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Within-exam automatic brain segmentation for accurate and reproducible geometry planning—An open-source tool, illustrated for MRS volume selection

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Introduction

Magnetic Resonance (MR) scan planning sometimes targets very specific anatomic regions. For brain characterization, the latter can be specified with reference to structural or functional brain areas as documented in canonical brain atlases, like the T1-based MNI atlas[1, 2]. Several MRI scanner manufacturers provide automatic scan geometry planning functionality, but often with limited options or necessitating some training to make their algorithm learn user-defined acquisition geometries. Nowadays, several powerful open-source tools are commonly used to realign individual brain images to reference atlases, allowing segmentation of individual brain images. We wanted to make such tools exploitable for supporting scan planning, importing individual brain segmentation results at the MR console to guide planning the geometry of scans acquired after the brain structural scan used for segmentation. After exposing the implemented steps, we illustrate the principle with a MR spectroscopy (MRS) application. The MRS Voxel of Interest (VOI) is usually large with respect to anatomical details and the tool we developed helps guiding its positioning and shaping to cover specific tissue targets, while composing with chemical shift-related displacements between metabolites and minimizing contamination from neighboring fat or CSF components.

Material and methods

The complete work-flow is illustrated in Figure 1. In addition to the MRI console (here an Achieva 3.0T dStream, R5.7.1.2, Philips, Best, The Netherlands) we use a processing workstation, connected to the same within-hospital network to help with data transfers. After a 3D T1w high-resolution brain scan (MP-RAGE, 256*256*160mm³ FOV, 1mm isotropic, 4'21''), we export (here in the proprietary XML/REC format and with the PRIDE tool developed by Philips) the image data to the workstation configured to run the AssemblyNet[3] docker image. This algorithm is capable of segmenting a large number of structures, allowing for a great flexibility in the choice of reference areas to represent.

A home-made python pipeline is used to convert the data to NIFTI format and retrieve the results obtained from AssemblyNet. The user can select, as a pipeline input, the labels corresponding to the regions of interest needed (lobes, macro-structures or structures). These selected regions are then extracted from the NiFTI produced by AssemblyNet and masked in the original T1w image with various levels of gray to distinguish them. Eventually, a new XML/REC pair of files is generated which can be re-imported into the MR console software through the PRIDE tool, and further used as geometry reference.

Results

Demonstration data were acquired on a volunteer under the MAP-IRMaGe protocol (NCT05036629, ID-RCB 2020-A03555-34). Figure 2 shows original and segmented images in the three directions. Note that the contrast is modified in the tissue to better distinguish the ROIs. Figure 3 presents an example of segmentation, along with a VOI intended to be used for a GABA-edition MRS sequence using a PRESS volume selection, and its maximum chemical shift. Using the segmentation obtained with our proposed tool, a compromise was found to cover as much as possible the combination of the structures while avoiding contamination of the signal by non-brain tissue.

The code required by PRIDE as well as the developed Python code will be available on github.com/IRMaGe-3T/segment-from-pride.

Discussion & Conclusion

In our configuration segmentation currently takes about 10', during which acquisitions not requiring very specific geometry planning are performed. Due to the complete separation between the acquisition and processing parts of the pipeline, possible via PRIDE, it should be straightforward to use a different segmentation algorithm, either to decrease the processing time, or to obtain a finer/more dedicated segmentation. We believe this tool could be precious to help both the accuracy in targeting a region for a single exam and the reproducibility of scan geometry in longitudinal studies, especially for users which are not expert in brain anatomy.

