq n$ using Eq.(10). ;

Step 2. Given a preset threshold T, split the pairs of features (t_i, t_j), where $(i \neq j,\ 1 \leq i, j \leq n)$, into two sets, where $F_1 = F \mid \rho_{ij} < T, i \neq j, 1 \leq i, j \leq n$ is a set that does not contain redundant features in F, and $F_2 = \{t_p, p \in \{i, j\}) \mid \rho_{ij} \geq T\}$ is generated by choosing either feature of a highly correlated pair. Selection can equally be random, or we kept the one that computed most efficiently.

Step 3 The final feature set after removing redundant components is given by $F' = F_1 \cup F_2$.

4.2 Performance based feature selection

After removing the redundant features from the vector, those remaining are largely independent. Further analysis is then performed to select the best features based on their discrimination performance. To evaluate the discrimination, the contribution to the correct classification for each feature is evaluated [7]. Given a sample set of skin lesions with manually labeled classes w_1 and w_2, representing benign moles and malignant melanomas respectively, the probability distributions $P(t_i \mid w_2)$, and $P(t_i \mid w_1)$ are evaluated for each feature. Suppose the prior probabilities $p(w_1)$ and $p(w_2)$ are equal, then the posterior probabilities $p(w_1 \mid t_i)$ and $p(w_2 \mid t_i)$ will be closely related to $p(t_i \mid w_1)$ and $p(t_i \mid w_2)$. The classification is perfectly separable when any value of $p(t \mid w_2) \neq 0$ has the corresponding value of $p(t \mid w_1) = 0$, and is absolutely inseparable when $p(t \mid w_2) = p(t \mid w_1)$ at any point [19].

However, medically, the probability of a benign mole $p(w_1)$ is larger than that of a melanoma $p(w_2)$. With the Bayesian rule, the discrimination can be stated: If

$p(x \mid w_1)p(w_1) > p(x \mid w_2)p(w_2)$, then $x \in w_1$. Here this is simplified to be

$p(x \mid w_1) > p(x \mid w_2)$ using $p(w_1) = p(w_2)$. This proposed simplification is justified when

$p(x \mid w_1)$ is located to the left side of $p(x \mid w_2)$. This is true as the features, measuring contour roughness, take smaller values in moles than that in melanomas. In addition, our rule has the same averaged error probability as the Bayesian, because if

$p(x \mid w_1) > p(x \mid w_2)$, $p(w_1) > p(w_2)$, then

$p(x \mid w_1)p(w_1) > p(x \mid w_2)p(w_1) > p(x \mid w_2)p(w_2) \Rightarrow p(x \mid w_1)p(w_1) > p(x \mid w_2)p(w_2)$

Generally conditional probabilities of the feature t_i for two classes will be overlapped. The degree of overlapping of the two probability distributions was used as a measure of classification error for any single feature t_i.

Suppose $F' = \{t_1, t_2, \cdots, t_r\}$ was the feature vector after redundancy removal. The steps used for performance based feature selection were:-

Step 1: Conditional probability distributions. For each feature $t_i \in F'$, calculate the

conditional probability distributions $p(t_i \mid w_1)$ and $p(t_i \mid w_2)$ for benign and malignant

lesions in the sample sets;

Step 2: Accumulated probabilities. Given a threshold T, find an appropriate value of k to

compute the accumulated probabilities $P_b^i = \sum_{j=1}^{k} p_j^b \geq T$ and $P_m^i = \sum_{j=k+1}^{N} p_j^m$ for each

feature t_i. Where p_j^b and p_j^m are the jth values of $p(t_i \mid w_1)$ and $p(t_i \mid w_2)$.

Step 3: Feature verification. For each feature $t_i \in F'$ ($1 \leq i \leq p$), If $P_b^i \geq T$ and $P_m^i \geq T$,

the feature t_i is verified with a classification error of less than 1-T, otherwise t_i is discarded. Where T is a preset value that is chosen to be large enough to secure a sufficient classification

accuracy. The final feature set is then $F^* = \{t_1^*, t_2^*, \cdots, t_q^*\}$, $t_i^* \in F'$ ($1 \leq i \leq q, q \leq p$).

