Evolving Breast Tissue Segmentation Models Using Genetic Programming and Fuzzy Logic

Technical Report No. CCC-22-007

by

Mc. Ingrid Aurora Valencia Hernández

Doctoral Advisors:

Dr. Carlos Alberto Reyes García, INAOE

Dra. Alicia Morales Reyes, INAOE

Instituto Nacional de Astrofísica, Óptica y Electrónica
©Coordinación de Ciencias Computacionales

July, 2022
Santa María de Tonantzintla, Puebla, CP 72840

Contents

1 Introduction

Image analysis is an area in computer vision to extract information found within digital images, an important operation in this area is image segmentation [1, 2]. Segmentation seeks to define boundaries within an image in order to identify, differentiate and classif objects as the human eye would [3]. Segmenting an image correctly helps to solve problems in medical, industrial, biometric, livestock, earth observation satellites, agriculture, and many other applications [4]. For these reasons segmentation is an extremely important task for solving image analysis problems. Several algorithmic techniques have been developed to improve image segmentation. However, not all segmentation methods work for all types of images. One of the problems in image segmentation is that the contrast between regions is sometimes not good. That is, they do not show a very clear border where the change of region can be clearly identified when going from one region to another has a smooth and gradual change [5] in addition to presenting combined pixels, which is a term used in image processing to define areas with more than one homogeneous coverage, in other words, that the pixels belong to more than one region in the image. This occurs in medical areas such as mammographic imaging, where differentiating the borders of the different tissues within the breast is difficult. It is worth mentioning that mammography images are used to classify breast density to study the relationship between breast density and the development of breast diseases such as breast cancer [6].

Many works focus on the automatic segmentation of mammography images, as is the work of D. Stylianos [7], who segments mammograms with Grayscale transformation, Image whitening, thresholding, and other operations for classification breast density, obtaining 92.17% accuracy. However, although he obtained a high ranking, not all mammography segmentation is automatic but requires an expert to search for parameters for operations manually. Therefore, performing a segmentation task with this method is extremely laborious. Another disadvantage of these methods is that it is not known if the operations used for segmentation are optimal and they do not deal with the problem of pixel combination (combination of fibroglandular tissue and fat), so a lot of information may be lost time to segment to image.

This work plans to find a segmentation method that optimally segments mammography images with the help of genetic programming. Since Genetic Programming has been shown to be an evolutionary algorithmic technique, it has developed highly complex segmentation models incorporating local and global image information and combining them in a strongly nonlinear manner[8]. Therefore, it is verified that genetic programming is an effective tool for image segmentation. GP is one of the principal techniques in Evolutionary Computation. One of the main advantages of evolutionary algorithms is their possibility to escape local minima during the searching process due to their stochastic nature. However, evolutionary algorithms depend on a number of solutions or population and their evaluation is computationally expensive [9].

In addition to using genetic programming to generate a segmentation method, it is sought to combine it with fuzzy logic due to its properties of identifying an object as more than one class [10], it is perfect for dealing with the segmentation problem of mammographic images in the areas where to find a combination of pixels. In addition, fuzzy logic has linguistically descriptive properties that can help identify the characteristics described by the ACR BI-RADS for its classification without extracting extra features, but only those described by doctors.

During this work, fuzzy logic is planned to be used as a fitness function in genetic programming. This is because evolutionary computation works they have used fuzzy logic as a fitness function and have had good results [11, 12]. In addition to the fact that by nature, it is not a heavy function, so it reduces the computational cost. Although they have been tested in other evolutionary computational works, no work has been found that combines genetic programming with fuzzy fitness functions.

Therefore, it is expected from this research to find a method of segmentation of mammographic images and to be able to differentiate the existing tissues in mammograms to extract the characteristics described in ACR BI-RADS and thus improve the automatic classification of breast density. Improving segmentation in mammography will help make automatic breast density classification better than the current state of the art. The Breast Imagine ACR Reporting and Data System (ACR BI-RADS) standard is the most widely used manual classification system in the medical field. It will be used as the basis for automatic breast density classification. In the same way, the search with fuzzy fitness functions is expected to provide an optimal segmentation process. Therefore, the objective of the research is to find an optimal segmentation method for mammography images by performing the search with genetic programming in conjunction with fuzzy fitness functions.

2 Background

This section introduces core elements that will be integrated in the proposed segmentation method. Thus, main aspects related to image segmentation, as well as concepts for Genetic Programming and Fuzzy Logic are presented. Finally, problem related considerations such as breast density and one of the main standards used in the medical arena the Breast Imaging Data and Reporting System (BI-RADS) are discussed.

2.1 Image Segmentation

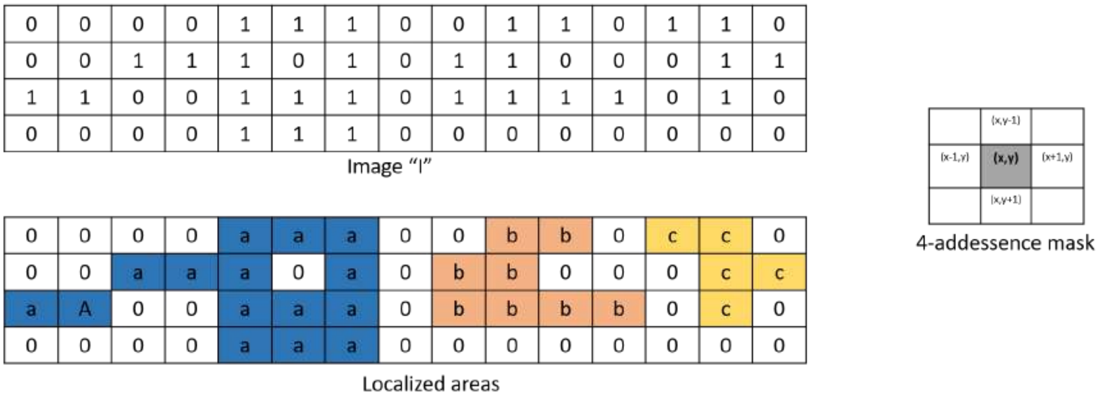
Image segmentation extracts and identifies objects within an image for further analysis [13]. Image segmentation is also defined as the classification of pixels within an image to separate objects of interest into independent regions to find helpful information [14]. The identification of objects in images can be made by distinguishing specific criteria such as pixel intensity, texture, edge identification, morphological operations, among others.

Image segmentation plays an important role in medical image analysis. It aims to divide an image into elementary parts with uniform and similar characteristics such as tissue density, tumors, or other abnormalities within the human body [11]. By having a good segmentation, it is possible to observe and differentiate soft and hard structures found in organs of the body that are not perceptible to the human eye; therefore, image segmentation in the medical arena play an important role as a support tool for medical experts.[14].

There are two ways to segment an image; the first consists of the segmentation of a specific region of the image (local segmentation). The second segmentation is performed on the entire image to detect several objects simultaneously (Global Segmentation). These forms of segmentation are used depending on what the problem requires and can even combine the two [15].

Some widely used techniques in image segmentation are briefly described below:

- **Pixel Connectivity** is used to delimit regions by establishing connectivity between two or more pixels [16]. For example, to find the components connected with four underlays of a binary image I, for a pixel at position (x,y), its neighbors would be: $(x-1, y)$, $(x+1, y)$, $(x, y-1)$ y $(x, y+1)$. Thus the image is processed from top to bottom resulting in regions located and labeled as shown in Figure 1.



0	0	0	0	1	1	1	0	0	1	1	0	1	1	0
0	0	1	1	1	0	1	0	1	1	0	0	0	1	1
1	1	0	0	1	1	1	0	1	1	1	1	0	1	0
0	0	0	0	1	1	1	0	0	0	0	0	0	0	0

Image “I”

0	0	0	0	a	a	a	0	0	b	b	0	c	c	0
0	0	a	a	a	0	a	0	b	b	0	0	0	c	c
a	A	0	0	a	a	a	0	b	b	b	b	0	c	0
0	0	0	0	a	a	a	0	0	0	0	0	0	0	0

Localized areas

	(x,y-1)	
(x-1,y)	**(x,y)**	(x+1,y)
	(x,y+1)	

4-addessence mask

Figure 1: Connectivity segmentation process in a binary image.

- **Thresholding segmentation based on histograms** aims is at finding a threshold that allows binarizing an image by adequately separating the background from the objects of interest [17]. The technique works by analyzing the histogram of the image; in this histogram, there are two sections or two peaks, one is the background, and the other is the object, the optimal threshold T is the one that separates these two areas, as shown in Figure 2.

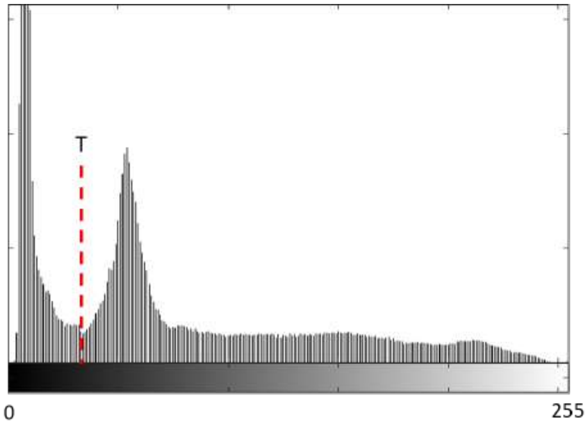


Figure 2: Histogram with optimal T threshold.

- **Region growing segmentation** groups and labels adjacent pixels of similar width as a single region [18]. A widely known method is given by Brice et al. [19] where pairs of quantized pixels are combined into atomic regions if these pixels are of the same amplitude. Subsequently, heuristic rules are applied to connect weak neighborhoods; a result example is observed in Figure 3, where two regions, R_1 and R_2, that have perimeters that have been previously joined.

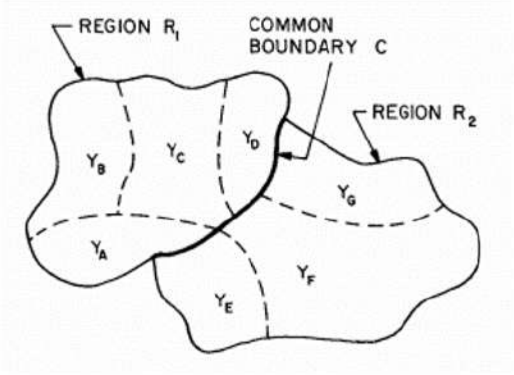


Figure 3: Image divided by region growth [18]

- **Texture segmentation** is based on visual texture that is defined as the roughness or smoothness due to tone variations within an image [20]. Measuring texture in a digital image is usually based on statistical values which can be of first or second order, and separate those different regions within images [21]; An example of this can be seen in Figure 4, where the texture is represented by different colors.

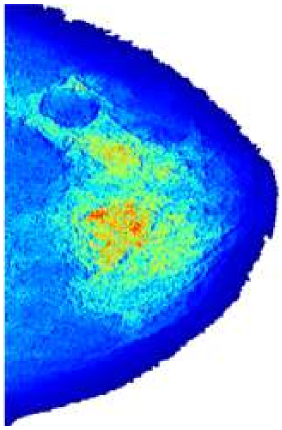


Figure 4: Different textures within a mammographic image.

Image segmentation is applied in different areas of science, such as image recovery, detection, and recognition, satellite analysis, medical image analysis, agriculture, among others. Therefore, image segmentation remains as a fundamental process for many related computer vision areas. Although a number of image segmentation methods have been developed to this day, it remains as an open problem due to the complexities of the application contexts such as medical imaging which is pursued in this research.

2.2 Genetic Programming

Genetic programming is one of the main algorithmic techniques in Evolutionary Computation. It is mainly used to evolve and search for models for different application contexts, such as machine learning tasks, electronic circuit development or programming codes for a specific task [8, 22]. Genetic programming has proven successful in evolving complex models for a variety of tasks such as image processing, where it is used for image enhancement, segmentation, understanding, classification, and registration [23]. Furthermore, programming is a tool where there is the possibility of representing strongly nonlinear models in the form of trees or graphs [24], in addition to the fact that it can combine information at different levels of complexity and scalability.

