A New Retinal Recognition System Using a Logarithmic Spiral Sampling Grid

Fabiola M. Villalobos Castaldi[1], Edgardo M. Felipe-Riveron[2], and Ernesto Suaste Gómez[1]

[1] Researches and Advanced Studies Center of the National Polytechnic Institute, Av. Instituto Politécnico Nacional # 2508, La Laguna Ticoman, Gustavo A. Madero, P.O. 07360, Mexico D.F., Mexico
{mvillalobos,esuaste}@cinvestav.mx
[2] Centro de Investigación en Computación, Instituto Politécnico Nacional, Av. Juan de Dios Batiz and Miguel Othon de Mendizabal P.O. 07738., Mexico D.F., Mexico
edgardo@cic.cin.mx

Abstract. The retinal vascular network has many desirable characteristics as a basis for authentication, including uniqueness, stability, and permanence. In this paper, a new approach for retinal images features extraction and template coding is proposed. The use of the logarithmic spiral sampling grid in scanning and tracking the vascular network is the key to make this new approach simple, flexible and reliable. Experiments show that this approach can achieve the reduction of data dimensionality and of the required time to obtain the biometric code of the vascular network in a retinal image. The performed experiments demonstrated that the proposed verification system has an average accuracy of 95.0 – 98 %.

Keywords: Logarithmic spiral sampling grid, spiral scan and sampling, biometry, retinal images, time series representations.

1 Introduction

It has been proposed a number of authentication methods based on the retina. These methods have focused primarily on selecting the appropriate features to represent the retina (bifurcations, ending points, etc.). But the final representation of the features has never been studied carefully [2-16]. Biometric representation (*template*) is a machine readable and understandable form of a biometric trait. It influences the system's accuracy and the design of the rest of the system. The machine representation of a biometric is critical to the success of the matching algorithm. In a practical authentication system, the database can contain records of millions of people. Choosing an appropriate representation of the features in order to make the data base smaller in size, having a rapid response search and while retaining high accuracy in the verification, is a vital task.

A relatively high number of personal authentication methods based on the blood vessel network of the retina have been recently developed as biometric. These

J.F. Martínez-Trinidad et al. (Eds.): MCPR 2014, LNCS 8495, pp. 241–250, 2014.

methods are based on determining a given number of appropriate features that represent uniquely the retina.

From previous studies, the retina's features used for authentication can be classified into three main categories: structural, statistical and algebraic features. Some typical structural features include main lines (centerlines), branching points, crossing points, termination points, positions, angles, diameters, etc. [12], [33]. Some statistical features are the texture moments that were used in [2] and the random values that were used in [31]. Likewise, the algebraic features, such as band-tree based radial partition, the ring method, etc., were proposed in [26].

The general procedure of biometric systems for personal authentication based on the retinal vascular network comprises the following seven steps:

1. Acquisition of the eye fundus image.
2. Image enhancement (noise smoothing, contrast enhancement, size normalization)
3. Creation of the conditions for doing the next stage invariant to translation, rotation and scale at least in a narrow range. This step may include eventually the segmentation of the optic disc and the macula luteal.
4. Probably, the vascular network segmentation. Eventually, its skeletonization is also required.
5. Extraction of the structural characteristics to obtain a code which differentiate it.
6. Classification on the basis of the code previously found.
7. Authentication for recognizing/identifying the person.

Some algorithms do not segment the vascular network in order to save computational time (stage 4). In this paper we discuss mainly the novelty of the approach related to the steps 3, 4 and 5 and evaluation of the feature extraction method to be used for authentication of individuals (stages 6 and 7).

The main contribution of this paper is the implementation of a new biometric representation method based on coding blood vessel segments, through a new scanning and tracking algorithm by using a logarithmic spiral. Data obtained from the sampling of the vascular network constitute local features that are conformed in time series representations. The time series have been studied extensively in data mining, bioinformatics and pattern recognition in biometrics [1].

