

A Geomatics and Genetic Programming Approach for the Segmentation of Medical MR Images

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Abstract: - Medical image segmentation is currently performed by qualified medical personnel who, however, often must deal with large amounts of work, often in emergencies. Therefore, there is a need for automatic and reliable methods to analyze medical images, particularly magnetic resonance imaging, with high precision. There are several methods in the literature that are mainly based on the use of 3D atlases or convolutional neural networks, subject to several disadvantages. The present research work focuses on the development of an alternative and innovative method for the segmentation of medical images using a bilateral filter, a genetic programming algorithm developed ad hoc, the CLAHE algorithm, and the Watershed segmentation algorithm, typically used for geo-topographic images. The results obtained by the following methodology allow us to conclude that the proposed approach provides comparable results with a smaller dataset of images compared to the most common neural networks used in the field. The integration of the genetic algorithm represents a highly innovative solution, improving the local quality of the contrast and reducing the noise of the images, and allowing for optimizing the Watershed segmentation.

Key-Words: - Segmentation, Medical Imaging, Watershed, CLAHE, Genetic Programming, Magnetic Resonance

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1 Introduction

Ultrasound imaging is a promising approach in medicine because it is a non-intrusive technique with the ability to obtain important data from a large number of patients. Despite its potential, images generated using this technique are still severely corrupted with high levels of noise, especially speckle, which hinders their further processing. There is a growing interest in machine learning in the field of both medical image denoising and segmentation, mainly due to the fact that it allows for better generalize to new datasets compared to existing techniques. Despite neural networks being the most important algorithm being employed in this field; their widespread adoption is limited by their need for large amounts of data being used in the training phase. Alternative techniques like algorithms and Cellular Automata have then been studied in

more detail, not suffering from this limitation. For example, in [1], a genetic algorithm has been employed to remove speckle noise from Optical Coherence Tomography (OCT) images, with the main purpose of optimizing the wavelet transform coefficients. These are of fundamental importance in the definition of wavelets, the latter being a decomposition of a given signal, of which the Fourier Transform can be interpreted as a particular case. The importance of evolutionary algorithms is also emphasized in a critical review of bio-inspired techniques being used in medical image processing [2].

Cellular automata are another interesting approach being employed in the field of image denoising, which also does not have the need for a large dataset for training, although there are few studies regarding this topic. In [3], a cellular

automata approach for despeckling of medical images is introduced. It operates on the basis of a threshold value calculated on a Moore neighborhood (i.e., a 3X3 kernel centered around a central pixel): if the threshold is higher than a given value, the single individual calculates the median of the pixels; otherwise, it calculates their median.

Related to the use of cellular automata with small datasets, there are also several articles in which an emphasis is put on their conjunction with neural networks in order to improve performance in this particular case: in [4], good performance of U-Nets with small training data is noticed. The article also emphasizes how these nets' performance can be affected when the distribution of data changes. Particularly impressive is the fact that this integration can allow a three-order reduction in network size. Integration is made possible by the fact that the neural network generates rules automatically, instead of the common approach in which Cellular automata use a fixed ruleset. In [5], there is a further application of these techniques in the field of medical image denoising. Despite cellular automata being a valid approach, albeit still an unexplored approach to image denoising and more generally to other fields, they can have drawbacks such as requiring a longer time for inference. Genetic algorithms and Genetic Programming (GP) can be an alternative to this approach, despite requiring more computationally intensive training, and many experimentations to find the optimal evolutionary parameters (i.e, crossover, mutation, population size, number of generations, and in the specific case of genetic programming, also functions being used by the algorithm). Besides [6], there have been other studies employing genetic programming to denoise medical images. In [7] a GP approach has been employed to remove speckle noise from ultrasound: one thing to notice is how GP was in this case, applied to filter noise directly, by using several statistics as input to the GP tree and common mathematical functions as primitives. Many of the statistics used in this study are taken directly from [7], even though the GP is applied solely to detect noisy pixels, not to filter them, a concept referred to as the 'switching scheme' in literature. This approach is motivated by the fact that directly applying a filter to the image may lead to the corruption of clean pixels [8]. In [9], GP is applied to MRI images, in the particular case of removing Rician Noise.

