

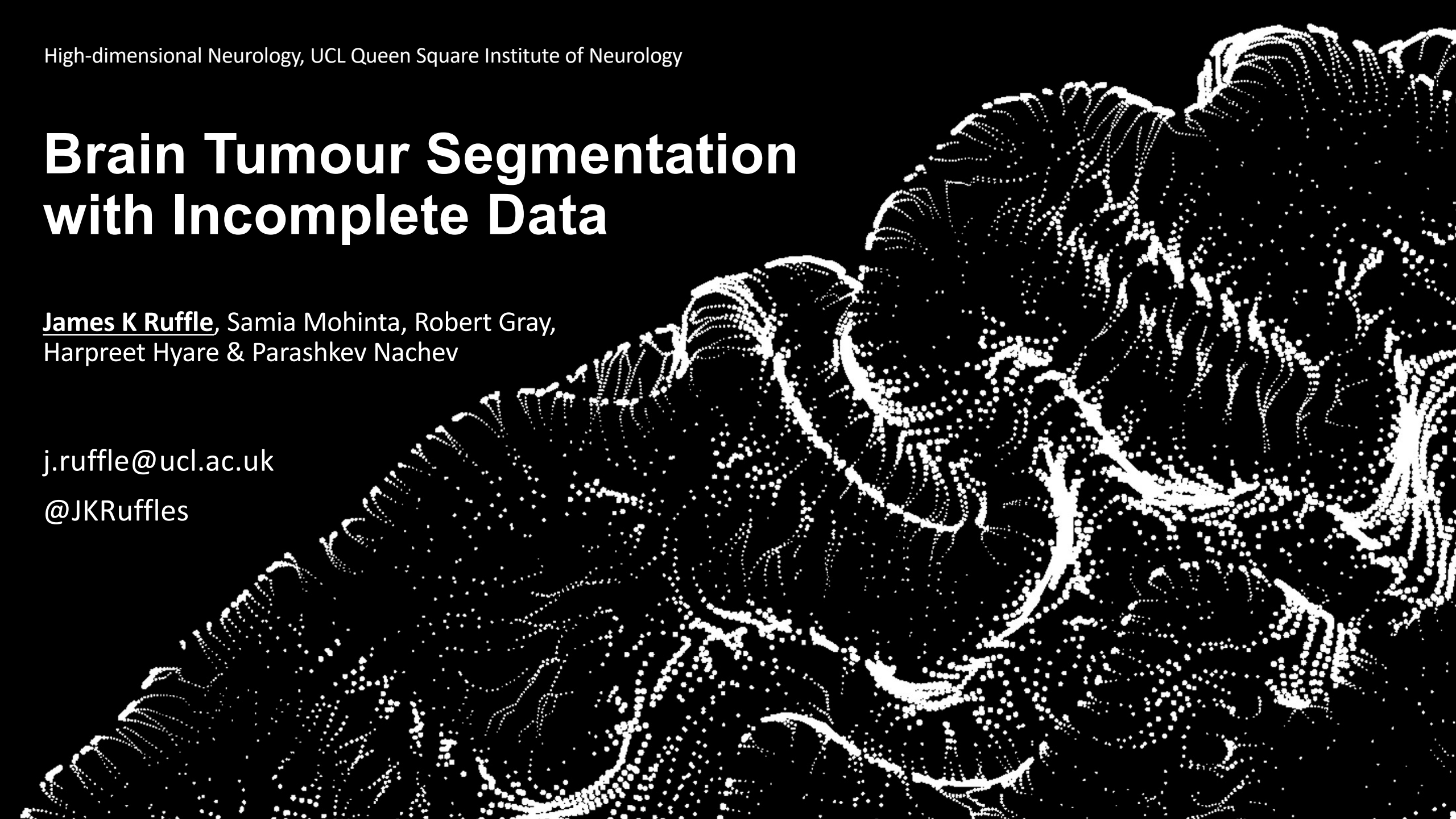
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Brain Tumour Segmentation with Incomplete Data

