An Efficient Classification for Detecting Diabetes Mellitus and Nonproliferative Diabetic Retinopathy by using PSVM Classifiers

M.Arun Jothi, C. Thirumoorthi, M. Hasina Banu

Abstract

Diabetes mellitus (DM) and its cause’s diabetic retinopathy (DR) are major health problems. To combat this approaching epidemic, proposes a noninvasive automated method to detect DM and NPDR by distinguishing Healthy/DM and NPDR/DM sans NPDR (DM without NPDR) samples using an array of tongue features consisting of color, texture, and geometry. The various tongue features like color, texture, and geometry are extracted from the human tongue can used to diagnose disease. Tongue images were captured using an especially designed in-house device taking into consideration color correction. Each image was segmented in order to locate its foreground pixels. With the relevant pixels located, three groups of features namely color, texture, and geometry were extracted from the tongue foreground. The tongue color gamut represents all possible colors that appear on the tongue surface representing 12 colors. The color features are extracted from the sample tongue image. The texture features are extracted from the tongue image. To extract the texture value of each block, the 2-D Gabor filter is applied. The texture of tongue images separate eight blocks that categorize the nine texture features of the tongue. Here the Healthy samples having a higher texture value and DM samples have lower texture values. Also, 13 geometry features are extracted from tongue images. These features are based on measurements, distances, areas, and their ratios. Finally by applying 34 features, Proximal Support Vector Machine (PSVM) classifier used for classification instead of SVM classifier by comparing with the normal tongue features. Classification was performed between Healthy versus DM in addition to NPDR versus DM-sans NPDR initially using every feature individually (from the three groups), followed by an optimal combination of all the features. A dataset consist of 296 Diabetes Mellitus samples consisting of 267 DM-sans NPDR and 29 NPDR processed among three features and identify the accuracy of 95% result respectively.

Keywords: Detecting Diabetes mellitus (DM), Detecting non-proliferative diabetic retinopathy (NPDR), tongue color features, tongue geometry features, tongue texture features.

I. INTRODUCTION

Diabetes mellitus (DM), also known as simply diabetes, is a group of metabolic diseases in which there are high blood sugar levels over a prolonged period. This high blood sugar produces the symptoms of frequent urination, increased thirst, and increased hunger. Untreated, diabetes can cause many complications.

Two main types of DM exist, Type 1 DM and Type 2 DM. People with Type 1 DM fail to produce insulin, and therefore require injections of it. Type 2 DM is the most common type and can be categorized by insulin resistance. Currently, there is no cure for Type 1 DM or Type 2 DM. However, Type 2 DM can be managed by eating well, exercising, and maintaining a healthy lifestyle.

A fasting plasma glucose (FPG) test is the standard method practiced by many medical professionals to diagnose DM. FPG test is performed after the patient has gone at least 12 h with-out food, and requires taking a sample of the patient’s blood (by piercing their finger) in order to analyze its blood glucose levels. Even though this method is accurate, it can be considered invasive, and slightly painful (piercing process). Diabetic retinopathy (DR) is a micro vascular complication of DM that is responsible for 4.8% of the 37 million cases of blindness in the world, estimated by WHO [1]. In its earliest stage known as non-proliferative diabetic retinopathy (NPDR), the disease if detected can be treated to prevent further progression and sight loss. Various imaging modalities such as red-free [2], angiography [3], [4], and color [5]–[10] fundus imaging are used to examine the human retina in order to detect DR and subsequently NPDR. These methods are based on the detection of relevant features related to DR, including but not limited to hemorrhages, micro aneurysms, various exudates, and retinal blood vessels. These imaging modalities themselves can be regarded as invasive, exposing the eye to bright flashes or having fluorescein injected into a vein in the case of angiography. Therefore, there is a need to develop a noninvasive yet accurate DM and NPDR detection method.

