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Leukemia recognition with evolutionary vision and knowledge transfer

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Abstract. Leukemia is a health problem that affects the world population causing thousands of kills. Visual analysis is a diagnostic method required for leukemia detection. Evolutionary vision models are useful to understand the solutions found because they make it possible to identify how the image recognition process develops. In this work, we analyze the performance of an evolutionary vision model named brain programming, in which we use a multi-class classifier embedded into the model, to lead the evolutionary process. Furthermore, we use a type of knowledge transfer to improve the recognition task. Results suggest that the knowledge transfer allow an adequate model performance to solve the problem of leukemia recognition. In addition, the structure of the model provides some degree of explainability to the approach, and the structure of the solutions found is amenable to interpretation, which is a desirable aspect of the leukemia recognition problem.

Keywords: Evolutionary vision · Knowledge transfer · Leukemia recognition

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1 Introduction

Artificial Vision models offer excellent alternatives for solving major problems in diverse fields [1,2,3]. Particularly, in the medical area, one of these problems is opportune cancer detection, whose cost of diagnosis is significantly elevated. Acute Leukemias (AL) are a type of cancer that requires greater attention due to their indolent course and short evolution, with an average annual lethality of 3 to 5 cases per 100,000 population and with a marked upward trend [4]. Morphological classification of AL is useful in the early stages of diagnosis, however in at least 20% of cases human errors can be made [5], so the use of Computer Vision techniques is useful to decrease these failures.

In this work, we use an evolutionary symbolic learning model called brain programming (BP) in which we use a multi-class classifier selected in previous work [6] to address the problem of leukemia recognition. Furthermore, we use a type of knowledge transfer to improve the recognition rate in different types of leukemia.

In the next section, the Related Works are described. Section 3 presents the Theoretical Background and the section 4 shows the Methodology. In section 5, Experiments and Results are shown. Conclusions and Future Work are included in section 6.

2 Related Work

The problem of leukemia classification based on visual analysis has been widely used using handcrafted approaches [2,7,8,9]. In these approaches, the features such as color, shape, distribution of cellular components, and the number of cells are taken into account since they are considered in the medical literature for the recognition of various hematological diseases [9]. On the other hand, automatic approaches such as deep learning neural networks have also shown satisfactory results in the leukemia classification problem [11,12,13,14]. However, there are serious limitations when use them this technology due to the scarcity of images for the adequate performance of these models, as well as the lack of transparency in their learning process.

Other approaches that have also demonstrated competitive results in various vision applications are those based on evolutionary computation [15,16], and represent an alternative in the sense of providing a certain level of transparency and interpretability in the learning process. On the other hand, an inherent problem in any image recognition and classification approach is achieving adequate classification rates. In this regard, transfer learning is an alternative to address this problem [17,18,19].

Since the problem of leukemia recognition and classification has been little addressed using evolutionary computational approaches, this paper proposes using an evolutionary vision model in which a form of knowledge transfer is incorporated to handle the problem of classification rate improvement. In addition, aspects of transparency and interpretability of the learning done by the model are presented.

3 Theoretical Background

In this section, we provide some words about the materials we propose using for solving the abovementioned problem. First of all, we breafly describe a model of evolutionary computing named brain programming as a symbolic learning technique. Secondly, we describe the knowledge transfer applied in the BP.

3.1 Symbolic Learning and Brain Programming

Symbolic learning analyzes methods based on high-level symbolic representations of problems, logic, and search. Such high-level representations are characterized as being human-readable [20]. Brain Programming (BP) is an evolutionary computer vision paradigm that look for a set of operations using an optimization process, in which the operations are embedded within a hierarchical process called the Artificial Visual Cortex (AVC). Genetic Programming (GP) is the method used by BP to discover a set of evolutionary Visual Operators (VOs) embedded within the AVC [21]. These VOs are functions for the description of the image classes, which are shown in Table 1.

