

Automated MRI Based Pipeline for Glioma Segmentation and Prediction of Grade, IDH Mutation and 1p19q Co-deletion

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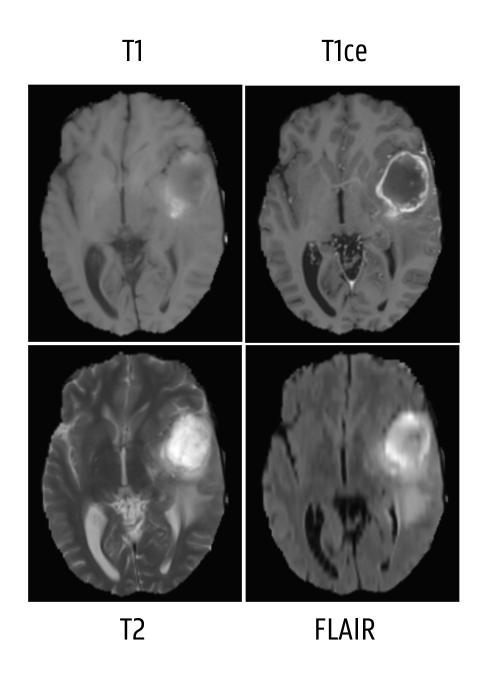




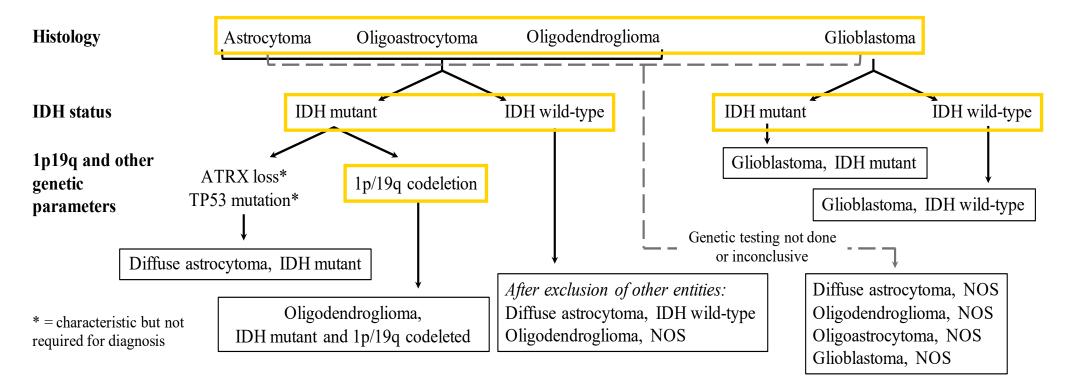




Motivation



WHO classification of glioma¹:

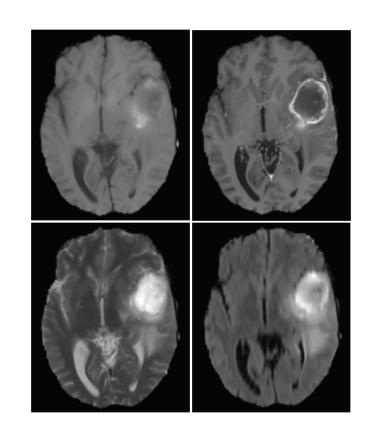


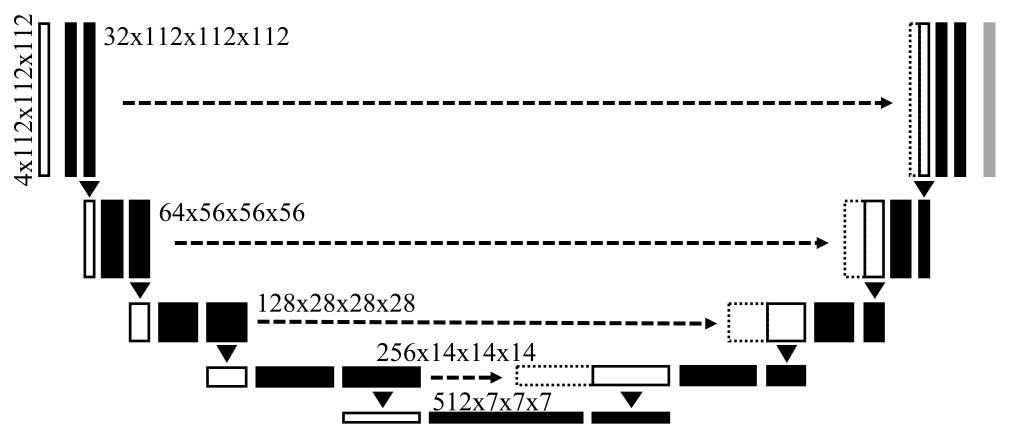
- WHO Grade, IDH mutation and 1p19q co-deletion are important markers for optimal therapy planning and prognosis
- Biopsies involve risks and negatively impact overall survival
 - → Need for non-invasive, accurate and automatic CAD systems

