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BrAInXplore: Automated 3D Delineation and Structural Analysis of Brain MRI Data

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Abstract—Magnetic Resonance Imaging (MRI) is fundamental for the diagnosis of neurological disorders, as by isolating specific regions of the brain allows easier detection of possible anatomical alterations. In recent years, the use of deep learning (DL) approaches spread in clinics for automated and accurate segmentation of brain tissues and structures. This work presents BrAInXplore, a DL-based graphical user interface (GUI) designed for automated anatomical delineation, 3D reconstruction, and qualitative and quantitative brain MRI analysis. The tool integrates a previously developed DL segmentation algorithm into a user-friendly and extensible framework. BrAInXplore is mainly structured in two windows: the main window, which serves as the main application interface, and an operating window, called “3D Viewer”, which performs 3D reconstruction of brain tissues and structures from MRI data. The GUI automatically delineates and visualizes in 3D six anatomical components (grey matter, white matter, basal ganglia, cerebellum, ventricles, and brainstem), also providing their volumes. BrAInXplore can handle both labelled and blind input data, depending on whether annotations on brain anatomical components are available or not. The GUI may find application in both research and educational contexts. Moreover, its design ensures extensibility and ease of modification, allowing for future improvements.

Keywords— brain structure automatic segmentation; deep learning; neuroradiology; magnetic resonance imaging; radiodiagnostics; volume measure analysis

I. INTRODUCTION

Nowadays, one of the most robust imaging techniques for the diagnosis of neurological disorders and the analysis of alterations in brain structures is Magnetic Resonance Imaging (MRI) [1]. Thanks to its non-invasiveness, it allows the detection of structural and functional changes in the brain in a safe manner for the patient [1]. Most neurological and neurodegenerative disorders are characterized by alterations in specific brain regions. For example, multiple sclerosis is characterized by the presence of lesions in the white matter, Parkinson’s disease is characterized by shrinkage of brain stem, Alzheimer’s disease is characterized by atrophy in grey matter [1]. For diagnostic purposes, imaging analyses typically focus on the basal ganglia, cerebellum, ventricles, and brain stem, together with separation of grey and white matter [2]. The anatomical isolation of brain regions is referred to as parcellation, whereas the separation of different

tissue types (such as grey matter and white matter) is known as segmentation. Although they represent distinct processes, parcellation and segmentation are complementary operations in brain image analysis and are both useful for investigating pathological brain alterations. Both parcellation and segmentation processes are usually carried out manually by the clinician, but they are strongly dependent on the clinician’s expertise, thus suffering from inter- and intra-expert variability [3]. Thus, automatization of these processes can support the clinician in decision-making, improving the diagnostic performance [1].

In this context, this work aims to present a DL-based graphical user interface (GUI), called BrAInXplore and designed for automated anatomical delineation, 3D reconstruction, and qualitative and quantitative analysis of brain tissues and structures from MRI data. BrAInXplore is built upon a previously developed deep learning (DL) segmentation algorithm, which has been integrated into a user-friendly and extensible framework [4]. Specifically, the DL segmentation algorithm was proposed in 2023, consisting in a double-stage 3D U-Net for on-cloud brain extraction and multi-structure segmentation of MRI data from [2].

II. THE MAIN AVAILABLE TOOLS IN THE FIELDS

To the best of our knowledge, the most used publicly available tools for the segmentation of brain regions are Statistical Parametric Mapping 12 (SPM12) [5], FMRIB Software Library (FSL) [6], and FreeSurfer [7].

SPM is a software developed for the analysis of different imaging modalities [8]. The latest version of the software is SPM12, and it was updated in January 2020 [8]. The classification of MRI volumes into different tissue types relies on tissue probability maps derived from anatomical atlases, which encode the probability of each tissue type at a given spatial location, together with voxel intensity information. [5,8]. Specifically, it relies on the spatial location and on the intensity information of each voxel of the MRI input volume. Since each tissue type does not have a uniform and specific intensity distribution, it is represented by several Gaussian intensity distributions. Hence, each tissue class is represented by a distribution given by a mixture of Gaussians [5]. To classify the input volume into several tissue types, the likelihood of each voxel’s intensity is evaluated under the intensity distributions associated with

each tissue class. This likelihood, together with the voxel's spatial location, determines the probability that the voxel belongs to a specific tissue type [5]. This procedure is accompanied by a bias-field correction process that helps improve the uniformity of each tissue intensity, by removing artifacts [5]. The tissues that can be segmented through SPM are grey matter, white matter, cerebrospinal fluid, bone, soft tissues, and air (background) [5]. SPM has also a tool for the lesion segmentation, called LST [5].

