11-1-2018

# DenseNet for Anatomical Brain Segmentation

Ram Deepak Gottapu

Cihan H. Dagli
*Missouri University of Science and Technology*, dagli@mst.edu

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Ram Deepak Gottapu[a]* , Cihan H Dagli[a]

*Missouri University of Science and Technology, Rolla, MO, USA*

## Abstract

Automated segmentation in brain magnetic resonance image (MRI) plays an important role in the analysis of many diseases and conditions. In this paper, we present a new architecture to perform MR image brain segmentation (MRI) into a number of classes based on type of tissue. Recent work has shown that convolutional neural networks (DenseNet) can be substantially more accurate with less number of parameters if each layer in the network is connected with every other layer in a feed forward fashion. We embrace this idea and generate new architecture that can assign each pixel/voxel in an MR image of the brain to its corresponding anatomical region. To benchmark our model, we used the dataset provided by the IBSR 2(Internet Brain Segmentation Repository), which consists of 18 manually segmented MR images of the brain. To our knowledge, our approach is the first to use DenseNet to perform anatomical segmentation of the whole brain.

*Keywords:* convolutional neural network (CNN), Dense Net, segmentation

* Corresponding author. Ram Deepak Gottapu
  E-mail address: rgrk6@mst.edu

## 1. Introduction

Quantitative analysis of brain magnetic resonance image (MRI) is necessary for the diagnosis of many neurological diseases and conditions. For instance, abnormal shapes of certain anatomical regions of brain have been found to be associated with many disorders such as Alzheimer's and Parkinson's [4,5]. Segmentation i.e. labelling of each pixel (2D)/voxel (3D) plays a critical role in this analysis which led many researchers to design mathematical models that can accurately automate the process of segmentation. A popular approach for segmentation before the deep learning algorithms includes the use of atlases [7,8] and pattern recognition methods [6]. In order to perform anatomically accurate segmentation, these methods use explicit spatial and intensity information which are manually created features.

The explicit definition of such features can be avoided with the use of convolutional neural networks (CNNs). CNNs have shown excellent results in many computer vision tasks such as ImageNet [9]. In recent years, convolutional neural networks (CNNs) have become a dominant machine learning approach for MRI segmentation because of their self-learning ability and generalization over large amounts of data [17]. CNNs were initially used for medical image analysis in [10-15], where they were able to provide accurate segmentations of various abnormalities without the use of hand crafted features. This motivated the researchers to develop many new CNN architectures for various segmentation tasks on MRI.

CNNs have also been used for brain MRI segmentation in [16], where the authors presented a CNN architecture to accurately segment the white matter, gray matter and cerebrospinal fluid in infants. In addition, a number of competitions were created by MICCAI in last few years where datasets were provided to segment different brain MRIs. In the recent MICCAI challenges of neonatal and adult [2], the best accuracy was not produced by single architecture. It was shown that different architectures are good at segmenting different aspects of the brain. In [2], the authors tried to develop a more general approach that is not biased towards one aspect of the brain. Considering the results from all these challenges, it was obvious that there are a lot of inaccuracies in the developed architectures and there is a lot of space for improvement.

In this paper, we present a new architecture for automated brain segmentation based on the concept presented in DenseNet [1]. DenseNet is the present state-of-the-art CNN architecture which gave the best results on CIFAR-10, CIFAR-100 and ImageNet datasets using only a fraction of parameters compared to its predecessors [1]. The idea behind DenseNet is to connect each layer to every other layer behind it to improve the information flow within the architecture. This gives CNN the capability to make decisions based on all of the layers rather than a single final layer. By using this approach for brain segmentation, we perform the segmentation which can further be used to identify abnormalities in brain.
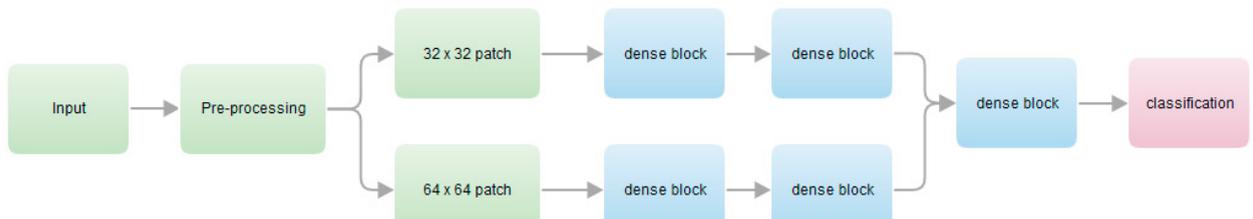


