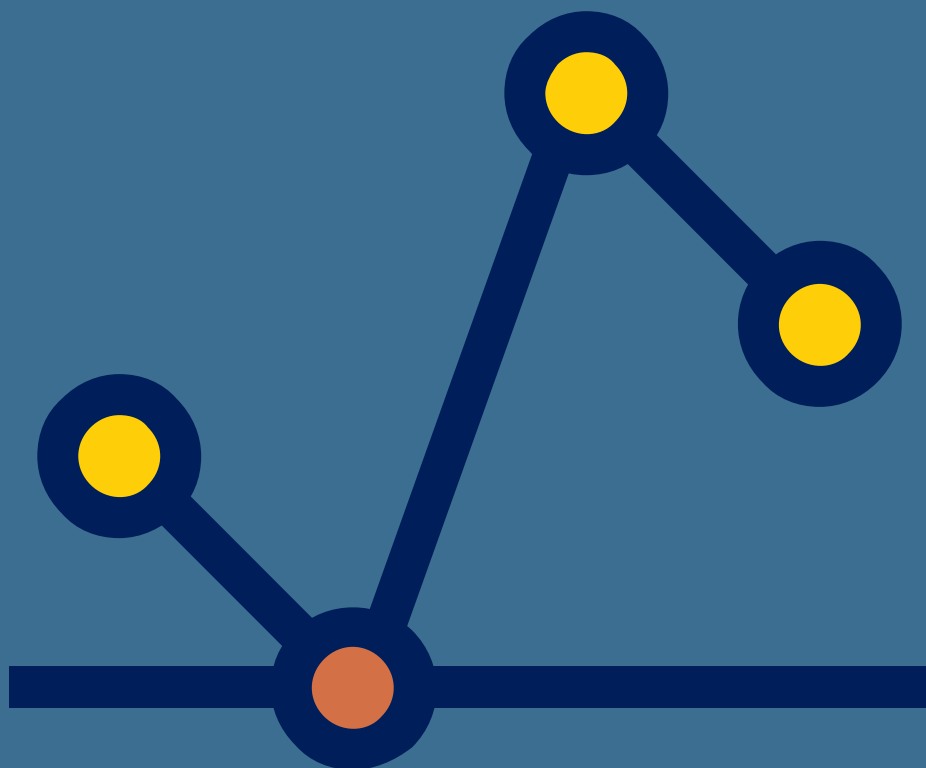

Edited by
Paola Cerchiello · Arianna Agosto
Silvia Osmetti · Alessandro Spelta

Proceedings of the Statistics and Data Science Conference



Copertina: Cristina Bernasconi, Milano

Copyright © 2023 EGEA S.p.A.
Via Salasco, 5 - 20136 Milano
Tel. 02/5836.5751 - Fax 02/5836.5753
egea.edizioni@unibocconi.it - www.egeaeditore.it

Quest'opera è rilasciata nei termini della Creative Commons Attribution 4.0 International Licence (CC BY-NC-SA 4.0), eccetto dove diversamente indicato, che impone l'attribuzione della paternità dell'opera e ne esclude l'utilizzo a scopi commerciali. Sono consentite le opere derivate purché si applichi una licenza identica all'originale. Il testo completo è disponibile alla pagina web <https://creativecommons.org/licenses/by-nc-sa/4.0/deed.it>.

Date le caratteristiche di Internet, l'Editore non è responsabile per eventuali variazioni di indirizzi e contenuti dei siti Internet menzionati.

Pavia University Press
info@paviauniversitypress.it – www.paviauniversitypress.it

Prima edizione: maggio 2023
ISBN volume 978-88-6952-170-6

The use of magnetic resonance images for the detection and classification of brain cancers with D-CNN

Davide Mascolo, mascolo.2001991@studenti.uniroma1.it
Leonardo Plini, plini.2000543@studenti.uniroma1.it
Alessandro Pecchini, pecchini.1824164@studenti.uniroma1.it
Margaret Antonicelli, margaret.antoniceili@uniroma1.it

Sapienza University of Rome, Italy

Abstract Among the various oncological pathologies, brain cancer continues to be one of the most wide-spread, as well as lethal, diseases. Within this paper we used Keras and Tensorflow to implement state-of-the-art convolutional neural network (CNN) architectures, such as EfficientNetB0, Res-Net50 and VGG16, using Transfer Learning to detect and classify three types of brain tumors namely say – Glioma, meningioma, and pituitary. The dataset we used consisted of 3264 2-D MRI images and 4 classes. Due to the small number of images, various data augmentation techniques were used to increase the size of the dataset. Our proposed methodology consists not only of data augmentation, but also of various techniques of image denoising, skull strip-ping, cropping and bias correction. In our working proposal, the EfficientNetB0 architecture gave the best results providing a very high accuracy. The purpose of this document is to distinguish between normal and abnormal pixels and classify them more accurately.