When generating a genetic programming algorithm, it is necessary to declare several essential elements. The first element to be considered is the evolutionary component that will be the input of the genetic program and will be defined by the problem to be solved. For example, if one wants to solve an image processing problem, the evolutionary components would be images or pixels. In genetic programming, the individuals generated are possible solutions to the problem in question and are represented in the form of trees or graphs. The possible solutions are randomly generated to obtain the first population to evolve. To create individuals other than the evolutionary components, a set of terminals and functions is needed, which can be variables, constants, or functions. The evolution of the genetic program is carried out on the basis of fitness functions that are responsible for evaluating the quality of the individuals. Evolution is performed by crossing two individuals taken as parents or with a mutation; whether either of the two evolution operations is performed depends on the probability defined by the user. The selection, evaluation, and evolution process is performed iteratively until a stopping criterion is met; the criterion may be finding the optimal solution or a maximum number of iterations [25, 26]. The general process of the genetic programming algorithm can be observed in the following flow diagram (Figure 5).

All elements involved in genetic programming are described next [8, 26, 28].

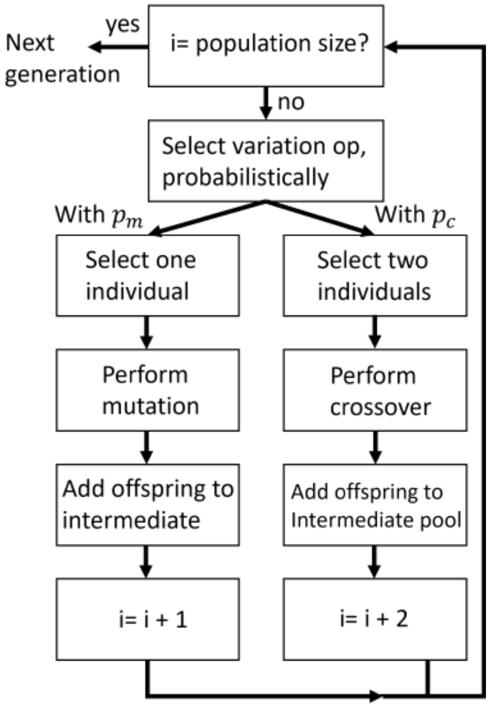


Figure 5: Genetic Programming general flow chart [27]

- **Individuals**: Representation of individuals is made through parse trees. Parse trees are individuals or solutions. These are defined by internal and terminal nodes. Internal nodes are functions, while terminal nodes are variables or constants. In GP, solutions represented by parse trees are initialized randomly after both sets of functions and terminals; These can be randomly generated, or the user can predetermine them. An example is shown below: There is an operation like the following $MAX(X * X, X + 3 * Y)$, it would be represented as a tree as in the following Figure 6.

- **Functions set**: Depends on the task to solve. These can be arithmetic operations ($*$, $-$, $/$, %) or functions used in programming (For, $Else$, $Switchcase$, If). The functions are internal nodes, in the trees that represent the individuals.

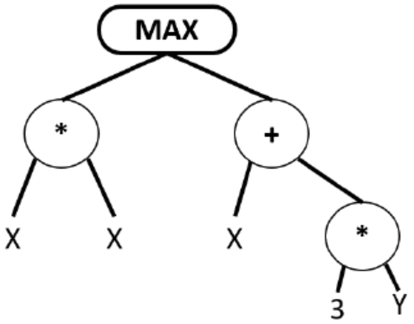


Figure 6: GP's solution or individual example represented by a parse tree.

- **Set of terminals**: They are variables of a function that will be the input to the genetic program. Entries can be constant or random. For example, the set of terminals for image processing could be raw pixel values, full images, and even pre-processed images in image processing. The set of terminals is represented in the trees as leaves.

- **Fitness function**: Also called an objective function, it assigns a score to every individual with in the population depending on the targeted problem. In single objective optimization problems, the fitness function draws the search space of the mathematical function to be solved. Genetic Programming approaches a variety of computational tasks. For example, in ML learning tasks such as data classification, performance metrics such as accuracy are normally used as the fitness scores for every individual within a population. In this research, Genetic Programming will be explored to evolve image segmentation models for mammographic images, therefore performance metric associated to this task will be used, such as jaccard index, F1 measure and relationship signal/noise. Therefore, the fitness function of the genetic program is a fundamental operation since it defines the search space for the optimal solution.

- **Selection methods**: During the searching process, individuals undergo selection, once as a parents for mating and as survivors for the next generation:

  - Parental selection: A selection criterion is defined in order to choose pairs of solutions normally with high fitness scores for reproduction.Individuals selected on the basis of fitness function are taken as new parents to be crossover.
  - Replacement criterion: Once offspring or new solutions are created, a replacement criterion determine which individual from both solutions sets, parents and children, remain in the population for the next generation. There are two widely known replacement criteria: steady state in which a reduced number of new solutions or children are selected to replace the worst parents in the current population; and generational replacement, where the children replace the parents completely.

- **Genetic operations**: Genetic operations are the core of the evolutionary process. In GP, parents are recombined or mutated according to a predefined probability. Recombination or crossover allows information exchange at the genotypic level. In GP, for example, parse-trees can exchange a sub-tree or a branch among parents. Mutation allows the introduction of diversity by randomly modifying the genotype of a solution; in GP, a sub-tree or a branch of an individual can be randomly modified.

Genetic Programming has demonstrated to be a powerful algorithmic technique to target problems where inputs and expected outputs are known and the model is unknown. GP allows the evolution of strongly non-linear models and the flexibility to incorporate and to operate data information from different available resources. For example, in image processing tasks, image data at local and global level can be can be represented by GP solution.

2.3 Fuzzy Logic

Lofti Zadeh introduced the concept of fuzzy logic in 1965 to represent qualitative linguistic expressions mathematically [10, 29]. Fuzzy logic can be defined as an extension of Boolean logic that indicates whether an object belongs to one set or another. However, unlike Boolean logic, fuzzy logic can give the membership of an object to more than one set to varying degrees ranging from [0,1] [30]. In Figure 7a. It is observed how the Boolean logic classifies the pixels of an image in black or white; Opposite case of the Figure 7b. where fuzzy logic classifies the pixels in an image so that they are not black or white, but rather have different degrees of gray.

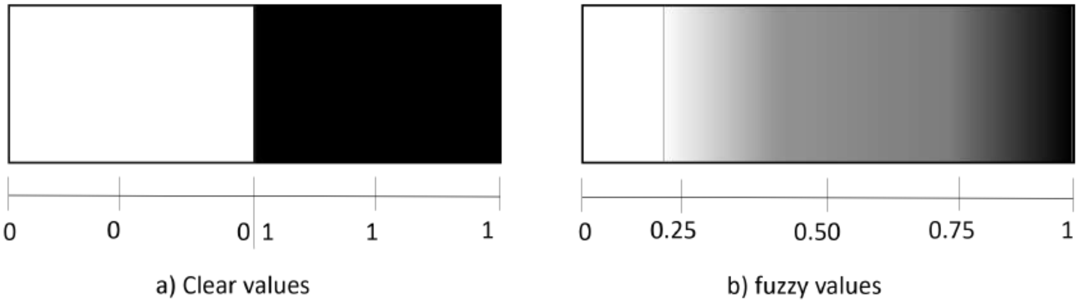


Figure 7: Representation in tree form of an operation.

The elements that fuzzy logic needs to be able to give membership to an object are described below [31]:

- **Fuzzy Sets**: Formalize linguistic expressions. These expressions define the degree of ambiguity such as: "Very little," "Little," "Medium," "Much," etc. This degree of ambiguity mathematically can be given from [0-1], with 1 being the largest membership and 0 that the element does not belong to the set. Fuzzy sets perform operations to calculate this ambiguity, the most used are: union, intersection, and complement.
- **Membership functions**: They serve to express fuzzy sets and quantify imprecise and subjective words. Membership functions are made up of:

- **Height of a fuzzy set (height)**: The largest value of its membership function:$sup_{x\varepsilon X} H(X)$.
- **Normalized Fuzzy Set (normal)**: If there is some element $x\varepsilon X$, such that it belongs to the fuzzy set totally, that is, with degree 1, Or also, that:$Height(H) = 1$.
- **Support of a fuzzy set (support)**: Elements of X that belong to H with a degree greater than 0: $supp(H) = \{x\varepsilon X|H(x) > 0)\}$.
- **Nucleus of a Fuzzy Set (core)**: Elements of X that belong to the set with degree 1:$Core(H) : \{x\varepsilon X|H(x) = 1)\}$

  Logically,$Core(H) \subseteq supp(H)$
- α-**Cut**(cut): Values of X with degree minimum α:$H_\alpha = \{x\varepsilon X|H(x) \geq \alpha\}$

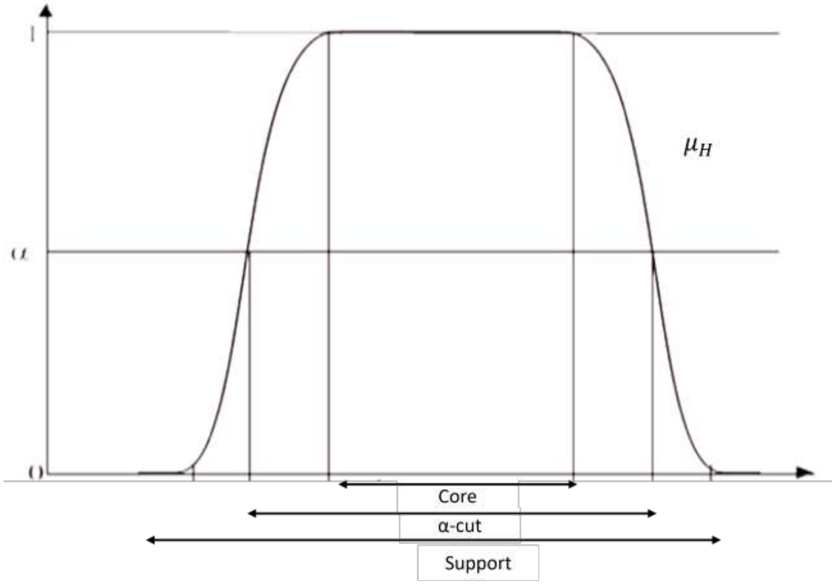


Figure 8: Membership role structure.

- **Fuzzy Rules**: It is a set of propositions with the IF-THEN expression by default. These rules express the relationship between the different sets and are represented in logical implications. Fuzzy rules have to be created as follows:

If X is A then Y is B

Being A and B fuzzy sets are defined in X and Y ranges.

- **Fuzzy Inference**: It is the process of obtaining output for a fuzzy input value. There are two models to carry out this process: Mamdani and Takagi, Sugeno.

Fuzzy logic is used to solve problems where Boolean logic is not a viable option; a clear example of this is medical images as they may contain tissues that do not always belong to a specific type of tissue as there may be a combination of different tissues.

2.4 Breast Density

Breast density is defined as the ratio of fibroglandular tissue and fatty tissue found within the breast of women. Fibroglandular tissue is made up of ducts and lobes [6]. Breast density is studied using mammography, a technique that obtains a flat image of the breast using X-rays. This technique seeks to visualize the lesions found within the breast and to study breast density, and its relationship with developing breast cancer [32]

In a mammogram, fibroglandular tissue is seen as white areas because its attenuation coefficient is radiologically dense and blocks X-rays; on the other hand, adipose tissue has a minimal attenuation coefficient, which is why it is observed in mammography as dark areas [33], this representation can be seen in Figure 9 b.

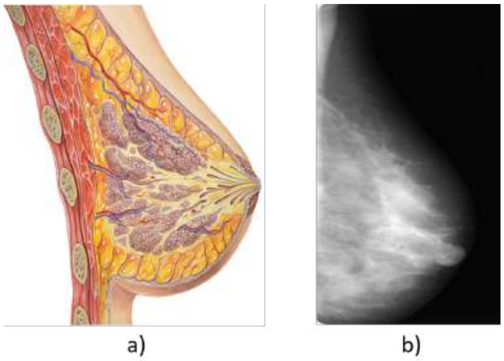


Figure 9: a) Breast compositions, b) Breast density in mammography.

The percentage of breast density is the ratio of fibriglandular tissue to the total surface of the breast. This means that when a breast has more fibroglandular tissue than adipose tissue, it is defined as high density. On the contrary, when the adipose tissue covers more of the breast, it is defined as low density [34]. An example of these two cases can be seen in Figure 10.

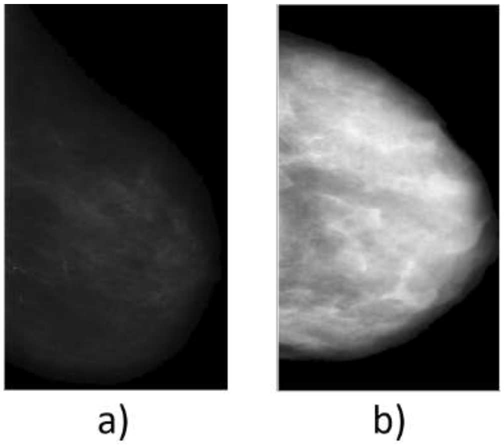


Figure 10: a) Breast density low in mammography, b) breast density high in mammography.