As a result, this paper deals with the aforementioned problems and proposes a noninvasive automated method to detect DM and NPDR by distinguishing Healthy/DM and NPDR/DM-sans NPDR (DM without NPDR) samples using an array of tongue features consisting of color, texture, and geometry. To remove these qualitative aspects, quantitative feature extraction and analysis from tongue images can be established. To the best of our knowledge, there is no other published work to detect DM or NPDR using tongue color, texture, and geometry features.
Tongue images were captured using an especially designed in-house device taking into consideration color correction. Each image was segmented in order to locate its foreground pixels. With the relevant pixels located, three groups of features namely color, texture, and geometry were extracted from the tongue foreground. Classification was performed between Healthy versus DM in addition to NPDR versus DM-sans NPDR initially using every feature individually (from the three groups), followed by an optimal combination of all the features.

Section II describes the tongue image capture device, color correction, and tongue segmentation, while Section III discusses tongue color feature extraction. In Section IV, tongue texture feature extraction is given in detail; with tongue geometry feature extraction presented in Section V. Section VI describes the experimental results and discussion, followed by concluding remarks in Section VII.

II. CAPTURE DEVICE AND TONGUE IMAGE PREPROCESSING

The capture device, color correction of the tongue images, and tongue segmentation are given in this section. Fig. 1 shows the in-house designed device consisting of a three-chip CCD camera and two D65 fluorescent tubes kept symmetrically around the camera to deliver a uniform light. The angle made between the incident light and reflected light is 45°, (CIE). During image capture, patients placed their chin on a chinrest while showing their tongue to the camera. The images captured in JPEG format that ranged from 257 × 189 pixels to 443 × 355 pixels were color corrected [26] to eliminate any variability in color images caused by changes of illumination and device dependence. This allows for consistent feature extraction and classification in the following steps. The idea based on the Munsell ColorChecker is to map a matrix generated from the input RGB vector to an objective RGB vector, thereby obtaining a trans-formation model. Compared with the retinal imaging modalities mentioned previously, this capture device is noninvasive, neither requiring a bright flash nor injection of dye into a patient’s blood stream.

Once the tongue images are captured, automatic segmentation is next applied to each image in order to separate its foreground pixels from its background. This is accomplished by combining a bielliptical deformable template (BEDT), and an active contour model known as bielliptical deformable contour (BEDC). In [27], the segmented tongue is obtained by first minimizing the energy function of BEDT, followed by the energy function of BEDC. BEDT captures the overall tongue shape features, while BEDC can be deformed to match the local tongue details. The result is a binary tongue image clearly defining foreground pixels (tongue surface area and its edges) from its background pixels (area outside the tongue edges). This allows for three groups of features, color, texture, and geometry to be extracted from a tongue foreground image in the proceeding steps.

III. TONGUE COLOR FEATURES

The following section describes how color features are extracted from tongue images. The tongue color gamut is initially compressed in Section III-A. In Section III-B, each foreground pixel of the tongue is compared with 12 colors and assigned to its closest color. It creates the color features.

A. Tongue Color Gamut

The tongue color gamut represents all possible colors that appear on the tongue surface, and exists within the red...
TABLE I
RGB AND CIELAB VALUES OF THE 12 COLORS

<table>
<thead>
<tr>
<th>Color</th>
<th>[R G B]</th>
<th>[L A B]</th>
</tr>
</thead>
<tbody>
<tr>
<td>C (Cyan)</td>
<td>[188 188 188]</td>
<td>[76.0693 0.5580 1.3615]</td>
</tr>
<tr>
<td>R (Red)</td>
<td>[189 99 91]</td>
<td>[52.2540 34.8412 21.3002]</td>
</tr>
<tr>
<td>B (Blue)</td>
<td>[183 165 180]</td>
<td>[69.4695 9.5423 5.4951]</td>
</tr>
<tr>
<td>P (Purple)</td>
<td>[226 142 214]</td>
<td>[69.4695 42.4732 23.8880]</td>
</tr>
<tr>
<td>DR (Deep red)</td>
<td>[136 72 49]</td>
<td>[37.8424 24.5593 25.9396]</td>
</tr>
<tr>
<td>LR (Light red)</td>
<td>[227 150 147]</td>
<td>[69.4695 28.4947 13.3940]</td>
</tr>
<tr>
<td>LP (Light purple)</td>
<td>[225 173 207]</td>
<td>[76.0693 24.3246 9.7749]</td>
</tr>
<tr>
<td>LB (Light blue)</td>
<td>[204 183 186]</td>
<td>[76.0693 7.8917 0.9885]</td>
</tr>
<tr>
<td>BK (Black)</td>
<td>[107 86 56]</td>
<td>[37.8424 3.9632 20.5874]</td>
</tr>
<tr>
<td>GY (Gray)</td>
<td>[163 146 143]</td>
<td>[61.6542 5.7160 3.7317]</td>
</tr>
<tr>
<td>W (White)</td>
<td>[200 167 160]</td>
<td>[70.9763 10.9843 8.2952]</td>
</tr>
<tr>
<td>Y (Yellow)</td>
<td>[166 129 93]</td>
<td>[56.3164 9.5539 24.4546]</td>
</tr>
</tbody>
</table>