1.1 Logarithmic Spiral

The spiral is a curve that winds itself around a given point. While not being a circle, the radius will vary along the angle [20], [21]. The logarithmic spiral is that in which the radius grows exponentially with the rotation angle. The logarithmic relation between radius and angle leads to the name of logarithmic spiral. In this curve the distances where a radius from the origin meets the curve increases in geometric progression. In polar coordinates the logarithmic curve can be expressed matematically as (Eq. 1):

$$r = ae^{b\theta} \tag{1}$$

where r is the distance from the origin, θ is the angle from the horizontal x-axis, e is the base of natural logarithms, and a and b are arbitrary positive real constants. The constant $\boldsymbol{a}$ is the increasing rate of the spiral and its sign determines the rotation direction of the spiral (in this work $\boldsymbol{a}$ is known as the spiral roll). The logarithmic spiral is also known as the growth spiral, equiangular spiral, and spiral mirabilis. The logarithmic spiral is remarkable because of its unique self-similarity, that is, it is invariant after a similarity transform. After any scaling (uniformly increasing or decreasing the size) logarithmic spirals can be rotated and always match the original figure.

The retinal circulation of the normal human retinal vasculature is statistically self-similar, fractal and the Murray optimization principle is valid. Studies from several groups present strong evidence that the fractal dimension of the blood vessels in the normal human retina is approximately 1.7. This is the same fractal dimension found for a diffusion-limited growth process, which is consistent with the hypothesis that the development of human retinal vessels involves a diffusion process [34]. Fractal analysis provides a method for the quantitative study of changes in the retinal vascular network [33]. It has been suggested that fractal models are simple to encode genetically because the same branching mechanism is used repeatedly. All fractals have scale and rotational invariances, and any fractal formed from a process that has a non-zero rotational component will include logarithmic spiral forms [35].

1.2 Advantages of the Logarithmic Spiral Sampling Grid

In this work the scanning and tracking step is based on a sparse logarithmic spiral sampling grid, which has a log-polar geometry, meaning that the density of the sampling points decreases exponentially with the distance from the center. Such non-uniform sampling pattern, with frequency decreasing from the center to the periphery, shares the same geometric progression that the retinal vascular network has. This sampling grid offers the following advantages:

1. The data dimensionality is reduced because the retinal vascular network is represented by a sequence of only two real valued data [29].
2. Discontinuities caused by sampling the blood vessels are eliminated from the data [32]. This problem occurs when concentric flatted circles or other sampling methods are used [28].
3. Only data related to detected points of the vascular network along the spiral grid are encoded and not the entire region (blood vessels and background). The information of every point P extracted by the spiral is used as feature descriptors of the vascular network structure [31].
4. The vascular network travels and distributes across the retina in the same way as does the logarithmic spiral mapping grid. The most problematic area is located within the optical disc which is previously removed [39-41].
5. The most robust and stable structure of the vascular network is coded, that is, the vessel segments of the vascular network. Bifurcations and crossings of the venous and arterial networks are eliminated in order to avoid coding errors [22-26].

6. It is not necessary to take into account whether a given vessel is a vein or an artery; only the midpoint of every vessel segment is used as the feature descriptor.
7. The amount of coded information is increased because it is possible to extract more than one feature from the detected vessels along the spiral path [31].
8. The size of the spiral grid is determined by the number of necessary points that ensures the subject's individuality [30]. The sampling is done in the thinned retinal blood vessels. This provides invariance to small changes in the scale.

2 The Recognition System

In our retinal recognition system, fundus images are analyzed with a logarithmic spiral sampling grid, and the geometrical characteristics of the retinal vascular network are coded using a time series approach. The retina images contained in the publicly available VARIA database were used to implement the recognition system and to assess its performance. The VARIA database is a set of retinal images used for authentication purposes. The database currently includes 233 images, from 139 different individuals. The number of images per subject is not constant. The images have been acquired with a TopCon non-mydriatic camera NW-100 model and are optic disc centered with a resolution of 768x584 pixels [38]. The detailed description of the system follows.

