ADT-3D Tumor Detection Assistant in 3D

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Abstract — The present document describes ADT-3D (Three-Dimensional Tumor Detector Assistant), a prototype application developed to assist doctors diagnose, detect and locate tumors in the brain by using CT scan. The reader may find on this document an introduction to tumor detection; ADT-3D main goals; development details; description of the product; motivation for its development; result's study; and areas of applicability.

Key Words — ADT-3D, Briain tumor, CT Scan, image processing, Jaimes' algorithm, Kmeans, Matlab, segmentation, tumor, Visual Intelligence.

I.INTRODUCTION

A.A piece of history on Computerized Tomography

According to *Tomografia Computerizada* [1] on October 1st, 1971 the first brain scan was performed in a London hospital. From then on, there has been a quick development on the field. In 1973, the EMI Scanners, developed by Electrical Musical Instruments Co. headed by Hounsfield, expanded rapidly to the US and Europe. After which the brain scan adopted different names such as CT Scanner (Computerized Tomography) by Anglo-Saxons, TDM (Tomodensiometry) or CAT Scan (Computerized axial tomography); all of which were also known as X-ray scanners.

Since Hounsfield begun the investigations, there have been many changes on the discipline. The improvements try to shorten the swap time and refine the image quality. Xavier Vila [2], on its website, explains quickly, easily, and visually the evolution of those changes. X. Vila states that there are four different machinery ages.

At the early stages on tomography there was only one detector, which rotated opposite to the X-ray tube, which is how tomography was reached. Then, these machines were upgraded to decrease rotation times and maximize the angle of rotation from 180 degrees up to 360 degree.

B.Computerized Tomography

The CT technology was developed in order to carry out head studies, but previous advances made possible the study of the whole body. Nowadays, the CT can be used for any region of the body.

The CT core are X-rays¹. The main difference is how they are used. For CT Scans the X-rays are applied over small body slices. Therefore, instead of a body projection, CT obtains a full resolution slice. Many manufactures have developed different CT machines, building up the different generations, from the first to the very last fourth scanner generation. Generations differ from each others on the tube-detector system. The most use CT scan generation is the 3rd which is illustrated on the following picture.

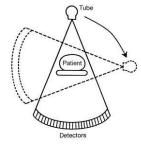


Fig 1. "Schematic drawing of tube-detector system of 3rd generation CT scanner. The X-ray tube emits a sharply collimated fan beam of X-rays which passes the patient and reaches an array of detectors. Tube and detector array rotate together around the patient; one exposure often comprises 360° rotation."[3]

The X-rays are emitted from the scanner as thin telescopic fan shaped beam, making a regular angle with the patient long side. The distance between the patient and the tube must mach with the fan projection. The thickness of the fan could be selected creating thicker or thinner slices, form one to ten mm.

Each slice is divided into a constant number of volumes, socalled voxels (Figure 2). Each single voxel value is obtained by combining the values of several projections. Each projection is done rotating the tube around the patient, for each rotation the values are received by the array of detectors which are on the opposite side the tube (Figure 1). When the voxel is represented as a two-dimensional image, it becomes a pixel. The pixel value, position, and size represent the whole voxel data. As an image, the value will be a represented in the grey scale, depending on the selected brightness. The higher the attenuating voxel the less quantity of rays have crossed through it, e.g. bone, which are brighter in the grey scale, closer to white. On the other hand, the less dense tissue, which more amount of X-rays cross through, the darker the voxel representation is.

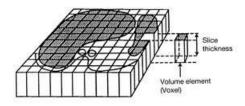


Fig 2. "The imaged slice of tissue divided into volume elements, voxels. The attenuation in each voxel determines the brightness (shade of grey) of the corresponding pixel in the final two-dimensional image."[3]

The relationship of bones as white and air as black voxels is obtained from the Hounsfield Scale. The Scale links each voxel value with a grey shade scale. The default numbers are -1,000 to represent air, 0 for water, and +3,000 for dense

¹X-rays: The oldest and best known of the medical imaging techniques. X-rays, discovered by Röntgen more than 100 years ago, are high energy radiation produced in a special type of lamp called an X-ray tube. X-rays are also a form of electromagnetic radiation, but with a much shorter wavelength and a higher frequency than visible light.[4]

elements, such as bones. The brain tissues average is between 60 and 120. The unit uses is called HU, Hounsfield Unit. In fact, each manufacturer use its own scale but always referred to Hounsfield Scale, see the picture below.