Fig 1: Architecture for brain MRI segmentation

## 2. Method

Fig 1 shows an overall schematic of our proposed architecture. Considering the complexity of brain MRI, we use patches for inputs rather than sending the whole image as input to the architecture. The pre-processing steps include the normalization of the MRI images and generating concentric patches. The central pixel/voxel will be target which the architecture has to classify using the patches. The larger patch provides spatial information as they are large enough to understand where the central pixel is located. The smaller patch provides the detailed information about the neighborhood of the central pixel. Fig 2 shows an example of concentric patches.
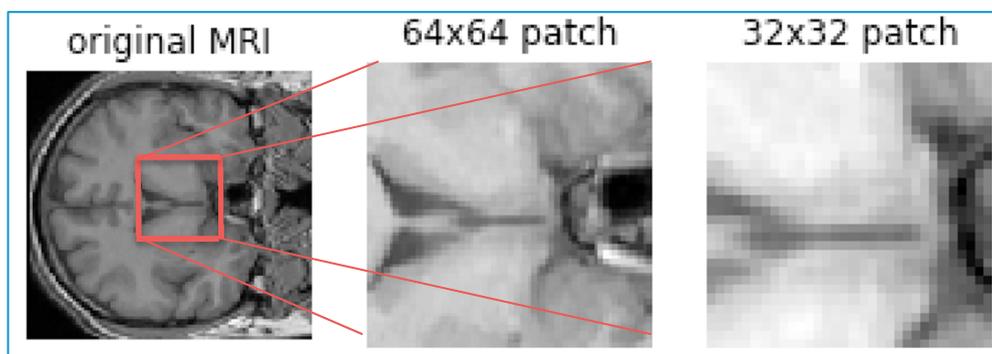


Fig 2: MRI with 64 and 32 size patches

There are two parallel paths for each patch where it goes through two dense blocks. The two paths are then concatenated and passed through a final dense block before the classification layer. Fig 3 shows the schematic of the dense block. The layers in dense block form a composite function [1]. It consists of three consecutive operations: batch normalization (BN) [18], followed by a rectified linear unit (ReLU) and a 3 × 3 convolution (Conv). The transition layers are placed in between the blocks for spatial reduction. It consists of batch normalization and an 1x1 convolution followed by 2x2 pooling layer.

**Growth Rate**: An important feature in DeseNet is the use of growth rate which describes the rate at which the size of each layers inside the dense block grows. The growth rate regulates how much information is passed at each layer to the future layers. The colored connection in Fig 3 shows how the information is passes between the layers in dense block. For e.g., a growth rate k=12 implies that a filter size of 12 is used for each layer and therefore the output size of each layer will be $12 + n * 12$ where $n$ is the layer number. Experiments have shown that a small value of k is sufficient to efficiently transfer the information between the layers [1]. In our approach, we set the growth rate at 10.

**Bottlenecks**: It was shown in [19,20] that a 1×1 convolution can be introduced as bottleneck layer before each 3×3 convolution to reduce the number of input feature-maps, and thus to improve computational efficiency. In our approach, we used bottlenecks before convolutional and pooling layers

**Compression**: The compression feature reduces the number of feature maps at the transition layer and also to improve computational efficiency. Since we used only two layers inside each dense block, there is no advantage to use compression for reducing feature maps. However, we observed that our architecture performs better when the compression is set at $\theta = 0.5$.
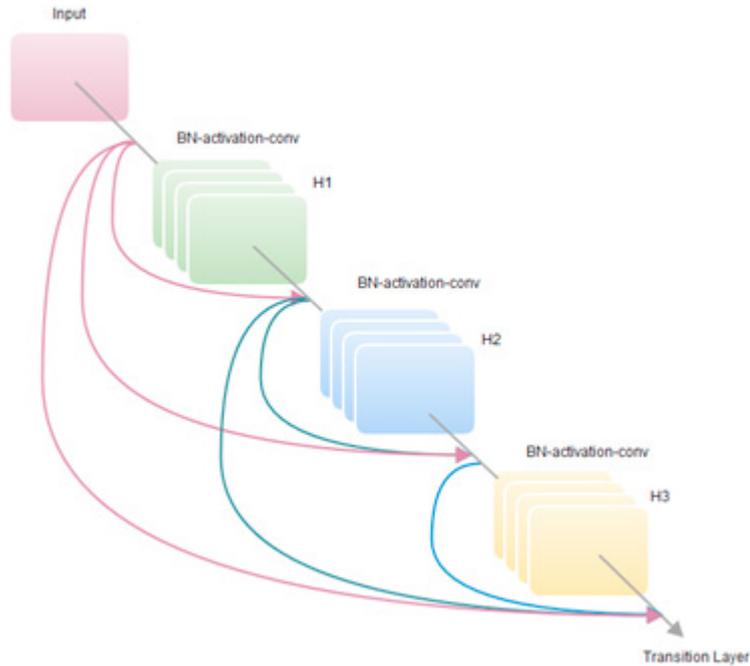
Fig 3: Dense Block

## 3. Data

The IBSR (http://www.cma.mgh.harvard.edu/ibsr) dataset consists of 18 manually segment MR images of brain. Fig 4 shows an MRI of brain with the corresponding segmentation. The goal of our architecture is to perform segmentation identical to the manual approach. The quality of our segmentation is measured using the mean dice coefficient over the anatomical regions. All computations were run in-memory using a single NVIDIA Tesla K40 GPU with 12GB memory.

