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Automatic retiming method based on genetic algorithm for the detection and the follow-up of dental lesions

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In dental surgery, a great number of pathologies (cysts, granuloma…) presents clinical, radiological and evolutionary aspects considerably polymorphic. Medical imagery and particularly oral imagery, by the means of the digitized images and the image analysis algorithms, constitutes an essential element which leads to a precise presumptive diagnosis. The technique of retiming per subtraction can be thus used to recognize in two-dimensional images evolution of the pathological zones (lesions, tumours). From this point of view, a method of automatic retiming was developed by genetic algorithm to follow the evolution of the pathological zones after parodental treatment. In this article the traditional technique of retiming by specifying its disadvantages for our application and then an automatic model of retiming, which offers promising results, are presented. This tool will make it possible to distinguish, identify, and visualize automatically the form of the pathological structures and their evolution in time. An analysis of form and texture of these structures will allow the identification type of pathology.

1. INTRODUCTION

In spite of the high rate of success met with the parodental treatments, complications or failures can occur. In which relates to the early complications, absence of stability primary of the implant, the surgical trauma, the bacterial contamination presurgical and occlusal overloads constitute the major common advanced etiologies. The majority of the authors report that the late failures are the principal origin. Like the parodontal diseases, the inflammatory lesions develop secondarily with accumulation of bacterial plate and are characterized by clinical and microbiological signs similar to those of the parodontopathies. The clinicians should consequently encourage the preventive measures in order to reduce incidence of these potential etiological factors. The therapeutic ones aim at the establishment of balance established between the mechanisms of defence and bacterial aggression. To this end, the major difficulty lies in the detection of the pathological processes and the installation of the diagnosis. Concurrently to clinical evaluation, radiographic images interpretation constitutes one of the most reliable procedures of diagnosis and most used for evaluation of the pathological structures and their evolutions. The care of support and the treatments belong to a global therapeutic solution relating to the lesions and are usually lavished with regular

times intervals. The rigorous follow-up appears particularly significant, it conditions maintains of long-term therapeutic effect.

However the various anatomical structures likely to present small structural modifications, under effects of inflammatory phenomena with a bacterial or traumatic origin, became difficult to detect by radiographic image. This difficulty becomes more significant when one knows the limited space resolution and the disturbed character of the conventional radiological images. The limitation of analysis, based on a simple radiological visualization image [1] as well as the current clinical practice, resulting in handling more radiological images, pushed the researchers, to develop numerical image tools for increasingly powerful treatment and image analysis. Indeed, the analysis which is based primarily on the visual human capacity, which distinguishes only 30 to 40 gray levels, is an unable to appreciate in his totality the information quantity contained in a rough digital image with 256 gray levels [2]. However the comparisons of the images resulting in same or various sources are often carried out mentally by the expert aiming to validate, or not, a therapeutic procedure according to the evolution of the pathological area. The mathematical algorithms and the techniques of image analysis, in particular the image retiming technique by subtraction, becomes difficult to circumvent in order to extract from these rough images, the necessary elements to diagnostic and therapeutic (evolution of the lesions and treatment planning). However, the reliability of subtraction results is dependent on the development of techniques likely to cure all the possible problems (geometrical and photometric conditions) without speculating too much in the radiological material quality [3].

In this article we will present the traditional retiming techniques, by specifying the difficulties of their implementation. We will then present a more elaborated technique, allowing an automatic retiming by the genetic algorithms, which offers promising performances and results for the analysis, the diagnosis and the follow-up of the pathological areas.

