Celiac Disease Detection from Videocapsule **Endoscopy Images Using Strip Principal Component Analysis**

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Abstract—The purpose of this study was to implement principal component analysis (PCA) on videocapsule endoscopy (VE) images to develop a new computerized tool for celiac disease recognition. Three PCA algorithms were implemented for feature extraction and sparse representation. A novel strip PCA (SPCA) with nongreedy L1-norm maximization is proposed for VE image analysis. The extracted principal components were interpreted by a non-parametric k-nearest neighbor (k-NN) method for automated celiac disease classification. A benchmark dataset of 460 images (240 from celiac disease patients with small intestinal villous atrophy versus 220 control patients lacking villous atrophy) was constructed from the clinical VE series. It was found that the newly developed SPCA with nongreedy L1-norm maximization was most efficient for computerized celiac disease recognition, having a robust performance with an average recognition accuracy of 93.9%. Furthermore, SPCA also has a reduced computation time as compared with other methods. Therefore, it is likely that SPCA will be a helpful adjunct for the diagnosis of celiac disease.

Index Terms—Celiac disease, Medical image analysis, Nongreedy L1-norm maximization, Principal component analysis, Videocapsule endoscopy

1.INTRODUCTION

eliac disease patients suffer from an autoimmune reaction to dietary gluten that primarily affects the small intestine, and occurs in about 1% of the population worldwide [1, 2]. The patient symptoms are systemic and reproductive, can affect neurological, endocrine, hematologic, cardiovascular, and other systems [3, 4]. The resulting immune reaction of celiac disease often damages the small intestinal mucosa, in particular the proximal portions including the duodenum and jejunum. The small intestinal villi, which absorb nutrients, can become blunted, resulting in poor absorption of nutrients. As a consequence, the small intestinal mucosa exhibits fissuring, a mosaic appearance, and scalloping of mucosal folds [3, 5].

The current gold standard for celiac disease diagnosis includes an initial serological testing for antibodies to followed tissue transglutaminase, by upper gastrointestinal endoscopy with duodenal biopsy. However, this procedure is invasive and possibly misses mucosal pathology that can be present in the distal small intestine, as well as pathology that is subtle to visual

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inspection [6]. Videocapsule endoscopy (VE) or capsule endoscopy, is a comparatively new clinical tool for gastrointestinal examination, and it is particularly advantageous for bowel bleeding, inflammation, and even cancerous manifestation [7, 8].

Utilized in celiac disease diagnosis, VE enables the examination of the entire small intestine, allowing for the visualization of mucosal villous architecture in detail. Therefore, outputted the VE images enable gastroenterologists to visually assess the extent and severity of villous atrophy, an important indicator of celiac disease. By analyzing VE images of the small intestinal mucosa, it is possible to assess the degree of villous atrophy in untreated celiac patients, as well as in recovering, treated celiac patients. The presence of villous atrophy may be subtle, it may in fact be present in most or even all untreated celiac patients, and it is an important marker for diagnosing the disease. However, the visual assessment procedure mainly depends upon gastroenterologist knowledge and experience. It can be laborious and time consuming to analyze the image series manually. That is why computerized analysis and automatic classification of VE images are of increasing interest and attention for study in recent years [7, 9-15].

Computerized VE image analysis remains challenging when considering that the camera angle and illumination with respect to the intestinal wall are not controllable. At the same time, interfering opaque fluids and air bubbles may appear anywhere in the image series. Since villous atrophy is one of the most significant manifestations, most prior works focused on the computerized quantification of mucosal features.

Several methods have been used for quantitative analysis, including frequency or spectral analysis. The variance computed over many video frames can be used to estimate the frequency spectrum, which is defined as 1545-5963 (c) 2019 IEEE. Personal use is permitted, but republication/redistribution requires IEEE permission. See http://www.ieee.org/publications_standards/publications/rights/index.html for more

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the degree of periodicity over a unit time interval [13]. The areas with greater pathology as measured by increased degree of texture in celiac patients tend to have longer periodicity, which is indicative of a lesser mobility. A more advanced tool using the wavelet transform was also introduced for scale invariance of textural description [9]. Implementing this technique, it was possible to improve mucosal-based classification of celiac disease by correcting endoscopic distortion. Many paradigms for quantitative analysis are implemented pixel-by-pixel. This however may render them susceptible to noise and artifacts. In addition, although the image-to-pixel methods have been shown to work well for some kinds of medical images [16], it is also known that the underlying spatial or structural information is ignored.

