STUDIA INFORMATICA 2003
Volume 24 Number 4 (56)

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# GENETIC FEATURE SUBSET SELECTION FOR CLASSIFICATION OF EYE-CUP REGION IN FUNDUS EYE IMAGES

**Summary**. In this paper the new method of feature subset selection for eye-cup classification in fundus eye images based on genetic algorithms is proposed. We also proposed a new, suitable fitness function used in reproduction stage. The proposed method enables to reduce the classifier error rate significantly.

**Keywords**: feature selection, genetic algorithms, classifier, glaucoma

# SELEKCJA CECH Z WYKORZYSTANIEM ALGORYTMU GENETYCZNEGO DO KLASYFIKACJI WNĘKI NACZYNIOWEJ NA CYFROWYCH OBRAZACH DNA OKA

**Streszczenie**. W artykule przedstawiono nową, wykorzystującą algorytmy genetyczne metodę selekcji cech do automatycznej klasyfikacji wnęki naczyniowej na cyfrowych obrazach dna oka. Zaproponowano również nową funkcję celu używaną w fazie reprodukcji algorytmu genetycznego. Metoda pozwala znacznie zmniejszyć prawdopodobieństwo błędnej klasyfikacji.

**Słowa kluczowe:** selekcja cech, algorytmy genetyczne, klasyfikator, jaskra

## 1. Introduction

Glaucoma is a group of diseases characterized by the proceeding optic nerve neuropathy which leads to the rising diminution in vision field, ending with blindness. The correct eye-disk structure contains *neuroretinal rim* of pink color placed on the *eye-disk* circuit and centrally placed yellowish *eye-cup* [6] (Fig. 1). Glaucomatous changes in retina appearance

embrace various changes in neuroretinal rim and eye-cup, as the result of nerve fibers damages.

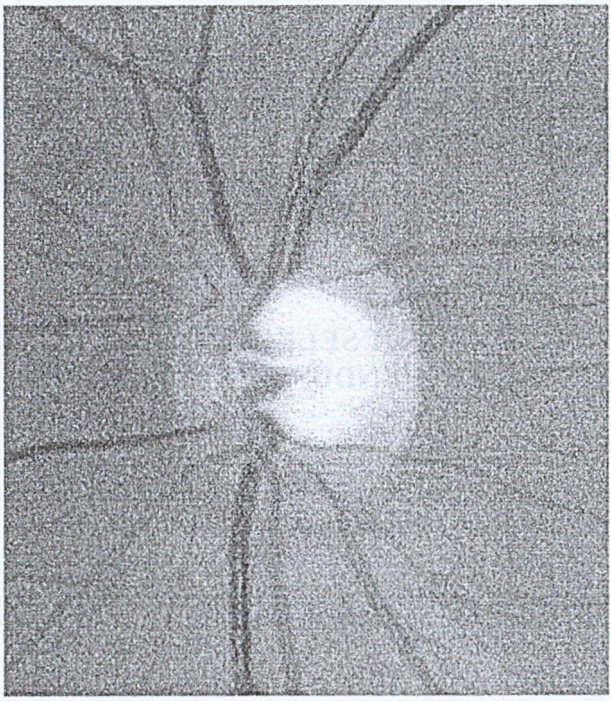

Fig. 1. The initial fundus eye image with the eye-cup area in the central part
Rys. 1. Wejściowy obraz dna oka z wnęką naczyniową w centralnej części

The existing methods of qualitative analysis (i.e. based on ophthalmoscope and slit lamp with Volk lens) [6] are very subjective, while quantitative methods of eye-disc morphology evaluation (cup to disc ratio, neuroretinal rim area) do not result in full diagnosis. The new methods of morphologic analysis based on laser scanning ophtalmoscopy [6] are expensive and accessible only in specialized ophtalmic centres.

Thus, there is a need for better, cheaper and more objective methods of quantitative eye-disc structures evaluation which are based on methods of automatic analysis and recognition of digital images.