5. Experimental results

Three experiments were performed:- Significant wavelet sub-band selection; Reconstruction of skin lesion contour from wavelet decompositions; And an evaluation of the proposed multi-scale descriptors of contour irregularity using a combined classifier based on a back projection neural network

The test data comprised 134 images of skin lesions, with 72 melanomas and 62 moles.

They were downloaded from the Dermnet Skin Disease Image Atlas database at
http://www.dermnet.com/. The images were randomly selected from the database, after viewing
to remove some images that contained defocussed patches. Most images were of size 120x120
pixels, and if not, they were converted to this size by resampling. Each was converted from
color to gray level before processing. For the purpose of classification, a training set was formed
by randomly selecting 31 moles and 36 melanomas from the sample set, with the remaining
samples being used as test samples. The experiments were implemented using MATLAB 7.6.

5.1 Significant level selection and reconstruction of the structural component of a contour
Based on the procedure for significant sub-band selection described in Section 2.2.2, the
significant levels were identified using the training set and the 'db3'wavelet. The maximum
level of decomposition was preset to 10. Then the HD between the averaged sub-band energies
of the wavelet detail coefficients for each class was measured at each level. The distribution is
shown in Fig.4 where it can be seen that levels 1 to 5 have a low flat distribution, levels 6 to 9
have a monotonically increasing HD, and that the HD at level 10 has decreased again.
The coefficients in levels D^1 to D^5 cover the higher frequencies where there are similar small
textural variations for both moles and melanomas. The detail coefficients in D^{10} locate at the
low frequencies where there is some basic structure, but for computational efficiency it was
found to be better to use this when included in the approximation set A^9. Therefore, as expected,
with HDs up to 3.1, the middle-frequency bands represented by D^6 to D^9 have been shown to
contain significant discrimination information, and these were selected as the significant levels.
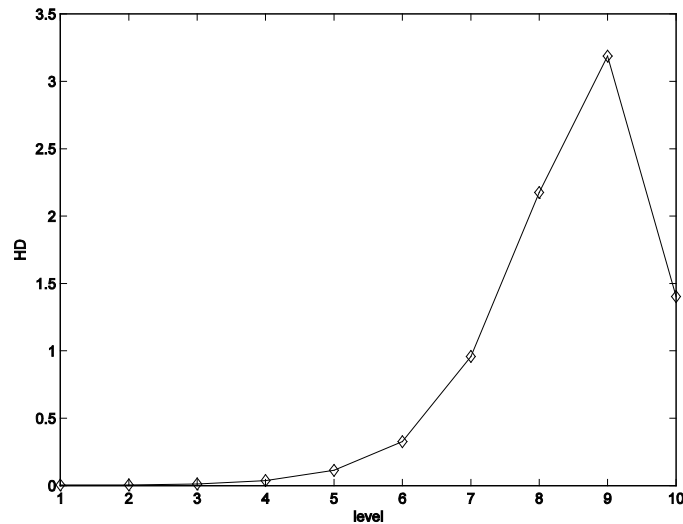

Fig.4 HD distribution of wavelet detail signals v. level

It is simple to reconstruct the structural components of the contour after the significant levels in
the wavelet decomposition stack have been determined. Fig.5 shows the extracted contours of a
mole (a,b,c) and a melanoma (d,e,f), where Fig.5 a) and d) are the original contours. Fig.5 b)