The second type of technique for quantitation is metric analysis. For example, a simple metric was proposed in [13] by using the standard deviation or variance in pixel brightness over a specified image area, which is effective to detect bowel fissuring and mottled appearance which is characteristic of pathologic regions in celiac disease. Another metric is the length of mucosal fissures per unit area [11]. It was found that this metric increases from Marsh grade II to IIIa, IIIb and IIIc, respectively, and is therefore correlative. The techniques are implemented in a block-based statistical way, and are thus robust to artifact. However, every block is simplified to a variance or color model [12], which may sometimes be insufficient to extract the salient information required for VE image analysis. For example, a shape-from-shading model was proposed to quantify the number and width of villous protrusions [10]. In practice, they were found useful to distinguish blunted villi in celiac patients versus the normal villi of control patients.

Herein, principal component analysis (PCA) is introduced for computerized VE image analysis [17-19]. PCA is a subspace learning algorithm and is capable of extracting expressive features. Differing from the pixel-bypixel techniques, modular PCA is implemented on a block-by-block basis for robust VE image analysis. To this purpose, high-dimensional information is automatically extracted in every block. The spatial information is exploited using a two-dimensional PCA (2DPCA) [19, 20] and the recent block PCA (BPCA) [21]. BPCA is a windowed 2DPCA, as a result that BPCA transforms into 2DPCA if the blocks are acquired as the row vectors. It was hypothesized that these methods would be more robust to small-scale outliers and interfering artifacts. Furthermore, celiac disease often leads to fissuring, mosaic appearance and scalloping of mucosal folds. Therefore, a special form of BPCA, hereafter termed strip PCA (SPCA), was incorporated into the system for VE image processing and celiac disease analysis. In particular, a recent scheme of the nongreedy L1-norm maximization was investigated for expeditious optimization of the PCA output [22].

The rest of the paper is organized as follows. Section 2 elaborates upon involved methods. Experimental results are reported in Section 3. Section 4 includes a discussion on the experiments and also reports further results concerning supervised celiac disease recognition

methodology. The concluding remarks are provided in Section 5.

2.METHODS

2.1. Videocapsule Endoscopy

All clinical VE images were acquired at Columbia University Medical Center using the PillCam SB2 system. Included in the study were twelve celiac patients and eleven control patients. Both the celiac patients and control patients underwent VE in addition to the standard endoscopy, because the origin of all symptoms was not resolvable by the standard endoscopy technique. VE provides images of the entire small intestine, whereas the standard endoscopic technique only images the duodenum. Detection of additional mucosal abnormalities, including presence of adenocarcinoma, ulcerative jejunoileitis or intestinal T-cell lymphoma is also done with VE [23]. All celiac patients had been confirmed to have the disease by bowel biopsy, prior to VE. Although there was no gold standard available, indirect evidence was available to gauge efficacy of the VE quantitation technique; the degree of villous atrophy at the level of the duodenal bulb was known from the standard endoscopy with biopsy. Informed consent was obtained from each participant prior to VE examination.



Fig. 1. Selected VE images from celiac patients (upper two rows) and controls (lower two rows) in this study.

The VE system - PillCamSB2 - was manufactured by Given Imaging (Yoqneam, Israel) which is now part of Medtronic (Parsippany, NJ). It is comprised of a disposable mini-endoscopic capsule, an external receiving antenna array and a console with dedicated software for interpretation. The endoscopic capsule has dimensions of 11mm × 26mm and weighs 3.7g. The mini-camera has a 140° field of view, a 1.30mm depth of view, 1:8 magnification and approximately 1 millimeter resolution. The battery life is about 8 hours for a continuous 2 frames per second image acquisition.

After a 12-hour fast, each subject swallowed the videocapsule in the morning with 200ml water and 80mg of simethicone. The external recorder received the radioed images as the capsule passed through the gastrointestinal tract. Following examination, the recorder was detached and the data was downloaded to the console. All videos

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were reviewed and interpreted by experienced gastroenterologists. They also de-identified and clipped the video data for retrospective computerized analysis. This procedure was approved by the Internal Review Board at Columbia University Medical Center.

