An evolutionary algorithm for the segmentation of muscles and bones of the lower limb.

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Abstract. In the field of medical image segmentation, muscles segmentation is a problem that has not been fully resolved yet. This is due to the fact that the basic assumption of image segmentation, which asserts that a visual distinction should exist between the different structures to be identified, is infringed. As the tissue composition of two different muscles is the same, it becomes extremely difficult to distinguish one another if they are near. We have developed an evolutionary algorithm which selects the set and the sequence of morphological operators that better segments muscles and bones from an MRI image. The achieved results shows that the developed algorithm presents average sensitivity values close to 75% in the segmentation of the different processed muscles and bones. It also presents average specificity values close to 93% for the same structures. Furthermore, the algorithm can identify muscles that are closely located through the path from their origin point to their insertions, with very low error values (below 7%).

1. Introduction
Image segmentation has been traditionally done in two ways: one way is tracing each required structure manually in each image in the study. The results obtained with this process precisely represents the anatomy, but are inefficient due to the large amount of time required for obtaining each structure. Another method is to use computer programs that perform this process in an automatic or semi-automatic way, reducing processing times and therefore increasing the efficiency. Furthermore these methods allow reproducibility, feature that cannot be achieved with manual methods. Therefore, the objective is to make these computational methods reach anatomical representations comparable to those obtained manually. It is important to note that with exception of the manual segmentation, there is not yet a universal semiautomatic or automatic segmentation technique that can be used at any application, so it is necessary to adapt the available segmentation techniques to each specific application.

In the field of medical image segmentation, muscles segmentation is a problem that has not been fully resolved yet. This is due to the fact that the basic assumption of image segmentation, which asserts that a visual distinction should exist between the different structures to be
identified, is infringed. As the tissue composition of two different muscles is the same, it becomes extremely difficult to distinguish one another if they are closely located [1].

The algorithms based on mathematical morphology are widely used in the field of digital image processing in the process of extracting information about the geometry and topology of an unknown set of pixels. This is achieved through the use of a test element whose shape and size are known. This element allows to compare and quantify if it is contained or not, within the image. This element is called Structuring Element (SE). For example this kind of algorithms have been used as an aid in the segmentation of the pectoral muscle from mammography studies [2], for the segmentation of computed tomography images [3], among others.

Evolutionary algorithms are adaptative heuristic search algorithms based on the evolutionary ideas of natural selection and genetics. These algorithms use an intelligent exploitation of a random search for solving an optimization problem. However, they are not in any way random, on the contrary they rather use historical information to direct the search to a region of better performance within the search space [4]. Evolutionary algorithms simulate the Charles Darwin principle of Survival of the fittest, i.e., through several generations the fittest individuals survive to achieve the solution of the problem. Each generation consists of a population of sequences of characters that are analogous to the chromosomes of DNA. Each individual represents a point in the search space and a possible solution to the problem. These individuals are taken through the process of evolution, where they compete with each other and the fittest will be more likely to generate offspring. The genes of the best individuals then tend to spread through the population so that two good parents produce in some combinations, offsprings with better performance than their parents [4]. Thus it is expected that the last generation would obtain individuals that carry the best solutions to the initial

In this article we have developed an evolutionary algorithm that aims to identify the set and order of application of different morphological operators, which under a defined set of evolution conditions, may achieve the best segmentation of a group of muscles and bones of the lower limb; from a set of magnetic resonance images (MRI).

2. Evolutionary Algorithm
The developed evolutionary algorithm is based on the algorithm proposed by Janc et al. [5] for the segmentation of trabecular and cortical bone. Jancs’s algorithm has been modified to also achieve the segmentation of muscles. The algorithm presented in this article, aims not only to achieve the segmentation of bone structures, but also muscle structures through morphological operators. Noraini Geraghty [6] describes the general scheme of an evolutionary algorithm. The algorithm presented in this paper uses this scheme, and the functions contained in the Matlab’s digital Image Processing Toolbox (IPT) , for the application of the different morphological operators over the set of MRI. The features of the developed evolutionary algorithm are:

2.1. Chromosome:
The chromosome is the descriptor of the characteristics that determine each one of the individuals that represent a solution to the problem to be solved. For this algorithm was defined a chromosome consisting of 3 different processing blocks located one after the other. The three blocks add up seventy five genes.