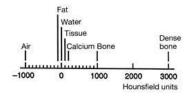


Fig 3. "Scale of Hounsfield units (HU). The approximate scale locations of different substances are indicated. (By "tissue" is meant most fat-deficient soft tissues and parenchymal organs.) Reference points: -1,000 HU for air, 0 HU for water."[3]

CT scan resolution is far greater than older radiography techniques, but moreover, the spatial resolution is lower. The voxels thickness is as large as the slice. If the scanning setup asks for a normal study of the patient, the number of slices to determinate the patient's head will be lower than forty. If the head is represented using computer programs there will be many gaps between slices. The empty gaps are fill by using the average value among the surrounding voxels. The process is called interpolation, the added gaps are in fact not real data. This is called the spatial loss of CT scannig. This spatial loss could be resolved using thinner and more slices. Consequently, longer CT examinations will be needed.

A thin slice resolves the spatial loss, but also requires higher amount of radiation to obtain a usable slice. The process of thinner slices will multiply the radiation levels.

In CT scanning is crucial the relationship between quality, time, radiation, and area covered.

C. Technological approach

Nowadays, the contribution of technology to any field is fundamental but especially indispensable on medicine. It is clear the close relationship between medicine and technology since the manipulation of high complex medical equipments is part of the technological progress made up to date.

A vertiginous advance on science has characterized last fifty years, causing all technologies to advance rapidly. For those whose professions involve the utilization of the technologies, it's being difficult to stay on top of the rapid changes. Technological developments have positively altered medicine, since it has enabled the better comprehension of the multiple processes, which explain the symptoms of several illnesses. Therefore, it has help on the understanding of many symptoms and repercussions on the human body.

A classic classification of medical technologies could be: diagnosis, preventive, therapy, rehabilitation, and management.

D.Medical approach

A brain tumor is "a benign or malignant growth in the brain. Primary brain tumors arise in brain tissue. Secondary brain tumors are cancers that have spread to the brain tissue (metastasized) from elsewhere in the body. Brain tumors can and do occur at any age" [5]. A brain tumor is still very difficult to diagnose. According to the University of California, San Francisco [6], the doctor would first ask about family medical history and perform a complete physical examination. Then, depending on the results obtained, it may be possible that the doctor request a CT scan, MRI, Brain Scan or other test. Unfortunately, neither CT Scan nor MRI provides complete accurate data about the presence of a tumor.

II. MAIN GOAL

By utilizing the group of slices obtained from a CT Scan of the head, the ADT-3D is able to recognize a brain tumor. To perform this task it will be necessary to generate a 3D representation of the sections or slices. Once the threedimensional image has been generated the ADT-3D will proceed to study the different regions using Artificial Intelligence Vision methods and algorithms such as Kmeans and Jaimes' segmentation algorithms.

The result of all these processes should help to differentiate visually the tumor from the rest of the brain mass. The visual differentiation would make it easier to study the properties of tumors.

III. DEVELOPMENT DETAILS

A.Functionality

The main goal of ADT-3D is to assist doctors during the brain tumor detection and the possible diagnosis on patients who undergo the CT Scan. ADT-3D fulfils the 3D analysis of the possible tumors. The utilization of these three-dimensional images enables tumor location on XYZ axis for their later examination.

B.Development tools

1)MATLAB R2007b

MATLAB is a development environment based on MATLAB language. "MATLAB® is a high-level language and interactive environment that enables you to perform computationally intensive tasks faster than with traditional programming languages such as C, C++, and Fortran." [7]. This language can be used in many different fields such as signal or image processing; communications; test and measurement, as well as other scientific fields of investigation.

On this development environment it is possible to manage code, files, and data. It includes many functions for statistics, optimization, and numeric data integration and filtering. There are also great amounts of functions that facilitate the manipulation of bi-dimensional, and three-dimensional images.

2)MATLAB Newsgroup [8]

Software developers may have to face problems to which are not able to find a solution. The *MATLAB Newsgroups* is a website tool offered by Mathworks. It allows software developers to have a common point of contact to solve programming problems. The *Newsgroup* has an extensive database with hundreds of conversations, about the programming language, concerning troubleshooting.

C.Data Manipulation

ADT-3D data input consist on a variable number of DICOM images, which represent the brain mass in consecutive slices. An example of this is shown on Figure 4. The utilization of such technique on CT Scans allows first, to store data about the patient's head. Secondly, to manage a 3D body in a group of slices.

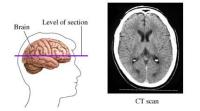


Fig 4. The figure represents one of the DICOM images that form the data input of ADT-3D.