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and e) are the corresponding contours reconstructed from A^9 and D^1 to D^5. The approximation coefficient, A^9 has been included to give the basic structure of the contour onto which the more complex textural part has been superimposed. Fig.5 c) and f) are reconstructed from A^9 and D^6 to D^9 ($s = 9$, $s_t = 6$), that is the boundaries representing the structural portion of the original lesion. With the textural information removed, these have the property of the highest discrimination between different lesion classes. In the remainder of the paper these significant sub-bands will be referred to as the structural sub-bands.
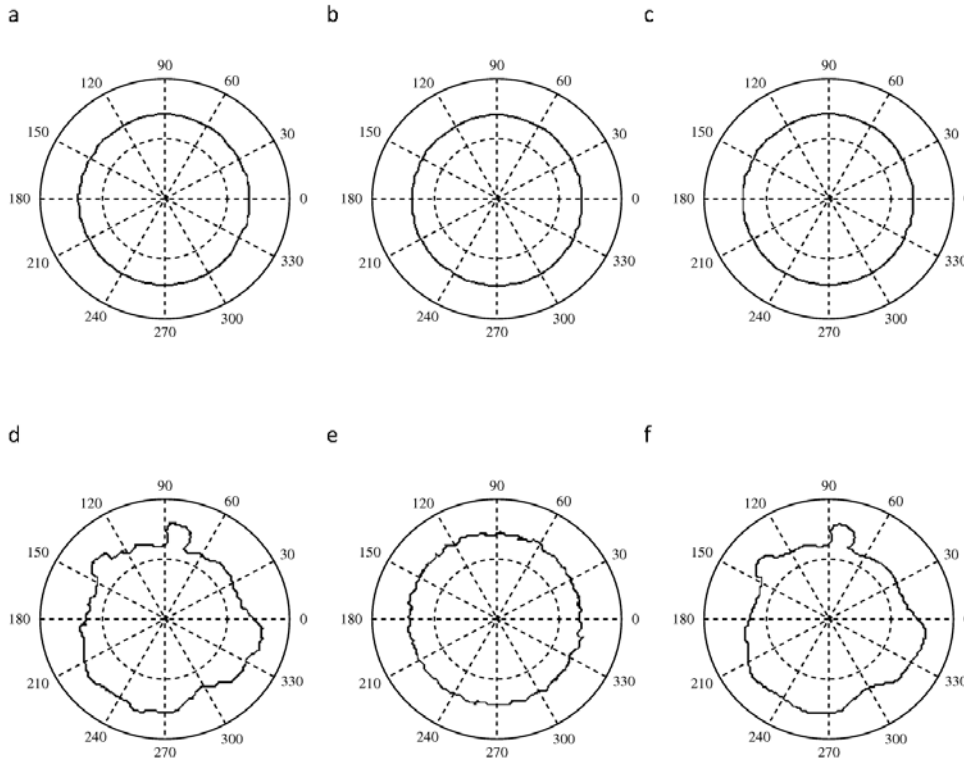

Fig.5 Contours after wavelet reconstruction. (a) Mole - original, (b) Mole - textural, (c) Mole – structural, (d) Melanoma – original, (e) Melanoma – textural, (f) Melanoma – structural. (Angle in degrees and Radius in pixels, with inner dotted circle at 100 and solid circle at 200).

5.2 Results of feature selection

As described in Section 4, the original feature vector consisted of 25 irregularity features that were formed from seven measures, six of which were applied at each of four significant sub-bands. At the first stage of feature selection, correlation analysis, nine of these features were removed to decrease redundancy. Table 1 shows the retained (tick) and removed (cross) features. The average energy, wavelet entropy and ultimate width were reliable features at most levels of the significant sub-bands. The other independent features retained included the variance at the two higher levels (8 and 9), the radial deviation at level 6, the contour roughness at level 7, and the irregularity measure at level 6.

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Wavelet Level	Averaged energy	Wavelet entropy	Ultimate width	Variance	Radial deviation	Contour roughness	Irregularity measure
6	√	√	√	x	√	x	√
7	√	√	√	x	x	√	
8	√	√	x	√	x	x	
9	√	√	√	√	x	x	

