

# DoctorEye: A multifunctional open platform for fast annotation and visualization of tumors in medical images

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**Abstract**—This paper describes a flexible and easy-to-use annotation platform (GUI) for quick and precise identification and delineation of tumors in medical images. The design of the platform is clinically driven in order to ensure that the clinician can efficiently and intuitively annotate large number of 3D tomographic datasets. Both manual and well-known semi-automatic segmentation techniques are available in the platform allowing clinician to annotate multiple regions of interest at the same session. Additionally, it includes contour drawing, refinement and labeling tools that can effectively assist in the delineation of tumors. Furthermore, segmented tumor regions can be annotated, labeled, deleted, added and redefined. The platform has been tested over several MRI datasets to assess usability, extensibility and robustness with promising results.

## I. INTRODUCTION

CANCER is a leading cause of fatality among other diseases. Still, there is no known way of preventing cancer, but early detection allows treatment before cancer is metastasized to other parts of the body.

Modern tomographic systems like the new Magnetic Resonance Imaging (MRI) scanners, offer clinicians high resolution images allowing a more specific look at radiologic anatomy. They offer the ability to detect masses and distortions of tissue better, quicker and more efficiently than ever before. This makes MRI imaging a very popular technique in cancer imaging, allowing doctors to extract critical pathophysiological information in order to establish early diagnosis and assess the stage of the disease.

A radiological department and specifically oncologists often deal with a large number of MRI multi-frame slides where tumor identification and delineation can be a thorny and time consuming process. Numerous existing projects are

developing specialized platforms and tools to speed up the process of data analysis in different biomedical applications. Such medical image-annotation representative systems include VANO [1], CMAS [2], Hybrid System [3], Annotor [4] and Amiravis [5].

DoctorEye is a novel, open access, more flexible and easy to use platform, for intuitive annotation and / or segmentation of tumor regions. Its development is clinically driven and follows an open modular architecture focusing on plug-in components. The main advantage of the proposed platform is that the user can quickly and accurately delineate complex areas in medical images in contrast with other platforms that do not facilitate the delineation of areas with complicated shapes. Additionally, multiple labels can be set to allow the user to annotate and manage many different areas of interest in each selected slide. The close collaboration with clinicians in designing the platform has ensured that it can be effectively used in the clinical setting.

Another feature that adds value to the platform is that it allows computational “in-silico” models of cancer growth and simulation of therapy response to be easily plugged in, in order to provide a future integrated platform for modeling assisted therapy decision making. Currently, our group is working towards incorporating such models in the platform and the new version will also be freely available. In this context, the platform could also serve as a validation environment where the simulation predictions could be compared with the actual therapy outcome in order to achieve a global optimization of the modeling modules. This tool is part of the “Contra Cancrum” EU-ICT research project and in its first stage serves as an intuitive 3D annotation system.

## II. METHODOLOGY

### A. Platform design

The platform was developed from scratch based on the .NET framework architecture [6] and can be used in any Windows-based computer with the .NET framework ver. 2.0 or later. However, .NET framework permits, in concept, the porting of the application in many other Linux based environments, using the Mono project [7] functionality and libraries, so the user can run an application using the No-Touch Deployment [6].

Its basic functionality is described below:

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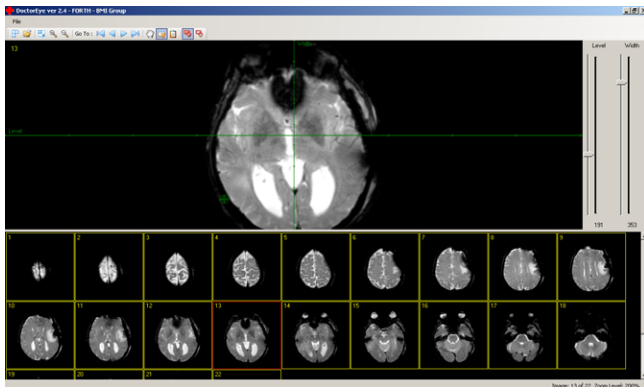


Fig. 1: DicomEye: Snapshot of the main window. The user is able to easily navigate through the available slides and select the one to process.