## 4. Experiments

We started our experiment by normalizing the given data and generating the concentric patches for training. The outer patches were of dimensions 64x64 and the inner patches were of dimension 32x32. We trained our architecture for 200 epochs with a batch size of 32 using SGD optimization. We also use l2 regularization with dropout to prevent overfitting. The testing was done on the test images using dice coefficient. In order to get the best architecture from training, we used early stopping to the error rate on validation data with a patience limit of 10 epochs.

Table 1. Architecture Details

| Layer | Configuration |
|---|---|
| Input (64 x 64 and 32 x 32) | 2 |
| Dense block (1) x 2 | $\binom{1x1}{3x3}x2$ |
| Transition layer (1) x 2 | 1x1 conv and 2x2 pool |

| | |
|---|---|
| Dense block (2) x 2 | $\binom{1x1}{3x3}x2$ |
| Transition layer (2) x 2 | 1x1 conv and 2x2 pool |
| Merge layer | |
| Dense block (3) x 1 | $\binom{1x1}{3x3}x2$ |
| Transition layer (3) x 1 | 1x1 conv and 2x2 pool |
| Classification layer | 4D Fully Connected |

Fig 5 shows the results for few frames of a single patient. The results show that our architecture was able to accurately segment majority of the brain tissue. The borders show some unwanted segmentation which will be removed in future work.
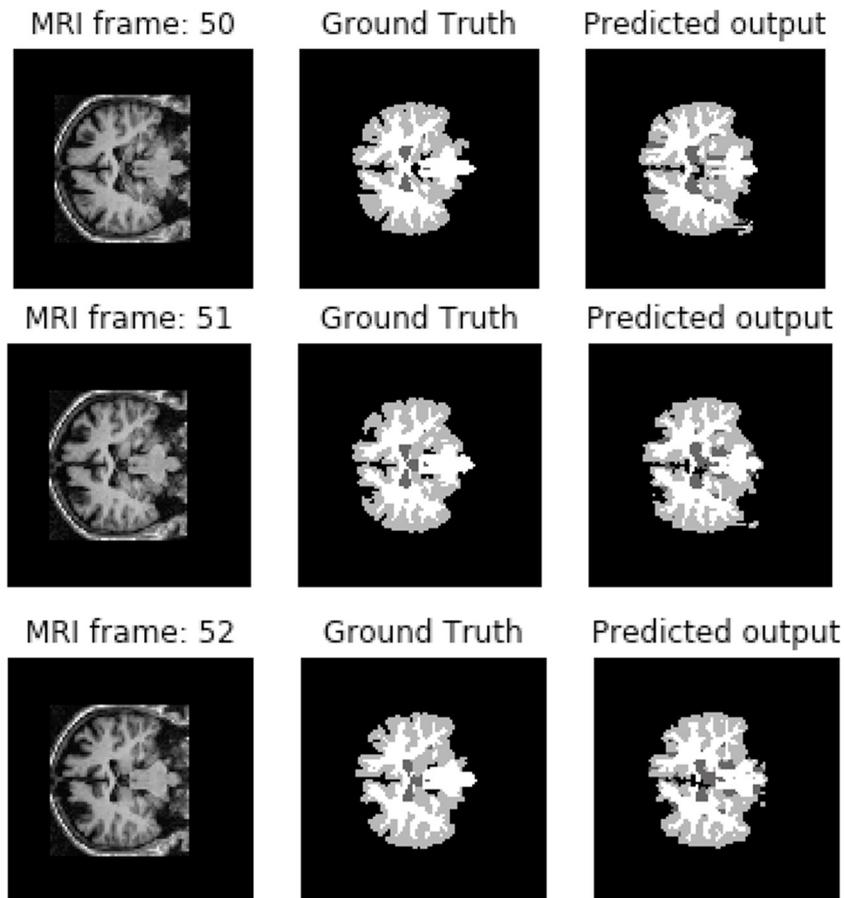
Fig 4: Original Scans (left row) , manual segmentation (middle row) , predicted segmentation (right row)

Table 2. Results

| Layer | Loss | Accuracy |
|---|---|---|
| Architecture without compression | 0.5972 | 0.9052 |
| Architecture with compression | 0.4577 | 0.9253 |

The results in table 2 show the values obtained on validation data. Here it is observed that using compression slightly improves the accuracy of the model which is in accordance with the DenseNet architecture. We evaluated our model on 5 test MRIs and achieved a dice coefficient of 0.673. Note that we achieved this level of accuracy with only ∼ 0.4M parameters which is a significantly low number for CNN architectures.

## 5. Conclusion

In this paper, we have performed the MRI brain segmentation using the DenseNet architecture. The results show that our approach can accurately perform the segmentation. We plan to improve the accuracy of this approach and use it for Parkinson's MRI segmentation in the future work.

## 6. Acknowledgement

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