FSL software performs segmentation through FMRIB Automated Segmentation Tool (FAST) [8, 9]. Differently from SPM, in FSL, tissue segmentation can only be performed on brain-extracted volumes; therefore, an explicit brain extraction step is required prior to segmentation [9]. It can segment the following tissues: grey matter, white matter, cerebrospinal fluid, and some anomalies in case of pathology (e.g., lesions) [9]. Similarly to SPM, in FSL the intensity histogram of each tissue class is modeled using a mixture of Gaussian distributions. Voxel classification is based not only on intensity but also on spatial coherence with neighboring voxels through a Markov random field model [9]. Thus, unlike SPM segmentation, by default, FAST does not use atlas priors and instead relies on intensity modeling and the spatial information of neighboring voxels [9]. FSL has also another tool for the segmentation of sub-cortical structures, called FIRST, that, differently from FAST tool, is atlas- and model- based [8].

Unlike SPM and FSL, which primarily focus on tissue segmentation, FreeSurfer not only performs tissue segmentation but also allows the parcellation of specific anatomical brain structures, including cortical and subcortical regions [7]. To do this, FreeSurfer exploits not only probabilistic atlas and intensity information, but also the position and the relationships between subcortical structures [8]. With the implemented pipeline, up to 40 labels can be assigned to each voxel, each one corresponding to a specific brain region/structure. In last years, the pipeline has been extended to segment also 9 amygdala nuclei and 13 subfields of hippocampus [8].

Although SPM, FSL and FreeSurfer are widely used for segmentation tasks, they suffer from some limitations: they are atlas-based and not learning-based, this means that, to improve their performance, new atlases are needed, which generally need to be manually created; they lack accuracy in the precise delineation of the boundaries of brain structures; image artifacts may lead to coarse segmentation of brain structures; abnormal contrast or gross morphological alterations may lead to misinterpretation [8,10]. In recent years, DL-based approaches have emerged as the preferred methods, as they enable fully automated and accurate segmentation of both tissues and anatomical structures, reducing reliance on manual atlases and preprocessing steps. Specifically, convolutional neural network (CNN) showed to be the most efficient DL-algorithm in this field, as proven by Sun et al. [11], Wang et al. [12], Bontempi et al. [10], Ramzan et al. [13], and Laiton-Bonadiez et al. [14]. CNN exploits contextual information from the input volume to perform voxel-wise classification without relying on hand-crafted features. Hence, it is able to learn directly from data, without relying on prior atlas, as it is able to extract the most relevant features from the input volume by itself. If trained on a sufficiently large dataset, these models can generalize well with new data. Recently, 3D CNNs for brain MRI

segmentation have been used, implementing patch-based or fully volumetric approaches [10, 11, 12, 13, 14]. Most of these approaches use an encoder-decoder network with skip connections, enabling the decoder to incorporate both high-level features and fine-grained spatial information from the encoder at each corresponding layer. [10, 11, 12, 13, 14]. This sub-kind structure of CNN is called U-Net. However, despite the high performance, these approaches cannot have direct applicability in real practice due to the unavailability of user-friendly interfaces, which are well-suited for prompt usage.

III. BRAINXPLORE

BrAInXplore is developed using Python 3 (version 11) programming language on the TensorFlow backend. The GUI is developed using PyQt5, which is a comprehensive set of Python bindings for Qt (version 5), efficient in building graphical user interfaces and applications [15-16]. The architecture of BrAInXplore is designed to allow easy access to the users through a powerful but lightweight interface.

Once launched, the main window of BrAInXplore (Fig.1, left panel) appears, serving as a main application interface. Clicking on the brain icon, the working window (Fig.1, right panel), called "3D Viewer", opens and allows the interactions of the user to reconstruct 3D brain structures. The top tab contains GUI components that enable the users to access all possible operations of the GUI. Specifically, five buttons are included for the following operations: load the MRI data, visualization of brain structures, full screen visualization, reset and saving.

