

Finding Similarity between the Left and Right Retinal Images of an Individual Using Legendre Moments

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Abstract: Many researchers in medical science studied the similarity between the left and right retina of a patient. On the contrary, many retina-based biometric researchers consider that an individual's left and right retinas are different. Therefore, few works were reported in retina-based biometric for finding similarities between the left and right retina of an individual. This research intends to find similarities between an individual's left and right retina using orthogonal Legendre moments from a biometric perspective. Here, we use orthogonal Legendre moments for feature extraction and dimensionality reduction and cosine distance to measure similarity between the Legendre moments-based vectors extracted from the left and right retina. We perform experiments on two publicly available data sets named CHASE_DB1 and Messidor-2. We show that the Legendre moments can preserve almost all the retinal image information in few coefficients, and there exists a noticeable similarity in the Legendre moments extracted from the left and right retinal images of an individual.

Key Word: Legendre moments, retina, cosine similarity, biometric.

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I. Introduction

The retina is a neural tissue that helps to form images in our brain by converting electromagnetic signals into neural signals. It plays an important role both in our vision and biometric. Pathology in the retina can be the cause of irreversible partial or complete vision loss. Therefore, patients' retina is one of the focusing points for ophthalmologists, medical researchers, and computer-aided diagnostic devices. The tree structure of the central retinal blood vessels remains unchanged during a person's lifetime unless being affected by severe retinal pathology. The external environment cannot affect it since its location is inside our eye [1]. Therefore, the retina was studied as a reliable biometric to ensure high security in an environment with massive interest by biometric researchers since 1899 [2-19].

The similarity between the left and right retina can benefit medical science in two ways. First, it allows ophthalmologists to use one retina as a proxy for the other retina during the post-surgery and post-treatment analysis. Second, it helps to track pathology progress in a retina compared to the other retina. If two retinas have any similar anatomical feature, then dissimilarity in that feature indicates pathology development in the retina. For example, the presence of unevenness between the optic nerve cup of the two eyes of an individual is considered an early sign of glaucomatous damage [20][21] and is a predictor of future damage in ocular hypertensive patients [22]. Therefore, many researchers explored the similarity between the left and right retina in many works in medical science [23-28].

On the contrary, few researchers worked on the similarity issue between the left and right retina from a biometric perspective. Except for the works done by Biswas and her colleagues, no other works can be found in the literature regarding this issue. Biswas et al. turned the problem of finding the similarity in the left and right retina into a verification problem and reported experimental results in [29-33]. If a system (either human or a machine learning algorithm) decided that a pair of retinal images of the left and right retinas was captured from a single subject, they assumed that the system found substantial similarity in that pair. On the other hand, if the system decided that a pair of left and right retinas belongs to two different subjects, they assumed that the system did not see any similar properties in that pair. By manual and automatic verification, they investigated to what extent their assumptions are correct in [29-33]. In [29], [34] Biswas et al. also discussed the similarity between left and right retina as an identification problem. They assumed that if the left and right retinas, captured from a single subject, then the pair of the left and right retinal images would have lower cosine distance or higher cosine similarity compared to the pairs made by taking a left and right retinal images from two different subjects. The cosine similarity can be easily measured after reshaping two 2D images of blood vessels or 3D RGB retinal images to vectors. However, these vectors are so long that the cosine similarity suffers from the curse of high dimensionality. Before measuring the cosine similarity, two neural network-based embedding techniques along with three non-neural network-based embedding techniques were investigated to

reduce dimension: principal component analysis (PCA), locally linear embedding (LLE), and isometric mapping (Isomap). Embedding is a mapping of a high dimensional variable into a low dimensional variable.

This research aims to explore a Legendre moments based non-neural network-based feature other than PCA, LLE and Isomap for finding similarities between an individual's left and right retinas. The Legendre moments are orthogonal and scale, translation and rotation invariant. Hence, they represent various features of the retina. However, finding the best set of Legendre moments for assessing the degree of similarities between an individual's left and right retinas is very challenging.

We organize this paper as follows. In Section 2, we describe briefly Legendre moments. Then in Section 3, we describe data sets that we use in experiments. We devote Section 4 to the cosine distance-based similarity measurement between Legendre moments based features extracted from the left and right retina. We present evaluation results in Section 5. Finally, concluding remarks are given in Section 6.