Then, each single image on the group of input images is transform into a bi-dimensional matrix. The next step is to create a three-dimensional matrix out of the group of 2D matrixes. The created volume matrix is used for holding the patient's data, which is used as the numeric input to ADT-3D.

The process of transformation from image into numeric values is done through dicomread(), a function provided by MATLAB environment. As long as the input argument of the function is a DICOM image, then the output argument will be an square matrix containing the voxel values. An example of this transformation is seen on Figure 5.

	124	135	141	255
	110	120	128	141
	108	115	120	135
	98	110	119	128

Fig 5. It shows the numeric values corresponding to the given image when MATLAB's dicomread() is used.

During the process of converting images into figures, each bi-dimensional matrix is added to a three-dimensional matrix. The size of its third dimension will be equal to the number of images conforming the brain scan. The outcome it's a 3D matrix, containing all data acquired during the CT Scan, becoming the initial unit of work.

D.Segmentation

The segmentation is a computer technique "*in computer vision in which an image is divided into regions*" [9]. Also defined as: "*the act of dividing or partitioning; separation by the creation of a boundary that divides or keeps apart*" [10]. What about image segmentation? If the term segmentation is applied to the word image, tImage Segmentation is the act of dividing or partinioning an image into regions defined by the creation of a threshold.

There are many different segmentation algorithms, each one uses different characteristics from the studied object. There are four common approaches used with intensity images (e.g. Dicom images which use voxel values). The four approaches are: threshold techniques, edge-based methods, region-based techniques, and connectivity-preserving relaxation methods.

ADT-3D uses Jaimes' algorithm for segmentation. The algorithm is explain in more detail below. Jaimes' algorithm uses Kmeans algorithm as part of the process, but since Kmeans does not divide the data with the needed accuracy, it applies other filters.

E.Jaimes' Algorithm

1)Differentiate a tumor from brain mass

The main goal of ADT-3D is the identification of brain tumors. How could it be done? The answer is on the segmentation of the image. Image segmentation, as part of Visual Intelligence, is responsible for discrimination on different pictures. DICOM's protocols differentiate tumors from other brain masses by using the Hounsfield Unit Scale. Based on Hounsfield Unit Scale, tumors score diverse values than the rest of brain mass.

2)Kmeans

Kmeans algorithm divides any image into k number of different classes. The k value can be determinate by using other algorithms such as Chain-Map or Max-Min over the image. Kmeans algorithm, applied to a DICOM data collection, allows a maximum k value of five. It denotes that Kmeans will give five different centroids, and each pixel matrix will be related to one of these centroids. Unfortunately, a classification using only five types of classes is not enough to differentiate tumors from other brain masses.

3)Variables

- Mdata: It is a three-dimensional matrix that contains the input data for both Kmeans segmentations.
- Mclasses: Is the result of the application of Kmeans to Mdata.
- Mresult: The output data of the application of Jaimes' algorithm is stored in this 3-D matrix.

4)Iteration I

Mdata is the input information to Jaimes' algorithm, a matrix containing the original numbers. Kmeans allows us to classify raw data contained in Mdata based on a scale from 1 to k elements. As it was stated above k value is equal to 5. The following figure is an example of this step:

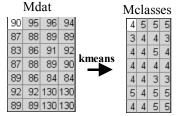


Fig 6. The first table represents the data input values, where the four bottomright hand corner values represent a simulated brain tumor. Unfortunately, the estimated outcome should be such that only those four values should have a value of five. Moreover, there are other extra 5's not related to a brain tumor. Thus, the idea is to improve this first segmentation.

The application of Kmeans is executed using the following code.

```
For nc=1:60
X = Mdata(:,:,nc);
k = 5;
[idx, partialClasses] = kmeans(X,k);
Mclasses(:,:,nc)= partialClasses;
End
```

Fig 7. Kmeans brings forward two values: idx and PartialClasses. The former contains centroid values and the latter saves the data related to each element's classification.

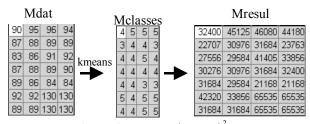
5)The Adjustment

The previous step has achieved a decent approximation. Nevertheless, it has confused certain brain masses also as tumors. How could be possible to isolate the tumor? The exponential function solves this problem by applying the $f(x) = x^2$ function for each matrix pixel:

5 ()	
$\forall x_1 \Box R$	Example :
$\forall x_2 \square R$	$x_1 = 92$
$f(x) = x^2$	$x_2 = 130$
$\Delta(x_1,x_2) \Box \Delta(.$	$(x_1), f(x_2)$ $\Delta_1(92, 130) = 38$
, (,	$\Delta_2(f(92), f(130)) = \Delta(8464, 16900) = 8436$

Fig 8. Two different numbers from the same class could be distanced by using the exponential function f

The distance between numbers will be increase if the f function is applied. It does not matter if the element belongs to the same class. Once the function is applied, it is also multiplied by the Mclasses number k. In this way, a hypothetical second iteration will distinguish tumors from brain mass values. The following function represents how the adjustement is done for a selected group of data.