Breast density is an essential factor in different diseases diagnosis, including breast cancer, since there are studies that affirm that before breast cancer develops (cancerous nodules), there is a change in breast density, first decreasing and then gradually increasing [33].

For that reason, there are standards that are used to classify and study the relationship of breast density to breast cancer. These standards have been developed by physicians in different parts of the world. These standards can be qualitative or quantitative, where the qualitative ones classify breast density with regards to tissue distribution and shape. Quantitative standards only focus on the amount of tissue and fat found within the breast. Some of the best-known standards are:

- **Wolfe**: Classifies breast density depending on the morphology of the breast tissue. In other words, it is classified qualitatively [35].
- **Boyd**: It focuses on classifying breast density depending on the percentage of existing tissue and fat. Therefore its classification is quantitative [36].
- **Tabar**: Its classification is qualitative depending on the linear patterns of tissue, homogeneous tissue that does not contain a specific structure [37].
- **Breast Image Reporting And Data System (BI-RADS)**: The classification is both quantitative and qualitative [38].

Although they all have different qualities, the so-called gold standard is the Breast Image Reporting And Data System (BI-RADS). In addition to its quantitative and qualitative classification, it also classifies anomalies found, such as nodules or microcalcifications.

2.5 ACR-Breast Image Reporting And Data System (BI-RADS)

The Breast Imaging Data and Reporting System (BI-RADS) standard is the most widely used manual by clinicians for analyzing breast density. It is the only one approved by doctors worldwide since it allows quantitatively and qualitatively breast density classification. In addition to categorizing breast density, the BI-RADS standard also classifies items that do not match breast tissue, such as nodules, calcifications, and breast asymmetry [38].

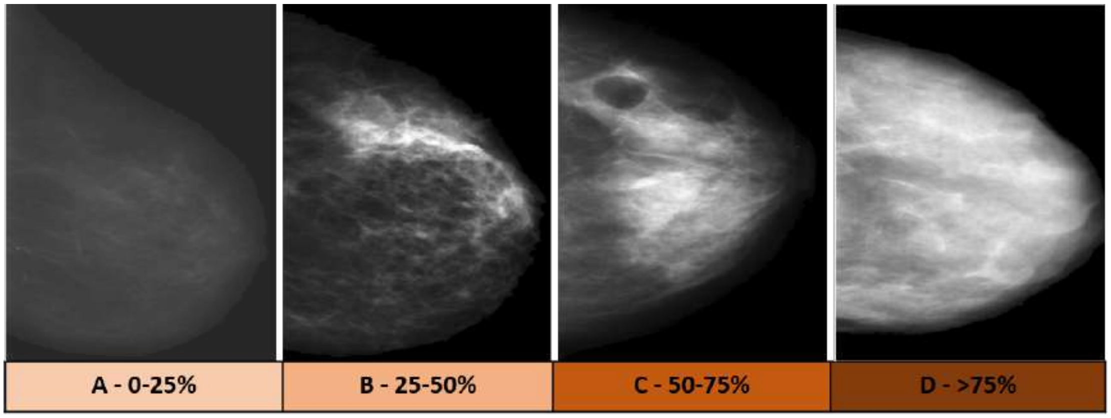


Figure 11: Representation of the classes ACR BI-RADS.

BI-RADS has excellent diagnostic quality, making it the gold standard. Using the same terminology and exact words in each class facilitates communication between physicians, radiologists, and patients by standardizing the description of breast lesions. It is worth mentioning that the BI-RADS classification is performed on mammographic images.

BI-RADS is a manual that is divided into four different sections [39]: (i) Lexicon, is where the findings are described through images: these findings are the abnormalities found in addition to the different types of breast density; (ii) this section provides a detailed description of how to report findings found in mammography; (iii) lays the foundation for imaging diagnosis and monitoring; (iv) the last section provides forms, as well as guidance or information that may be of use to the specialist who will be available to make a diagnosis. The Bi-RADS classification is mandatory for breast cancer diagnosis, treatment and monitoring.

Breast density classes are given in ACR BI-RADS as breast density without including any abnormality description.The classes that ACR BI-RADS handles are shown and described in the following Table 2.5.

Table 1: Classes and description of breast density according to ACR BI-RADS [40]

Class	Description
A	The breast consists almost entirely of fat.
B	The breast tissue is dispersed in the breast.
C	The tissue is more heterogeneous and occupies more space within the sinus.
D	The tissue occupies almost the entire breast area

.

3 State of the art

This section discusses work related to the main topics of this technical report, which are genetic programming (GP) for image segmentation, fuzzy logic combined with evolutionary algorithms, and breast density classification.

3.1 GP for image segmentation related work

In the work of J. Liang et al.[41], three different structures were used to segment images based on GP, using primitive operators (filters). The proposed method was divided in three main stages: 1) images pre-processing, 2) segmentation, 3) post-processing. Weizman's image data set was used for empirical validation. It contains images of aircraft and horses. The functions set contained a) arithmetic operators (filters and a threshold operator) and b) morphological operators (Laplace, image histogram, Gaussian filter, histogram equalization, among others). The F1 metric as the testing accuracy was set as the objective function. F1 is used to combine the precision and recall measurements into a single value. The best result obtained in the GP work reaches an F1 of 0.57+-0.035.

J. Liang et al. [42] created a method for feature construction and selection with GP. This algorithm carries out the evolution of subtrees that create multiple simultaneous characteristics for the segmentation of images at the pixel level (classification of pixels). The algorithm randomly captures a series of pixels in images for training. Training guarantees the same number of pixels for objects and background. It is worth mentioning that the characteristics selected by the GP are from low and half level. The Fitness function used is the accuracy to observe that pixels are classified correctly with those characteristics selected by the GP. The result obtained is a significant reduction in the number of features compared to the state of the art while maintaining a similar performance, reaching an accuracy of 83.13% + -0.60.

In Liang et al.[43], This is an extension of the work of Ling [44]. Therefore they penalize the complexity of the solutions with the help of multi-objective techniques and Pareto force evolutionary algorithms for image segmentation. The terminal set of the program will be the characteristics of the image pixels instead of raw pixels. Features are 320 from Gabor. For the set of functions, arithmetic and conditional operators are used. For the evaluation, used the measure F1. Several experiments were carried out with the different databases. The highest F1 reached by the genetic program was with the Brodatz database, with an F1 of 0.94.

In Liang et al. [45] proposes an image segmentation method that separates the object from the background using GP. GP works as a feature selector to classify image pixels into two classes (background or objects). The set of functions is standard arithmetic operators and five conditional operators. The set of terminals is the texture, brightness, shape, and color of the image. The fitness function is measured by the precision obtained from the classification of the pixels in the image. The result was a significant reduction in the number of characteristics and an accuracy of 75.40%.

In Liang et al. [44], a new solution for complexity and size penalization of solutions and new image segmentation methods for object and background separation within images are developed. Standard arithmetic operators and conditional operators, all of which are low-level, are used for the function set. The terminal set is the pixels of the images, so the segmentation, like the aforementioned works, is based on pixel classification. The fitness function is based on the accuracy of pixel classification. To determine the solution complexity, the weighted sum together with the accuracy obtained in the fitness function penalizing the size of the solutions is used to adjust the fitness evaluation of the solutions. The experiments were performed on two databases. The first is for Weizmann images, obtaining an accuracy of 98.0%; for Pascal images, obtaining an accuracy of 95.0%.

In Meng et al. [46], previous work, texture is also used to perform a fully automated algorithm that segments the corpora lutea of other objects in ultrasound images using GP. The set of functions used are operations: $-$, max, $>$, $<$. The texture classifier to evolve is a Local Binary Pattern (LBP). The fitness function used to guide the search was the classification accuracy. It should be noted that this fitness measure was used because segmentation was based on pixel-to-pixel classification. The result of the developed algorithm was a accuracy of 86.93%.

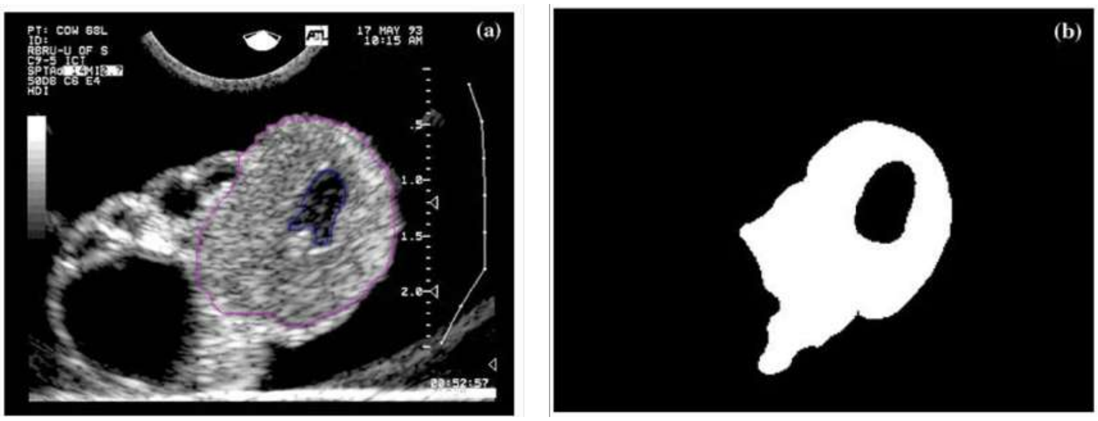


Figure 12: Images of Bovine Luteal Ovaries in ultrasound images [46]

.

Singh et al. [13] developed a method for medical images segmentation based on GP. This work uses two types of input images: original cells images (Figure 13) and binarized images of the same size and format. The binarized images are used to train the algorithm; medical experts proposed the threshold selected to binarize the images. The operators used to evolve the GP are basic arithmetic operations, morphological operations, and image segmentation filters. Image segmentation is based on a pixel-by-pixel classification, so the objective function is the accuracy. Binarized images by the expert were treated as the ground truth for pixels classification. As a result, a 98.76% accuracy was obtained.

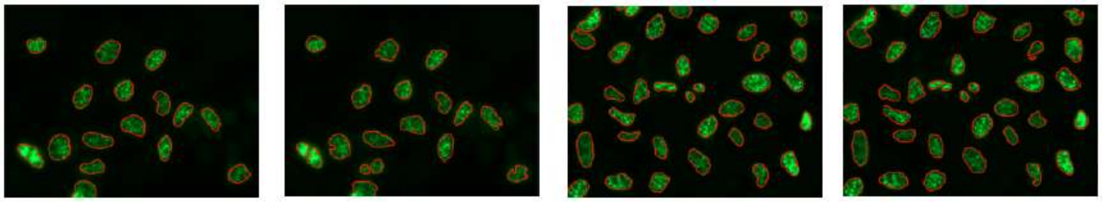


Figure 13: Image representation of Singh's work [13].

In [47] texture classifiers were evolved with GP for image segmentation. The algorithm performs image segmentation by evolving texture classifiers without extracting additional characteristics but the texture. The testing data were satellite images. This process was supervised, so the input images are already previously tagged by experts. The set of functions for the GP was formed by basic arithmetic operations $(+,--,*,/)$. The set of terminals were image pixels. The fitness function was defined as the texture classification accuracy achieved by the GP. Texture classifiers evolved in this work were two Bitmap textures and Brodatz textures. An accuracy of 97.48% was achieved.

In [48] GP was used for the segmentation of histological skin images. The set of functions used in this work consists of morphological operations, logical operations, region intensity functions, edge filtering, thresholds for the set of terminals of the input images, and numerical pixel values. The fitness function was defined by the specificity and sensitivity measures while having a balance between true positives, true negatives, false positives, and false negatives. The results achieved were 97% for sensitivity and 81% for specificity.

In Poli et. al.[8], effective filters and optimal thresholds are selected to extract features from magnetic resonance images, which will try to segment the brain. In this work, arithmetic operations and macros that allow the construction of filters are used as a set of functions. The set of terminals are the image pixels, so it is a segmentation based on pixel classification. The fitness function that is used is based on a symbolic regression that is the sum of the absolute errors made by the program for all the pixels of the images. Finally, the results obtained by genetic programming are compared with a neural network, obtaining similar results, proving that genetic programming is a potential tool to develop algorithms for image segmentation.

