Jeevn-Net: Brain Tumor Segmentation using Cascaded U-Net & Overall Survival Prediction

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Abstract - *This paper proposes a new architecture "Jeevn-Net" a cascaded u-net for Brain tumor Segmentation & Overall Survival Prediction from the features extraction of the segmented tumor image. MRI scans are processed and optimization techniques are applied for improving the accuracy. Extracted features from the segmented image are classified based on the properties using Random Forrest Regressor. Survival prediction algorithm works accurately to predict the survival of the patient. Our Network Architectural model is inspired & based on enhancements of previous work & Results of the BraTS competition. This Noval model is a complete State oF Art Architecture (SOTA) segmentation algorithm for the Brain Tumor Detection.*

*Key Words***:** Brain Tumor Segmentation, U-Net, CNN, Cascaded U-Net, Random Forrest Algorithm, Medical Radiology, Deep Learning, etc

1. INTRODUCTION

Glioma is one of the most common diseases in the Brain Tumor disease family. Tumor causes a large number of casualties every year both adults and younger ones[10]. Diagnosis of Brain tumor is a very long, time-consuming, expensive process[10]. Our proposed algorithm will help to improve accuracy of the tumor detection and reduce the time required for diagnosis.

MRI(Magnetic Resonance) Images are used for diagnosis of the brain tumor in medical radiology. Tumor has own features such as size, age, etc this features can be extracted using MR image processing. This features can be used to calculate the overall survival of the patient based on which doctors and Radiologist can take required actions.

1.1 MOTIVATION

Our main motive is to build a fast, robust and efficient algorithm which will improve the accuracy of Diagnosis and tumor segmentation.

2. RELATED WORK

Since Deep Learning techniques are widely used for image segmentation, CNN had been the most used. There are several techniques such as FCN, BFCN, DRN, etc are present for the brain tumor segmentation. However Two Pathway architecture[14] for feature extraction works well, the series of upsampling can not refine the segmented image in FCN[1], downsampling & removing Pooling in Traditional CNN may give results well but Time & Memory Consumption issue of DRN is still present. Classical U-Net CNN architecture Ronnenberger [10] applies the skip-connections between encoder and decoder part which ultimately improve overall decode operation. H. Dong [17] U-Net architecture based on application of loss in Dice Score in loss function. But our proposed architecture outperforms all techniques. Our Algorithm is a successor to the winning architecture of the BraTS 18 winner paper[7] with addition of cascaded U-Net structure. Encoder and Decoder [9] architecture is based architecture for most of the U-Net image segmentation algorithms. Our algorithm based on the cascading of U-Net and implementation of the Auto-Encoder Regularization[7] on both the Encoder and Decoder part of the proposed architecture. Combing these architectures and developing new architecture performs well over its other variants. [6], [13], etc.

3. PROPOSED SYSTEM ARCHITECTURE

3.1 JEEVN-NET: CASCADED U-NET

Jeevn-Net is State Of The Art, Noval deep learning algorithm mainly focusing on brain tumor segmentation. This new architecture is influenced from its parent architecture of Cu-Net[1], AutoEncoder regularization[8], and the U-Net[10]. Large distributed Fully Connected Network of U-Net, Auto-Encoder regularization and benefits from total group normalization & modified de-coding CNN Units and finally symmetrical adding features, concatenating the results from each U-Net Combines to

form Jeevn-Net. The Input Image Is of size 240 X 240 X 155 resolutions with Voxel size of 1 X 1 X 1. i.e. every MR image will consist of length and breadth both 240 x 240. There are 155 images per batch are taken. While performing, the batch image size must be less than the number of training images due to GPU limitations. As per the data, we used X4 sub-types of the tumor images each batch making total dimensions as 4 X 240 X 240 X 155 as input data image dimensions. Our Proposed architecture uses the 32 X 32 input feature map with 4 channel 3-d channels with 3 X 3 X 3 convolution of 32 filters.