- *Slide Selection and Presentation Context*

The user can select any number of medical images in DICOM format, from a group of thumbnails to process. These thumbnails will appear in a resizable area at the bottom of the screen as shown in Fig. 1. At this point, the user can also adjust the level and width values by using a system of axes. Two options are also available here. The first allows the user to zoom in or out and the second to shift the position of the selected image on the screen in order to have a better view of the regions of interest.

- *Annotation tools and Segmentation algorithms*

The user can activate the “Annotations” panel to delineate either areas or contours of potential tumors in the selected medical image. These areas can be annotated, categorized,

deleted, added and redefined as depicted in Fig. 2. The steps involved are described below.

The user must first create a label in order for the segmentation method to begin. This label will correspond to the area which will be identified by the algorithm. The user may also label the selected region with a chosen color and define the “working area” where the segmentation method will be applied (Fig. 2). Two different segmentation methods are currently available in the platform as discussed in section II-B.

Finally, contour refinement is possible by using the “eraser” and “pencil” tools, where any mistakenly selected or ignored pixel can be removed or added, respectively, in order to end up with the best possible delineation of the identified tumor.

The label that had been given at the beginning of the process is now available in the “annotations” panel corresponding to this specified tumor. It can be selected and the specified tumor will be displayed.

The platform also gives the ability to select and delineate multiple tumors (i.e. in the case of metastasis) with different labels and colors, either in the same or any other slide as shown in Fig. 3.

- *Annotation Storage*

Finally, the selected areas are saved in an .xml file and can be accessed and displayed from the main menu at any time. The platform keeps a record of both regions and contours of the delineated tumors.

