Classification of brain tumor types by deep learning with convolutional neural network on magnetic resonance images using a developed web-based interface

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***Abstract*— Automated machine learning (AutoML) algorithms developed using deep learning algorithms have been the focus of interest in many studies recently. This study aims to develop a free web-based software based on deep learning that can be utilized in the diagnosis and detection of brain tumors (Glioma/Meningioma/Pituitary) on T1-weighted magnetic resonance imaging. The Keras library, which is used in Python programming language, is utilized in the construction of the deep learning algorithm in this software. The experimental results show that this software can be used for the detection and diagnosis of three types of brain tumors. This developed web-based software can be publicly available at http://biostatapps.inonu.edu.tr/BTSY/ in both English and Turkish.**

Keywords*— *brain tumors, classification task, deep-learning strategy, Keras, magnetic resonance imaging.

I. INTRODUCTION

A brain tumor is formed by uncontrolled increase of and development of cells in the skull. Since the brain is the control center of the human body, developing tumors can put pressure on the skull and cause negative human health [1]. The number of deaths due to brain tumors are increasing day by day. Therefore, early diagnosis is important for all brain tumors, as in all diseases. Early diagnosis of brain tumor is often made by magnetic resonance imaging (MRI) [2]. MRI is a non-invasive diagnostic technique, that does not require any medication to cause sensitization in the human body, painless and does not use radioactive x-ray. In brain tumors, MRI is usually performed in three different planes: axial, coronal and sagittal. Thanks to the MRI imaging, the three different planes provides more precise information about the shape, tissue and volume of the brain tumors. MRI imaging in three different planes is given in Figure 1.

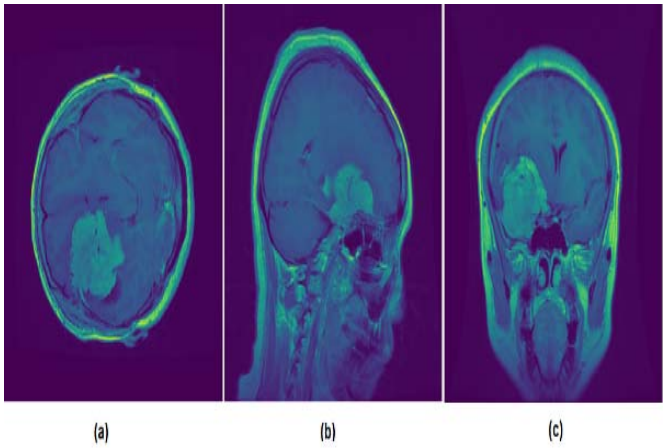

Fig. 1. Brain MRI imaging in three different planes (a) axial plane (b) coronal plane (c) sagittal plane

Tumor tissue which has different biological structure may not be possible to identify by a single-sequence MR imaging. In order to have more accurate information about tumor tissue, MR images are performed in two different sequence; T1-weighted and T2-weighted. T1-weighted MR imaging technique is used to visualize the anatomical structure of brain tumors. On the other hand, T2-weighted MR imaging technique is used to visualize the pathological structure of brain tumors.

Brain tumors in the brain can occur in tissues close to it. Therefore, the tumors are named according to the cells in which they are occurred. Glioma, meningioma and pituitary tumors are the most common brain tumors. Glioma is a type of tumor that occurs in the brain and spinal cord. Glioma-typed tumors occur in glial cells, which are the supporting tissue of the brain [3]. Meningioma, another type of brain tumor, is a tumor that surrounds the brain, protects it, and originates from the membrane called the dura mater. It is one of the most common tumors in the brain. It is generally known that they

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constitute 15-20% of brain tumors [4]. Finally, a pituitary tumor develops in the pituitary gland, which maintains hormonal balance, maintains the reproductive cycle, and has an important role in regulating the functioning of other glands [5]. T1-weighted MR images of three tumor types on three different planes are shown in Figure 2.