Many of the same techniques can be applied to medical image segmentation, with the addition of other techniques, like the watershed transform, directly borrowed from the field of geomatics. In [10], Genetic Programming is used in the form of Cartesian Genetic Programming, i.e., a

representation in which different functions are represented as belonging to a Cartesian grid, with assigned coordinates, and with different applications to image processing in general. The motivation for the use of this paradigm is here as well explained as the feasibility of using a limited dataset, and a clear interpretability of the models: regarding the latter, an example is provided in the fact that the algorithm is able to find the correct sequence of operators (for example Gaussian Blur, difference between images, and Median Blur) to get a more precise segmentation. As in other GP studies, particular emphasis is put on the choice of the most appropriate functions and parameters. The study is also open to the possibility regarding integration of data coming from different sources (one mentioned case of which is demographic data), not only from images, by the use of the so-called Mixed-Type Cartesian Genetic Programming (CGP) approach. Another application of GP to medical image segmentations is exposed in [11], with regard to blood vessels and brain Magnetic Resonance Imaging (MRI) images using simple functions (arithmetic functions, average filters). It is shown to outperform neural networks for the same task. GP is again used in [12] with applications in the medical field as well: it is of particular interest the evolution of programs which are relatively small in size for this kind of problem, an important issue in GP. It's also important to notice that these algorithms are not only an alternative to neural networks but can help in the design of better neural network architectures. In [13], Cartesian Genetic Programming is being employed to develop CNNs that require less training time and less computational resources for segmentation tasks. In our approach, we further use Contrast Limited Adaptive Histogram Equalization (CLAHE) to improve image segmentation, an approach already used in other studies [14], [15]. Similar results are found with another histogram equalization algorithm. In [16], an SNN is trained to recognize patterns of noise that hinder the Watershed segmentation process, with the latter being applied after denoising. The present work introduces several new contributions beyond that study: (i) a Genetic Programming-based selective denoising algorithm trained on a single image, capable of identifying and filtering only noisy pixels; (ii) integration of Contrast-Limited Adaptive Histogram Equalization (CLAHE) to improve segmentation precision and mitigate illumination variability; (iii) stabilization of the evolutionary process by enforcing determinism in BLAS backends; (iv) strongly typed primitives and anti-bloat strategies to ensure semantic consistency and structural diversity; and (v) a fitness formulation

explicitly balancing PSNR/MAE with runtime. These advances distinguish the current manuscript from the prior conference paper and extend its scope toward reproducible, interpretable, and resource-efficient segmentation. In [17], a switching filter is proposed for impulse noise, capable of filtering noisy pixels only.

In this context, we present a pipeline in which images are first filtered, focusing only on pixels with the most noise, followed by CLAHE histogram equalization and Watershed segmentation. Through genetic programming, the most appropriate sequence of filters for accurate segmentation of a given medical image is determined. The main differences with our study, however, lie in the fact that the proposed approach has been proven to use a single image for training, and in the fact that only selected pixels are being filtered.

2 Methodology

The main objectives achieved from this work are two:

- 1) Denoising of medical images obtained from ultrasound using a genetic programming algorithm.
- 2) Segmentation of the same images using an algorithm belonging to geomatics, the Watershed.

The genetic programming filter was chosen because it uses algorithms that are able to filter only noisy pixels and that can be trained using training sets of limited size. The Watershed was instead used because it has greater accuracy and a low execution time. The implementation was carried out using Python and the DEAP library, using images from the CAMUS dataset.

Figure 1 shows the proposed methodology.