In [10], we proposed a new method for automatic segmentation of eye-cup region from fundus eye images acquired from standard fundus camera. Fig. 2 shows the extracted eye cup region from sampled image shown in Fig. 1 by the segmentation method described in [10]. A successful eye-cup classification into normal and glaucomatous ones based on the suitable shape descriptors can boost the performance of applications supporting glaucoma diagnosing. Despite its importance, it has received no attention in the literature.

A new automatic feature selection method based on genetic algorithms (GA) for eye-cup classification is proposed in this paper. We argue that feature selection is important for eye-cup classification, and demonstrate that, by removing features that do not encode important eye cup information from it's representation (i.e. feature vector), the classifier error rate can be reduced significantly.

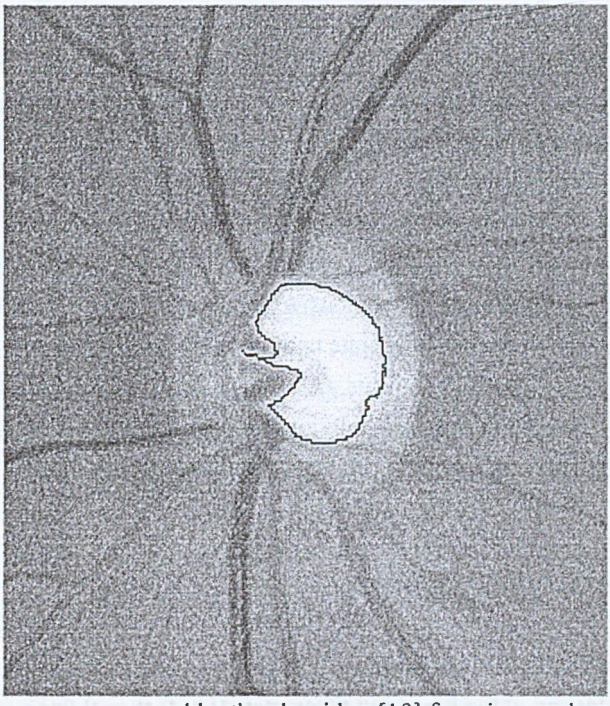

Fig. 2. The eye cup segmented by the algorithm [10] from image shown in Figure 1
Rys. 2. Wnęka naczyniowa wysegmentowana algorytmem [10] z obrazu na rys. 1

## 2. Background on genetic algorithms

Genetic algorithms (GA) [1,3] are a class of optimization procedures inspired by the biological mechanisms of reproduction. GA operate iteratively on a population of structures, each one of which represents a candidate solution to the problem at hand, properly encoded as a string of symbols (e.g. binary). Unlike classical hill-climbers it does not evaluate and improve a single solution but instead, it analyzes and modifies a population of solutions at the same time.

A randomly generated set of such strings forms the initial population from which the genetic algorithm starts its search. Three basic genetic operators guide this search: selection, crossover, and mutation. The genetic search process is iterative: evaluating, selecting, and

recombining strings in the population during each iteration (called generation) until reaching some termination condition.

Evaluation of each string is based on a fitness function that is problem-dependent. It determines which of the candidate solutions are better. Selection of a string, which represents a point in the search space, depends on the string's fitness relative to that of other strings in the population. It probabilistically removes from the population those points that have relatively low fitness.

Mutation, as in natural systems, is a very low probability operator and just flips a specific bit. Mutation plays the role of restoring lost genetic material. Crossover, in contrast, is applied with high probability. It is a randomized yet structured operator that allows information exchange between points. Its goal is to preserve the fittest individuals without introducing any new value. Selection probabilistically filters out solutions that perform poorly, choosing high performance solutions to concentrate on or exploit. Crossover and mutation, through string operations, generate new solutions for exploration.

