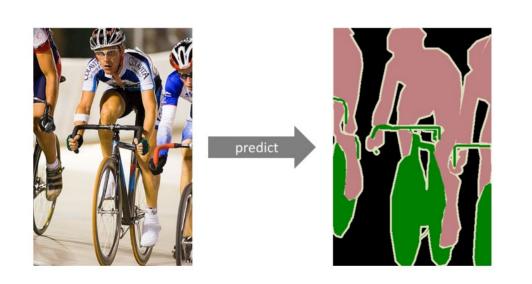
Automatic medical image segmentation with Unet and Unet++

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Semantic segmentation

 Classify each pixel in a picture in its class membership (Szeliski and Szeliski 2011).

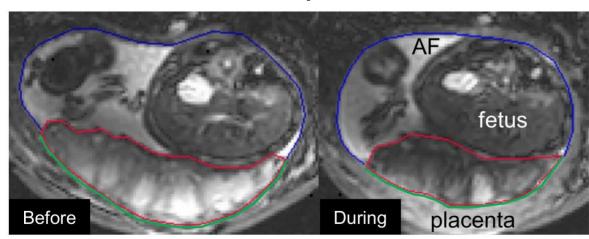


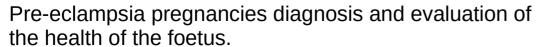
Person Bicycle Background

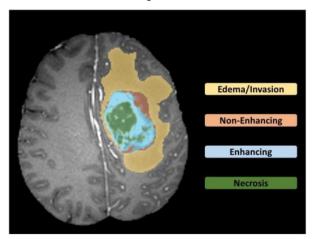
Segmentation in medical science Why?

It may be used to segment anatomical structures for further quantitative study.

(Szeliski and Szeliski 2011)







Prior to radiotherapy treatment segmentation mask, an image is used to mark the exact location of the cancerous tumour and to create a treatment plan

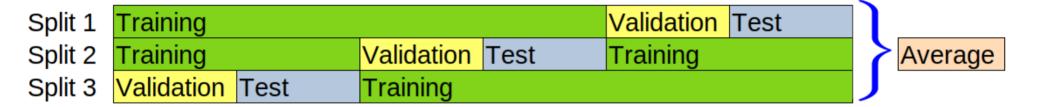
Aims and objectives

- Develop software python/pytorch for the implementation of model segmentation with Unet and Unet++ to each dataset.
- Segmenting the placenta from the utero-placental pump MRI images using Unet and Unet++
- Segmenting tumour in its specified regions whole tumour (WT), tumour core (TC), and enhancing tumour.
- For the placenta segmentation task one aim is to evaluate performance of the implementation obtained and compare them with previous work in the university. For the BraTS challenge the aim is to compare the results with previous ones in the field

Evaluation metrics

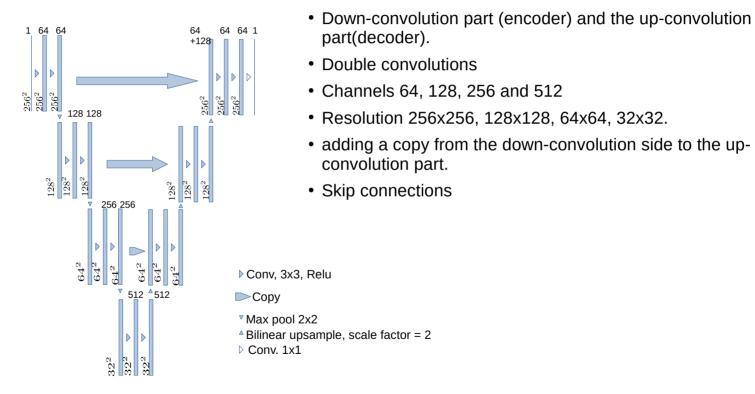
- Binary Cross Entropy: is the same loss function used with logistic regression (Bishop 2006) and it widely used for classification problems.
- Dice coefficient:is a similarity statistic and expresses the relation between pixel overlapping (between the predicted classes and the ground truth) and the total number of pixels of the prediction plus the ground truth.
- BCE-Dice loss: is a combination between binary cross entropy and dice loss.

k-fold cross validation

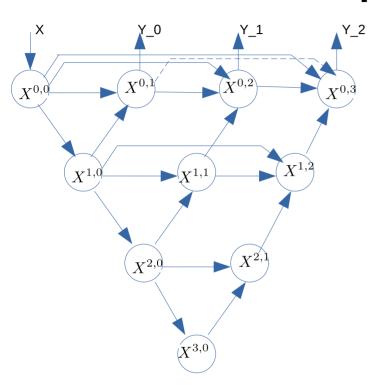


 Cross-validation is one of the most extensively used data resampling strategies for assessing a predictive model's generalisation capacity and preventing over-fitting.(Berrar 2019)