 $Mclass = kmeans(Mdata) Mresult = (Mdata)^{2} \circ Mclass.$

Fig 9. The Adjustment function is applied to Mdata after the First Iteration. Is easy to appreciate how the tumor pixels have grown more than the brain mass data pixels.

The Adjustment process is done by using the following MATLAB code.

```
Mresult=Mclasses;
dim = size(Mclasses)
for i=1:dim(3)
    for j=1: dim(2)
        for k=1: dim(1)
            Mresult(k,j,i) =
    Mdata(k,j,i)*Mclasses(k,j,i)*Mdata(k,j,i);
        end
    end
end
```

Fig 10. The Mresult matrix is the weighting output. Mresult will be used on the second Iteration.

6)Iteration II

Once the adjustment is done, the second Kmeans Iteration may proceed. As well as on the first Iteration, the number of centroids and classes will be five. The difference between iterations is that class five is reserved for high tumor probability pixels. The picture below shows how the second Iteration leads the tumor to the fifth class.

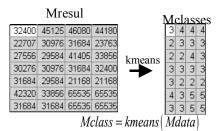


Fig 11. As well as the First Iteration, the Second Iteration returns a new Mclasses matrix. Now the accuracy is higher. Anyway, it is needed the last step to assure a precise result.

7)Smooth

The last algorithm's step has a crucial effect on the final results. Sometimes, depending on the working slice, other non-tumor related five class pixels could be detected. For sure, a tumor is a non-stoppable growing amount of cells. When smooth is applied to a group of pixels the result is that those isolated pixels loose importance. The smooth process is done over the Mclasses matrix. The objective is to penalize the spread pixels. It is done by giving more importance to the grouped fifth class pixels. Thus, the final matrix solution will increase the five class pixel groups using float numbers from 1 to 10. The smooth comparing data will be five. The higher concentration of fives that are closer to each other, the higher possibitily for that value to reach 10. The process will produce a final matrix like the following one.

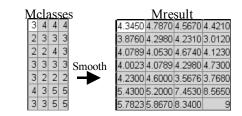


Fig 12. The final matrix is **finally** obtained. It could be appreciated how the tumor has been finally found out. The tumor related pixels values are clearly distant from the brain mass pixels.

The following matlab code represents how the smooth is implemented:

```
%Create the Mresult matrix
Mresult = Mclasses;
%patch smoothing factor
rfactor = 0.125;
%isosurface size adjustment
level = .8;
%useful string constants
c2 = 'facecolor';
c1 = 'edgecolor';
p=patch(isosurface(smooth3(Mresult ==5),level));
reducepatch(p,rfactor)
set(p,c2,0.8*[1,0.5,0.5],c1,'none');
```

Fig 13. The smooth is applied for the pixel value of 5. The reducepatch function with a rfactor lower than one perseveres the shape of the smoothed zone. The set line configures the output representation. The result is shown on Figure 3.

IV.ADT-3D COURSE OF ACTIONS

Thanks to the user interface, it is possible to monitorize each step on the process of tumor detection, recognition and isolation. The first step is Image load, which reads dicom images from the hard drive and transforms them into a threedimensional image. The second step is brain mass isolation consisting on two subprocesses such as noise reduction and bone exclusion. Third, it is Tumor simulation, due to the difficulty of finding head CT scans with tumors on them. The simulation, as explained later on, consists on the generation of a head tumor. The following step, Segmentation, is the most important since it divides the studied data (or head) into different classes for later envision and study. The next step is Class Visualization allowing the 3D visualization of the different classes obtained from the segmentation. Later on is *Class Plotting*; this step is used to display on a bi-dimensional image all the different classes resulting of the segmentation. Finally, it is Tumor Visualization, which is used to visualize the detected tumors isolated from the rest of brain mass. Two possible visualizations are offered to the user: a group of bidimensional images that represents the diverse slices of the detected tumors; and a three-dimensional representation of those tumors.

A. Constant Functions

Here can be found the different functions, which are present during the running time of the program. They can be executed at any given time to obtain the desired result. These results are display graphically, so the user of the system can acquire a better knowledge of them. The quantity of feedback given to users is vital. It simplifies the diagnosis process.

