Brain Tumour Segmentation with Incomplete Data

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Background & Aim

- Brain tumour segmentation is *difficult*
 - Imaging is very heterogenous
- Best imaged with MRI
 - 4 main structural sequences: FLAIR, T1-weighted, T2weighted, and contrast-enhanced T1-weighted sequences (T1CE).
- Current brain tumour segmentation research focuses solely on using deep learning models to automatically segment lesions when all four sequences are available.
 - But this 'perfect' and complete data is often rare in clinical practice.
 - For example, what about patients allergic to contrast, or those in renal failure who cannot receive it?
- Aim: How well do segmentation models perform with incomplete data?



T1CE



Method

- State-of-the-art tumour segmentation modelling based on nnU-Net¹
- Glioma population of 1251 patients
- All possible combinations of imaging modalities
 - Trained, and tested with five-fold cross-validation on the 2021 BraTS-RSNA dataset
 - 30 separate models

1. Isensee et al, Nature Methods, 2020



Results

- A) All models perform well
 - Close to current state-of-the-art
- B) Incremental gain with scanning time (TA) for additional sequences *is small*

A		One Sequence				Two Sequences						Three Sequences				Four Sequences		
Whole Tumor –	0.938	0.907	0.927	0.908	0.941	0.941	0.943	0.928	0.913	0.931	0.942	0.944	0.945	0.931	0.945		- 0.90	
Edema –	0.861	0.797	0.839	0.826	0.868	0.871	0.888	0.844	0.836	0.864	0.873	0.889	0.891	0.867	0.891		efficient efficient	
Enhancing Tumor –	0.764	0.756	0.759	0.874	0.784	0.783	0.875	0.774	0.877	0.875	0.79	0.875	0.877	0.877	0.876		C C 0.80 – 0.80 –	
Non-enhancing Tumor –	0.701	0.708	0.707	0.831	0.731	0.729	0.831	0.721	0.834	0.832	0.738	0.83	0.834	0.834	0.826		- 0.75	
B ≰-	1.77	3.1	1.52	3.1	4.87	3.28	4.87	4.62	6.2	4.62	6.38	7.97	6.38	7.72	9.48		- 7.5 (uiu) - 5.0 (Uiu) - 2.5 L	
C Whole Tumor – (0.531	0.293	0.611	0.293	0.193	0.287	0.194	0.201	0.147	0.202	0.148	0.119	0.148	0.121	0.0996		- 0.6 epin - 0.5	
Edema – (0.487	0.257	0.553	0.266	0.178	0.265	0.182	0.183	0.135	0.187	0.137	0.112	0.14	0.112	0.0939		ш бијис — 0.4 .iuc	
Enhancing Tumor –	0.432	0.244	0.501	0.282	0.161	0.238	0.18	0.168	0.141	0.19	0.124	0.11	0.137	0.114	0.0923		ber scal	
Non-enhancing Tumor – (0.397	0.228	0.466	0.268	0.15	0.222	0.171	0.156	0.134	0.18	0.116	0.104	0.131	0.108	0.0871		- 0.2 e O - 0 1	
FLA	$FLAIR T' T^{2} T1CE T' T1C$																	

Results

- Deep learning models without contrast-enhanced imaging (T1CE) available still accurately identify the enhancing tumour
- Moreover, their performance in doing so is close to models that do have it available.



Results

- Deep learning models without contrast-enhanced imaging (T1CE) available still accurately identify the enhancing tumour
- Near perfect prediction of enhancing tumour volume, despite no contrastenhanced imaging being provided to the model (R² range 0.953-0.976)



Conclusions

Acknowledgements

- Segmentation models can identify tumours with missing data
- Can be used in clinical situations where partial data is common.



Ground Truth



without Contrast



Inputs: FLAIR + T1 + T2

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