its label on top. Correspondingly, its RGB and CIELAB values are given in Table I.

B. Color Feature Extraction

For the foreground pixels of a tongue image, corresponding RGB values are first extracted, and converted to CIELAB [29] by transferring RGB to CIEXYZ using

\[
X = 0.4124 \cdot 0.3576 \cdot 0.1805 \cdot R \\
y = 0.2126 \cdot 0.7152 \cdot 0.0722 \cdot G \\
z = 0.0193 \cdot 0.1192 \cdot 0.9505 \cdot B
\]

followed by CIEXYZ to CIELAB via

\[
L^* = 166 \cdot f(Y/Y_0) - 16 \\
ar^* = 500 \left[ f(X/X_0) - f(Y/Y_0) \right]_0 \\
\]

where \( f(x) = x^{1/3} \) if \( x > 0.008856 \) or \( f(x) = 7.787x + 16/16 \) if \( x \leq 0.008856 \).

\( X_0, Y_0, \) and \( Z_0 \) in (2) are the CIEXYZ tristimulus values of the reference white point. The LAB values are then compared to 12 colors from the tongue color gamut (see Table I) and assigned the color which is closest to it (measured using Euclidean distance). After evaluating all tongue foreground pixels, the total of each color is summed and divided by the total number of pixels. This ratio of the 12 colors forms the tongue color feature vector, where \( v = [c_1, c_2, c_3, c_4, c_5, c_6, c_7, c_8, c_9, c_10, c_11, c_12] \) and \( c_i \) represents the sequence of colors in Table I. As an example, the color features of three tongues are indicated in visual structure (refer to Figs. 5–7) along with its extracted color feature vector, where the original image is decayed into one of the 12 colors. Fig. 5 shows a Healthy sample, Fig. 6 shows a DM sample, while an NPDR sample is given in Fig. 7. In these three samples, the majority of pixels are \( \hat{R} \).

The mean colors of Healthy, DM, and NPDR are displayed in Table II along with their standard deviation (std). DM tongues which have a higher ratio of \( DR, LR, \) and \( Y \) are greater in Healthy samples, and \( GY \) is higher in NPDR. The rest of the mean color features are similar.
IV. TONGUE TEXTURE FEATURES

Texture feature extraction from tongue images is presented in this section. To better represent the texture of tongue images, eight blocks (see Fig. 8) of size 64 × 64 strategically located on tongue surface are used. A block size of 64 × 64 was chosen.

Fig. 6. DM tongue sample, its tongue color feature vector.

Fig. 7. NPDR tongue sample, its tongue color feature vector.

