Segmentation of Brain Tumors and Patient Survival Prediction: Methods for the BraTS 2018 Challenge

Leon Weninger, Oliver Rippel, Simon Koppers & Dorit Merhof

Persented By: Ravi Kumar

November 7, 2019



Introduction

The challenge consists two tasks:

- tumor segmentation in 3D-MRI images of Brain Tumor patients
- Survival prediction based on MRI images

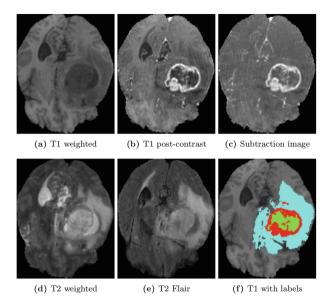
General brain tumors:

- Glioblastma (GBM / HGG)
- Low grade glioma (LGG)

Data-set contains 286 MRI-scans from 19 different patients,

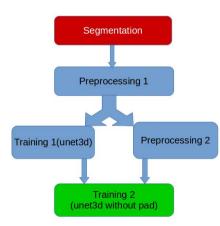
- T1 and T1 post-contrast(T1CE)
- T2 and T2 Fluid Attenuated Inversion Recovery(Flair)
- Hand annotated expert labels







Prepossessing & Training





Unet3d Model generalization used in figure

- Double Conv Block ->
 - Sequential(
 - (0): Sequential(
 - (0): Conv3d(in_channels, out_channels, kernel=, stride=)
 - (1): InstanceNorm3d(num_features=out_channels)
 - (2): ReLU()
 -)
 - (1): Sequential(
 - (0): Conv3d(in_channels, out_channels, kernel=, stride=)
 - (1): InstanceNorm3d(num_features=out_channels)
 - (2): ReLU()



Unet3d Model generalization used in figure

```
Trans Conv Block ->
```

Sequential(

(0): ConvTranspose3d(in_channels, out_channels, kernel=, stride=)

(1): InstanceNorm3d(num_features=out_channels)

(2): ReLU()

)



	Input 3D MRI scan
	Double conv Block
	(5,16,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
	(16,16,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
	MaxPolling3d(kerne=2,stride=2,padding=0,dilation=1)
	Double conv Block
	(16,32,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
	(32,32,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
	MaxPolling3d(kerne=2,stride=2,padding=0,dilation=1)
	Double conv Block
	(32,64,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
	(64,64,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
	MaxPolling3d(kerne=2,stride=2,padding=0,dilation=1)
-	Double conv Block
1	64,128,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
	128,128,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
~	Trans conv Block
C	128,128,kernel=(3,3,3),stride=(2,2,2),padding=(1, 1,1),
	output padding= $(1, 1, 1)$
	Double conv Block
(192,64,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
	(64,64,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
	Trans conv Block
	(64,64,kernel=(3,3,3),stride=(2,2,2),padding=(1, 1,1),
	output_padding=(1, 1, 1))
	Double conv Block
	(96,32,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
	(32,32,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
	Tráns conv Block
	(32,32,kernel=(3,3,3),stride=(2,2,2),padding=(1, 1,1),
	output_padding=(1, 1, 1)) Double.conv.Block
	(48,16,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
	(16,16,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
	Out conv3d
	(16,kernel=(3,3,3),stride=(1,1,1))
	Location of Brain Tumor Predicted
	Location of brain rumor Predicted



Patched Input and labels
Double conv Block
(5,32,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
(32,32,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
MaxPolling3d(kerne=2,stride=2,padding=0,dilation=1)
Double conv Block
(32,64,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
(64,64,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
MaxPolling3d(kerne=2,stride=2,padding=0,dilation=1)
Double conv Block
(64,128,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
(128,128,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
MaxPolling3d(kerne=2,stride=2,padding=0,dilation=1)
Double conv Block
(128,256,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
(256,256,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
Trans conv Block
(256,128,kernel=(3,3,3),stride=(2,2,2),padding=(1, 1,1),
(200, 120, 100, 100, 100, 100, 100, 100,
Double conv Block
(256,128,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
(128,128,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
Trans conv Block
(128,64,kernel=(3,3,3),stride=(2,2,2),padding=(1, 1,1),
output padding=(1, 1, 1))
Double conv Block
(128,64,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
(64,64,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
Trans conv Block
(64,32,kernel=(3,3,3),stride=(2,2,2),padding=(1, 1,1),
(04,02,001) output padding=(1, 1, 1))
Double conv Block
(64,32,kernel=(3,3,3),stride=(1,1,1),padding=(1, 1,1))
(32,32,kernel=(3,3,3),stride=(1,1,1),padding=(1,1,1))
Out conv3d
(32,4,kernel=(3,3,3),stride=(1,1,1))
Brain Tumor Type Predicted
Brain ramor Type Fredicted



Segmentation Results

Dataset	Dice			Sensitivity			Specificity			Hausdorff 95		
	ΕT	WT	TC	EΤ	WT	TC	ET	WT	TC	ET	WT	TC
Train set	0.763	0.860	0.817	0.747	0.784	0.787	0.998	0.998	0.998	5.63	7.01	7.88
Val set	0.712	0.889	0.758	0.757	0.887	0.735	0.998	0.995	0.998	6.28	6.97	10.91
Test set	0.621	0.844	0.728	*	*	*	*	*	*	10.5	8.71	13.3



Survival Prediction Features and Results

Features	MSE	Median Err.
Age (submitted)	95082	216
Age + gde	100941	224
Age + ed	99693	221
Age + nec	98826	216
Age + dist	100928	215
Age + gde + ed + nec	109817	222

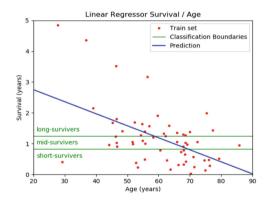


Survival Prediction Validation Result

Features	Accuracy	MSE	Median SE	stdSE	SpearmanR
Age	0.5	97759.5	46120.5	139670.7	0.267
$\mathrm{Age} + \mathrm{gde} + \mathrm{ed} + \mathrm{nec}$	0.536	101012.0	51006.5	140511.5	0.258



Survival Linear Regression Plot





Conclusion and My Opinion

- ► In paper splitting of dataset is not described.
- Patching part is missing from second step in paper.
- Overall paper well described and this into my master's work for result comparision.



Code & Paper Links

https://doi.org/10.1007/978-3-030-11726-9_1 https://github.com/weningerleon/BraTS2018



Thanks for attention!! Questions???

