Converting 2D magnetic resource imagining brain tumors to 3D structure using depth map machine learning techniques

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Article Info	ABSTRACT
	The use of medical imaging technology aids clinicians in recognizing and assessing patient problems, as well as improving treatment procedures. However, while conducting complex procedures such as the excision of brain tumors, the knowledge and biological research gathered from 2D images are insufficient. Converting 2D images to 3D images may assist doctors in determining the size, shape, and sharp area of tumor cells in the brain. The feasibility of translating 2D medical image data to a 3D model is described in this work. A suggested framework for predicting the size, shape, and location of a brain tumor using a minimized genetic machine learning method, and then converting the tumor information into 3D images using a depth map estimation approach after detecting the tumor information. When the tumor is located, the left and right view data are combined to form a 3D magnetic resonance imaging reconstruction. We used mixed reality methods to minimize file size while preserving the greatest quality of the model during a brain surgical operation. *This is an open access article under the CC BY-SA license.*
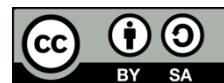
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1. INTRODUCTION

The medical image data are huge, the selection of features of interest is the most important and complex process that needs to be done on time. Usually, magnetic resonance imaging (MRI), computed tomography (CT) scans, etc are used as imaging sources for capturing the affected parts. It is also difficult for the physicians for analyzing the images which are usually in a two-dimensional format. The depth of the cancer-affected parts cannot be observed in two-dimensional images; hence a three-dimensional view is mandatory for finding the depth of the cancerous cell. The issue, in a few words, is the emergence of contaminants/noise generated during in the analysis and conversion of digital imaging and communications in medicine (DICOM) medical picture data [1], [2]. This motivates us to concentrate on the transformation of two-dimensional images to three-dimensional images. Here we intend to create a framework to predict the size, shape, and region of the brain tumor using minimized genetic machine learning algorithm, and later after identifying the tumor information, 2D images are converted into 3D images using the depth map estimation technique. MRI dataset is given as input to the preprocessing system in which histogram equalization technique is used to remove the signal to noise ratio in the MRI images [3], [4].

Bharathi *et al.* [5] have come up with a 2D to 3D conversion model which segments the input image group of objects by applying an effective grouping model. Using the depth gradient model, the depth model

can be assigned. Then the depth image-based rendering method for processing the filtered image. Kanchan and Mathur [6], Ellingson *et al.* [7] have discussed the algorithms for transforming 2D to 3D image conversion. They have analyzed the depth and developed an evaluating model for finding the relative position of the cell. Thus they have developed novel combined depth cues for analyzing the images. The conventional image acquisition is employed, with reduction maps and volumetric estimations being used to improve tumor cell visibility. Kayal and Ulusevik [8] used recognition and volume rendering techniques to create a 3D representation of tumor cells. They detected tumor cells using MRI pictures and converted them into the a 3D model. They created software to analyze MRI pictures in order to separate tumor cells from healthy brain regions. The volumes rendering model is then used to create a 3D picture of the discovered tumor cells. For converting a 2D picture to a 3D image, Guo-Shiang *et al.* [9] have developed an image conversion model.

Hnatkova *et al.* [10] present a technique for converting medical information from 2D to 3D then s actually it until it becomes able to publish three-dimensional models that are analogous to human anatomy using one of the advanced translation tools known as Mimics. Unfortunately, the appropriate and consistent does not operate including all DICOM file instance. Quang *et al.* [11], The author provides an overview of DICOM computer vision translation, and also a three-dimensional concept of digitized and bridge imaging and how to assess and develop it using the VTK library. Mazzotta *et al.* [12]. Present an overview of how to build a three-dimensional modeling of dental roots without using CBCT while decreasing the radiation rate to safeguard the patient's health and providing three-dimensional information with statistical and clinically acceptable accuracy. The crown of the parametric model, however, is of low quality when considering the multiple features (tendon length, root lengths, and widths) measured by CBCT and PAN. Cutters and bends were created during the creation of Bspline curves and free surfaces. Gonsai *et al.* [13] the "Cube Process" technique used in this study to identify the proper area for transformation to a three-dimensional model using a detonation algorithm. The "Cube Process" method is an effective technique that provides physician with a three-dimensional extending that comprises a series of data that can also be viewed from all angles.