Given an initial population of elements, GA use the feedback from the evaluation process to select fitter solutions, generating new solutions through recombination of parts of selected solutions, eventually converging to a population of high performance solutions.

## 3. Automatic feature selection

One of the most difficult and important problems in the design of automatic pattern classifiers is the *selection of* the measured parameters (i.e. *features*) upon which the classifier bases its determination of the classes of the observed objects. The problem of feature selection is defined as follows: "Given a data set of candidate features, select a subset that performs the best under some classification system". Devijer and Kittler [2] define feature extraction as the problem of: "extracting from the raw data the information which is most relevant for classification purposes, in the sense of minimizing the within-class pattern variability while enhancing the between-class pattern variability".

Proper feature selection can reduce not only the cost of recognition by reducing the number of features that need to be collected, but in some cases it can also provide a better classification accuracy due to finite sample size effects [5].

Formally, the problem of feature selection is to find a feature subset $X \subseteq Y$ such that

$$J(X) = \max_{Z \subseteq Y} J(Z)$$

where J is the feature selection criterion function. One possible criterion function is $(1-p_e)$ where $p_e$ denotes the probability of error. Exhaustive evaluation of possible feature subsets is

usually computationally prohibitive in practice (feature selection qualifies as an NP-problem [8]). A number of feature selection approaches have been proposed in the literature [5,8,9]. In general, these methods can be divided into two groups:

1) methods that guarantee to find an optimal solution
2) methods that may result in a suboptimal feature set.

The suboptimal methods are further divided into those that store just one "current" feature subset and make modifications to it (single solution methods), versus those that maintain a population of subsets (multiple solution methods). Another distinction is made between algorithms that are deterministic, producing the same subset on a given problem every time, and those that have a random element which could produce different subsets on every run (stochastic methods).

Genetic algorithms belong to the class of randomized heuristic search techniques, offering an attractive approach to feature subset selection. Siedlecki [9] presented one of the earliest studies of GA-based feature selection in the context of k-NN classifiers. Roth [7] has proposed extracting geometric features using GAs.

In our approach, 29 geometric features taken from [11] are computed on the extracted eye-cup region. GAs are then used to select the most significant features characterizing the shape of eye-cup region.

## 4. The features

The eye-cup can be represented by the spatial central moments of order p+q [4,11] (p, q are integers) of its intensity function:

$$m_{pq} = \sum_{i=1}^{m}\sum_{j=1}^{n}(i-I)^p (j-J)^q p(i,j)$$

where $I = \frac{m_{10}}{m_{00}}$, $J = \frac{m_{01}}{m_{00}}$

and p(i,j) is the intensity function representing the image. Normalized central moments of order p+q [4,11] are defined as:

$$\mu_{pq} = \frac{m_{pq}}{(m_{00})^{\alpha}}$$

$$\alpha = \frac{p+q}{2} + 1$$

The following 29 features were computed for each segmented eye-cup region. Seven Hu moment invariants [4,11]:

$$\phi_1 = \mu_{20} + \mu_{02}$$

$$\phi_2 = (\eta_{20} + \eta_{02})^2 + 4\eta_{11}^2$$

$$\phi_3 = (\mu_{30} + 3\mu_{12})^2 + (3\mu_{21} - \mu_{03})^2$$

$$\phi_4 = (\mu_{30} + \mu_{12})^2 + (\mu_{21} + \mu_{03})^2$$

$$\phi_5 = (\mu_{30} - 3\mu_{12})(\mu_{30} + \mu_{12})\left[(\mu_{30} + \mu_{12})^2 - 3(\mu_{21} + \mu_{03})^2\right] + (3\mu_{21} - \mu_{03})(\mu_{21} + \mu_{03}) \cdot \left[3(\mu_{30} + \mu_{12})^2 - (\mu_{21} + \mu_{03})^2\right]$$