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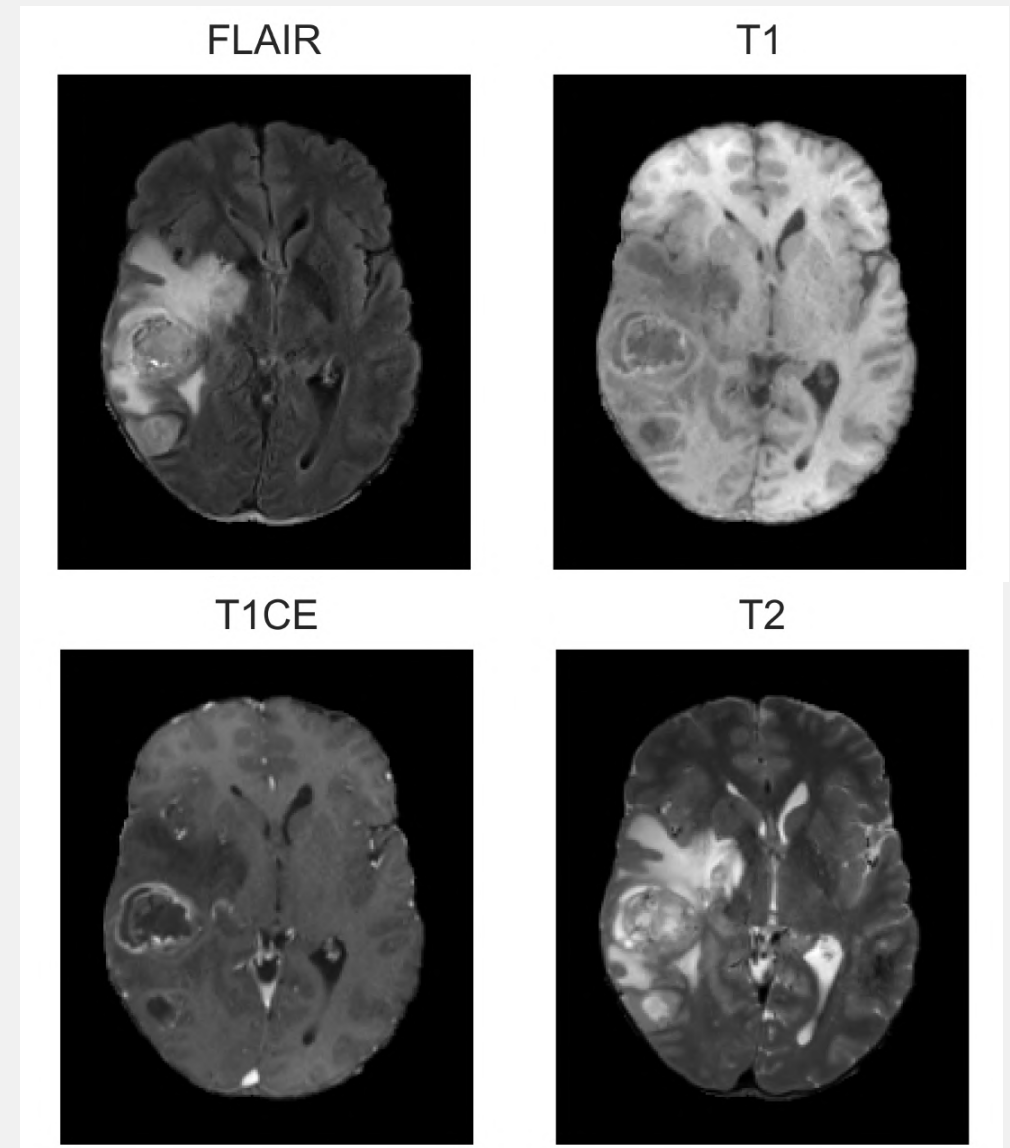