Table 1. Results of feature selection after correlation analysis

After removal of the redundant features identified by the correlation analysis, selection was taken further for the remaining 16 features by a classification performance analysis of each feature. As discussed in Section 4.2, the cumulative probability distribution of each feature was calculated for both the benign, $P_b = \sum_{i=1}^{k} p_i^b$, and the melanomas, $P_m = \sum_{i=k+1}^{N} p_i^m$, in the sample sets, where N was the largest observed value for that feature and k was a value satisfying $P_b = \sum_{i=1}^{k} p_i^b \geq T$. A threshold $T = 0.75$ was chosen experimentally that indicated correct classification for every feature when applied to the benign samples in the training set. Then the feature had to meet the requirement $P_m > T$ to be retained within the overall feature vector. Fig.6 presents the results of the final feature selection.
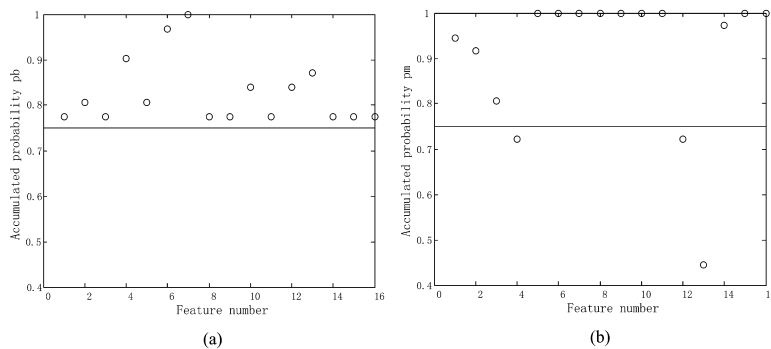

Fig.6 Plot of accumulated probabilities:- (a) P_b ; (b) P_m, for each of the 16 features

In Fig 6 it can be confirmed that all the features had a value of P_b larger than threshold $T = 0.75$ and there were three features with P_m values that were less than T. They were the averaged energy at level 9, and variances at level 8 and 9. These were discarded, leaving 13 features for

further classification. It was noticed that some P_m values approached 1.0, signifying there was little overlap between the probability distributions of the benign and melanoma sets for these features.

5.3 Combined classification results

The results of selections and tests on the individual features have been presented in Sections 5.1 and 5.2. In this section a Back Projection (BP) neural network is described that was used to perform classification of skin lesions based on a combination of the 13 selected features. The neural network had a structure of three layers:- input layer with 13 nodes; hidden layer with 3 nodes; and output with one node [20]. The training parameters were a preset training error of 0.01 and a maximum training number of 1000 iterations. As before, the main training set was formed by randomly selecting 31 moles and 36 melanomas from the sample set, with the remaining samples forming the testing set. A sub-set of the large training set was randomly formed to produce an alternative small training set of 9 moles and 9 melanomas. To study the discrimination ability of the proposed multi-scale based feature vector and to refine its operation, some classification experiments were performed to compare firstly single-scale with multi-scale features, and then multi-scale feature either before feature selection (25 features), or after (13 features). This was performed with both the small and large sized training sets to see which gave the best results.

5.3.1 Before feature selection

Four experimental schemes were tried for training the BP network:- (1) Multi-scale, with all 25 features and the small training set; (2) Single scale, with 7 features at level 9 and the small training set; (3) Multi-scale features and the large training set; and (4) Single scale features and the large training set. After each training and processing of the test data, their corresponding Receiver Operating Characteristic (ROC) plots were generated and are shown in Fig.7.

The input layer of the neural network has m values, where m is the number of features calculated from each sample in the test data set. The output of the network produces a single real value between 0 and 1 to indicate which class the sample belongs to for each of the S samples in the test data set. Overall the network produces an output vector with dimension S. Given a threshold value between 0 and 1, the output vector is converted to a binary vector with elements 0 and 1 indicating the class estimations. Each sample in the set has previously been classified by a clinician and so the TP and FP values for this threshold can be calculated. This process is repeated for a range of thresholds between 0 and 1 and the resulting FP,TP pairs plotted as an ROC curve that spans from the bottom left (1,0) to the top right corner (0,1).