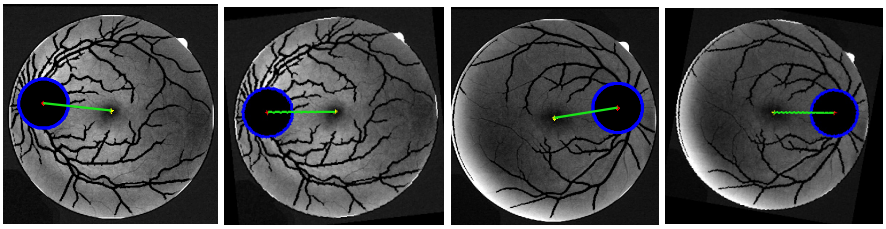
2.1 Logarithmic Spiral Sampling Grid

The recognition scheme proposed in this paper is based on a logarithmic spiral sampling grid which is positioned over the center of the optic disc. It travels throughout the retinal vascular network that surrounds the optic disc. For this, it is necessary to detect the optic disc and locate its center to be used as a reference point. The detection of the optic disc is carried out from the green plane of the color fundus image acquired in the RGB color space. This is because this plane presents more details and less noise with respect to the red and blue planes. Then a morphological opening and a morphological closing with a circular structuring element (disc) of 5 pixels diameter are performed to emphasize the areas of interest and to reduce the number of non-interesting ones. Once the optic disc is located it is hidden superimposing a black circular disc of a diameter 10% greater than the actual diameter of the optic disc.

2.2 Invariances of the Method

In order to couple the proposed scheme against eventual small rotation variations occurring during the image acquisition procedure, we use the macula center as another reference point, in order to link it with the optic disc center with a straight line (Fig. 1). To compensate the rotation variations, the image is then rotated accordingly so that the line is aligned with the horizontal axis. The methodology step by step for segmenting the optic disc and the macula, and to locate the centroid of both anatomic retina structures is beyond the scope of this paper [39-40]. The proposed method is

also invariant to small translation variations since we always relate the sampling to the center of the optic disc. If the retinal vascular network suffers some translation during the acquisition process of the image, the logarithmic spiral sampling is always referred to the same reference coordinates.



a) b) c) d)

Fig. 1. Experimental results of the reinforcement of the proposed method against translation and rotation in some typical images. a) and c) not compensated images, b) and d) processed images.

2.3 Feature Extraction

Since it is not a particular goal of this paper to segment the vascular network, the feature extraction process starts from a binary image having the vascular network already segmented using the method previously proposed and published by the authors [36].

2.3.1 Morphological Thinning

Vessels in the vicinity of the optic disc could have different diameter size. To overcome this inconvenience, retinal vessel thinning (through a skeletonizing procedure) was implemented using a morphological operator that reduces the width of vessels to single-pixel width line segments, while preserving the extent and connectivity of the original shape. The thinned representation of the vascular network is processed easily in later stages savings either computing time and storage complexity [12]. The spiral grid is mapped along the thinned retinal network starting from the center of the masked optic disc towards the periphery of the vascular network. This step transforms the irregular retinal structure into sequential data. It is necessary to evaluate now the potential benefit of adapting the mapping grid to the dimensions of the image, instead of placing a mapping grid of constant size. Thus, an exhaustive analysis of the spiral mapping grid must be performed in order to select the most suitable size of the mapping grid for obtaining the most adequate biometric template congruence.

We configured the logarithmic spiral grid in several sizes employing different spiral roll values. The spiral roll value should not be so small because the resulting spiral grid will travel very gently, the number of wings will increase and then the length of the feature vector and the required computational time to analyze the retinal network will increase. Moreover, the spiral roll value should not be so large, because

the resulting spiral grid travels so fast and the number of wings will be small and therefore, the length of the feature vector reduces and also the achieved data.

