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Slicer-DeepSeg: Open-Source Deep Learning Toolkit for Brain Tumour Segmentation

Abstract: Purpose Computerized medical imaging processing assists neurosurgeons to localize tumours precisely. It plays a key role in recent image-guided neurosurgery. Hence, we developed a new open-source toolkit, namely Slicer-DeepSeg, for efficient and automatic brain tumour segmentation based on deep learning methodologies for aiding clinical brain research. Methods Our developed toolkit consists of three main components. First, Slicer-DeepSeg extends the 3D Slicer application and thus provides support for multiple data input/ output data formats and 3D visualization libraries. Second, Slicer core modules offer powerful image processing and analysis utilities. Third, the Slicer-DeepSeg extension provides a customized GUI for brain tumour segmentation using deep learning-based methods. Results The developed Slicer-DeepSeg was validated using a public dataset of high-grade glioma patients. The results showed that our proposed platform's performance considerably outperforms other 3D Slicer cloud-based approaches. Conclusions Developed Slicer-DeepSeg allows the development of novel AIassisted medical applications in neurosurgery. Moreover, it can enhance the outcomes of computer-aided diagnosis of brain tumours. Open-source Slicer-DeepSeg is available at github.com/razeineldin/Slicer-DeepSeg.

Keywords: 3D Slicer, Brain tumour segmentation, Deep learning, Image-guided neurosurgery, MRI.

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1 Introduction

Treatment of malignant brain tumour is still among the most difficult challenges in cancer remedies [1]. Gliomas are the most common primary brain tumours representing 75% of primary brain malignancies among adults [1]. Due to the highly heterogenous appearance of Gliomas and their sub-regions, the prognosis remains very challenging despite recent advances in therapeutics. Pre-operative imaging is a key factor in the accurate definition of the tumour tissue and its peritumoral regions, and therefore, has a great impact on the overall survival rate [2]. Preoperative magnetic resonance imaging (MRI) provides superior image contrast and high-resolution soft tissue and thus can be essentially used for image-guided neurosurgery (IGN) [3].

Accurate tumour segmentation is crucial in the planning phase of IGN and contributes to the success of neurosurgery, for instance, it has an effect on the residual tumour mass and the post-operative follow-up treatment plan. Therefore, reliable and robust image analysis software is mandatory for precise and effective neuronavigational guidance. Although there are several commercial image analysis software platforms, these proprietary systems are typically built for specific applications and, due to their restrictive licenses, lack flexibility and extensibility, which are two main factors in developing cancer research toolkits. Some initiatives have been launched for open-source medical research toolkits, such as 3D Slicer [4], MITK [5], ITK-Snap [6], and NifTK [7]. These software programs provide manual or semiautomated tumour segmentation for neurosurgical planning and this process is associated with large processing time.

Deep learning methods have been developed recently outperforming previous classical approaches in many medical applications including segmentation [8, 9], registration [10], and classification [11]. 3D Slicer and MITK have recently integrated the artificial intelligence (AI) framework NVIDIA Clara [12] for automatic segmentation. NVIDIA Clara is a cloud-powered application framework that enables automatic tumour volume inference using some pre-trained models.

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Similarly, Mehrtash et al. [13] proposed DeepInfer, which is an application package developed as an extension for Slicer 3D to provide over-the-cloud deep learning models. Shortcomings of the above extensions include dependency on the network speed for uploading the MRI image data and downloading the predicted segmented model. Additionally, major privacy concerns become apparent since sensitive imaging data must be transferred over the internet before processed using the backend network.

In this study, we developed Slicer-DeepSeg toolkit as an open-source AI-powered extension for 3D Slicer. Slicer-DeepSeg allows users, developers, and clinical researchers to employ recent deep learning advances in brain malignancy imaging research. To the best of our knowledge, Slicer-DeepSeg is the first publicly available open-source 3D Slicer extension for automatic brain tumour segmentation and cancer research using self-contained deep learning methods.

2 Methods

The architecture of the Slicer-DeepSeg toolkit follows a modular approach, as presented in Fig. 1. The components of our developed system are described in the following subsections.

2.1 3D Slicer Core

3D Slicer is an open-source, cross-platform, and extensible software program for medical image computing and analysis [4]. Over two decades, 3D Slicer was implemented and developed through multi-institutional support from the National Institute of Health (NIH) as well as a worldwide developer community. Slicer 3D provides 2-, 3-, and 4-dimensional visualization capabilities for different imaging modalities (for example MRI, CT, and Ultrasound). Besides, 3D Slicer supports importing and exporting imaging data from multiple standard data formats including NIFTI, DICOM, and NRRD.

2.2 3D Slicer Core Modules

The 3D Slicer application follows a modular paradigm allowing developing additional modules for feature-specific functionalities. Numerous modules providing a wide range of medical applications are distributed with the standard 3D Slicer software. Core modules are primarily categorized according to their function. One example is the

Filtering module providing tools for basic pre-processing functions on medical images including arithmetic operations, Gaussian, bias field correction, and denoising filters.