The nearer the ROC trace is to the top left corner, the better the discrimination of a scheme [21,22,23]. Fig.7 shows that the worst plot, is the single scale with a small training set, and the best, that clearly locates towards the top left corner, was for the multi-scale features using the

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small training set. This had a better classification power than the multi-scale scheme using the large training set. The multi-scale features were always found to perform better than the single scale features. In addition, the multi-scale features provided a way of improving the discrimination when only a small sized training set was available.
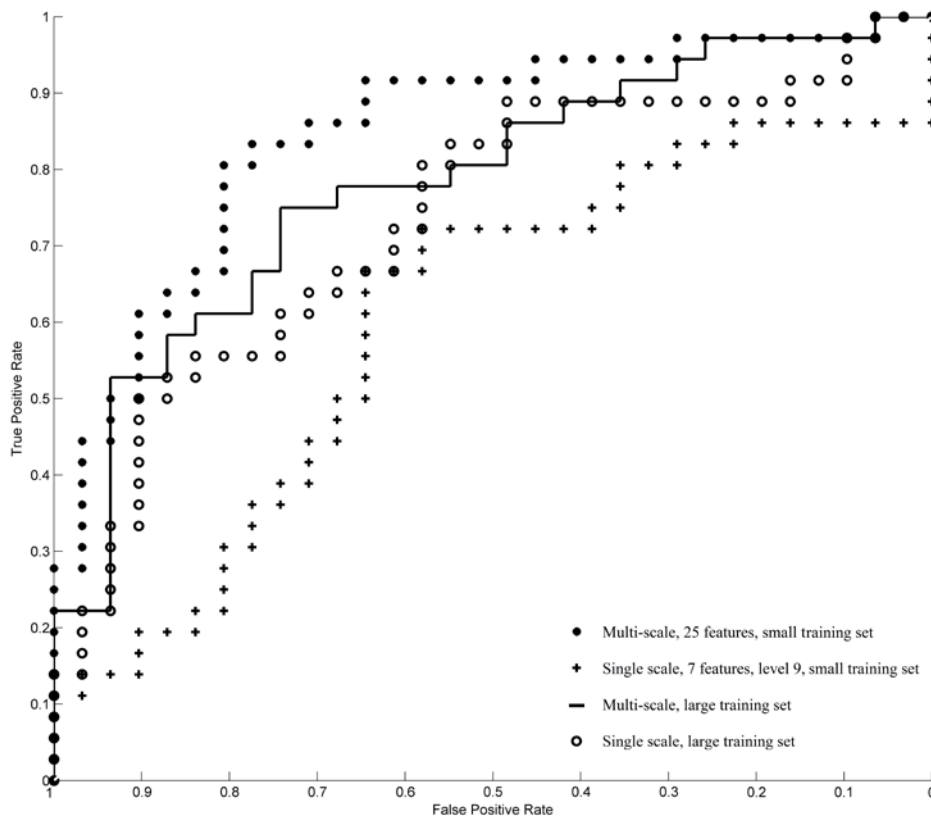

Fig.7 ROC plots of the different training schemes before feature selection.

5.3.2   After feature selection

In this section the classification performances of the features selected by the different schemes have been compared. Feature selection has only been reported for the multi-scale case as the results of Section 5.3.1 have already confirmed multi-scale processing to be superior. The following experiments were designed to compare the multi-scale features before and after selection using both the large and small training sets. In order to reach a generality for the small training set, an averaged ROC plot has been generated from 15 randomly selected possible small training sets of 9 moles and 9 melanomas. In effect this was achieved by providing 15 parallel neural networks, averaging their real valued outputs, converting this to binary at each threshold value from 0 to 1 and then plotting the TP, FP rates accumulated from all the test samples on the ROC. The number of combination of all possible sets was too big to test

at $\left(C_{36}^9 \times C_{31}^9 \right)$.

The ROC in Fig.8 gives a comparison of results when features are used at multiple-scales.