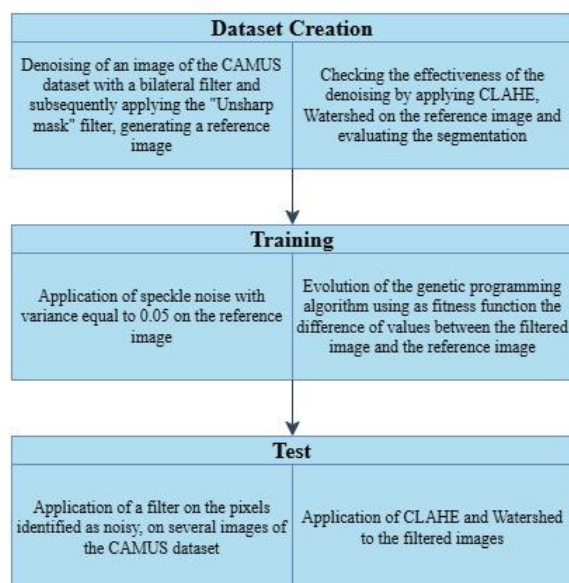


Fig. 1. Proposed methodology. Source: created by the authors.

The procedure used can therefore be summarized as follows.

Training image creation:

- Application of the bilateral filter on an image of the dataset → Application of the “Unsharp-masking” filter to the image filtered with the bilateral filter → Evaluation of the bilateral filter performance by first applying a histogram equalization algorithm and then the Watershed.
- Generation of speckle noise on the image obtained by the bilateral filter and the “unsharp-masking” filtering.

Training:

- Training of the genetic programming algorithm on the reference image, consisting of the application of the bilateral filter, unsharp masking, and speckle noise generation. The best individual of the evolution is the one whose denoising guarantees the highest (Peak Signal-to-Noise Ratio) PSNR/MAE ratio calculated between the image corrupted by speckle noise and the original image (image obtained by applying the bilateral filter and unsharp masking)

Test:

- Application of the filter obtained from the evolution of the genetic programming algorithm on the other images of the CAMUS dataset → Application of the CLAHE algorithm on the filtered image → Application of the Watershed.

The first phase of the methodology consists of the creation of the dataset. The training set creation process involves the creation of an image subjected to a series of algorithms, which will subsequently be used for the purposes of comparison with an original image (therefore not filtered), in the subsequent training phase. Considering that the images of the dataset are in .nii format, these are imported using the nibabel library. In a similar manner to what was done in [16], a stretch is performed on the central part of the image: the same motivation provided in the article just cited is reported, i.e., the fact that the stretching of the image in the central part allows for emphasizing this portion more.

The resulting image was converted into “unsigned 8-bit integer format, i.e., 8-bit integers, so that it could be used by OpenCV. We chose the bilateral filter, as the watershed segmentation performed provided more accurate results than the “Non local means denoising” filter.

The bilateral filter [18] represents a filter with the characteristic of preserving the edges and, at the same time, reducing the noise. It uses two kernels in particular: the range kernel and the spatial kernel. An example of such kernels can be the Gaussian function. They can be indicated respectively as f_r and g_s , obtaining interval and space weights (respectively space weight and range weight), which can be defined as (1), (2):

$$f_r(|I(x_i) - I(x)|), \quad (1)$$

$$g_s(|x_i - x|), \quad (2)$$

where x represents the pixel to be filtered, and x_i a pixel included in a window of the latter. For each pixel, a new value is obtained which is given by the sum of the pixel value by its weights in a window indicated as Ω , that is (3):

$$\sum_{x_i \in \Omega} I(x_i) f_r(|I(x_i) - I(x)|) g_s(|x_i - x|) \quad (3)$$

The obtained value is normalized, using as the normalization term the product of the kernel values for each pixel belonging to a window Ω . This can then be defined as (4):

$$W_p = \sum_{x_i \in \Omega} f_r(|I(x_i) - I(x)|) g_s(|x_i - x|) \quad (4)$$

The final value of the pixel will therefore be equal to the ratio between the two terms just mentioned (5).

$$I(x) = \frac{\sum_{x_i \in \Omega} I(x_i) f_r(|I(x_i) - I(x)|) g_s(|x_i - x|)}{\sum_{x_i \in \Omega} f_r(|I(x_i) - I(x)|) g_s(|x_i - x|)} \quad (5)$$

Despite its effectiveness, the bilateral filter is generally quite slow in its implementation, which can be a disadvantage in the case of applications that require rapid image processing.

To the filtered image (which will be used as a training image), a histogram equalization algorithm, and then the Watershed algorithm, were applied in order to evaluate the performance of the filter used.