<table>
<thead>
<tr>
<th>TABLE II</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>MEAN (std)</strong> OF THE COLOR FEATURES FOR HEALTHY (std&lt;sub&gt;Healthy&lt;/sub&gt; = 11.71), DM (std&lt;sub&gt;DM&lt;/sub&gt; = 12.50), AND NPDR (std&lt;sub&gt;NPDR&lt;/sub&gt; = 12.08)</td>
</tr>
<tr>
<td><strong>Healthy</strong></td>
</tr>
<tr>
<td><strong>C</strong></td>
</tr>
<tr>
<td>23.77 (3.76)</td>
</tr>
</tbody>
</table>
convolution. Responses of a block are combined to form a single output that represents the texture of a block by averaging the pixel values of the block. The Gabor filter is a linear filter used in image processing, and is commonly used in texture representation. To compute the texture value of each block, the 2-D Gabor filter is applied as

\[
R_k(x, y) = \frac{1}{\pi(\lambda^2 + \gamma^2)^{\frac{1}{2}}} \exp \left( - \frac{x^2 + y^2}{\lambda^2 + \gamma^2} \right) \cos \left( \frac{2\pi \lambda}{\lambda} \right) = \exp \left( - \frac{x^2 + y^2}{\lambda^2 + \gamma^2} \right) \cos \left( \frac{2\pi \lambda}{\lambda} \right)
\]

where \(\lambda\) is the wavelength, \(\gamma\) is the aspect ratio of the sinusoidal function, and \(\theta\) is the orientation. A total of three \(\theta\) (1, 2, and 3) and four \(\delta\) (0, 45°, 90°, and 135°) choices were investigated to achieve the best result. Each filter is convolved with a texture block to produce a response \(R_k(x, y)\):

\[
R_k(x, y) = G_k(x, y) \ast \text{im}(x, y)
\]

where \(\text{im}(x, y)\) is the texture block and \(\ast\) represents 2-D convolution. Responses of a block are combined to form \(R_k\), and its final response evaluated as follows:

\[
R_k(x, y) = \max (R_1(x, y), R_2(x, y), \ldots, R_N(x, y))
\]

which selects the maximum pixel intensities, and represents the texture of a block by averaging the pixel values of \(R_k\).

In the end, \(\sigma\) equal to 1 and 2 with three orientations (45°, 90°, and 135°) was chosen. This is due to the fact that the sum of all texture blocks between Healthy and DM had the largest distance of \(\sigma\) to its center. Fig. 9–11 illustrate the texture blocks for Healthy, DM, and NPDR samples, respectively. Below each block, its corresponding texture value is provided.

Table III depicts the texture value mean for Healthy, DM, and NPDR together with their standard deviation. Healthy samples have a higher texture value in Block 7, whereas NPDR texture values are greater for the remaining blocks. The mean of all eight blocks is also included as an additional texture value. This brings the total number of texture features extracted from tongue images to be 9.

V. TONGUE GEOMETRY FEATURES

In the following section, we describe 13 geometry features extracted from tongue images.

Width: The width \(w\) feature (see Fig. 12) is measured as the horizontal distance along the \(x\)-axis from a tongue’s furthest right edge point \((x_{\text{max}}, y)\) to its furthest left edge point \((x_{\text{min}}, y)\):

\[
w = x_{\text{max}} - x_{\text{min}}.
\]

Length: The length \(l\) feature (see Fig. 12) is measured as the vertical distance along the \(y\)-axis from a tongue’s furthest top edge \((x, y_{\text{max}})\) to its furthest bottom edge \((x, y_{\text{min}})\):

\[
l = y_{\text{max}} - y_{\text{min}}.
\]

Length–width ratio: The length–width ratio \(lw\) is the ratio of a tongue’s length to its width:

\[
lw = \frac{l}{w}.
\]

Smaller half-distance: Smaller half-distance \(z\) is the half distance of \(l\) or \(w\) depending on which segment is shorter (see Fig. 12):

\[
z = \min(l, w) / 2.
\]

Center distance ratio: Center distance ratio \(cd\) is ratio of \(\sigma\) to \(l\):

\[
\text{cdr} = \frac{\sigma}{l}.
\]

Area: The area \(a\) of a tongue is defined as the number of pixels found in the foreground area of the tongue:

\[
a = \frac{\pi}{r^2}.
\]
TABLE III
MEAN (std) OF THE TEXTURE FEATURES FOR HEALTHY (std_{Healthy} = 1.160), DM (std_{DM} = 1.238), AND NPDR (std_{NPDR} = 1.196)

