# Brain Tumor Segmentation with U-Net

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### **Implementation Details**

PL	Python 3.8
API	Tensorflow 2.4.0
Packages	os, numpy, matplotlib, imgaug, tf_Segmentation
GPU	M1
Github	None

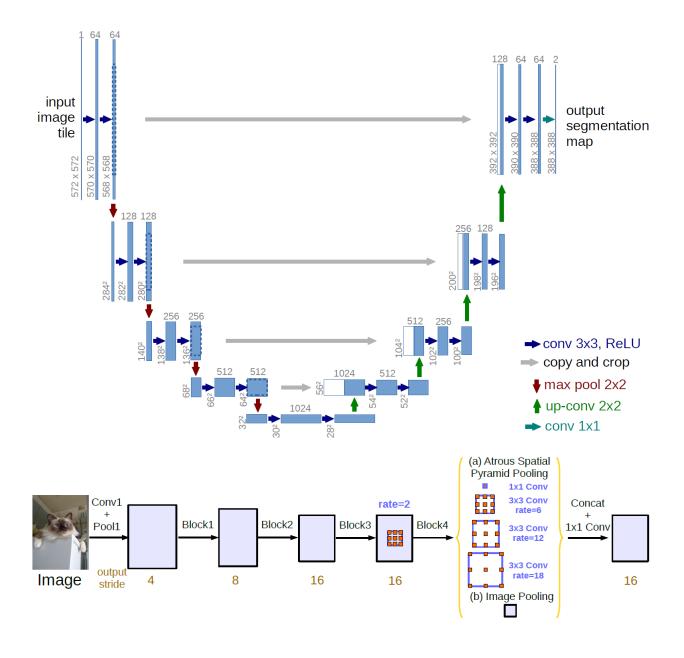
#### **Dataset**

Name	2021 Brain Tumor Segmentation Asia Championship Challenge
Content	MRI images and labelled images of 1600 patients
Source	https://aidea-web.tw/topic/a0264109-3fc6-49ea-9e4b-4b0a9433f02f
Size	512x512 pixels, channel number=3
Classes	Brain tumor region, none
Distribution	Train: 1280, validation: 160, test: 160

### **Experimental Design**

U-Net is an encoder-decoder-like model for semantic segmentation task; it contains several stacks of convolution and max pooling layers just as common CNN but also up-convolution layers and the action, copy and crop, like residual. The up-convolution layers and residual-like action help the model increasing the resolution of the output and localizing features in higher resolution layers.

DeepLabv3 is also a model for semantic segmentation task that improves upon DeepLabv2. To implement segmentation, modules were designed to employ atrous convolution in cascade or in parallel. Atrous convolution is quite different from common convolution; it enlarged size of kernel to capture feature instead of contracting. Other details are most identical to DeepLabv2.



## **Modified Parameters**

To have an insight into the cross-effect of input size and loss function to U-Net, I implemented the following four trials altering input size and loss function. Otherwise, with the interest in the performance of DeepLabv3, it also be tried to compare with U-Net.

Trial #	1	2	3	4	5
Architecture	U-Net	U-Net	U-Net	U-Net	DeepLabv3
Input size	416 × 416 × 3	416 × 416 × 3	512 × 512 × 3	512 × 512 × 3	512 × 512 × 3
Loss function	Dice	Crossentropy	Dice	Crossentropy	Crossentropy
Metrics	Accuracy	Dice coefficient	Accuracy	Dice coefficient	Dice coefficient

All the models were trained with Adam optimizer, 30 epochs, batch size=10, and learning rate=1e-5.

#### **Results**

## Trial 1:

Confusion metric	Tumor	None	Precision	Recall	F1-score
Tumor	107764	9647	0.0025	0.9178	0.0050
None	4148264	23423285	0.9996	0.8495	0.9185

## Trial 2:

Confusion metric	Tumor	None	Precision	Recall	F1-score
Tumor	112538	17462	0.0315	0.8657	0.0608
None	3259183	24099777	0.9993	0.8809	0.9364

## Trial 3:

Confusion metric	Tumor	None	Precision	Recall	F1-score
Tumor	25783	196340	0.0336	0.1161	0.0521
None	742701	40978216	0.9952	0.9822	0.9887

# Trial 4:

Confusion metric	Tumor	None	Precision	Recall	F1-score
Tumor	207693	6007	0.0216	0.9719	0.0353
None	9394094	32335246	0.9998	0.7749	0.8731

## Trial 5:

Confusion metric	Tumor	None	Precision	Recall	F1-score
Tumor	1573	100964	0.0030	0.0153	0.0050
None	528972	27057451	0.9962	0.9808	0.9884

## Reference

- 1. U-Net: Convolutional Networks for Biomedical Image Segmentation. <a href="https://arxiv.org/abs/">https://arxiv.org/abs/</a>
  <a href="https://arxiv.org/abs/">1505.04597</a>
- 2. Rethinking Atrous Convolution for Semantic Image Segmentation. <a href="https://arxiv.org/abs/1706.05587">https://arxiv.org/abs/1706.05587</a>