2. MATERIALS AND METHODS

2.1. Traditional method of retiming per subtraction

Radiographic image retiming by subtraction was applied successfully these last years [4, 5]. It requires a pair of images taken under the same geometrical conditions [6, 7]. It constitutes a good tool to visualize the lesions by eliminating the structural or anatomical noises. Any structure not having undergone a modification between two examinations will not be taken into account by the subtraction and will be thus affected of a neutral gray level. This technique was applied for the diagnosis of the osseous lesions, the carious lesions and the osseous changes around the implants [5, 8], but also to check the efficiency of the treatment of the parodontal diseases [9]. Unfortunately, it is often difficult to visualize the weak differences of the gray levels in the images resulting from a subtraction operation. The installation of the various means, allowing to lead to a better visualization of the weak contrasts of images, becomes very important. An undertaken study, for the detection of the small jaws lesions, and based on the pseudo-color made it possible to increase the interpretation efficiency of the subtraction images with a great insurance [9, 10]. Other

techniques which consist in applying, on images subtraction, a nonlinear raising of contrast [11] allowed a significant improvement as for the certainty with which the diagnosis is realised in the case of the proximal decays. These techniques gave results considered to be satisfactory in the case of the images of poor quality corresponding to the effects of the reduction of the exposition to x-rays level. However, other works showed that factors related to the noise structural caused by nonalignment of radiographies pair, can be more harmful with none detection of the pathological areas in the subtraction images, than the photometrical reasons [12]. However, in spite of the great potential of these techniques to improve visualization of the weak tissue variations, a great difficulty related to the geometrical and photometric conditions is to be raised, when applying subtraction operation. It is thus important to correct these last in order to not attribute wrongfully to drug action which is only an experimental imperfection. The subtraction method application, between two radiographic images, will have to give representative results of the real variations, in time, of a possible pathology and does not have to (in no case), give place to a corresponding result to a bad alignement or a contrast difference between radiographies. So, to prevent this geometrical alignement problem, a manual alignement method using a negatoscope and an image analysis system illustrated by Figure 1 was exploited for a long time. The radiological film is placed on the negatoscope which can be controlled by a micromanipulator able to carry out a rotation and an adjustment in the horizontal and vertical directions.

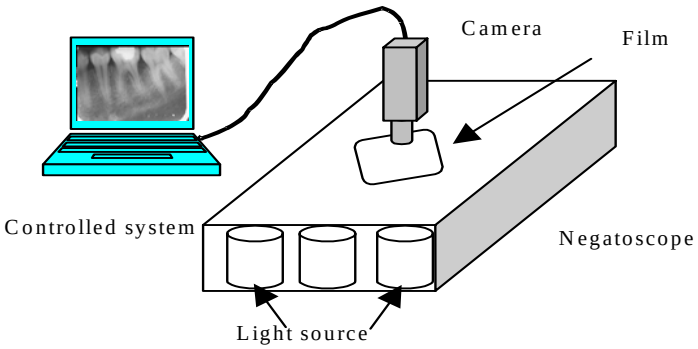


Figure 1. Negatoscope and acquisition system

A CCD camera makes it possible to convert illuminated radiological film to a digital image. After having captured the first image (radiography reference image), the second radiography image (source) must be readjusted on reference one (Figure 2).