<table>
<thead>
<tr>
<th>Feature</th>
<th>Block 1</th>
<th>Block 2</th>
<th>Block 3</th>
<th>Block 4</th>
<th>Block 5</th>
<th>Block 6</th>
<th>Block 7</th>
<th>Block 8</th>
<th>Mean of Blocks 1-8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Healthy</td>
<td>3.11 (0.397)</td>
<td>1.660 (0.632)</td>
<td>1.891 (0.677)</td>
<td>2.242 (0.875)</td>
<td>2.733 (0.999)</td>
<td>1.870 (0.650)</td>
<td>3.893 (1.167)</td>
<td>3.538 (1.326)</td>
<td>2.636 (0.486)</td>
</tr>
<tr>
<td>DM</td>
<td>2.952 (1.039)</td>
<td>2.142 (0.790)</td>
<td>2.539 (1.051)</td>
<td>2.114 (0.901)</td>
<td>2.522 (1.111)</td>
<td>1.859 (0.807)</td>
<td>3.740 (1.371)</td>
<td>3.887 (1.509)</td>
<td>2.768 (0.562)</td>
</tr>
<tr>
<td>NPDR</td>
<td>3.221 (1.118)</td>
<td>2.341 (0.777)</td>
<td>2.630 (0.892)</td>
<td>3.392 (1.333)</td>
<td>2.977 (1.130)</td>
<td>2.255 (1.255)</td>
<td>3.686 (1.343)</td>
<td>3.902 (1.133)</td>
<td>3.050 (0.521)</td>
</tr>
</tbody>
</table>

Fig. 12. Illustration of features 1, 2, and 4.

Fig. 13. Illustration of feature 5.

Circle area ratio: Circle area ratio (car) is the ratio of \( ca \) to \( a \):
\[
car = \frac{ca}{a}.
\]  
(13)

Square area: Square area (sa) is the area of a square defined within the tongue foreground using smaller half-distance \( z \) (refer to Fig. 15):
\[
sa = 4z^2.
\]  
(14)

Square area ratio: Square area ratio (sar) is the ratio of \( sa \) to \( a \):
\[
sar = \frac{sa}{a}.
\]  
(15)

Triangle area: Triangle area (ta) is the area of a triangle defined inside the foreground pixel of the tongue (see Fig. 16). The right point of the triangle is \( x_{max} \), the left point is \( x_{m} \) and the bottom is \( y_{max} \).

Triangle area ratio: Triangle area ratio (tar) is the ratio of \( ta \) to \( a \):
\[
tar = \frac{ta}{a}.
\]  
(16)

The mean geometry features of Healthy, DM, and NPDR are shown in Table IV along with their standard deviation.
VI. NUMERICAL RESULTS AND DISCUSSION

The ensuing section presents the numerical results. Healthy versus DM classification is first provided in Section VI-A. This is followed by NPDR versus DM-sans NPDR classification in Section VI-B.

A. CLASSIFICATION USING PSVM CLASSIFIER

Proximal Support Vector Machine is based on Support Vector Machine, it is simpler and faster than traditional Support Vector Machines algorithm, which is especially suitable for large amounts of data or image classification and operations.

On assumption that there are N training samples, such as, \((x_1, y_1), (x_2, y_2), \ldots, (x_N, y_N)\) among them, so the target function of Proximal Support Vector Machine can be denoted by

\[
\min_{\omega, e} \frac{1}{2} ||\omega||^2 + \frac{1}{2} ||w^T w + r^2
\]

Subject to : \(L(Aw - e) + y = e\)

\(C\) is the cost factor, \(y\) express the sample output, \(w\) figure the normal vector of the classification hyper plane, \(e\) is the units vector, \(g\) is the parameter which can ascertain the position of two dividing-line plane relating to the origin in Proximal Support Vector Machine; \(A\) is \(n \times m\) dimensional training data set, each sample is corresponding to a list \(A_1\).