For each subject, the de-identified video clips of 200 frames were acquired from five locations in the small intestine. The color data with a resolution 576 × 576 pixels were extracted and converted to a series of grayscale images by using MATLAB 2010b (MathWorks®, Natick, MA). Twenty images were selected and further downsampled to 96 × 96 pixels for celiac disease recognition (Fig. 1). Those images were selected according to the following rules:

1) The celiac images included features of fissuring, mosaic appearance, and scalloping of mucosal folds. 2) Excluded were the degraded images, such as those of low-contrast, or having air bubbles or overexposure. 3) The images covered the five regions (jejunum, duodenal bulb, distal duodenum, proximal ileum and distal ileum). The final dataset was composed of 460 images from 12 celiac patients versus 11 normal controls.

2.2. SPCA

The method of analysis can be derived as follows. Suppose that every image can be expressed as X^i , where *i* is the index of images (*i.e.*, *i* = 1, ..., *N*). The dimension of X^i is $r \times c$, where *r* and *c* symbolize the height and width of the image, respectively. In conventional PCA, all images $X = [X^1, \dots, X^N]$ must be converted into d-dimensional ($d = r \times c$) vectors $X = [x_1, \dots, x_N]$ by lexicographic ordering, where x_i is the vectorized version of X_i . As shown in Fig. 2e, lexicographic ordering means that the 2D pixel array is converted to a single d-dimensional vector. PCA attempts to find a projection matrix $U = [u_1, \dots, u_d] \in \mathbb{R}^{d \times d}$ that minimizes the mean square reconstruction error:

$$\arg\min_{U} \left\| U^T \hat{X} - X \right\|_2^2 \tag{1}$$

where the components of U are orthogonal with respect to each other, $\hat{X} = UX$, and $|| ||_2$ denotes the L2-norm. The Karhunen- Loève transform converts the optimization of (1) into an eigen decomposition problem of the scatter or covariance matrix:

$$S = \sum_{i=1}^{N} (X_i - \overline{X})^T (X_i - \overline{X})$$
⁽²⁾

where *X* is the mean of all images. Without loss of generality, it is possible to preprocess the images so that they are mean-centered, namely, $\overline{X} = (\sum_{i=1}^{N} X_i)/N = 0$.

Note that the size of the scatter matrix *S* in (2) is as high as $d \times d$. It is challenging in PCA to decompose *S* for eigenvalues and eigenvectors. As a consequence, 2DPCA [24] takes every row or column of an image as a single object so that the scatter matrix S could be reduced to size $r \times r$ (Fig. 2b). It is thus able to enhance computational efficiency in theory. Actually, the local blocks in an image

are prone to having strong correlation, which has been utilized in previous VE image analysis and celiac disease recognition methods [11, 15].

In this study, BPCA is taken advantage to divide every image X_i into the blocks of size $m \times m$ (Fig. 2c). It is then possible to stack every block in the lexicographic ordering and convert X_i into a vectorized version $\{x_1^{(i)}, \dots, x_{d/m^2}^{(i)}\}$. As shown in Fig. 2d, in order to capture the patterns of fissuring and mucosal folds, the novel SPCA that is proposed divides each image X_i into blocks of size $sn \times n$, where $s (\in [2,3, \dots r/n])$ is a scaling factor controlling the strip shape. Note that SPCA is asymmetric, and will be downgraded to BPCA when using the scaling factor s = 1. It is then possible to stack every block in the lexicographic ordering and convert X_i into a vectorized version.



Fig. 2. Alignment patterns of different PCA methods: (a) regular PCA, (b) 2DPCA, (c) BPCA, and (d) SPCA. (e) Lexicographic order of SPCA

It is however computationally inefficient to directly decompose the scatter matrix of SPCA for eigenvalues and eigenvectors. The L1-norm-based methods attempt to resolve this issue in a one-by-one way for optimization [24]. The special form of SPCA, hereafter termed SPCA-L1, aims to find the eigenvector $u_1 \in R^{sn^2 \times 1}$ by maximizing

$$u_{1} = \arg \max_{u_{1}} \sum_{i=1}^{N} \left\| X_{i} u_{1} \right\|_{1}$$

$$= \arg \max_{u_{1}} \sum_{i=1}^{N} \sum_{j=1}^{d/sn^{2}} \left| u_{1}^{T} x_{j}^{(i)} \right|, \text{ subject to } \left\| u_{1} \right\|_{2} = 1$$
(3)

where $\| \|_1$ denotes the L1-norm, and $x_j^{(l)}$ is a vector version of the image strip. The optimization problem can be solved in an iterative manner, i.e.:

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$$u_{1}(t) = \frac{\sum_{i=1}^{N} \sum_{j=1}^{d/sn^{2}} p_{j}^{(i)}(t-1)x_{j}^{(i)}}{\left\|\sum_{i=1}^{N} \sum_{j=1}^{d/sn^{2}} p_{j}^{(i)}(t-1)x_{j}^{(i)}\right\|_{2}}$$
(4)

where the polarity function at the $(t-1)^{th}$ iteration is given by:

$$p_{j}^{(i)}(t-1) = \begin{cases} 1, \ u_{1}^{T}(t-1)x_{j}^{(i)} \ge 0\\ -1, \ u_{1}^{T}(t-1)x_{j}^{(i)} < 0 \end{cases}$$
(5)

The convergence of this technique has been justified in [24]. It leads to a final eigenvector u_1 , once the objective value $\sum_{i=1}^{N} \sum_{j=1}^{d/sn^2} u_1^T(t) x_j^{(i)}$ is maximized.

After the first eigenvector u_1 is obtained, it is possible to extract the 2^{nd} eigenvector u_2 by simply updating the data as:

$$x_{ij}^{2} = x_{ij}^{1} - u_{1} \left(u_{1}^{T} x_{ij}^{1} \right), \ i = 1, \cdots, N \text{ and } j = 1, \cdots, d/sn^{2}$$
 (6)

The processes (4) and (5) are then applied to the updated data[$x_1^2, ..., x_N^2$] for u_2 . Such an efficient process of L1-norm maximization can be recursively applied for the subsequent eigenvector u_k with k > 2 on the updated data:

$$x_{ij}^{k} = x_{ij}^{k-1} - u_{k-1}(u_{k-1}^{T} x_{ij}^{k-1})$$
(7)

Note that the optimization of L1-norm maximization relies on a conventional greedy strategy. It is assumed that there must be an upper bound of dispersion. In each iteration of evolution, the sign function p(t) is calculated according to the current eigenvector $u_k(t)$, while the next $u_k(t+1)$ is updated with the current p(t). This iterative procedure is repeated until the monotonically increasing dispersion converges to a local solution. After updating all training data, the subsequent eigenvector is pursued with the same procedure. Therefore, the projection matrix is solved one-by-one in an iterative way.

The nongreedy approach for L1-norm maximization attempts to calculate all eigenvectors simultaneously without increasing the computational complexity [25]. In terms of SPCA, hereafter termed SPCA-L1-NG, the problem of optimization (U^*) is converted to

$$U^* = \arg\max_{U^T U = I} \sum_{i=1}^{N} \sum_{j=1}^{d/sn^2} (p_j^{(i)})^T U^T x_j^{(i)}$$
(8)

where $U \in R^{sn^2 \times sn^2}$, and $p_i^{(i)}$ is the sign function, namely $p_j^{(i)} = sgn(U^T x_j^{(i)})$. If M is denoted as M = $\sum_{i=1}^{N} \sum_{j=1}^{d/sn^2} x_j^{(i)} (p_j^{(i)})^T = XP^T \text{ , with } X \in \mathbb{R}^{sn^2 \times (d/sn^2)N},$ then $M \in R^{sn^2 \times d/sn^2}$ and $P = sgn(U^T X) \in R^{d/sn^2 \times (d/sn^2)N}$, so that (8) can be rewritten as

$$U^* = \arg \max_{U^T U = I} \operatorname{tr}(U^T M) \tag{9}$$

Where tr () is the matrix trace. Suppose that the singular value decomposition (SVD) of *M* is 1545-5963 (c) 2019 IEEE Personal use is permitted, but republication/redistribution requires IEEE permission. See http://www.ieee.org/publications_standards/publications/rights/index.html for more