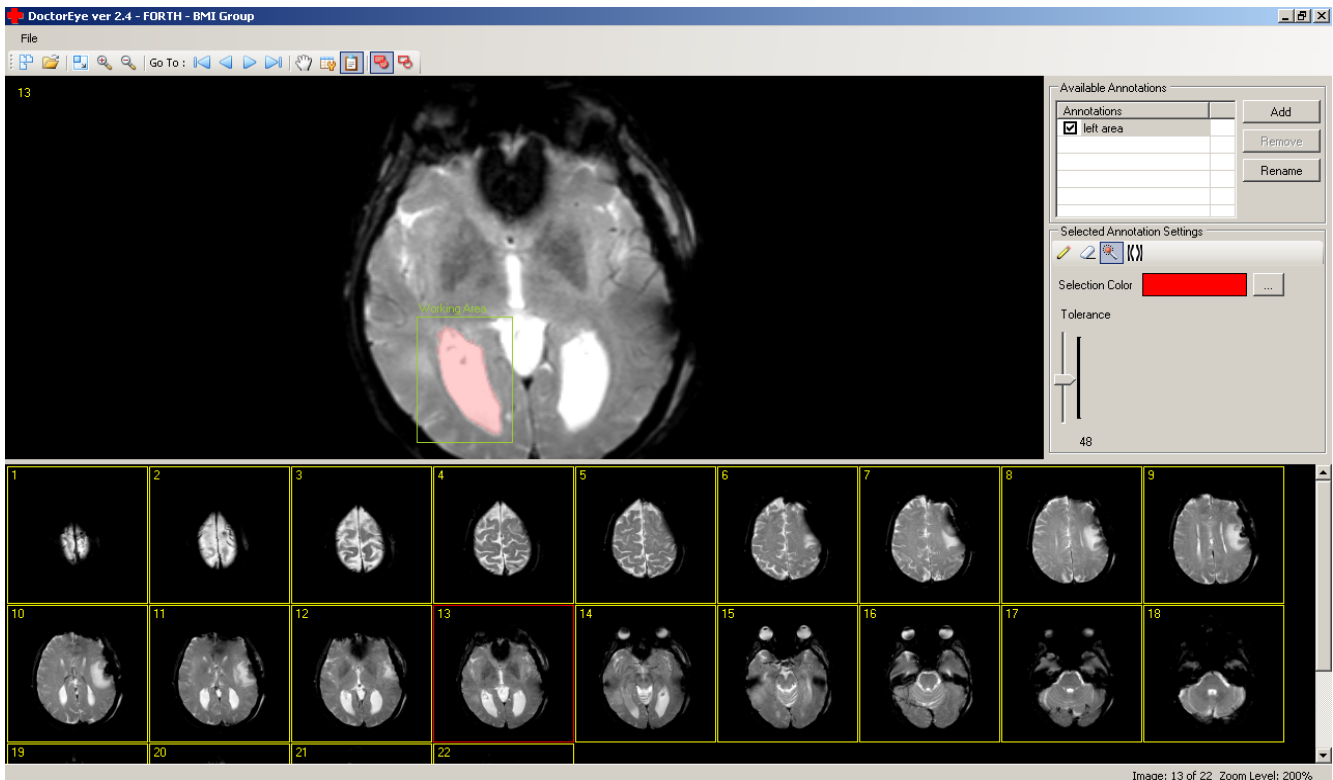


Fig. 2: A single slide is selected for further processing. A working area has been set (green rectangle) and the segmentation algorithm has been applied. The selected area is labeled in pink.

## B. Segmentation Methods Applied

Medical image segmentation has been a subject of vast research in the past years. Both the automatic and semiautomatic detection and delineation of tumors (glioma in this test case), typically involve different types of tissue and fuzzy boundaries rendering them difficult to segment. In this phase of the development we mostly focus on MRI imaging modality since MRI has been mostly used by the clinicians in the glioma case.

Two different, in terms of underlying theoretical concepts, segmentation algorithms are currently available in the platform: namely the “Magic Wand” and the “Active Contours”, while any other algorithm can be easily plugged-in as well. The first is based on image intensity, whereas the second is a model-based method.

### 1) THE MAGIC WAND ALGORITHM

The function of the Magic Wand Algorithm is based on finding and selecting all the pixels around a pre-specified user-selected initial point that are similar in gray intensity. A tolerance value can also be set by the user to determine how closely to match colors (higher tolerance ends up in a larger selection) [8]

All the points selected by the algorithm are automatically stored in an image mask of the same size as the original image. Each pixel in the image mask represents the position of the selected pixels in the original image and is used to label the delineated tumors.

To enhance its effectiveness, we have also implemented a faster version of this algorithm which excludes all the pixels that have already been examined, to ensure that the algorithm does not check them again.

### 2) THE ACTIVE CONTOURS ALGORITHM

An alternative method to perform segmentation in two-dimensional images is based on iterative evolution methods such as the discrete active contours algorithm. A number of methods are available to evolve active contours. The most commonly used ones are the variational approach [9] and the greedy algorithm [10], [11]. The platform implements the greedy algorithm, which minimizes the following discrete energy functional:

$$E(p'_i) = E_{\text{cont}}(p'_i) + E_{\text{curv}}(p'_i) + E_{\text{grad}}(p'_i) + E_{\text{bal}}(p'_i)$$

In contrast with the initial location  $p_i$ , we denote  $p'_i$  the search location, whose energy is a weighted sum of various internal and external energies [10]. Global minimization is done by means of successive local optimization. The *external energy* is supposed to be minimal when the snake is at the object boundary position. The user only need to add points in order to define an initial approximation. The following parameters can also be defined in order to achieve optimal segmentation results: Continuity, Curvature, Gradient and Pressure (or balloon).

However, segmentation errors are common, especially when at the bounds of the tumor, where the gray-level value

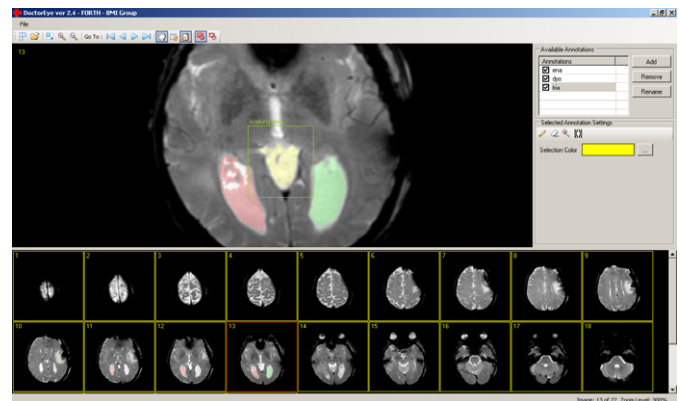


Fig. 3. Different areas of interest may be annotated accordingly using respective labels in different colors. This can be done in the same slide in the case of metastasis.