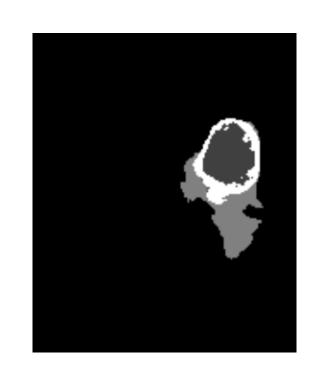


Segmentation









■ 3x3x3 Conv - IN - LReLU ▼ 2x2x2 Encoding: MaxPool Decoding: Trilinear Upsampling ■ 1x1x1 Conv - SoftMax

Data:

Training: BraTS 2019 Training set (335)

Test: BraTS 2019 Validation set (125)

(online evaluation platform¹)

Increased robustness to missing modalities through input channel dropout

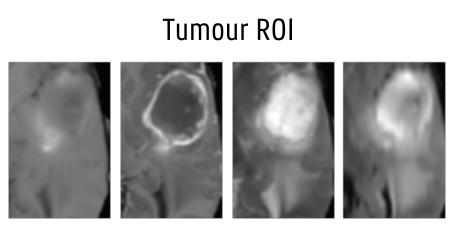
Available modalities	Dice Score			
	ET	WT	TC	
T1, T1ce, T2, FLAIR	75.7	89.8	83.2	
T1ce, FLAIR	74.4	89.4	82.7	
T1ce, T2	74.1	87.0	82.2	



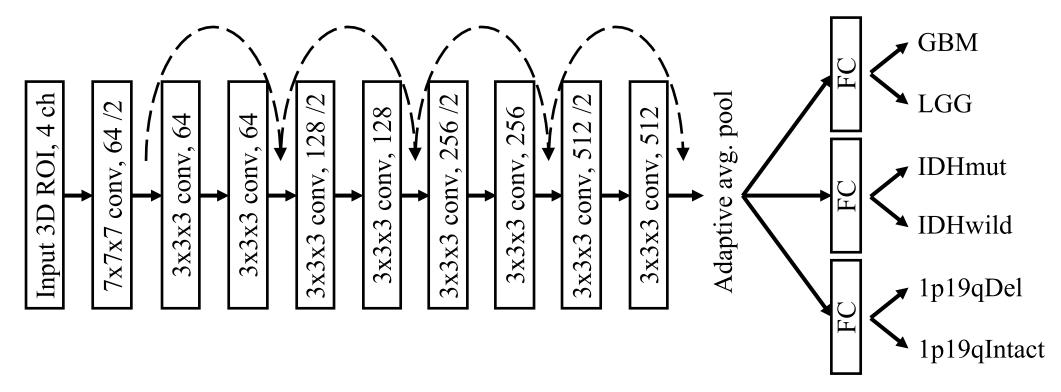
¹https://ipp.cbica.upenn.edu

Multi-task Glioma Classification









Public Data:

- TCIA: TCGA-GBM | TCGA-LGG | 1p19qDeletion BraTS 2019 (not already included in TCGA)
- 628 patients
- At least preoperative T1ce + T2 and/or FLAIR

	Training	Validation	Test
Glioblastoma	264	27	46
Lower-grade	194	43	54
IDH mutant	123	41	48
IDH wildtype	87	29	52
1p19q co-deleted	83	20	30
1p19q Intact	100	23	24
Total	458	70	100

Multi-task learning:

- + Reduce overfitting
- + Handle missing labels
 - → Train one network on all data



Results

TCIA Test set	AUC	Acc.	Sens.	Spec.
GBM vs. LGG	93.3	90.0	93.5	87.0
IDH mutation	94.0	89.0	89.6	88.5
1p19q co-deletion	82.1	83.3	86.7	79.2

GUH	AUC	Acc.	Sens.	Spec.
GBM vs. LGG	94.0	90.0	90.1	89.8
IDH mutation	86.2	75.6	84.4	70.4
1p19q co-deletion	86.6	75.0	58.3	82.1

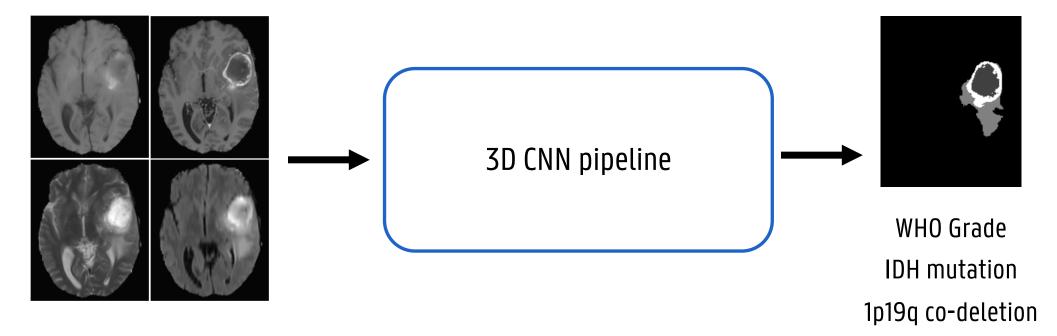


Independent Test Data Ghent University Hospital (GUH):

- 61 GBM + 49 LGG
- 32 IDH mutant + 54 IDH wildtype
- 12 1p19q co-deleted + 28 1p19q Intact
 IDH status assessed through immunohistochemistry

→ lower sensitivity compared to gene sequencing

→ lower specificity of network



- Non-invasive
- Accurate
- Fully automatic
- Robust to variations in imaging protocols and missing modalities
- Based on routine pre-therapy MRI

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