1. Gray Level Processing: This block refers to the gray level morphological processing of the image. It is represented by the first twenty-four genes of the chromosome , which in groups of four genes represent the parameters for each of the six possible morphological processes. The structure that represents each of the processes in the chromosome is shown in Figure.
Figure 1. Structure of the genes which encode gray level processing.

- Gene 1: this gene determines the type of SE used. This gene is defined by a number which refers to the geometry of SE. This gene can take the values: 1. Square, 2. Disk, 3. Diamond.
- Gene 2: this gene determines the size of the SE defined by the previous gene. 120 pixels is defined as the maximum size that can take the SE.
- Gene 3: this gene determines the type of processing to be applied. These processes are: 1. Erosion, 2. Dilatation, 3. Closing, 4. Opening, 5. Tophat, 6. Bothat.
- Gene 4: this gene defines the application of the processing. It may take 2 different values: 0. If the processing is not apply, 1. If the processing is applied.

2. Black and white processing: after applying the first processing block, a binarization of the resulting image is performed. This binarization is performed using the IPT’s function `im2bw`. For the determination of the binarization threshold the function `graythresh` is used, this function calculates the global threshold of an image using Otsu method. Once the image has been binarized, the same six processes defined for gray levels are applied; but this time applied to the black and white image. The genes that represent these six processes are determined by the group of genes located from the twenty-fifth gene up to the forty-eighth gene of the chromosome.

3. `bwmorph` function processing: these last processing block is applied to the resulting images of the previous black and white processing. The IPT’s function `bwmorph` allows to apply various morphological operators over black and white images. From all the different operators that this function allows to apply, nine were chosen each of which is represented by three genes of the chromosome. This latter processing block is defined by the group of pixels located from the forty-ninth gene up to the seventy-fifth gene of the chromosome. The structure which represents each of these processes in the chromosome is shown in Figure 2:

Figure 2. Structure of the genes which encode `bwmorph` function processing.

- Gene 1: this first gene determines the morphological operator to be applied over the image. It can take values from: 1. Bridge, 2. Fill, 3. Majority 4. Remove, 5. Shrink, 6. Skel, 7. Spur, 8. Thicken, 9. Thin.
- Gene 2: This gene determines the number of times the operator defined by the previous gene is going to be applied over the image. It was defined to be five the greatest number of times the operator can be applied.
- Gene 3: this gene defines the application of the processing. It may take 2 different values: 0. If the processing is not apply, 1. If the processing is applied.

2.2. Initial Population:
In this block the initial population of the algorithm is defined. The seventy five genes of the chromosome for each individual in the population are selected here. For each gene it is randomly
selected a number between 0 and the maximum value that can take this gene. It is important to clarify that all individuals generated in this block are viable.

2.3. Fitness Calculation:
In this block the fitness of each individual in the population being evaluated is calculated. As an initial step the original image is taken and each processing defined by the chromosome is applied. Then, the Dice coefficient [5] is calculated to measure the fitness of the resulting binary image. This coefficient is calculated as:

\[
Fitness = \frac{2n}{a + b}
\]  

Where, \( n \) is the number of pixels with value 0 which coincide in both images, \( a \) is the number of pixels with value 0 in the image found by the genetic algorithm, and \( b \) is the number of pixels with value 0 in the gold standard.

The obtained fitness values are in the range between 0 and 1. A value of 0 is assigned to images which have no matching pixels with the Gold Standard; and a value of 1 to images which are identical to the Gold Standard. The Gold Standard used in this article is the manual segmentation performed by the medical expert.