Algorithm 1 SPCA-L1 Nongreedy

Input: $[X^1, \dots, X^N]$, creating the training matrix X

Initialize $U^t \epsilon R^{sn^2 \times d/sn^2}$, subject to $U^T U = I_{d/sn^2}$, t = 1; while not converge do 1. $P = \operatorname{sgn}((U^t)^T X)$

2. Calculate the SVD of *M* as $M = W\Lambda V^{T}$; 3. Let $U^{t+1} = W \Big[I_{d/sn^2}; 0_{(sn^2 - d/sn^2) \times d/sn^2} \Big] V^T;$ 4.t = t + 1;end while Output: $U^{t+1} \epsilon R^{sn^2 \times d/sn^2}$

 $\overline{M = W \Lambda V^T}$, where $W \in \mathbb{R}^{sn^2 \times sn^2}$, $\Lambda \in \mathbb{R}^{sn^2 \times d/sn^2}$, and $V \in \mathbb{R}^{sn^2 \times d/sn^2}$ $R^{d/sn^2 \times d/sn^2}$. Then we have:

$$U^{*} = \arg \max_{U^{T}U=I} tr(U^{T}M) = \arg \max_{U^{T}U=I} tr(U^{T}W\Lambda V^{T}) =$$

$$\arg \max_{U^{T}U=I} tr(\Lambda V^{T}U^{T}W) = \arg \max_{U^{T}U=I} tr(\Lambda Z) = \sum_{i} \lambda_{ii} Z_{ii} \quad (10)$$

where $Z = V^T U^T W \in \mathbb{R}^{d/sn^2 \times sn^2}$, and λ_{ii} and Z_{ii} are the $(i, i)^{th}$ element of the matrices Λ and Z, respectively.

Since $ZZ^{T} = I_{d/sn^{2}}$, where I is a (d/sn^{2}) -dimensional identity matrix, it leads to $z_{ii} \le 1$. At the same time, $\lambda_{ii} \ge 0$ in that it is the *i*th singular value of *M*. In other words, the objective function (10) can reach its maximum only when $z_{ii} = 1$ ($1 \le i \le d/sn^2$), i.e., $Z = [I_l, 0]$. It leads to the optimal solution:

$$U = V^{T} Z^{T} W = W \Big[I_{d/sn^{2}} : 0_{(sn^{2} - d/sn^{2}) \times d/sn^{2}} \Big] V^{T}$$
(11)

The nongreedy SPCA algorithm will determine the projection matrix U directly by converging to a local solution, which is described in Algorithm 1. It is not necessary to further update the training data.

2.3. Classification

Both linear and nonlinear classifiers have been designed for computerized VE image analysis [9-14]. Those classifiers are generally initialized for sample separation, and then further optimized according to various training samples. In this work, the different PCA algorithms are introduced for self-adaptive dimensionality reduction and feature extraction of VE images. For fair evaluation, a non-parametric method - knearest neighbor (k-NN) - is employed by using the "knnclassify()" function in the Bioinformatics Toolbox of MATLAB for statistical classification [26]. Such instancebased k-NN does not involve any training or optimization. Its decision is determined by majority vote of k nearest neighbors. The computational efficiency is competitive in case of small-volume samples. Actually, it is in some sense similar to the polling protocol [10], and has been utilized for PCA-based image analysis and pattern recognition as a convention [19-22].

It is likely that the performance could be further

information.

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improved by introducing other methods such as the support vector machine (SVM) and artificial neural networks which are specially designed for optimal recognition and classification. A standard SVM classifier is therefore constructed for performance comparison. Recently, deep learning has also demonstrated for medical image analysis with promising outcomes [27-29]. As a consequence, a standard AlexNet classifier is also established to evaluate the feasibility of deep learning in celiac disease classification. The data for training and testing of SVM and AlexNet maintain consistency with the k-NN experiments.

3.EXPERIMENTS

To evaluate the performance, the novel SPCA algorithm was compared against several state-of-the-art algorithms including 2DPCA and BPCA, both of which were enhanced with respect to the L1-norm-based maximization and the nongreedy type. All algorithms, including 2DPCA-L1, 2DPCA-L1-NG, BPCA-L1, BPCA-L1-NG, SPCA-L1 and SPCA-L1-NG, were programmed and implemented in MATLAB R2010b. They ran on a ThinkCentre M9350z workstation (Lenovo®, Beijing, China) with Intel® Core i5 CPU 3.20GHz and 4.0GB RAM. All protocols including random data separation, principal component extraction and celiac disease recognition were repeated five times, and the results were averaged for fair performance evaluation. The dataset of 460 images was first randomly separated into 40% for training and 60% for testing. The number of principal components ranged from 1 to 60 with an incrementing stepsize of 5. The strip size s of SPCA was ranged in $(\in [2,3, ..., r/n])$. We used Grid Search to enumerate all candidate parameters and choose the best one. Finally, BPCA was configured with the block size 8×8 and SPCA had dimension 4×8 in this work.

