

NUMERICAL COMPUTATION IMPLEMENTATION OF DEEP NEURAL NETWORK FOR DETECTING BRAIN TUMOR

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Abstract - MRI is the most frequently used imaging technique to detect brain tumors. In this project, an automated approach has been proposed where MRI gray-scale images were incorporated for brain tumor detection. This project proposed an automated approach that includes enhancement at the initial stage to minimize gray-scale color variation. Filter operation can be used to remove unwanted noises as much as possible to assist better segmentation. Since we are testing grayscale images, threshold-based OTSU segmentation will be used instead of color segmentation. Finally, pathology experts provide feature information that can be used to identify the region of interest (Brain tumor region). We are proposing a novel architecture, named Xception, which enabled both high performance and reduced size and computational cost of deep neural networks using depth-wise separable convolution to develop a high-performance computer-aided diagnosis system for brain tumor detection from MRI. Preliminary assessment for the Xception model utilizing transfer learning demonstrated good performance with high accuracy and prediction probability. Interestingly prediction probabilities were different when different layers were relearned.

Key Words: Dataset, Machine learning-classification method.

1. INTRODUCTION

This study applied a novel architecture, named Xception, which enabled both high performance and reduced size and computational cost of deep neural networks using depthwise separable convolution to develop a high-performance computer-aided diagnosis system for brain tumor detection from MRI. Preliminary assessment for the Xception model utilizing transfer learning demonstrated good performance with high accuracy and prediction probability. Interestingly prediction probabilities were different when different layers were relearned.

By analyzing the patient's immune indications and basic indications, it is concluded that the recovery of cancer patients is related to physical conditions, daily activities, dietary intake, environmental conditions, and psychological factors. Correlation analysis is performed

on many factors related to the rehabilitation of cancer patients, and finally, six indicators are selected to generate the feature vector $\{x_1, x_2, x_3, x_4, x_5, x_6\}$ of the current user. In the prediction process of the cancer rehabilitation intelligent diagnosis system, the original behavior data of the patient can be directly used as the feature vector in the input system model sample. The feature vector is mainly obtained from various index indicators of cancer patients.

2. RELATED WORKS

[1] Hossam H, Sultan, Nancy M. Salem, and Walid Al-Albany, Multi-Classification of Brain Tumor Images Using Deep Neural Network, 2019 Brain tumor classification is a crucial task to evaluate the tumors and make a treatment decision according to their classes. The datasets include 233 and 73 patients with a total of 3064 and 516 images on T1-weighted contrast-enhanced images for the first and second datasets, respectively. The proposed network structure achieves a significant performance with the best overall accuracy of 96.13% and 98.7%, respectively, for the two studies. The results indicate the ability of the model for brain tumor multi-classification purposes. In the proposed structure, we have found that 10% and 20% dropout probabilities were the most suitable values for dropout layers 1 and 2 respectively. Finally, we have used three advanced layers; Fully Connected layer (FC), softmax layer and classification layer. The proposed CNN method is a segmentation-free approach as we load the brain tumor image to get the corresponding class directly. The authors have used only two convolutional layers with 64 kernels in each one. Moreover, they have used 4 dropout layers which are relatively high for the presented network. Despite Ertosun and Rubin have used pathological images to train the network, weak results have been obtained after using a combination of 2 classifiers.

[2] Ying, b, FujuanChena, YangZhaoa, ZhixingWua, ChaoZhanga, DongyuanWua, A Stacked Multi-Connection Simple Reducing Net for BrainTumor Segmentation, 2019 It is well known that the Unit has been widely used in the area of medical image segmentation because of the cascade connection in the up-sampling process. But it does not

perform well in dealing with complex medical images (Such as brain MRI). To achieve better segmentation performance by adopting the Unet, many researchers have paid more attention to stacking the Unet. However, the stacking process leads to a large increase in the number of parameters. This is not a good choice when considering the tradeoff between precision and efficiency. We propose a novel framework called Stack Multi-Connection Simple ReducingNet(SMCSRNet) which is stacked by some basic blocks called Simple ReducingNet(SRNet). We want to further modify Unet, to make it more suitable for stacking to brain tumor segmentation.