2.4. Selection:
Once the fitness of all individuals in the population has been calculated, a selection of the group of individuals which are going to reproduce for the generation of a new population must be performed. In this article a linear ranking selection method with selective pressure control is used. This method sorts individuals regarding their fitness, assigning the first position of the ranking to the individual with the lowest value of fitness, and the \( N \) position to the one with the highest fitness value. The probability of selecting the individual \( i \) is linear and is given by the expression:

\[
ProbS(i) = 2 - SP + 2(SP - 1) \frac{Pos - 1}{Nind - 1}
\]

Where:
- \( SP \): Selective Presion.
- \( Pos \): Position occupied by the individual \( i \) inside the ranking.
- \( Nind \): Number of individuals inside the population.

The value of SP controls the probability of the individuals with the lowest fitness values being selected, increasing their chance when assigning low SP values, and decreasing their chance with highest values. The expression used in this article allows to select SP values between 1 and 2.

2.5. Reproduction
The developed algorithm divides the reproduction block in two consecutive steps: a crossover followed by a mutation.

1. Crossover: In this first step the crossover between the individuals selected in the previous block is made. Figure 3 shows the crossover procedure. In this procedure three random cutting points over the chromosomes are defined, which take into account the division of the chromosome into the three blocks described above. i.e the first random number can take values between one and twenty four, the second value between twenty five and forty eight, and the third value between forty nine and seventy five. This is done in order to ensure that the offspring obtained from the crossover process are viable as their parents.
2. Mutation: mutation of the children generated during the crossover depends on a parameter called mutation probability \( MP \). If a random number between zero and one generated by the algorithm is greater than the value of the selected \( MP \), the mutation of the offspring’s chromosomes is generated. Selection of genes to be mutated is also random. The mutation of a gene is carried within the constraints determined during the generation of the initial population, this ensures that the mutated individuals remain viable. The mutation process is shown in Figure 4.

Once a new population is obtained from the reproduction of the selected individuals, the fitness values are calculated for the new individuals. If the Number of Generations (NG) determined as the stop restriction is reached, the algorithm stops; if not, the selection of the new parents to be reproduced is generated, and all the previously described blocks are applied once again until the NG restriction is reached.
Table 1. Selected working parameters for the evolutive algorithm for each segmented structure.

| Estructure | PopSize | NG     | MP     | SP     | Fitness | Dispersion |
|------------|---------|--------|--------|--------|---------|------------|
| Fem        | 30      | 200    | High   | Variable | 0.9417  | 0.0018     |
| GM         | 50      | 400    | Variable | Variable | 0.8675  | 0.0098     |
| BFCL       | 50      | 400    | Variable | Variable | 0.8205  | 0          |
| SemT       | 50      | 400    | Variable | High    | 0.9310  | 0.0021     |
| SemM       | 100     | 200    | Very Low | High    | 0.5936  | 0          |
| Sar        | 50      | 400    | Variable | High    | 0.8622  | 0          |
| RF         | 50      | 400    | Variable | Variable | 0.9097  | 0.0012     |
| Gra        | 30      | 400    | Variable | High    | 0.9139  | 0          |

From the characteristics of the previously described algorithm, it can be identified that the performance of the evolutive algorithms is influenced by a set of working parameters which defined both the efficiency and quality of the processing results. These parameters are: the Population Size (PopSize), the NG, the MP and the SP. The values used for these parameters in this article are shown in Table 1. These values were determined after analyzing the results obtained by the developed algorithm with different combinations of these four parameters in a randomly selected image of the MRI set. The selection criteria to determine the optimal set of working parameters were: the highest average fitness value and the lowest dispersion among the individuals inside the final generation obtained with the different combination of working parameters and for each segmented structure [7].

3. Performed Tests

Different tests on this article were performed over a set of 130 T2-weighted-spin echo images, with a Relaxation Time of 400 ms, Echo Time 17 ms, a Field of View of 20.48 * 20.48 cm (image size of 512 * 512 pixels and a resolution of 0.4 mm/pixel for both the x axis and the y axis), and a gap between images of 4 mm (z axis). These images were obtained using a 1.5 T Siemens Magnetom Vision device.

The anatomic structures segmented manually and using the developed algorithm were: the femur bone (Fem), and the muscles; Sartorius (Sar), Rectus Femoris (RecF), Gracilis (Gra), Biceps Femoris Long, Head (BFLH), Biceps Femoris Short Head (BFSH), Semitendinosus (SemT), Semimembranosus (SemM) and Gluteus Maximus (GM).