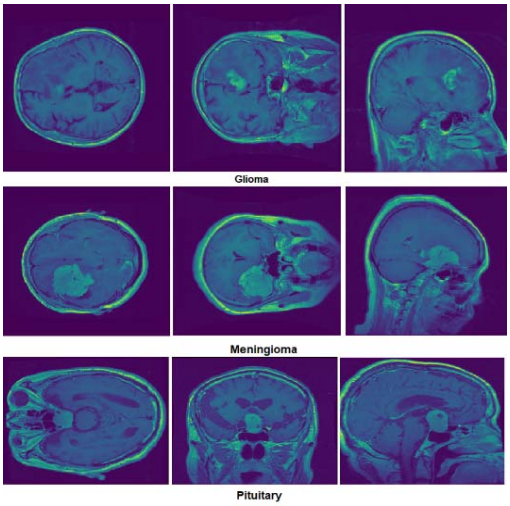

Fig. 2. T1-weighted MR images of three tumor types on three different planes

Diagnosis of brain tumors from MR images can lead to the waste of time and the misinterpretations for physicians. In recently, computer-aided automatic detection and diagnosis systems based on deep learning and image processing algorithms are used to minimize both the time of interpretation of MR images and the margin of error in the interpretation. It is an artificial intelligence method that uses multilayered neural networks in the fields of deep learning, object recognition and image classification and is one of the kinds of machine learning. Deep learning can learn automatically from icons of pictures, video, audio and text data instead of learning with coded rules, which is different from the classical machine learning methods [6].

The aim of this study is to develop a user-friendly, free web-based software that can classify brain tumors (glioma, meningioma, pituitary) and enable experts to make fast and accurate clinical decisions.

II. Material and Methods

A. Dataset

In this study, the studied images achieved from Nanfang Hospital and Tianjin Medical University General Hospital are an open source dataset downloaded from https://figshare.com. This data set consists of 3064 T1-weighted contrast-enhanced MR images from 233 patients, 708 meningioma, 1426 glioma, and 930 pituitary tumors [7].

B. Deep Learning

Machine learning is a data science approach that develops different methods enabling a system to decide on a specific problem. Deep learning, a sub-branch of machine learning, uses many non-linear processing unit layers for feature extraction and transformation. Artificial neural networks are a technique developed by mimicking the way the human brain works. This technique has many important features such as learning from data, generalization and working with many variables. Convolutional Neural Network (CNN), a deep learning algorithm, is inspired by artificial neural networks. This algorithm, like artificial neural networks, is forward-looking. However, unlike artificial neural networks, CNNs have a feature extraction layer. The CNN algorithm consists of one or more convolutional layers, subsampling layers, and one or more fully connected layers [8].

Auto-Keras is an automatic machine learning approach based on Keras library in Python. The goal in this system is to construct automatically deep learning structure(s) to classify/predict any target/label/dependent variable such as a disease (sick or healthy, present or absent, etc.) [9]. The detailed description of Auto-Keras system is given in Figure 3.

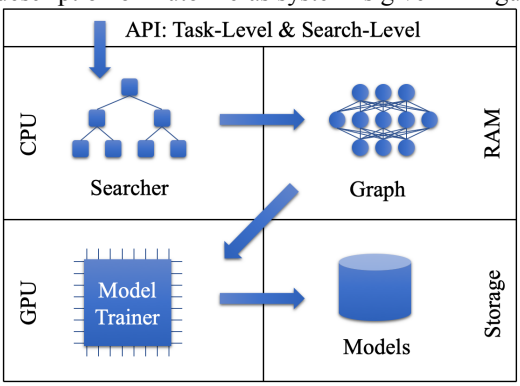

Fig. 3. The detailed description of Auto-Keras system [9]

There are a total of 3064 T1-weighted MR image scans for glioma, meningioma, pituitary brain tumors. 2599 instances of these T1-weighted MR images are used in the training phase and the remaining 465 in the testing phase. Keras/Auto Keras, one of the Python programming language libraries, is used in image pre-processing (image rotation, changing width and length, truncating images, rescaling, etc.) [9, 10]. Bayesian optimization technique is used to tune the hyperparameters of the model. Performance assessment of the developed model is performed based on the metrics described in the following sections.

C. The Developed Software

The developed web-based software can classify glioma, meningioma and pituitary types of brain tumors over T1-weighted MR images. Python programming language and TensorFlow [11], Keras [12], Scikit-learn [13], OpenCV [14], Pandas [15], NumPy [16], MatPlotLib [17], and Flask [18] libraries are used in the development of this software. The open source software can be publicly accessible at http://biostatapps.inonu.edu.tr/BTSY/. The developed software has two main web pages: English and Turkish languages. The

screenshot of the developed web-based software is given in Figure 4.