For each point that the spiral grid crosses with the thinned vascular network, two geometrical characteristics are encoded. For instance, we use as descriptor the radius from the origin to the blood vessel segment in the junction point (for simplicity "position"), and the angle that this blood vessel segment forms respect to the horizontal axis in that point (for simplicity "crossing angle"). For each feature mapped and coded, we created a sequence of real valued data; thus, we got two time series from each input retinal image.

We carried out the analysis in order to select the best mapping grid size varying the spiral roll value and computing the length of the resulting time series for each spiral roll value ranging from 0.01 to two. For example, if we choose 0.5 as the spiral roll value, the length of the resulting time series had 12 coded points, and the processing time to encode the retinal network was 0.8s. On the other hand, if we want to increase the time series length to 178, the spiral roll value must be 0.03 for which the system will require 3.9s. This let us to establish a range of allowed spiral roll values, without increasing the processing time while ensuring the efficiency of the recognition system based on the logarithmic spiral mapping grid. Based on the obtained results, we decided to select 0.2 as the most suitable spiral roll value that guarantees to encode an average of 50 points in a time of 1s; thus, the resulting time series length was 50 coded points. It means that the spiral grid was of a constant size for all the similar images contained in the database. Figure 2 shows both time series of a typical coded retinal image using a logarithmic spiral maping grid with a spiral grid value = 0.15942.

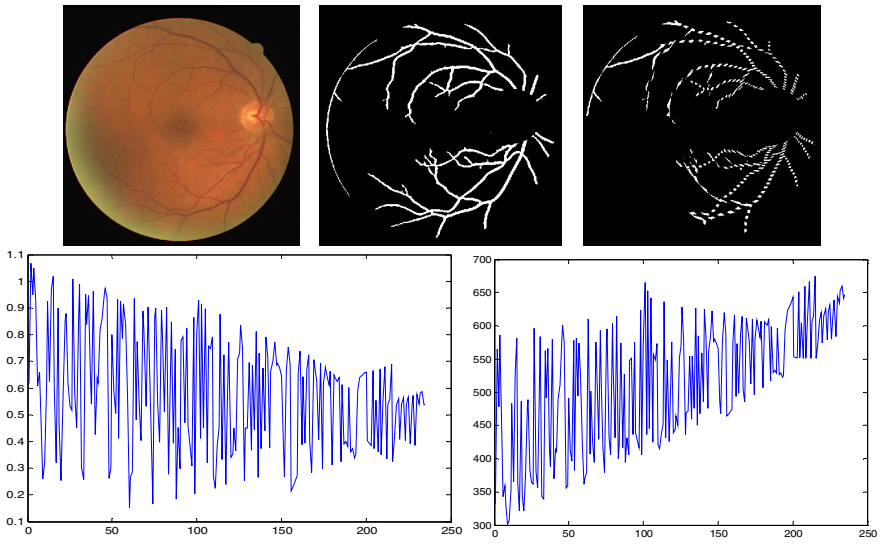


Fig. 2. Time series obtained with a spiral grid value = 0.15942

3 Experiments and Results

We use also a novel retinal recognition scheme to evaluate the discriminatory potential and the inter-individual differences based on the time series representation of the geometrical retinal network features, employing the logarithmic spiral as the sampling grid. In the recognition phase, we compare the presented biometric trait with the feature vector associated with the claimed ID stored previously in the database. Here, the user has to present his/her ID in order to retrieve the biometric feature template associated to his/her database. Then, the extracted feature vector from the input image (whose identity has to be recognized) is compared with the template retrieved from the database. The output of the comparison is an accept/reject decision. The recognition is positive if the distance between the claimed and the stored feature vector is less than a given threshold value. The metric used for the proposed recognition system is the Euclidean distance.

