Paper #93

AUTOMATIC SEGMENTATION OF BRAIN TUMOR PARTS FROM MRI DATA USING A RANDOM FOREST CLASSIFIER

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Motivation

- Why detect brain tumor?
  - 100k++ people die of brain tumor yearly
  - Early detection helps the survival

- Why is it useful?
  - There are not enough human experts
  - Automatic segmentation of brain tumor helps the diagnosis
  - Automatic segmentation of tumor parts helps therapy planning
  - Also useful in follow-up studies after intervention

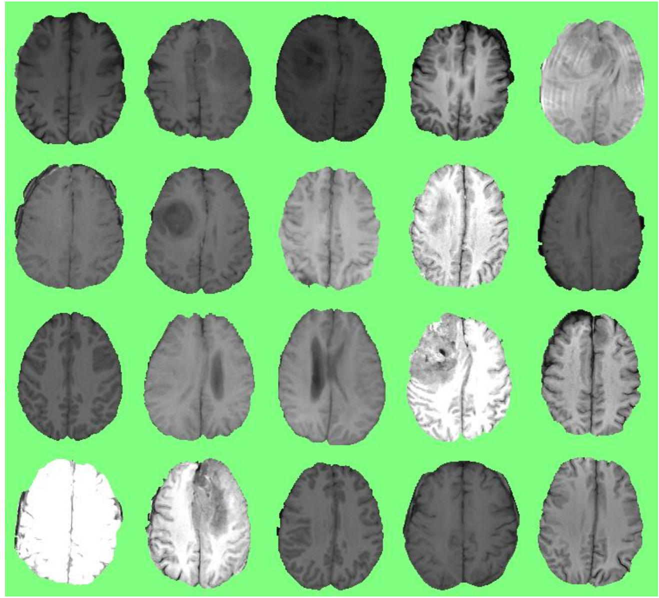
- Random forest approach

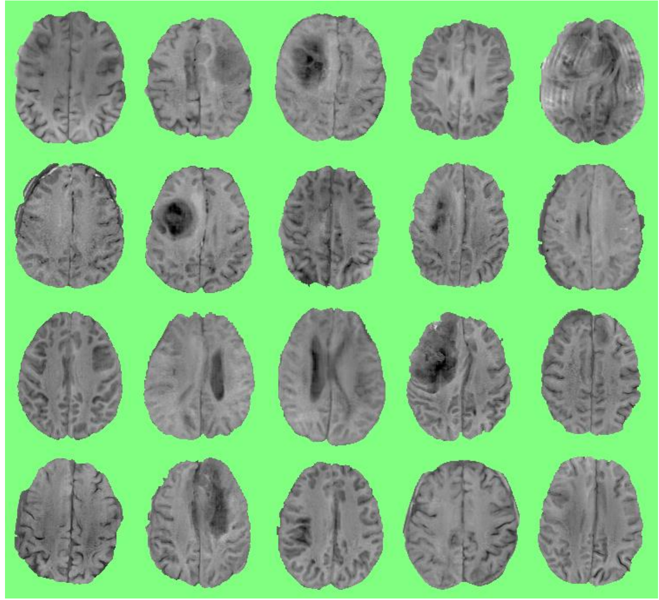
Input Data

- Medical Image Computation and Computer Aided Interventions (MICCAI)
- Brain Tumor Segmentation Challenge (BraTS) since 2012
- BraTS train dataset 2015
  - 54 low-grade (LG) and 220 high-grade (HG) volumes
- Multispectral (T1, T2, T1C, FLAIR)
- 155 x 240 x 240 image volxels
- Ground truth (GT): negative, enhancing core, tumor core, edema
- Skull removed
- This study uses the HG volumes only, because LG contains no enhancing core

Difficulties

- Tumors have a great variety in
  - Size
  - Shape
  - Appearance
- Histograms need normalization
- Intensity inhomogeneity





Proposed Procedure

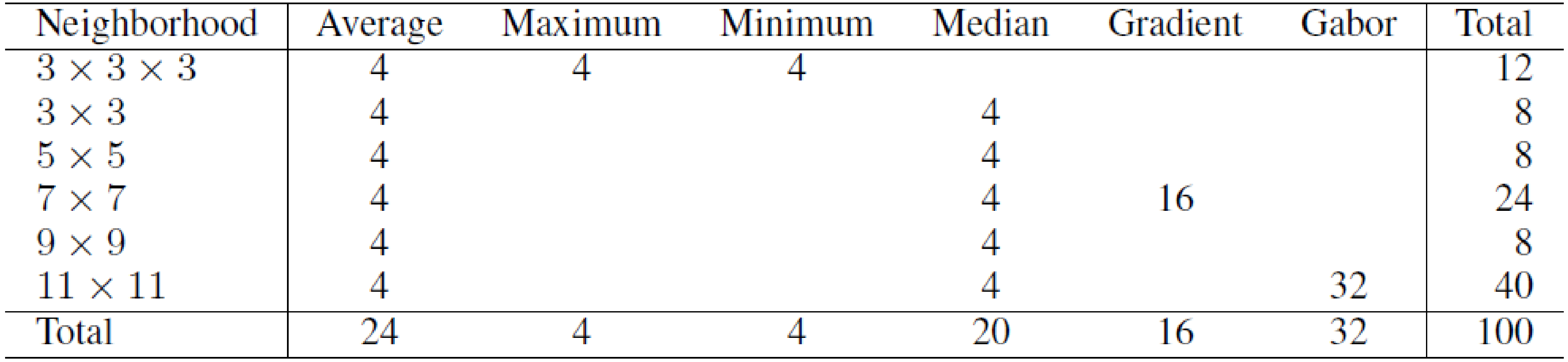
- Preprocessing
  - Histogram normalization
  - Feature generation
- Classification
  - Random forest
    - Four classes according to BraTS ground truth
  - No post processing, this time we are interested in the accuracy of the classifier
- Statistical evaluation
  - Accuracy indicators for whole tumor, enhancing core, tumor core, edema