The image obtained with the bilateral filter was subsequently applied to the “unsharp masking” filter [19], [20] to increase the number of details visible in the image, subtracting from it an image to which the Laplacian filter was applied. A speckle noise was created on the resulting image, using the “scikit-learn” library.

In the second phase, the genetic programming code was later implemented. In this work, a genetic programming algorithm for speckle noise removal from degraded images has been designed and

implemented by building and evolving individuals representing complex mathematical functions applied locally on the image pixels. Each individual consists of a syntactic tree containing mathematical primitives and logical functions acting on arrays representing local image properties, such as variance, standard deviation or median on central windows of size 3x3 or 5x5, combined with values from the original image and pre-filtered versions of it. The individual is transformed into an executable function that is evaluated pixel by pixel on the noisy image to generate a binary mask: pixels for which the function returns a value greater than or equal to a threshold are labelled as noisy and are replaced with a filtered value (e.g. via smoothing), while the others are kept unchanged (6).

$$mask(x) = \begin{cases} 1 & \text{se } f(x) \geq threshold \\ 0 & \text{se } f(x) < threshold \end{cases} \quad (6)$$

For each individual, the quality of the resulting filtered image is evaluated with respect to a noise-free reference image through the metrics Peak Signal-to-Noise Ratio (PSNR), Structural Similarity Index Measure (SSIM) and Mean Absolute Error (MAE), while the fitness function is defined as the ratio between PSNR and MAE, possibly penalized by the execution time (7).

$$Fitness = \frac{PSNR}{MAE} \times 1/T \quad (7)$$

As known, PSNR is a metric used to evaluate the quality of image reconstruction by comparing the original image with a modified version; SSIM is a more complex metric that aims to measure the perceived similarity between two images and generally takes into account the characteristics of structure, brightness and contrast; finally, MAE represents how much on average the predictions or modified images differ from the real ones.

During the development phase, a non-deterministic behaviour of the algorithm was observed, i.e. multiple executions on the same input produced slightly different results, making the metrics non-reproducible and compromising the stability of the genetic selection. This behaviour was initially attributed to error propagation in floating point calculations, since operations on real numbers are subject to rounding errors and do not respect the associative property, but even the use of arbitrary precision arithmetic via the decimal library did not solve the problem. The investigation subsequently identified the multi-threaded behaviour of the underlying numerical libraries (such as Basic Linear

Algebra Subprograms (BLAS) or OpenBLAS used by Numpy) as the real cause of the problem, since the concurrent execution of threads introduces variability in the order of elementary operations, influencing the final result. To ensure the determinism of the execution, the constraint of using only one thread for the BLAS backend was imposed, thus avoiding race conditions and uncontrollable execution orders. The best individuals were saved via binary serialization using the Pickle library to be reused later without having to repeat the training phase. The entire evolutionary process was implemented using the Distributed Evolutionary Algorithms in Python (DEAP) library, with the construction of a primitive set strongly typed in which the primitives are rigorously typed and can only act on certain types of input, in order to ensure the semantic consistency of the generated trees. Primitives include protected arithmetic operations, trigonometric, logarithmic, sigmoidal functions, and a logical "decide" function that returns a binary array based on a point-to-point comparison between two arrays. The evolutionary tree is constructed so that the root node is always the decision function, intermediate nodes are unary or binary functions operating on arrays, and terminals are constant values or functions that compute local properties of the image. To avoid bloating, the initial generation of individuals was performed using the GenGrow method [21], with variable depth, which allows for greater structural diversity than the GenFull method. Finally, evolution was driven by an evaluation function that takes into account both the quality of the reconstructed image and computational efficiency, so as to favor individuals that produce high-quality results in short times, avoiding unnecessarily complex or computationally expensive solutions.

As for the average filter, it is a linear filter used for noise removal. Its main advantage is that it is relatively fast (computational complexity equal to $O(n)$, where n is the number of pixels in an image), however it is particularly sensitive to noise, since a pixel with a value very different from the others within a window can cause the average to assume a value that is also very different from the original one, resulting in pixel values that can be very different from those expected. It also has the disadvantage of blurring the edges, characteristics that generally make it more appropriate to use other filters, such as those already mentioned in this paragraph. During the experiments, it was particularly effective, both in terms of PSNR and SSIM, with PSNR values even higher than 60 dB. The median filter is instead based on the use of a median, calculated on a 3X3 or 5X5 window. Compared to the mean filter, the sorting

algorithm used to calculate the median filter places pixels with outliers from the mean in the first or last position in the array used for this purpose.