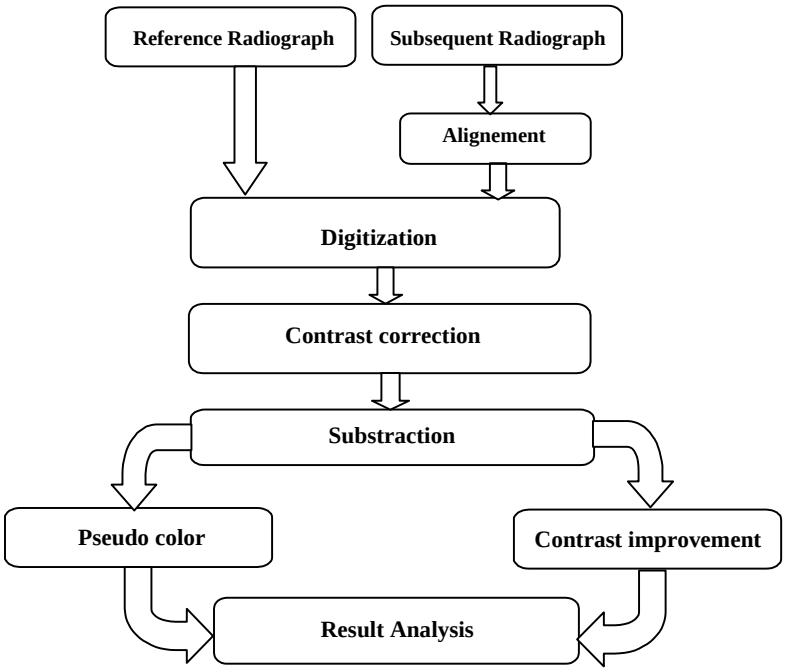


Figure 2. Procedure for digital subtraction

The retiming of the follow-up image is made manually and consists of 4 features:

In the *first step* of coarse alignment, the stored image is binary-transformed, and an algorithm is applied that outlines the edges of the teeth, root structures or implant. The dark parts of the image become invisible, and the follow-up image can be adjusted manually so that its bright parts (teeth, implant) correspond to those of the stored baseline image. Radiographs not containing enough bright parts are aligned by inverting the binary-transformed part, which makes only the dark parts of the image visible. A third possibility is to achieve the alignment with the help of edge enhancement and edge detection of the structures on the image. The first image can even remain partly visible, thus allowing sufficient reference to align the follow-up image.

In a *second stage*, the baseline image is divided into a chessboard format (Figure 3). The follow-up image is then shifted and rotated until the two images are superimposed, displaying on the monitor 50% from the stored baseline image and 50% from the follow-up radiograph.

The next feature (*third stage*) consists in changing the display from the baseline to the follow-up image, in a flickering manner (moving image). The second image is then shifted, until the two images are perceived as one stable image on the monitor.

The finest adjustment (*fourth stage*) is made by using the real-time subtraction image manner (moving image). By means of micrometer screws and subtle translateral and rotational movements, the best possible alignment is achieved. The objective of the alignment of the images is to obtain complete cancellation of the stable anatomical landmarks (such as implant or teeth) [13].

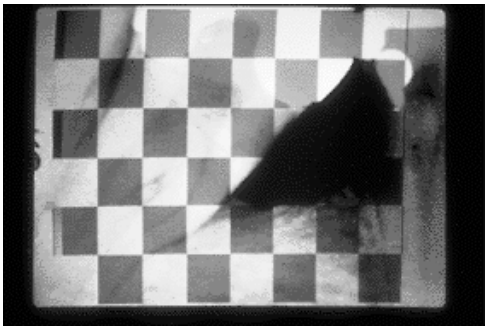
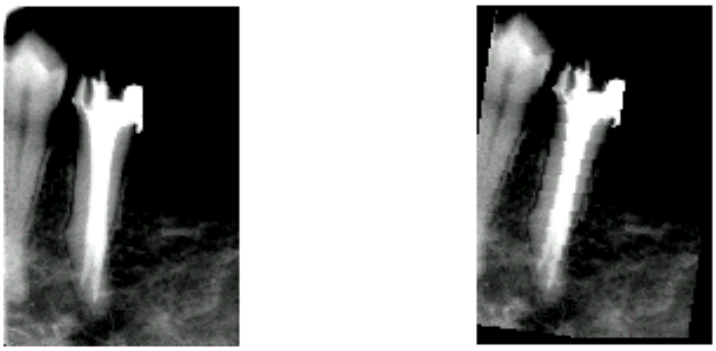


Figure 3. Chessboard format showing 50% of the squares originaly from the stored image and 50% of the squares originaly from the radiograph to be superimposer and viewed by the video camera [13]

Finally, the follow-up image is captured using the same principles with those applied for the first image. In order to achieve the minimum difference in grey levels, regions of assumed identical intensity are defined on the two images, from which histograms, mean values and standard deviations of the grey level values allow to grab the follow-up image with the nearest possible contrast and brightness compared with the baseline one.