Fig.1-Jeevn-Net (Cascaded U-Net)
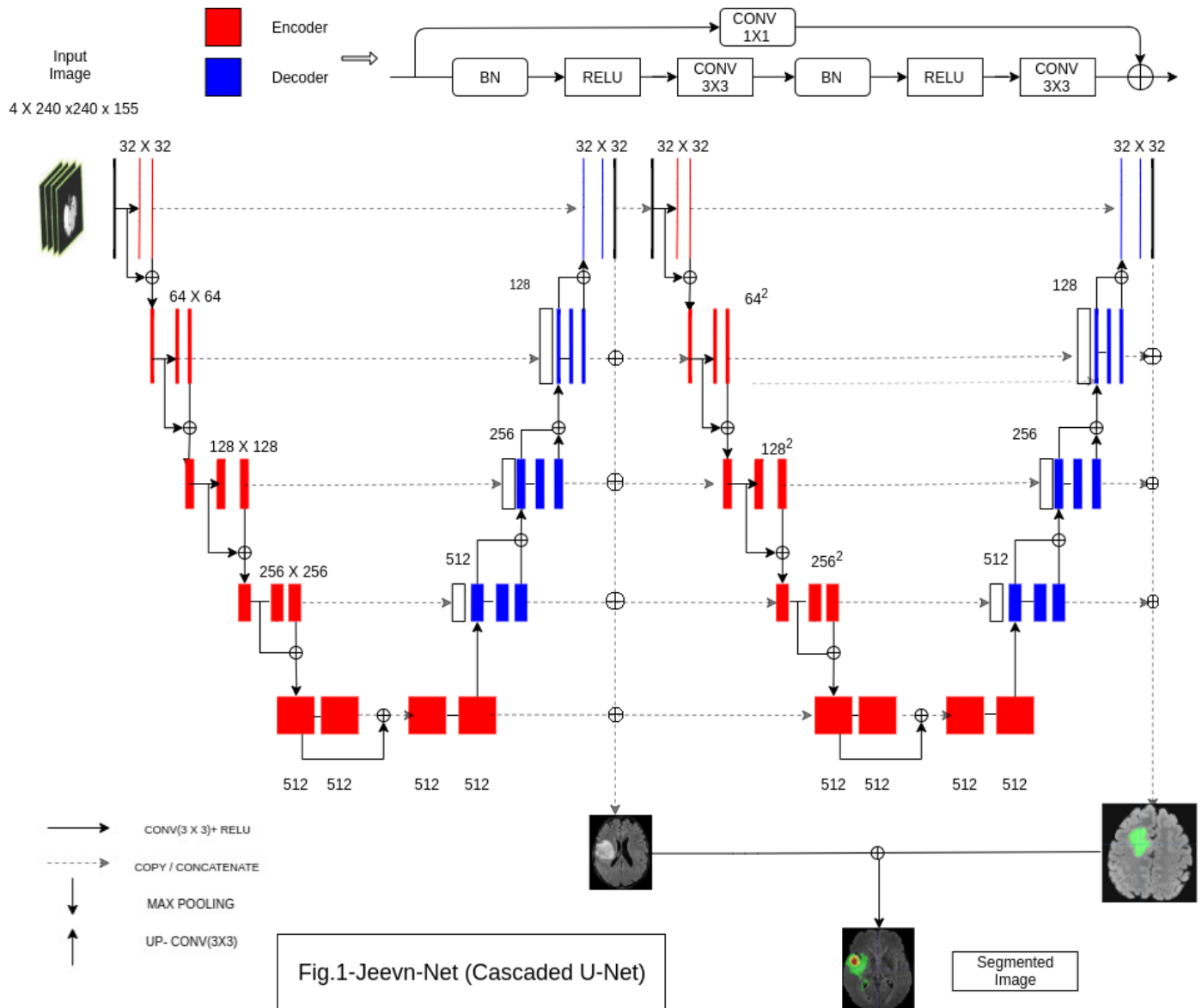
3.2 ENCODER

Architecture is consist of similar looking two parts as Encoder and Decoder. Encoder consists of the total 4 down-sampling with keeping the same resolution for more better convolution. The basic building block of this architecture is CNN as a RES-Net with Two 3 X 3 CNN with Relu and the Batch Normalization. Each block is provided forward sampling to Implementing 1 X 1 Convolution. Final image at bottom is having the dimension as 512 X 32 X 32 I.e 512 feature maps having resolution as 32 X 32.

3.3 DECODER

Decoder part of enhances the details reduces the number of feature maps 2 and adding the concatenated output image of the previous stages. Convolution matrix is of size 1 X 1 X 1 for better details and it is done by doubling spatial dimension using 3-d Bilinear Up-sampling.