II. Legendre Moments

Legendre moments are used in a lot of image processing and pattern recognition applications such as blurred image recognition [35]. They belong to the class of orthogonal moments. They use Legendre polynomials as basis set. The two-dimensional Legendre moments of order (p, q) , with an image intensity function $f(x, y)$, are defined on the square $[-1, 1] \times [-1, 1]$ as

$$L_{pq} = \lambda_{pq} \iint_{-1}^1 P_p(x)P_q(y)f(x, y)dx dy \tag{1}$$

where $\lambda_{pq} = \frac{(2p+1)(2q+1)}{4}$, $p, q = 0, 1, 2, \dots, \infty$, and $P_p(x)$ is the p th order Legendre polynomial defined by

$$P_p(x) = \sum_{k=0}^p \left\{ \frac{(-1)^{\frac{p-k}{2}} x^k (p+k)!}{2^p k! \left(\frac{p-k}{2}\right)! \left(\frac{p+k}{2}\right)!} \right\}, p-k = \text{even} \tag{2}$$

And, the recurrent formula of Legendre polynomials is

$$\begin{cases} P_{p+1}(x) = \frac{2p+1}{p+1} x P_p(x) - \frac{p}{p+1} P_{p-1}(x) \\ P_1(x) = x, P_0(x) = 1 \end{cases} \tag{3}$$

The Legendre polynomials are a complete orthogonal basis set on the interval $[-1, 1]$. The relation of orthogonality is defined as

$$\int_{-1}^1 P_p(x)P_q(x)dx = \frac{2}{2p+1} \delta_{pq} \tag{4}$$

where,

$$\delta_{pq} = \begin{cases} 1 & \text{if } p = q \\ 0 & \text{if } p \neq q \end{cases} \text{ is the Kronecker symbol.}$$

The orthogonal property of Legendre polynomials implies no redundancy or overlapping of information between the moments with different orders. This property enables the contribution of each moment to be unique and independent from the information in an image [36].

To compute Legendre moments of a digital image, the integrals in Equation (1) are replaced by summations and the coordinates of the image are normalized into $[-1, 1]$. Therefore, the numerical approximate form of Legendre moments, for a discrete image of $M \times N$ pixels with image intensity function $f(x, y)$, is [37]

$$L_{pq} = \lambda_{pq} \sum_{i=0}^{M-1} \sum_{j=0}^{N-1} P_p(x_i)P_q(y_j)f(x_i, y_j) \tag{5}$$

where $\lambda_{pq} = \frac{(2p+1)(2q+1)}{M \times N}$, x_i and y_j denote the normalized pixel coordinates in the range of $[-1, 1]$.

III. Data Sets

The publicly available retina data sets are mainly prepared for tasks other than finding similarities between an individual's left and right retina, e.g., automatic pathology detection; segmentation of anatomical structures such as optic disc, macula, and central retinal blood vessels; assessing the image quality; and retinal image registration. Most of the data sets have images from only one side and one session. Therefore, most of the data sets are not appropriate for our purpose. Few data sets have images from both side retinas, among which we choose two data sets to do the identification: (1) Child Heart Health Study in England (CHASE) data set and (2) Methods to Evaluate Segmentation and Indexing Techniques in the field of Retinal Ophthalmology-2 (Messidor-2) data sets. These two public data sets have a pair of left and right retinal images per subject. Two example pairs of these data sets are shown in Figure 1.

CHASE_DB1 [38], [39] contains 14 pairs of colored retinal images (i.e., 28 RGB retinal images in total), captured by a Hand-held Nidek NM-200-D camera, with 999×960 pixels. It is a subset of retinal images captured from multi-ethnic children.

Messidor-2 [40] contains 874 pairs of images captured from the left and right retina of 874 subjects using a Topcon TRC NW6 non-mydratic fundus camera with a 45-degree field of view having 1440x960, 2240x1488, and 2304x1536 pixels.