2.2. Automatic retiming by the genetic algorithms

The manual method of retiming shows significant constraints as for its practical application: tact of the expert and time of realization. To overcome these very restrictive constraints, of the above mentioned method, we propose an automatic method based on the genetic algorithms [14, 15] and the concepts of refines estimate movement [16, 17, 18] with knowing rotation, the translation and the scale factor (Figure 4).



teeth treated source image retiming

Figure 4. Effects of closely connected transformation

This method of retiming consists in carrying out a connection between the frames of reference $\{X\}$ and $\{X'\}$ of the two images taken at different times. It is given by a $X' = h(X,T)$ transformation, where T expresses the vector of parameters [19]. The elements of the vector T describe connection between two successive images I_n and I_{n+1}. If the structure of the transformation $h(x,T)$ is known, this transformation must be single and invertible.

The transform $h(x,T)$ mainly depends on two factors [20, 21]:

- the matrix rotation R and a vector of translation d given by the following equation:

$$X' = RX + d, \tag{1}$$

where $X = (x, y, z)^T$, $X' = (x', y', z')^T$ are the three-dimensional coordinates;

- the transform:

$$x' = \frac{(1-a_1)x + a_2 y + a_3}{a_7 x + a_8 y + 1}; \qquad y' = \frac{a_4 + (1+a_5)y + a_6}{a_7 x + a_8 y + 1} \tag{2}$$

describes the connection of the coordinates $\{(x,y)^T\}$ and $\{(x',y')^T\}$ in the camera plane when central projection is utilized. The surface of the moving object is assumed to be planar $(z = ax + by + c)$. The vector parameters is $T = (a_1, a_2, a_3, a_4, a_5, a_6, a_7, a_8)^T$ implicitly contain retiming parameters (R, d) and the surface information (a, b, c).

To obtain an appropriate estimate $\hat{T}$ of the parameter vector T of the transformation $h(x,T)$, model adaptive parameter estimation techniques are used. For this purpose, the image $I_{n+1}(x)$ which results from $I_n(x)$ through the transform $h(x,T)$ with the unknown retiming vector T is rebuilt with a model image $I_m(x,\hat{T})$. This model image results from image $S_n(x)$ through the same transform $h(x,T)$ as $I_{n+1}(x)$ using the model vector $\hat{T}$. The difference $e(\hat{T})$ between the predicted feature $S_m(x,\hat{T})$ and $S_{n+1}(x)$ is described by an error function $J\{e(\hat{T})\}$ which can be minimized by modified Newton algorithm combined with quasi-Newton method [15]. In additional to the computational requirement, the practical use of this algorithm faces serious problems:

– The retiming estimation may not work well, if the starting value of $\hat{T}$ is too far away from the true value T. Thus, the algorithm might converge to a wrong minimum of the error function, namely to a local one instead of the global one.
– When the Hessian has no inverse, not all parameters can be estimated because the error function does not have a unique minimum.

To overcome this disadvantage we propose a minimization by a genetic algorithm to obtain the optimal $\hat{T} = T^*$. With this minimization the object $S_m(x,\hat{T})$ is moved towards $S_{n+1}(x)$ according to the transform $h(x,T)$. Thus $S_m(x,\hat{T})$ is becoming closer to $S_{n+1}(x)$. At the optimum of the error function when the estimated vector $\hat{T} = T^*$ equal the true vector T, $I_m(x,\hat{T})$ and $I_{n+1}(x)$ will be similar. As $S_m(x,\hat{T})$ moved toward $S_{n+1}(x)$, it is possible to say that $I_m(x,\hat{T})$ is the predicted image when trying to predict $I_{n+1}(x)$ from $I_n(x)$. Thus, it is possible to predict $I_{n+1}(x)$ exactly from $I_n(x)$ if the correct transform $h(x,T)$ is chosen and $\hat{T}$ is estimated correctly.