Computational efficiency is important in medical image processing and analysis. Actually, both the L1-norm maximization and the nongreedy scheme are likely to improve the computational efficiency of PCA methods. Fig. 3 shows the average running periods of PCA algorithms with respect to the different principal



Fig. 4. Average reconstruction error versus principal component number obtained by 2DPCA, BPCA and SPCA.

component values. Here the performance in seconds (s) was measured by the stopwatch timer function in MATLAB. It is obvious that, no matter whether 2DPCA, BPCA or SPCA is utilized, the new strategy of nongreedy L1-norm maximization is able to enhance their computational efficiency substantially. Meanwhile, SPCA always achieved the best performance of computational efficiency for image feature extraction and celiac disease recognition.

PCA is mainly developed for dimensionality reduction and feature extraction. In order to evaluate the capability of PCA methods to characterize sparse images, the average reconstruction error is defined by referring to [22].

$$e = \frac{1}{N} \sum_{i=1}^{N} \left\| x_i - \left((x_i - \bar{x}) U U^T + \bar{x} \right) \right\|_F$$
(12)

where $\| \|_{F}$ is the Frobenius norm. Both image-as-vector and image-as-matrix PCA methods can be evaluated in this way. Fig. 4 shows the average reconstruction errors of 2DPCA-L1, 2DPCA-L1-NG, BPCA-L1, BPCA-L1-NG, SPCA-L1 and SPCA-L1-NG. It can be found that all imageas-matrix methods achieved very similar performances in terms of average reconstruction error. In particular, the



Fig. 3. Computational efficiency versus principal component number obtained by 2DPCA, BPCA and SPCA.



Fig. 5. Average recognition accuracy versus principal component number obtained by 2DPCA, BPCA and SPCA.

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nongreedy scheme does not contribute to reconstruction error.

increased. SPCA were more robust than 2DPCA, BPCA and regular PCA with respect to recognition accuracy.



Fig. 6. Average recognition accuracy and run time versus principal component number obtained by PCA, 2DPCA, BPCA and SPCA.

Fig. 5 shows the average recognition accuracy over different principal components in 2DPCA, BPCA, and SPCA. The recognition accuracy was computed as the rate of correct classification. The definition of recognition accuracy (RC) is:

$$RC = (TP + TN)/(TP + FN + FP + TN)$$
(13)

where TP, TN, FP and FN refer to the number of true positive, true negative, false positive and false negative examples, respectively. As shown in Fig. 5, the PCA methods enhanced by L1-norm maximization could not achieve a stable performance. On the contrary, the recent scheme of nongreedy L1-norm maximization was very effective to enhance the PCA methods in celiac disease recognition. In particular, SPCA-L1-NG achieved a robust performance of celiac disease recognition, with an average recognition accuracy of 94%. However, it is noteworthy that other PCA methods, in terms of self-adaptive degraded with increasing recognition, principal component number. In other words, addition of principal components may not lead to better performance in classification. Actually, this has also been recognized in studies using other techniques, for example, linear discriminant analysis (LDA), locality preserving projections (LPP) [30, 31] and manifold learning [32]. For capturing the spatial information of an image, PCA commonly vectorizes the image or treats the row vectors of the image as computational samples. To better preserve image characteristics, a tradeoff between the row spatial information and columns emerges. SPCA is a special form of BPCA developed by introducing a scaling factor to control the strip shape. Additionally, we made a comparison between regular PCA, 2DPCA, BPCA, and SPCA in runtime and recognition accuracy. As shown in Fig. 6, SPCA exhibited a lesser time cost compared with other PCA variants as the principal component number



Fig. 7. Celiac disease recognition with a standard AlexNet classifier.