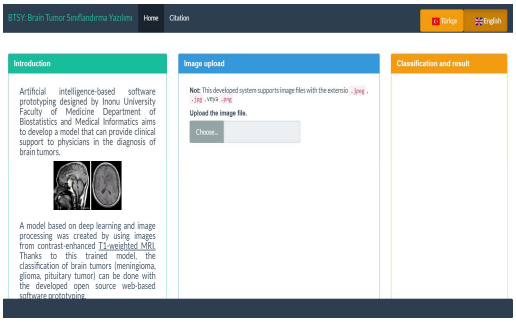

Fig. 4. Screenshot of the English web page

This web-based software consists of two main menus: “Home” and “Citation”. There are three sub-menus in “Home” main menu: "Introduction", "Image Upload" and "Classification and Result". The "Introduction" submenu contains information about the software. T1-weighted MR image of the brain tumors to be analyzed is uploaded to the software in the "Image Upload" submenu. Finally, in the "Classification and Result" submenu, the type of brain tumor is predicted by the uploaded T1-weighted MR image. The developed software supports .jpeg, .jpg and .png extension image files. If a file extension other than these three file extensions is uploaded to the system, the following screen appears in the "classification and Result" submenu.

Fig. 5. Unsupported file extension type error

A min-max filter code is formed to identify irrelevance images loaded into the software. The mxn pixel matrix of each image is calculated for this filter. Then, all the components of this matrix are summed with the following formula.

$$A_F = \sum_{i=1}^{m} \sum_{j=1}^{n} a_{ij}$$

A range of minimum and maximum values is determined from the obtained A_F values. If the A_F value of the new image loaded into the software falls outside this range, it is detected as an irrelevant image.

PSEUDO-CODE I. MIN-MAX FILTERING

A, B and C are matrices of each RGB channels of uploaded image.

```
if (A, B and C are not all equal){
  return ("Irrelevant image")
} else {
  if (AF not in range [192249, 293860]) {
    return ("Irrelevant image")
  }
  else {
    return ("Relevant image")
  }
}
```

D. Evaluation Metrics

In training and testing stages, accuracy, precision, sensitivity, specificity, F-Score, Matthew's Correlation Coefficient (MCC) and G-mean metrics together with 95% confidence interval (CI) levels are calculated in the assessment of classification performance of the model developed by using deep learning algorithm. DTROC: Diagnostic Tests and ROC Analysis Software, which we developed, are used to calculate performance metrics and 95% confidence intervals for these metrics [19]. The formulas for these performance criteria are given below.

$$\text{Accuracy} = (TP + TN) / (TP + TN + FP + FN)$$
$$\text{Sensitivity} = TP / (FN + TP)$$
$$\text{Specificity} = TN / (FP+TN)$$
$$\text{G-mean}=(\text{Sensitivity}*\text{Specificity})^{1/2}$$
$$\text{F1-score}= 2TP/(2TP+FP+FN)$$
$$\text{MCC}=(TP*TN-FP*FN)/ ((TP+FP)*(TP+FN)*(TN+FP)*(TN+FN))^{1/2}$$

In these formulas, TP represents the true positive number, TN defines the true negative number, FP explains the false positive number and FN describes the false negative number [20].

III. Experimental Results

The performance metrics on the training and testing datasets of the system constructed using the Keras library and the 95% confidence intervals for these metrics are given in Table I and Table II.

TABLE I. PERFORMANCE METRICS AND 95% CONFIDENCE INTERVAL FOR THE TRAINING DATASET

Metrics	*Training Value (%) (95% CI)*		
	Meningioma	***Glioma***	***Pituitary***
Accuracy	99.81 (99.64-99.98)	99.77 (99.58-99.95)	99.65 (99.43-99.88)
Precision	99.84 (99.68-99.99)	99.92 (99.81-99.99)	98.98 (98.60-99.37)
Sensitivity	99.35 (99.05-99.66)	99.58 (99.34-99.83)	99.87 (99.73-99.99)
Specificity	99.95 (99.86-99.99)	99.93 (99.83-99.99)	99.56 (99.31-99.81)
F-Score	99.60 (99.35-99.84)	99.75 (99.56-99.94)	99.43 (99.14-99.72)
MCC	99.47 (99.19-99.75)	99.54 (99.27-99.80)	99.17 (98.83-99.52)
G-Mean	99.65 (99.43-99.87)	99.75 (99.56-99.94)	99.71 (99.51-99.92)