Farzana and Sathik [14] research demonstrates how to convert 2D DICOM MRI to 3D using one of the matrices-based conversion algorithms, as well as the beginnings of the result obtained using the K Algorithm Method, which would be a subset of artificial intelligence that act as strolling blocks, choosing the best results for achieving a high rate of accuracy, confidentiality, and sensitivity in data. According to Liuet *et al.* [15], they have meant a skillful approach for the transformation of two-dimensional video to three-dimensional youtube clip adaption based on structure from motion, or SFM. The project's main components are the piecewise SFM approach and novel nonlinear depth warping algorithms, which embody the distinctiveness of stereoscopic 3D. To construct a more manageable CT image, deep thickness maps were created and subsequently handled with color segmentation [16], [17].

The findings show that develop a computer representation in which the dimension of each patient's heart is the same irrespective of background or health status, and is clean of sounds, to aid the doctor/surgeon in dealing with the sickness via the three-dimensional model and the brain. To handle this problem, we should go through many procedures and employ a set of equipment: 2D to 3D conversion, model, segment calculations, and sometimes during comparison of images.

2. RESEARCH METHOD

The proposed model intends to create a framework to convert 2D medical images of brain tumors into a three-dimensional structure to analyze the size and the depth of the tumor using machine learning and 3d reconstruction technique. In general, the brain tumors of the patients are scanned and detected using an MRI scanning machine. The images produced by the MRI scans are 2 dimensional, which can only show the height and width of the tumor. But it will not clearly show the depth or the exact location of the tumor. Such information is very much important before the physician operates or starts the treatment.

Explaining research chronological, including research design, research procedure (in the form of algorithms, Pseudocode or other), how to test and data acquisition [5]-[7]. The description of the course of research should be supported references, so the explanation can be accepted scientifically [2], [4]. Figure 1 and Figure 2 are presented center, as shown below and cited in the manuscript [13]. Theeffects ofelectrical discharges to acidity of HVNE and NELV has been illustrated in Figure 2.

2.1. Datasets

The proposed method takes 256×256,512×512-pixel size of MRI brain image dataset as input and converts the image into grayscale for further enhancement. The collection comprises of example images of five patients who were treated with all available modalities. The information was gathered through digital

imaging and communication in the medical dataset. In total 25 images were taken and 18 were affected from a brain tumor and 7 images are of normal brains.

2.2. Preprocessing

Aspects of the parameters include an increase in the signal-to-noise ratio, an improvement in the visual appearance of magnetic resonance images, the elimination of irrelevant noise and background from unwanted portions, smoothing areas of inner parts, and the preservation of important edges. In this case, the histogram equalization method is utilized to enhance the quality of the MRI images taken using the scanner. Histogram Equalization is a computer-based image processing method that is used to enhance the contrast of MR images. When the useful data in an image is represented by near contrast values, this technique is often used to enhance the global contrast of the image. This enables regions with lower local contrast to acquiring a greater contrast in areas with higher local contrast. Steps involved in preprocessing (Histogram equalization):
−   Create a grayscale version of the input image and calculate the frequency of occurrence for each pixel value, i.e. the histogram of an image (values for any grayscale image are in the range [0, 255]).
−   Calculate the cumulative frequency of all pixel values.
−   Multiply the cumulative frequencies by the total number of pixels in the image and divide the result by the highest gray count (pixel value) in the image.

2.3. Segmentation of image

Brain tumor segmentation is the process of separating a tumor from surrounding normal brain tissue. The segmentation procedure divides an MRI into distinct areas based on the information included in the image. Certain requirements must be met, such as the segmentation being intact, which means that every pixel must be included inside the area, every point within the regions must be linked in some way, and the regions must be disjointed, among other things.

They have utilized the K-means segmentation method to segment the MRI in this instance. One of the most important data analysis techniques, K-means clustering is extensively utilized in a broad range of practical applications in developing fields. Clustering is the act of identifying groups of items in such a way that the objects in a group are similar to one another but distinct from the objects in other groups. It is a technique used in data mining. To use the K-means method, we must first determine the number of clusters to be used (k). Then k cluster centers are selected at random from the remaining cluster centers. The distance between each pixel and the center of each cluster is computed and shown. The distance may be a simple Euclidean function. The distance formula is used to compare each pixel to all of the cluster centers. Steps in K-Meains algorithm:

Step 1: Determine the number of clusters to be used, K.
Step 2: Make a random selection of K points and locate their centroids.
Step 3: Assign each data point to the centroid that is closest to it, resulting in K clusters.
Step 4: Calculate and place the new centroid of each cluster in its proper location.
Step 5: Reassign each data point to the centroid that is now the closest to it.
         If there was any reassignment, go to step 4, otherwise, the model is complete.