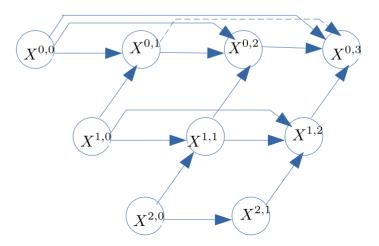
Model implementation - Unet



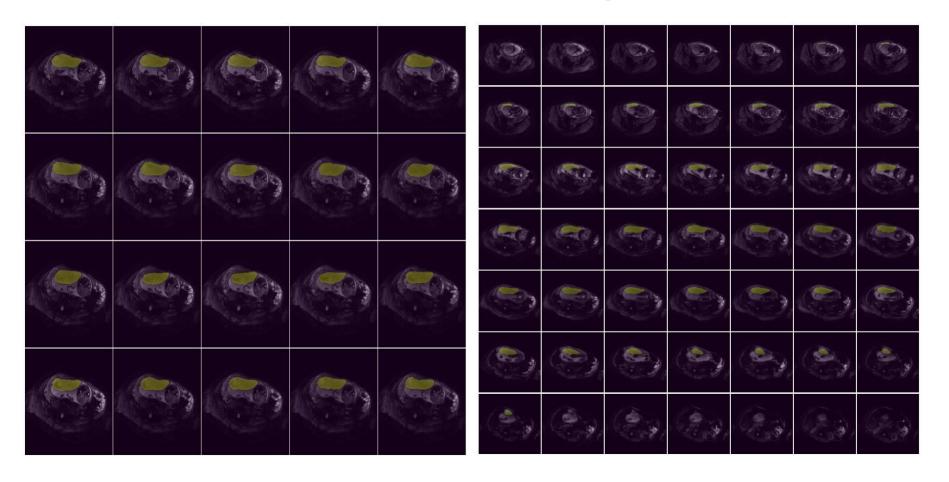
Model implementation - Unet++



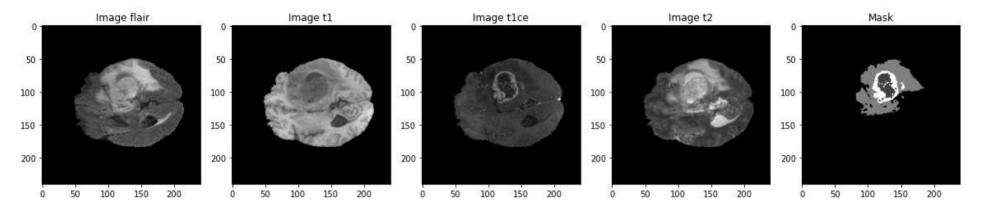
- Down-convolution part (encoder) and the up-convolution part(decoder).
- Double convolutions
- Channels 64, 128, 256 and 512
- Resolution 256x256, 128x128, 64x64, 32x32.
- adding a copy from the down-convolution side to the up-convolution part (pass forward with a dense convolutional block from the encoder to the decoder).
- · Skip connections redesigned.
- · Deep supervision.
- Model pruning.



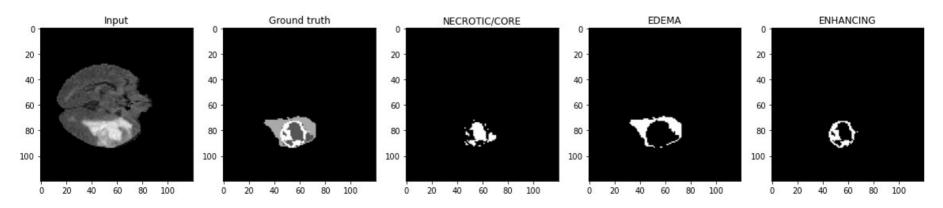
Data analysis



Four modes –Image flair, Image t1, Image t1ce and Image t2



One hot encoding



Summary of results

dataset	model	dice	training time	validation time
placenta	Unet	0.900	16.284	2.808
placenta	Unet+ +	0.915	13.814	2.228
BraTS	Unet	0.714	274.230	88.068
BraTS	Unet+ +	0.706	276.419	85.931

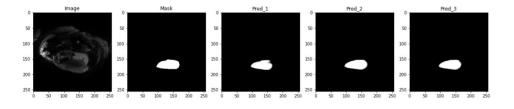
Model pruning results

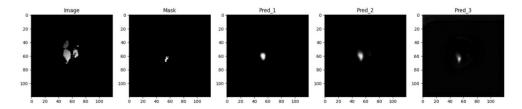
Placenta

pruning	parameters	dice	Inference time (seconds)
0	259,869	0.891	12.424
1	1,478,750	0.916	28.936
2	6,571,039	0.915	51.523

BraTS

pruning	parameters	dice	Inference time (seconds)
0	259,983	0.699	65.962
1	1,478,994	0.703	186.209
2	6,571,413	0.706	364.806





Comparison of results with previous studies

Source	DATA	DICE
(Alansary et al. 2016)	* Placenta MRI	0.72
(Looney et al. 2017)	* Placenta ultrasound	0.73
(Twickler et al. 2020)	* Placenta MRI	0.82
Unet 2020	Placenta MRI	0.87
Unet 2021	Placenta MRI	0.9
Unet++ 2021	Placenta MRI	0.92
(Henry et al. 2020)	BraTS	0.84
(Fidon, Ourselin, and Vercauteren 2021)	BraTS	84.8
Unet 2021	BraTS	0.71

Conclusion / areas of improvement / limitations

- u-net and u-net++ implemented with Python and Pytorch framework.
- Increasing the depth of the network, other data normalization technique, some regularization technique such as drop-out, data augmentation technique.
- Placenta data comes from just one clinical institution.
- Results obtained for the BraTS data set are quite limited computing capacity

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