TABLE II. PERFORMANCE METRICS AND 95% CONFIDENCE INTERVAL FOR THE TESTING DATASET

Metrics	*Testing Value (%) (95% CI)*		
	Meningioma	***Glioma***	***Pituitary***
Accuracy	96.29 (94.57-98.01)	96.08 (94.31-97.84)	97.14 (95.62-98.65)
Precision	94.51 (92.43-96.58)	96.97 (95.41-98.53)	91.61 (89.09-94.13)
Sensitivity	87.76 (84.78-90.73)	95.32 (93.40-97.24)	99.24 (98.45-99.99)
Specificity	98.61 (97.55-99.67)	96.88 (95.29-98.46)	96.27 (94.55-97.99)
F-Score	91.01 (88.40-93.61)	96.14 (94.39-97.89)	95.27 (93.34-97.20)
MCC	88.77 (85.90-91.64)	92.17 (89.73-94.61)	93.38 (91.12-95.64)
G-Mean	93.02 (90.71-95.34)	96.09 (94.33-97.85)	97.75 (96.40-99.10)

When performance metrics are considered, the performance of the proposed system to classify brain tumors (Glioma/Meningioma/Pituitary) is promising in both the training data set and the test data set.

In order to illustrate the working principle of the software, when the T1-weighted MRI image of a patient with a glioma brain tumor is uploaded to the web-based software, the output of the classification prediction is obtained in Figure 6. The same result can be obtained in Turkish language for the patient concerned.

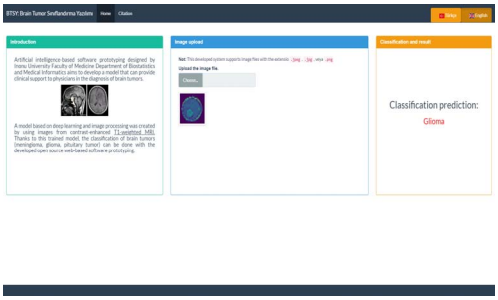

Fig. 6. The output of the classification prediction for a patient with glioma in English

IV. CONCLUSION

The aim of this study is to develop a web-based software that can classify brain tumors (glioma, meningioma, pituitary) based on high-precision T1 contrast magnetic resonance images using convolutional neural network from deep learning algorithm. Thanks to the free web-based software developed, it is believed that medical professionals and other health professionals can classify brain tumors faster and more accurately. In this aspect, the software can be used as a clinical decision support system in the classification of brain tumor types (i.e., glioma, meningioma, pituitary).

According to the experimental results, all the calculated performance metrics are higher than 98% for classifying the types of brain tumors on the training dataset. Similarly, all the performance metrics are higher than 91% except for sensitivity and MCC performance metrics for meningioma brain tumor on the testing dataset. When considering the calculated performance metrics from the CNN model on the training and testing stages, the proposed model is successfully capable of classifying brain tumor types.

A recent study has developed a deep learning system established on CNN for classifying brain tumors on public data sets, containing 233 and 73 patients with a total of 3064 and 516 images on T1-weighted contrast-enhanced magnetic resonance images. The developed system in the study realizes a important performance with the best total accuracy rates of 96.13% and 98.7% for the two datasets, respectively and can successfully classify for brain tumor multi-classification tasks [21].

In another article, a new deep learning algorithm has been constructed for classifying brain tumors into grade I, grade II, grade III and grade IV on the CNN deep learning algorithm. The new deep learning algorithm consists of three stages: tumor segmentation, data augmentation and deep features extraction/classification. Experimental results in the studied paper point out that the proposed algorithm has better performance than the present methods when it is applied to the augmented and original datasets [22].

Machine learning and deep learning algorithms have been reported to perform well in the classification and prediction of T1-weighted magnetic resonance images of brain tumors in the previous studies. However, when considering the machine learning/data mining applications of the reported studies in recent years, the selection and creation of these algorithms may require a lot of time and experience. Therefore, automatic

machine learning and different modeling systems have been commonly developed in recent years [23].

In a nutshell, the current study presents a novel public web-based software for classifying the types of brain tumors based on T1-weighted MR image scans by CNN algorithm of deep learning. In the following stages, it is envisaged to develop a system that can classify data sets containing brain images of healthy individuals in addition to the images of the brain tumors of patients examined in this study.

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