The result of 1st U-Net is provided as input to the 2nd U-Net one. The summation of this U-Nets gives the final segmented image. This segmented image contains features which will be used further.

3.4 AUTO-ENCODER REGULARIZATION

Auto-Encoder Regularization is based on the measured architecture of the usage of the more features while downsampling in encoder part and adding comparatively smaller sized convoluted matrix with more feature maps while up-sampling in decoder part. Input of each block of the RES-Net is forward sampled and concatenated to the output.

3.5 ALGORITHM

This proposed algorithm takes input as 4 sub-types of the brain tumor annotated MR images & outputs the segmented image with the features associated with it and overall survival prediction based on features. First U-Net with Auto-Encoder Regularization and concatenation is done using parsing each output image of the RES-Net to its corresponding Decoder level. Output of the first image is given as input to second level with same procedure. Advantage is of the adding concatenated output image on the same decoder level with forward sampling block is it improves accuracy & segmentation. Each RES-Net contains forward sampling with CONV.(1X1)with Relu layer and Batch Normalization. Output of all the layers in Encoder and Decoder is added to obtain the final Segmented Image. Finally, both outputs of U-Nets are concatenated to output final segmented image.

```
Input: BRATS Dataset 2018
Output: Tumor Segmentation and Survival prediction
Steps:
    1. Start
    2. Read: Training Dataset
       Read: Test Dataset
    3. Apply: Preprocessing
       X: Preprocessed Data

       //Tumor Segmentation
    4. Train: Model
       Apply Model
       Input: A
         Apply:  1. U-Net_1
                 2. Auto-Encoder Regularization
                 3. Concatenation
         Output: Segmented Image of U-Net 1
                 X ← Segmented Image of U-Net 1
       Input: X
         Apply:  1. U-Net_2
                 2. Auto-Encoder Regularization
                 3. Concatenation
         Output: Segmented Image of U-Net 2
                 Y ← Segmented Image of U-Net 2
    5. Final Output: Z  where Z← X + Y

       //feature Extraction
    6. Input: Z
       Apply: Random Forest Regressor ( Z )
       Output: Extracted Features
       K← Extracted Features

       //survival Prediction
    7. Input: K
       Apply Support Vector Machine: SVM (K)

       If Class Label > 15 months

           Print: "Long Survival"

       If Class Label < 10 months

           Print: "Short Survival"

       If Class Label < 15 months OR Class Label > 10 Months

           Print: "Mid Survival"

       Output: Survival Prediction
    8. End
```