This property makes the median filter quite resistant to single noisy pixels. Another important advantage of this algorithm is the possibility of retaining edges, compared to other filters: it should be noted, however, that this property is not verified in the case where there is a large amount of noise, such as to require a larger filter window. During the tests carried out, it was found that it was not as effective as the other filters, in particular, the average filter: a possible reason could be the fact that the median filter requires more iterations in the case of strong noise, such as that studied in these images. In order to avoid any race condition phenomena (which could occur in the case where the filter values are calculated on a different image at each iteration, instead of being calculated starting from a single image), it was decided to limit the tests to a single iteration.

In the last phase, the bilateral filter, the adaptive histogram equalization algorithm (CLAHE), and the Watershed were applied.

The CLAHE algorithm [22], [23], [24], [25], as already mentioned, is based on the histogram equalization performed in an adaptive way. It starts with the division of the images into smaller blocks, indicated as "tiles", in the literature, for each of which the histogram is calculated. The values exceeding a certain threshold are "redistributed" in the lower part. A cumulative distribution function is then used to normalize the values of the obtained image, the blocks are then joined together.

The phases of the algorithm are the following:

- Division of the image into smaller blocks (indicated as "tiles" in the literature).
- Following the calculation of the histogram, the values exceeding a certain threshold (generally indicated as "clip limit") are redistributed in the lower part.
- Normalization of the values using a cumulative distribution function.
- Union of the different blocks.

During the various experiments (both in the training image creation phase and in the validation phase of the evolutionary algorithm trained for image filtering purposes) it was observed that the application of a histogram equalization algorithm allowed the generation of better results in terms of segmentation. A better precision of the Watershed algorithm is also noted, which indicates the need to insert an

equalization algorithm of this type, or more generally, a contrast enhancement algorithm.

Watershed is a technique that has its origins in geomatics [26], [27], [28], [29], [30], [31] and is based on the flooding of certain areas, that is, the flooding of these areas is simulated through the application of different colors, which will then be segmented into areas of interest. Its main advantage consists of having a high execution speed, which makes it ideal for use in real-time applications. However, it can present the disadvantage of excessive segmentation, defined in literature as over-segmentation [32], [33].

The segmentation process starts with the definition of a sure background by applying morphological operators such as aperture and dilation. At this point, a sure foreground is determined, which can be obtained by threshold-based algorithms, such as Otsu's algorithm. Alternatively, there are other techniques, such as the gradient-based algorithm, that can be applied to identify the foreground.

The foreground image is then refined by morphological operations, such as erosion, or by the distance transform algorithm. In the specific work, the distance transform algorithm was chosen; however, since the objects to be segmented (in this case, the different areas of the heart) do not overlap, it was preferable to apply the erosion algorithm to obtain the final foreground image. Subsequently, a decision threshold is applied to define the exact contours of the area of interest. The sure background is obtained through the dilation algorithm, which expands the initially defined background area, thus ensuring a clear separation between the foreground and the background.

As for the unknown area, which does not belong to either the foreground or the background, it is used as a marker for the watershed algorithm. The unknown area is essential for the subsequent segmentation phase.

Subsequently, the flooding process is applied, which represents the operation of filling the image starting from the markers, which correspond to the local minimum points. In practice, flooding fills the areas surrounding each marker with the same value, simulating a "flooding" process similar to that which occurs in a watershed. The algorithm uses a FIFO (First In-First Out) priority queue, which manages pixels based on certain characteristics. Pixels are then inserted and removed from the queue in order of priority, and the surrounding area is filled as the marker values expand.

This process ensures precise segmentation of areas of interest, effectively separating regions and reducing the risk of over-segmentation.