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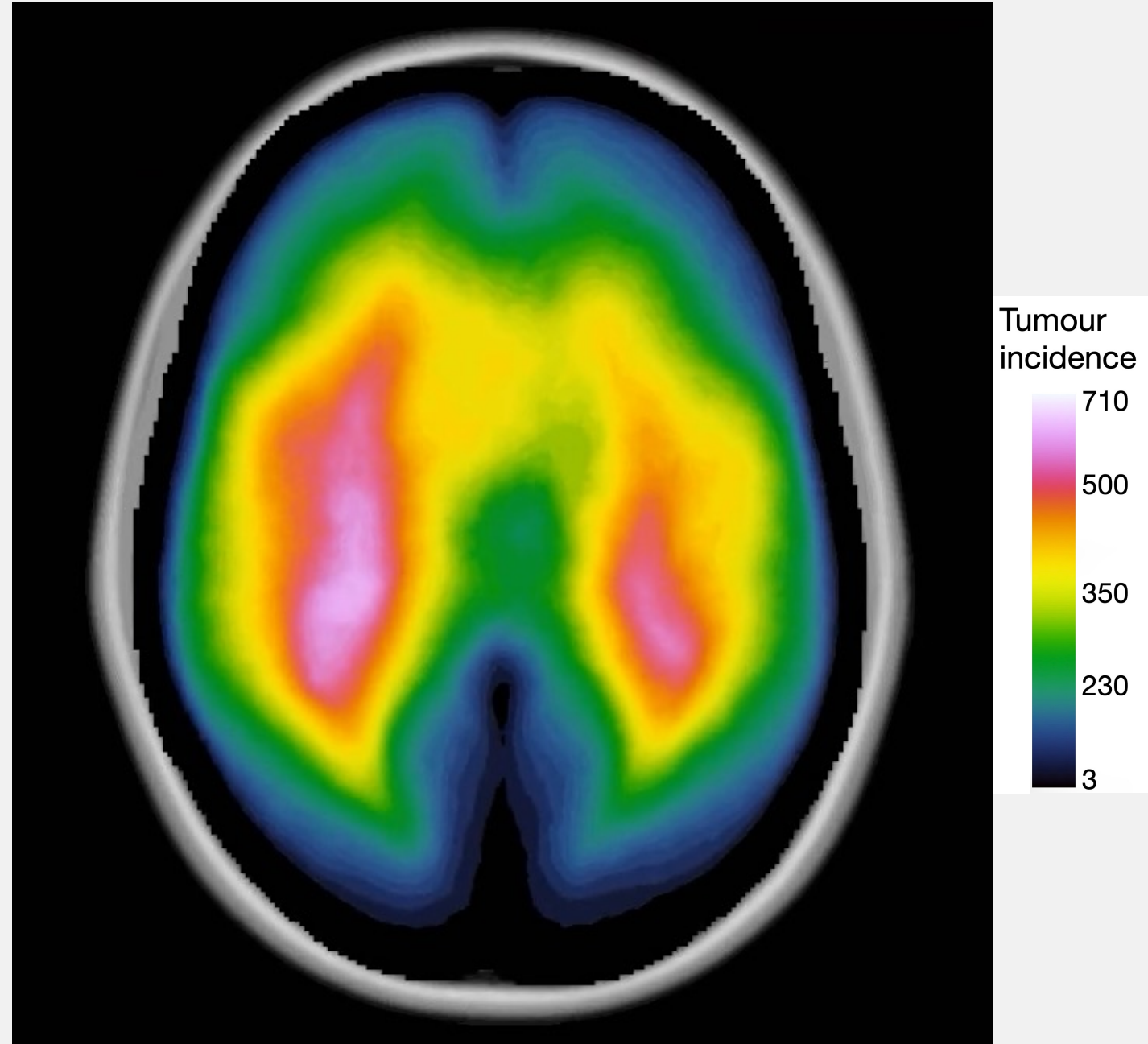
Background & Aim

