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ABSTRACT

Data reduction procedures and classification via support vector machines (SVMs) are often associated with multi or hyperspectral image analysis. In this paper, we propose an automatic method with these two schemes in order to perform a classification of skin hyper-pigmentation on multi-spectral images. We propose a spectral analysis method to partition the spectrum as a tool for data reduction, implemented by projection pursuit. Once the data is reduced, an SVM is used to differentiate the pathological from the healthy areas. As SVM is a supervised classification method, we propose a spatial criterion for spectral analysis in order to perform automatic learning.

Index Terms— spectral analysis, data reduction, projection pursuit, Support vector machine, skin hyper-pigmentation

1. INTRODUCTION

Spectral analysis of the skin is important for dermatologists to evaluate the quantities of particular chromophores in order to quantify diseases. To this end, multi and hyperspectral images allow the integration of both spectral properties and spatial information of pathological areas.
In the literature, several methods for skin analysis propose to select regions of interest in the spectrum [1, 2]. Then the disease is quantified using small numbers of bands. In fact, in Fig.2, one can see that in the q-bands and in the Soret band haemoglobin absorbency presents maxima, and that melanin has an almost linear absorbency for wavelengths between 600 nm and 1000 nm. That is why the main idea to evaluate the quantity of haemoglobin with multi-spectral data is to compensate the influence of melanin in the q-bands by a band around 700 nm where the absorbency of haemoglobin is weak compared to the melanin absorbency [1]:

$$M_h = -log(b_q/b_{700}), \quad (1)$$

where M_h represents the resulting haemoglobin quantification map, b_q an image taken in one of the two q-bands and b_{700} the image taken from a band at the wavelength of 700 nm. To extract a representative cartography of melanin, a method is proposed in [2]. It consists in modelling the melanin response as linear between 600 nm and 700 nm. Then, the linear coefficient gives a melanin quantification map.
Contrary to the spectral analysis methods based on physics, methods like principal component analysis (PCA) or independent components analysis (ICA) enable to extract the most statistically important information of the spectrum.
In this paper, we propose to use data reduction [3, 4, 5] in order to avoid the Hughes phenomenon [6] and classification by SVM [7, 8] since this combination is known to provide good results [9]. In our application, we analyse multi-dimensional data whose variations are linked to physics. That is why we choose Projection Pursuit (PP) to perform the data reduction. Projection pursuit algorithms [3] merge the data in K groups with equal number of bands and project each group in a unique vector by maximising an index I between the projected groups. K appears as a setting parameter.
Thus as shown in Fig.1, we propose a spectral analysis to estimate both a spectral partitioning for data reduction by projection pursuit and a training set for classification by SVM. The paper is organized as follows. In section 2, we expose a spectral analysis method with a spectral gradient index. In section 3, we present the projection pursuit for data reduction. In section 4, we propose a method to extract a training set for SVM from the spectral analysis. In section 5, we present obtained results. In section 6, we consider perspectives of further development within this framework.

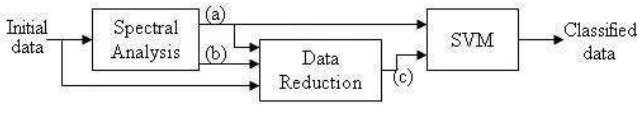

Fig. 1. Scheme of the processing. Arrows represents: (a) data learning set, (b) spectrum partition, (c) reduced data.

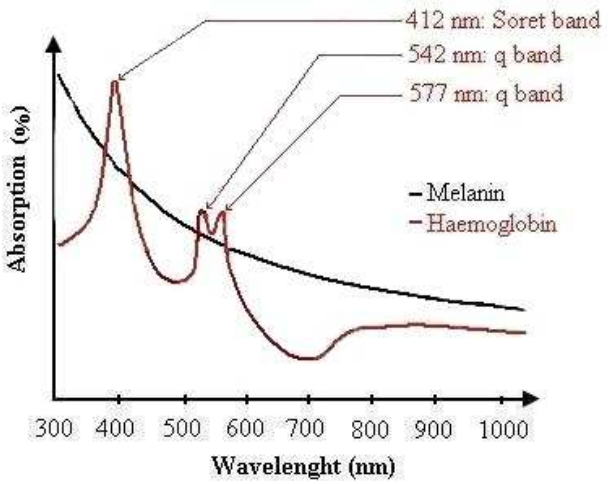

Fig. 2. Absorption of melanin and haemoglobin depending on the wavelength.