3.1 Evaluation of the Recognition System

The performance of the recognition phase depends on how good was created the biometric representation of the biometric feature and how good is the matching scheme. As it was mentioned previously, we coded the geometrical features of the retinal network and arranged them in a sequence of real valued data. We saved these time series as the feature vectors in the database along with the provided user ID. The distance measured is the matching score that cuantifies the response of the matching scheme. Based on the matching scores, and a predefined threshold value, it is possible to estimate the accuracy of the proposed logarithmic spiral sampling grid-based recognition system. The results of the accuracy of the proposed retinal recognition system are presented as follows: we considered each retinal fundus image in the database as one of a different user. We matched all retina feature vectors against each other. Based on the 233 images from 139 registered subjects in the VARIA database, the total amount of comparisons was ((233*232)/2) = 27028. With this total number of comparisons it is now possible to compute the FAR (False Accepted Rate), the FRR (False Rejected Rate) and the thresholds. We carried out the evaluation of the recogniton system using separately each time series as the feature descriptor, i.e., the time series of the position and that of the crossing angle. It was concluded from the experimental results that we obtain lower error rates using as the feature vector the position time series; this result is consistent with that obtained by [27] concluding that the position of the blood vessel as a descriptor is the main contribution to retina template entropy. If the FAR and FRR rates for a series of threshold values are obtained, it is possible to plot these rates as a Receiver Operating Curve (ROC), where one axis displays FAR rates and the other displays FRR rates. Based on such a curve, it is possible to make tradeoff decisions regarding what FAR/FRR values that is desirable for a system. The graph is shown in Fig. 3. From this curve it is possible to observe that in a very small FAR we have large values of FRR for identification.

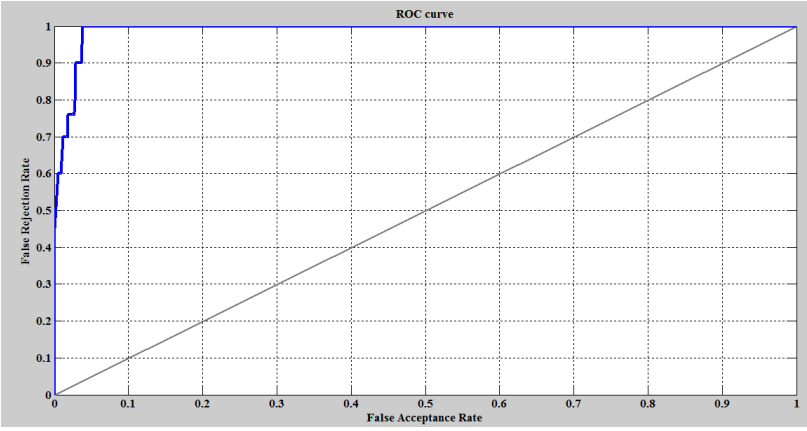


Fig. 3. Roc curve

4 Conclusion

A novel approach for the vascular network biometric coding based on a logarithmic spiral mapping grid was proposed. The main contribution of this proposal is the implementation of the logarithmic spiral mapping grid as the scan and tracking pattern method. This methodology share the fractal and geometrical characteristics that retinal network has; it is very flexible to implement since the spiral parameters, the geometrical retinal features and the size of the spiral sampling grid can be easily adjusted according to different system requirements; the time series representation makes it very convenient for the implementation of multi-biometrics using feature fusion, and the logarithmic spiral scan and sampling representation reduce the data dimensionality of the original retinal image to a real sequential data. Finally; the method reduces the computational time required for the template representation and the matching step. We obtained a maximal performance of the proposed system of 95 -98%, which is relatively high. The experimental results showed that the novel proposed retinal recognition system is an effective approach in biometric identification applications.

Acknowledgement. The authors of this paper would like to thank the COFAA, Postgraduate and Research Secretary, Centro de Investigación en Computación del Instituto Politécnico Nacional (IPN), CONACyT and Researchers National System (SNI), for their economic support to carry out this work.