The problem of image classification from the point of view of data modeling through GP is how the BP performs image recognition. In this way, the BP can be considered as a symbolic learning approach. The learning process of BP is defined since a minimization problem requires finding a solution $P_{min} \in S$ such that $\exists P_{min} \in S : f(P_{min}) \leq f(P)$. Since the direct mapping between the domain and codomain is unknown or not well defined, the model takes several steps. Thus, the classification problem through BP is defined as in equation 1.

$$min\ (y - f(\mathrm{x}, \mathbf{F}, \mathbf{T}, \mathbf{a})) \tag{1}$$

where (y, x) are the label and the image from dataset, respectively; $f(.)$ represent the classifier, **F**, **T**, and **a** refer to function and terminals sets, and the parameters controlling the evolutionary process. The criterion for minimization in terms of a classification problem allows to discover an optimal solution to the problem. In this work, we evaluate the performance of the classifiers SVM, RF, and MLP to learn a mapping $f()$ that associates descriptors d_i created by the AVC to labels y_i in the multi-class classification problem.

Table 1. Functions and Terminals for the visual operators (*VO*).

Color Functions (OV_C)	Color Terminals
$A+B, A-B, A*B, A/B, k+A, k-A, k*A, k/A, A^2$, $thr(A)$, $round(A)$, $\lfloor A \rfloor$, $\lceil A \rceil, \sqrt{A}, log(A), (A)^c, exp(A)$	$I_r, I_g, I_b, I_c, I_m, I_y, I_k,$ $I_h, I_s, I_v, Op_{r-g}(I_{rgb})$
Orientation Functions (OVo)	Orientation Terminals
$A+B, A-B, A*B, A/B, \mid A+B \mid, \mid A-B \mid, inf(A,B), sup(A,B),$ $\sqrt{A}, A^2, log(A), thr(A), round(A), \lfloor A \rfloor, \lceil A \rceil, G_{\sigma=1}(A), G_{\sigma=2}(A), \mid A \mid,$ $D_x(A), D_y(A), k+A, k-A, k*A, k/A$	$I_{color} = I_r, I_g, I_b, I_c, I_m, I_y, I_k, I_h,$ $I_s, I_v\ I_x \in I_{color}, G_{\sigma=1}(I_x), D_x(I_x),$ $D_y(I_x), D_{yy}(I_x), D_{xx}(I_x), D_{xy}(I_x)$
Shape Functions (OV_S)	Shape Terminals
$A+B, A-B, A*B, A/B, k+A, k-A, k*A, k/A, thr(A), \lfloor A \rfloor,$ $round(A), \lceil A \rceil, A \ominus SE_d, A \ominus SE_s, A \ominus SE_s, A \ominus SE_{dm}, Sk(A),$ $A \oplus SE_s, A \oplus SE_s, A \oplus SE_{dm}, Perim(A), A \circledast SE_{dm}, A \circledast SE_d,$ $A \circledast SE_s, T_{hat}(A), B_{hat}(A), A \odot SE_s, A \odot SE_s$	$I_r, I_g, I_b, I_c, I_m, I_y, I_k,$ I_h, I_s, I_v
Mental Maps Functions (OV_{MM})	Mental Maps Terminals
$A+B, A-B, A*B, A/B, \mid A+B \mid, \mid A-B \mid, \sqrt{A}, A^2, log(A), \mid A \mid,$ $D_x(A), D_y(A), k*A, G_{\sigma=1}(A), G_{\sigma=2}(A)$	$MC_d, D_x(MC_d), D_y(MC_d),$ $D_{yy}(MC_d), D_{xx}(MC_d), D_{xy}(MC_d)$

BP consists of two stages. During the first stage, the goal is to discover functions to optimize complex models adjusting operations within them. In the second stage, the parts (programs) are applied to a hierarchical model for the feature extraction. Figure 1 presents the general scheme of the model. The evolutionary process starts with an initial random population in which an individual represents a program. Each individual (symbolic solution) consists of four types of functions, one for each *VO* visual operator. These operators are selected from the set of functions and terminals in Table 1. Each individual is composed of a variable number of syntactic trees whose range is from 4 to 10, where 3 correspond to the visual operators of orientation, color, and shape; and from 1 to 7 correspond to the visual operators of the MM mental maps shown in Figure 1.

