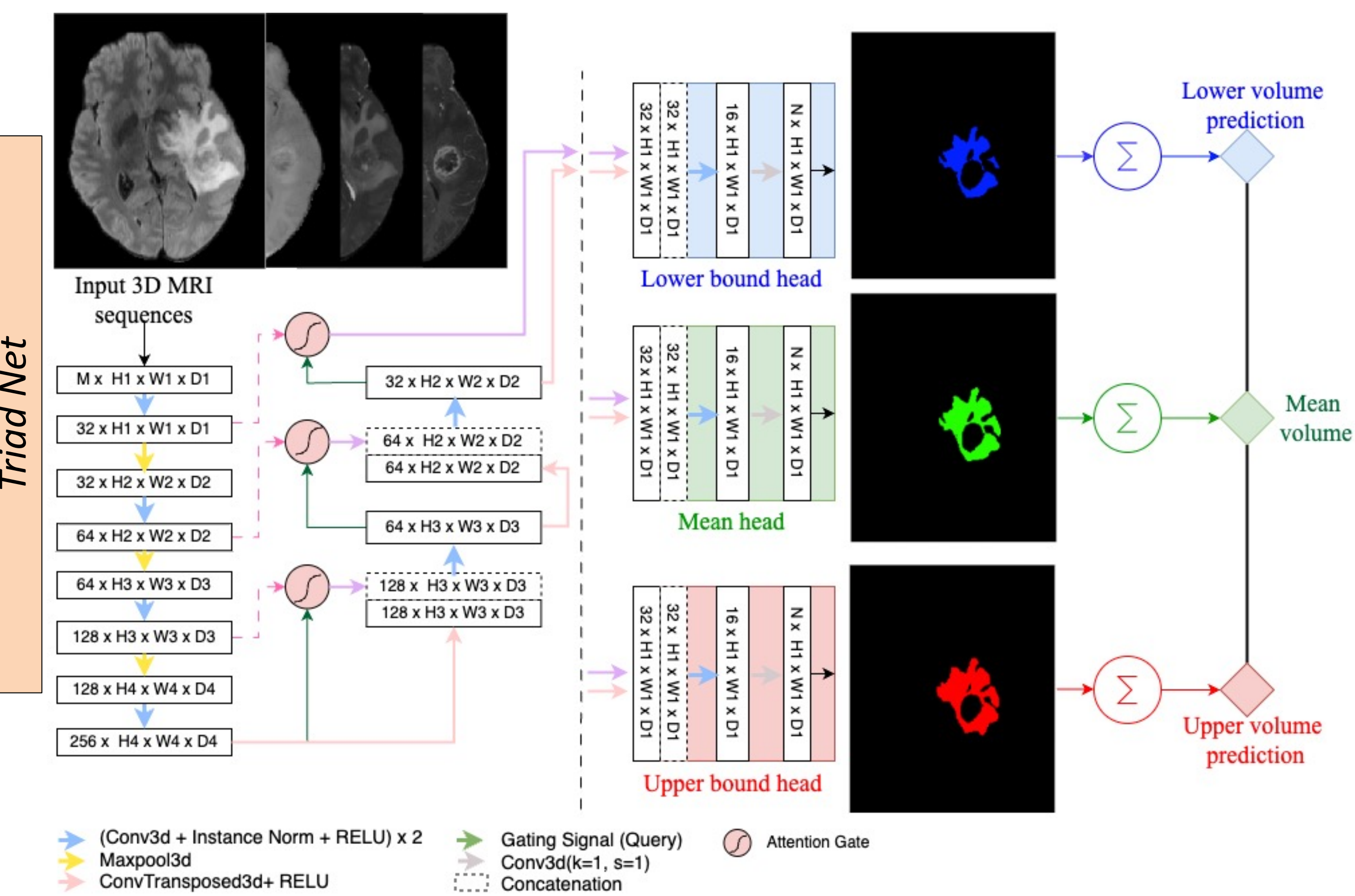