A. Data Loading

BrAInXplore is able to detect from MRI data (in standard NIfTI format) six structures of the brain, that are grey matter (GM), white matter (WM), basal ganglia (BG), cerebellum (CB), ventricles (VEN), and brain stem (BS).

MRI data (Fig. 2) can be blind or labelled, according to the absence or presence of brain structures annotations, respectively. The button "Blind MRI" allows the loading of blind MRI data. Once the MRI data are loaded, BrAInXplore automatically applies the trained DL model proposed in [4] in order to segment the image in the six brain structures. While the button "Labelled MRI" allows the loading of MRI data with its own annotations. Once loaded, the six brain structure information are derived from the annotations. When obtained brain structures, their 3D visualization is displayed (Fig 3.A), together with their anatomical volumes in cm^3 .

B. Visualization of Brain Structures

The brain structures can be visualized by selecting in the "START" and "END" spin boxes the number of the corresponding structure. Specifically, number 1 corresponds to GM (Fig 3.B), number 2 corresponds to WM (Fig 3.C), number 3 corresponds to BG (Fig 3.D), number 4 corresponds to CB (Fig 3.E), number 5 corresponds to VEN (Fig 3.F), and number 6 corresponds to BS (Fig 3.G). By default, the "START" spin box value is equal to 1 (i.e., GM) and the "END" spin box value is equal to "6" (i.e., BS), in order to ensure the visualization of all brain structures. If the values of both "START" and "END" spin boxes are the same, only the corresponding brain structure is visualized; while if the values of "START" and "END" spin boxes differ, all the brain structured included in the range are visualized (example at Fig 3.H).

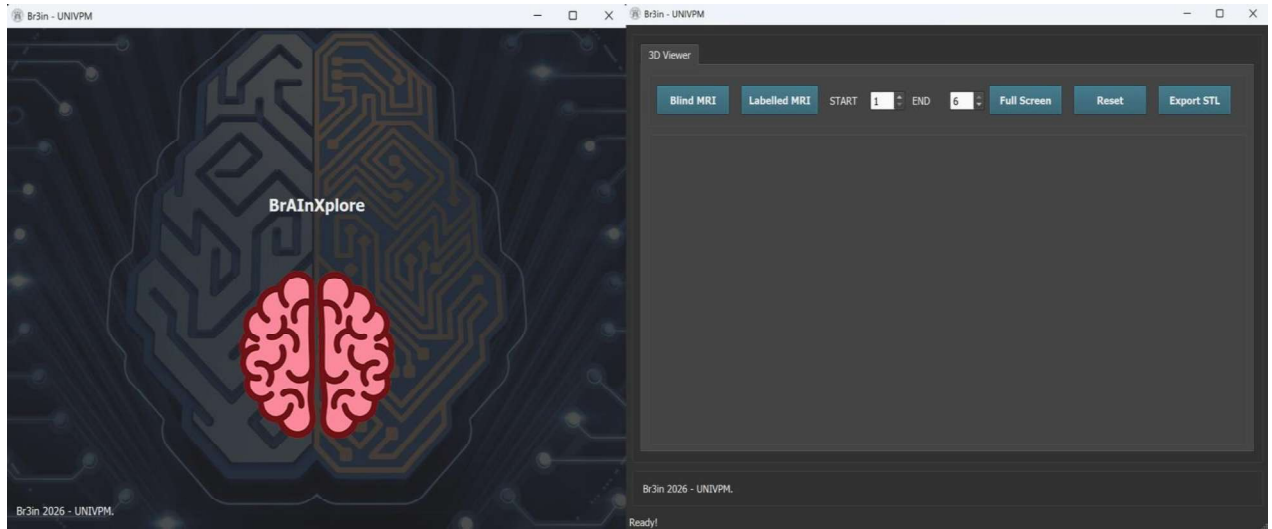


Fig. 1. Representation of the GUI structure of BrAInXplore. On the left, the main window. Clicking on the brain icon, “3D Viewer” opens up, with the following buttons: “Blind MRI” and “Labelled MRI” for the loading and starting the 3D reconstruction of the chosen brain structure(s) of blind and labelled MRI data, respectively; “Full Screen” for the visualization of the 3D rendering in full screen mode; “Reset” to clean the 3D viewer to start with a new analysis; and “Export STL” to save the annotations of brain structures in STL format. Additionally, two spin boxes are present, called “START” and “END”, respectively, which allow to select the number(s) of the chosen brain structure(s) to be visualized. The numbers 1, 2, 3, 4, 5, and 6 correspond to GM, WM, BG, CB, VEN, and BS.