Feature extraction is performed by the AVC whose hierarchical structure finds salient points in the image to generate an image descriptor that is subsequently used for classification. The set $I_{color} = \{I_r, I_g, I_b, I_c, I_m, I_y, I_k, I_h, I_s, I_v\}$, is created from multiple color channels whose elements refer to the color components of RGB, HSV, and CMYK color spaces. The decomposition of the image into its relevant features is performed by applying the VOs, the output of which is an image called visual map VM. The next step, called center-surround, consists of the scale-invariant features are extracted and stored in a conspicuity map (CM).

The CM is calculated as the difference between the different scales that are obtained through a pyramid of 9 levels: $P_d^\sigma = \{P_d^{\sigma=0}, P_d^{\sigma=1}, P_d^{\sigma=2}, \dots, P_d^{\sigma=8}\}$. A Gaussian smoothing filter is used on each VM to calculate each pyramid. This produces an image that is half the size of the input map. The process is repeated 8 times to obtain the 9-level pyramid. In the next step, the differences with respect to each pyramid level in P_d^σ are calculated using equation 2 as follows:

$$Q_d^j = P_d^{\sigma=\left\lfloor \frac{j+9}{2} \right\rfloor+1} - P_d^{\sigma=\left\lfloor \frac{j+2}{2} \right\rfloor+1} \tag{2}$$

where $j = 1, 2..6$. Each level of P_d^σ is normalized and scaled to the dimensionality of the VM using polynomial interpolation. Finally, the six levels are combined into a single map with a summation operation, and a CM is obtained for each dimension. Later, a mental map (MM) is built from the CMs using equation 3, where d is the dimensionality and k is the cardinality of the set EVO_{MM}. This MM discriminates unwanted information, highlighting the most salient features of the object. VOs are defined through syntactic trees, and the MMs occupy the fourth position of the tree onward.

$$MM_d = \sum_{i=1}^{k} EVO_{MM_1}(CM_d) \tag{3}$$

The generated program is applied to each image from the MMs obtained and concatenated with the rest of the syntactic trees. Then, the n highest values are used to define the descriptor vector v for the input image in turn. The next step is to train a classifier using the feature vectors obtained from the data set. In this way, the classifier creates a model $f(x)$ that maps a set of descriptor vectors x_i to their corresponding labels y_i, satisfying equation 1. The selection, crossover, and mutation processes are performed as suggested in [21]. Finally, the stopping conditions are (1) the algorithm reaches a predefined number of generations, or (2) the fitness of the algorithm reaches an optimal value; in this case, all images are correctly classified.