$$\phi_6 = (\mu_{20} - \mu_{02})\left[(\mu_{30} + \mu_{12})^2 - (\mu_{21} + \mu_{03})^2\right] + 4\mu_{11}(\mu_{30} + \mu_{12})(\mu_{21} + \mu_{03})$$

$$\phi_7 = (3\mu_{21} - \mu_{30})(\mu_{30} + \mu_{12})\left[(\mu_{30} + \mu_{12})^2 - 3(\mu_{21} + \mu_{03})^2\right] + (3\mu_{12} - \mu_{30})(\mu_{21} + \mu_{03}) \cdot \left[3(\mu_{30} + \mu_{12})^2 - (\mu_{12} + \mu_{03})^2\right]$$

Fifteen compound invariant moments [4,11]:

$$I_1 = \mu_{20}\mu_{02} - \mu_{11}^2$$

$$I_2 = (\mu_{30}\mu_{03} - \mu_{21}\mu_{12})^2 - 4(\mu_{30}\mu_{12} - \mu_{21}^2)(\mu_{21}\mu_{03} - \mu_{12}^2)$$

$$I_3 = \mu_{20}(\mu_{21}\mu_{03} - \mu_{12}^2) - \mu_{11}(\mu_{30}\mu_{03} - \mu_{21}\mu_{12}) + \mu_{02}(\mu_{30}\mu_{12} - \mu_{21}^2)$$

$$I_4 = \mu_{30}^2\mu_{02}^3 - 6\mu_{30}\mu_{21}\mu_{11}\mu_{02}^2 + 6\mu_{30}\mu_{12}\mu_{02}(\mu_{11}^2 - \mu_{20}\mu_{02}) + \mu_{30}\mu_{03}(6\mu_{20}\mu_{11}\mu_{02} - 8\mu_{11}^3) + 9\mu_{21}^2\mu_{20}\mu_{02}^2 - 18\mu_{21}\mu_{12}\mu_{20}\mu_{11}\mu_{02} + 6\nu_{21}\mu_{03}\mu_{20}(2\mu_{11}^2 - \mu_{20}\mu_{02}) + 9\mu_{12}^2\mu_{20}^2\mu_{02} - 6\mu_{12}\mu_{03}\mu_{11}\mu_{20}^2 + \mu_{03}^2\mu_{20}^3$$

$$I_6 = (\mu_{20} - \mu_{02})^2 + 4\mu_{11}^2$$

$$I_7 = (\mu_{30} - 3\mu_{12})^2 + (\mu_{03} - 3\mu_{21})^2$$

$$I_8 = (\mu_{30} + \mu_{12})^2 + (\mu_{03} - \mu_{21})^2$$

$$I_9 = (\mu_{30} - 3\mu_{12})(\mu_{30} + \mu_{12})[(\mu_{30} + \mu_{12})^2 - 3(\mu_{03} + \mu_{21})^2] + 3(\mu_{21} - \mu_{03})(\mu_{03} + \mu_{21}) \cdot [3(\mu_{30} + \mu_{12})^2 - (\mu_{03} + \mu_{21})^2]$$

$$I_{11} = 3(\mu_{21} - \mu_{03})(\mu_{30} + \mu_{12})[(\mu_{30} + \mu_{12})^2 - 3(\mu_{03} + \mu_{21})^2] + (3\mu_{21} - \mu_{03})(\mu_{30} + \mu_{12})[(\mu_{30} + \mu_{12})^2 - 3(\mu_{03} + \mu_{21})^2] + (3\mu_{12} - \mu_{30})(\mu_{03} + \mu_{12})[3(\mu_{30} + \mu_{12})^2 - (\mu_{03} + \mu_{21})^2]$$

$$I_{12} = \mu_{40}\mu_{04} - 4\mu_{31}\mu_{13} + 3\mu_{22}^2$$

$$I_{13} = \mu_{40}\mu_{22}\mu_{04} - 2\mu_{31}\mu_{22}\mu_{13} - \mu_{40}^2\mu_{13} - \mu_{04}\mu_{13}^2 - \mu_{22}^3$$

$$I_{14} = \frac{I_4}{\mu_{00}I_2}$$

$$I_{15} = \frac{I_1^2}{\mu_{00} I_3}$$

$$I_{16} = \frac{I_1 I_3}{I_4}$$

2 circular coefficients:

$$R_{C1} = 2 \cdot \sqrt{\frac{S}{\pi}}$$

$$R_{C2} = \frac{L}{\pi}$$

S – object area,

L – object perimeter

Area to perimeter coefficient:

$W_{SL}$=S/L

Danielsson coefficient

$$R_D = \frac{S^3}{\left(\sum_i l_i\right)}$$

$l_i$ – minimal distance of pixel *i* from object contour

Haralick coefficient:

$$R_H = \sqrt{\frac{\left(\sum_i d_i\right)^2}{n \cdot \sum_i d_i^2 - 1}}$$

$d_i$ – distance of contour pixel *i* from center of gravity of the object

n – number of contour pixels

Blair–Bliss coefficient:

$$R_{BB} = \frac{S}{\sqrt{2\pi \sum_i r_i^2}}$$

$r_i$ distance of object pixel *i* from the center of gravity of the object

Feret coefficient:

$$R_F = \frac{L_h}{L_v}$$

$L_h$ – maximal diameter in horizontal direction

$L_V$ - maximal diameter in vertical direction

A question that arises very naturally is: "which features are most suitable for eye-cup region classification ?". In the next subsection we propose the new method for automatic selection of a subset of good features which is based on genetic algorithms.

## 5. Genetic feature selection algorithm

Genetic algorithms are employed to select features that encode important eye-cup information and improve classification performance. A given feature subset is represented as a binary string (a chromosome) of length n, with a zero or one in position i denoting the absence or presence of feature i in the set (n is the total number of available features). A population of chromosomes is maintained. Each chromosome is evaluated to determine its "fitness", which determines how likely the chromosome is to survive and breed into next generation. New chromosomes are created from old chromosomes by the process of:

1) crossover, where parts or two different parent chromosomes are mixed to create offsping
2) mutation, where the bits of a single parent are randomly perturbed to create a child.

A high level algorithmic description of the proposed feature selection method is given below in the following pseudocode.

```
Procedure Genetic_feat_sel
begin
t:=0                        /* current number of generations */
KrZak =: V_krZak            /* counter */
P^0 initialization          /* P^t current population */
P^0 evaluation
while not (KrZak = 0 or t = max_pok) do
/* max_pok – maximal number of generations */
   begin
      /* T^t O^t temporary populations */
      T^t := reproduction P^t
      O^t := crossover and mutation T^t
      ff [1, ..., popul] =: Evaluation O^t      /* ff table of fitness values for
                                                   chromosomes in a current generation */
      P^(t+1) := O^t
      t:=t+1
      if Max ff[1, ..., popul] > 0.9 x Mean ff[1, ..., popul]    /* popul population size */
          KrZak := KrZak +1
            else
              KrZak := KrZak -1
   end
end
```

Encoding

Each image (the extracted eye-cup region) is represented as a vector of values of the described 30-ty features:

$$(\phi_1,...,\phi_7, I_1,...,I_{16}, R_{c1}, R_{c2}, W_{SL}, R_D, R_H, R_{BB}, R_F)$$

In our encoding scheme, the chromosome is a bit string whose length is determined by the number of features (i.e. 30). Each feature is associated with one bit in the string. If the $i^{th}$ bit is 1 then the $i^{th}$ feature is selected, otherwise, that component is ignored. Each chromosome thus represents a different feature subset.

Initial population

In general, the initial population is generated randomly – each bit in an chromosome is set by flipping a coin. In this way, however, we will end up with a population where each chromosome contains the same number of 1's and 0's on the average. To explore subsets of different numbers of features, the number of 1's for each chromosome is generated randomly. Then, the 1's are randomly scattered in the chromosome.