2.3. Genetic implementation

Genetic Algorithms (GAs) [14, 15], are pseudo-stochastic search methods whose derive their fundamental ideas and terminology from the Darwinian "Natural selection" theory, according to which individuals that are better fit to a given environment are more likely to survive.

Unlike conventional techniques, GAs can be successfully applied to problems characterized by a large and irregular search space. In those cases, they have been shown to compare favorably, in terms of applicability and efficiency, with other methods, such as simulated annealing. Furthermore, GAs do not require that the search space be continuous, but can act effectively in discrete and mixed discrete/continuous spaces.

While solving an optimization problem using GAs, each solution is usually coded as an alphabet string of finite length called chromosome. Each string or chromosome is considered as an individual. A collection of M individuals is called population. GAs start with a randomly generated population of size M, and in each iteration, a new population of the same size is generated from the current population by applying operators, termed selection, crossover, and mutation, that mimic the corresponding processes of natural selection.

In this section we describe in detail the genetic algorithm that we propose in the learning stage. First initial population and fitting function for the problem under consideration are discussed. Then the genetic operators and the way they are used are stated. The last part of this section deals with stopping criteria for GA.

Initial Population: To solve this geometrical alignement problem with GAs, we encode the parameter vector $T=(a_1, a_2, \ldots a_8)$ of the transformation $h(x,T)$ in a way that allows manipulation by genetic work. Therefore, we consider the chromosome representation individuals as a binary string of finite length. The phenotype of each individual is defined by

a_0	a_1	. . .	a_8

The corresponding genotype (chromosome representation):

$\alpha_1, \alpha_2, \ldots \alpha_K$	$\alpha_{K+1}, \ldots \alpha_{2K}$	. . .	$\alpha_{7K+1}, \ldots \alpha_{8K}$

where α_i is the binary value, i=1 . . . K bits.

The initial population of parameter vectors is generated randomly. There exist no guidelines for choosing the appropriate value of the size (M) of the initial population, this parameter is fixed throughout the training stage. There is the intuitive dilemma that is shown in [15], which provide that a large number of individuals in the population can speed up the convergence of the GA toward the optimal string.

Fitting Function: Each individual is evaluated by his fitness value. The evaluation function specifies the quality of the estimate. To this end, knowledge of the signal and noise statistics should be incorporated. The most general approach is given by a maximum-likelihood estimate. If the noise is not too strong, a simpler error is given by:

$$J\left\{e(\hat{T})\right\} = \frac{1}{2} E\left\{(S_m(x,\hat{T}) - S_{n+1}(x))^2\right\}, \tag{3}$$

i.e. the variance of the model error is sufficient. The expectation value $E\{.\}$ is obtained by summing over the object and dividing by the number of pixels on the image region.

Selection: The 'selection' operator identifies the fittest individuals of the current population to serve as the parents of the next generation. The fitness value of each individual is given by a problem-dependent function. The selection mechanism can take many forms, but it always ensures that the best individuals have a higher probability to be selected to produce and form a new generation. Here strings are selected from a population to create a mating pool. The size of the mating pool is taken to be the same as that of the population (M).

The probability of selection of a particular individual is directly or inversely proportional to the fitness value, depending on weather maximization or minimization problem.

Crossover: The 'crossover' is the key operator for GA. This operator randomly chooses a pair of individuals among those previously selected to breed and exchange tracts of their DNA (corresponding substrings) to generate offspring. For example, let $parent_1$ and $parent_2$ be two chromosomes that selected randomly from the mating pool to be mated:

$Parent_1$	α_1	α_2	...	α_N
$Parent_2$	β_1	β_2	...	β_N

where β_i is a binary value, $i=1 \ldots N$.