[3] Chao Ma, Gongning Luo, Concatenated and Connected Random Forests With Multiscale Patch Driven Active Contour Model for Automated Brain Tumor Segmentation of MR Images, 2018 Segmentation of brain tumors from magnetic resonance imaging (MRI) data sets is of great importance for improved diagnosis, growth rate prediction, and treatment planning. In this paper, we introduce a new methodology that combines random forests and an active contour model for the automated segmentation of the gliomas from multimodal volumetric MR images. Results reported on public benchmarks reveal that our architecture achieves competitive accuracy compared to the state-of-the-art brain tumor segmentation methods while being computationally efficient. Once trained, the approximated elapsed time of the brain tumor multiphase segmentation is around 5 min. Therefore, the ccRFs-mpAC model achieves more advantages in terms of accuracy and computational efficiency.

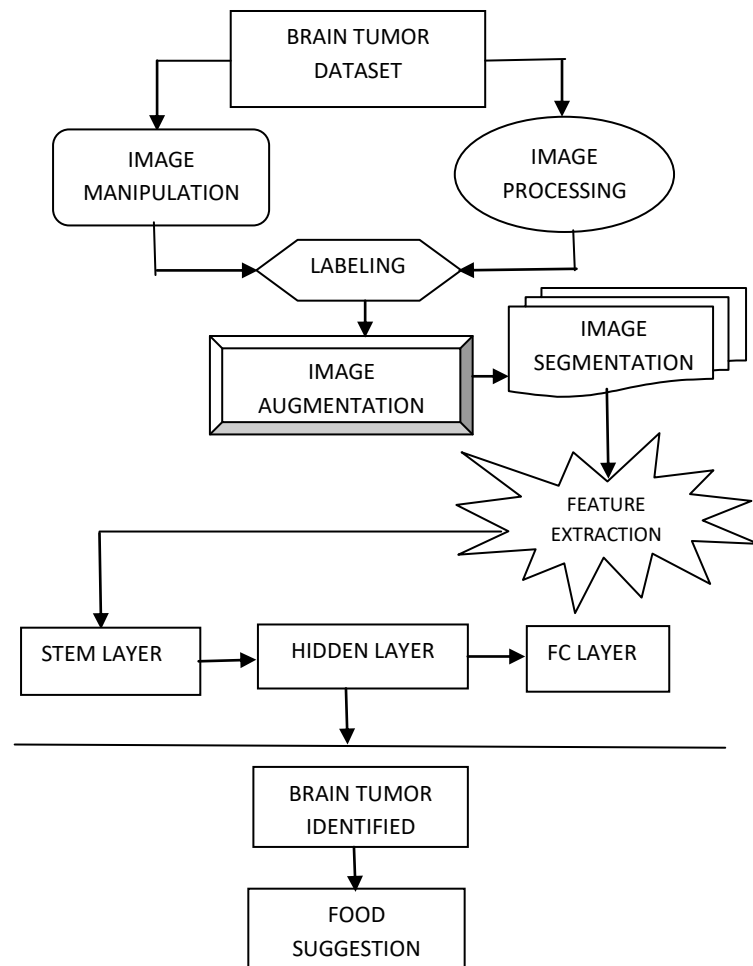
[4]A. Bhandari, A. Bansal, A. Singh, and N. Sinha¹, Transport of liposome-encapsulated Drugs in Voxelized Computational Model of Human Brain Tumors, 2017 There are many obstacles to the transport of chemotherapeutic drugs to tumor cells that lead to irregular and non-uniform uptake of drugs inside tumors. The study of these transport problems will help inaccurate prediction of drug transport and optimizing treatment strategy. This model utilizes dynamic contrast enhanced-magnetic resonance imaging (DCE-MRI) data to account for heterogeneity in tumor vasculature. The porosity of the interstitial space inside the tumor and normal tissue is determined voxel-wise by processing the DCE-MRI images by General Tracer Kinetic Model (GTKM). The CFD model is applied to predict the transport of two different types of liposomes (Stealth and conventional) in tumors.

□

3. PROPOSED SYSTEM

The proposed system consists of five parts. They are the Import and Preprocessing, Augmentation, Model building, Performance and Recommendation of food. The below figure describes that the data sets have been imported and processing technique is used to remove the unwanted noises from the images and it sharpens the images with equal edges, then it will train each image that consists of some algorithms. Finally, it predicts the output as a Brain tumor is found or not, then it recommends the nutritional food for tumor patients.