Results are with and without feature selection, and for large and small training image sets. From Fig.8 the best classification performance is for 13 selected multi-scale features with a small training set. It should be noted that this ROC plot has resulted from the averaged outputs of the 15 separately trained neural network classifiers using the test set. The next best is for the 13 selected multi-scale features with a large training set, followed by the 25 original multi-scale features using the large training set, and finally the 25 original multi-scale features using the small training set.
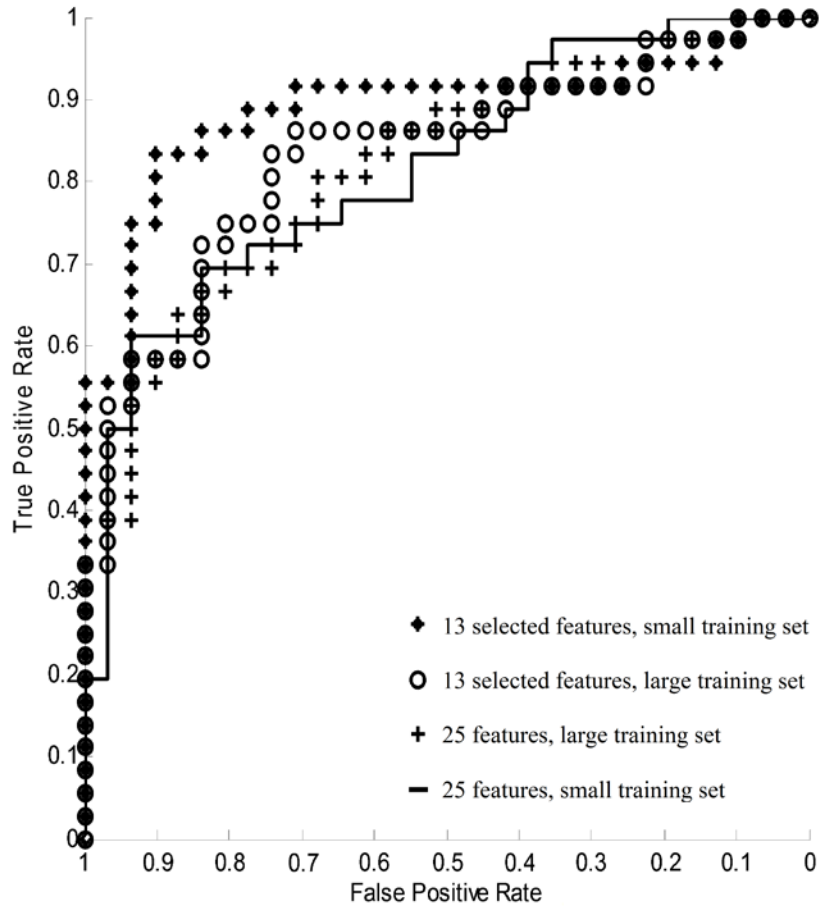

Fig.8 ROC plots for feature selection using multi-scale features

5.3.3 Design of parallel classifiers using small training sets
The results in Fig 8 have indicated that the averaged output of 15 neural classifiers using small training sets can outperform a single classifier using a large training set. However a single classifier using a small training set may or may not outperform that with a large training set. The following experiments were performed to ascertain the optimum size of the training set.
For the many neural networks produced by training using randomly chosen small data sets, an ROC plot from their averaged outputs was compiled after feeding the test data to each of them in turn. To find the optimum size of the training set, sizes of small training sets of melanomas

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plus moles were chosen at 3+3, 6+6, 9+9, 16+16, 23+23, 30+30, and tested together with the large training set of 36+36. In the experiments 15 training sets were randomly selected for each size from the full set of training data. Fig.9 presents the performance using the area under the ROC plot against training set size for the pre- and post-selection schemes. The trace marked by diamonds is for a ROC plot from the averaged outputs of the 15 classifiers before feature selection whereas that marked by circles is post feature selection.