Herein, a novel SPCA method was specially designed for VE image processing and celiac disease analysis. The extracted principal components were sent to a 1-NN for self-adaptive classification, in consideration of the smallscale dataset. As shown in Fig. 3, Fig. 4 and Fig. 5, it was found that the nongreedy L1-norm maximization was able to improve the PCA methods in recognizing the presence of villous atrophy in celiac patients from the VE images. Interestingly, reconstruction errors and recognition accuracy do not always correlate; the reconstruction error measures the dissimilarity in reconstruction of the original image by principal components, while the recognition accuracy measures the differentiation ability of principal components to classify celiac disease patients versus controls.

The decision of k-NN is achieved via a majority vote of k nearest neighbors. Although the performance of recognition with 1-NN is satisfactory, it was of interest to further analyze the impact of the k values. As reported in Table I, the performance of recognition is quite similar among 1-NN, 3-NN and 5-NN. It is noteworthy that a larger value of k did not lead to a higher recognition rate. The non-parametric k-NN classifier is an instance-based classifier. The decision of this classifier comes from the majority vote of k nearest sample, and the nearest samples increases with increase of k value due to the vote mechanism. However, the samples with different label which are far away from the test samples can affect the vote result, leading to the increase in vote error. This adds to the evidence that the 1-NN method is likely valid.

The k-NN classifier is non-parametric and does not require training. In contrast, SVM is a well-established method for optimal recognition and classification. Nevertheless, coming to a high-dimensional small-scale dataset, its performance against k-NN is uncertain. Therefore, we also employed the Bioinformatics Toolbox

TABLE I Impact of The Number of Nearest Neighbors				
k Features	1	3	5	
15	93.91 ±0.70	92.83±1.19	91.88±1.27	
30	93.84±0.57	92.68 ± 1.04	91.52±1.22	
45	93.48±0.44	92.46±1.01	90.80±1.51	

* k represents the k samples near the test sample.

** k-NN classification of different SPCA features.

*** mean ±standard deviation of five-time statistical results.

to establish a SVM classifier for celiac disease recognition. It was created by using the "symtrain()" function. With the "crossvalind()" function, the benchmark dataset was randomly separated into 40% for training and 60% for testing. The different numbers of principal components extracted by 2DPCA-L1-NG, BPCA-L1-NG and SPCA-L1-NG were imported to SVM as the features for training and testing. The "quadratic kernel" function was chosen to map raw data into a new kernel space. The results of classification were obtained directly from the "svmclassify()" function in the same toolbox. Similarly, all protocols were repeated five times for robust evaluation. The statistical results are reported in Table II. Overall, the average recognition rate of 89.45% is smaller than that in Table I (i.e., 92.60%). Consequently, it is reasonable to use k-NN rather than SVM for celiac disease recognition in this work.

In terms of deep learning, due to different application scenes, there is no universal neural network to deal with different problems. Herein, a representative AlexNet classification network [33] without fine tuning was constructed with 5 convolution layers and 3 fullyconnected layers. The network input VE images were of dimension 96 × 96 pixels. For system initialization and optimization, 30% of VE images were randomly selected for training and 10% were used for validation. The remaining 60% were utilized for system testing. After a 100-epoch evolution, the system became stable, with a validation recognition accuracy of 90.63% (Fig. 7). This AlexNet classifier eventually achieved a recognition accuracy of 89.98% with respect to the test dataset based on five statistics. As we known, the dataset of ImageNet Large-Scale Visual Recognition Challenge (ILSVRC) relied on millions of images. The ImageNet dataset has thousands of categories for different scenes except celiac disease. On the other hand, deep learning is a timeconsuming technology to process the dataset. To realize a rapid and specialized analysis methodology in such a limited dataset, SPCA is a better choice in this work.

A. Noise and Artifacts

It is a different problem from face recognition to analyze villous atrophy in celiac disease using VE images and PCA. There are a series of new challenges in terms of computerized VE image analysis. For example, most PCA methods in the published literature were evaluated based upon some well-established benchmark datasets [19-22, 24], including but not limited to the Columbia Object Image Library (COIL), Face Recognition Technology

TABLE II CLASSIFICATION BY SVM				
Method Features	2DPCA-L1- NG	BPCA-L1-NG	SPCA-L1-NG	
15	91.23 ± 1.29	90.36±2.33	89.06±2.96	
30	89.42±2.59	89.35±0.79	89.42±2.63	
45	86.67 ± 1.57	89.13±1.72	90.43 ± 1.07	

* SVM classification of different PCA methods with different numbers of features.