3 Results

As mentioned, the first phase of the proposed methodology involved the creation of the dataset by applying the bilateral filter. The parameters used for the bilateral filter, the CLAHE filter, and GP algorithm (Table 1):

Table 1. Pipeline parameters. Source: created by the authors.

Filter/ Algorithm	Parameter	Value	Description
Bilateral Filter	Spatial Sigma (σ)	2.0	Controls the size of the neighborhood used for filtering.
	Range Sigma (σ)	50.0	Controls the intensity difference between pixels for filtering.
	Diameter of the Pixel Window	5	Size of the local neighborhood (in pixels) used for the filter operation.
CLAHE (Contrast-Limited Adaptive Histogram Equalization)	Tile Size	8x8	Size of the tiles in which local histograms are calculated.
	Clip Limit	2.0	The contrast limit for the histogram equalization step.
	MaxSlope	3.0	Determines the maximum slope in the adaptive

			histogram equalization.
Genetic Programming (GP)	Population Size	200	Number of individuals in the initial population.
	Generations	50	Number of generations for the evolutionary process.
	Crossover Rate	0.8	Probability of applying crossover between individuals.
	Mutation Rate	0.1	Probability of mutation during each generation.
	Tournament Selection Size	3	The size of the tournament for selecting parents in the evolutionary process.
	Fitness Function	PSNR/MAE Ratio	Evaluates the fitness of individuals based on PSNR and MAE ratios.
	Arithmetic Operators	+, -, *, /, %, sin, cos, exp, log	The set of arithmetic operators available for individuals to build their functions.
	Local Properties	Variance, Standard Deviation, Median	Features computed over local image windows are used for filtering.

Evolutionary Method	Generational, Tournament Selection	The type of genetic programming method used for evolving the population.
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The algorithm evolved to generate a binary mask, where each pixel is assigned a value of 1 if it is considered noisy, and 0 if it is uncorrupted. If the mask value is 1, a Gaussian filter of size 5x5 is applied to that pixel; if the mask value is 0, the pixel remains unchanged. This approach enables selective denoising, focusing only on noisy pixels while preserving the original values of non-noisy ones.

To evaluate the effectiveness of the algorithm, we use the PSNR/MAE ratio as the fitness measure, which has been commonly employed in similar studies [1]. Additionally, we explored an alternative evaluation method based on segmentation performance, comparing the segmented images to a reference image. For this comparison, standard metrics such as the adapted Rand error or Dice score are used to quantify the similarity between the predicted segmentation and the reference segmentation.

Figure 2 illustrates the evolution of the genetic programming algorithm over 30 generations, showing the improvement in the fitness measure and segmentation performance as the algorithm iterates. The gradual refinement of the filtering process indicates the algorithm's ability to adapt and optimize for better noise removal and segmentation quality.

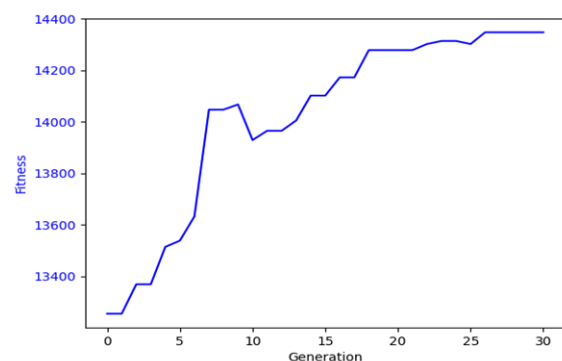


Fig. 2. Evolution of the genetic programming algorithm for 30 generations. Source: created by the authors. Source: created by the authors.

For testing the algorithm, we stretch the central part of the test images, as in the training part of our study, then we run the best evolved individual obtained

from the genetic programming algorithm, and conclude by applying Watershed segmentation. We also confronted the segmentation by using CLAHE after denoising and without CLAHE. All images are taken from the CAMUS dataset [34] (Figure 3). We also plan to extend this algorithm to other medical datasets, as well, the latter containing a limited amount of data. The results are as follows in the following images.