Although the works mentioned give good image segmentation results, they have the disadvantage that the images evaluated in some of the works do not have the complexity observed in mammographic images. Another disadvantage is that the search for solutions is a slow process because the evaluation of individuals with traditional aptitude functions is a long process. Although there are also works in the state of the art that use mammography images only try to classify the images into cancer and cancer-free. But so far, no genetic programming work has been found that uses mammography images to try to segment the different tissues and fat within mammograms. This is due to the nature of mammography, where it isn't easy to detect the transition from one tissue to another because there are patterns of tissue combination. This segmentation problem makes the classification of breast density not as good as doctors would like for the early diagnosis of breast diseases. Therefore, this work seeks to solve the limitations of the aforementioned works.

3.2 Fuzzy logic with evolutionary computation

The work of Shashwati et al. [49] describes an approach to medical image segmentation where a genetic algorithm is combined with fuzzy logic; This technique is based on finding the optimal values of various thresholds for magnetic resonance imaging. In this work fuzzy logic is used as an objective function to find the most suitable individuals to solve the problem. The objective function is called the fuzzy fitness function; This function calculates the entropy using the probability obtained by applying certain fuzzy membership functions. Membership functions give values that are used separately to find the entropy of the image and indicate the fitness value of each individual. With the fuzzy fitness function used in this work, the search time

Table 2: GP for image segmentation related work

Work	Function sets	Segmentation type	Fitness function	Results
J.Linag, 2020	Arithmetic operators Morphological operators	Full image	F1	0.57
J.Liang, 2020	High level features Low level characteristics	Classification of pixels	Accuracy	83.13%
Liang, 2019	Arithmetic operators Conditional operators	pixel characteristics	F1	0.94
L. YuYu, 2017	Arithmetic operators Conditional operators	Classification of pixels	Accuracy	75.40%
Liang, 2016	Arithmetic operators Conditional operators	Classification of pixels	Accuracy	98%
Meng, 2013	Algorithm's of Texture $-$,Max,$>$,$<$	Classification of pixels	Accuracy	86.93%
Singh, 2009	Arithmetic operators Morphological operations Segmentation filters	Classification of pixels	Accuracy	98.76%
Song, 2008	Arithmetic operators	Full image	Accuracy	97.48%
E. Mark, 2003	Logic operators Morphological operators Filters	Full image	Specificity Sensitivity	97% 81%
Poli, 1996	Arithmetic operators Macros	Classification of pixels	Symbolic regression	—%

was reduced and the accuracy of the genetic algorithm was competitive with the state of the art.

In Cruz et al. [50], is used as a fitness function in conjunction with a genetic algorithm. However, unlike the other works, in this case, fuzzy logic is used to generate fuzzy granules and thus reduce the fitness evaluations of individuals. Diffuse granulometry avoids the use of multiple fitness assessments in individuals with similar characteristics. The results of this work are the reduction of evaluations by approximately 80%, significantly reducing the processing time to find the optimal solution.

In Basabi et al.[51], a genetic algorithm is combined with a fuzzy fitness function to find optimal characteristics for image classification. The fuzzy fitness function tries to find intraclass and interclass ambiguity. Ambiguity is calculated with fuzzy entropy of the classes considered as fuzzy sets. If the intraclass ambiguity is minimal and there is a maximum interclass ambiguity, it is considered that the individual has the best trait for solving the problem. The fuzzy fitness function is calculated using the following Equation 1, which represents the ratio of the ambiguity values of the classes (fuzzy sets) represented by a set of characteristics $1, 2, \ldots, q$ instead of just the characteristic q. The classification results with the characteristics extracted from the genetic algorithm were of accuracy of 97.5%.

The work of Bhandari et al. [52], As in previous works, combines a genetic algorithm with fuzzy logic for image enhancement; it tries to automatically select an optimal set of 12 parameter values from a generalized image enhancement function. Fuzzy logic was used as an objective function based on the fuzzy entropy and the area coverage index, these factors are taken as quantitative indices to evaluate the image quality.

$$FSEI_j = \frac{d(1,2,...,q)_{,j} + d(1,2,...,q)_{,k}}{d(1,2,...,q)_{,jk}} \tag{1}$$

In the works reviewed in the state of the art, we can observe that fuzzy logic in conjunction with genetic algorithms is a tool that can obtain promising and competent results with the state of the art. Fuzzy logic is used in different ways as an objective function in the works and in most of these, it has the advantage of being less heavy so that finding the optimal solution is faster than techniques with a conventional objective function. Since the efficiency of fuzzy logic as an objective function of genetic algorithms has been proven; In this work, we will try to integrate them with genetic programming since so far no job has been found to do it.

3.3 Breast density classification related work

A number of previously proposed approaches for breast density classification have been developed considering other algorithmic approaches. Although good results have been achieved, the proposed algorithmic approach based on genetic programming lead by a fuzzy fitness function aims at improving reported results. Next, related works are analyzed.

In the work of Deng et al. [53], a database of digital mammograms obtained at the "First Hospital of Shanxi Medical University" was used, containing 18,157 mammography images, all classified into the different BI-RADS classes. The classification for comparison of results was performed manually by several specialized radiologists. The methodology is based on the following steps: first, the image was segmented by removing the background and the pectoral area of the breast. This process was performed manually. Then enhance the image with some image processing techniques such as image whitening. Then extracted the feature vector. Finally, the breast density was classified with a convolutional neural network (CNN) based on the four categories of the BI-RADS standard: A class which is mainly fat with less than 25 % tissue within the breast, B sparse breast tissue with a percentage of 25- 50 % breast tissue, C heterogeneously dense tissue and 50-75 % breast tissue. Finally, there is class D, where the tissue covers almost the entire breast or has a percentage of tissue more significant than 75 %. The overall percentage of classification obtained in this work is 92.17% accuracy.

E. Matsuyama et al. [54], segmented the mammograms manually with the help of an expert who separated the breast from the fundus and the pectoral area, then used a convolutional neural network (CNN) model obtained from the AlexNet article [55], Matsuyama uses the AlexNet model to generate a new CNN network, for the extraction of features, the information of the spectral image of the mammogram obtained with the Wavelet transform is used, the work obtains a percentage of 88.3 % accuracy. However, it does not make use of the BI-RADS classification but instead creates and classifies into the following categories; a) sparse density (benign), b) sparse density (malignant), c) heterogeneously dense (benign), and d) heterogeneously dense (malignant). The database used for this work is DICOM, obtained from The Cancer Imaging Archive (TCIA) and composed of 1170 mammography images that were manually labeled and segmented by an expert radiologist.

The work of A. Rampun et al. [56], is based on the segmentation of mammographic images where the breast and the pectoral area are separated using the method of Rampun's [57] work in which, utilizing active contours, he estimates the limit of the breast and with the growth of regions he estimates the pectoral area. For the extraction of the patterns, a 3X3 window was used. The operators that were selected and defined as the vector of characteristics were: local binary patterns (LBP), local ternary patterns (LTP), local quinary patterns (LQP), and local septenary patterns (LSP). The set of patterns that would have the greatest significance when classifying was then selected; for breast density classification, it was classified into the four BI-RADS classes using a support vector machine (SVM) classifier with an accuracy of 83.3% was obtained. The databases used in this work were: MIAS and InBreast.

In I. Valencia [58], breast density is classified with a Takagi-Sugeno type classifier, obtaining an overall accuracy of 84.20%. The classification is based on the BI-RADS standard. Therefore, the classes are A, B, C and D. The segmentation of the breast is performed by thresholding with Otsu, which separates the objects found on mammography (fundus, pectoral and breast). Subsequently, an area criterion is taken into account to select the most significant and rounded regions of the image, which is the breast area. In the article by D.

Stylianos[7], the image is segmented giving orientation to the breast, this means that all mammograms are normalized so that they have the same orientation in this case the pectoral area has to be in the upper left corner of the image, the change of orientation is so that the image segmentation can be carried out automatically, later the breast is extracted from the pectoral area and finally, filtering techniques are applied to improve the image, once the image is segmented the characteristics vector is extracted, some of the characteristics include: the mean and variation of the intensity values of the back area, the intensity of the pixels in the tissue area. For the classification of breast density, a vector support machine classifier (SVM) was used where precision of 84.47% is obtained, the classes obtained are Fat (F), fat-glandular (G) and dense glandular (D). The database used for this work is miniMIAS, which contains 161 images from analog mammograms and subsequently digitized.

In the article by D. Stylianos et al. [7] the image is segmented giving orientation to the breast, this means that all mammograms are normalized so that they have the same orientation in this case the pectoral area has to be in the upper left corner of the image, the change of orientation is so that the image segmentation can be carried out automatically, later the breast is extracted from the pectoral area and finally, filtering techniques are applied to improve the image, once the image is segmented the characteristics vector is extracted, some of the characteristics include: the mean and variation of the intensity values of the back area, the intensity of the pixels in the tissue area. For the classification of breast density, a vector support machine classifier (SVM) was used where precision of 84.47% is obtained, the classes obtained are Fat (F), fat-glandular (G) and dense glandular (D). The database used for this work is miniMIAS, which contains 161 images from analog mammograms and subsequently digitized.

In Table 3.3 comparison of breast density classification papers is observed. Most of the papers have a good classification; however, some are not based on the BI-RADS standard. This is a problem since there is not an easy and homogeneous interpretation for physicians and patients. In addition, the works that classify the different tissues observed in mammograms have low accuracy, which can improve this accuracy percentage. Therefore, it is important to identify how the breast tissue is distributed within the breast to detect changes in breast density, which is intended to alert the radiologist to the change in density so that he can observe and define whether the change could have serious consequences, such as the development of breast cancer or another type of breast disease.

Table 3: Related works chart.

Work	Tecnique semgentation	Clasificator/ Accuracy	Clasification	Database
I.Valencia, 2021 [58]	-Otsu -Area criterion	Takagi-sugeno 84.20%	-BI-RADS	Breast Cancer Digital Repository (BCDR)
J. Deng, 2020 [53]	-Segmentation manual -Grayscale transformation. -Random cropping and angle rotating -Image whitening	CNN 92.17%	-BI-RADS	First Hospital of Shanxi Medical University
E. Matsuyama, 2020 [54]	-Segmentation manual	CNN 88.30%	-Disperse density (benign) -Disperse density (malignant) -Heterogeneously dense (bening) -Heterogeneously dense (malignant)	The Cancer Imaging Archive (TCIA)
A. Rampun, 2020 [56]	-Active Contours -Pixel-wise multiplication	SVM 80.02%	-BI-RADS	Mammographic Image Society (MIAS)
D. Stylianos, 2011 [7]	-Row and column interface -Thresholding -Iterative cliff detection	SVM 84.47%	-Fatty (F) -Fatty Glandular (G) -Dense Glandular (D)	Mammographic Image Society (MIAS)

4 Research Proposal

This section will describe the problem statement, research questions, hypotheses, general and specific objectives, limitations of the work, contributions, and describe the steps we will follow during the proposed research methodology.

4.1 Problem Statement

Segmentation in image analysis is a major problem in computer vision. Image segmentation is a task that attempts to group pixels that belong to one region or another. Although there are many good techniques for image segmentation, the problem remains open because not all methods are suitable for all types of images.

One of the problems that remain open is the segmentation of mammograms for breast density classification, where segmenting fat tissue is a difficult task due to the nature of mammograms where we can observe areas where there are combined pixels (combination of adipose tissue and fibroglandular tissue).

Correctly segmenting a mammogram generates a good breast density classification since the gold standard ACR Breast Image Reporting And Data System (ACR BI-RADS) is based on the distribution of the breast tissue and the fat found in the breast. Therefore, it is important to have a good segmentation of tissue and fat on the mammogram to obtain a description of the distribution of the breast tissue for a correct classification of breast density.

Traditional methods that segment mammography images for subsequent classification cannot differentiate pixels belonging to one or the other group in the case of a combination of tissues (combined pixels). Furthermore, the segmentation methods tested in the state of the art have no way to verify that they are optimal for breast tissue segmentation. Therefore, this doctoral research proposes a method based on genetic programming with fuzzy fitness function for segmenting breast tissues, even if they are combined.

4.2 Research Questions

- Can Genetic Programming integrated and adapted to be guided by fuzzy fitness functions evolve competitive state of the art image segmentation models for mammographic images?
- What is the best abstraction level for solutions representation in Genetic Programming to tackle images segmentation of mammographic images?
- How can a fuzzy fitness function be generated to guide the genetic programming search of a segmentation algorithm for breast density?
- What are the most appropriate evolutionary operations according to solutions representation and population dynamics in Genetic Programming for mammographic images segmentation ?
- What is the most suitable set of functions and terminals to generate an optimal segmentation model for breast density?