Fig.2- Algorithm

3.6 FEATURE EXTRACTION

Obtained segmented image contains several features such as circularity, area, perimeter, shape, age, contrast, texture, etc. These features need to be extracted from the image and must be classified for prediction. This is done by applying Random Forest Regressor over approx. 14 features and tabulated in structured format.
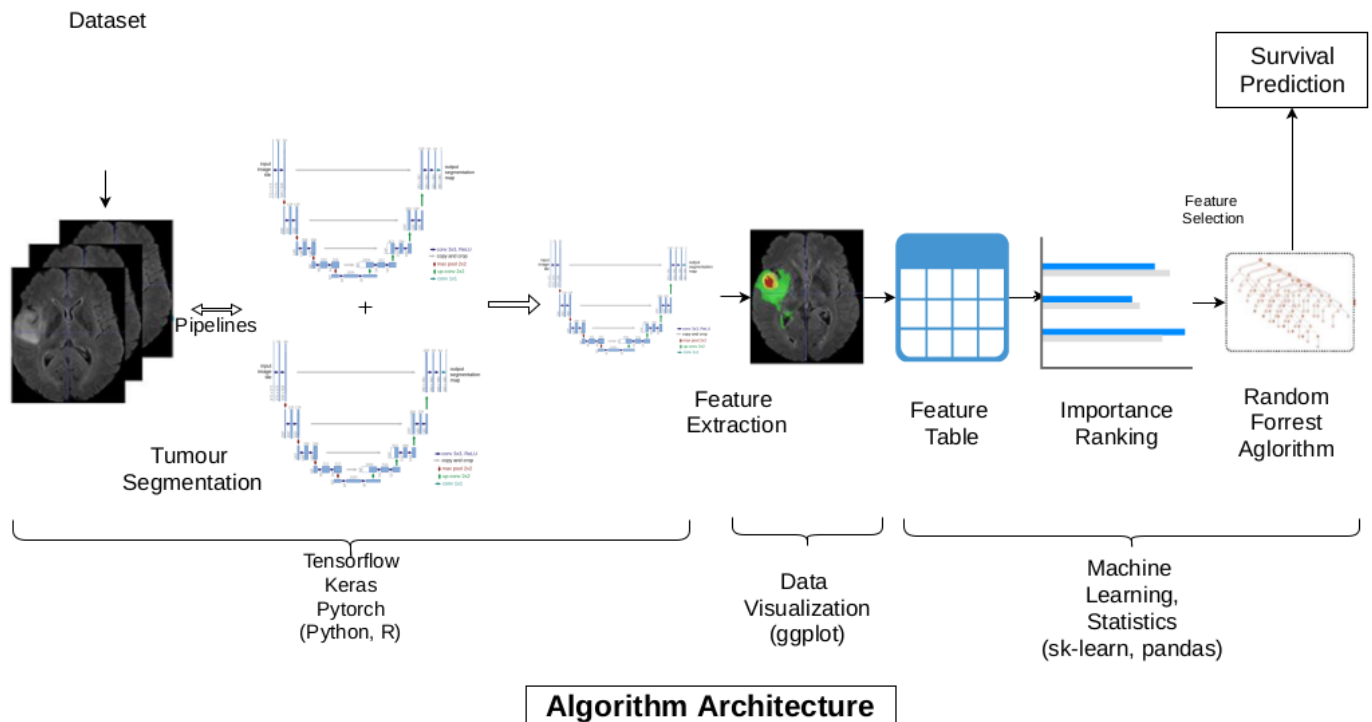
3.7 ALGORITHM ARCHITECTURE

Fig. 3- Algorithm Architecture

This architecture is a complete pictorial representation of the Jeevn-Net. Feature tables are very useful while working in the supervised learning domain.

3.8 HISTOGRAM IMPORTANCE RANKING

Using pandas a statistical computational library all the features are analysed based on their importance. Histogram Mapping being the most widely used technique for the feature mapping across the extracted features. Graphs and Data-Visualization tools such as ggplot and very helpful in analyzing and providing dynamic accessibility over the visualization of the segmented image.

3.9 SURVIVAL PREDICTION

Survival prediction of the patient is very important in terms of this kind of disease where patient needs to be diagnosed. The survival prediction of the patient is broadly classified into 3 subcategories such as long survivals, survival more than 15 months, mid-survivals between 10-15 months and short survival, survival less than 10 months.[7] Support vector machine easily can classify the features based on classmarking and importance ranking.
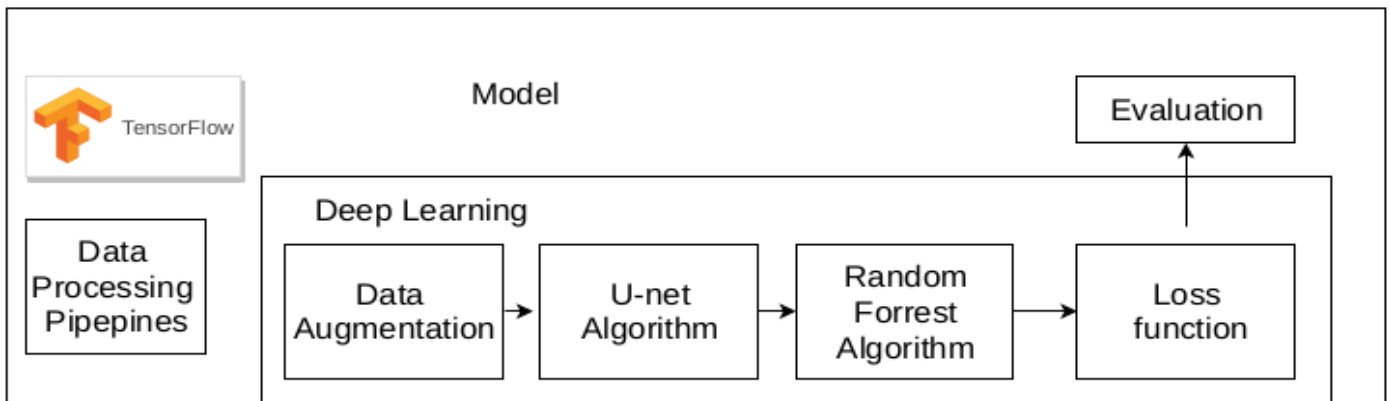
3.10 SOFTWARE ARCHITECTURE