2.4. Shape-based feature extraction

After the images are segmented, the next step is to perform feature extraction. As the proposed scheme deals with the depth of the tumor, a shape-based feature extraction algorithm is used to extract the features. The size of a region in a digital image is defined as the sum of the number of pixels in the region in which the region appears. Mark the pixels that are inside the area with $f(x, y) = 1$ and the pixels that are outside the region with f (x, y)=0. Then the area may be computed based on the data $A = \sum_{} (x, y \in R)/1$.

Roundness: The regional area and the length of the border are often used to define the form of the target when the size of the interest region remains constant. When it comes to fixed area images, the narrower the perimeter, the closer the target is to the center of the circle. Roundness is $C = (4\pi A) / P2$; Here, P is the perimeter of the regional bounder, A is the regional area. When the region is circular, C takes the maximum value of 1. When the region is a long and thin strip or more complex, the C value is smaller.

2.4. Feature selection using minimalist genetic algorithm

Through uniform mutation over a specified number of generations, the minimalist genetic algorithm (MGA) produces an encoded binary text that can be decoded. Using fewer features in the classification process will improve the accuracy of the classification and therefore the classification accuracy. Many processes, such as encoding, initialization, and modification, are included in this category.

2.4.1. Encoding

The MGA employs a representation method based on bit strings. The string has a length of $L = 124251$, which is the same as the total number of features in the game. The string will be encoded in binary format once it has been decoded. The character "1" in the encoding indicates that the feature has been chosen, while the character "0" indicates that the feature has not been selected. The encoding will be done in the following manner, $010\ldots100$.

2.4.2. Initialization

During the first generation, each of the genes is assigned a value of 1 with a probability Pin for generating a random initial solution. The number of selected features can be controlled by Pin in the initial individual. It is set based on the domain knowledge as it is problem-dependent.

2.4.3. Fitness function Evaluation

One of the objectives of the study is to obtain the highest possible accuracy in categorization. To accomplish a balance between accuracy and the number of chosen features, overfitting is avoided at all costs. The fitness F of the person I under consideration is determined as (1).

$$F(I) = C(I) - \frac{n_I}{L} \tag{1}$$

Where $C(I)$ is the accuracy of the classification and n_I is the number of features selected in the individual I which denotes the number of 1s in the representation which is encoded. L denoted the size of the string. the number of features selected is divided over the total length of the chromosome to maintain the balance between the features.

2.4.4. Mutation

To see the variation in each of the genes, the uniform random mutation method is employed, with the likelihood of change denoted by the letter rm. Following the uniform distribution, a random number between 0 and 1 is generated using a random number generator. The value of the gene is changed from 1 to 0. If the value produced is less than rm, the value of the gene is modified in the other direction, from 1 to 0. Because the second random number produced is 0.001, the second gene of person I on the left is changed from 0 to 1 in the following example:

$$I = 01\ldots10 \rightarrow I' = 00\ldots10$$

$$rand(): 0.236, 0.001, \ldots, 0.385, 0.798$$

The MGA is comprised of many stages, such as the generation of a random starting solution I, followed by the repetition of the following steps until the criterion is satisfied. Then, until the halting criteria are satisfied, the following stages are performed repeatedly: In I the child I' is produced for the individual I via mutation by representing the existing solution, and, if the offspring has a better fitness value than the person I, the new current solution is retained; otherwise, the current solution is not altered. The process comes to an end after a certain number of iterations, which is indicated by the symbol $MGen$.