1)3D Visualization

The function's name is self-explanatory. Provided that the user of the system has executed correctly the step in which this function is attached; then, the outcome will be a threedimensional representation of the results obtained. Nevertheless, this process takes more time than users might expect, due to the fact that the process of transformation from a three-dimensional matrix into a 3-D representation requires reading each single item on the matrix. Moreover, since usually the dimensions of a matrix are 256x256x60, it results on a composition of almost four million elements.

MATLAB handles the representation of any volumetric data, but in order to perform a proper representation it requires the programmer to establish certain information related to color map, axis aspect, and other elements.

Once the user has the 3D illustration of the results, the view can easily be rotated; amplified or reduce its scale; and even change the color map. Automatically all these functionalities are included by MATLAB. An example of this type of representation can be seen on Figure 14.

2)Video Visualization

Is a function that makes possible a dynamic bidimensional visualization of three-dimensional matrixes. The process is simple and requires fewer time compared to the 3D visualization function. In order to decide how the data is going to be sliced, the function's data input has to be a three-dimensional matrix. The decision is done by sizing the matrix and by selecting the smallest dimension. The next step is to show the first 2D slices on the stack, then a counter is set up to count a number of milliseconds. Once this is done then the second 2D slice is shown and so on. The final output is a dynamic movie simulation, which exhibits correlating images.

Since this functionality is directly perform by implay(), a MATLAB function. It is not strange to assume that color map, velocity, and other aspects of the movie could be easily changed.

3)Image Closure

The main purpose of this function is to close all other open images but the interface, which is also considered a figure. Some processes, such as 2D visualization of tumors, can generate too many figures. Deleting the images one-by-one could be boring and time-consuming for the user. Thus, *Image closure* is provided to close all open images except the user interface, making it fast and easy.

On the one hand, some users might find this function unnecessary and useless. On the other hand, its users would surely benefit from its features.

B.Image Load

If *Image Load* is not the first procedure ever to be executed on the system, then any other action would have no reaction. The reason for this is that this process is in charge of reading the data input images. As stated above, Dicom images have to be store in the computer or in a server and they have to be reachable by this procedure.

It is not required that the input images enclose a common string name including an identification number (e.g "ImageName"+num+".FileExtention"). However, the use of a common string name would facilitate loading images into the system, at least to the programmer. In any case this would affect on response times from this process, but it would help, on one hand, the organization of images belonging to the same patient, and on the other hand, the programming code used to read and load the images. This way, it could be a more autometized and simplier process.

C.Brain Mass Isolation

The intention of this process is to isolate brain mass from the rest. Now that images have been loaded into a matrix, it is possible to get rid of all those parts that are not needed to detect a brain tumor. The process is done in two steps: first, *Noise Reduction* and second *Bone Exclusion*. Both procedures will be explained below with plenty details.

1)Noise Reduction

The apparition of noise on images is usually unwanted and random, causing a variation of values in the image's pixels. It can be originated, for example, on electronic devices such as radios, sensor devices (e.g. cameras). Unfortunately, CT Scans are not an exception to the apparition of noise. The problem of noise reduction was deeply studied by Hanson [11]. He differentiates three different types of noises: random, artifactual and structural. He also classifies random noise into statical, electronic and roundoff noise.

In relation, noise reduction was applied in two different

steps. First, the voxel values lower than twenty are assigned a zero. A study of voxel values were done to check that those values under twenty could be easily erase without the loss of information. The second step is to delimitate brain mass boundaries meaning that those values over the skull and under the patients' jaw are equalize to zero. This would prevent those values to interfere on the system.

2)Bone Exclusion

The second step on *Brain Mass Isolation* is in charge of minimizing bone tissue. The brain's surrounding bone complicates the process of tumor detection, recognition, and isolation; therefore, it has to be minimized as much as possible.

An extensive bone tissue values should be completed to perform appropriately the bone exclusion. Such study includes bone original Voxel values and the calculation of the bone mass average. Then, the average bone values are used to check that no other brain mass might be also affected.

In the end, bone tissue is excluded from the CT Scan three-dimensional matrix. If the matrix is now delineated either onto two or three dimensions, the representation would show the brain.

D. Tumor Simulation

As hard as it is to find a digital CT Scan example, getting one with a tumor is even more difficult. For this reason, tumors on ADT-3D have to be simulated. Simulating brain tumors is not an easy task owing to the fact that they are supposed to seem real, at least to the system. ADT-3D is tested based on its capability to recognize brain tumors, meaning that the most desirable features are accuracy and effectiveness.