References

1. Keogh, E., Chakrabarti, K., Pazzani, M., Mehrotra, S.: Locally Adaptive Dimensionality Reduction for Indexing Large Time Series Databases. In: Proceedings of ACM SIGMOD Conference on Management of Data, Santa Barbara, CA, May 21-24, pp. 151–162 (2001)

2. Jung, E., Hong, K.: Automatic Retinal Vasculature Structure Tracing and Vascular Landmark Extraction from Human Eye Image. In: Proceedings of the International Conference on Hybrid Information Technology. IEEE Computer Society (2006)
3. Hill, R.B.: Retina Identification, Portland, OR, USA (1992)
4. Hill, R.B.: Apparatus and method for identifying individuals through their retinal vasculature patterns. U.S. Patent No. 4109237 (1978)
5. Simon, C., Goldstein, I.: A new scientific method of identification. New York State. J. Medicine 35(18), 901–906 (1935)
6. Tower, P.: The fundus oculi in monozygotic twins: Report of six pairs of identical twins. Arch. Ophthalmol. 54, 225–239 (1955)
7. Marshall, J., Usher, D.: Method for generating a unique and consistent signal pattern for identification of an individual. U.S. Patent No. 6993161 (2006)
8. Derakhshani, R., Ross, A.: A Texture-Based Neural Network Classifier for Biometric Identification using Ocular Surface Vasculature. In: Appeared in Proc. of International Joint Conference on Neural Networks (IJCNN), Orlando, USA (2007)
9. Golden, B.L., Rollin, B.E., Switzer, J.R.V.: Apparatus and method for creating a record using biometric information. U.S. Patent No. 028343 (2004)
10. Ortega, M., Gonzalez, M.F.: Automatic system for personal authentication using the retinal vessel tree as biometric pattern, PhD. Thesis, Department of Computer Science of the Faculty of Informatics of the University of Coruña (2009), downloaded from: http://www.varpa.es/ (revised on June 10, 2012)
11. http://www.absoluteastronomy.com/topics/Retinal_scan (revised on June 10, 2012.)
12. Bevilacqua, V., Cambó, S., Cariello, L., Mastronardi, G.: Retinal Fundus Hybrid Analysis Based on Soft Computing Algorithms. Communications To Simai Congress 2 (2007) ISSN 1827-9015
13. Usher, D., Tosa, Y., Friedman, M.: Ocular Biometrics: Simultaneous Capture and Analysis of the Retina and Iris. Advances in Biometrics Sensors, Algorithms and Systems, 133–155 (2007)
14. Usher, D.B.: Image analysis for the screening of diabetic retinopathy, PhD thesis, University of London (2003)
15. Fukuta, K., Nakagawa, T., Yoshinori, H., Hatanaka, Y., Hara, T., Fujita, H.: Personal identification based on blood vessels of retinal fundus images (Proceedings Paper). In: Medical Imaging, Image Processing, Proceedings, vol. 6914 (2008)
16. Lee, S.S., Rajeswari, M., Ramachandram, D., Shaharuddin, B.: Screening of Diabetic Retinopathy - Automatic Segmentation of Optic Disc in Colour Fundus Images. In: Proc. 2nd International Conference on Distributed Frameworks for Multimedia Applications, pp. 1–7 (2006)
17. MacGillivray, T.J., Patton, N., Doubal, F.N., Graham, C., Wardlaw, J.M.: Fractal analysis of the retinal vascular network in fundus images. In: Proceedings of the 29th Annual International Conference of the IEEE EMBS, Cité Internationale, Lyon, France (2007)
18. Barry, R.: Fractal analysis of the vascular tree in the human retina, Masters. Annu. Rev. Biomed. Eng. 6, 427–452 (2004), doi:10.1146/annurev.bioeng.6.040803.140100
19. Taylor, R.P.: Chaos, Fractals, Nature: a New look at Jackson Pollock, Fractals Research, Eugene OR (200&)
20. http://mathworld.wolfram.com/LogarithmicSpiral.html (revised on September 20, 2012)
21. http://www.2dcurves.com/spiral/spirallo.html (revised on September 20, 2012)