2. SPECTRAL ANALYSIS

Usually, for data reduction, the number K of desired groups to partition the spectrum is manually fixed after an analysis of the classification problem. To partition the data with respect to spectrum absorbency variations, a solution is proposed in [5]. After an initialisation with K groups with the same number of bands, the borders of each groups are iteratively re-estimated minimizing the internal variance inside each group. In order to remove the constraint on the number of groups K, we propose to partition the spectrum using a function F_I. The spectral analysis method is to browse the wavelengths with an index I, such as the variance or Kullback-Leibler, and deduce interest parts in the spectrum from variations of I. Then, let define the F_I function as:

$$F_I(k) = I(k-1,k), \qquad k = 2, ..., N_b \tag{2}$$

where k is the index of the spectral band and N_b the total number of spectral bands. Analysing the F_I function enables to determinate spectral bands where absorption changes appear. In fact, if the spectrum is stationary between two bands, the index I measures only noise whereas it quantifies the variations when the spectrum is not stationary. Assuming that the noise measured by I in a stationary spectrum is Gaussian, we can use the mean value and the standard deviation of the distribution to detect the spectral variations. Thus, a non stationary area in the spectrum is detected when $F_I(k)$ is above the threshold T_1 or below the threshold T_2:

$$\begin{aligned} T_1 &= \mu_{F_I} + t\sigma_{F_I}, \\ T_2 &= \mu_{F_I} - t\sigma_{F_I}, \end{aligned} \tag{3}$$

where μ_{F_I} and σ_{F_I} are the mean value and the standard deviation of F_I respectively, and t the setting parameter of the proposed method estimated once for all the data set. The spectrum partitions are deduced from the analysis of the F_I function. Local extrema of F_I above the threshold T_1 or below the threshold T_2 are the borders of the groups. It is better to choose the parameter t than the parameter K for spectral partitioning. In fact, in our data set of skin diseases, it is interesting to get the spectral partitioning without a fix number of group K because the spectral bands of interest can varied depending on the disease.

The spectral analysis with a statistic index does not enable a training set for classification. That is why, we propose a spatial index I_s for each voxel neighbourhood to have a spatial mapping of the spectral variations (see Fig.3). In our application, skin hyper-pigmented areas do not present a specific pattern. That is why we propose a spectral gradient as index I_s computed on 3×3 square area denoted v:

$$I_s(k-1,k) = \frac{1}{N} \sum_{i,j \in v} \big|S(i,j,k) - S(i,j,k-1)\big|, \tag{4}$$

where N denotes the number of pixels in v, k the index of the studied band or projected group and $\forall i,j \in v, S(i,j,k)$ is the intensity of the pixel at position (i,j) in the band or group k. for spatial indices, let denote F_{I_s} the F_I function:

$$F_{I_s}(k) = I_s(k-1,k), \qquad k = 2, ..., N_b. \tag{5}$$

F_{I_s} is a 3D function. For every couple of bands, F_{I_s} computes a spatial map of spectral variations. To perform the spectral analysis mentioned above to partition the spectrum, we use a spatial integration of F_{I_s}. Thus the proposed function analysis is done with the function:

$$F^{\mathcal{A}}_{I_s}(k) = \mathcal{A}\big(F_{I_s}(k)\big), \qquad k = 2, ..., N_b \tag{6}$$

where $\mathcal{A}$ denote the area of the detected changed pixels. A method to extract training pixels from F_{I_s} is proposed in section 4.

3. DATA REDUCTION BY PROJECTION PURSUIT

Usually, to compute a projection subspace by PP, an index I is maximized between the whole projected groups. In our application, we expect healthy/pathological skin classification. That is why, we prefer to compute the maximization of the index I between the projected classes as proposed in [4]. Conventionally, the Kullback-Leibler distance is used for projection pursuit. If i and j represent the classes which are to be discriminated, the Kullback-Leibler distance can be written as follows:

$$D_{kb}(i,j) = \frac{H_{kb}(i,j) + H_{kb}(j,i)}{2}, \tag{7}$$

with

$$H_{kb}(i,j) = \int f_i(x) ln \frac{f_i(x)}{f_j(x)} dx, \tag{8}$$

where f_i and f_j are the distributions of the two classes. For Gaussian distributions, the Kullback-Leibler distance or index I takes the following form [5]:

$$I(i,j) = \frac{1}{2}\big((\mu_i-\mu_j)^t(\Sigma_i^{-1}+\Sigma_j^{-1})(\mu_i-\mu_j)\big) + \frac{1}{2}tr(\Sigma_i^{-1}\Sigma_j+\Sigma_j^{-1}\Sigma_i-2Id), \quad (9)$$

where μ and Σ represent the mean value and the variance respectively of each class and tr is the trace. This way the index I enables to measure the variations between two classes on two bands or two groups.

In our process, we initialize the projection pursuit with the spectral partitioning given by the spectral analysis, and then we compute the projection subspace by maximizing the Kullback-Leibler distance between the two classes defined by the training set. The method to select this training set is proposed in the next section.

4. SVM CLASSIFICATION

SVM [7, 8] technique results in a supervised algorithm which performs a classification in two classes. Thanks to a training set defining the two classes an optimal class separator is computed. Each data point is then classified according to its position to the separator. We propose to use spectral analysis with the spatial index I_s to find the training pixels for the SVM. In fact, as described in section 2, spectral analysis with a spatial index gives a spatial map of the spectral changes between two consecutive bands. For training the SVM, we select one of the $F_{I_s}(k)$ maps. This map can be the one revealing the most changes in the whole spectrum, i.e the global extrema of $F_{I_s}^{\mathcal{A}}$, or the global extrema of $F_{I_s}^{\mathcal{A}}$ in a region of interest of the spectrum. Afterwards, in the selected map $F_{I_s}(k)$, the N nearest pixels to the concerned threshold T_1 or T_2 are extracted for training the SVM. Among the N training pixels, half are selected above the threshold and half below the threshold.

To summarize, the proposed classification method consists in two steps. The first one is a rough automatic classification performed in a few number of spectral bands selected by spectral analysis. In the second step, the SVM enables to improve the previous classification by reconsidering the whole reduced data cube by PP. Thus the classification scheme is (see Fig.1) : spectral analysis to partition the data into spectral groups and extract a training set, then, data reduction by projection pursuit with the Kullback-Leibler distance maximized between the classes and, finally, classification by SVM.

5. EXPERIMENTAL RESULTS

The experiments have been conduced on multi-spectral images containing 18 bands from 405 nm to 970 nm with an average step of 25 nm. These images are about 900×1200 pixels. To partition the spectrum, we use the $F_{I_s}^A$ function analysis with the spatial index I_s. In the 18 bands data cube containing both hyper-pigmented and healthy skin, spectral analysis gives $K = 5$ groups. In Fig.3, binary images on the borders of the five groups obtained by thresholding the $F_{I_s}(k-1,k)$ images by T_1 and T_2 are shown. As one can see, the pattern of the hyper-pigmented area appears in the images b, e and f which corresponds to the wavelengths around 470, 660 and 700 nm. For these wavelengths the haemoglobin absorbency becomes significantly lower than the melanin absorbency. Moreover, the images c and d partition the spectrum in the two q-bands where the Haemoglobin absorbency becomes higher than the melanin one (see Fig.2). In this example, in order to classify hyper-pigmentation, the training set is extracted from the image e. The 50 nearest pixels w.r.t. the concerned threshold T_2 are selected to construct the training set.

Fig.4 shows the hyper-pigmentation cartography automatically obtained by data reduction with SVM, melanin representative source by ICA, and melanin concentration obtained by using Stamatas algorithm [2]. For the SVM method, we assume that the distance between a pixel and the separating hyperplane is proportional to the degree of hyper-pigmentation. Then, the cartography given by data reduction combined with SVM is obtained with the SVM decision function values [7]. As one can see in Fig.4, the SVM based method gives as accurate cartography as the Stamatas method and ICA melanin representative source with the advantage of computing automatically a boundary to separate the healthy and pathological areas. This boundary corresponds to the separating hyperplane.