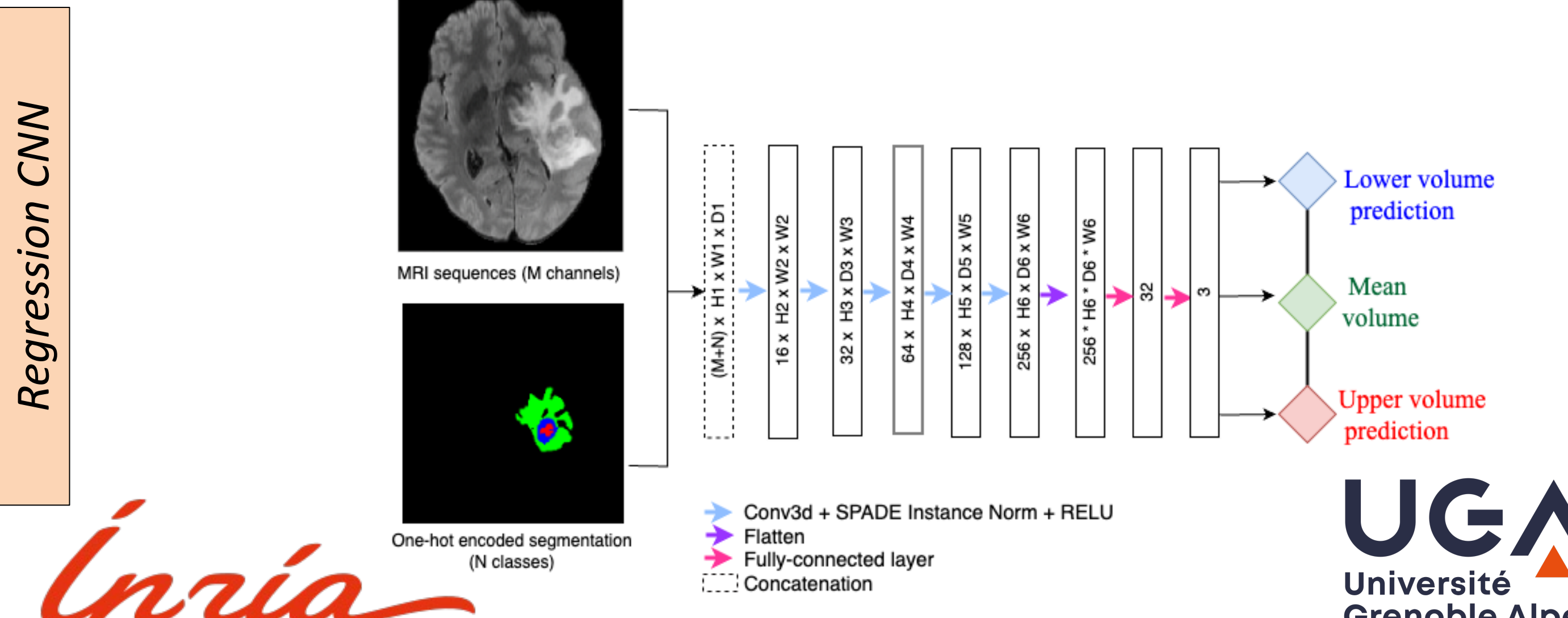