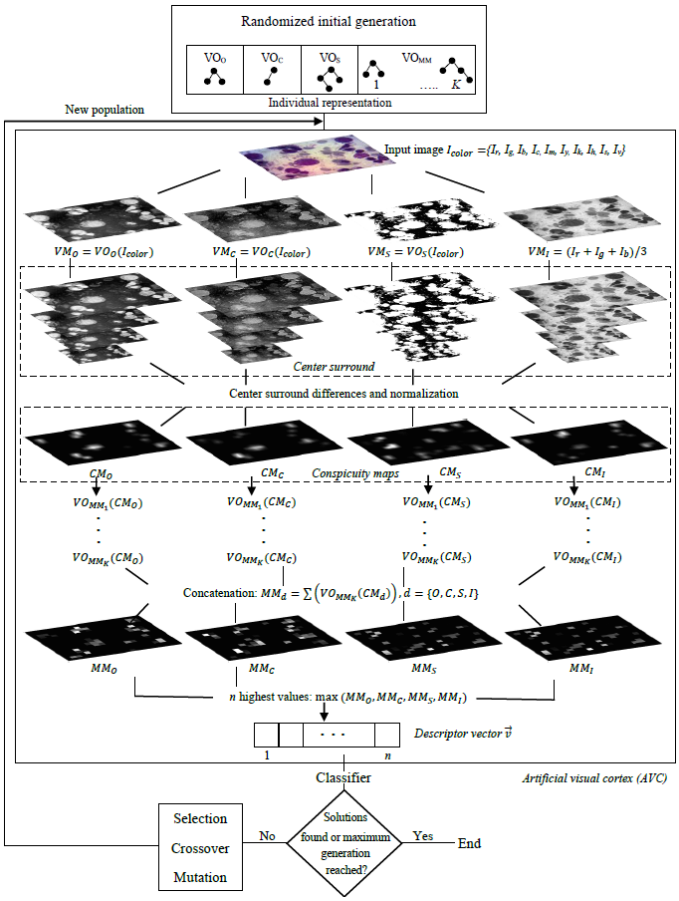


Fig. 1 General flowchart of brain programming.

3.2 Knowledege transfer in the Brain Programming

Since BP is a methodology based on genetic programming, aspects mentioned in the literature regarding the use of transfer learning in GP are taken into account [17,18,19]. Furthermore, considering that the goal of transfer learning is to improve learning in new tasks from previously acquired knowledge to solve similar problems; there are evident advantages of its use, among which we can point out the following:

A. The initial performance of the new task
B. The consumption of time to complete the learning of the new task
C. The final performance achieved, as compared to the final result when transfer learning is not used.

In the same vein, taking up the work of [22] in which aspects of hands-on artificial evolution through BP are presented, in this section we propose to use a percentage of the best solutions (individuals) discovered in previous experiments, as the initial population for a new set of experiments. In this way, the knowledge that represents the previously achieved learning is used for the recognition of a new dataset of images.

4 Methodology

The baseline method used to solve the classification problem is the BP described in section 3.1. Since BP has been commonly used in bi-class problems using a Support Vector Machine (SVM) as a classifier to guide the evolutionary process [21,22], in this work, we use a Multi-Layer Perceptron (MLP) that was selected from previous work [6] to address the problem of multi-class classification.

On the other hand, two groups of experiments are proposed to evaluate the impact of knowledge transfer in the model. In the former, the BP is tested with three different datasets (1) L1, L2, and L3, (2) M3, M4, and M5, (3) M2, M3, M4, and M5.

In the second group of experiments, a percentage of the best solutions (or individuals) derived from the three tested datasets is used as the initial population. To construct the initial population for the new experiments, the following steps are considered:

1. The new population is the same size as the population used in previous experiments, in this case 30 individuals
2. The number of previous experiments (runs) can range from 10 to 30
3. The number of best solutions (individuals) to take from each previous experiment is given by *population size/number of experiments*

In this work three individuals are taken from each previous experiment, since 10 experiments are considered initially. Thus, the knowledge representing the previously achieved learning is used for image recognition of the dataset composed by the classes M2, M3, M4, and M5. Figure 2 shows a scheme of this process.