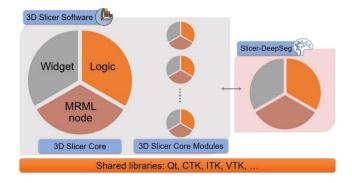


Figure 1: A high-level overview of the Slicer-DeepSeg architecture and its relationship with 3D Slicer software and core modules.

2.3 DeepSeg 3D Slicer Extension

The modular design of 3D Slicer allows the development of additional modules for delivering further feature-specific functionalities. The core of Slicer is written in C++ programming language, however, the APIs of the core modules are also implemented in Python programming language allowing great support for rapid and simple prototyping applications.

Fig. 2 displays Slicer-DeepSeg, which is implemented as an external 3D Slicer extension coded in Python as a scripted module. Slicer-DeepSeg extends the functionality of the 3D Slicer providing the following main functions. First, Slicer-DeepSeg uses the CTK and Qt libraries to create a custom user interface for brain tumour segmentation using deep learning. Second, the input MRI volumes are pre-processed using the Numpy, SITK, and ITK libraries for image processing, resampling, and registration. Third, the tumour boundaries are segmented using pre-trained deep learning models and visualized in both 2-and 3-dimensional formats.

3 Results and Discussion

3.1 Data and Pre-processing

This study was validated using the MICCAI Brain Tumour Segmentation Challenge 2020 (BraTS) dataset [14, 15], which contains 369 training and 125 validation multi-site

patients. All cases have been manually annotated by one to four raters and comprise the non-enhancing tumour (label 1), edema (label 2), and the enhancing tumour (label 4). For every patient, BraTS 2020 provides four different MRI data, which are: T1-weighted, post-contrast enhanced T1-weighted, T2-weighted, and fluid-attenuated inversion recovery T2-weighted (FLAIR) in addition to the ground truth tumour segmentation. It is important to mention that Slicer-DeepSeg is a general brain tumour segmentation toolkit and can be utilized to predict tumour boundaries in other MRI databases as well.

Before the tumour boundaries are automatically segmented using our Slicer-DeepSeg toolkit, a pre-processing stage is essential since MRI data are acquired using different clinical protocols, come from different MRI scanners, and multiple institutions. First, all input images are resampled to an isotropic resolution of 1x1x1 mm³ using SITK. Then, the input data is cropped to the brain region and resized to an image dimension of 192×224×160. Finally, we apply z-score normalization by subtracting the mean value and dividing by the standard deviation individually for each input MRI image.



Figure 2: Slicer-DeepSeg extension during visualization of the resultant tumour boundaries. The GUI panel is shown on the left, where the user can specify inputs, output volumes, model parameters, other 3D visualization options. Brain tumour segmentation results (*in red*) of a sample HGG case from BraTS 2020 challenge are presented on the right. The application layout shows the axial (*top middle*), sagittal (*bottom middle*), coronal (*bottom right*), as well as 3D views (*top right*).

3.2 Use Case Example

In order to demonstrate the capabilities of using Slicer-DeepSeg extension with 3D Slicer for addressing brain cancer research problems, a sample high-grade glioma (HGG) case from the BraTS 2020 dataset was employed.

The user must install the Slicer 3D program and then download the Slicer-DeepSeg extension via the 3D Slicer Extension Manager. After that, Slicer-DeepSeg can be selected from the machine learning category in the modules list. The default parameter settings include two different pre-trained deep learning models based on the input MRI image modalities. The first model is our previous work, DeepSeg [9] which requires only the T2-FLAIR MRI data

as an input and automatically predicts the tumour region. The second model is the winning approach in the segmentation task of MICCAI BraTS 2020 challenge, nnU-Net [16], which requires the four MRI modalities like the BraTS challenge: FLAIR, T1, T1ce, and T2.

After the Slicer-DeepSeg installation, the user can choose one model, specifies its input data, creates a new segmentation volume, and presses the "apply" button, as shown in Fig. 2. Then, an automatic pre-processing stage, including resampling, cropping and registration, is applied before the resultant tumour region is predicted using the specified pre-trained deep neural networks. Finally, the segmented tumour is displayed in both Slicer 2- and 3D scenes as presented in Fig. 2.

3.3 Runtime Results

Table 1 lists the time runtime speed analysis for the two built-in neural networks, namely, DeepSeg and nnU-Net. The experiments were run on a computer with AMD Ryzen 2920X (32M Cache, 3.50 GHz) CPU, 32 GB RAM, and a single NVIDIA RTX 3060 GPU 12GB GDDR6. Slicer 3D version 4.11 was used with Python 3.6 running on 64-bit Ubuntu 18.04. Each measurement has been repeated 10 times and the average values are reported. Outstandingly, Slicer-DeepSeg was able to detect and localize the tumour region in an average of 1.87 and 4.25 seconds using DeepSeg and nnU-Net models, respectively. Compared to other cloud-based Slicer 3D extensions such as NVIDIA Clara and DeepInfer which take about 2 to 3 minutes for Slicer-DeepSeg demonstrates performance advantages using pre-trained local models.