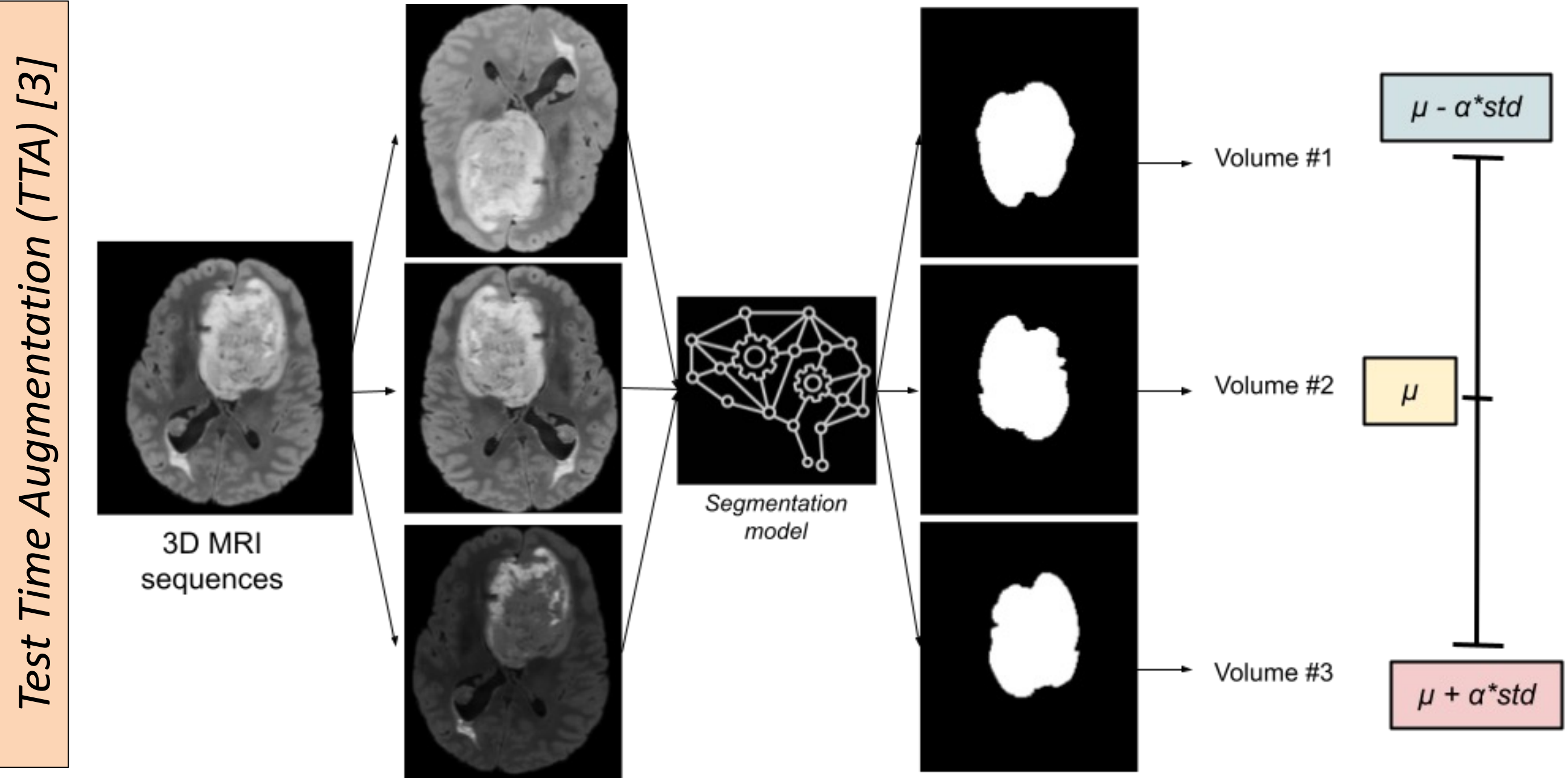