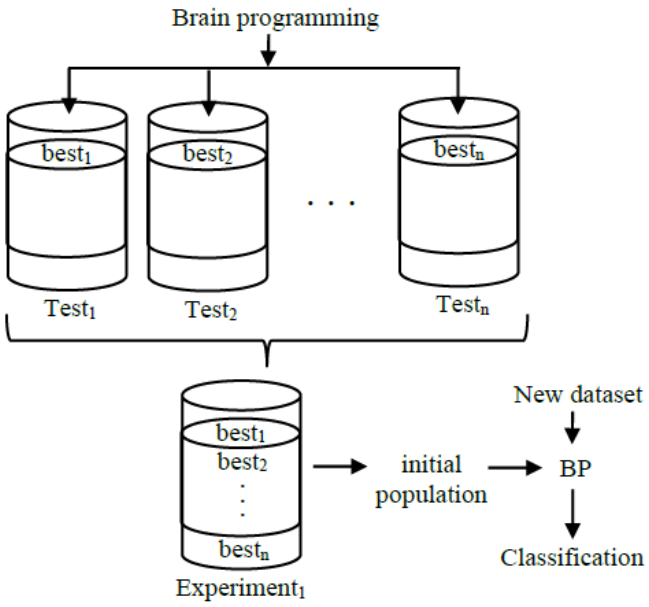


Fig. 2 Scheme of the proposed methodology.

It is to note that in Figure 2, the brain programming implies to performance the process described in Figure 1. Thus, at the beginning the BP is applied for *n* times (tests) with a dataset. Then, the best solution for each test is used to built the initial population to classify either the same or new dataset.

5 Experiments and Results

The experiments were performed on Windows10 Enterprise Edition operating system and MATLAB. Initialization values for the algorithm are: population size 30 individuals, crossover rate 0.4, mutation 0.1, tree

max length 50 levels, selection of roulette wheel, tree creation by ramped half-and-half, and elitism keep the best inividual. The evolutionary loop ends until the classification rate is 100% or the algorithm reaches the maximum number of 30 generations. To evaluate the model using knowledge transfer, two groups of experiments are performed with different datasets.

The datasets used are composed of bone marrow smear images of acute lymphoblastic leukaemia (ALL): L1, L2, and L3, and acute myeloid leukemia (AML): M2, M3, M4, and M5. The images were selected from an own dataset [23], they are in BMP format with resolutions of 1280 × 1024 pixels and resized to 256×320 pixels using bicubic interpolation. For each class, were used sets of 217 images that are shown in Figure 3.

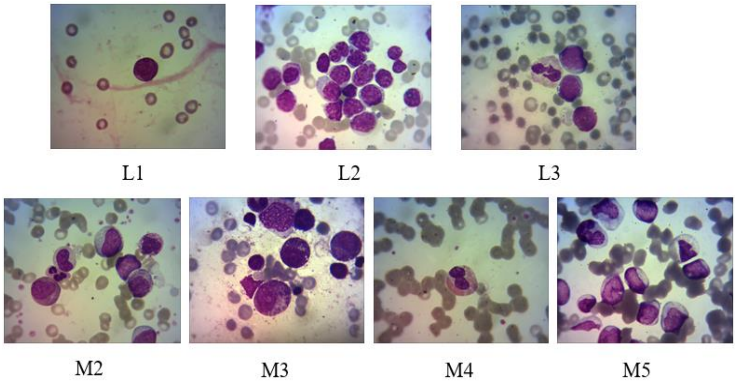


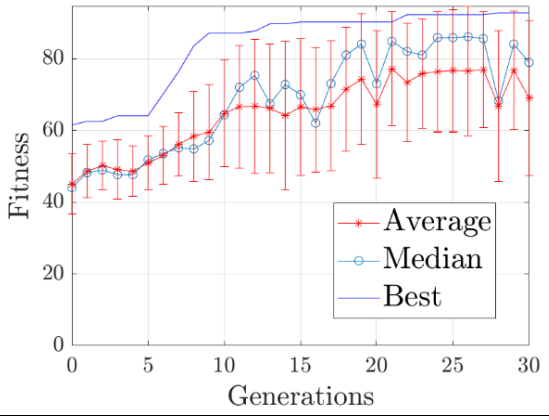
Fig. 3 Types of acute lymphocytic and myeloid leukemia.