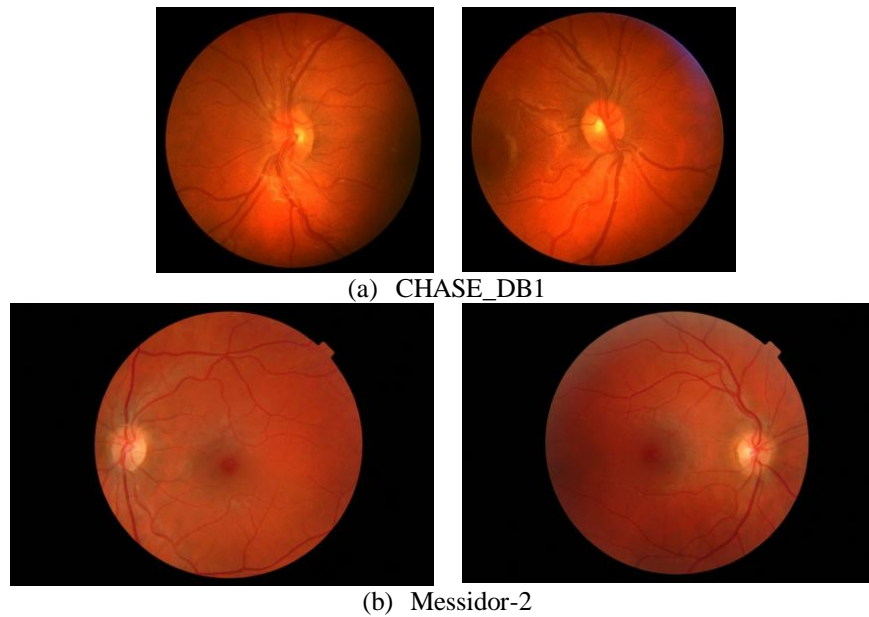


Figure 1: Two Example Pairs of Left and Right Retinal Images of the Datasets (a) CHASE_DB1 and (b) Messidor-2

IV. Legendre Moments based Similarity Measurement

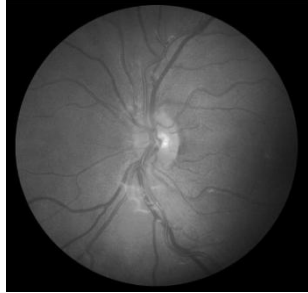
At first we convert each 3D RGB retinal images of a data set (i.e., CHASE_DB1 and Messidor-2) into 2D grayscale images by performing a weighted summation of three color channels in the following way



$$\text{Grayscale} = 0.299 \times \text{Red} + 0.587 \times \text{Green} + 0.114 \times \text{Blue}.$$

Except that no other preprocessing (such as image enhancement, background cropping, or denoising) is done on any retinal image. After that we represent each grayscale retinal image by a sequence of Legendre moments $L_S, \{L_0, L_1, L_2, L_3 \dots L_S\}$ where S is the order of the moments. We set $S = 15$ assuming that the computation of cosine distance between the low dimensional Legendre feature vectors will not suffer from the curse of high dimensionality.

Two sample left retinal images and one right retinal image of the CHASE_DB1 data set along with their corresponding 15 order Legendre moments are shown in Table 1.

Table 1: Fifteen Legendre Moments of Two Left and One Right Retinal Images

| Retina | Image | Legendre moments |
|--------|---|---|
| Left1 |  | -2.54883216644013, -39.1841405357075, 0.519517186326675, 1.09555006610562, -0.195206187674502, -0.024244949300752, 0.001774621167093, -0.111701953187058, 0.042335373583012, 0.068560284172142, -0.019016578815481, 0.112713784523971, 0.014495142325508, 0.229014184160956, -0.016658880384136 |

| | | |
|--------|---|--|
| Right1 |  | -2.44195690601696, -40.1609229725178, 0.465676337493098, 0.251467346822934, 0.2029634304591, -0.401027841891579, -0.249114685951248, 0.152025985269091, 0.120675467962824, -0.002092193401076, -0.10904412968962, 0.079295887598107, 0.063789838410484, 0.269551196825741, -0.05992901829815 |
| Left5 |  | 0.14553990681233, -54.815478285092, -0.233357897290385, 2.34639643397884, 0.159220891497932, -1.07689549183256, -0.141497894945793, 0.284929316863294, 0.06730653926678, 0.069482533010556, -0.046496802781095, 0.004889504051136, -0.022685093949874, 0.327549539105079, -0.016335496559562 |

After extracting orthogonal Legendre moments based feature vectors for all the left and right retinal images of a data set, we estimate the cosine distance for each possible pair of left and right retina in the following way

$$\cos\theta = \frac{\vec{L} \cdot \vec{R}}{\|\vec{L}\| \|\vec{R}\|} = \frac{\sum_{i=1}^n L_i R_i}{\sqrt{\sum_{i=1}^n L_i^2} \sqrt{\sum_{i=1}^n R_i^2}} \quad (6)$$

where $\vec{L} \cdot \vec{R}$ is the dot product between the Legendre feature vector of the left and right retina and n is the dimension of the vectors. The cosine distance between five pairs of left and right retinal images of CHASE_DB1 are shown in Table 2. Each diagonal cell belongs to a pair of left and right retinal images from a single subject, whereas each non-diagonal cell belongs to a pair of left and right retinal images from two different subjects. The smallest value in the first diagonal cell indicates that the correct right retina (i.e., Right1) has the smallest cosine distance with the left retina (i.e., Left1). It means that the left retina (i.e., Left1) of Subject1 is more similar to the right retina of Subject1 (i.e., Right1) than the right retinas of other subjects (i.e., Subject2, Subject3, Subject4, and Subject5). Same thing happens to Left2, Left3, and Left4. Such cases are the examples of correctly identified right retinas for left retinas. The ideal case is that all diagonal cells of Table 2 have the smallest cosine distance comparing to other cosine distances in that row. However, for Left5 it happens that the smallest value is not in the diagonal cell. In the fifth row (i.e., for L5 retina), the smallest cosine distance is found in the first cell, i.e., with R1 retina. Such case is an example of wrongly recognized right retina for a left retina.