Key words: Deep Learning, Convolutional Neural Network, Glioma, Meningioma, Pituitary, Transfer Learning

1 Introduction

A brain tumor is an abnormal growth of cells in brain tissue, which can be benign or malignant. The central nervous system is part of the brain and consists of two parts: the brain and the spinal cord. Together they control both voluntary functions, such as walking, talking, etc., and involuntary functions, such as breathing, digestion, and so on. The central nervous system is also the basis of sensory functions (sight, smell, touch, hearing and taste), of emotions and of all the so-called higher activities such as memory and learning. Typically, the process of diagnosing a brain tumor begins after the patient has seen their general practitioner about the onset of symptoms. The doctor then evaluates the need for an in-depth study with the neurology specialist or prescribes instrumental diagnostic tests. In some cases, however, the onset of symptoms is sudden and requires urgent evaluation in the emergency department. Magnetic resonance imaging (MRI) of the brain is the main test in case of suspicion of a brain tumor. Compared to CT, nuclear magnetic resonance (MRI) with and without the use of paramagnetic contrast medium (gadolinium), allows to identify lesions and nodules, provides 3D (three-dimensional) images, allows to identify the site, the dimensions, the extension of the disease and the relationships with the surrounding structures, the so-called "eloquent" areas. Furthermore, the use of functional methods in MRI (diffusion and perfusion) can provide further information on the cellularity and vascularization of the analyzed regions. Based on 3264 2-D MRI images, advanced analysis models will be evaluated, with the support of machine learning techniques, with the aim of distinguishing between normal and abnormal pixels and classifying them more accurately.

2 Method

Recently, deep learning methods have demonstrated excellent performance in analyzing medical images compared to traditional machine learning methods.[3] This is mainly due to the ability to extract features during the learning process and to the possibility of optimizing the network parameters in order to minimize the error committed. For this study several networks based on the CNNs architecture were used: more in details, two convolutional networks were implemented from scratch which represent the benchmark with respect to compare the pretrained networks ResNet50, VGG16 and Efficient-NetB0, used through the transfer learning technique[1]. The typical pipeline of an image-based cancer classification study using CNNs[2] is shown in Fig. 1.

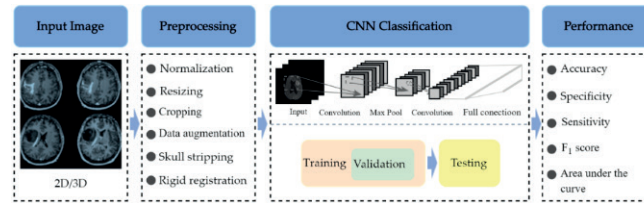


Fig. 1: Pipeline of CNNs-based Brain Cancer Classification

2.1 Pre-processing

As a first operation, the dataset was split into Training Set and Test Set. Subsequently the preprocessing operations were applied only on the Training data and during the training of the models, 10% of the Training data was used as Validation Set for parameters tuning. Fig. 2 shows the data split.

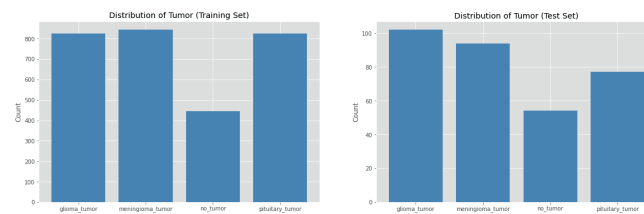


Fig. 2: Distribution of classes for Training Set and Test Set

2.1.1 Pre-processing of the image

1. **Resize:** The first pre-processing operation applied was to resize the image to a size of (150, 150).
2. **Noise Reduction:** To change the resolution of the original images, a Gaussian filter has been applied to reduce noise and blur the images.