Preprocessing

- Histogram normalization
  - Widely used method of Nyúl et al, works with a batch of MRI records
    - Aligns all histograms to the same milestones that have averaged positions
  - Our solution: context dependent linear transform
    - The 25 and 75 percentile values are transformed to some predefined constants
    - Coefficients of transform extracted from these two fixed point
    - Transform applied to all pixel intensities
    - New values cut at both limits of the predefined target interval

Feature generation

- 4 observed features (T1, T2, T1C, FLAIR)
- 4 x 25 = 100 computed features



Neighborhood	Average	Maximum	Minimum	Median	Gradient	Gabor	Total
$3 \times 3 \times 3$	4	4	4				12
3×3	4			4			8
5×5	4			4			8
7×7	4			4	16		24
9×9	4			4			8
11×11	4			4		32	40
Total	24	4	4	20	16	32	100

Random forest

- Python Scikit package
- Classification of individual pixels, 104 features
  - 4 classes according to ground truth
- Number of trees: 150
- Maximum depth: 18
- Train data size
  - 10k pixels from each train volume
- Half of the volumes used as train data, the other half as test data
  - These two halves took turns

Measuring accuracy

- Ground truth of record *i*: set of positives $\Gamma_i^{(\pi)}$ and set of negatives $\Gamma_i^{(\nu)}$
- Segmentation result of record *i*: set of positives $\Lambda_i^{(\pi)}$ and set of negatives $\Lambda_i^{(\nu)}$
- Accuracy indicators for each record
  - Sensitivity (true positive rate, TPR)
  - Specificity (true negative rate, TNR)
  - Dice score (DS)
  - Accuracy (ACC)

$$\mathrm{TPR}_i = \frac{|\Gamma_i^{(\pi)} \cap \Lambda_i^{(\pi)}|}{|\Gamma_i^{(\pi)}|} \qquad \mathrm{TNR}_i = \frac{|\Gamma_i^{(\nu)} \cap \Lambda_i^{(\nu)}|}{|\Gamma_i^{(\nu)}|}$$

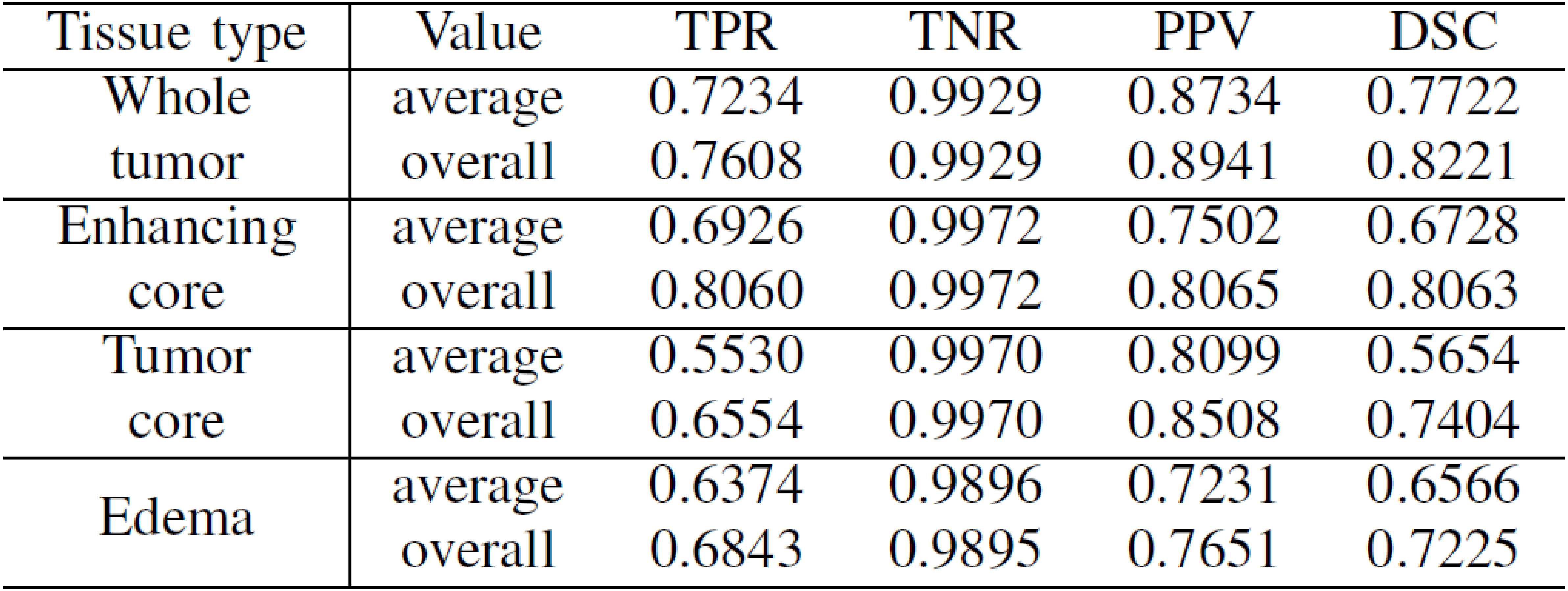
$$\mathrm{DS}_i = \frac{2 \times |\Gamma_i^{(\pi)} \cap \Lambda_i^{(\pi)}|}{|\Gamma_i^{(\pi)}| + |\Lambda_i^{(\pi)}|}$$

$$\mathrm{ACC}_i = \frac{|\Gamma_i^{(\pi)} \cap \Lambda_i^{(\pi)}| + |\Gamma_i^{(\nu)} \cap \Lambda_i^{(\nu)}|}{|\Gamma_i^{(\pi)}| + |\Gamma_i^{(\nu)}|}$$