Table 1: Runtime measurement comparing the two integrated deep neural networks: DeepSeg and nnU-Net on both CPU and GPU implementations.

Process	DeepSeg (s)	nnU-Net (s)
Loading data and pre-processing	0.07	0.70
Building deep neural network	0.58	0.81
Tumour prediction	1.20	2.35
Results visualization	0.02	0.02
Total time	1.87	4.25

3.4 Software Access

Both of Slicer-DeepSeg and 3D Slicer are distributed under the BSD-style license that allows free use for both academic and commercial purposes without any restrictions. Source codes are available on the project website (github.com/razeineldin/Slicer-DeepSeg), where users, developers, data scientists, clinical researchers are welcome to contribute and add their models and comments.

4 Conclusion

We developed an open-source deep-learning toolkit, called Slicer-DeepSeg, for brain tumour segmentation in MRI images. With its simple GUI, easy installation guide, and range of available modules, Slicer-DeepSeg gives users and clinical researchers the opportunity to utilize advanced deep learning approaches within brain cancer research without the need for advanced programming skills or detailed knowledge of several software packages.

Furthermore, Slicer-DeepSeg has a flexible, modular, and open-source structure enabling biomedical engineers and clinical researchers to develop novel brain cancer applications using the advances of deep learning.

Author Statement

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References

- [1] Lapointe S, Perry A, Butowski NA. Primary brain tumours in adults. Lancet. 2018;392:432-46.
- [2] Coburger J, Merkel A, Scherer M, et al. Low-grade Glioma Surgery in Intraoperative Magnetic Resonance Imaging: Results of a Multicenter Retrospective Assessment of the German Study Group for Intraoperative Magnetic Resonance Imaging. Neurosurgery. 2016;78:775-86.
- [3] Miner RC. Image-Guided Neurosurgery. J Med Imaging Radiat Sci. 2017;48:328-35.
- [4] Fedorov A, Beichel R, Kalpathy-Cramer J, et al. 3D Slicer as an image computing platform for the Quantitative Imaging Network. Magn Reson Imaging. 2012;30:1323-41.
- [5] Goch CJ, Metzger J, Nolden M. Abstract: Medical Research Data Management Using MITK and XNAT. Bildverarbeitung für die Medizin 20172017. p. 305-.
- [6] Yushkevich PA, Piven J, Hazlett HC, et al. User-guided 3D active contour segmentation of anatomical structures: Significantly improved efficiency and reliability. NeuroImage. 2006;31:1116-28.
- [7] Clarkson MJ, Zombori G, Thompson S, et al. The NifTK software platform for image-guided interventions: platform overview and NiftyLink messaging. International Journal of Computer Assisted Radiology and Surgery. 2014;10:301-16.
- [8] Ronneberger O, Fischer P, Brox T. U-Net: Convolutional Networks for Biomedical Image Segmentation. Medical Image Computing and Computer-Assisted Intervention – MICCAI 20152015. p. 234-41.
- [9] Zeineldin RA, Karar ME, Coburger J, et al. DeepSeg: deep neural network framework for automatic brain tumor segmentation using magnetic resonance FLAIR images. Int J Comput Assist Radiol Surg. 2020;15:909-20.
- [10] Zeineldin RA, Karar ME, Coburger J, et al. Towards automated correction of brain shift using deep deformable magnetic resonance imaging-intraoperative ultrasound (MRI-iUS) registration. Current Directions in Biomedical Engineering. 2020;6:20200039.
- [11] Zhang J, Xie Y, Wu Q, et al. Medical image classification using synergic deep learning. Medical Image Analysis. 2019;54:10-9.

- [12] Zhu W, Zhao C, Li W, et al. LAMP: Large Deep Nets with Automated Model Parallelism for Image Segmentation. Cham: Springer International Publishing; 2020. p. 374-84.
- [13] Mehrtash A, Pesteie M, Hetherington J, et al. DeepInfer: Open-Source Deep Learning Deployment Toolkit for Image-Guided Therapy. Proc SPIE Int Soc Opt Eng. 2017;10135.
- [14] Menze BH, Jakab A, Bauer S, et al. The Multimodal Brain Tumor Image Segmentation Benchmark (BRATS). IEEE Transactions on Medical Imaging. 2015;34:1993-2024.
- [15] Bakas S, Akbari H, Sotiras A, et al. Advancing The Cancer Genome Atlas glioma MRI collections with expert segmentation labels and radiomic features. Scientific Data. 2017;4.
- [16] Isensee F, Jäger PF, Full PM, et al. nnU-Net for Brain Tumor Segmentation. Cham: Springer International Publishing; 2021. p. 118-32.