As indicated in Fig.9, the scheme using the averaged outputs of the 15 classifiers post-feature selection performs best. It was noticed from the experiments that the averaged output value of all networks, using a combination model of many parallel network classifiers, may overcome the weakness of any single classifiers in the case of small training sets. The peak area of the ROC for the averaged outputs of the neural network classifiers, post-feature selection was for a training set of 9 melanomas plus 9 moles, indicating this to be the optimum size.
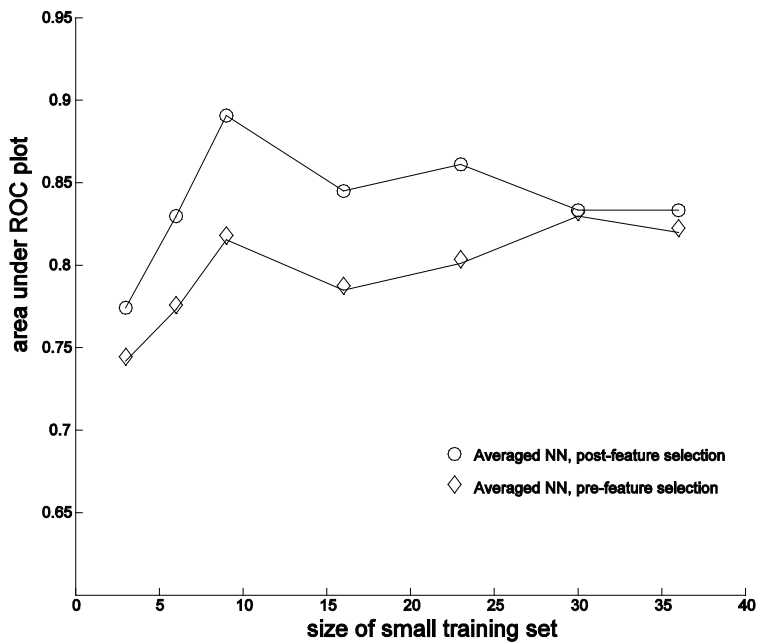

Fig.9 Performance against size of training set

Table 2 lists the ROC performances for each of the two single scale and the four multi-scale schemes tested. The performance is indicated by the measures of the sensitivity, specialty and area covered by each ROC plot, where the paired values of sensitivity and specialty are the True Positive Rate (TPR) and False Positive Rate (FPR) coordinates of the point on each ROC plot closest to the top left corner [21,22,23]. With the lowest values, the single scale features with the small training set have the worst results, and the multi-scale features after feature selection and using the small training set the best.

Scheme	Specialty	Sensitivity	Area of ROC
Single scale features with small sample set	0.64566	0.69444	0.69534
Single scale features with large sample set	0.87903	0.55556	0.75179
Original multi-scale features with small sample set	0.83871	0.69444	0.81541
Original multi-scale features with large sample set	0.80645	0.69444	0.81989
Selected multi-scale features with large sample set	0.74194	0.83333	0.83333
Selected multi-scale features with small sample set	0.90323	0.83333	0.89068

Table 2. Comparison of classification performances

5.3.4 Discussion

In general, Fig.8 and Table 2 indicate that multi-scale features have better discrimination than single scale features, and that, after feature selection, multi-scale schemes have better performances than schemes without selection. The best ROC plot was for multi-scale selected features using the small training set. It outperformed the corresponding scheme using the large training set. There are two reasons for this in that each of the 13 selected multi-scale features had a good individual performance when used for skin contour irregularity measurement and so a small training set was probably sufficient. Secondly the performance of a neural network with a BP training algorithm can be degraded by using a large training set that may cause a solution to become stuck in a local minimum [24].

6 Conclusions

A method that examines the structural content of the contour of skin lesion images has been proposed that determines if the lesion is a melanoma or a benign mole. The contour contained both structural and textural information, but it was demonstrated that the structural information was most important in the determination.

The 1D contour signal was filtered into sub-bands using the discrete wavelet transform (DWT) down to level 9. The structural information was found to lie mostly at the lower frequencies, in the detail levels from 6 to 9 plus the approximation at level 9. These were denoted as significant levels, and the information within them was shown to provide the best classification separation between sets of melanomas and moles. The DWT was found to enable efficient processing of the signals.

A number of statistical and geometric feature descriptors of contour irregularity were developed. These were computed in each of the significant sub-bands. To enable an efficient system, these features were selected using a two stage process. Firstly correlation analysis was used to remove redundant features, and secondly the performance of each feature in separating sets of melanomas and moles was measured and compared.

A classifier using a combination of features was designed using a back-projection neural network. The system was optimized to obtain the maximum true positive rate and minimum false positive rate for separation. Issues of training were explored, and a small, randomly chosen, sub-set of 9 melanoma and 9 mole images found to provide the best results. Of the seven available features, six were applied in four significant sub-bands and one in a single sub-band, forming twenty five measurements in total. As described above these had been ranked in order of effectiveness, and it was found the best combined classifier resulted when just the best thirteen measures were used.

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