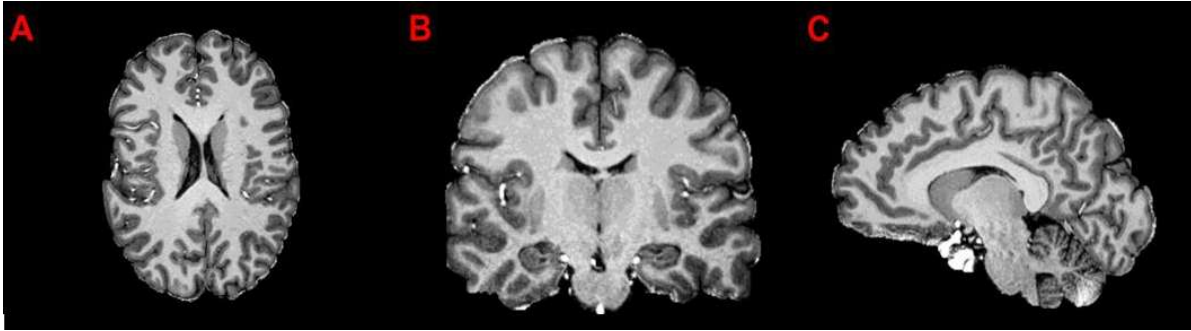


Fig. 2. Example of blind MRI data. Panel A: axial plane; panel B: coronal plane; panel C: sagittal plane; of the same MRI data.

C. Full Screen Visualization, Reset and Saving

The “Full Screen” button allows users to visualize the selected structures in a full screen mode (Fig. 4) and to move the 3D rendering in an interactive way. “ESC” button on the keyboard allows to close full screen mode. The “Reset” button allows users to clean the entire “3D Viewer” and to restore the interface visualization to its initial state in order to start with a new analysis. The “Export” button allows users to save the annotations of brain structures if needed (in standard STL format).

IV. DISCUSSION

Precise tissue segmentation and brain structure parcellation from MRI scans are crucial for diagnosing neurological disorders, as isolating brain regions improves detection and characterization of abnormalities. BrAInXplore is a DL-based GUI designed to automatically delineate brain structures, render them in 3D, and provide quantitative and qualitative analyses. It builds on a DL model previously developed by [4] and tested on the dataset released by Svanera et al. [2], achieving mean test Dice scores of $90.24 \pm 1.04\%$ (GM), $93.82 \pm 0.87\%$ (WM), $87.55 \pm 0.83\%$ (BG), $91.53 \pm 1.96\%$ (CB), $85.77 \pm 4.16\%$ (VEN), and $89.95 \pm 2.63\%$ (BS). BrAInXplore can automatically strip the skull, delineate brain structures, compute volumes, and visualize results in 3D within seconds. By providing a user-friendly

interface and addressing challenges of existing automatic and DL-based tools, such as limited accessibility and workflow complexity, BrAInXplore improves the interpretation and usability of segmentation results. Unlike SPM12, FSL, and FreeSurfer, it preserves both whole-brain and structure-specific inspection, as in manual segmentation. Moreover, the tool ensures interoperability, being NIfTI and STL two standard formats for neuroimaging data and for 3D surface representation, respectively. BrAInXplore generalizability has not yet been tested on a wide range of subjects, which will be ensured for subsequent versions. BrAInXplore demonstrated high performance in the processing of MRI data, the quality of which was not preliminarily checked. Moreover, as a DL approach, it can adaptively learn from data; however, its generalization capability remains unproven without validation on heterogeneous MRI datasets, despite promising preliminary results. Hence, the integration of BrAInXplore in the clinical scenario could serve as valid support for improved patient care, being the first to allow the volume measure analysis of the delineated brain structures and tissues.