- Brain tumour segmentation is *difficult*
 - Imaging is very heterogenous
- **Best imaged with MRI**
 - 4 main structural sequences: FLAIR, T1-weighted, T2-weighted, 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?



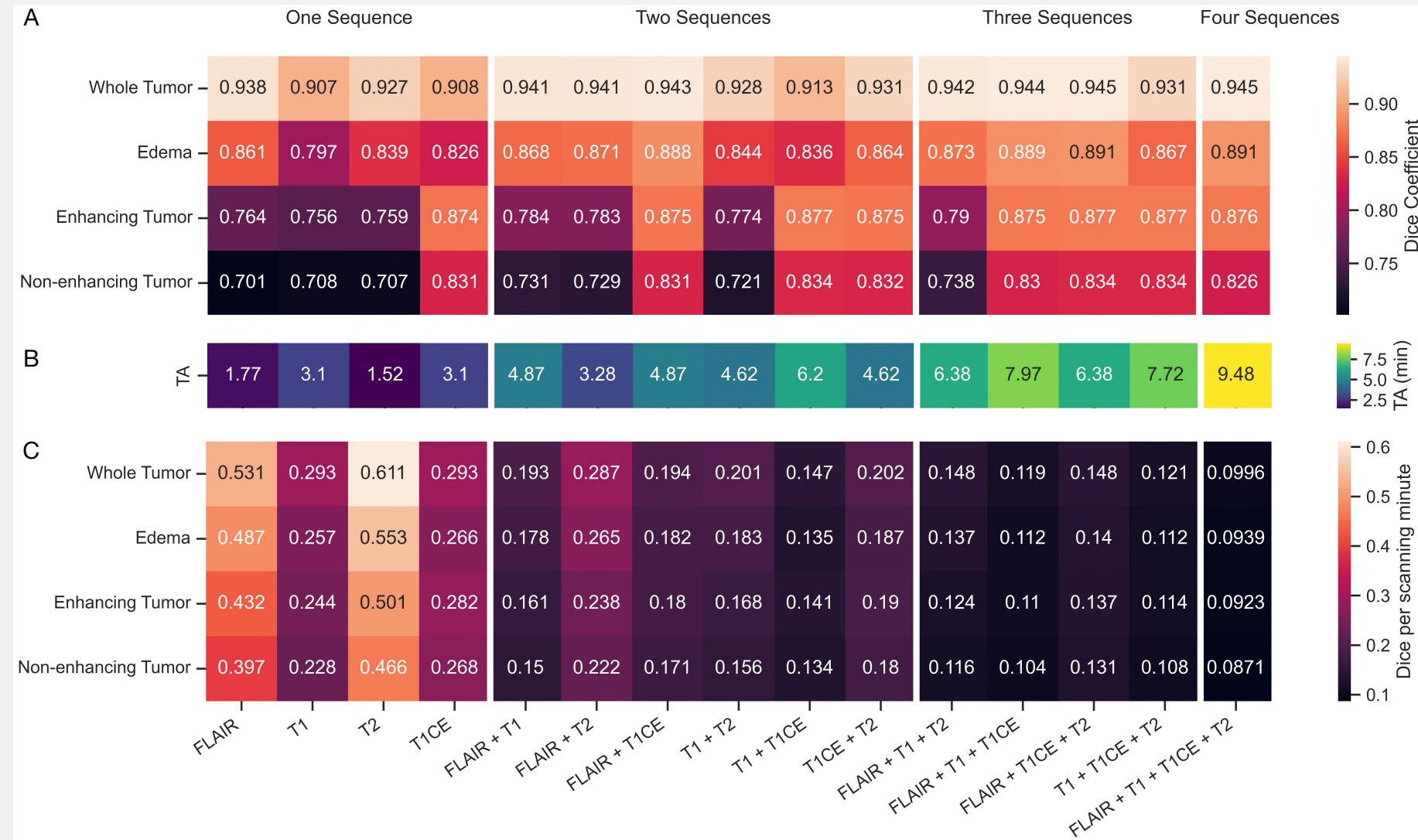
Method

- 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