The tumors are simulated based on voxel density values. Brain tissues were found to be between 60 and 120, raising the question of which value had to be used. Various alternatives such as above, below, and inside the stated limits. The final decision was to simulate three different brain tumors. The main characteristics for all three is dissimilararity from each other. It can be accomplish by using dispare voxel values, location, and size. Such specifications intend to test the system to its maximum capacity.

E.Segmentation

The segmentation algorithm used on ADT-3D is called *Jaimes*. This algorithm is explained on further details on section *Jaimes' Algorithm*, included on *Development Details*. This algorithm provides a better differentiation of the original input data and thus a better segmentation is achieved. Based on Kmeans segmentation algorithm classifies the input data into five different classes. On the fifth class is where detected tumors can be found.

Segmentation is the most time-consuming process due to the fact that almost twelve million digits are used (three element's iteration for each item on a three dimensional matrix of 256x256x60). It supplies information to Class K Visualization, Class Plotting, and Tumor Visualization.

F.Class K Visualization

There is a simple but tedious requisite demanded by this function. The requisite is the correct execution of *Segmentation*. By using this function it is possible to represent, in a three dimensional environment, the specified K class given as an input value.

The data input is *Segmentation's* data output, thus only a matrix is given. In order to represent one of the classes contained on the matrix all values different to K are equalized to zero for the representation, but then the values are restored. Otherwise, it could only be possible to delineate the first class.

G.Class Plotting

Segmentation's output matrix is used as input data, thus Class Plotting uses the same matrix than Class K Visualization. In this case the intention is to visualize a determined matrix slice on a two dimensional draft. The difference with Class K Visualization relays on the fact that now all the different classes are shown on a 2D picture.

Class Plotting introduces the idea of individual segment visualization. Such technique increases the feedback given to the user of the system. As said before, is better to have an informed user than an ignorant one.

H.Tumor Visualization

Segmentation supplies Tumor Visualization the necessary information to envision tumors. Recalling Jaimes' algorithm outcome is a three-dimensional matrix containing the belonging of each element to a K class, on a range of 1 to 5. It is possible to say that tumors are localized on the fifth class. Tumor detection, diagnosis, and recognition are done on Segmentation. It is time to picture the result to the user, usually a doctor, who would have the last word on this matter. ADT-3D assist the process of detection, and under that circumstance, offers the detailed information achieved. 1)Tumor's 3D Visualization

Tumor's 3D Visualization function is only in charge for the 3D representation of the detected tumors. The only difference with *3D Visualization* is the data input. *2)Tumor's 2D Visualization*

Tumor's 2D Visualization is in charge for generating a bidimensional image of tumors location in a similar way to *Video Visualization*. The idea is to display a variable number of 2D images, not in video, each one of them containing different parts of the tumors.

V.REASONS

ADT-3D (Three-dimensional Tumor Detection Assistant) came up as a scientific proposal for tumor detection. The main purpose was to offer information related to the possible infected areas. In this matter it facilitates, complements, reduces time, lowers cost, and sets up an entry point to other further advanced systems.

A.Facilitates

Nowadays, CT Scans display for doctors the gained data

from patients. The data can be presented in different formats, chosen by the doctors depending on the situation. Adding the ADT-3D inside CT Scans would facilitate and greatly improve the detection and diagnosis of tumor because it is specifically designed for this mission.

B.Adds functionality

Doctors around the world would agree, "Medicine is not an exact science". During the diagnosis process, most doctors will contact colleges to discuss a series of events that point towards a final judgment. The insertion of ADT-3D in a CT Scan may lead to a greater efficiency detection tumors and diagnosing each single patient. The improvement in efficiency would utilize better the time doctors' work diagnosing the patient. Therefore, there would be more time to expend curing the tumor.

C.Economizes

As a result of the implementation of ADT-3D system into CT Scan there is a smaller delay for the results, but on the other hand, since the data was processed and studied by the ADT-3D, it saves time. The economization of time and money is always seen as a positive asset. In any case, the implementation of the ADT-3D would only improve and advance the process. The addition of the new system would never become a disadvantage. The possible high cost of the new ADT-3D would be cover by the time savings on doctors and patients' time, and ever greatly it would be more than justified by the lives that it would save.

D.Clarifies

For image diagnosis the most common method used by doctors is the ocular identification of unknown shapes and forms. Unfortunately, in few cases, this type of identification cannot be used because the affected areas are particularly small. If we take tumors as an example, it is expected that first stages of the illness cannot be detected because of the difficult location and the small size of the tumor. ADT-3D assist doctors with the detection and diagnosis phase, which includes early stages since it's a computerized system that can access all the data from the patient, even the smallest piece. The figure 3 represents how easily a tumor could be shown with ADT-3D.