If pos denote an integer position generated from the range of $[1, N–1]$, then two chromosomes produced after mating will be:

$offspring_1$	α_1	. . .	α_{pos}	β_{pos+1}	. . .	β_N
$offspring_2$	β_1	. . .	β_{pos}	α_{pos+1}	. . .	α_N

The crossover operation is performed as a rate controlled by the probability p_c, which usually has a high value close to 1. The operation stated above, is referred to as single-point crossover [22].

Mutation: The mutation has an important role in the generation process [22]. It main function to restore diversity that may be lost from the repeated application of selection and crossover. This operator randomly introduces a new genes by flipping one or more allele value (1 into 0 or 0 into 1). Following nature's example the probability p_m of applying the mutation operator is very low compared to the probability of applying the crossover operator p_c, p_m is chosen to have a value in the interval [0, 0.5].

Elitist Strategy: In simple GA, the old population is completely replaced by the offspring population after reproduction, crossover, and mutation. In this way, it is possible that the best chromosome in the old population disappears in the current generation. A reasonable improvement is reached by preserving the best string obtained so far in a separate location outside the population so that the algorithm may report the best value found, among all solution inspected during the whole process. In the present work, we have used the elitist model of De Jong [22] where the best string in the previous iteration is copied into the current population. We have implemented this strategy in the following way:

Step 1: Copy the best chromosome ch_0 of the initial population p_0 in a separate location.
Step 2: Perform selection, crossover and mutation operations to obtain a new population p_1.
Step 3: Compare the worst chromosome ch_1 in p_1 with ch_0 in terms of their fitness values. If ch_1 is found to be work than ch_0 , then replace ch_1 by ch_0.
Step 4: Find the best chromosome ch_2 in p_1 and replace ch_0 by ch_2 .

Note that a string ch_1 is said to be better than another string ch_2 , the fitness value of ch_1 is less than that of ch_2 , since the problem under consideration is a minimization problem.

Stopping Criteria: There exists no criterion in the literature [14, 15], which ensures the convergence of GAs to an optimal solution. Usually, two stopping criteria are used in Genetic Algorithms. In the first, the process is executed for a fixed number of iterations and the best individual obtained is taken to be the optimal one. In the second, the algorithm is terminated if no improvement in the fitness value of the best individual for a fixed number of iterations, and the best chromosome is taken to be the optimal one.

The images of the Figure 5 represent an example of retiming effect. It is to be stressed that for this example, all interest is related to the dental structure, the bony structure is not taken into account.

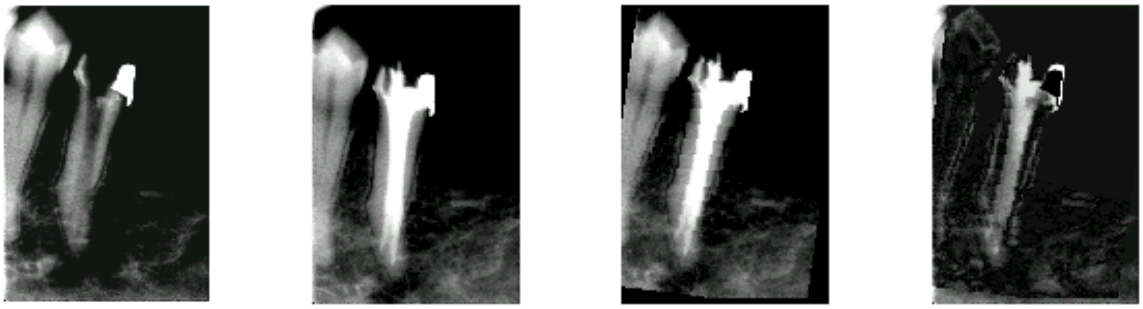
3. EXPERIMENTAL RESULTS

This method is of a great interest in dental radiodiagnosis. To illustrate its importance we present three examples below: the first one was selected to show in a very clear way, the result of the subtraction for images taken ideally under the same geometrical and photometric conditions. In the selected example, these conditions were carried out artificially by taking an image test on which we create an artificial resorption (Figure 5a and 5b). The result of the subtraction is shown by the Figure 5c.