4.3 Hypothesis

Integrating genetic programming with a fuzzy logic-based fitness function could guide the search for a segmentation method for the different breast tissues visualized in mammography images to generate a quantitative and qualitative breast density description based on ACR Breast Image Reporting And Data System (ACR BI-RADS), increasing the classification of breast density compared to state of the art.

4.4 General objective

Design and develop a fuzzy logic based fitness function that can integrate into a genetic programming algorithm to generate a breast density segmentation method capable of efficiently differentiating the different breast tissues found in mammography images and generating a quantitative and qualitative description of these based on the ACR BI-RADS standard.

Specific objectives

- Select strategic and terminal set representation functions for Genetic Programming considering the challenges involved in mammographic image segmentation.
- Select custom genetic operations for the representation of proposed solutions to improve GP search capabilities.
- Design and develop a fuzzy fitness function that incorporates the strengths of fuzzy logic elements to improve tissue discrimination in mammography.
- Design an optimal experimental setup for the proposed algorithm to reduce the high computational cost involved in evolutionary algorithms.
- Validate the proposed algorithmic approach for mammography image segmentation by considering standard benchmarks used in medical and computer science communities.

4.5 Scope and Limitations

- This paper proposes a segmentation scheme for breast tissue segmentation in mammographic images based on Genetic Programming using a fuzzy logic fitness function.

- Only Genetic Programming will be explored as the algorithmic technique to build a mammography image segmentation model.
- Breast tissue (adipose tissue and fibroglandular tissue) will be segmented and described from the breast density database to be used, so no cancerous nodules or microcalcifications will be segmented.
- A classifier for breast density will be used only to check that the images segmented with the selected method by genetic programming and fuzzy logic match the description of the ACR BI-RADS standard without using other characteristics than those described in that standard.

4.6 Expected Contributions

As a result of this thesis, the following items are expected to be completed:

- To develop a fuzzy logic-based fitness function that works with genetic programming for mammogram segmentation.
- A mammogram segmentation model based on GP that integrates fuzzy logic to improve the state-of-the-art performance of previously proposed segmentation algorithmic techniques.
- An image analysis system for determining mammogram tissue density according to the ACR BI-RADS standard.
- A detailed study on the interpretability of the ACR BI-RADS standard in the medical community and how its criteria may influence the development of algorithmic techniques to assist as diagnostic support tools.

5 Methodology

This subsection presents the methodology for this research proposal.

1. A review of the state of the art of different works in image segmentation with genetic programming will be carried out, also in works where fuzzy logic is used as a fitness function in an evolutionary computation approach and works in the field of classification and segmentation of mammography images.
2. Mammography images will be preprocessed to be tested in the genetic programming algorithm. We plan to remove the background and the pectoral area to obtain only the breast and avoid noise when generating the breast tissue segmentation model.
3. Selecting the terminal sets and functions for the genetic programming algorithm is essential to exploring the search space and finding the appropriate segmentation method for the breast tissue.
4. A fitness function will be designed based on the properties of fuzzy logic that is suitable to be integrated with genetic programming and generates a suitable segmentation method for mammary tissues.
5. A study will be carried out to select the values to be used in the different parameters that make up genetic programming.
6. The proposed genetic programming algorithm with fuzzy fitness function will be validated using the images generated by the segmentation method selected by the said algorithm. The ACR BI-RADS characteristics will be extracted from the segmented images for subsequent classification and comparison with state of the art.
7. The algorithm will first be tested on two datasets: the Breast Cancer Digital Repository (BCDR), which has a collection of 1010 mammography images.

The images were analyzed and labeled based on BI-RADS by a group of expert radiologists. In addition, the Mammographic Image Analysis Society (MIAS) dataset contains 322 mammography images labeled and evaluated by expert physicians in the United Kingdom. An example of the images from the BCDR dataset.

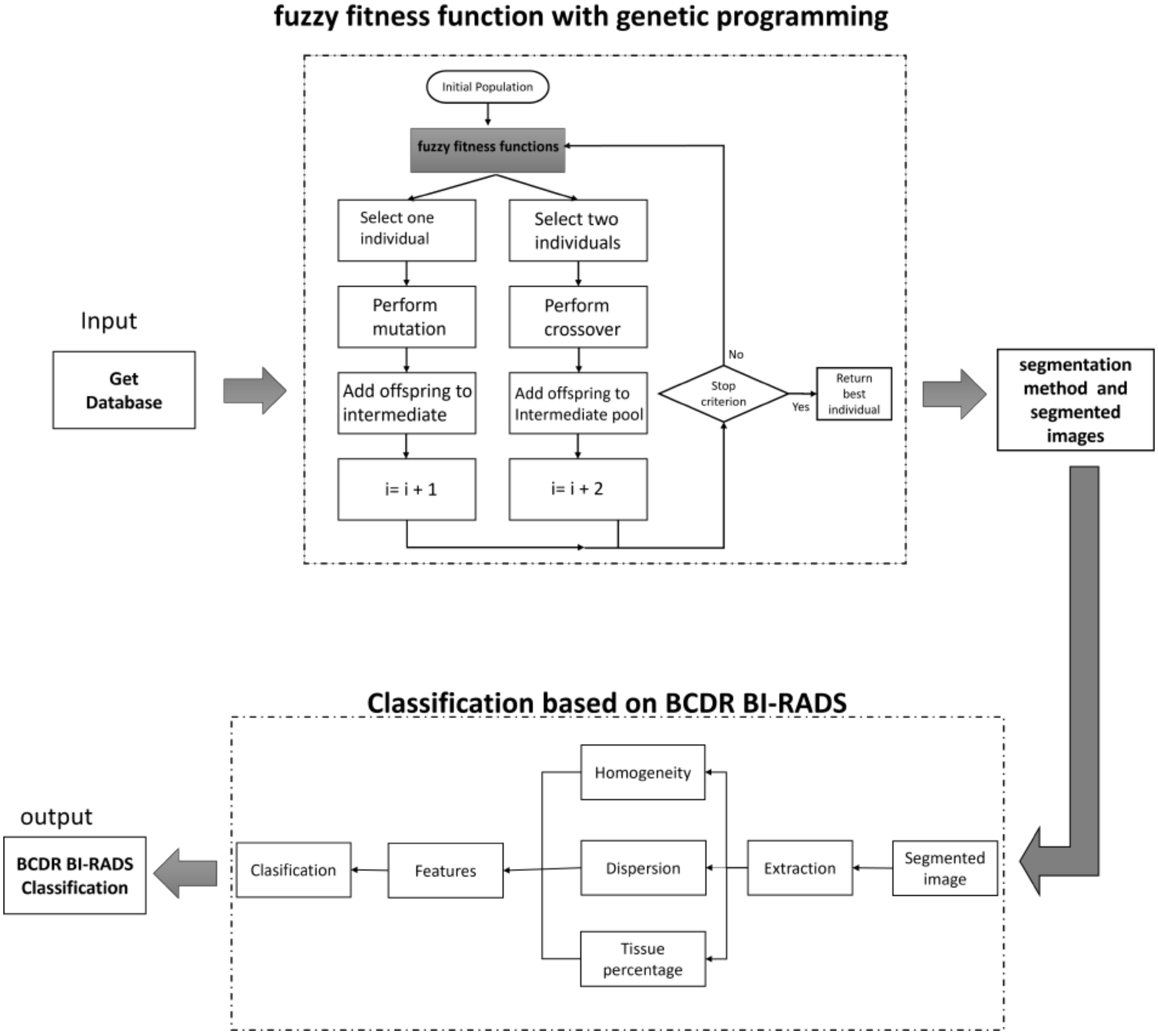


Figure 14: General methodology.

6 Preliminary Results

In Subsection 5.1, the extraction of the breast area is describes, removing the pectoral region and the labels placed by the radiologists found on the mammograms.

In Subsection 5.2, the initial experiments with GP for mammograms segmentation are details. Our experimental designs consists of the following experiments:

- The first experiment modified the genetic programming toolbox for breast tissue segmentation. The first test was performed with general image processing operations for segmentation, such as histogram equalization and contrast enhancement, among others. These operations were used as input functions to the genetic program to generate the segmentation method. In this experiment, accuracy was used as a function of the fitness that qualified the individuals in each population.
- For the second experiment, the set of input functions was modified using more specific operations described in the state-of-the-art for breast tissue segmentation, such as homogeneity, correlation, and local binary patterns, among others. The fitness function was changed to be more consistent with image segmentation. The fitness function used to evaluate individuals in this experiment was the Jaccard index.
- The last experiment was based on generating a new fitness function using fuzzy logic. The new fitness function is based on three evaluation metrics used in image processing Jaccard Index, Signal to Noise Ratio (SNR), and F1 measure that are combined with fuzzy logic. This last experiment aims to verify that fuzzy logic can be used as a fitness function in a genetic program. It is worth mentioning that in this experiment, we used the same set of functions as in the previous experiment.

Results from experiments 2 and 3 were compared in order to assess the effectiveness of integrating fuzzy logic in the fitness function that leads the search for the mammogram segmentation model.

6.1 Mammogram images preprocessing and labeling

Mammographic images were obtained from The Breast Cancer Digital Repository database. Before entering the genetic programming algorithm, these images are preprocessed to remove the pectoral area and the labels placed by the radiologist that can generate noise during segmentation. The pectoral area is not used since only tissue and fat found in the chest are of interest. In this process, the pectoral area is not used since it is only interested in segmenting the tissue and fat of the breast. An example of labels and the pectoral area can be seen in Figure 15, where the areas marked in red belong to the pectoral area and the labels placed by the radiologist.

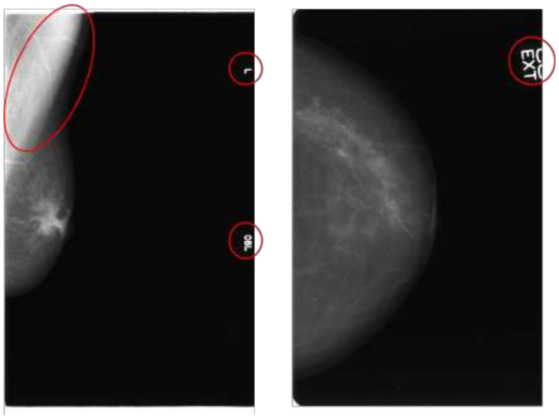


Figure 15: Mammogram images containing labels and pectoral area.

For the experiments carried out, 376 mammograms were preprocessed, which are divided into the different classes of ACR BI-RADS. The distribution can be seen in the Table 6.1.

Table 4: Mammograms used in experimentation.

Class ACR BI-RADS	Description	Num.Mammograms
Class A	The breast is composed almost entirely of fat, with <25% fibroglandular tissue.	94
Class B	Breast tissue is scattered throughout the breast, 26-50% fibroglandular tissue.	94
Class C	The fabric is more heterogeneous and occupies more space inside the breast, from 51 to 75% of fibroglandular tissue.	94
Class D	The tissue occupies almost the entire breast area, >75% fibroglandular tissue.	94

Thresholding was applied to the image and thus be able to better observe the blobs within it. Objects smaller than 1000 pixels were selected and eliminated with an area criterion. In the case of mammograms, the objects with such dimensions are labels and noise in general in the image. An example of this process can be seen in Figure 16.

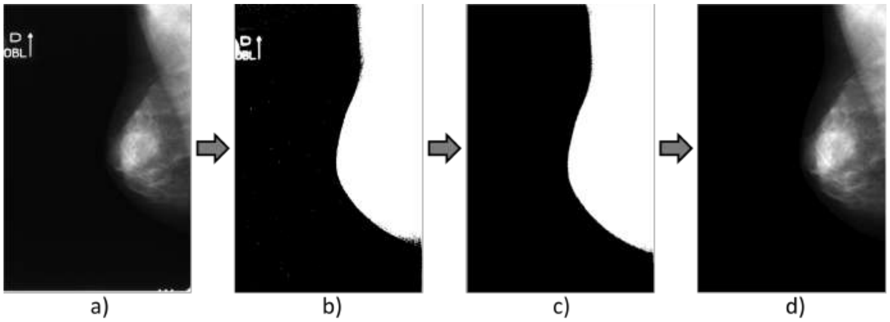


Figure 16: Procedure to remove labels and noise in general from the image: a) Original image, b) Thresholded image, c) Objects smaller than 1000 pixels are removed, d) Results.

In order to extract the pectoral area of the breasts, the images were placed in the same horizontal direction since not all mammograms come in only one direction. Some breast were attached to the right side and others to the left; this made it difficult to extract the pectoral area. Therefore the breast were glued to the left side for better manipulation.