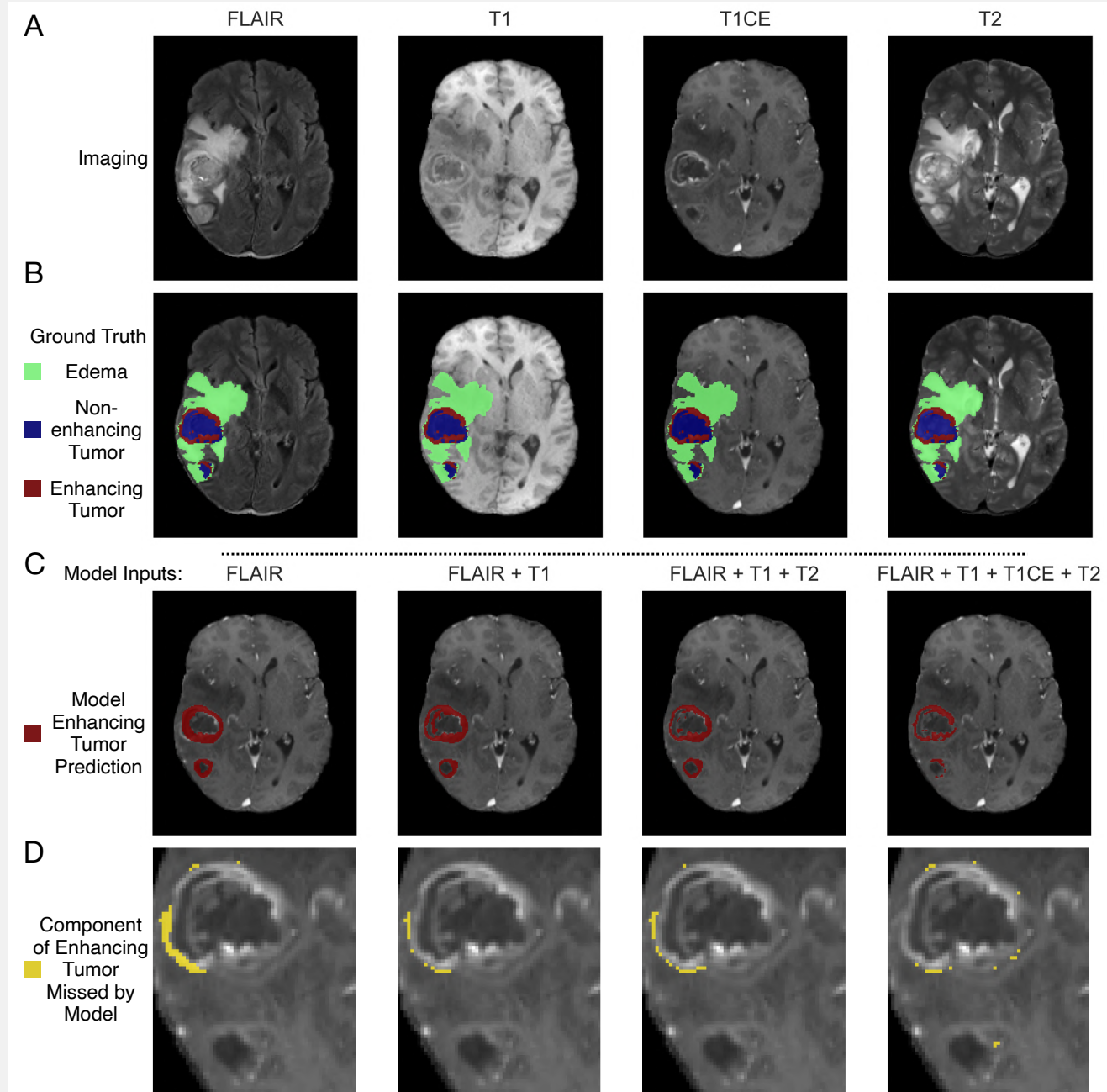
Results

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



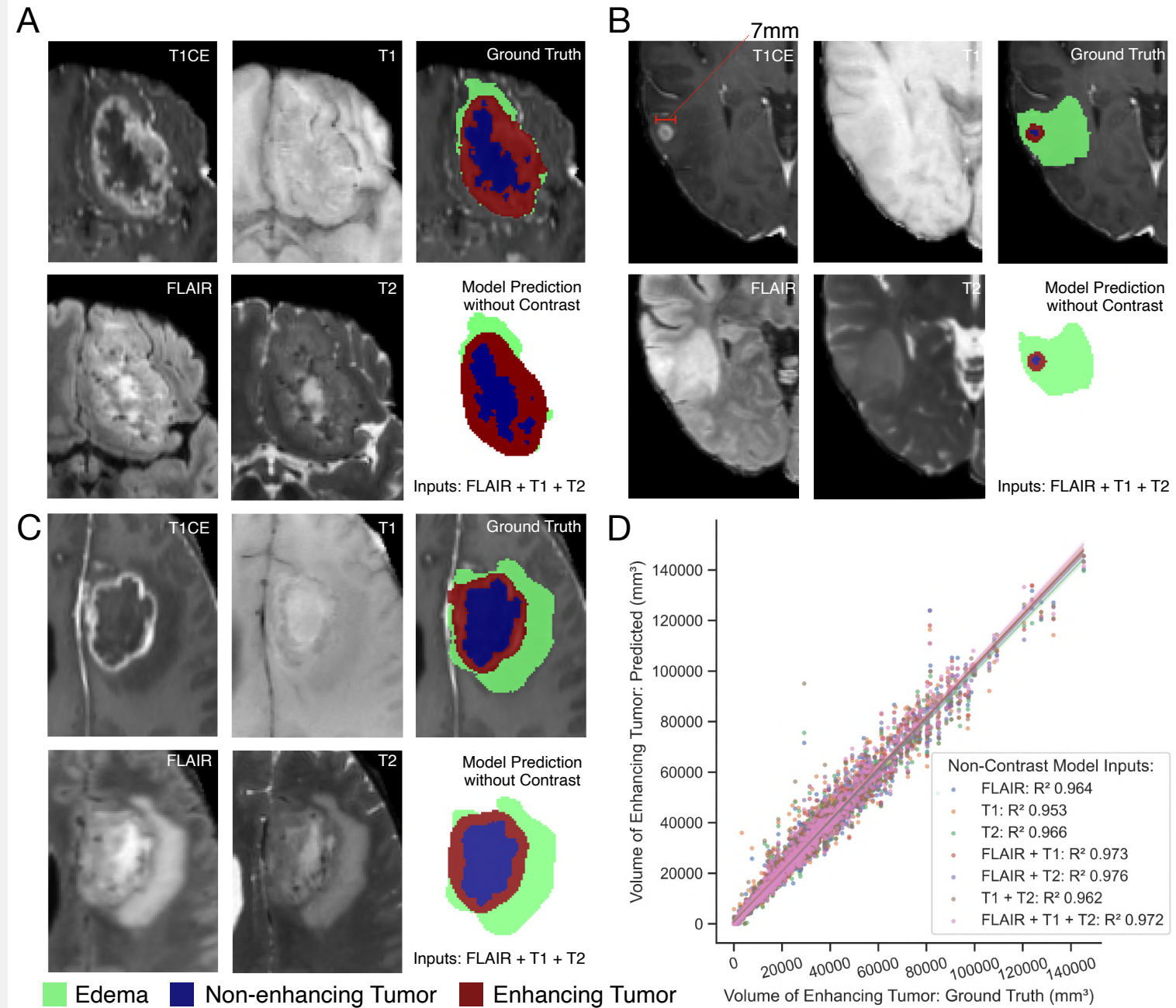
Results

- 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.



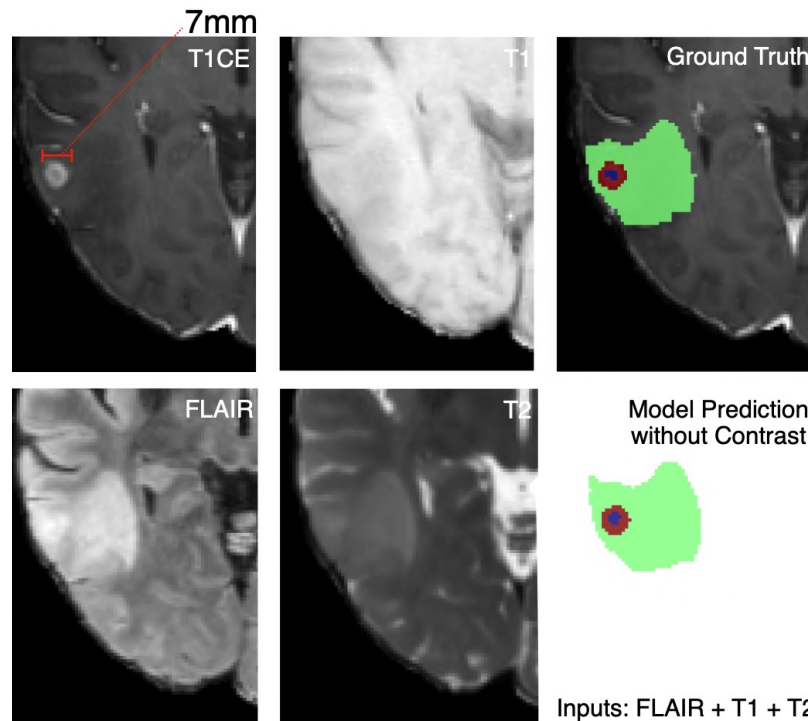
Results

- Deep learning models **without contrast-enhanced imaging (T1CE)** available still accurately identify the enhancing tumour
- Near perfect prediction of enhancing tumour volume, despite no contrast-enhanced imaging being provided to the model (R^2 range 0.953-0.976)



Conclusions

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



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