- Average of individual values
- Overall Dice score

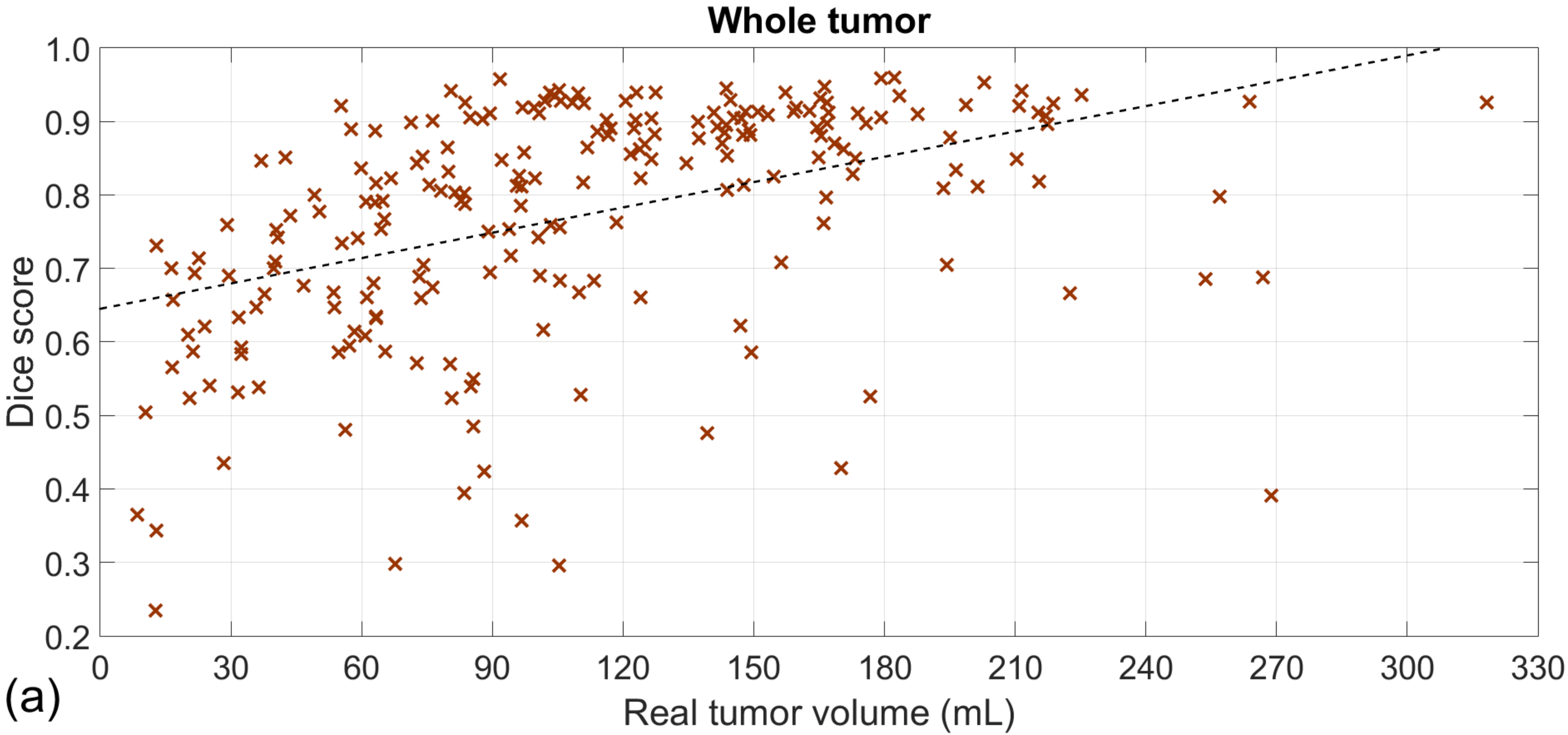
$$\widetilde{\mathrm{DS}} = \frac{2 \times \left| \bigcup_{i=1}^{n_V} \Gamma_i^{(\pi)} \cap \bigcup_{i=1}^{n_V} \Lambda_i^{(\pi)} \right|}{\left| \bigcup_{i=1}^{n_V} \Gamma_i^{(\pi)} \right| + \left| \bigcup_{i=1}^{n_V} \Lambda_i^{(\pi)} \right|}$$

