Deep Learning-based Type Identification of Volumetric MRI Sequences

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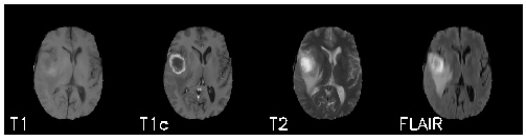
Introduction

Through techniques of Magnetic Resonance Imaging (MRI), professionals can properly analyse the progress of brain tumors, which can, when malignant, affect human physical and cognitive abilities and are a common cause of cancer death. MRI enables highlighting different parts of a brain volume, depending on the MRI sequence type applied (AMIN et al., 2020; SAJJAD et al., 2019; WIDMANN et al., 2017; LENZ et al., 2000; TOĞAÇAR; CÖMERT; ERGEN, 2020). Figure 1 exemplifies some of the most common MRI sequence types.

Figure 1 – Examples of different MRI sequence types (T1, T1c, T2 and FLAIR) associated to the same brain volume (volumes from the publicly available BraTS dataset; no license information found).

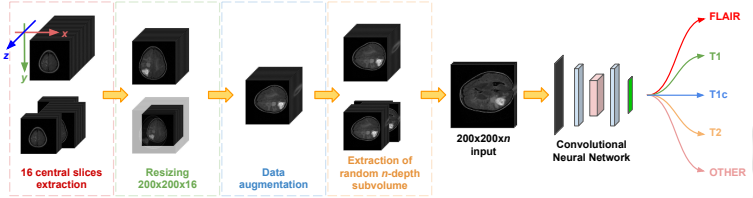


The interest on automatizing the process of tumor progression monitoring is hindered by the highly unstandardized naming protocols among different clinical centers. Based on this, we propose a deep classifier of MRI sequence types, based on a Convolutional Neural Network and capable of distinguishing the given input brain volumes among their respective types precisely. The proposed system achieves a macro-accuracy close to 97%.

Proposed System

Figure 2 shows an overview of the proposed system.

Figure 2 – Overview of the proposed system (volumes from the publicly available TCGA-GBM dataset, distributed under the CC BY 3.0 license (https://creativecommons.org/licenses/by/3.0/)).



- MRI volumes with different dimensions and orientations are loaded and have their 16 central slices extracted;
- The 16-depth volume is resized to have 200 pixels of both width and height;
- To increase the data variability during the training phase, some augmentation, including rotation, translation, blurring, noising and brightness adjustment are applied to the volume;
- Then, a random sequential n-depth subvolume, where n is a parameter defined by the user, is provided to the Convolutional Neural Network, which classifies the input as a FLAIR, T1, T1c or T2 sequence type if belonging to any of these classes, or as OTHER if not.

Experiments

The experiments performed consist in analysing the impact of:

- the impact of the input subvolume depth ($n = 1, 2, \ldots, 16$);
- the impact of using pre-processed data.

The public available brain volume datasets BraTS (MENZE et al., 2014; BAKAS; AKBARI, et al., 2017; BAKAS; REYES, et al., 2018; KISTLER et al., 2013) and TCGA-GBM (SCARPACE et al., 2016; CLARK et al., 2013) were used as, respectively, pre-processed (skull-stripped) and non-pre-processed data. The following custom datasets were assembled:

Table 1 – Custom datasets assembled for the experiments

Pre-processed data (BraTS)	Non-pre-processed data (TCGA-GBM)	Classes	Resulting dataset
✓		4 (no OTHER)	BRATS4
	✓	4 (no OTHER)	TCGA4
	✓	5	TCGA5
✓	✓	5	BRATS+TCGA4
✓	✓	5	BRATS+TCGA5

Results and Discussion

The results are summarized in Figure 3 and Tables 2 and 3.

Figure 3 – Validation accuracy (%) across the tested input volume depths n. The best result is obtained for $n = 4$.

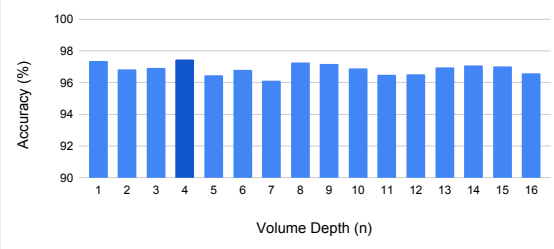


Table 2 – Testing accuracy (%) for the four-classes datasets with $n = 4$ (best validation accuracy).

Train Datasets	Test Datasets BRATS4	BRATS+TCGA4	TCGA4
BRATS4	99.27	82.90	62.44
BRATS+TCGA4	98.98	96.36	93.30
TCGA4	42.59	65.01	92.99

Table 3 – Testing accuracy (%) for the five-classes datasets with $n = 4$ (best validation accuracy).

Train Datasets	Test Datasets BRATS+TCGA5	TCGA5
BRATS+TCGA5	96.81	94.51
TCGA5	52.68	94.66

Figure 3 shows that the subvolume input depth n has very little impact on the sytem's performance, i.e., a single slice is enough to identify the MRI sequence and using more do not impair the classification. Meanwhile, the tables show that the performance of models trained with only one kind of data (pre-processed or not) is better as the proportion of that kind is bigger in the test set. Mixing data is the most viable option, yielding satisfactory results in all cases.

Conclusions

- It is possible to use a Convolutional Neural Network to classify among different MRI sequence types accurately;
- Mixing pre-processed and non-pre-processed data provides better generalization to the model;
- The system may be further improved:
  - for better distinction between the similar T1 and T1c classes;
  - by adding more distinguishable classes.

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Acknowledgments

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