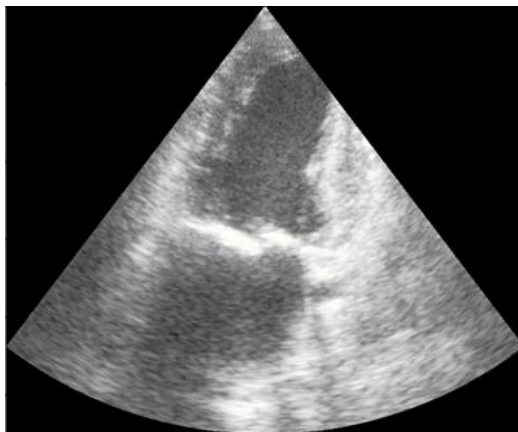


Fig. 3. Raw image from the CAMUS dataset. Source: created by the authors.

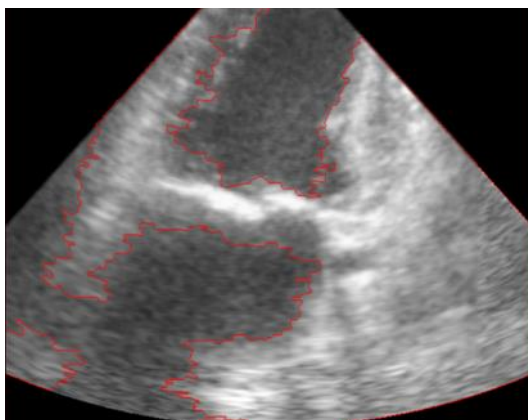


Fig. 4. Segmentation was performed on the image, with denoising applied to each pixel. Source: created by the authors.

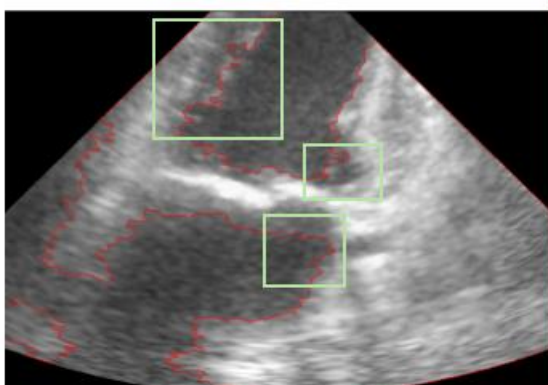


Fig. 5. Segmentation is performed by applying the genetic programming algorithm on selected pixels. Source: created by the authors.

In Figure 5, with green rectangles, closer alignments of Watershed lines are highlighted compared to those of the previous figure (Figure 4).

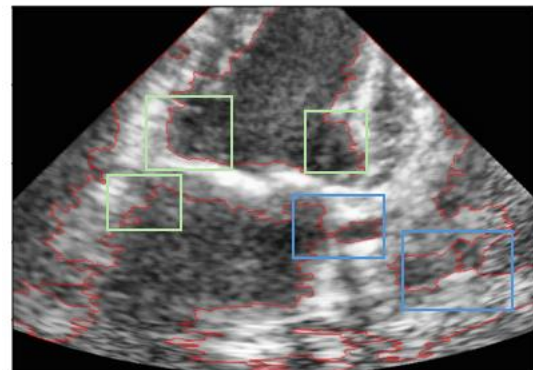


Fig. 6. Watershed segmentation is applied after denoising on pixels identified as noisy and CLAHE histogram equalisation. Source: created by the authors.

Again, in Figure 6, green rectangles show closer alignment to the edges, while blue rectangles show oversegmentation areas.

From the images studied, it appears that often it is the differences in illumination that are relevant in the quality of the segmentation, and not only the noise itself. It follows that a possible improvement of the approach used must necessarily consist of an algorithm that also considers these differences. Addressing the problem of differences in illumination only using CLAHE does not provide results suitable for use in a real case, although it has allowed for obtaining a much more accurate segmentation in many images.