Algorithm for MGA
```
Step 1: Input: Initialization of random individual (I);
Step 2: Function:
Step 3: Evaluate I;
Step 4: nGen = 0;
Step 5: while nGen < MGen
Step 6: do
Step 7: Apply mutation to I → I';
Step 8:          Evaluate I';
Step 9: if F(I') > F(I)
Step 10:         then
Step 11:         I = I';
Step 12: end if
Step 13: nGen + +;
Step 14: end while
```

2.5. Conversion of 2D to 3D using depth map estimation

The conversion of a two-dimensional image to a three-dimensional image may be accomplished following the selection of characteristics by using three distinct appealing techniques, including greyscale analysis, relative spatial setup, and multiple view 3D rendering, among others. Using a color image of the tumor afflicted portion, one intensity value G with grayscale is retrieved and transformed to one intensity value G:

$$G = \frac{(G_r + G_g + G_r)}{3} \tag{2}$$

where r, g, b denotes the base intensity of the colors red, green, and blue. The greyscale G can be extended to G' for an 8-bit word with a range from 255 to 0 by (1) and (2).

$$G' = \frac{(G - G_{min}) \times 255)}{G_{max} - G_{min}} \tag{3}$$
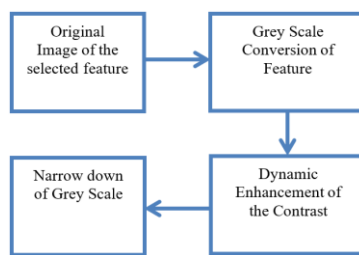
Figure 1. Grey scale conversion
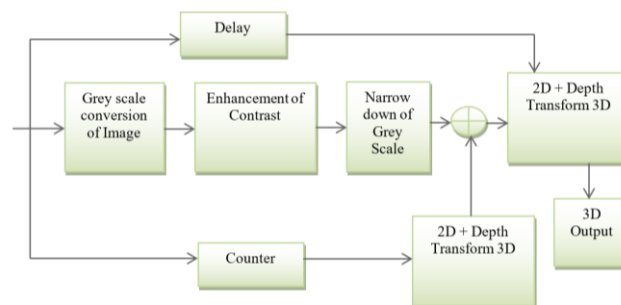
Figure 2. Conversion of 2D to 3D image

The greyscale conversion is carried out for the feature retrieved from the tumor-affected portion, and the regions with the highest concentration of RGB are the ones that are converted. The grayscale (see Figure 1) converted portion is next subjected to contrast enhancement, which allows the viewer's attention to be drawn to the specific tumor afflicted area, which will be highlighted in white. The scale range is then reduced down to the numbers 0-63. In the next phase, the brightness of the whole image is reset by assigning a reduced luminance to the top part of the image, which gradually becomes brighter as it moves toward the bottom section. The remarkable sense of the depth of the image is communicated via the use of an increasing grayscale (see Figure 2) toward the bottom portion of the image [18], [19]. Concerning the low intense statistics, it likewise retracts. This depth augmentation works by counteracting the spot of the image at any depth that reflects light, giving the impression of a shallower depth than it is. Following the depth map, the four views are divided into two views, with the depths given to each pair differing from the other [20], [21].

3.   RESULTS AND DISCUSSION

The dataset is collected from cancer image archive. The size of the dataset is 21 Gb. Here the image dataset is preprocessed by selecting the sample of the images. The dataset includes more than 400 patient data in which 4 different images are been selected for observing the change of two-dimensional images to a

three-dimensional image. The segmentation is the second step in which the sample selected from the dataset is segmented to observe the region where the cancer is been affected. The third step is the feature selection, here the region where cancer exists is found. In Figure 3, we can observe that the cancer-affected part is been colored differently to observe it easily. Here Figures 3(a)-(d), denotes different cancer-affected brains. The top row shows the greyscale image of cancer affected part and the bottom part shows RGB-colored cancer-affected parts of the brain [22]-[25].
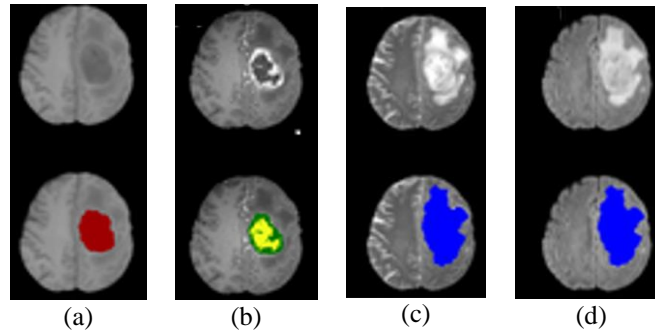
Figure 3. Greyscale and RGB applied feature selection of cancer affected module, (a) original image segment part, (b) detect the tumor, (c) inner layer detection, and (d) inner and outer layer detection