In Fig. 3 it's possible to see an example of an image filtered.

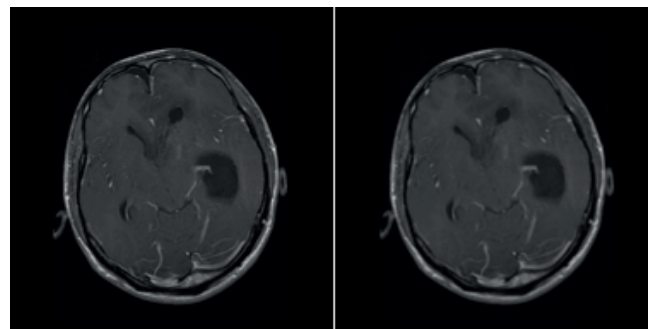


Fig. 3: Original Image and Filtered Image with Gaussian Method

3. **Data Augmentation:** To make the proposed methods more robust and reduce the overfitting effect, Data Augmentation was applied with various transformations, in particular:

- rescale
- rotation with an angle of 30 degrees
- vertical and horizontal shift
- image zoom
- horizontal flipping

In Fig. 4 it is possible to observe the example of an original image and the respective transformations.

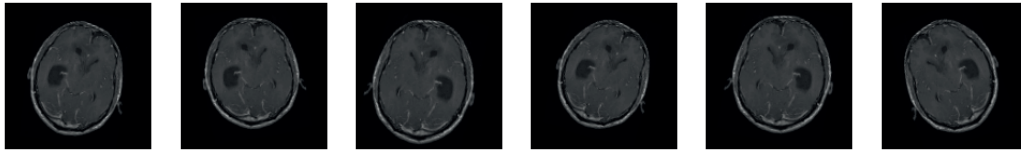


Fig. 4: Example of Original Image and Respective Transformations

4. One-Hot Encode: The last operation carried out was the transformation of the reference variable which was originally coded as numeric into a categorical variable.

2.2 Proposed Methodology

We chose to use a CNN architecture over any other model because CNN employs several convolutional filters to scan the whole feature matrix and perform dimensionality reduction, hence making them well suited for image processing and classification. Famous CNN architectures like VGG16, ResNet and EfficientNet-B0. All these architectures were implemented using Transfer Learning.

2.2.1 Configuration Model

To make it possible to compare the different classifiers, the same parameter configuration was used for the different models. To speed up the training a batch size of 32 was used and the models were trained for 15 epochs. The optimization algorithm chosen to train the models is Adam, because it is computationally efficient, easy to implement and works well for problems that involve large amounts of data or parameters.

The chosen loss function is the Categorical Loss-Entropy that is used to calculate and minimize the error of the model during the optimization process. This is a typical choice for a multi-class classification model.

The loss is defined by:

$$\sum_{i=1}^{outputsize} y_i \log(\hat{y}_i) \quad (1)$$

To avoid overfitting and save the model with the best performance on the validation set, a model checkpoint procedure has been implemented. During the training epochs, the validation loss is monitored and if it does not decrease for two consecutive epochs, the Learning Rate is reduced. The parameters used were: factor = 0.3, patience = 2 and minimum value of delta = 0.001.

For the convolutional networks implemented from scratch, in addition to the above configuration, several techniques have been used to improve their performance. The first model contains 5 layers including input and output layers. Each layer consists of 2D convolution, Max Pooling 2D, Batch Normalization and Dropout operation. The final layer (Fully Connected Layer) is composed of 128 neurons connected to the 4 output neurons (one for each class to be provided) and managed by the softmax function. The activation function chosen is the ReLU function. For the dropout operation, the value of p is 0.2 and 0.3 for the fully connected layer.

In order to improve the performance of the first model, the second one contains 6 layers including input and output layers and the final layer is composed of 1024 neurons. In this case, the value of p is 0.25 and 0.4 for the fully connected layer. For performance evaluation, the following metrics were used: Precision, Recall, F1-Score.

3 Results and Discussion

In order to see the predictions of the models we employed a confusion matrix and drew conclusions from it. In this study we want to maximize the number of True Positive which means correctly classifying patients with the disease and minimizing False Negative, i.e. reducing the risk of not treating patients who are actually ill.