We investigate for how many left retinas can find the smallest cosine distance in k nearest neighbors of right retinas. There is a correspondence between the value of k and the degree of similarity. Smallest value of k represents a high degree of similarity. In contrast, largest value reports a low degree of similarity.

Table 2: Cosine Distances Measured between the Left (L) and Right (R) Retinal Images.

| Right \ Left | Right1 | Right2 | Right3 | Right4 | Right5 |
|--------------|-------------------|-------------------|-------------------|-------------------|------------|
| Left1 | 0.00038761 | 0.00273396 | 0.00443778 | 0.00421216 | 0.00556403 |
| Left2 | 0.00781619 | 0.00112177 | 0.00865895 | 0.00128904 | 0.00218104 |
| Left3 | 0.00060657 | 0.00459435 | 0.00013687 | 0.00050906 | 0.00767014 |
| Left4 | 0.00177693 | 0.00688795 | 0.00656728 | 0.00091488 | 0.00123844 |
| Left5 | 0.00054917 | 0.00089887 | 0.00078071 | 0.00065637 | 0.00109431 |

V. Results and Discussion

It is found in the experiments that the lower orders of Legendre moments mainly contain fundamental retinal image information, while the higher orders of Legendre moments preserve more detailed retinal image information. Only lower-order or only higher-order moments have few significant effects on the similarities

measurement. A set of both lower-order and higher-order moments is taken from the whole retinal image. However, it is experimentally observed that all the parts in the whole image cannot contribute equally. Part-based Legendre moments are calculated from both retinas of an individual and from the two different persons. In most of the cases similar or very close Legendre moments are found from the same parts of the left and right retinas of an individual based on cosine distance. On the other hand, different Legendre moments are found from the same parts of the two different persons' eyes. Moreover, in some cases Legendre moments of some parts in the left and right retinal images of an individual cannot influence our similarity assessment task. Part-based Legendre moments are not used in this work.

The probability of finding the correct right retina among the k-nearest right retinas for a left retina is shown in Table 3. Note that the probability of retrieving the correct right retina for a left retina by chance is $1/14 = 0.0714$ for CHASE_DB1 and $1/874 = 0.0011$ for Messidor-2. As shown in Table 3, the probability of retrieving the correct right retina for a left retina is 0.61 for CHASE_DB1 and 0.22 for Messidor-2, respectively. Among five nearest neighbors, the probability of being the actual right retina for a left retina is 0.92 and 0.71, respectively. These values are much higher than by chance. It indicates that a subject's left and right retinas have more similarities than those from two different subjects. There is a significant difference in the performances of the two datasets. One reason behind this phenomenon might be the size difference of the two datasets. As the number of subjects increases, it becomes increasingly difficult for the system to accurately find the right retina for a left retina.

Table 3: Probability of Finding Similarity of Left Retina in k-nearest Right Retinas

| Dataset | Values of k | Probability |
|------------|---------------|------------------------------|
| CHASE_DB1 | 1, 2, 3, 4, 5 | 0.61, 0.82, 0.89, 0.91, 0.92 |
| Messidor-2 | 1, 2, 3, 4, 5 | 0.22, 0.34, 0.53, 0.6, 0.71 |

VI. Conclusion

In this paper, for the first time, we have shown that the orthogonal Legendre moments can be used as a feature vector to find substantial similarity between the left and right retinal images captured from a single subject. We perform experiments on two publicly available data sets (i.e., CHASE_DB1 and Messidor-2) with a pair of left and right retina for each subject. By estimating orthogonal moments for both left and right retinal images at first and then estimating cosine distance between estimated moments, we have shown that a left retina has the lowest cosine distance from a right retina when they are from the same subject than when they are from two different subjects. Performing experiments on a database having more pairs of left and right retinal images than the Messidor-2 (i.e., more pairs than 874 pairs) and multiple pairs for each subject captured in different settings is necessary for figuring out more exciting information about the similarity of an individual's left and right retina. This task can be a good research direction in the future.

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