22. Zana, F., Klein, J.C.: Robust Segmentation of Vessels from Retinal Angiography. In: International Conference on Digital Signal Processing, Santorini, Greece, pp. 1087–1091 (1977)
23. Zhoue, L., Rzeszotarski, M., Singerman, L., Cokreff, J.: The detection and quantification of retinopathy using digital angiograms. IEEE Transaction on Medical Imaging 13-4, 619-626 (1994)
24. Matsopoulos, G.K., Mouravliansky, N.A., Delibasis, K.K., Nikita, K.S.: Automatic retinal image registration Scheme using global optimization techniques. IEEE Trans. Information Technology in Biomedicine 3 (1999)
25. Wang, L., Bhalerao, A.: Model based segmentation for retinal fundus images. In: Bigun, J., Gustavsson, T. (eds.) SCIA 2003. LNCS, vol. 2749, pp. 422–429. Springer, Heidelberg (2003)
26. Farzin, H., Abrishami-Moghaddam, H., Moin, M.: A Novel Retinal Identification System. EURASIP Journal on Advances in Signal Processing, Article ID 280635, 10 pages (2008), doi:10.1155/2008/280635
27. Arakala, A., Culpepper, J.S., Jeffers, J., Turpin, A., Boztaş, S., Horadam, K.J., McKendrick, A.M.: Entropy of the Retina Template. In: Tistarelli, M., Nixon, M.S. (eds.) ICB 2009. LNCS, vol. 5558, pp. 1250–1259. Springer, Heidelberg (2009)
28. Fuhrmann, T., Hammerle-Uhl, J., Uhl, A.: Usefulness of Retina Codes in Biometrics. In: Wada, T., Huang, F., Lin, S. (eds.) PSIVT 2009. LNCS, vol. 5414, pp. 624–632. Springer, Heidelberg (2009), doi:10.1007/978-3-540-92957-4_54.
29. Che Azemin, M.Z., Kumar, D.K., Wu, H.R.: Shape Signature for Retinal Biometrics. In: 2009 Digital Image Computing: Techniques and Applications, DICTA 2009, pp. 382–386 (2009)
30. http://www.biometricnewsportal.com/retina_biometrics.asp
31. Chen, J., Moon, Y.-S., Wong, M.-F., Su, G.: Palmprint authentication using a symbolic representation of images. Image and Vision Computing 28, 343–351 (2010)
32. http://en.wikipedia.org/wiki/Connected_space#Path_connectedness
33. MacGillivray, T.J., Patton, N., Doubal, F.N., Graham, C., Wardlaw, J.M.: Fractal analysis of the retinal vascular network in fundus images. In: Proceedings of the 29th Annual International Conference of the IEEE EMBS, Cité Internationale, Lyon, France (2007)
34. Barry, R.: Fractal analysis of the vascular tree in the human retina, Masters. Annu. Rev. Biomed. Eng. 6, 427–452 (2004), doi:10.1146/annurev.bioeng.6.040803.140100.
35. Taylor, R.P.: Chaos, Fractals, Nature: a New look at Jackson Pollock, Fractals Research, Eugene OR (200&)
36. Villalobos, F.M., Felipe, E.F.: A Fast Efficient and Automated Method to Extract Vessels from Fundus Images. Journal of Visualization, J. Vis. 13, 263–270 (2010) ISSN: 1343-8875, doi:10.1007/s12650-010-0037-y
37. http://en.wikipedia.org/wiki/Macula_of_retina (last acceced, June 2013)
38. http://www.varpa.es/varia.html
39. Yu, H., Barriga, S., Agurto, C., Echegaray, S., Pattichis, M., Zamora, G., Bauman, W., Soliz, P.: Fast Localization of Optic Disc and Fovea in Retinal Images for Eye Disease Screening (2008), http://visionquest-bio.com/index.html
40. Youssif, A.A.A., Ghalwash, A.Z., Ghoneim, A.A.S.A.: Optic Disc Detection From Normalized Digital Fundus Images by Means of a Vessels' Direction Matched. IEEE Transactions on Medical Imaging 27(1), 11–19 (2008)