Fig. 5: Confusion Matrix

In Table 1 is possible to see the performances of the models,

Model	Precision	Recall	F1-Score
CNN (V.1)	0.79	0.78	0.78
CNN (V.2)	0.90	0.92	0.91
VGG 16	0.74	0.77	0.74
ResNet 50	0.95	0.97	0.96
Efficient Net - B0	0.97	0.95	0.97

Table 1: Comparison of performances

As we can observe from the table the best model is Efficient Net-B0, the result is not surprising considering the advanced architecture and the recent study of it. It is also interesting to note that the second convolutional network from scratch performs almost similarly to the ResNet 50 network and even better than VGG 16. Despite several attempts and parameter configurations, the big loser is VGG 1 probably the poor performance is due to the few images contained in the dataset and to the network architecture. In Figure 7 it is possible to observe the plot of the various metrics considered with respect to the number of epochs. In Figure 8 we can see the Confusion matrix.

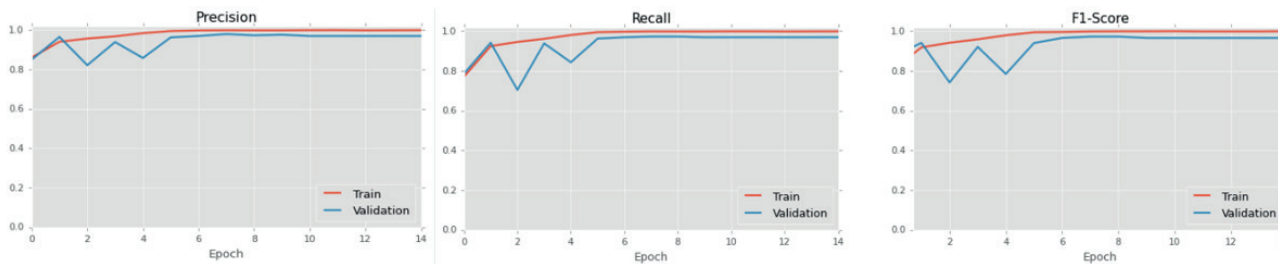


Fig. 6: Performance Metrics Vs. Epochs

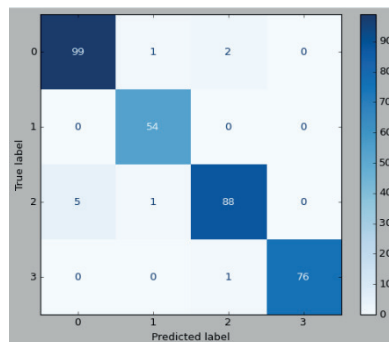


Fig. 7: Confusion Matrix Efficient Net - B0

For the interpretation of the confusion matrix, we remember that:

- 0: Glioma Cancer
- 1: No Cancer
- 2: Meningioma Cancer
- 3: Pituitary Cancer

4 Conclusions and Future Works

This study represents only one of the possible approaches to this type of problem. As we have seen, using a pretrained network does not always guarantee better performance than a network implemented from scratch and the results obtained strictly depend on the preprocessing operations carried out. In fact, for future works other preprocessing techniques could be applied such as image cropping, i.e. a technique that allows to modify the image by removing a portion that is not considered useful and focus attention on the part of the image needed for classification. Another improvement could be to perform object detection, i.e. detecting the actual location of the cancer with bounding boxes using segmentation and sophisticated detection algorithms such as YOLO (You Only Look Once) and SSD (Single-Shot Detector). In conclusion, future studies in this area may lead to better results, possibly using other pre-processing methods and further refining the model hyperparameters.

References

1. François Chollet. “Xception: Deep learning with depthwise separable convolutions”. In: Proceedings of the IEEE conference on computer vision and pattern recognition. 2017, pp. 1251–1258.
2. Nyoman Abiwinanda et al. “Brain tumor classification using convolutional neural network”. In: World congress on medical physics and biomedical engineering 2018. Springer. 2019, pp. 183–189.
3. Stefan Bauer et al. “A survey of MRI-based medical image analysis for brain tumor studies”. In: Physics in Medicine Biology 58.13 (2013), R97.