The manually segmented regions were inserted into the evolutive algorithm in order to be used as training structures for this algorithm. The developed algorithm calculates the centroid and the area of the inserted regions. With this information an automatic subsampling of the image is performed and the morphological operators contained inside the chromosome of each individual on the population are applied only to the subsampled image. The subsampled image is defined as the square region whose central point is located in the calculated centroid for the manually segmented region, and whose sides have a size of three times the calculated radius for the manually segmented region.

The quality of the results obtained with the developed algorithm for the segmented anatomical structures, were quantified using the Receiver Operating Characteristic (ROC) analysis [8]. From this analysis the algorithm’s Sensibility and Specificity values were calculated. The confusion matrix for the segmented anatomical structures was also calculated. This matrix shows the algorithm’s ability to distinguish different structures.
4. Results Discussions

Figure 5 shows an example of segmenting the Gra muscle using the working parameters in Table 1. As mentioned above, the segmentation process starts with an automatic subsampling of the image (Figure 5-A). This subsampling is based on the information obtained from the manual segmentation made by the medical expert (Figure 5-B). Once the subsampling of the image has been made, the developed algorithm starts the evolving phase and if the final population is reached, the individual with the highest fitness value inside this population is selected. The information contained by the chromosome of the selected individual, are the set and the sequence of the morphological operators that better segment the muscle. Figure 5-C shows the resulting binary image of the application of the morphological operators over the subsampled image. Figure 5-D shows the region obtained for Gra muscle with the developed algorithm and the manually segmented region.

![Figure 5](image)

**Figure 5.** Gra Muscle Segmentation Process. A) Original MRI, the blue dotted square shows the location of the Gra muscle in the image. B) Gra Manual Segmentation (Gold Standard). C) Gra. Binary image obtained from the morphological processing. D) Segmented Regions Comparison, blue + symbols represents Gra gold standard segmentation and red * symbols represents Gra morphological segmentation.

Table 2 shows the mean calculated values of Sensibility (pixels’s true positive fraction), Specificity (pixels’s true negative fraction), pixels’s False Positive Fraction (FPF) and pixels’s False Negative Fraction (FNF). These values were obtained as the average of the calculated values of sensitivity, specificity, PFP and PFN for each structure in all images where it was present. From the data contained in this table, it can be seen that Sensibility values obtained for all the segmented structures are close to 75%; these values show the good capability of the algorithm on identifying those pixels that actually belong to the muscle that has been segmented. On the other hand, the values obtained for the Specificity (close to 93% in all the segmented structures), and the low values obtained for the FPF (with average value less than 7%); show the good capability of the algorithm on identifying those pixels that actually do not belong to the muscle that has been segmented. These values were expected because the developed algorithm uses the *a priori* knowledge about the location and shape of the segmented muscles.

Despite of the good global results shown by the algorithm, the values obtained for the FPF (close to 20%) shown the tendency that the algorithm have of sub-segment different structures. It can be seen that structures with high cross-sectional area (e.g GM and RecF muscles) presents
the highest values of FPF. This may be because of the initial restriction which determines that the maximum size that the SE can take is 120 pixels. This size could be smaller than the necessary one for representing the actual area of the structures in all the MRI set. The initial maximum size restriction was set based on the resulting maximum areas of the segmented structures, in a preliminary test of the developed algorithm over a randomly selected group of images which belong the set of MRI.

