An Automated MRI Analysis Tool to Measure the Tumor Volume and Assess the Treatment Response for Glioblastoma

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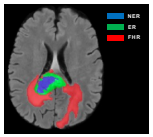
1. INTRODUCTION

- Glioblastoma (GBM) is the most common and aggressive grade IV glioma tumor[1].
- The median survival rate is up to **20.9 months** for patients enrolled in clinical trial[2].
- MRI is the most used imaging modality to identify the tumor's location, extent and aid in surgical planning.
- During surgery complete tumor removal is impossible due to tumor's irregular shape and could be infiltrate into adjacent brain tissue.
- Follow-up MRIs can measure residual tumor volume, detect tumor recurrence, and assess treatment effects.



Subregions of GBM:
Non-Enhancing Region (NER)- the center of the tumor and contains the dead cells.
Enhancing Region (ER)- contains a rim of growing tumor cells.
FLAIR Hyperintense Region (FHR)- the outer most part which contains the swelling or inflammation of tumor.

2. MOTIVATION

Challenges for accurate measurement of residual tumor volume in follow-up MRIs

- Tumors' irregularity and the presence of necrosis
- Presence of acute blood product within surgical bed
- Tumor recurrence can present as tiny lesions
- Correct diagnosis depends on individual experience and knowledge.
- Error-prone and time-consuming.

3. Aim

Utilize deep learning-based framework to

- Estimate the residual tumor volume considering the brain structural variations
- Assess the efficacy of the therapy utilizing imaging and clinical features
- Decrease variation and harmonize image interpretation
- Quantify the uncertainty in model's prediction.
- Provide a consistent and interpretable solution.

4. Dataset

- **419** pre-surgical and **310** follow-up segmented MRIs
- Four MRI modalities- T1, T1+Gd, T2, T2-FLAIR
- T1 and T1+Gd are necessary for enhancement and non-enhancement region prediction
- T2 and T2-FLAIR are important to predict flair hyperintense region
- The segmentation labels encompass FLAIR hyperintense region, contrast-enhancing tumor, and non-enhancing core.

5. METHODS

Image Preprocessing

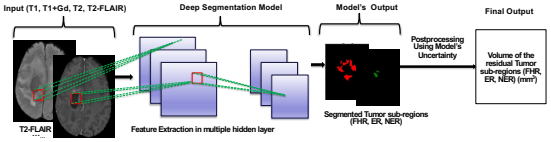
- Skull-stripping
- Registration
- Bias Correction

Encoder-Decoder based Model Development using Follow-up MRIs

- Encoder utilizes contrastive learning schemes to identify tumor location and shape
- Decoder's Bayesian layer quantifies the uncertainty in model's prediction

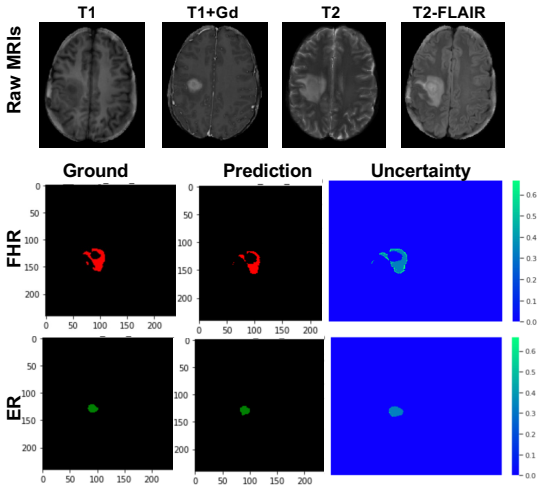
Post Processing

- Several image analysis method utilized to improve the prediction considering the model's uncertainty
- The volume of residual tumor sub-regions was calculated



6. RESULTS

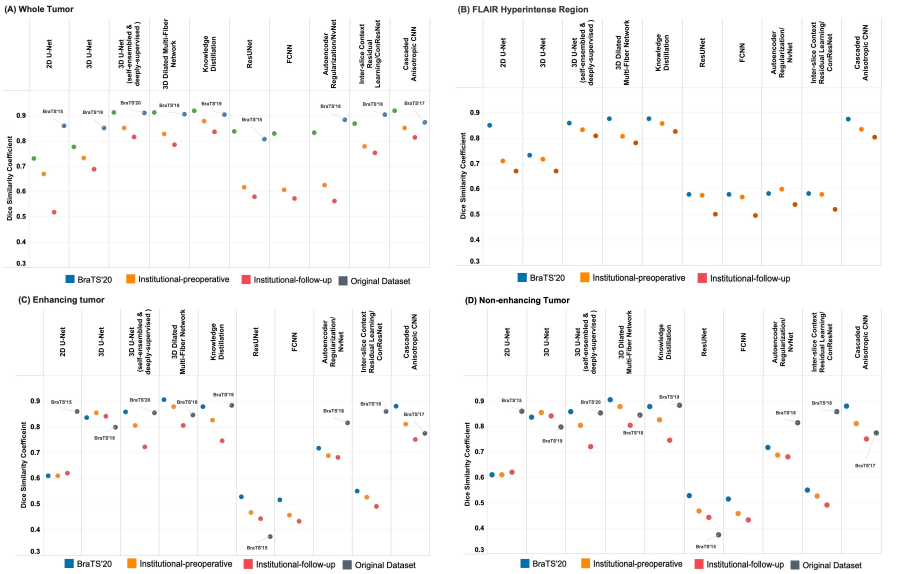
1. Segmentation Model Performance: The average dice similarity coefficient for FHR is 0.85 and ER is 0.88.



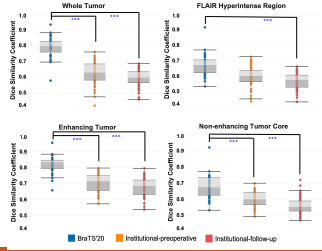
6. RESULTS

2. The state-of-the-art AI segmentation models trained on pre-surgery MRIs suffer from a 3-20% performance drop on follow-up MRIs for segmenting tumor subregions.

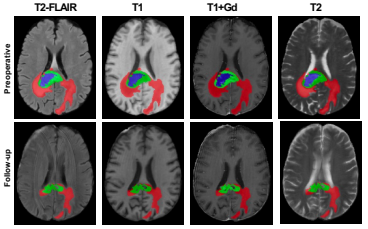
State-of-the-art Model Performance on Follow-up MRIs



3. A significant drop in generalizability and consistency on independent MRIs (*p-value<0.05*)



4. The similarity between the preoperative and follow-up MRIs drop by 20% due to morphological differences of brain and tumor.



7. CONCLUSION

- The first fully interpretable model for segmenting tumor sub-regions using follow-up MRIs.
- The proposed model demonstrated high accuracy and reliability.
- Identified a significant generalization gap between deep learning models in tumor segmentation for preoperative and follow-up images.
- The proposed framework has a significant applicability in clinical assessment for GBM patients.

9. REFERENCES

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8. ACKNOWLEDGEMENTS

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