Global accuracy indicators for various tissue types

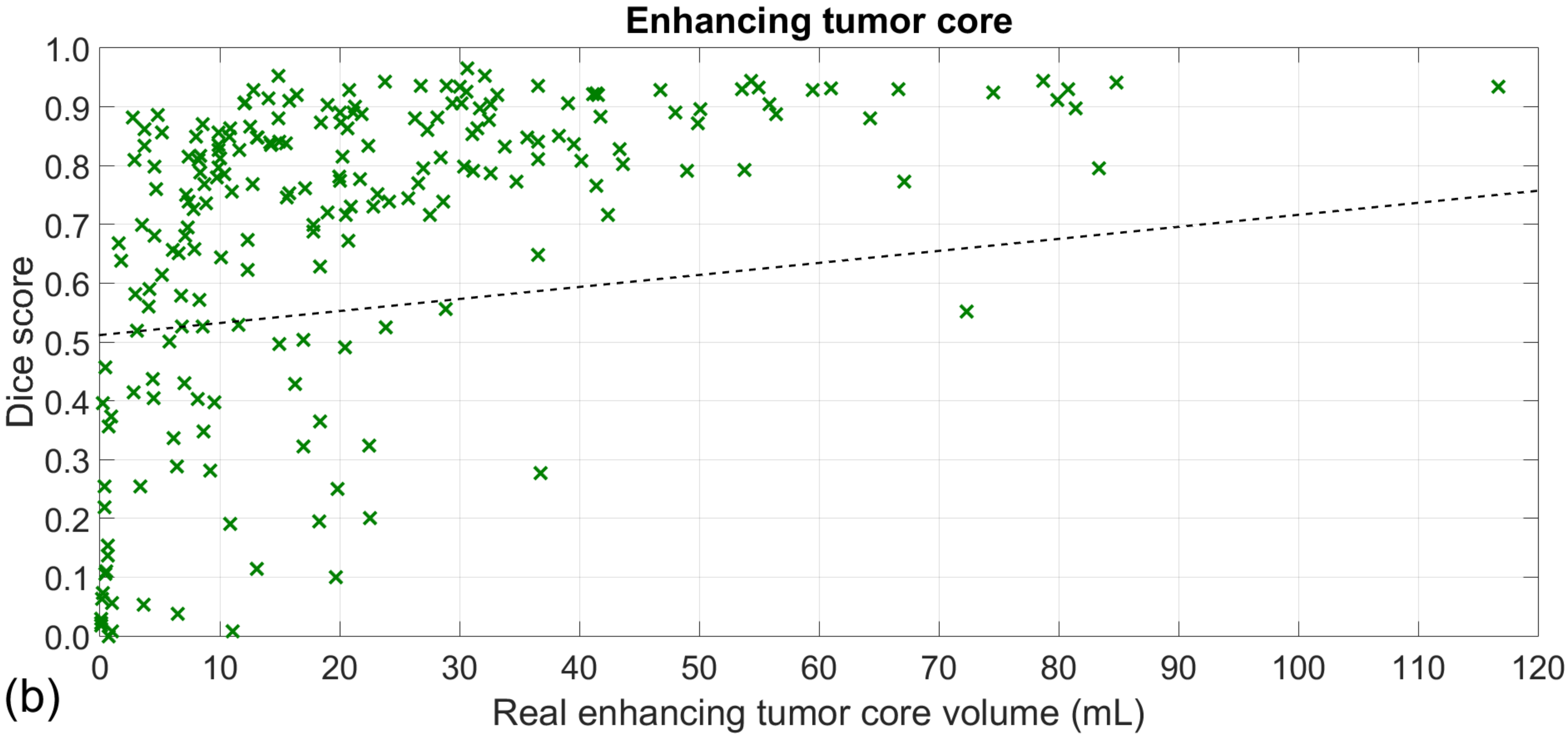


Tissue type	Value	TPR	TNR	PPV	DSC
Whole tumor	average	0.7234	0.9929	0.8734	0.7722
	overall	0.7608	0.9929	0.8941	0.8221
Enhancing core	average	0.6926	0.9972	0.7502	0.6728
	overall	0.8060	0.9972	0.8065	0.8063
Tumor core	average	0.5530	0.9970	0.8099	0.5654
	overall	0.6554	0.9970	0.8508	0.7404
Edema	average	0.6374	0.9896	0.7231	0.6566
	overall	0.6843	0.9895	0.7651	0.7225

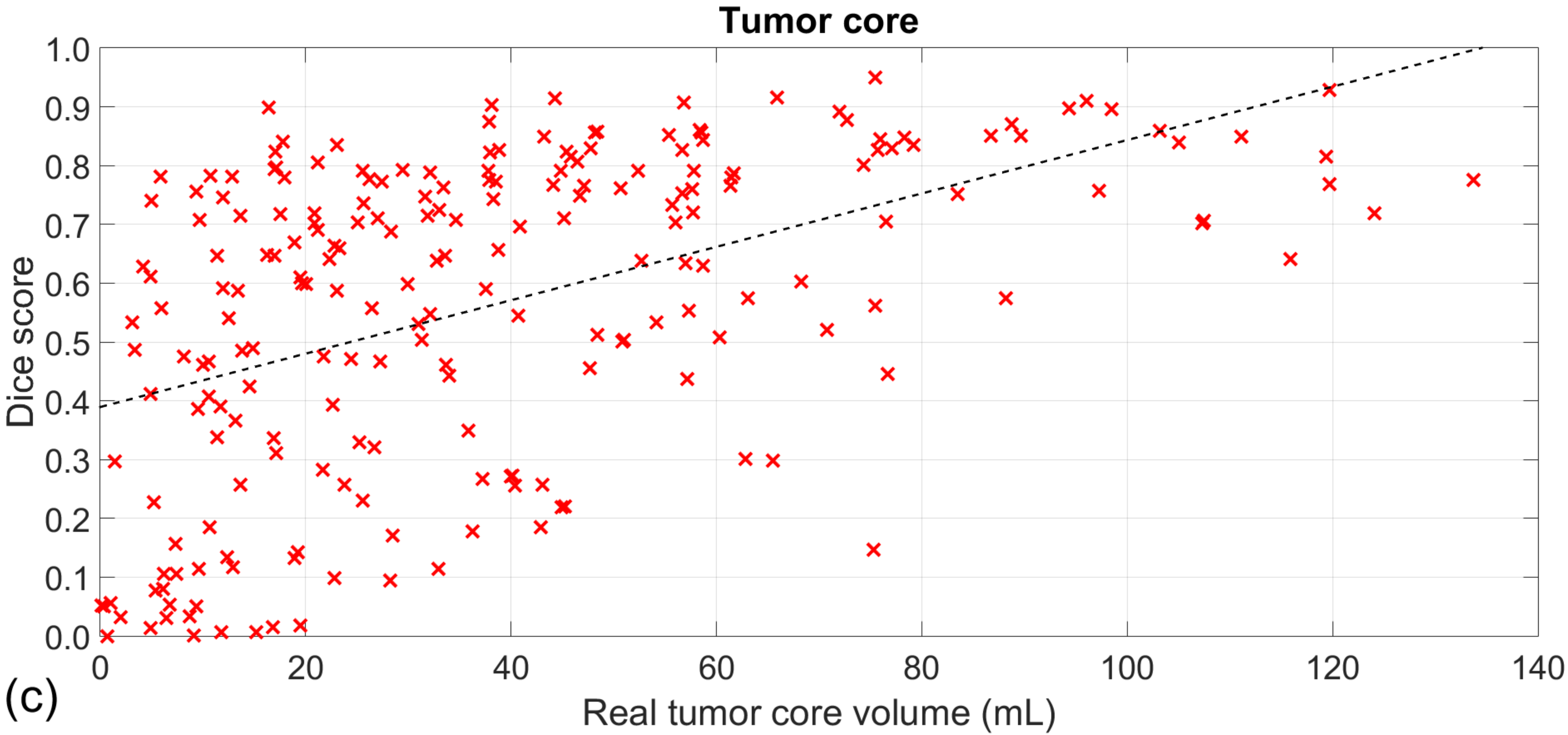
Individual Dice Score vs Tumor Part Size