For each experiment, the datasets were divided into three parts: a learning set, a validation set, and a testing set as in previous work [24]. To obtain reliable fitness values, each new individual is estimated by the average classification error rate with the classifier using five-fold cross validation. The learning set is randomly divided into five equal parts, five training cases are evaluated with the MLP on 4 out of 5 of these parts, and the result is computed with the remaining validation set. To select the best-performing solution, we test the classification error for every fold on validation set. Hence, we select one solution with the best validation error as the (near-) optimal feature descriptor for the final testing result. Finally, the test set is divided five-fold with the aim of computing the statistical results of the best solution discovered in the previous stage. The classifiers MLP and Random Forest (RF) are used to evaluate best solution. We apply the same process for the learning set, and the overall classification result is calculated as the average of the 5 classifier test accuracies.

5.1 Evolutionary vision for the leukemia recognition

Two groups of experiments were done to show the performance of the evolutionary vision model described in section 3.2. In the first, the objective is to recognize the types of leukemia: (a) L1, L2, and L3, (b) M3, M4, and M5; and (c) M2, M3, M4, and M5. The results of the first experimental group are shown in Table 2, where it is observed that adequate performance is achieved when classifying sets of 3 classes, obtaining a maximum accuracy of 86.67 for classes L1, L2, and L3; and 86.59 for classes M3, M4, and M5. When including one class the accuracy achieved decreases to 79.60 for the dataset of classes M2, M3, M4, and M5. Figure 4 shows the behavior of the best solution from Table 2, in which we can see that all classes were classified with more than 80% of accuracy.

Based on the behavior observed in Table 2, in the second group of experiments, 10% of the best solutions from the experiments of the first experimental group is used as the initial population for the recognition of leukemia types M2, M3, M4, and M5. Since in group 1 experiments 10 runs were made for each dataset, then the three best solutions of each run are chosen to build an initial population of 30 individuals. The population obtained for each dataset is used independently for the recognition of M2, M3, M4, and M5 leukemias. In this way, the knowledge that represents the learning achieved in previous experiments is used for the recognition of these four leukemia classes. Table 3 presents the results of this second group of experiments.



(a)

			Accuracy of L1, L2, L3
15.54	0	1.86	89.31
0.02	15.7	1.68	90.23
1.7	1.7	14	80.46
			86.67

(b)

Fig. 4 Results for the best solution from Table 2. (a) Convergency graph, (b) Confusion matrix.

Table 2. Results of test accuracy for the first group of experiments using the classifiers MLP and RF for evaluating the model. The best results are highlighted in bold. (a) Classes L1, L2, L3, (b) Classes M3, M4, M5 (c) Classes M2, M3, M4, M5.

No. Run	(a)		(b)		(c)	
	MLP	RF	MLP	RF	MLP	RF
1	84.56	82.87	78.89	79.78	72.76	75.55
2	79.47	83.37	76.65	80.19	64.83	69.44
3	**86.67**	86.43	81.10	82.34	72.46	74.53
4	77.15	84.65	59.21	60.29	78.63	**79.60**
5	81.73	83.79	76.17	79.09	73.37	75.81
6	77.48	78.89	81.69	80.98	68.85	72.16
7	82.48	84.02	83.97	84.57	76.01	77.13
8	79.94	81.99	78.49	79.15	73.33	73.64
9	74.38	80.33	74.12	80.53	70.89	73.31
10	78.33	80.45	82.95	**86.59**	75.29	77.90
Average	80.22	82.68	77.33	79.35	72.64	74.91
σ	±3.69	±2.28	±7.09	±7.12	±3.85	±2.96
Outliers	0	0	0	0	0	0
Critical value Z	2.28	2.28	2.28	2.28	2.28	2.28

As can be seen from Table 3, the best solutions from previous experiments for the 4-class classification are useful to improve the recognition accuracy in all cases. Although in one experiment the best solutions from the dataset were used with classes L1, L2, L3, which are different from the 4 classes to be recognized (M2, M3, M4, M5), the performance was higher than when the best solutions were not used as the initial population. It can also be noted that in one case the best solutions of 3 known classes (M3, M4, M5) provided better results, reaching an accuracy of 83.64. However, the best average performance was achieved by using the best solutions of the 4 classes from previous experiments. This suggests that features obtained for classes M3, M4, M5, M5 provide better knowledge for the classification of these classes.