Once all images were in the same direction, they were rotated 30° to be able to make a straight cut that will eliminate the pectoral area. After making the straight cut, the image is returned as it was previously, leaving the image with only the breast area. The turning and cutting process can be seen in the Figure 17.

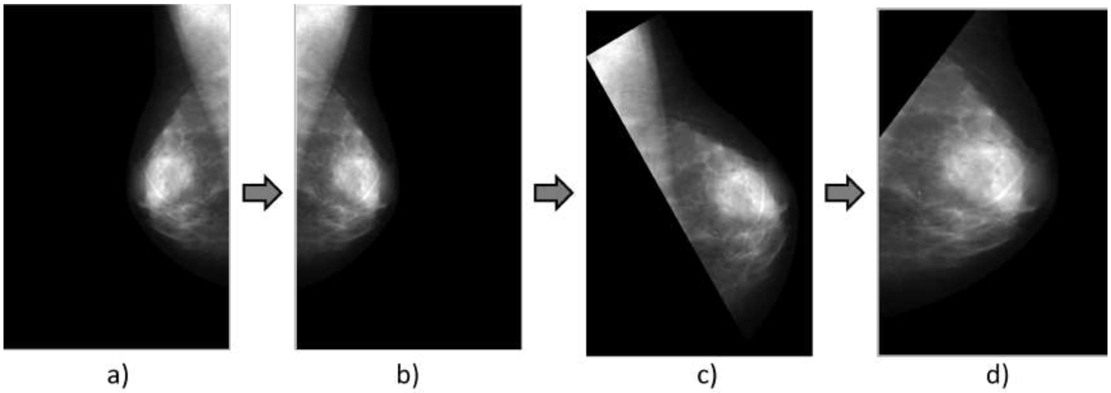


Figure 17: Extraction process of the pectoral area: a) original image, b) rotated image, c) rotated image 30°, d) image result without pectoral.

They selected 75 previously preprocessed mammography images for training. The image used was 19 of each ACR BI-RADS class.

Fibroglandular tissue patches and fat were extracted from the selected images for training. The patch extraction process was performed with the MATLAB Image Labeler application [59]. This application allows to label regions of interest to extract important areas and train or validate algorithms.

The labeling process is carried out manually, so in this case, only the areas known as fibroglandular tissue or fat were labeled; An example of the process can be seen in Figure 18, where two marked areas are observed, an orange area is tissue and blue area blue is fat. Both areas are labelled as 1 and 2, where 1 is fat and 2 is tissue.

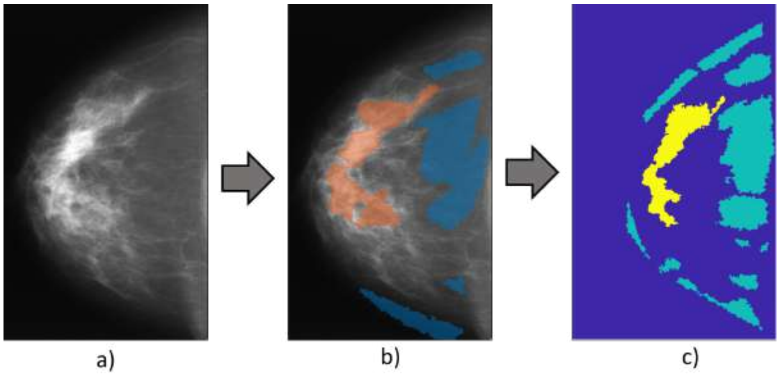


Figure 18: Fat and tissue patch extraction process: a) original image, b) manually labeled image, c) segmented image.

6.2 GP experimental setup

In this first experiment, we explore and become familiar with the genetic programming algorithm for mammography image segmentation. This experiment also aims to verify that genetic programming can first segment mammograms into two classes, breast tissue, and fat.

We started working with genetic programming and mammography images. We used the GPLAB toolbox for Matlab, which was modified to be able to use the images as our set of terminals. Once GPLAB was modified, the set of terminals was determined, which consisted of 16 mammography images for segmentation and 16 previously manually segmented mammography images, which would serve as background.

Subsequently, the operations that would constitute the set of functions for the genetic program were selected. Most of these operations are generally used for image segmentation, and we also use arithmetic operations Table 5. The fitness function used for this experiment was accuracy. The images used as ground truth are compared with the images segmented with the segmentation method generated by the genetic program, and the accuracy of this comparison is obtained. Other elements of genetic programming such as population size, number of generations, tree size constraints, crossover, and mutation were used as they were by default in GPLAB.

Table 5: Set of functions used for the first experiment.

Functions	**Operations**
Arithmetic operators	$*,/,+,-$
Image processing operations	Threshold, Edge Detector, Gaussian Filter, Laplacian Filter, Image Complement, Contrast, Histogram Equalization.

In the experiment with 16 mammography images, it was observed that the genetic program performed the tissue and fat segmentation acceptably, obtaining an accuracy of 67.52%. However, the accuracy of the fitness function can be improved by using another metric to qualify the image segmentation. Therefore, once the results of the first experiment were observed, we carried out other experiments with other types of operations for the set of functions, and the fitness function was changed, in addition to using a set of larger images to test the algorithm of genetic programming better.

6.2.1 Experiment 2: Jaccard index as a fitness function

For the second experiment, we proposed to use a fitness function more specific to image processing to evaluate the individuals in the genetic program. The measure used for this experiment was the Jaccard index. It measures the similarities between sets to evaluate the correct classification between two binary images, A and B. Therefore, the Jaccard Index is defined in Eq. 2

$$JI = \frac{TP}{TP + FP + FN} \tag{2}$$

Where the TP are the true positives, or those pixels marked as 1 in A and B. FP false positives or those values marked as 1 in A and 0 in B. And FN the false negatives between A and B, being 0 in A and 1 in B.

In the case of this experiment, mammogram images already processed with the method selected by the genetic program were used as the A element. For the B element, we used manually segmented images of each input image.

The used set of functions more specific operations that gave good results in state-of-the-art breast density segmentation. Among the selected operations are filters, morphological operations, and arithmetic operations. The complete set of functions used is shown in the Table 6.

Table 6: Functions set for GP

Set of functions	
Morphological operations	Image enhancement features
Erosion	Subtraction
Dilatation	Histogram equalization
Opening	Image intensity
Lock	Entropy
Top Tophat	General texture
Tophat bottom	Edge detection
Connectivity	Co-occurrence matrix with window of 3,5
Region fill	Co-occurrence matrix with window of 7,9
Perimeter of images	Co-occurrence matrix with window of 15

The terminal set consists of 75 mammography images and their respective manual segmentation. Therefore, the terminal set consists of 150 images. Manual segmentation separates breast tissue and fat. These segmented images are used for the fitness function of the Jaccard index to evaluate the individuals. Genetic programming is a stochastic algorithm. Therefore, several experimental samples are required to demonstrate their robustness. For the initial empirical evaluation, 5 runs of the proposed algorithm were performed. The GP configuration is shown in the Table 7. Genetic programming is a computationally expensive algorithmic technique, so in this initial phase of the research, small population size and number of generations were set as stopping conditions. The rest of the parameters were set according to a standard GP.

Table 7: Running parameters of GPLAB to perform the experiments.

Population size	50 individuals
Generations	50 generations
Initialization	6-depth full initialization
Operator probabilities	crossover = 0.5, mutation = 0.5
Bloat control	17-depth limit
Selection	Lexicographic tournament of size 5
Elitism in parents selection	Keep best individual

As a result of this experiment, in addition to the segmented mammogram images, a segmentation method represented as a tree given by the genetic program was obtained. The segmentation method generated by each run of the genetic programming algorithm was tested with 300 more mammography images. One of the results of this segmentation can be seen in the Figure 19, where four mammograms can be observed, each corresponding to each ACR BI-RADS class. The yellow areas correspond to tissue, and the green areas to fat.

Based on the results obtained from the breast tissue segmentation from the 300 images, breast density classification was performed by extracting the tissue and fat characteristics described in the ACR BI-RADS. This proved that the different breast tissues could be selected and classified using the methods generated by genetic programming. A Support Vector Machine (SVM) classifier was used for classification. It is worth mentioning that the mammography images are already labeled with

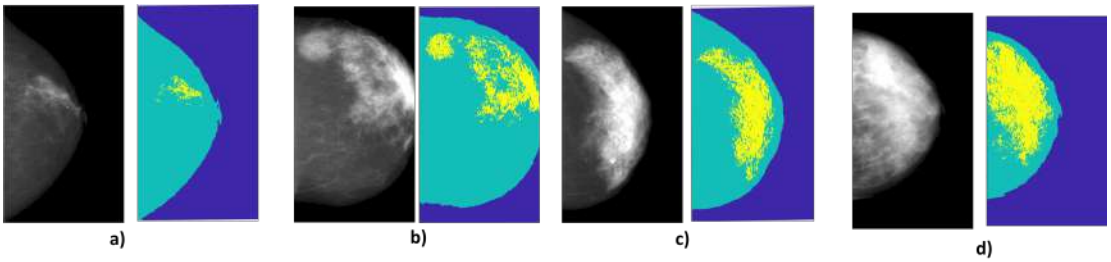


Figure 19: Segmented mammography with the method generated by genetic programming with fitness function Jaccard Index.: a) original image and segmented image of class A, b) original image and segmented image of class B, c) original image and segmented image of class C, d) original image and segmented image of class D.

their respective ACR BI-RADS class given by experts. Therefore, the labels were the validation of the classifier. The classification results can be seen in the Table 8.

Table 8: Results of breast density classification with fitness function Jaccard Index.

Number of runs	**Population size**	**Number of generations**	**Accuracy**
1	50	50	75.00%
2	50	50	74.05%
3	50	50	76.70%
4	50	50	75.21%
5	50	50	75.50%
Mean			**75.29%**

6.2.2 Experiment 3: Fuzzy fitness function

In the last experiment, we changed the fitness function to explore our possibilities with fuzzy logic as a fitness function. Therefore we generated a fitness function based on fuzzy logic to observe how it behaves in combination with genetic programming. The fitness function is based on the combination of three metrics used in image processing that rate how well the segmentation of an image is performed. The metrics that combined were the Jaccard index already explained above, and the other metrics are described below:

- Signal to Noise Ratio (SNR) is used in image processing to characterize the quality of an image mathematically expressed in the Equation 3 where μ_{sing} is the mean value of the signal and σ_{sing} is the standard deviation of the signal

$$SNR = \frac{\mu_{sing}}{\sigma_{sing}} \tag{3}$$

- F1 measure is a combination of precision measurement and recall in a single value is mathematically expressed in the Equation 4

$$F1 = 2 * \frac{precision * recall}{precision + recall} \tag{4}$$

The three metrics were integrated into a fuzzy model to generate a single fitness function that drives the search process of the tissue and fat segmentation method. To generate this single function, we started by defining a set of fuzzy rules to relate the results of the numerical segmentation metrics to the quality of the evolved segmentation model.

To generate the fuzzy rules, we have to give fuzzy sets defined by the membership functions that will be the inputs of our fuzzy fitness function. An example can be seen in Figure 21, where three membership functions are defined according to the segmentation value extracted by the Jaccard Index. The membership functions indicate whether the segmentation is of a low, medium, or high quality. Therefore, the fuzzy outputs were defined as High segmentation quality (high fitness), Medium segmentation quality (medium fitness), Low segmentation quality (low fitness), and Very low fitness (very low fitness). Depending on the aptitude obtained by each individual in the population, the solutions will remain or not for the next generation.

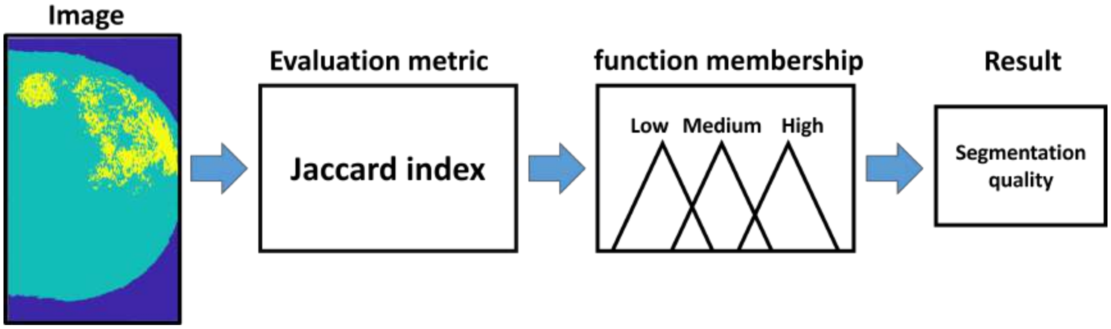


Figure 20: Jaccard Index Membership Features.