In fact, evaluating the brain anatomical variations, especially if related to specific brain regions, is essential in monitoring the progression of neurological pathologies, such as Alzheimer, Parkinson and Multiple Sclerosis [1]. Through the use of BrAInXplore, neuroradiology researchers can

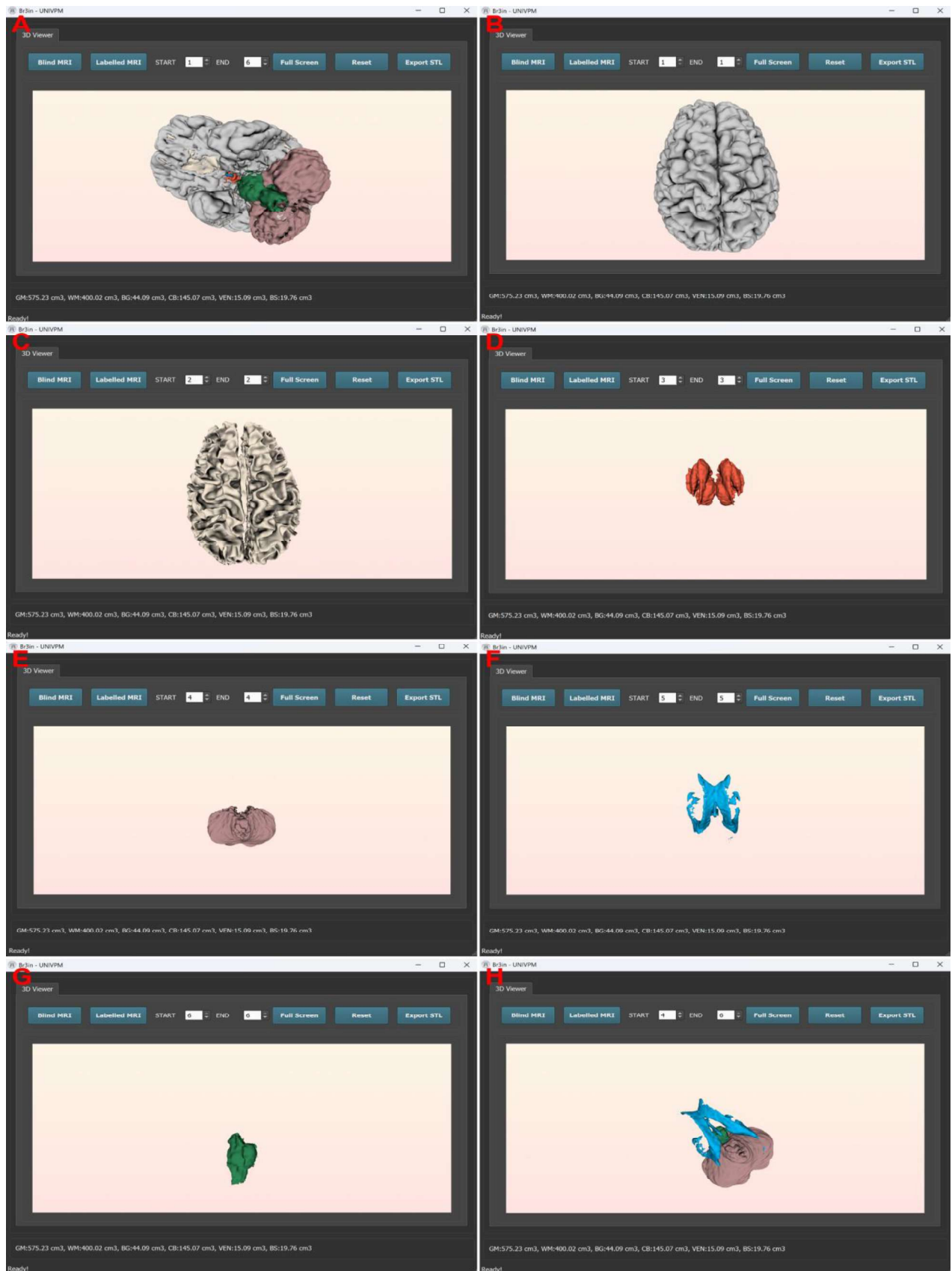


Fig. 3. Illustrative example of BrInXplore. The figure shows the 3D rendering of the segmented brain structures together with their corresponding volumes in cm^3 . Specifically, from left to right and top to bottom, the following panels are reported: A) all the predicted brain structures in different colors, B) GM; C) WM; D) BG; E) CB; F) VEN; and G) BS. On the H) panel also an example of the selection of only some structures is reported, specifically: CB, VEN, and BS. On the top row of each panel, it is possible