Table 2. Sensibility, Specificity, FPF, FNF values, calculated for each processed structure.

| Structure | Sensibility [%] | Specificity [%] | FPF [%] | FNF [%] |
|-----------|-----------------|-----------------|---------|---------|
| BFLH      | 76.41           | 94.31           | 5.69    | 23.59   |
| BFSH      | 74.38           | 95.20           | 4.80    | 25.62   |
| Fem       | 76.96           | 90.63           | 9.37    | 23.04   |
| GM        | 72.81           | 86.80           | 13.20   | 27.19   |
| Gra       | 82.96           | 98.17           | 1.83    | 17.04   |
| RecF      | 74.79           | 95.75           | 4.25    | 25.21   |
| Sar       | 81.04           | 98.00           | 2.00    | 18.96   |
| SemM      | 72.03           | 87.54           | 12.46   | 27.97   |
| SemT      | 83.78           | 98.25           | 1.75    | 16.22   |

Table 3 shows the confusion matrix calculated for the segmentation of the full MRI set. From this table it can be seen, in the same way as with the ROC analysis, the good performance of the developed algorithm in segmenting the processed structures (Matrix’s Diagonal). Furthermore, it also can be seen the algorithm’s capability to correctly segment muscles which during their path from the origin to the insertion, are closely located. This is the case of the SemM and SemT muscles. For these muscles the confusion matrix shows that the developed algorithm incorrectly classified 2.97% of the processed pixels as belonging to the SemM muscle when actually belonged to the SemT muscle; and 1.94% of the processed pixels in the opposite case. This same situation can be analysed for BFSH and BFLH muscles.

The Column Others in Table 3 refers to the fraction of pixels which the algorithm identified as belonging to one of the processed structures; but the Gold Standard identified as not belonging to any of these structures. These fractions of incorrectly segmented pixels may belong to other tissues inside the set of MRI (e.g adipose tissue), or to other muscles or bones not processed in this article.

Conclusions
In this study we present an algorithm for segmentation of muscles and bones from a series of MRI. This algorithm uses the concepts of evolutionary algorithms to identify the set and order of application of different morphological operators for segmenting each of the muscles and bones. The results obtained from the application of the algorithm to the different structures are consistent with those reported by Janc et al. [5] for identifying spongy and trabecular bone. The results obtained in this study are the bases for the posing in future works, a Model Based segmentation algorithm. This latter algorithm could allow to perform the segmentation of a new serie of MRI using the statistical information collected from the different morphological operators that better segmented the processed structures in a set of training images series; e.g the MRI set processed in this article. In addition, increased use of this statistical information could lead to the selection of the constraints for the algorithm (e.g the maximum size of SE)
Table 3. Results Confusion Matrix.

| Should be Classified as: | Estructura | BFSH | BFLH | Fem | GM | Gra | RecF | Sar | SemM | SemT | Otros |
|--------------------------|------------|------|------|-----|----|-----|------|-----|------|------|-------|
| Were Classified as:      |            |      |      |     |    |     |      |     |      |      |       |
| BFSH                     | 74.38      | 5.91 | 0.11 | 1.33| 0.00| 0.00| 0.00 | 0.00| 0.00  | 0.00 | 18.27 |
| BFLH                     | 1.23       | 76.41| 0.04 | 1.21| 0.00| 0.00| 0.00 | 0.00| 0.00  | 5.19 | 15.92 |
| Fem                      | 0.72       | 0.00 | 76.96| 2.01| 0.00| 0.00| 0.00 | 0.00| 0.00  | 0.00 | 20.31 |
| GM                       | 1.82       | 0.46 | 1.02 | 72.81| 0.02| 0.00| 0.00 | 0.00| 0.00  | 0.00 | 23.87 |
| Gra                      | 0.00       | 0.00 | 0.00 | 0.00| 82.96| 0.00| 0.00 | 0.14| 0.00  | 16.90|       |
| RecF                     | 0.00       | 0.00 | 0.00 | 0.00| 0.00 | 74.79| 3.20 | 0.00| 0.00  | 22.00|       |
| Sar                      | 0.00       | 0.00 | 0.00 | 0.00| 0.00 | 0.00 | 81.04| 0.32| 0.00  | 18.64|       |
| SemM                     | 0.01       | 0.00 | 0.00 | 0.00| 0.00 | 0.00 | 0.00 | 72.03| 2.97  | 24.56|       |
| SemT                     | 0.00       | 3.31 | 0.00 | 0.34| 0.00 | 0.00 | 0.00 | 1.94| 83.78 | 10.63|       |

that better suited to the actual characteristics of the segmented structures and therefore may achieved better results in segmenting muscles and bones.

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