Table 3. Results of test accuracy for classes M2, M3, M4, and M5 using the classifiers MLP and RF for evaluating the model. The best results are highlighted in bold. (a) Evolution from best solutions of classes L1, L2, L3 (b) Evolution from best solutions of classes M3, M4, M5 (c) Evolution from best solutions of classes M2, M3, M4, M5.

No. Run	(a)		(b)		(c)	
	MLP	RF	MLP	RF	MLP	RF
1	70.07	69.53	70.64	73.90	77.48	79.50
2	76.56	81.14	71.42	75.78	80.30	**81.15**
3	74.32	78.18	73.08	77.33	80.64	80.87
4	78.81	**81.44**	72.25	73.59	77.23	79.94
5	71.27	73.76	**83.64**	82.96	73.08	76.72
6	73.97	78.34	75.62	76.54	76.90	79.92
7	76.64	80.60	77.27	79.70	77.67	79.48
8	79.08	81.58	75.07	80.50	76.43	80.22
9	78.19	79.66	71.03	81.29	76.18	80.06
10	76.26	76.94	75.79	81.83	76.27	78.81
Average	75.52	78.12	74.60	78.34	77.22	79.67
σ	±3.07	±3.87	±3.91	±3.36	±2.14	±1.23
Outliers	0	0	0	0	0	1
Critical value Z	2.28	2.28	2.28	2.28	2.28	2.28

6 Conclusions and Future Work

In this work, we have presented an evolutionary vision technique named brain programming to address the problem of acute leukemia type recognition. In the first phase, the BP is applied to two datasets with three classes of leukemia, and one dataset with four classes. Results depict that the classification accuracy decreases slightly as the number of classes increases.

To handle this problem it was proposed a form of knowledge transfer in which the best solutions from previous experiments were used for the recognition of the dataset consisting of four leukemia classes. The results show that in all cases, the use of previously acquired knowledge improves the performance of the model for 4-class recognition.

On the other hand, the hierarchical structure of the model and the use of genetic programming provide a certain degree of explainability because in the evolutionary process it is possible to identify how the salient regions in the image that are useful for the generation of the features are useful for recognition are generated. In addition, the functional structure of the solutions provides the possibility of interpreting these solutions by identifying which visual operators are relevant for image classification.

Future work considers adjustments to the model regarding the use of visual texture operators, as well as the use of different mechanisms for the generation of the descriptors used in the classification process embedded in the model. We also intend to explore the use of parallel programming in the model implementation.