References

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Figures

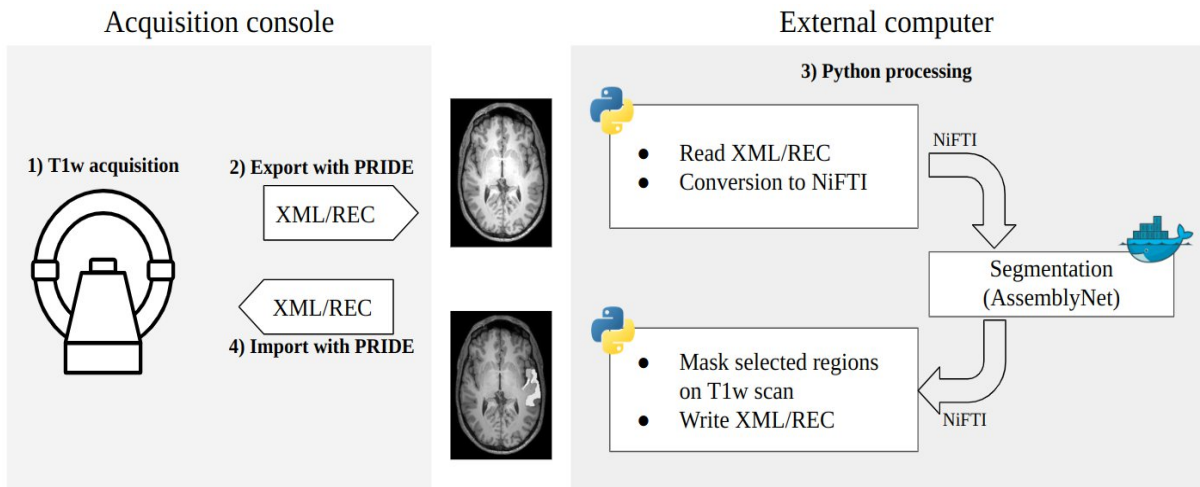


Figure 1. Illustration of the proposed work-flow. The PRIDE tool allows for a complete separation between the acquisition and processing parts of the pipeline, allowing for a great flexibility in the processing steps.