In proximal support vector machine (PSVM) instead of dividing the space into disjoint regions for each class, the feature points are assigned according to the proximity to the hyper planes that are separated as far as possible. This leads to a very fast and simple algorithm. The cost function is given as follows:

\[
\min_{\omega, b, \xi} f(\omega, b, \xi) = \frac{1}{2} ||\omega||^2 + \frac{C}{2} \sum_{i=1}^{m} ||\xi_i||^2
\]

\(s.t.\ y_i(\omega^T \phi(x_i) + b) = 1 - \xi_i\)

The minimization of cost function leads to maximization of margin in \((\omega, b)\) space. It also uses the equality constraint and minimizes the squared error like LS-SVM. The PSVM works much faster than SVM as well as give performance similar to SVM. The Lagrangian of the cost function is given as:

\[
\sum_{i=1}^{m} \alpha_i - \frac{1}{2} \sum_{i=1}^{m} \sum_{j=1}^{m} \alpha_i \alpha_j y_i y_j \phi(x_i)^T \phi(x_j)
\]
is the lagrangian multiplier due to equality constraint. The cost function is differentiated with respect to $\omega, b, \xi$ and $\alpha$ which gives:

**B. Healthy Versus DM Classification**

Healthy person samples were examined through a blood test. If indicators from these tests fall inside a certain extent, they were considered as healthy. In the DM class, FPG test was used to diagnose diabetes.

Half of the images were randomly selected for training, while the other half was used as testing. This process was repeated five times. Classification was performed using $k$-nearest neighbor ($k$-NN) \[30\] (with $k = 1$) and a proximal support vector machine (PSVM), where the kernel function (linear) mapped the training data into kernel space. To measure the performance, average accuracy was employed

$$\text{Average Accuracy} = \frac{\text{sensitivity} + \text{specificity}}{2}$$

with the average of all five repetitions recorded as the final classification rate. In the first step, each individual feature (from the three groups) was applied to discriminate Healthy versus DM. This result can be seen in Tables V–VII. It should be noted that both $k$-NN and PSVM achieved the same average accuracy for all 34 features.

In the next step, optimization by feature selection using sequential forward selection (SFS) was performed. SFS is a method based on maximizing some criterion $J$, and terminates when all features have been added. In this, $J$ is the average accuracy of the classifier ($k$-NN and PSVM). Tables VIII ($k$-NN) and IX (PSVM) illustrate this result applied to each of the three main feature groups. From color features, the best combination is 3 and 12, which obtained an average accuracy of 68.76% using PSVM (see Table IX). In texture features, 14, 15, 16, and 17 attained an average accuracy of 67.67%, again using the PSVM. With geometry features, 22, 30, 32, 33, and 34 distinguished Healthy versus DM with an average accuracy of 69.09% (in Table IX). Combining the features in these three groups by applying SFS, an average accuracy of 77.39% was achieved in Table IX using 3, 12, 14, 15, 17, 22, 30, 32, 33, and 34. Finally, by examining the best combination from all features (SFS), the highest average accuracy of 85.52% can be accomplished (via PSVM), with a sensitivity of 90.77% and a specificity of 70.27%.

For completeness, NPDR versus Healthy classification was also conducted. An average accuracy of 87.14% was accomplished using SFS with the PSVM, achieving a sensitivity of 89.66% and a specificity of 84.62% via features 3, 9, 15, 16, and 33.

<table>
<thead>
<tr>
<th>TABLE VII</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLASSIFICATION RESULT OF $k$-NN AND PSVM USING EACH GEOMETRY FEATURE INDIVIDUALLY TO DISCRIMINATE HEALTHY VERSUS DM</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Feature Number</th>
<th>Feature Name</th>
<th>Average Accuracy (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>22</td>
<td>w</td>
<td>60.81</td>
</tr>
<tr>
<td>23</td>
<td>l</td>
<td>50.25</td>
</tr>
<tr>
<td>24</td>
<td>lw</td>
<td>58.44</td>
</tr>
<tr>
<td>25</td>
<td>z</td>
<td>53.33</td>
</tr>
<tr>
<td>26</td>
<td>cd</td>
<td>60.29</td>
</tr>
<tr>
<td>27</td>
<td>cdr</td>
<td>61.61</td>
</tr>
<tr>
<td>28</td>
<td>a</td>
<td>43.76</td>
</tr>
<tr>
<td>29</td>
<td>ca</td>
<td>55.02</td>
</tr>
<tr>
<td>30</td>
<td>car</td>
<td>59.15</td>
</tr>
<tr>
<td>31</td>
<td>sa</td>
<td>55.02</td>
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<td>32</td>
<td>sar</td>
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<tr>
<td>33</td>
<td>ta</td>
<td>66.26</td>
</tr>
<tr>
<td>34</td>
<td>tar</td>
<td>64.68</td>
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</table>