In Figure 4, the feature extraction is done. The feature extraction is implemented to extract cancer-affected parts from the original image. Here Figure 4(a) shows the 3D feature extracted cancer affected part using Volumetric Algorithm model, Figure 4(b) shows the 3D feature extraction of cancer affected part using an existing algorithm, and Figure 4(c) shows the 3D feature extraction of cancer affected part using the proposed model.
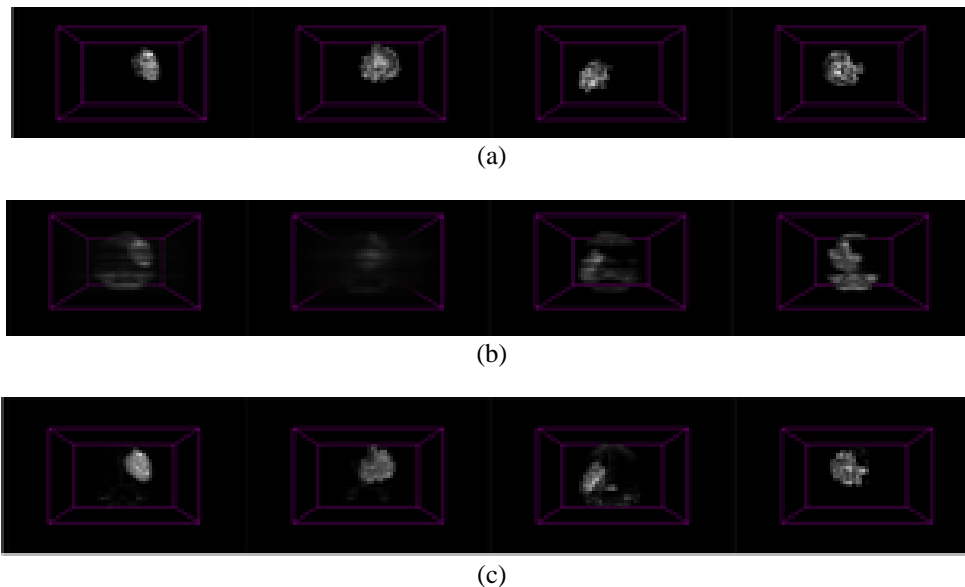

Figure 4. Feature extraction of an affected part after conversion to 3D (a) feature extraction using PR model, (b) feature extraction using BA model, and (c) feature extraction using proposed MGA model

The recall and probability, as well as the PR and BA, of our proposed 3D method, are calculated across these thresholded saliency maps, and the results are compared. The precision-recall and receiver operating characteristic (ROC) curves are shown in Figure 5 after averaging the collection of images. In the case of the suggested method, the corresponding area under curve (AUC) values for ROC are 0.993 0.01, and

0.01 respectively. The values obtained by the proposed method are almost identical to the values obtained from hand detection of the images, which is a significant improvement. The AUC values for algorithm PR and algorithm BA, on the other hand, are 0.93 0.1 and 0.91 0.2, respectively. Because of this, it is possible to notice that the new 3D method produces statistically superior precision-recall and ROC curves when compared to the previous 3D saliency approach of PR and BA models. From Figures 5 and 6, as we can see, the suggested model has a low false-positive rate and a high true positive rate when compared to the current algorithms PR and BA, which indicates that the proposed model is more accurate. In addition, while comparing the proposed MGA to the current algorithms PR and BA, it is discovered that the accuracy and recall are both excellent.
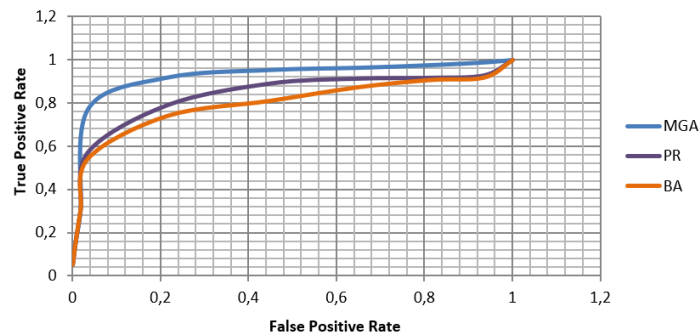