4. PROPOSED ARCHITECTURE



5. MODULES AND DESCRIPTION

5.1 Data Import and Preprocessing

Preprocessing is a common name for operations with images at the lowest level of abstraction both input and output are intensity images. The aim of pre-processing is an improvement of the image data that suppresses unwanted

distortions or enhances some image features important for further processing. Convert color images to grayscale to reduce computation complexity in certain problems to find it is useful to lose unnecessary information from your images to reduce space or computational complexity. For example, converting your colored images to grayscale images. This is because, in many objects, color isn't necessary to recognize and interpret an image. Grayscale can be good enough for recognizing certain objects. Because color images contain more information than black and white images, they can add unnecessary complexity and take up more space in memory (Remember how color images are represented in three channels, which means that converting it to grayscale reduces the number of pixels that need to be processed). One important constraint that exists in some machine learning algorithms, such as CNN, is the need to resize the images in your dataset to a unified dimension. This implies that our images must be preprocessed and scaled to have identical widths and heights before fed to the learning algorithm.

5.2 Data Augmentation

We use effective methods that can use to build a powerful image classifier, using only very few training examples—just a few hundred or thousand pictures from each class want to be able to recognize. To make the most of our few training examples, we will "augment" them via many random transformations, so that our model would never see twice the same picture. This helps prevent overfitting and helps the model generalize better. The right tool for an image classification job is a convent, to train one on our data, as an initial baseline. Overfitting happens when a model exposed to too few examples learns patterns that do not generalize to new data, i.e. when the model starts using irrelevant features for making predictions.

Data augmentation is one way to fight to overfit, but it isn't enough since our augmented samples are still highly correlated. The main focus for fighting to overfit should be the entropic capacity of your model --how much information your model is allowed to store. A model that can store a lot of information has the potential to be more accurate by leveraging more features, but it is also more at risk to start storing irrelevant features. Meanwhile, a model that can only store a few features will have to focus on the most significant features found in the data, and these are more likely to be truly relevant and to generalize better. There are different ways to modulate entropic capacity. The main one is the choice of the number of parameters in your model, i.e. the number of layers and the size of each layer.

Another way is the use of weight regularization, such as L1 or L2 regularization, which consists of forcing model weights to take smaller values.

5.3 Model Building

The input to cov1 layer is of fixed size 224 x 224 RGB image. The image is passed through a stack of convolutional (Conv.) layers, where the filters were used with a very small receptive field:3x3 (which is the smallest size to capture the notion of left/right, up/down, center). In one of the configurations, it also utilizes 1x1 convolution filters, which can be seen as a linear transformation of the input channels(followed by non-linearity). The convolution stride is fixed to 1 pixel; the spatial padding of Conv. Layer input is such that the spatial resolution is preserved after convolution, i.e. the padding is 1-pixel for 3x3 conv. layers. Spatial pooling is carried out by five max-pooling layers, which follow some of the Conv. layers (not all the Conv. layers are followed by max-pooling). Max-pooling is performed over a 2x2 pixel window, with stride 2. Model Checkpoint helps us to save the model by monitoring a specific parameter of the model. In this case, it monitors validation accuracy by passing val_acc to Model Checkpoint. The model will only be saved to disk if the validation accuracy of the model in the current epoch is greater than what it was in the last epoch.

5.4 Model Performance

As we train the classification predictive model, we want to assess how good it is. Interestingly, there are many different ways of evaluating performance. Most data scientists that use Python for predictive modeling use the Python package called sci-kit-learn. Scikit-learn contains many built-in functions for analyzing the performance of models. Confusion_matrix: Given an actual label and a predicted label, the first thing we can do is divide our samples into 4 buckets:

True positive – actual = 1, predicted = 1

False positive – actual = 0, predicted = 1

False negative – actual = 1, predicted = 0

True negative – actual = 0, predicted = 0

5.5 Recommendation System

The most common ingredients in each one are closely related to characteristics of the region, such as the climate. This plays a big influence in the availability of each of the components present in the local recipes. Some molecules are known to have a positive effect on health, namely, in

fighting cancer. Being able to identify which ingredients contain the higher concentrations, may help us treating and preventing the disease. Moreover, by including these ingredients in tasty and affordable meals, it can promote a shift in the nutritional habits of the population. In a world where fast food consumption is rising, it is clear that additionally to the two previous points, speed of preparation is also an important factor. Our system will propose the best food for the patient who diagnosed with Brain Cancer.