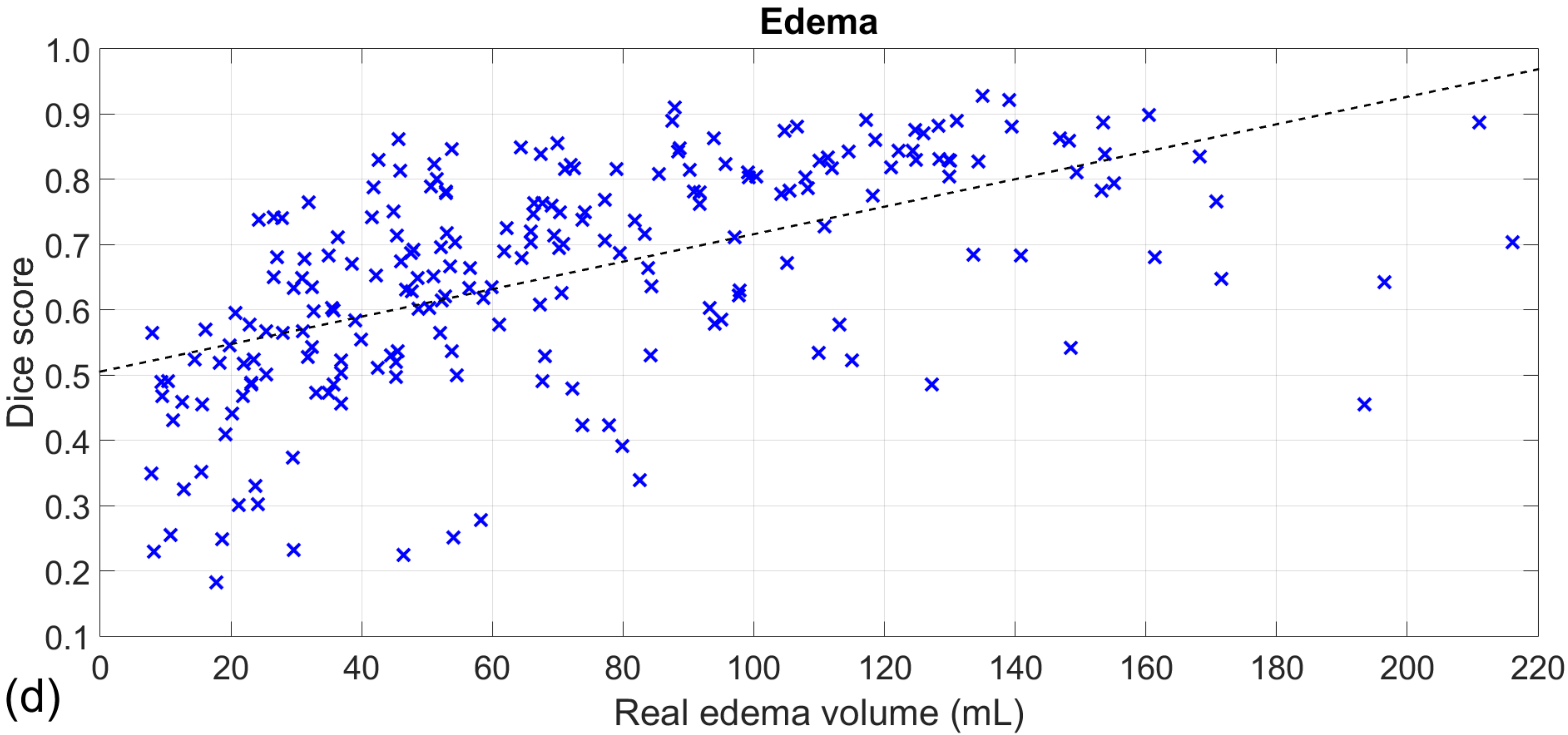
Individual Dice Score vs Tumor Part Size