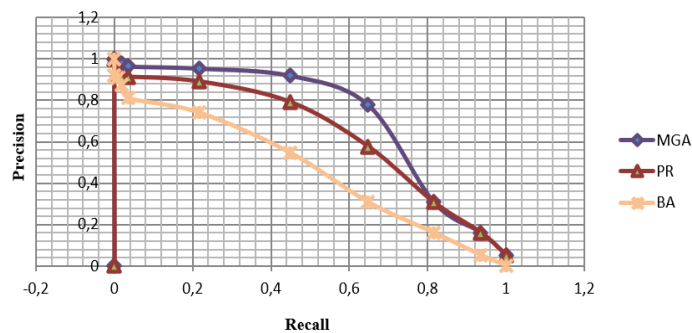Figure 5. Comparison of PR, BA, and proposed MGA based on ROC curves

Figure 6. Precision-recall comparison of PR, BA, and proposed MGA

4.   CONCLUSION

Thus converting 2D scanned images to 3D images can help the physicians to exactly identify the size, shape, and sharp region of the tumor cells in the brain. In this work, we have created a framework to predict the size, shape, and region of the brain tumor using minimized genetic machine learning algorithm, and later after identifying the tumor information, 2D images are converted into 3D images using a depth map estimation technique. MRI dataset is given as input to the preprocessing system in which histogram equalization technique is used to remove the signal to noise ratio in the MRI images. Later feature extraction and selection are performed to exactly identify the location and shape of the tumor. It is also observed that the proposed model produces good precision and recall rate when compared to the existing models.

REFERENCES

[1]   P. Grandhe, S. R. Edara, and V. Devara, "Adaptive analysis & reconstruction of 3D DICOM images using enhancement based SBIR algorithm over MRI," *Biomedical Research,*vol. 29, no. 4, 2018, doi: 10.4066/biomedicalresearch.29-17-1723.
[2]   C. Q. T. Thanh and N. T. Hai, "Trilinear interpolation algorithm for reconstruction of 3D MRI brain image," *American Journal of Signal Processing,* vol. 7, no. 1, , pp. 1–11, 2017, doi: 10.5923/j.ajsp.20170701.01.
[3]   N.-E. Yang, J. W. Lee, and R.-H. Park, "Depth map generation using local depth hypothesis for 2D-To-3D conversion," *International Journal of Computer Graphics & Animation*, vol. 3, pp. 1. 2013, doi: 10.5121/ijcga.2013.3101.
[4]   Jung, Cheolkon, L. Wang, X. Zhu, and L. Jiao, "2D to 3D conversion with motion-type adaptive depth estimation," *Multimedia Systems*, vol. 21, no. 5, pp. 451-464, 2015, doi: 10.1007/s00530-014-0375-z.
[5]   S. Bharathi and A. Vasuki, "2D-to-3D conversion of images using edge information," *IJCA Proceedings on International Conference in Recent trends in Computational Methods, Communication and Controls (ICON3C 2012),* no. 2, 2012, pp. 27-32.