Fitness evaluation

The goal of feature subset selection is to use fewer features to achieve the same or better performance. Therefore, the fitness evaluation contains two terms; 1) accuracy from the validation data and 2) number of features used.

Only the features in a selected subset is used to train a classifier. The classification experiment makes use of the k-NN classifier [2] (k=5) assuming Euclidean distance between feature vectors. The performance of the classifier is estimated by the k-fold cross-validation method [2] with k=10. The fitness function is given as:

$$\text{Fitness} = 10^4 \times \text{accuracy} + 0.4 \times \text{zeros}$$

where accuracy is the accuracy rate that the given subset of features achieves (i.e. the performance of a classifier measured by k-fold cross-validation method [2] on a given subset of features), zeros is the number of zeros in the chromosome. Overall, higher accuracy implies higher fitness. Fewer features used imply a greater number of zeros, and as a result, the fitness increases.

Reproduction

Reproduction (selection) is based on a random choice according to a fraction with repetitions method [3]. Each chromosome $i$ has its fitness value $f_i$ computed, and is given a probability $p_i$ of being selected proportional to its fitness value:

$$p_i = f_i / \sum_{j \in P^t} f_j \tag{1}$$

For each chromosome $i$ the number of its copies created in the next generation $P^{t+1}$ is an integer part of the expression:

$$p_i = f_i / \sum_{j \in P^t} f_j * popul$$

(*popul* is the number of all chromosomes in a population) being an expected value of the number of copies of a given chromosome in the next generation. Usually, the number of chromosomes created as above is less then *popul.* The missing chromosomes are generated in a series of *popul* Bernoulli's experiments with a probability of success according to (1) until the population reaches *popul* number of chromosomes.

Crossover and mutation

The crossover operation consists of:

1) randomly selecting pairs in the population
2) for each pair of chromosomes performing a crossing operation with a probability $p_k$.

If the crossing is not performed bit strings of chromosomes are not changed. Mutation is a very low probability operator and just flips a specific bit in a chromosome with a probability $p_m$.

Stopping condition

At the beginning a counter KrZak is initialized on a certain value VKrZak, being a parameter of the genetic algorithm. After each new reproduction, its value is incremented only if the maximal value of the fitness function in a population is greater than:

(0.9 * mean value of the fitness function in a population)

Otherwise the value of KrZak is decremented. The algorithm is stopped if one of the following conditions is satisfied:

1) KrZak = 0
2) number of generations = maks_pok

where *maks_pok* is the maximal number of generations and is the parameter of the algorithm.

## 6. Experiments and results

We have performed a number of experiments and comparisons in order to demonstrate the performance of the proposed approach to feature selection for eye-cup region classification. The dataset used contained 100 fundus eye images: 50 of patients with glaucoma which where previously examined by conventional methods (perimetry, slit lamp with Volk lens) and 50 of normal patients. On the acquired from Canon CF-60Uvi fundus camera images, the eye cup region is automatically detected by the method described in [10]. Fig 1 shows the sampled fundus eye image, while Fig 2 the resulting eye-cup region obtained by the method described in [10].

29 geometric features described above are computed on the extracted eye-cup region. Normalization of the dimension $v$ of the feature space was performed by a coefficient:

$$\lambda_v = \frac{1}{\max\limits_{x \in U} x_v - \min\limits_{x \in U} x_v},$$

where U is the set of all vectors representing the extracted eye-cups.