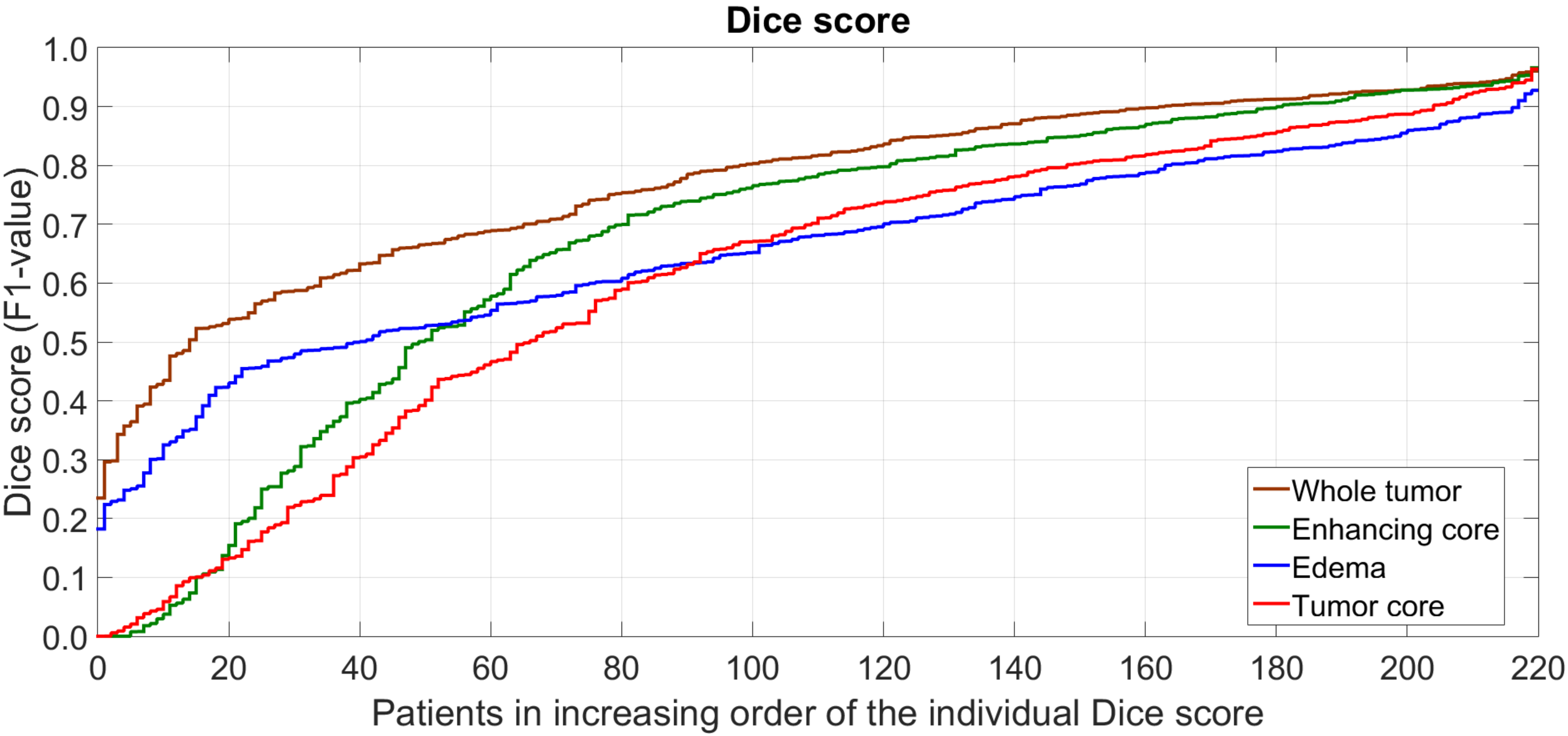
Individual Dice Score vs Tumor Part Size



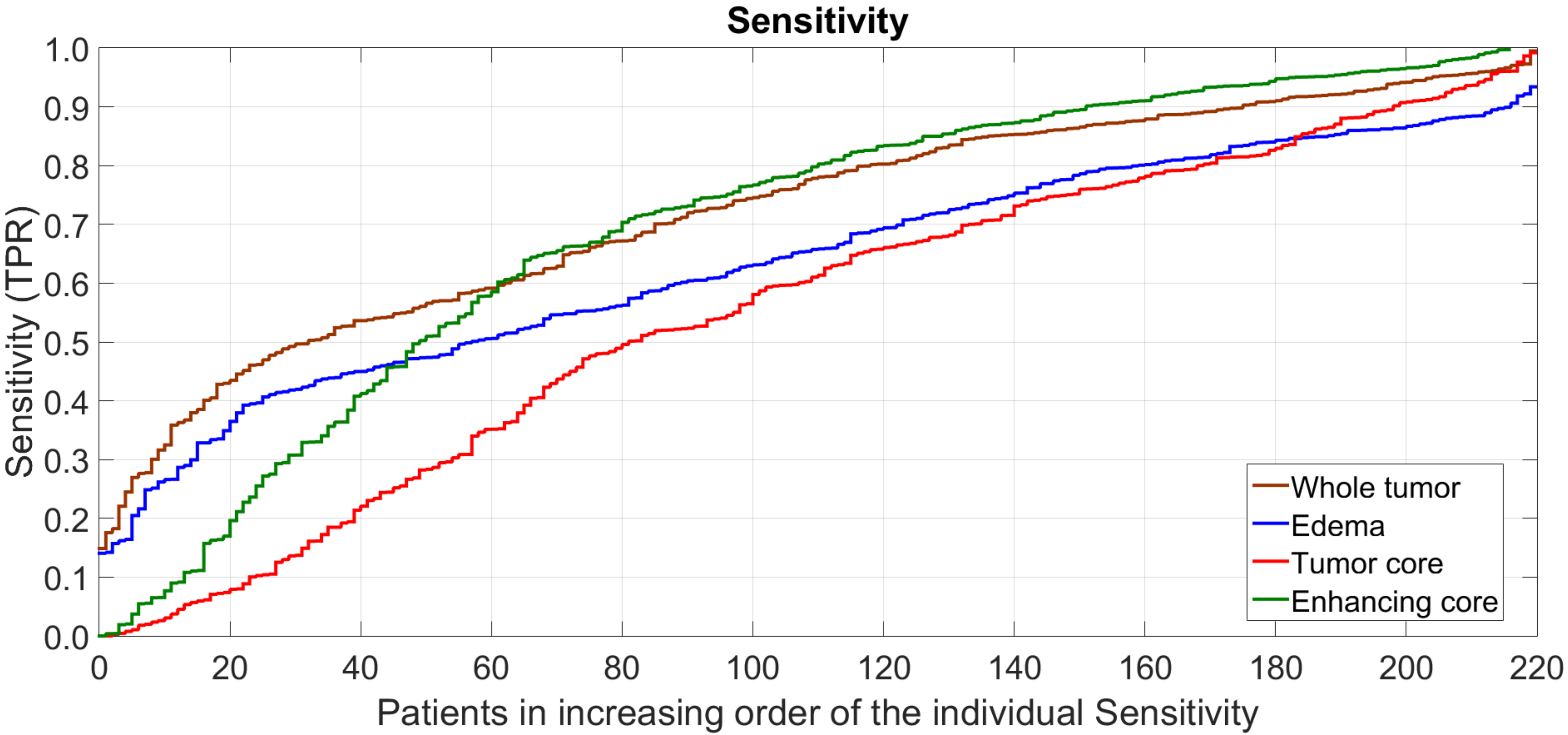
Individual Dice Score vs Tumor Part Size