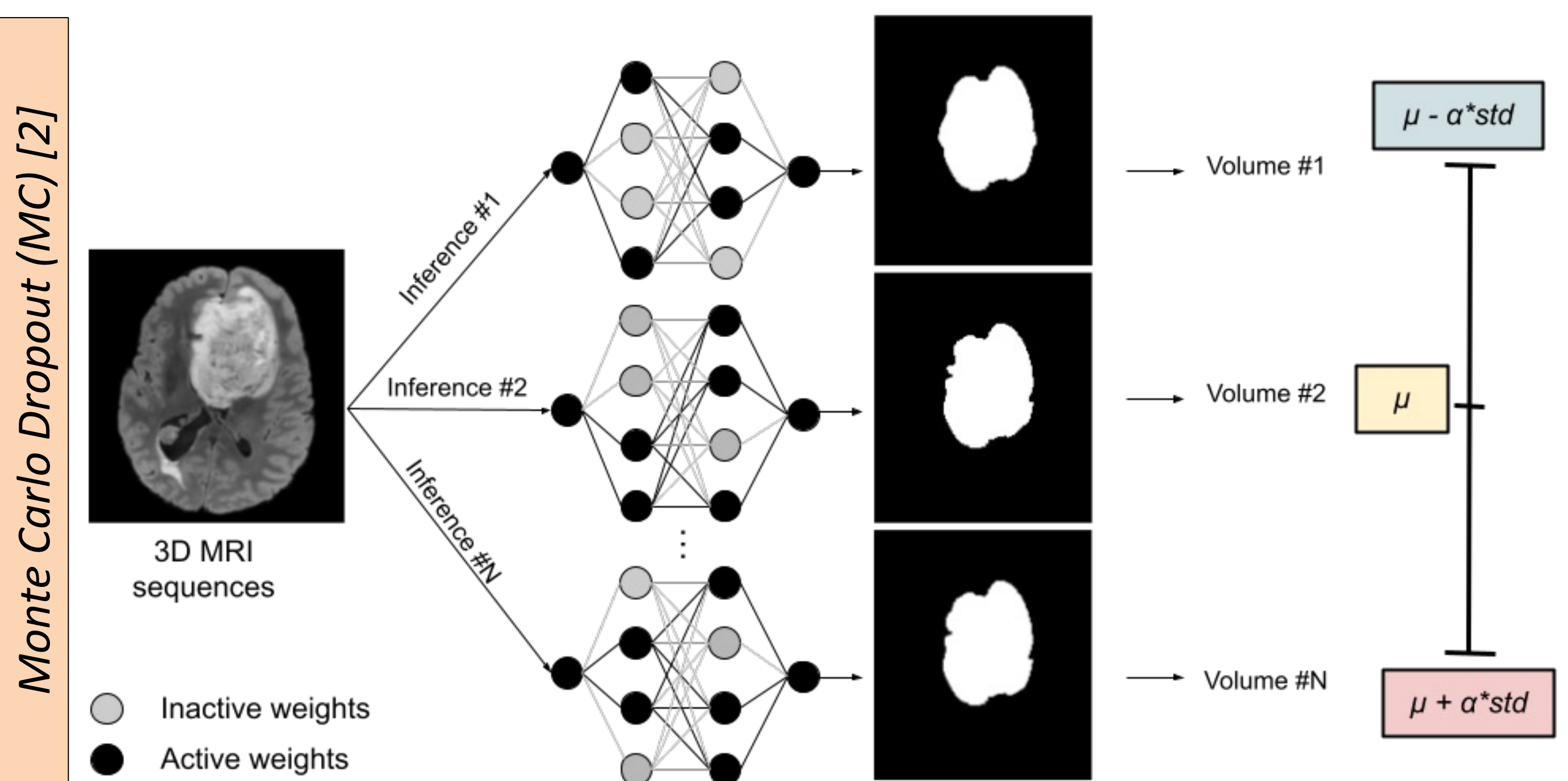
Motivation