5a. Original Image 5b. Image obtained after an artificial resorption 5c. Subtraction result

Figure 5. Subtraction result with artificial resorption

The second example corresponds to the automatic control of the obturation material used in a canal treatment



6a. Tooth decay 6b. Tooth treated 6c. Retiming result of original image 6d. Subtraction of original image and aligned one

Figure 6. Canal description treatment by the proposed retiming technique

In this case, all interest is related to the dental structure, the bony structure is not taken into account. The result of the subtraction of the aligned images by the suggested method is more manifest because of the significant radiopacity of the obturation material. The result of the subtraction is given by the Figure 6d.

The third application example consists with a radiological evaluation of parodontal treatment. It is a question of quantifying the evolution of the jaws lesion by the alignment proposed method (Figure 7). The two images were taken under different conditions, as the Figure 7a and 7b show it.

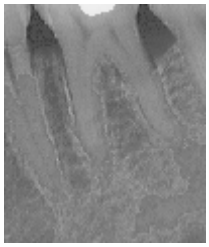
7a. Image before treatment 7b. Image after parodontal treatement

Figure 7. Example of image taken before and after parodontal treatment

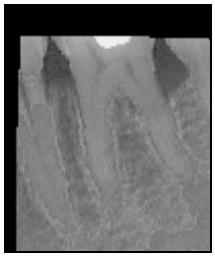
The subtraction cannot be made only when correction of the grey levels and geometrical alignment was be done. The correction of the grey levels of the images represented by the Figure 7a and 7b is carried out by equalisation of histogram of the bony areas in the two images.

The result of the suggested method, to carry out the geometrical alignement image represented by the Figure 7b while taking as reference the image represented by the Figure 7a, is given by the image Figure 8c.

8a. Original Image before parodontal treatment



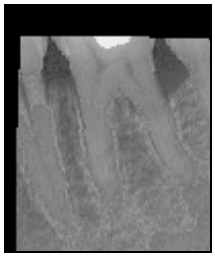
8b. Image after parodontal treatment with grey level correction



8c. Image alignement result of automatic retiming

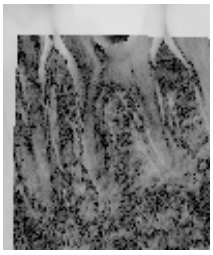
Figure 8. Result of alignement by proposed method

9a. Original Image before parodental treatement



9b. Image after parodontal treatement and grey level correction

9c. result of the alignement image by automatic retiming method



9d. Image after arising contrast

Figure 9. Result of automatic retiming method

The result of the subtraction of the image of Figure 8c and the image of Figure 8a is given by the image Figure 9c. However, to increase the effectiveness of dental diagnostic one applies a raising logarithmic curve of contrast to the image resulting from the subtraction, the result is illustrated in Figure 9d.

One notices the reappearance of the bony cortical between the first molar and the second premolar, a regeneration tissue in junction area, a bony affixing on the angular lesion bottom which exists between the two molars. One also notes the disappearance of the bony sclerosis in the vicinity of the apexes of the teeth which appear on the result of the subtraction image by differences in density.

CONCLUSION

In this article, we presented the method of retiming per subtraction of two radiological images which can be taken under different geometrical and photometric conditions. This method brings back the alignement problem the minimization of an evaluation criterion. To carry out this minimization we proposed the application of the genetic algorithms. Our proposed method was applicated to two principal types of treatment. The first one is related to the automatic control of the obturation material used in a canal treatment, whereas the second corresponds to the evaluation of the parodontal treatment results. The results presented show the performances of genetic approach of retiming per subtraction which includes at the same time geometrical standardization and the photometric standardization in an automatic way. This technique makes it possible to open a broad prospect for the follow-up and classification for areas according to their degrees for gravity with the aim of building an expert system leading to an adequate treatment.

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