To assess the reliability of the proposed methodology, the average results from the comparisons are presented in the following Table 2. These results evaluate performance by varying the number of randomly sampled pixels and the classifiers used. The performance of the proposed methodology and the goodness of the segmentation was compared with the segmentation performed by a commonly used segmentation software in this field called ITK-SNAP, a software that is used for manual and semi-automatic segmentation of medical images, using the Intersection over Union metric; From the latter metric, it was obtained a value of 0.94, demonstrating a very good correspondence in some areas compared to others of the segmentation method used in this work. In our fitness formulation, runtime is penalized through the multiplicative factor $1/T$,

where T denotes execution time. To assess the sensitivity of the evolutionary process to this term, we performed ablation experiments varying the exponent α in $1/T^\alpha$. Results show that lower values of α (≤ 0.5) favor individuals with higher PSNR/MAE ratios but longer inference times, while higher values (≥ 1) bias the population toward faster yet less accurate filters, occasionally increasing over-segmentation in Watershed segmentation. The absence of the time penalty yields the best reconstruction quality but leads to bloated individuals and impractical runtimes. These findings confirm that the time penalty factor plays a crucial role in balancing image quality and computational efficiency and justify the choice of in the final implementation.

In parallel, the performance of the proposed methodology is compared with other commonly used segmentation techniques applied to different regions of the images (Table 2), still highlighting different performances in different areas and image conditions. We highlighted that the comparison results were obtained by running the methods on the same dataset with the same experimental setup [35], [36], [37], [38].

Table 2. Comparison of the proposed methods with other common segmentation techniques. Source: created by the authors.

Method	Accuracy	Precision	Recall
Thresholding	0.85	0.80	0.75
Convolutional Neural Network (CNN)	0.95	0.92	0.90
Self-Normalising Neural Network (SNN)	0.93	0.91	0.88
Genetic Programming	0.90	0.91	0.92

4 Conclusion

In this work, a genetic programming algorithm was applied only on some pixels considered to be affected by speckle noise, training the algorithm on a single image. The images of the test set were subsequently processed with a histogram equalization algorithm (CLAHE). Although the evolution was not very marked (about 10%), an improvement in segmentation was noted in some areas and a higher level of segmentation (over-segmentation) in others: this last problem is, however, encountered only when using CLAHE. It was found that denoising performed

with this algorithm allows for better segmentation as it results in less jagged lines; however, a big difference in terms of areas was not noted, if compared to the other methods. One point on which this algorithm can be improved, in order to obtain optimal conditions of brightness and contrast, consists of the inclusion of functions such as CLAHE itself, gamma correction within the evolution.

It has also been noted that, even considering the implementation in Python language and not in C/C++, the algorithm has quite high calculation times, due to the calculation of the terminal functions (Median Absolute Deviation (MAD), absolute deviation of the quantile, etc.). However, this can be improved by using terminals that require shorter calculation times. For example, the median can be calculated starting from the values of the histogram, obtaining a linear calculation time ($O(1)$). The same considerations apply to the Gaussian filter. Another possibility that has been evaluated was to study the evolution by replacing the functions Quantile absolute deviation, and the functions MAD5 and Absolute deviation median 5, characterized by a computational complexity higher than the others, with functions obtainable in linear time.

Our approach aligns with the paradigm of single-image or few-shot learning in medical imaging, as the Genetic Programming filter is trained on a single reference image and then generalized to other cases. However, it extends beyond existing methods in several ways. First, the evolved decision trees are interpretable, combining local statistics (variance, median, standard deviation) with protected arithmetic operations, unlike black-box neural few-shot models. Second, the pipeline explicitly optimizes denoising for downstream Watershed segmentation, ensuring that improvements in image quality translate into more accurate anatomical delineation. Third, selective denoising reduces the risk of corrupting clean pixels, a limitation often encountered in global filtering or CNN-based denoisers trained with limited data. Finally, the inclusion of runtime in the fitness function operationalizes efficiency, making the method suitable for deployment in resource-constrained environments. These characteristics position our work as a complementary and interpretable alternative to meta-learning and few-shot neural approaches.

The proposed methodology therefore, represents an unconventional technique in the field of medical segmentation. The advantages that emerged from this work compared to current approaches are a better management of small and limited datasets, a reduction in the risk of overfitting, greater generalizability and a lower computational cost. The

results, in fact, show that this method is absolutely comparable with more established methods, distinguishing itself by the fact that it combines traditional techniques with evolutionary methods to create a lighter, more interpretable and effective pipeline even with small datasets.

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