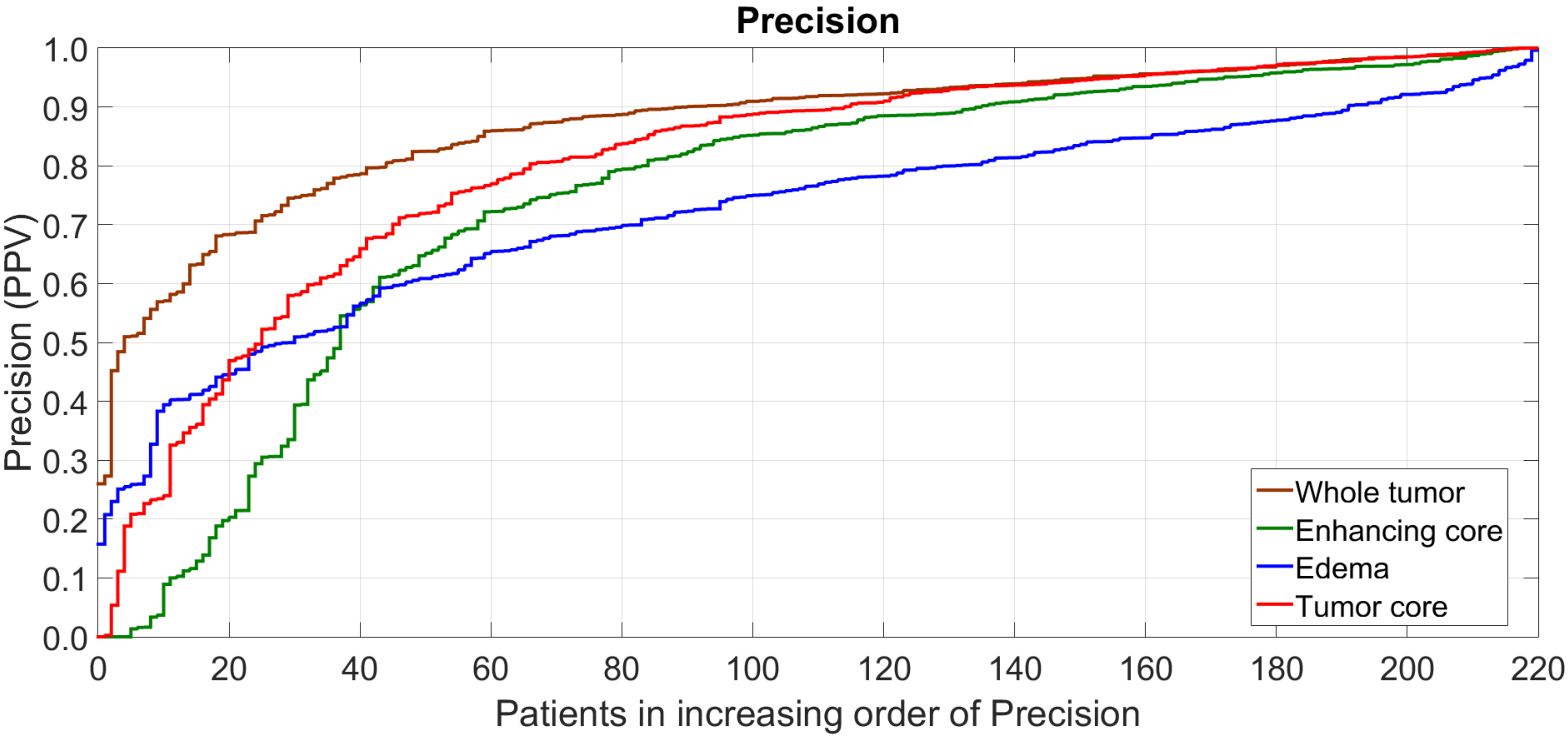
Individual Dice Scores for Various Tumor Parts



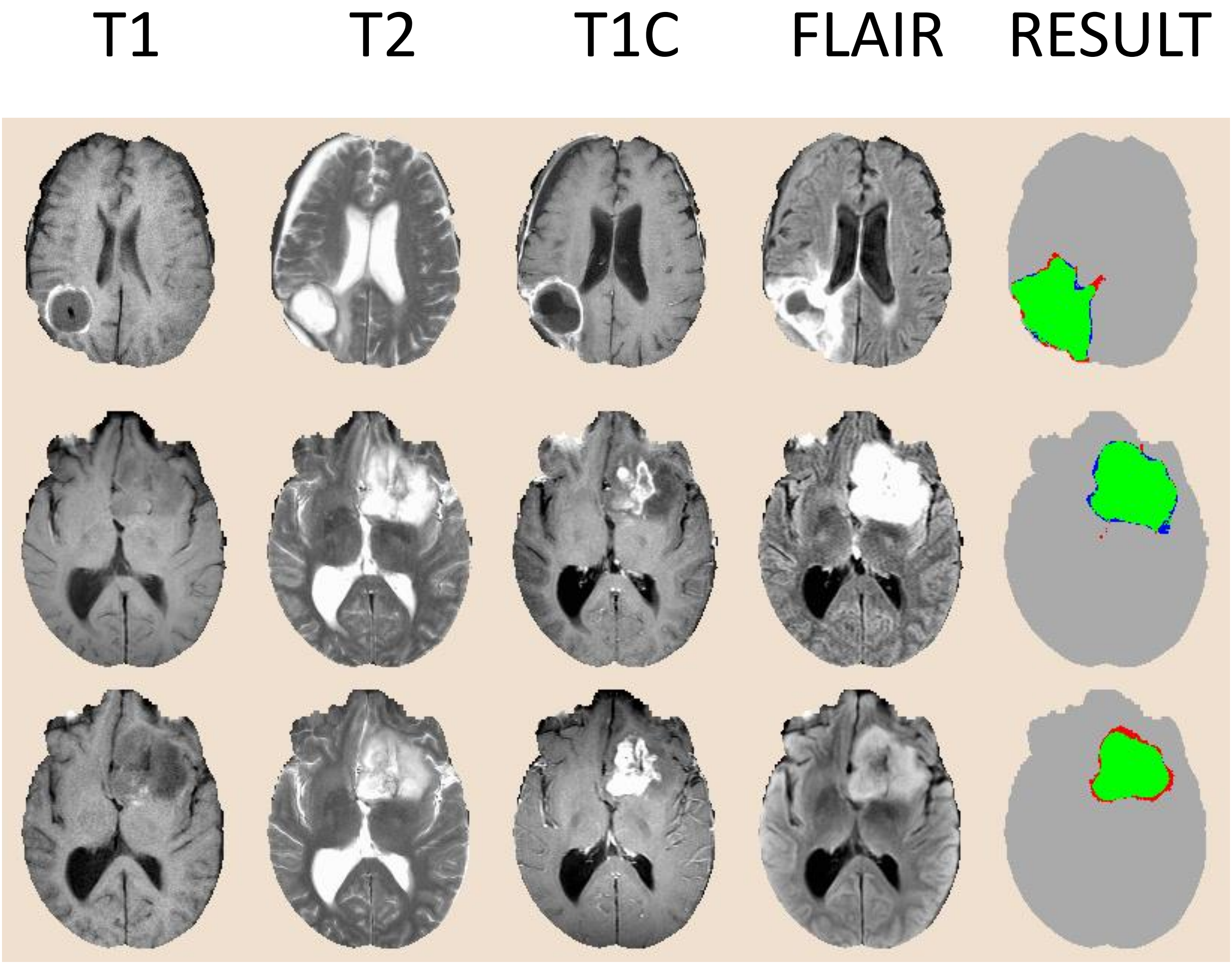
Individual Recall Values for Various Tumor Parts