<table>
<thead>
<tr>
<th>TABLE VIII</th>
</tr>
</thead>
<tbody>
<tr>
<td>OPTIMIZATION OF HEALTHY VERSUS DM CLASSIFICATION USING FEATURE SELECTION WITH $k$-NN</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Grouping</th>
<th>Feature(s) Number(s)</th>
<th>Feature(s) Name(s)</th>
<th>Average Accuracy (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Color</td>
<td>12</td>
<td>Y</td>
<td>64.78</td>
</tr>
<tr>
<td>Texture</td>
<td>14, 17, 16, 19</td>
<td>Blocks 2, 4, 5, 9</td>
<td>67.48</td>
</tr>
<tr>
<td>Geometry</td>
<td>22-30, 32-34</td>
<td>w-car, sar-tar</td>
<td>67.87</td>
</tr>
<tr>
<td>Best of Color, Texture, and Geometry</td>
<td>12, 14, 16, 17, 19, 22-30, 32-34</td>
<td>Y, Blocks 2, 4, 5, 9, w-car, sar-tar</td>
<td>67.87</td>
</tr>
<tr>
<td>All Features</td>
<td>1-30, 32-34</td>
<td>C-car, sar-tar</td>
<td>67.87</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>TABLE IX</th>
</tr>
</thead>
<tbody>
<tr>
<td>OPTIMIZATION OF HEALTHY VERSUS DM CLASSIFICATION USING FEATURE SELECTION WITH THE PSVM</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Grouping</th>
<th>Feature Numbers</th>
<th>Feature Names</th>
<th>Average Accuracy (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Color</td>
<td>3, 12</td>
<td>B, Y</td>
<td>68.76</td>
</tr>
<tr>
<td>Texture</td>
<td>14-17</td>
<td>Blocks 2-5</td>
<td>67.67</td>
</tr>
<tr>
<td>Geometry</td>
<td>22, 30, 32-34</td>
<td>w-car, sar-tar</td>
<td>69.09</td>
</tr>
<tr>
<td>Best of Color, Texture, and Geometry</td>
<td>3, 12, 14, 15, 17, 22, 30, 32-34</td>
<td>B, Y, Blocks 2, 3, 5, w-car, sar-tar</td>
<td>77.39</td>
</tr>
<tr>
<td>All Features</td>
<td>3, 5, 12, 15, 22, 27, 30, 33, 34</td>
<td>B, DR, Y, Blocks 3, w-car, sar-tar, ta, tar</td>
<td>80.52</td>
</tr>
</tbody>
</table>

For completeness, NPDR versus Healthy classification was also conducted. An average accuracy of 87.14% was accomplished using SFS with the PSVM, achieving a sensitivity of 89.66% and a specificity of 84.62% via features 3, 9, 15, 16, and 33.
VII. CONCLUSION

In this paper, a noninvasive approach to classify Healthy/DM and NPDR/DM-sans NPDR samples using three groups of features extracted from tongue images was proposed. These three groups include color, texture, and geometry. A tongue color gamut was first applied such that each tongue image can be represented by 12 colors. Afterward, eight blocks strategically located on the tongue were extracted and its texture value calculated. Finally, 13 geometry features from tongue images were extracted. By applying each feature individually to separate Healthy/DM, the highest average accuracy achieved (via PSVM) was only 66.26%. However, employing SFS with the PSVM, nine features (with elements from all the three groups) were shown to produce the optimal result, obtaining an average accuracy of 90.52%. As for NPDR/DM-sans NPDR classification, the best result of 90.33% was attained using five features: three from color, one from texture, and one from geometry.

REFERENCES