6. RESULT

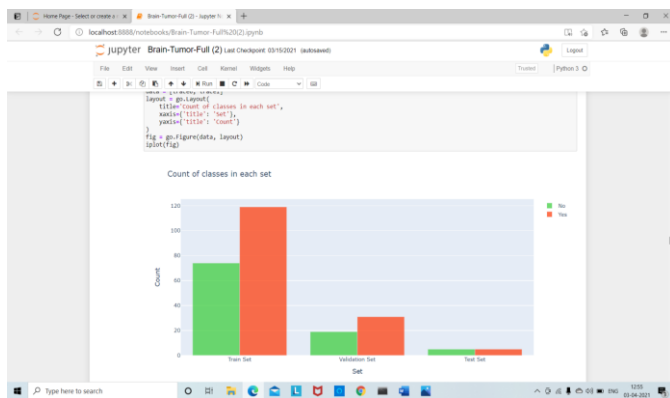


Fig -2: Model Creation

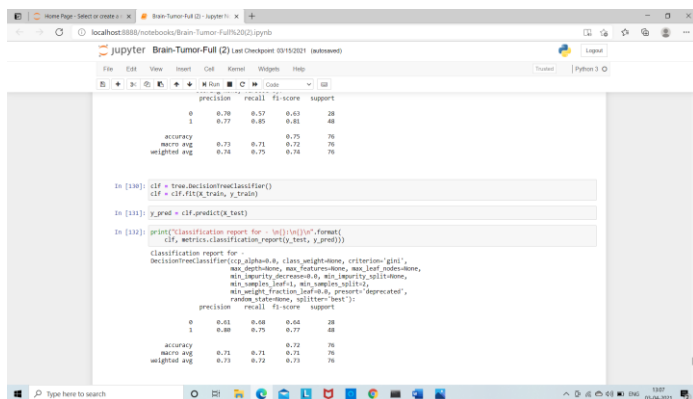


Fig -3: Validation and accuracy of decision tree algorithm

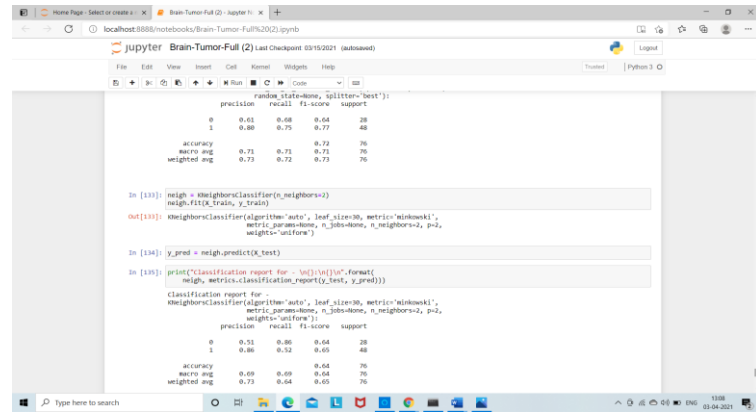


Fig -4: Validation and accuracy of KNeighborsClassifier algorithm

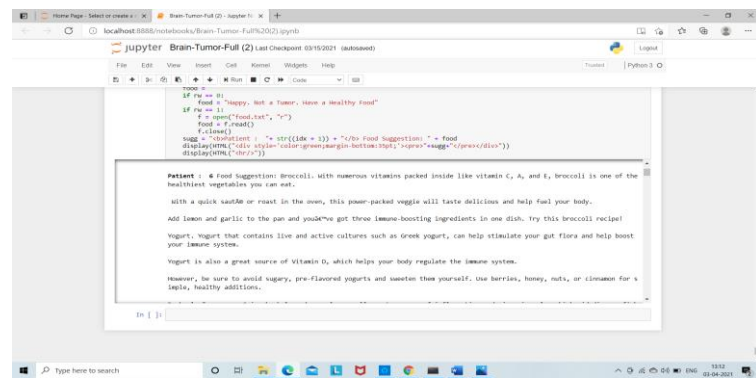


Fig -5: Food suggestion

7. CONCLUSIONS

This project proposes a Faster R-neural network for the classification of two-dimensional MRI brain tumor images. The real MRI brain images are obtained from Jansons MRI Diagnostic center. Initially, the local feature information is extracted using this method and the overall global features are extracted using the Faster-RNN method. By these methods, the brain images are fully illustrated from local and global. The feature sub selection is done by statistical technique. The features with the highest variance are considered for classification. In this project, we have proposed an enhancement to the method for image thresholding. Our method uses a Gamma distribution rather than a Gaussian distribution. This approach solves the problem of non-symmetric histograms of images. We have also implemented our algorithm and applied it sequentially to make the threshold value converges to be the optimal value.

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