Deep Learning-based Type Identification of Volumetric MRI Sequences

Jean Pablo Vieira de Mello*, Thiago M. Paixão, Rodrigo F. Berriel, Mauricio Reyes, Claudine Badue, Alberto F. De Souza, Thiago Oliveira-Santos

SUPPORT AND ACKNOWLEDGMENTS

UNIVERSIDADE FEDERAL DO ESPÍRITO SANTO

lcad LABORATÓRIO DE COMPUTAÇÃO DE ALTO DESEMPENHO

INSTITUTO FEDERAL Espírito Santo

UNIVERSITÄT BERN

CAPES

CNPq Conselho Nacional de Desenvolvimento Científico e Tecnológico

FAPES FUNDAÇÃO DE AMPARO À PESQUISA E INOVAÇÃO DO ESPÍRITO SANTO

SPHN Swiss Personalized Health Network

NVIDIA

krebsliga schweiz

* jeanpvmello@gmail.com

Introduction

- Magnetic Resonance Imaging (MRI):
    - Analysis of brain tumor progression:
        - Interest on automating the process.
- MRI sequences must be well identified:
    - However, unstandardized naming protocols.
- Proposed solution:
    - Convolutional Neural Network (CNN) to classify among MRI sequence types.

Related works

- Noguchi *et al.* (2018):
    - MRI classification based on the first or central slice of the volumes;
    - Small dataset.
- Ranjbar *et al.* (2019):
    - Single-slice classification;
    - No guarantee that slices from the same volume do not occur in train and test sets;
    - Missing/contradictory information;
- Also, both works use private datasets, hindering comparability.

Proposed solution

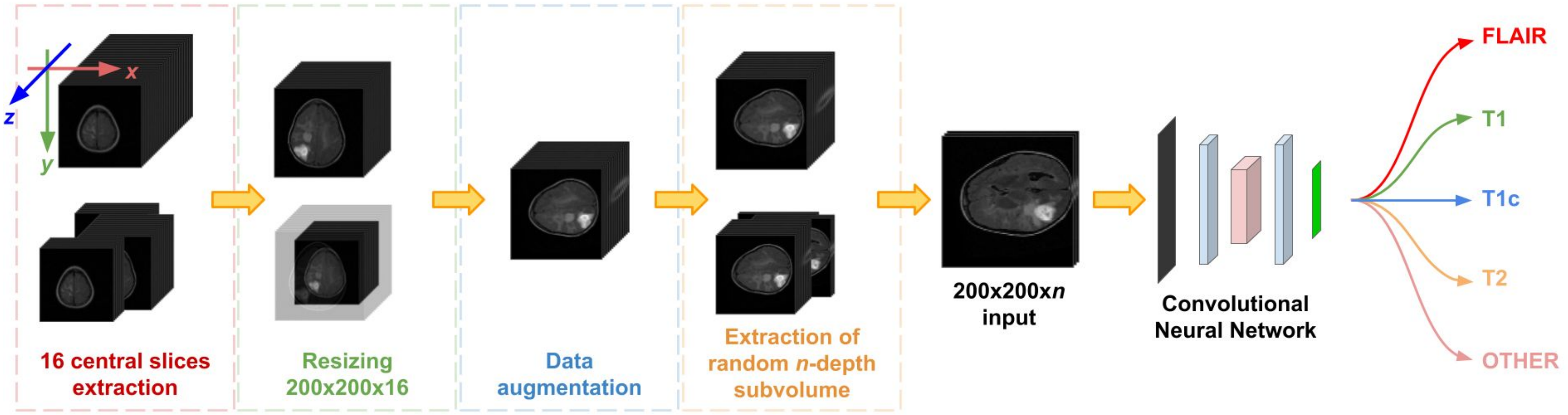

Figure 1: Overview of the proposed method (volume from TCGA-GBM* dataset)