** mean ± standard deviation of five-time statistical results.

these datasets, all objects have been calibrated carefully for consistent feature extraction and pattern recognition. For example, all face images in the Olivetti Research Laboratory (ORL) Face Data Set were aligned according to the center points of the eyes [19]. However, the camera angle and illumination of videocapsule endoscopy with respect to the intestinal wall are uncontrollable. In other words, PCA has to work with the images without realignment and calibration.

On the other hand, the PCA methods were often repeatedly evaluated on the benchmark datasets with different outlier proportions, ranging from 10 to 40% [19, 22, 24]. In other words, an artificial rectangle with the pixel value being either 0 or 255 was overlaid on the benchmark images in a random place. Although such artifacts seem complicated, they are totally different from ambient objects. In contrast, there are various interfering fluids and bubbles that naturally appear in VE images. From the analytic point of view, this kind of interference may be more challenging to PCA. Actually, it has been noticed [17] that the outliers might bias the mean of all images in (2) and thus impair the optimization process for nongreedy L1-norm maximization.

B. Limitations

The study should be repeated with greater sample size N to verify the results. Since the establishment of a deep learning solution often relies on tens of thousands of training data, it would not be applicable to the small-scale benchmark dataset utilized thus far. We would need to collect more data to integrate SPCA and deep learning methods for celiac disease recognition in future work. Another limitation of the current work is that the selection of VE images was implemented by a single expert gastroenterologist from the Celiac Disease Center of Columbia University Medical Center. Thus intra- and inter- observer variability cannot be measured. As a consequence, the results should be interpreted cautiously from the perspective of advanced quantitative analysis. Future studies should include additional expert gastroenterologists for VE analysis of celiac disease.

The purpose of this work was to introduce the latest PCA methods for celiac disease recognition from VE images. PCA is a general technique and does not require a specific data dimension. However, the larger the data dimension, the longer the processing time. Therefore, the sizes of images in most benchmark databases of computer vision (e.g., COIL, FERET and USPS) are often rescaled smaller than size 64 × 64 pixels [16, 20, 22]. Herein, the (FERET), and US Postal (USPS) Handwritten Digits. In resolution of all VE images used in this paper was 1545-5963 (c) 2019 IEEE. Personal use is permitted, but republication/redistribution requires IEEE permission. See http://www.ieee.org/publications_standards/publications/rights/index.html for more

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downsampled. Thus, some subtle yet important information may be lost in the procedure. Furthermore, colored VE images were converted to grayscale, which can diminish the available diagnostic information [12]. It would thus be interesting to extend the PCA methods to include color VE images in future work.

5.CONCLUSION

The principal component analysis of VE images was investigated for computerized celiac disease recognition. We constructed a benchmark dataset of 460 clinical VE images (240 from celiac disease patients versus 220 from control patients) acquired from the Columbia University Medical Center. Three PCA algorithms were developed with the improvement of the L1-norm maximization and the nongreedy strategy. They were evaluated on the celiac dataset. It was found that the novel SPCA method achieved a satisfactory performance in terms of computational efficiency, dimensionality reduction and self-adaptive classification. In particular, the enhanced SPCA-L1-NG had a robust performance ($\approx 93.9\%$) and superior efficiency for computerized celiac disease recognition. The non-parametric k-NN classifier (\approx 92.60%) outperformed two advanced classifiers, namely SVM (\approx 89.45%) and AlexNet (\approx 89.98%) with respect to this small-scale celiac disease dataset, too.

Currently, there is much interest in incorporating quantitative technology for VE image analysis in the design of programs for celiac disease diagnosis and treatment. In fact, endoscopy is an auxiliary analysis tool in the general diagnostic process of celiac disease. The main step is a serological test for antibodies to tissue transglutaminase [35], followed by biopsy. However, the use of automated programs would be assistive to detect the subtle presence of villous atrophy not evident by visual inspection. It may also be useful to assess the degree of improvement of celiac patients on a gluten-free diet, the main treatment method for stopping the autoimmune process and improving the state of the small intestinal villi.

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