profile may be similar to that of the tumor itself. This defect can be reduced by re-adjusting the tolerance level (when using the Magic Wand option), which yields a more precise delineation of the tumor region. This can be done in real time by the user adjusting a slider in the GUI. Finally, segmentation errors can also occur when using the Active Contours algorithm, mostly because it is not easy to adjust the algorithm parameters in an automated way.

## III. RESULTS

There are four basic features that characterize the platform. It is flexible, easy to use, fast to operate and freely distributed for testing upon request.

The application interface is flexible and can be easily adjusted to suit different viewing setups by adjusting the width and height of the thumbnail and the main window by sliding the window separator bar. Therefore, the user can actively alter the number of the thumbnails that appear on the screen as well as the size of the selected image. The resolution and size of the screen are also taken into account for ensuring an optimal representation.

It is easy to use, as the platform is designed as a GUI environment with standard menus and buttons. Moreover, it enables the user to view the effects of the functions that are being implemented in the selected medical image while the user is experimenting with various parameters.

It is fast to operate due to the fact that the algorithms used are fully integrated in the platform and run “on the fly” and not as calls to external programs.

Finally, it is distributed free to test and requires no registration or activation, thus not limiting its use in any way [12].

Currently, the platform is being tested by engineers on 15 annotated MRI datasets and the results will be reported in the near future. By visual inspection of the results, the system yields precise semi-automatic annotations as perceived by the developers. At a later stage, further clinical testing will be conducted by pathologists, to corroborate results.

#### IV. DISCUSSION

This tool facilitates the 3D annotation of features such as cancer from MRI datasets and can be extended to any other tomographic modality. In its current form, it can be used as a flexible and practical annotation system, providing quick and precise delineation of tumors.

Future work focuses on incorporating even more tumor specialized segmentation algorithms and measuring the performance of the later. This requires the knowledge of the true borders of the tumor under investigation and a precisely defined validation metrics utilizing both statistical and geometrical properties. Nevertheless, in medical image processing society there is no established method to define the correctness of a segmentation result thus a manual segmentation done by one or more neurosurgical experts will serve as a standard for the validation. It is expected that a larger number of human raters is needed for a validation [13].

Although the platform has been designed by clinicians for clinicians it is crucial to design several validation experiments that will deal a) with the functionality / usability of the algorithms and b) with the effectiveness of the tools in annotating tumors / ROIs. The latter requires to compare the annotations of experts (used as gold standard) to the generated segmentations and report the sensitivity / specificity score.

The initial assessment of the methods used indicates that the “Magic Wand” method exhibits greater ease of use and is more applicable to medical images when the gray tone on the contour of the delineated tumor is not similar to that of the surrounding area. In the later case, diffusion can occur and the use of the “Active Contours” segmentation method is more advisable. This method however, is non intuitive, in the sense that the user may find it difficult to interpret the physical meaning of the related parameters and predict the best possible values to be selected and adjusted individually for every tumor case.

A problem currently under consideration is the size of the xml file that is used to store the different labels and segmented regions. Currently this file serves also as a database for all the exported data from the processed medical images. A more sophisticated data management system is planned to be developed in order not to create data files that are large and difficult to handle. Plug-in extensibility will be thoroughly addressed in the next available version.

#### V. CONCLUSIONS

In this paper we presented a novel, open access platform that can assist doctors to identify any number of distinct 3D features such as tumors in complex medical images and annotate them individually. Due to the scalable architecture of the platform it can serve as the basis of an integrated system for visualizing cancer in three dimensions, as well as hosting models of cancer growth or response to therapy.

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