First, k-NN classifier was tested using k-fold cross-validation method (k=10) [2] on three different, manually selected subsets of features giving the mean error rate is 35%.

| features: | error percentage (%) |
|---|---|
| $(\phi_1,....,\phi_7)$ | 35 |
| $(\phi_1,....,\phi_5, I_1,...., I_7)$ | 33 |
| $(\phi_1,\phi_4, I_{11},...., I_{16}, R_{cl}, R_F, R_D, R_H, W_{SW})$ | 37 |

GAs are then used to select the most significant features (i.e. the optimum subset of features) characterizing the shape of eye-cup region. The GA parameters we used in all experiments are as follows:

1) the length of each chromosome: 30,
2) population size popul = 120,
3) max nr of generations: max_pok = 500,
4) cross-over rate $p_{kr}$: = 0.6,
5) mutation rate: $p_m$ = 0.005,
6) $V_{KrZak}$ = 60.

GA converged to the final solution after 150 generations. It should be noted that after only 20 generations all chromosomes are very similar to each other and in the next generations they change very little.

We thus took the best 120 chromosomes the algorithm found during the execution, and we selected the best chromosome – that means the chromosome which was the most frequent among those chromosomes (it makes almost whole population – 99%):

**00100001100101000000100011000 0**

The associated percentage error was 6% (i.e. classifier performance 94%) while the value of the fitness function for the best chromosome was 58575.19.

We are now able to determine what features played a significant role for the classification of eye-cup region and what features are useless, or even disturbing the classifier. So we can see that among 30-ty computed features the following 8 features:

$$(\phi_3, I_1, I_2, I_5, I_7, I_{14}, R_{c2}, W_{SL})$$

are the most significant than the others. This corresponds to the 26% of the information contained in the whole set of 30-ty features.

The results illustrate clearly that the feature subset selected by the GA have reduced the error rate of the classifier significantly: from 35% to 6%.

## 7. Conclusions

We have presented the method of selecting suitable features for eye-cup classification in fundus eye images which is based on genetic algorithms. We showed that some features are more significant than others. By reducing irrelevant information and using only selected features the classifier showed significant performance improvements which is very important for application supporting glaucoma diagnosing.

Our method could provide valuable insights into other pattern classification problems – how to extract and use only the relevant features for a particular pattern classification task, especially when the number of training examples is limited.

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Recenzent: Dr inż. Henryk Palus

Wpłynęło do Redakcji 23 lipca 2003 r.

**Omówienie**

W artykule zaproponowano nową metodę selekcji cech do celów klasyfikacji wnęki naczyniowej na cyfrowych obrazach dna oka, wykorzystującą algorytmy genetyczne. Nowa metoda pozwala uzyskać lepszą sprawność klasyfikacji wnęk naczyniowych na normalne i objęte jaskrą, co ma ogromne znaczenie dla różnorodnych aplikacji wspomagających diagnozowanie jaskry.

Obszar wnęki naczyniowej zostaje automatycznie wyekstrahowany z pozyskanych za pomocą funduskamery Canon CF-60Uvi cyfrowych obrazów dna oka korzystając z opracowanej metody automatycznej segmentacji opisanej w [10]. Na wysegmentowanych obszarach wnęk zostaje obliczonych 29 cech geometrycznych. Następnie, spośród tych cech za pomocą algorytmów genetycznych zostaje wybrany suboptymalny wektor cech, pozwalający zachować tylko cechy zawierające najważniejszą informację o kształcie wnęki naczyniowej.

Wektor cech reprezentowany jest w algorytmie w postaci łańcucha zer i jedynek (tzw. chromosomu). Dla każdego chromosomu obliczana jest wartość funkcji przystosowania, która określa prawdopodobieństwo przeżycia chromosomu i przeniesienia go do następnej generacji. Nowe chromosomy zostają utworzone ze starych poprzez procesy krzyżowania i mutacji. Najlepszy w sensie sprawności klasyfikacji chromosom zostaje wybrany jako efekt wykonania algorytmu genetycznego.

Zaproponowana metoda udowodniła, że poprzez odrzucenie cech nieistotnych, które nie przenoszą ważnej informacji dotyczącej kształtu wnęki naczyniowej, sprawność klasyfikatora może zostać w sposób znaczący podniesiona.

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