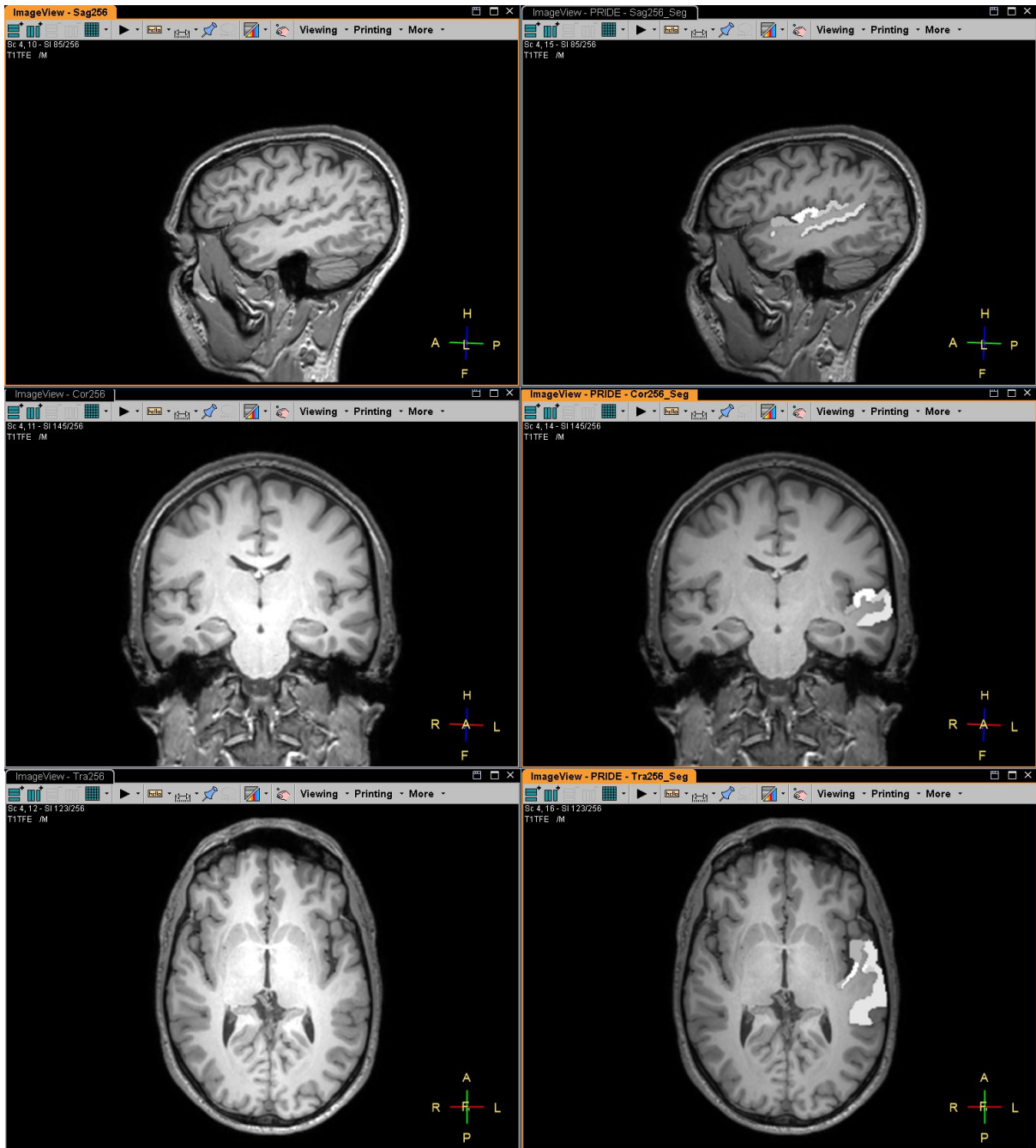


Figure 2. Screen-shots from the console. Each rows shows one of the three orientations. The left column shows the original acquisition, the right column shows the masked and re-imported version. The same slice was selected each time.

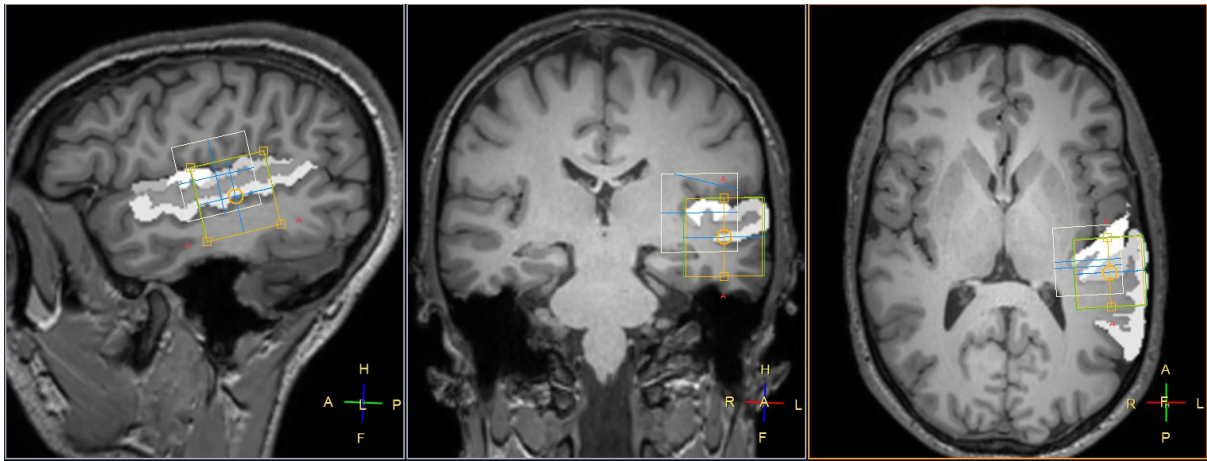


Figure 3. Screenshot from the console. The segmented scan can be used for acquisition planning.