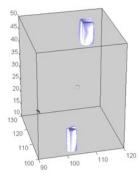


Fig 14. The figure represents the tumors detected in a brain example. There are two cubes that represent two experimental tumors.

E.Sets up an entry point

At the moment there is no other product similar to ADT-3D in the market. Its broadcasting could be inspirational for people with especial interest, attracting better facilities or more time and money. The utilization of this system can, positively improve the quality of life for many people. Present CT Scan or MRI's do not include any kind of Artificial Intelligence algorithms. The expansion of Artificial Intelligence to other fields has improved their main features and client satisfaction; therefore, the inclusion of AI methods and algorithm in Medicine would also help any patient

VI.RESULTS

1)Introduction

First of all, it should be said that ADT-3D is a prototype. As a prototype, the goal is achieved; the brain tumor is found, located, and shaped.

ADT-3D objective is to find a brain tumor, excluding any other CT scan elements such as bone, face, neck or skin. ADT-3D works only with the brain mass.

There is a limitation in ADT-3D results because it has only tested with data source in which the experiments were done. As said before, in the experiment the tumors were simulated through data.

The following test were run after the matrix was obtained, delimitated, and the tumors were added. Unfortunately, it was impossible to find any CT scan examples which had tumors. Neither on the net, nor at any Madrid's hospital tried.

2) Tumor density equal to brain average.

Once known the source protocol, it depends on the CT manufacturer; the non-meaningful value is selected. The test consists on adding a simulated tumor value similar to the brain tissue. If ADT-3D works properly, this kind of tumor cannot be detected by the system. The following picture shows where the simulated tumor was added.

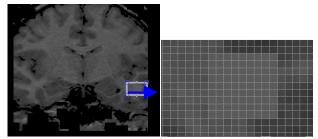


Fig 15. The simulated tumor has a value of 90, which is really close to brain tissue. It is not simple to distinguish where the tumor begins.

The simulated tumor could only be distinguished because of the shape, but never by comparing it to the voxel density levels. In order to recognize the tumor, another kind of artificial intelligence algorithm could be use to target shape oriented recognition.

An example of the detected tumors can be seen on Fig 14. In the sample (Fig 14), the 33rd slice does not show the tumor with value 90 because the density difference is almost equal to the surrounding brain tissue.

The following picture represents how the tumor is segmented by Jaimes' Algorithm.

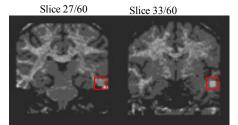


Fig 16. The tumor values are exactly the same, but due to the low value, for each slice the tumor is classified by the segmentation algorithm on different classes, instead of the same class.

Figure 16 shows how the Jaimes' Algorithm perceives the simulated tumor. For each slice the Kmeans class changes. In this way, it is impossible to join all the squares into a 3D image or a five class section for 2D recognition.

3)Intermediate Tumor Value

The Intermediate Tumor Value runs a simulation slightly above the average brain tissue density values. The tumors with density values above 90, the average, are easily recognized by ADT-3D. Tumors will be distinguished but the smoothen step is crucial here. Without image smoothing many spread pixels would be perceive as tumors.

The next picture represents how is a 110 value tumor is represented.

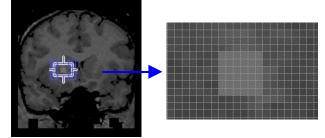


Fig 17. The tumor is seen better now because there is more distance comparing to the brain average value.

Once our Algorithm is applied the tumor is automatically detected. On Figure 14 the top part of the cube shows a tumor. The 2D result is shown below.

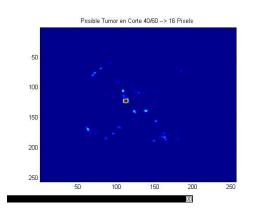


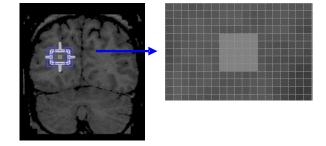
Fig 18. The 2D solution represents with garnet color the possible tumors and the number of pixels that satisfied the tumor condition.

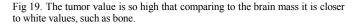
Therefore, the case illustrates the ADT-3D objective, to automatically find tumors otherwise undetected by conventional CT Scans.

4)High Tumor Value

The last test is done to ensure the recognition of highdensity tumor values. The voxel density selected is 130, which is hardly ever found merged into brain tissue. It could be said that any other value higher than 130 will be surely recognized, because the algorithm performs better in voxel density values above and beyond 130.