Proposed solution

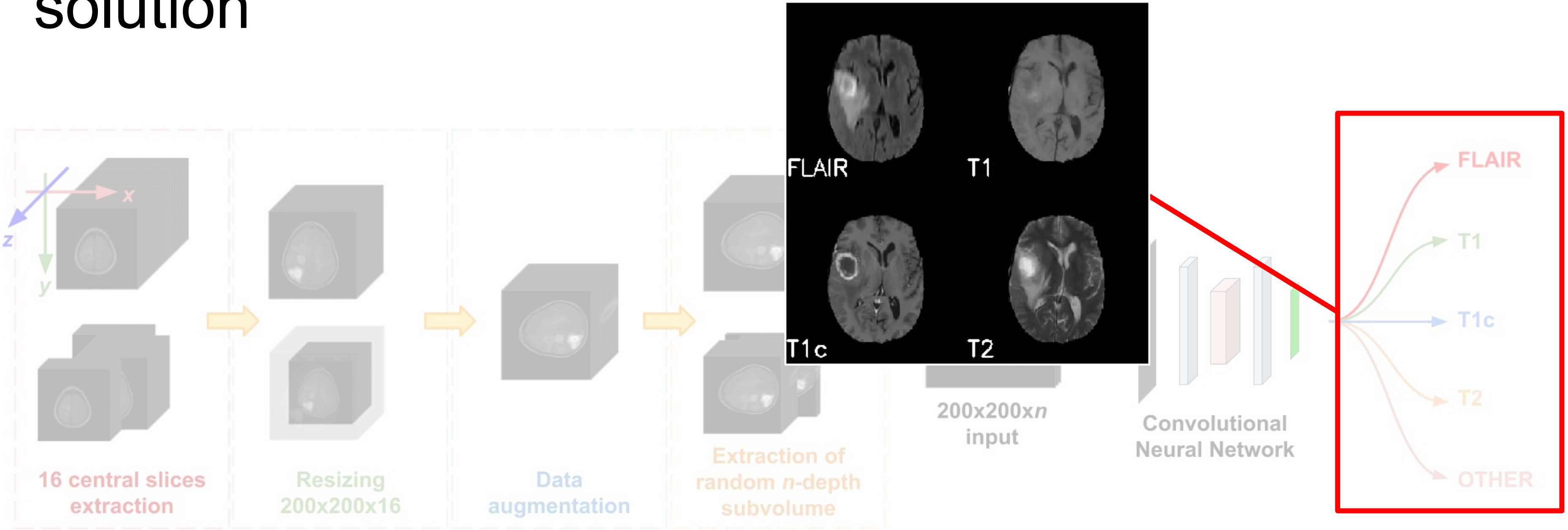

Figure 2: Distinction between the main sequence types recognized by the classifier (volume from TCGA-GBM dataset in the overview and from BraTS* dataset in the foreground)

*Publicly available. No license information found.

Experiments

- Datasets:

	BraTS (pre-processed data)	**TCGA-GBM (non-pre-processed data)**	**BraTS + TCGA-GBM (mixed data)**
All five classes	-	TCGA5	BRATS+TCGA5
No “OTHER” class	BRATS4	TCGA4	BRATS+TCGA4

Table 1: Datasets assembled for the experiments

Experiments

- Study on the input volume:

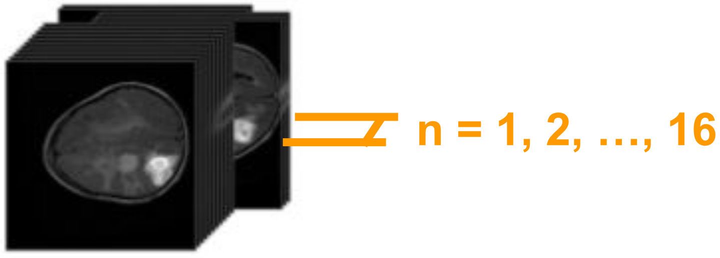

Figure 3: Study on the input volume: random *n*-depth subvolume from 1 to 16 slices (volume from TCGA-GBM dataset)

- Study on the use of pre-processed data:

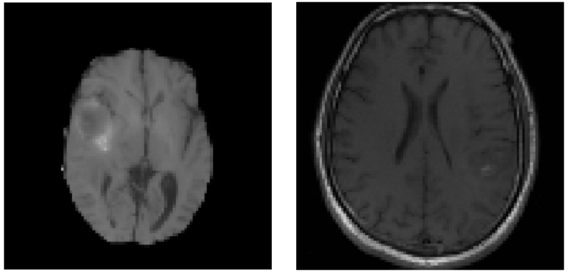

Figure 4: Slices from a pre-processed volume (left; from BraTS dataset) and from a non-pre-processed volume (right; from TCGA-GBM dataset)