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References

1. Hemaanand, M. et al. (2020). Smart surveillance system using computer vision and internet of things. Journal of Computational and Theoretical Nanoscience 17, 68–73.
2. Benomar, L. et al. (2018). Multi features based approach for white blood cells segmentation and classification in peripheral blood and bone marrow images. International Journal of Biomedical Engineering and Technology 1, 1–19.
3. Tian, H. et al. (2020). Computer vision technology in agricultural automation —a review. Information Processing in Agriculture 7(1) 1–19.
4. Cancer: World Health Organization (2021).
5. Ruiz Argüelles, G.J. and Ruiz Delgado G.J. (2014). Fundamentos de Hematología. 5 edn. Panamericana. ISBN: 9786079356088.
6. Ochoa-Montiel, R., Sossa, H., Olague, G., Sánchez-López, C. (2022). Machine Learning and Symbolic Learning for the Recognition of Leukemia L1, L2 and L3. In: Vergara-Villegas, O.O., Cruz-Sánchez, V.G., Sossa-Azuela, J.H., Carrasco-Ochoa, J.A., Martínez-Trinidad, J.F., Olvera-López, J.A. (eds) Pattern Recognition. MCPR 2022. Lecture Notes in Computer Science, vol 13264. Springer, Cham. https://doi.org/10.1007/978-3-031-07750-0_33.
7. Bodzás, A. et al. (2020). Automated detection of acute lymphoblastic leukemia from microscopic images based on human visual perception. Frontiers in Bioengineering and Biotechnology.
8. Ghadezadeh, M. et al. (2021). Machine learning in detection and classification of leukemia using smear blood images: A systematic review. Scientific Programming, 1–14.
9. Dasariraju Satvik et al. (2020). Detection and Classification of Immature Leukocytes for Diagnosis of Acute Myeloid Leukemia Using Random Forest Algorithm. Bioengineering (Basel, Switzerland). 7. 10.3390/bioengineering7040120.
10. Rodak, B.F. and Carr, J.H. (2016) Clinical Hematology Atlas. W. B. Saunders Co. ISBN: 9780323322508.
11. Huang Furong et al. (2020). AML, ALL, and CML classification and diagnosis based on bone marrow cell morphology combined with convolutional neural network: A STARD compliant diagnosis research. Medicine. 99. e23154. 10.1097/MD.0000000000023154.
12. Schouten Jens et al. (2021). Tens of images can suffice to train neural networks for malignant leukocyte detection. Scientific Reports. 11. 10.1038/s41598-021-86995-5.
13. Vogado L. et al. (2021). Diagnosis of Leukaemia in Blood Slides Based on a Fine-Tuned and Highly Generalisable Deep Learning Model. Sensors. 21(9):2989. https://doi.org/10.3390/s21092989.
14. Bianconi F et al. (2021). Colour and Texture Descriptors for Visual Recognition: A Historical Overview. Journal of Imaging.; 7(11):245. https://doi.org/10.3390/jimaging7110245.
15. I. Jannoud et al. (2021). "Genetic Algorithm for Image Recognition in Smart Systems Applications," 2021 IEEE 1st International Maghreb Meeting of the Conference on Sciences and Techniques of Automatic Control and Computer Engineering MI-STA, pp. 897-901, doi: 10.1109/MI-STA52233.2021.9464406.
16. Schulte RV et al. (2021). Genetic Algorithm for Feature Selection in Lower Limb Pattern Recognition. Front. Robot. AI 8:710806. doi: 10.3389/frobt.2021.710806.
17. M. Iqbal et al. (2017). “Cross-domain reuse of extracted knowledge in genetic programming for image classification,” IEEE Transactions on Evolutionary Computation, vol. PP, pp. 1–1, 01 2017.
18. M. Iqbal et al. (2019). “Genetic programming with transfer learning for texture image classification,” Soft Computing, vol. 23.
19. H. Dinh et al. (2015). “Transfer learning in genetic programming,”, pp. 1145–1151.
20. Haugeland J. (1985). Artificial Intelligence: The Very Idea. Cambridge, Mass: MIT Press.
21. Olague G. et al. (2014). Evolving an artificial visual cortex for object recognition with brain programming. In Schuetze, O., Coello, C.A.C., Tantar, A.A., Tantar, E., Bouvry, P., Moral, P.D., , Legrand, P., eds.: EVOLVE - A Bridge between Probability, Set Oriented Numerics, and Evolutionary Computation III. Volume 500 of Studies in Computational Intelligence. Springer Heidelberg 97–119.
22. Olague G. and M. Chan-Ley (2020). Hands-on Artificial Evolution Through Brain Programming, pp. 227–253.
23. Ochoa-Montiel Rocio et al. (2021). Dataset leukemia. Copyright 03-2021-112413373300-01.
24. Ochoa-Montiel Rocio et al. (2021). Symbolic learning using brain programming for the recognition of leukaemia images. Computación y Sistemas 25(4).