The segmentation of medical images allows the extraction of high-level metrics such as the volume of a lesion. However, these estimations are rarely equipped with **predictive intervals**, which limits the reliability of the algorithm. In this work, we propose a novel segmentation model, **Triad Net**, allowing to obtain the segmentation and predictive intervals associated to volumes, in **less than 1 second**. The advantages of our approach are demonstrated on a brain tumor segmentation task.

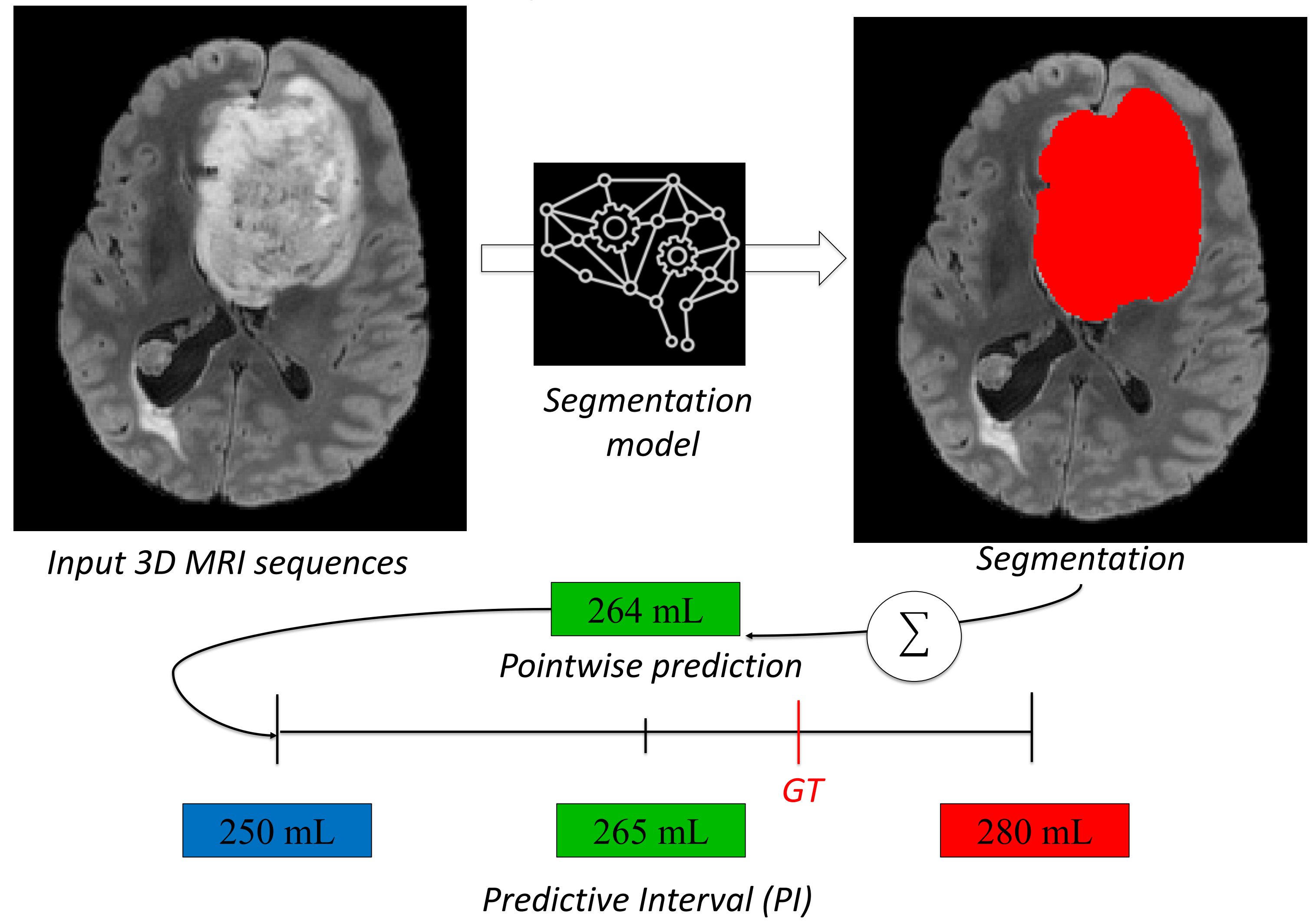


TriadNet in 3 key points

- ★ The segmentation architecture is modified by copying the output block **3 times**
- ★ TriadNet predicts **3 different masks**: one for the lower bound, one for the mean value, and one for the upper bound.
- ★ To learn to generate these 3 masks, we leverage the penalties (α , β) applied to False Positives (FP) and False Negatives (FN) in the Tversky loss [1]:

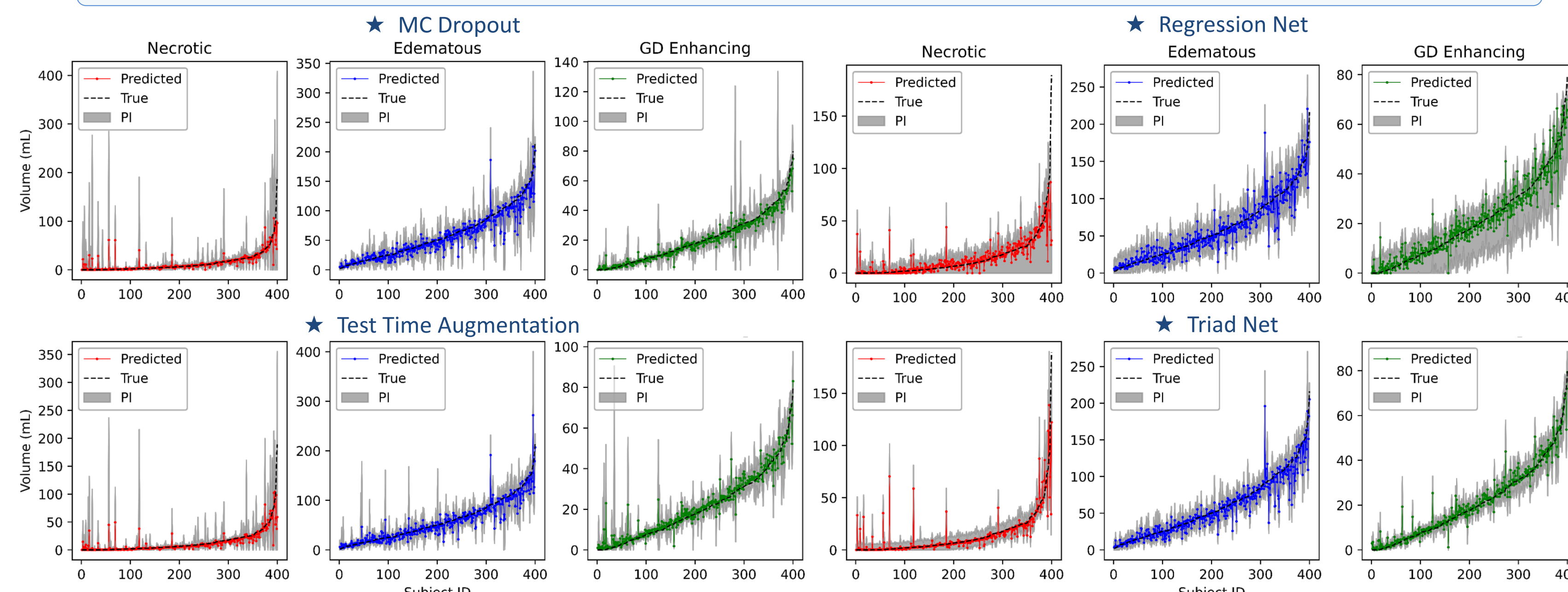


What is the volume of the lesion ? Can we associate a predictive interval with it ?



Material & Methods

- ★ We focus on **90%** predictive intervals.
- ★ The study is based on the BraTS 2021 dataset [4] for tumor segmentation in brain MRI (N=1251)
 - 651 for training, 200 for validation/calibration, 400 for testing
- ★ 4 input sequences: T1w, T2w, FLAIR, T1ce and 3 classes: necrotic part, enhancing tumor, edematous
- ★ **Evaluation** : the quality of the segmentation is assessed using the Dice score, and the precision of the volume estimation is assessed using the Mean Average Error (MAE). The quality of PIs is estimated with 2 metrics: the average interval width (W) and the empirical coverage (f).



Necrotic part	Dice	MAE (mL)	f (%)	W (mL)	Edematous	Dice	MAE (mL)	f (%)	W (mL)	GD Enhancing	Dice	MAE (mL)	f (%)	W (mL)
MC	0.76	3.2	95.6	20.6	MC	0.84	7.5	90.0	31.8	MC	0.85	1.9	93.5	10
TTA	0.76	3.5	96.3	25.0	TTA	0.85	7.7	91.3	34.9	TTA	0.85	2.0	93.0	10.6
RegCNN	0.76	6.3	96.1	25.8	RegCNN	0.85	9.2	91.7	41.9	RegCNN	0.85	3.2	90.7	22.2
TriadNet	0.76	3.2	93.4	13.7	TriadNet	0.85	7.2	91.6	30.2	TriadNet	0.85	1.8	94.2	8.9