to see how, changing the “START” and “END” spin boxes values, the displayed 3D rendering changes according to the corresponding numbers. While, on the bottom row of each panel, the volumes in cm^3 of each brain structure is reported.

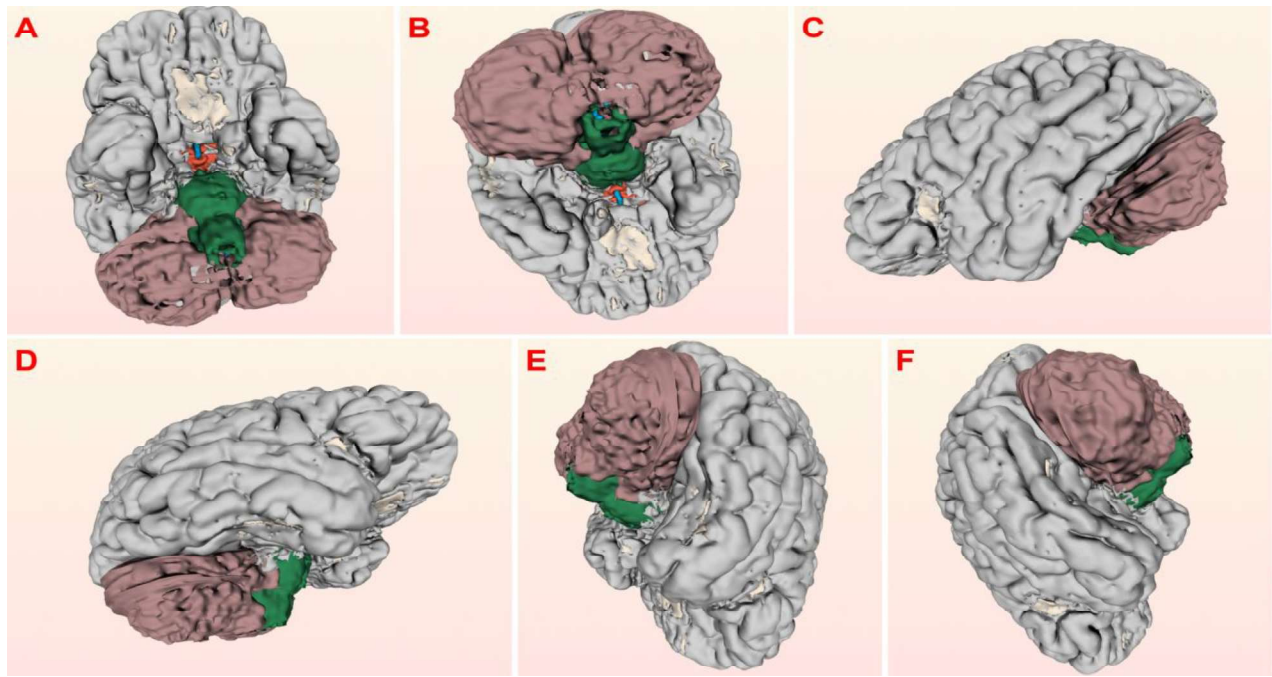


Fig. 4. Full-screen interactive visualization of the segmented brain structures. The panels A, B, C, D, E, and F, demonstrate how the user can use BrAInXplore in an interactive way, allowing a better and more detailed visualization of the selected brain structures.

better understand the underlying morphological patterns of neurological disorders. The impact BrAInXplore can extend beyond research, finding applications in educational contexts, such as high schools and universities, where students can interact with its functionalities to better understand brain anatomy.