Fig. 4- Name of the figure

Data processing pipelines maintains the flow of the data into the deep learning model. This whole architecture uses Tensorflow 2.0 as the base implementation with Keras serving as back-end. Deep learning model connecting with database with the help of data pipelines. MR data continuously being transferred into model with typically 4 separate pipelines as T1, T1-CE, T2, FLAIR for each sub-types of the data.

Data Augmentation and per-processing is done in very first step of execution. Each MR images of the size 240 X 240 is firstly cropped into more feasible size for algorithm as channels of 32 filters.

4. DATA AND IMPLEMENTATION

The BraTS competition provides pre-processed and annotated data-Set contain of 285 Cases. Total 75 Low grade (LGG) and 210 High grade (HGG) Gliomas sub-types out of which 67 were validation and 192 were testing MRI. These images are collected from 92 institutions and has higher quality resolution[18]. Doctors and radiologist have annotated and provided the dataset[18]. High-grade Gliomas are more dangerous than Low-grade ones. The dataset contains 4 types of the MR data, T1 MR, T1 (Weighted), T2 and FLAIR (Fluid Attenuation Inversion Recovery). The input size of Each MRI image is 240 X 240 X 150, i.e. 150 images of size 240 X 240. The annotations were comprising of the 3 regions, Whole Tumor (WT), Tumor Core (TC), Enhancing Tumor (ET).

Our proposed architecture will be implemented on the Intel Dev-Cloud which having Xeon Scalable Processors with 96 GB of On platform DDR4 ram with inbuilt integrated Python 2.0/ 3.0 and Tensorflow libraries, etc. Estimated time for training will be less than 6 hours for 300 epoch.

Loss function uses Stochastic gradient descent(SGD)as Adam Optimizer to calculate the loss and changing the parameter as per the whole training. Changing the parameters based on learning from the output stage given as input is very efficient process. This process needs less number of batch size as parameter can only change only one after the training is completed.

This kind of Encoder-Decoder architectures is defined only over less number of sample training batch size. Less number of training samples with high computation power such as Intel Dev-Cloud it is possible to handle such computational heavy tasks as well.

5. EVALUATION & VALIDATION

Brain tumor segmentation output is cross-checked by validating the trained model with testing data. Tumor segmentation accuracy is validated by using Dice Score, Sensitivity and specificity. Results need to be calculated over 3 sub-parts 1) Whole Tumor (WT), 2)Tumor Core (TC), 3) Enhancing Tumor (ET). The Dice Score (A, B) where A is segmentation results and B labels, P stands for positive counts and N stands for the negative counts in the training.

$$Dice(A, B) = \frac{2|A_P \wedge B_P|}{|A_P| + |B_P|}$$

Dice Score

Dice Score calculates the overall accuracy of the model. A_p & B_P denotes the positives in the result and the labels.

$$Sens(A, B) = \frac{|A_P \wedge B_P|}{|A_P| + |B_P|}$$

Sensitivity

Sensitivity defines as the positive accuracy of the model which is calculated w.r.t. Positives labels.

$$Spec(A, B) = \frac{|A_N \wedge B_N|}{|B_N|}$$

Specificity

Specificity is the amount of the negatives present in the sample batch w.r.t negative labels.

6. CONCLUSIONS

Brain tumor is one of the most fatal disease known and diagnosis of such diseases are much expensive. Jeevn-Net will help to improve the accuracy of the diagnosis and faster & robust algorithm will speed-up the diagnosis process.

Above Mentioned algorithm comes up with the ideology that even with the less number of the input data, image segmentation can be performed with the same accuracy and precision compared to ground truth. This architecture is capable of scaling to the number of feature maps as per requirements. Also, same architecture is flexible and can be applied across any other disease image segmentation. Jeevn-Net has a very strong encoder and decoder application with cascaded so it becomes very effective. survival prediction based on real extracted features is the most important feature of this architecture. In the near future, Jeevn-Net with its wide application, accuracy and scalability it will surely serve major computational systems.

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