Results

- Study on the input volume:

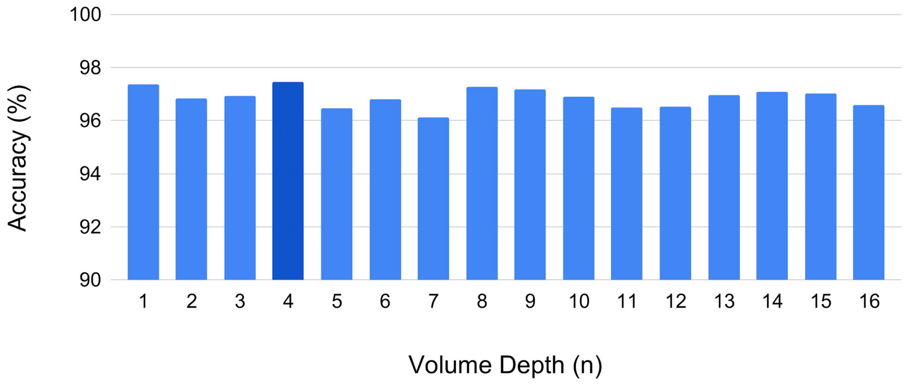

Figure 5: Validation macro-accuracy across the considered volume depths (*n*). **The highest accuracy is obtained for *n* = 4**

- Study on the use of pre-processed data:

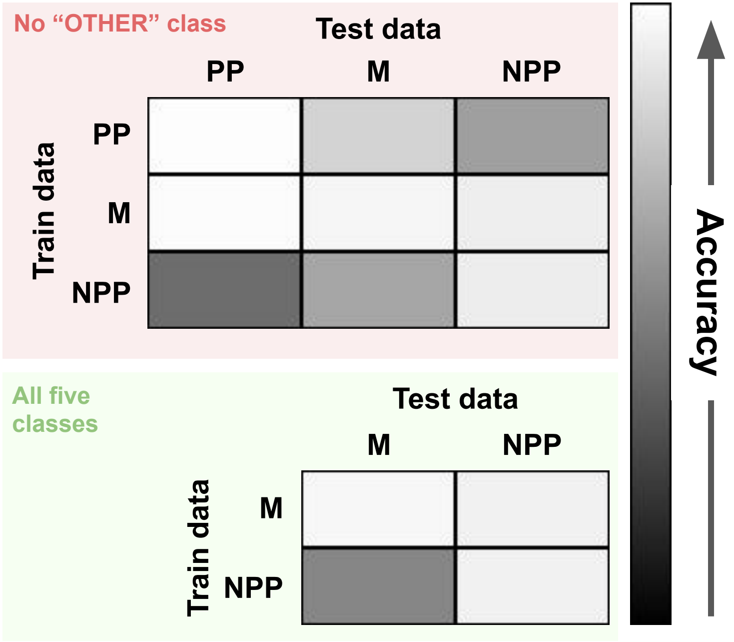

Figure 6: Test macro-accuracies regarding the use of pre-processed data

PP: **pre-processed** **M:** **mixed**
NPP: **non-pre-processed**

Conclusions

- High accuracy on classifying among MRI sequence types:
  - Even considering several acquisition protocols.
- Better generalization by mixing pre-processed and non-pre-processed data;
- Possible improvements:
  - Better distinguishing between T1 and T1c;
  - Recognition of more sequence types.

Thanks!

Jean Pablo Vieira de Mello*, Thiago M. Paixão, Rodrigo F. Berriel, Mauricio Reyes, Claudine Badue, Alberto F. De Souza, Thiago Oliveira-Santos

SUPPORT AND ACKNOWLEDGMENTS

UFES
UNIVERSIDADE FEDERAL DO ESPÍRITO SANTO

lcad
LABORATÓRIO DE COMPUTAÇÃO DE ALTO DESEMPENHO

INSTITUTO FEDERAL
Espírito Santo

UNIVERSITÄT BERN

CAPES

CNPq
Conselho Nacional de Desenvolvimento Científico e Tecnológico

FAPES
FUNDAÇÃO DE AMPARO À PESQUISA E INOVAÇÃO DO ESPÍRITO SANTO

SPHN
Swiss Personalized Health Network

NVIDIA

krebsliga schweiz

* jeanpvmello@gmail.com