Some examples of the fuzzy rules proposed for creating our fuzzy fitness are describe next:

- IF Jaccard Index is high and SNR is high and F1 is high THEN fitness is high.
- IF Jaccard Index is medium and SNR high and F1 high THEN aptitude high.
- IF Jaccard Index is medium and SNR medium and F1 high THEN medium fitness.
- IF Jaccard Index is medium and SNR medium and F1 medium THEN medium fitness.
- IF Jaccard Index is medium and SNR low and F1 high THEN aptitude low.
- IF Jaccard Index is low and SNR is low and F1 is low THEN very low fitness.

Therefore, the proposed fuzzy fitness function showed how well the search for the tissue and fat segmentation method is being performed. In the fig- you can see how the structure of the fuzzy fitness function is in a general way.

Once the new fitness function was generated, we performed experiments using the terminal set with 75 mammography images and manually segmented images. The function set was the same as the one used in the previous experiment and

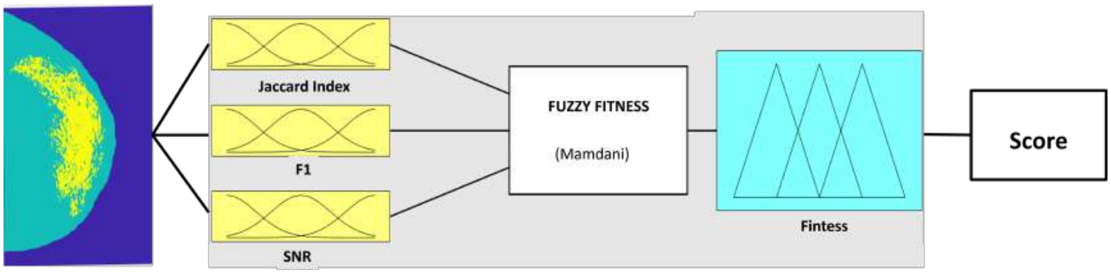


Figure 21: General fuzzy fitness function process.

can be seen in the Table 7. Five experimental runs were performed to check that they did not randomly generate the result. Subsequently, we tested each of the segmentation methods provided by the genetic program in each run. This was done with 300 more mammography images, and from the images generated with each segmentation method, the extracted features defined in ACR BI-RADS for further classification. The results can be seen in Table 9.

Table 9: Fuzzy fitness function result.

Number of runs	Population size	Number of generations	Accuracy
1	50	50	78.74%
2	50	50	79.51%
3	50	50	79.45%
4	50	50	80.11%
5	50	50	80.75%
Mean			**79.71%**

In the Figure 22a, you can see an original mammogram that went through the segmentation method given by the genetic program. In the Figure 22b, we can see the result of the segmentation. In the areas that are yellow are those that contain tissue, and these are extracted the number of components to see the dispersion that has these areas of tissue. Likewise, the image was applied homogeneity, and the yellow pixels and green color were counted to extract the percentage of tissue.

These were the characteristics that entered the SVM classifier, obtaining the results that can be seen in the table above.

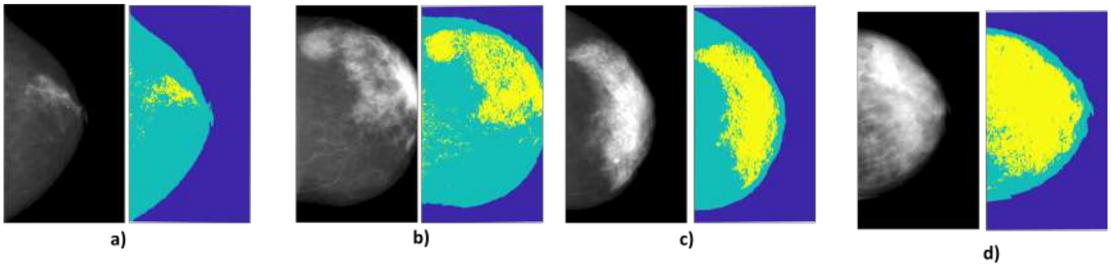


Figure 22: Segmented mammography with the method generated by genetic programming: a) original image and segmented image of class A, b) original image and segmented image of class B, c) original image and segmented image of class C, d) original image and segmented image of class D.

6.2.3 Results discussion

In Figure 23, results are compared the results obtained from the two fitness functions proposed to guide the search for the breast density segmentation method. As we can see, the upper images are the results of the Jaccard Index, and the lower images are obtained with the fuzzy fitness function. When comparing the two results visually, it can be seen that the diffuse fitness function gives a better result to segment the tissue as it detects better where it is located. However, in the results with the fitness function with the Jaccard index, it can be seen that there are areas within the mammogram that cannot detect tissue even if it is present.

Results obtained from genetic programming with Jaccard Index as a fitness function obtained an average of 75.29% and the genetic program guided by fuzzy fitness functions obtained an average of 79.71%. These results showed that a tailored design fitness function based on fuzzy logic to guide the search for a segmentation model of breast tissue supports an improvement in the classification of mammograms density. This research proposal relies on the computational strengths of genetic

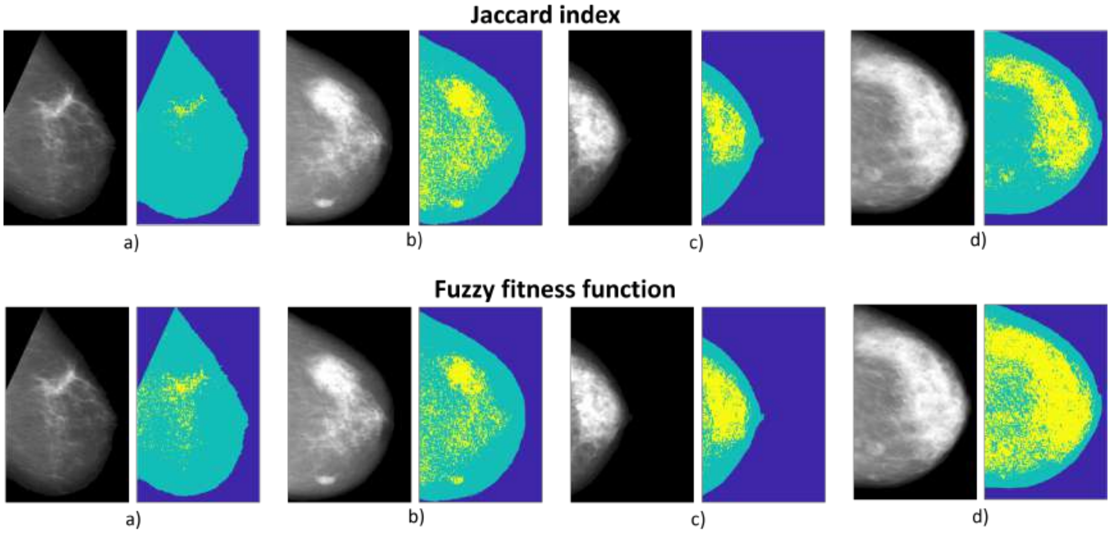


Figure 23: Segmented mammography with the method generated by genetic programming: a) original image and segmented image of class A, b) original image and segmented image of class B, c) original image and segmented image of class C, d) original image and segmented image of class D.

programming and fuzzy logic in problems such as image segmentation. On the one hand, genetic programming allows to evolve strong non-linear models while being able to represent not only local but global image data. On the other hand, fuzzy logic can optimally detect those non-crisp boundaries at image regions as those commonly present in mammograms.

Table 10: Results comparison

Fitness function	**Accuracy**
Jaccard Index	75.29%
Fuzzy fitness	79.71%

7 Conclusions

This proposal will develop a segmentation model based on genetic programming in combination with fitness functions based on fuzzy logic to evaluate individuals. The purpose of generating a segmentation model for mammography images is to aid in the automatic classification of breast density and provide a detailed description of how the breast tissue is distributed to help the physician provide a better diagnosis. Genetic programming has the qualities of being flexible and robust. It can generate linear and non-linear solutions. The operations they use can be low, medium, and high level, giving us better possibilities to generate an optimal mammographic image segmentation method. Fuzzy logic identifies objects that can belong to more than one class. As a fitness function, it will help us with the segmentation of images into pixels that belong to a single class but also with the combined pixels that belong to more than one class. Due to the nature of mammograms, in which we can observe a mixture of tissues, not belonging to one type of tissue or another. Fuzzy fitness functions will help guide the search of the genetic programming algorithm to find an optimal and descriptive segmentation method for mammography images.

Although there are mammography segmentation techniques, many of them are not performed automatically and require an expert to select the program's values to segment the images. In addition, they do not treat the areas where the tissues are combined (fibroglandular tissue and fat), so information can be lost in these areas, and a correct segmentation cannot be carried out.

7.1 Publications Plan

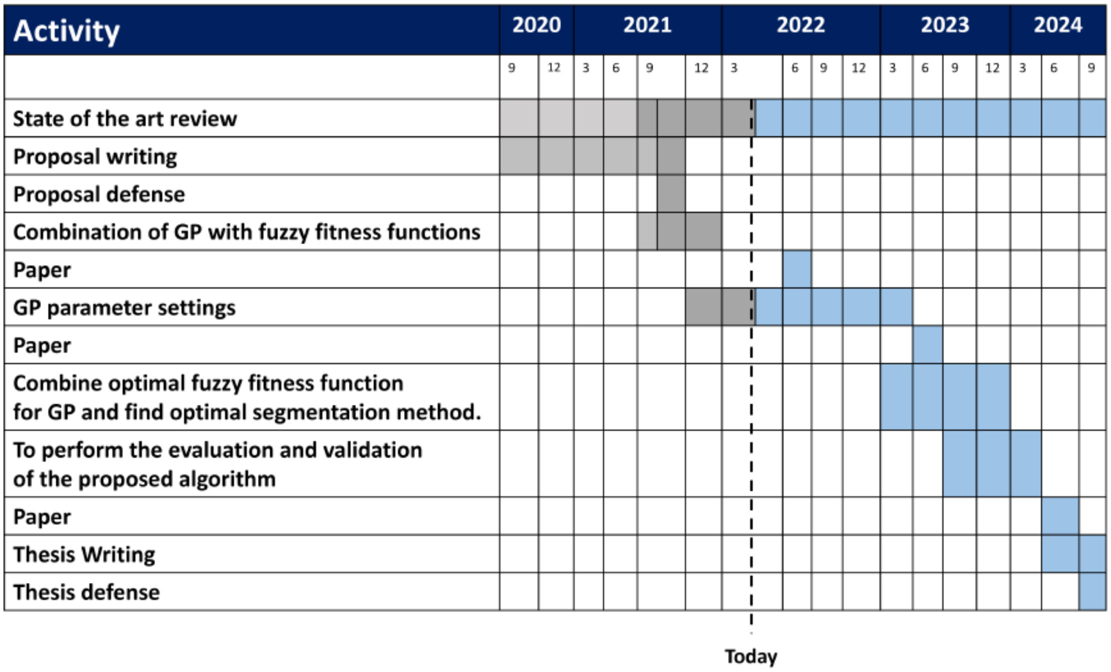
We aim to publish three articles, two from journals and one from an international congress during the doctorate. The dates, together with the name of the journals and the congress, can be seen in the Table 7.1.

Table 11: Publication plan table.

Date	Topic	Congress/Journal
05/06/2022	Genetic programming using fuzzy fitness functions.	-Journal Applied Soft Computing
01/10/2022	Breast tissue segmentation with genetic progrmaming	-Computer Methods and Programs in Biomedicine. -Journal of bimedical Informatics
01/03/2023	Breast density classification with a new approach to breast tissue segmentation using genetic programming and fuzzy fitness functions.	-International Instrumentation & Measuement Technology (IEEE)

7.2 Schedule of activities

The schedule of activities and progress to date can be seen in the figure 24.



Activity	2020		2021				2022				2023				2024		
	9	12	3	6	9	12	3	6	9	12	3	6	9	12	3	6	9
State of the art review	▨	▨	▨	▨	▨	▨	▨🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦
Proposal writing	▨	▨	▨	▨	▨												
Proposal defense					▨												
Combination of GP with fuzzy fitness functions					▨	▨											
Paper								🟦									
GP parameter settings						▨	▨🟦	🟦	🟦	🟦	🟦						
Paper												🟦					
Combine optimal fuzzy fitness function for GP and find optimal segmentation method.											🟦	🟦	🟦	🟦			
To perform the evaluation and validation of the proposed algorithm													🟦	🟦	🟦		
Paper																🟦	
Thesis Writing																🟦	🟦
Thesis defense																	🟦

Figure 24: schedule of activities.