It is important to emphasized how the simulated tumor is contrasted differently to the brain mass. The following images demonstrate the difference in contrast.





The 3D result obtained is shown on the Figure number 13. There are two cubes. This tumor is represented as the lower cube. The 2D recognition representation for one slice is on figure .

When comparing figures 18 and 20 is easily perceive that the higher the tumor density the less number of elements will be represented in a 2D picture. Figure 18 has more noise, more irrelevant information, while Figure 20 has only the tumor and two small data zones.

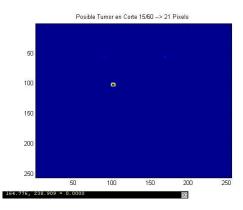


Fig 20. The tumor on slice 15 is shown as a garnet square with 21 high chance tumor pixels.

5)Results Analysis

These three simulated tumors were use to check ADT-3D performance. The first test verified ADT-3D detection capabilities for tumors with voxel density values equal to brain tissue. The second test tested ADT-3D capacity to find tumors with density voxel values slightly above brain tissue average. Finally, ADT-3D was tested for tumors with voxel density levels above 130.

The three tests reinforced the usage of Jaimes' algorithm on ADT-3D for brain tumor detection. Anyways, the prototype has to be further tested and CT scan voxel density values have to be collected to better understand and improve the process.

VII. PRODUCT LIMITATIONS

Unfortunately, any prototype has its drawbacks and limitations. The positive aspect is that it is possible to learn from them so that future updates can overtake them. Once ADT-3D was finalized, it was studied and tested in further detail to analyze its outcome. The negative side carries some limitations that could be divided into two independent categories: Physical and Software limitations.

A.Physical Limitations

Physical limitations concern the hardware devices in which ADT-3D is launched. Ram memory, processor speed, and similar features affect directly to the velocity of execution but never to the effectiveness. As a matter of fact ADT-3D is a very demanding project in terms of hardware requirements. It needs at least 1 Gb of RAM, and a processor equal or higher to 2,5GHz to work properly. The results of investing in hardware would mean better response times, which is always desirable.

B.Software Limitations

Software limitations are related to the effectiveness of the program. ADT-3D uses density values to discriminate classes during the segmentation process. There could be tumor areas which densities are too similar to densities on the surrounding areas, this would make impossible to detect that tumor. This is an important software limitation of ADT-3D but doctors already face this problem. Doctors many times detect tumors using their visual perception on a CT Scan, which also shows density values.

C.Area of Applicability

ADT-3D is a remarkably peculiar product which requires specific data from a CT Scan. Its main goal is to assist with tumor detection. For this reason the only possible application in the field could be Medicine. It is in radiology where the product is more feasible because its implemented into CT scans. Computer applications have revolutionized every area of Medicine, but they have to be updated.

VIII.CONCLUSION

Although additional studies are necessary to provide ADT3D more capabilities, it is clear that this project represent the very start of computing software applied to medical area.

Nowadays it is known that there are many applications dealing with medical stuff recognition using Artificial Intelligence. Each IT company focused on TC develops not only in the hardware, but also in software to deal with the achieved data. ADT3D tries to be cross-platform software able to work with any kind of raw data acquired by a CT machine, no matter its firm.

The current ADT3D is a prototype, an introduction of what could be done. The whole project could be improved, from the GUI to the core. The Jaimes' Algorithm, or the core as it was said, is a mathematical approximation to the tumor recognition which must be studied and improved. The present algorithm only works for simple cases where the whole tumor has a constant value.

Visual Intelligence Computing branch is getting more and more significant, acquiring new people day by day. The applicability of this computing area is enormous because it could be used easily as a human tool, not only for medical stuff, but also, for car identification numbers, people identification, optical character recognition ...

Developing ADT3D has been a great challenge during the last eight months. During the development of this project, MATLAB has been our third coworker. Matlab is a great prototype oriented application with a clear advantage: find much information on the Internet. Internet research has been also important to achieve the goal of recognition, so, as well as people provide their free code on the internet, ADT3D will be for free for all on the Internet.

Upgrades are an important part on each project or prototype. ADT-3D particularly could improve the user interface. The GUI was developed to perform the desired task but user interaction with it was not taken into account. User experience is key to many applications, upgrading the actual interface could make easier and simpler the understanding of the process.

New functionality could be added so that ADT-3D performs new tasks as acquiring data from the computer or servers to treat it as input data. Many additional functions could improve the productivity and capabilities of the system.

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