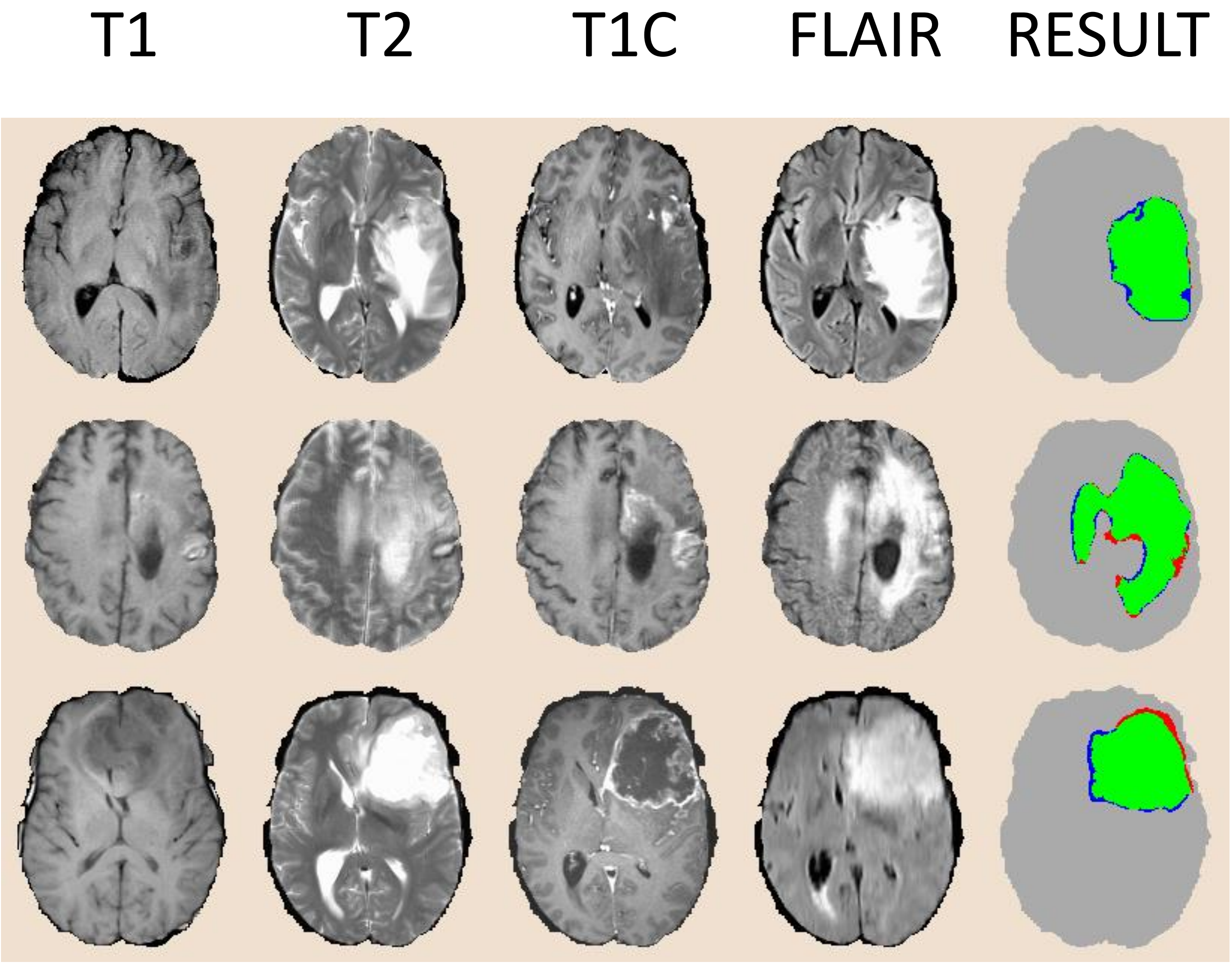


Individual Precision Values for Various Tumor Parts



Detected whole tumors: TP FP FN





Conclusions

- As preliminary result the achieved accuracy is promising
- Fine tuning and post processing will improve accuracy

- Future:
  - CNN + deep learning methods

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