The version presented in this work is the first (v1.0) and a series of improvements are possible: extending the label range beyond 1–6; leveraging the GUI's extensible design; integrating additional DL models possibly developed for the same purpose. These models can be embedded in two modalities, further enhancing flexibility: (1) running in parallel for performance-based self-selection; (2) providing users with the possibility to select a specific model. Potential commercial applications would require targeted market analysis and data collection. Since BrAInXplore has only been internally validated, the research manager (Laura Burattini, l.burattini@staff.univpm.it) can be contacted by stakeholders interested in obtaining for free the tool to conduct further testing or research proposes.

V. CONCLUSIONS

This work aimed to propose BrAInXplore: an easy-to-use, powerful and lightweight DL-based GUI for automatically delineating, rendering in 3D, and analyzing, both qualitatively and quantitatively, multiple brain tissues and structures from MRI data. Being DL-based, BrAInXplore overcomes limitations of existing software and tools, providing an accurate and efficient instrument for the analysis of brain tissues and structures.

REFERENCES

- [1] Zhao, X., & Zhao, X. M. (2021). Deep learning of brain magnetic resonance images: A brief review. *Methods*, 192, 131-140.
- [2] Svanera, M., Benini, S., Bontempi, D., & Muckli, L. (2021). CEREBRUM-7T: fast and fully volumetric brain segmentation of 7 Tesla MR volumes. *Human brain mapping*, 42(17), 5563-5580.
- [3] Kazancı, E., Prchkovska, V., Rodrigues, P., Villoslada, P., & Igual, L. (2018). Multiple Sclerosis Lesion Segmentation using Improved Convolutional Neural Networks. In *VISIGRAPP (4: VISAPP)* (pp. 260-269).
- [4] Tomassini, S., et al. (2023). A Double-Stage 3D U-Net for On-Cloud Brain Extraction and Multi-Structure Segmentation from 7T MR Volumes. *Information*, 14(5), 282.
- [5] Ashburner, J., et al. (2014). SPM12 manual. *Wellcome Trust Centre for Neuroimaging, London, UK*, 2464(4), 53..
- [6] Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., & Smith, S. M. (2012). Fsl. *Neuroimage*, 62(2), 782-790.
- [7] Fischl, B. (2012). FreeSurfer. *Neuroimage*, 62(2), 774-781.
- [8] Singh, M. K., & Singh, K. K. (2021). A review of publicly available automatic brain segmentation methodologies, machine learning models, recent advancements, and their comparison. *Annals of neurosciences*, 28(1-2), 82-93.
- [9] Smith, S. M., et al. (2004). Advances in functional and structural MR image analysis and implementation as FSL. *Neuroimage*, 23, S208-S219.
- [10] Bontempi, D., Benini, S., Signoroni, A., Svanera, M., & Muckli, L. (2020). CEREBRUM: a fast and fully-volumetric Convolutional Encoder-decoder for weakly-supervised sEGmentation of BBrain strUctures from out-of-the-scanner MRI. *Medical image analysis*, 62, 101688.
- [11] Sun, L., Ma, W., Ding, X., Huang, Y., Liang, D., & Paisley, J. (2019). A 3D spatially weighted network for segmentation of brain tissue from MRI. *IEEE transactions on medical imaging*, 39(4), 898-909.
- [12] Wang, L., Xie, C., & Zeng, N. (2019). RP-Net: a 3D convolutional neural network for brain segmentation from magnetic resonance imaging. *IEEE Access*, 7, 39670-39679.
- [13] Ramzan, F., Khan, M. U. G., Iqbal, S., Saba, T., & Rehman, A. (2020). Volumetric segmentation of brain regions from MRI scans using 3D convolutional neural networks. *IEEE Access*, 8, 103697-103709.
- [14] Laiton-Bonadiez, C., Sanchez-Torres, G., & Branch-Bedoya, J. (2022). Deep 3D neural network for brain structures segmentation using self-attention modules in MRI images. *Sensors*, 22(7), 2559.
- [15] What is PyQt?. Available online: <https://www.riverbankcomputing.com/software/pyqt/intro> (accessed on 28 January 2026).
- [16] Lazar, G., & Penea, R. (2018). *Mastering Qt 5: Create stunning cross-platform applications using C++ with Qt Widgets and QML with Qt Quick*. Packt Publishing Ltd.