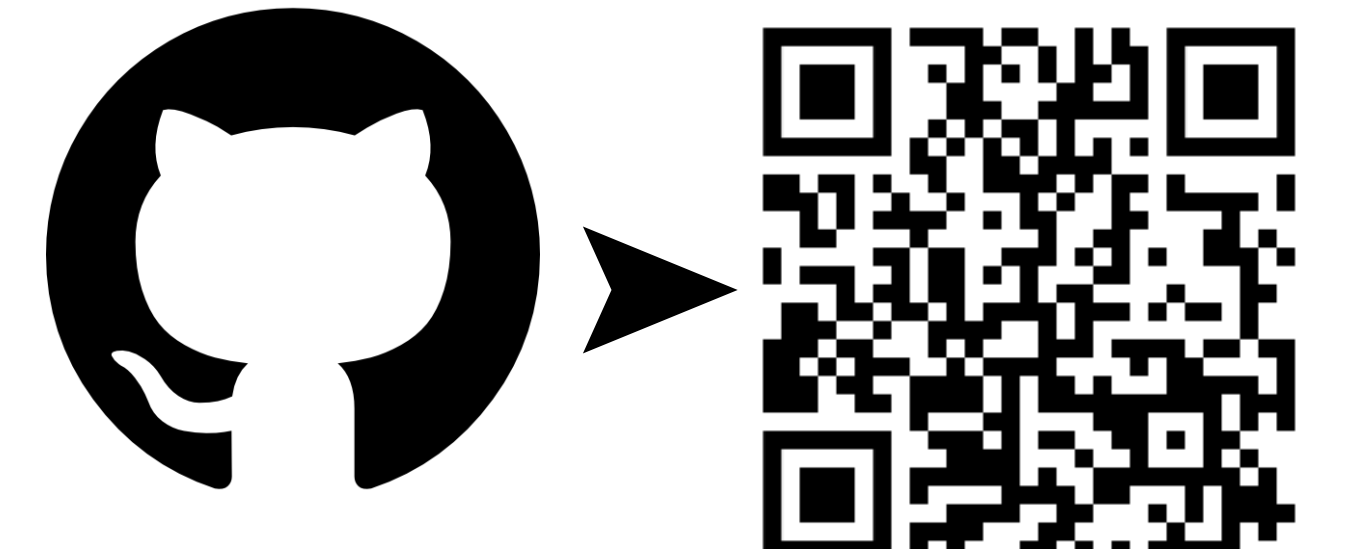
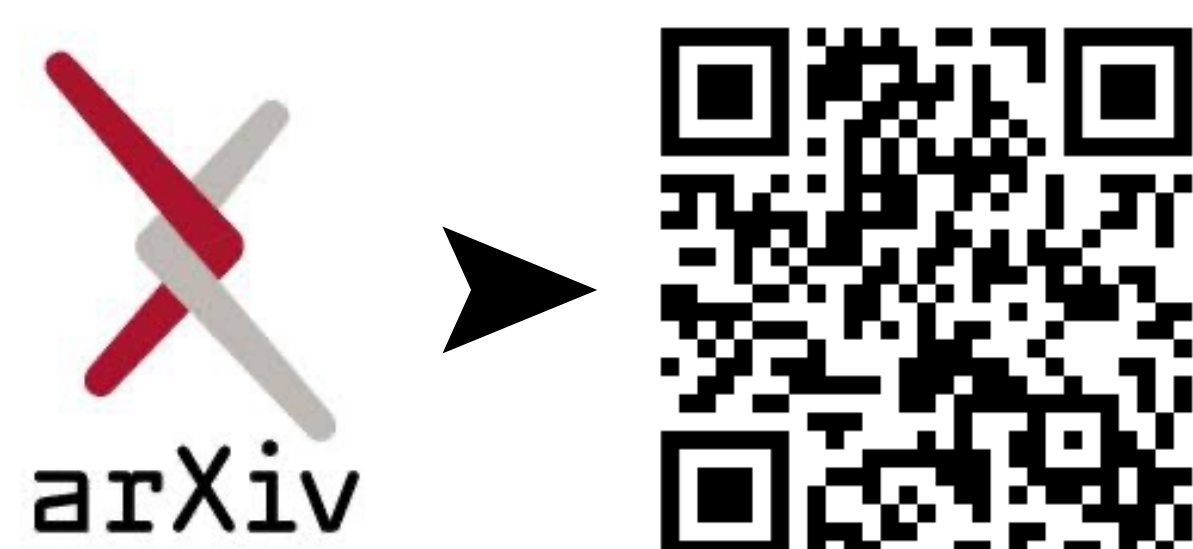
Table 1 : Metrics and inference time averaged over 5 runs

Results and Conclusion

- ★ PIs computed by Triad Net are **narrower** and thus **more informative** than other approaches
- ★ The computation is **much faster** (10x faster than MC dropout, 30x faster than TTA)
- ★ It only requires a slight modification of the segmentation architecture to make-it multi-head

Paper on arXiv

Project GitHub



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