References

[1] R. M. Haralick and L. G. Shapiro, "Image segmentation techniques," *Computer vision, graphics, and image processing*, vol. 29, no. 1, pp. 100–132, 1985.

[2] A. Landström, *Elliptical Adaptive Structuring Elements for Mathematical Morphology.* PhD thesis, Luleå tekniska universitet, 2014.

[3] C. G. Escalona, "Problemas de segmentación y deteción de bordes en imagenes digitales con información borrosa," *Tesis doctoral, Universidad Complutense de Madrid*, pp. 1–135, 2019.

[4] P. Q. imbeni, "Procesamiento digital de imágenes," *Universidad Nacional del Sur, Argentina*, pp. 1–5, 2015.

[5] S. Minaee, Y. Y. Boykov, F. Porikli, A. J. Plaza, N. Kehtarnavaz, and D. Terzopoulos, "Image segmentation using deep learning: A survey," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 2021.

[6] V. P. Neira, "Densidad mamaria y riesgo de cáncer mamario," *Revista Médica Clínica Las Condes*, vol. 24, no. 1, pp. 122–130, 2013.

[7] S. D. Tzikopoulos, M. E. Mavroforakis, H. V. Georgiou, N. Dimitropoulos, and S. Theodoridis, "A fully automated scheme for mammographic segmentation and classification based on breast density and asymmetry," *computer methods and programs in biomedicine*, vol. 102, no. 1, pp. 47–63, 2011.

[8] R. Poli, "Genetic programming for feature detection and image segmentation," in *AISB Workshop on Evolutionary Computing*, pp. 110–125, Springer, 1996.

[9] A. Khan, A. S. Qureshi, N. Wahab, M. Hussain, and M. Y. Hamza, "A recent survey on the applications of genetic programming in image processing," *arXiv preprint arXiv:1901.07387*, 2019.

[10] L. A. Zadeh, “Fuzzy logic,” *Computer*, vol. 21, no. 4, pp. 83–93, 1988.

[11] L. M. Sharma, Neeraj y Aggarwal, “Técnicas automatizadas de segmentación de imágenes médicas,” *Journal of medical physics / Association of Medical Physicists of India.*

[12] I. Cruz-Vega, C. A. R. García, P. G. Gil, J. M. R. Cortés, and J. d. J. R. Magdaleno, “Genetic algorithms based on a granular surrogate model and fuzzy aptitude functions,” in *2016 IEEE Congress on Evolutionary Computation (CEC)*, pp. 2122–2128, IEEE, 2016.

[13] T. Singh, N. Kharma, M. Daoud, and R. Ward, “Genetic programming based image segmentation with applications to biomedical object detection,” in *Proceedings of the 11th Annual conference on Genetic and evolutionary computation*, pp. 1123–1130, 2009.

[14] “Una revisión de los algoritmos de segmentación de imágenes médicas,” *Transacciones respaldadas por EAI sobre tecnología y salud generalizadas.*

[15] S. D. Yanowitz and A. M. Bruckstein, “A new method for image segmentation,” *Computer Vision, Graphics, and Image Processing*, vol. 46, no. 1, pp. 82–95, 1989.

[16] P. F. Nacken, “Image segmentation by connectivity preserving relinking in hierarchical graph structures,” *Pattern recognition*, vol. 28, no. 6, pp. 907–920, 1995.

[17] S. Patra, R. Gautam, and A. Singla, “A novel context sensitive multilevel thresholding for image segmentation,” *Applied soft computing*, vol. 23, pp. 122–127, 2014.

[18] “Segmentación automática de imágenes por crecimiento de región dinámica y fusión de múltiples resoluciones,” *transacciones IEEE sobre procesamiento de imágenes.*

[19] C. R. Brice and C. L. Fennema, "Scene analysis using regions," *Artificial intelligence*, vol. 1, no. 3-4, pp. 205–226, 1970.

[20] J. R. Irons and G. W. Petersen, "Texture transforms of remote sensing data," *Remote Sensing of Environment*, vol. 11, pp. 359–370, 1981.

[21] J. Ríos-Díaz, J. J. Martínez-Payá, and M. E. del Baño Aledo, "El análisis textural mediante las matrices de co-ocurrencia (glcm) sobre imagen ecográfica del tendón rotuliano es de utilidad para la detección cambios histológicos tras un entrenamiento con plataforma de vibración.(textural analysis by means of a grey level co-occurrence matrix method on patellar tendon ultrasonography is useful for the detection of histological changes after whole-body vibration training).," *Cultura, Ciencia y Deporte*, vol. 4, no. 11, pp. 91–102, 2009.

[22] C. Devarriya, Divyaansh y Gulati, "Clasificación de datos de cáncer de mama desequilibrada utilizando funciones de aptitud novedosas en la programación genética," *Expert Systems with Applications.*

[23] A. Khan, A. S. Qureshi, N. Wahab, M. Hussain, and M. Y. Hamza, "A recent survey on the applications of genetic programming in image processing," *Computational Intelligence*, vol. 37, no. 4, pp. 1745–1778, 2021.

[24] W.-J. Choi and T.-S. Choi, "Genetic programming-based feature transform and classification for the automatic detection of pulmonary nodules on computed tomography images," *Information Sciences*, vol. 212, pp. 57–78, 2012.

[25] J. Wang and Y. Tan, "Morphological image enhancement procedure design by using genetic programming," in *Proceedings of the 13th annual conference on Genetic and evolutionary computation*, pp. 1435–1442, 2011.

[26] W. Smart and M. y. o. Zhang, "Estrategias de clasificación para la clasificación de imágenes en la programación genética," in *Actas de la conferencia sobre computación de imágenes y visión.*

[27] A. E. Eiben, J. E. Smith, *et al.*, *Introduction to evolutionary computing*, vol. 53. Springer, 2003.

[28] K. Neshatian and M. Zhang, "Genetic programming and class-wise orthogonal transformation for dimension reduction in classification problems," in *European Conference on Genetic Programming*, pp. 242–253, Springer, 2008.

[29] "Computación blanda y lógica difusa," in *Conjuntos difusos, lógica difusa y sistemas difusos: artículos seleccionados de Lotfi a Zadeh*, World Scientific.

[30] "¿se necesita lógica difusa?," *Ciencias de la información.*

[31] B. Kosko and S. Isaka, "Fuzzy logic," *Scientific American*, vol. 269, no. 1, pp. 76–81, 1993.

[32] J. A. Harvey and V. E. Bovbjerg, "Quantitative assessment of mammographic breast density: relationship with breast cancer risk," *Radiology*, vol. 230, no. 1, pp. 29–41, 2004.

[33] "Densidad mamaria y riesgo de cáncer de mama: una revisión práctica," in *Mayo Clinic Proceedings.*

[34] B. T. Nicholson, A. P. LoRusso, M. Smolkin, V. E. Bovbjerg, G. R. Petroni, and J. A. Harvey, "Accuracy of assigned bi-rads breast density category definitions," *Academic radiology*, vol. 13, no. 9, pp. 1143–1149, 2006.

[35] "Patrones mamarios como índice de riesgo de desarrollar cáncer de mama," *American Journal of Roentgenology.*

[36] J. W. Byng, N. Boyd, E. Fishell, R. Jong, and M. J. Yaffe, "The quantitative analysis of mammographic densities," *Physics in Medicine & Biology*, vol. 39, no. 10, p. 1629, 1994.

[37] I. T. Gram, E. Funkhouser, and L. Tabár, "The tabar classification of mammographic parenchymal patterns," *European journal of radiology*, vol. 24, no. 2, pp. 131–136, 1997.

[38] L. Liberman and J. H. Menell, "Breast imaging reporting and data system (bi-rads)," *Radiologic Clinics*, vol. 40, no. 3, pp. 409–430, 2002.

[39] C. y. B. D'Orsi, "Sistema de datos e informes de imágenes de mama (bi-rads)," *Atlas de imágenes de mama.*

[40] M. Lopez, N. Posada, D. C. Moura, R. R. Pollán, J. M. F. Valiente, C. S. Ortega, M. Solar, G. Diaz-Herrero, I. Ramos, J. Loureiro, *et al.*, "Bcdr: a breast cancer digital repository," in *15th International conference on experimental mechanics*, vol. 1215, 2012.

[41] J. Liang, J. Wen, Z. Wang, and J. Wang, "Evolving semantic object segmentation methods automatically by genetic programming from images and image processing operators," *Soft Computing*, pp. 1–14, 2020.

[42] J. Liang, Y. Xue, and J. Wang, "Genetic programming based feature construction methods for foreground object segmentation," *Engineering Applications of Artificial Intelligence*, vol. 89, p. 103334, 2020.

[43] Y. Liang, M. Zhang, and W. N. Browne, "Figure-ground image segmentation using feature-based multi-objective genetic programming techniques," *Neural Computing and Applications*, vol. 31, no. 7, pp. 3075–3094, 2019.

[44] Y. Liang, M. Zhang, and W. N. Browne, "Multi-objective genetic programming for figure-ground image segmentation," in *Australasian conference on artificial life and computational intelligence*, pp. 134–146, Springer, 2016.

[45] Y. Liang, M. Zhang, and W. N. Browne, "Image feature selection using genetic programming for figure-ground segmentation," *Engineering Applications of Artificial Intelligence*, vol. 62, pp. 96–108, 2017.

[46] M. Dong, M. G. Eramian, S. A. Ludwig, and R. A. Pierson, "Automatic detection and segmentation of bovine corpora lutea in ultrasonographic ovarian images using genetic programming and rotation invariant local binary patterns," *Medical & biological engineering & computing*, vol. 51, no. 4, pp. 405–416, 2013.

[47] A. Song and V. Ciesielski, "Texture segmentation by genetic programming," *Evolutionary Computation*, vol. 16, no. 4, pp. 461–481, 2008.

[48] M. E. Roberts and E. Claridge, "An artificially evolved vision system for segmenting skin lesion images," in *International Conference on Medical Image Computing and Computer-Assisted Intervention*, pp. 655–662, Springer, 2003.

[49] S. Mishra and M. Panda, "Medical image thresholding using genetic algorithm and fuzzy membership functions: A comparative study," in *Research Anthology on Multi-Industry Uses of Genetic Programming and Algorithms*, pp. 896–916, IGI Global, 2021.

[50] I. Cruz-Vega, C. R. Garcia, H. J. Escalante, J. de Jesus Rangel-Magdaleno, and J. M. R. Cortes, "Surrogate modeling based on granular models and fuzzy aptitude functions," *Applied Soft Computing*, vol. 65, pp. 21–32, 2018.

[51] B. Chakraborty, "Genetic algorithm with fuzzy fitness function for feature selection," in *Industrial Electronics, 2002. ISIE 2002. Proceedings of the 2002 IEEE International Symposium on*, vol. 1, pp. 315–319, IEEE, 2002.

[52] D. Bhandari, S. K. Pal, and M. K. Kundu, "Image enhancement incorporating fuzzy fitness function in genetic algorithms," in *[Proceedings 1993] Second IEEE International Conference on Fuzzy Systems*, pp. 1408–1413, IEEE, 1993.

[53] "Clasificación de las categorías de densidad mamaria según las redes neuronales se-attention," *Métodos y programas informáticos en biomedicina.*

[54] E. Matsuyama, M. Takehara, D.-Y. Tsai, *et al.*, "Using a wavelet-based and fine-tuned convolutional neural network for classification of breast density in

mammographic images," *Open Journal of Medical Imaging*, vol. 10, no. 01, p. 17, 2020.

[55] A. Krizhevsky, I. Sutskever, and G. E. Hinton, "Imagenet classification with deep convolutional neural networks," *Advances in neural information processing systems*, vol. 25, pp. 1097–1105, 2012.

[56] A. Rampun, P. J. Morrow, B. W. Scotney, and H. Wang, "Breast density classification in mammograms: An investigation of encoding techniques in binary-based local patterns," *Computers in Biology and Medicine*, vol. 122, p. 103842, 2020.

[57] A. Rampun, P. J. Morrow, B. W. Scotney, and J. Winder, "Fully automated breast boundary and pectoral muscle segmentation in mammograms," *Artificial intelligence in medicine*, vol. 79, pp. 28–41, 2017.

[58] I. Valencia-Hernandez, H. Peregrina-Barreto, C. Reyes-Garcia, and G. Lopez-Armas, "Density map and fuzzy classification for breast density by using bi-rads," *Computer Methods and Programs in Biomedicine*, vol. 200, p. 105825, 2021.

[59] Matlab, "Get started with the image labeler,"