[6]   A. Kanchan and T. Mathur, "Recent trends In 2D To 3D image conversion: Algorithms at a glance," *International Research Journal of Engineering and Technology*, vol. 4, no. 4, pp. 3480-3484, 2017.
[7]   B. M. Ellingson, M. Bendszus, A. G. Sorensen, and W. B. Pope, "Emerging techniques and technologies in brain tumor imaging," *NeuroOncology*, vol. 16, pp. 12-23, 2014, doi: 10.1093/neuonc/nou221.
[8]   D. Kayal, and U. Çevik, "Detection and 3d modeling of brain tumors using image segmentation methods and volume rendering," in *Natural and Engineering Sciences*, vol. 3, no. 3, pp. 79-86, 2018.
[9]   G.-S. Lin, H.-W. Liu, W.-C. Chen, W.-N. Lie, and S.-Y. Huang, "2D to 3D image conversionbased on classification of background depth profiles," *PSIVT 2011: Advances in Image and Video Technology*, vol. 7088, 2011, pp. 381-392.
[10]   E. Hnatkova, P. Kratky and Z. Dvorak, "Conversion of 2D medical scan data into 3D printed models," *Advances in Environmental Sciences Development and Chemistry*, pp. 315–318, 2014.
[11]   V. S. Nguyen, M. H. Tran and H. M. Q. Vu, "A research on 3D model construction from 2D DICOM," in *2016 International Conference on Advanced Computing and Applications (ACOMP)*, 2016.
[12]   L. Mazzotta, M. Cozzani, A. Razionale, S. Mutinelli, A. Castaldo and A. S. Biavati, "From 2D to 3D: Construction of a 3D parametric model for detection of dental roots shape and position from a panoramic radiograph—A preliminary report," *Hindaw iPublishing Corporation, International Journal of Dentistry*, 2013, doi: 10.1155/2013/964631.
[13]   H. S. Bhatt and S. K. Gonsai, "3D modelling and volume rotation of 2D medical images," *International Journal of Advanced Research in Electrical, Electronics and Instrumentation Engineering,* vol. 3, no. 3, pp. 8082-8086, 2014.
[14]   A. Farzana and M. M. Sathik, "Analysis of 2D to 3D reconstruction techniques over brain MRI," *International Journal of Innovative Research in Computer and Communication Engineering*, vol. 5, no. 5, pp. 9370-9376, 2017.
[15]   W. Liu, Y. Wu, F. Guo, and Z. Hu, "An efficient approach for 2D to 3D video conversion based on structure from motion," *The Visual Computer*, 31, no. 1, pp. 55-68, 2015, doi: 10.1007/s00371-013-0904-3.
[16]   M. U. Akram, A. Khanum, and K. Iqbal, "An automated system for liver CT enhancement and segmentation," *ICGST-GVIP Journal*, vol. 10, no. 4, pp. 17-22, 2010.
[17]   H. Shi and R. Fahmi, "Energy minimization within the F.E. framework to predict liver tissue deformation," *ICGST International Conference on Graphics,Vision and Image Processing(GVIP-05),* 2005, pp. 541-547.
[18]   S. Mitra, S. Banerjee, and Y. Hayashi, "Volumetric brain cancer detection from MRI using visual saliency," *PLOS ONE*, vol. 12, no. 1, pp. 1–14, 2019, doi: 10.1371/journal.pone.0187209.
[19]   M. Erihov, S. Alpert, P. Kisilev, and S. Hashoul, "A cross saliency approach to asymmetry-based tumor detection," *MICCAI 2015: Medical Image Computing and Computer-Assisted Intervention,* vol. 9351, 2015, doi: 10.1007/978-3-319-24574-4_76.
[20]   S. Banerjee, S. Mitra, B. U. Shankar, and Y. Hayashi, "A novel GBM saliency detection model using multi-channel magnetic resonance imaging (MRI)," *PLOS ONE*, vol. 11, no. 1, pp. 1-16, 2016, doi: 10.1371/journal.pone.0146388.
[21]   J. Konrad, M. Wang, and P. Ishwar, "2D-to-3D image conversion by learning depth from examples," in *Proc. IEEE Comput. Soc. CVPRW*, 2012, pp. 16-22.
[22]   P. Ji, L. Wang, D. Li, and M. Zhang's, "An automatic 2D to 3D conversion algorithm using multi-depth cues," *2012 International Conference on Audio, Language and Image Processing,* 2012, pp. 546-550 doi: 10.1109/ICALIP.2012.6376677.
[23]   M. Kanmani and M. Pushparani, "Identification and classification of brain tumors," *International Journal of Current Research (IJCR)*, vol. 8, no. 5, pp. 31334-31337, 2016.
[24]   K. M. Toum, Z. A. Mustafa, B. A. Ibraheem, and A. O. Hamza, "Magnetic resonance imaging scans of the brain for tumor segmentation," *Journal of Clinical Engineering*, vol. 42, no. 3, pp. 115-120, 2017, doi: 10.1097/JCE.0000000000000223.
[25]   Y. Sun, B. Xue, M. Zhang, G. G. Yen, and J. Lv, "Automatically designing CNN architectures using the genetic algorithm for image classification," *IEEE Transactions on Cybernetics*, vol. 50, no. 9, pp. 3840–3854, 2020, doi: 10.1109/TCYB.2020.2983860.

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