6. DISCUSSION AND FUTURE WORK

In this paper we have proposed a method to automatically analyse the spectrum in order to reduce the redundant information and extract the approximative shapes of areas of interest. Using the obtained segmentation for training an SVM, applied to the reduced data cube by projection pursuit, gives a precise classification of skin hyper-pigmentation. In our application, we use an index without prior assumption since the hyper-pigmented areas exhibit no particular pattern. If it was not the case a spatial index including a prior shape could have been used such as, for example, a line prior to detect blood vessels.

The computation time of this spectral analysis method grows linearly with the number of spectral bands. Nevertheless, as the spatial index I_s evaluates the changes in local spatial neighbourhoods, the algorithm is easily implemented for parallel computation.

The main perspective of this work is to adapt the proposed method to hyper-spectral data. The presented spectral analysis is relevant for multi-spectral data since the gap between spectral bands is sufficient to measure significant variations using the F_I function. To adapt this method to hyper-spectral

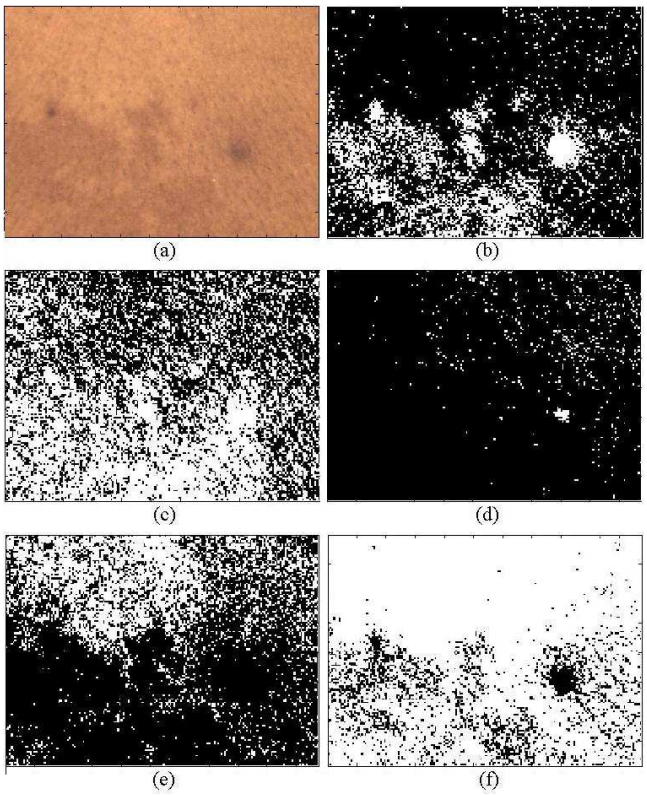

Fig. 3. Images of group borders obtained with the index I_s. The thresholding parameter t is equal to 0.5. Reconstructed color image(a), I_s at the border of the first group (b), I_s at the border of the second group (c), I_s at the border of the third group (d), I_s at the border of the fourth group (e), I_s at the border of the fifth group (f).

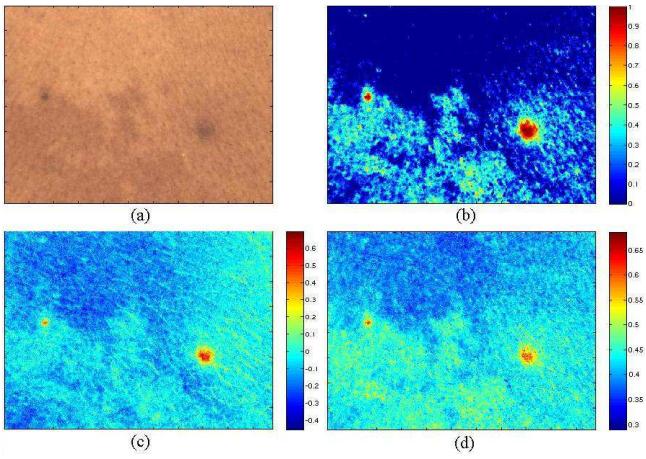

Fig. 4. Reconstructed by spectral integration color image (a). Hyper-pigmentation cartographies obtained by data reduction with SVM (b), by ICA (c), by Stamatas algorithm (d).

data, we need to introduce a parameter n in the F_I function in order to measure variations not between consecutive bands but between two bands with an offset n. Then the F_I function becomes $F_I = I_s(k-n, k)$ with $k = n+1, ..., Nb$. A process to estimate the parameter n will be studied.

7. ACKNOWLEDGEMENT

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