

TMTV-NET

Evaluation of the model on CHU de Nantes's database

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① Metrics

② Results

③ Code Modifications

1 Metrics

Dice Similarity coefficient

Hausdorff's distance

Normalized Surface Coefficient

Border Jaccard Index

TMTV recall and precision

Lesionwise recall and precision

2 Results

3 Code Modifications

1 Metrics

Dice Similarity coefficient

Hausdorff's distance

Normalized Surface Coefficient

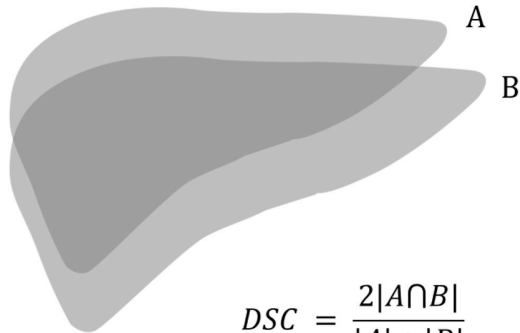
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$$DSC = \frac{2|A \cap B|}{|A| + |B|}$$

DSC: Dice similarity coefficient

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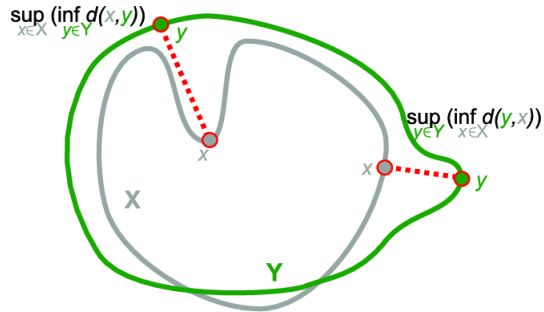


Figure. 1: We take the max of the two

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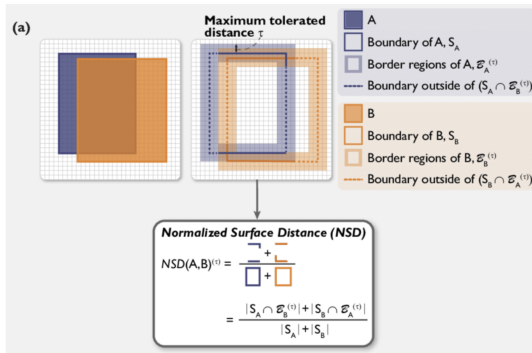
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$$TP_{B_{gt}}^c = \sum_{x \in B_{gt}^c} z \text{ with } z = \begin{cases} 1 - (d(x, S_{ps}^c)/\theta)^2 & \text{if } d(x, S_{ps}^c) < \theta \\ 0 & \text{otherwise.} \end{cases} \quad (12)$$

$$FN^c = |B_{gt}^c| - TP_{B_{gt}}^c \quad (13)$$

$$TP_{B_{ps}}^c = \sum_{x \in B_{ps}^c} z \text{ with } z = \begin{cases} 1 - (d(x, S_{gt}^c)/\theta)^2 & \text{if } d(x, S_{gt}^c) < \theta \\ 0 & \text{otherwise.} \end{cases} \quad (14)$$

$$FP^c = |B_{ps}^c| - TP_{B_{ps}}^c \quad (15)$$

Then, the score for class c , which we call *Boundary Jaccard* (BJ^c) is defined according to the Jaccard index:

$$BJ^c = \frac{TP^c}{TP^c + FP^c + FN^c}. \quad (16)$$

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TMTV recall and precision

TP TMTV : The total volume of correctly predicted lymphoma in milliliters

FN TMTV : The total volume of unpredicted lymphoma in milliliters

FP TMTV : The total volume of wrongly predicted lymphoma in milliliters

These measures allow us to establish precision and recall for each patient.

$$recall = \frac{TP}{TP+FN}, precision = \frac{TP}{TP+FP}$$

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We count FP, FN and TP in terms of lesions. Two approaches:

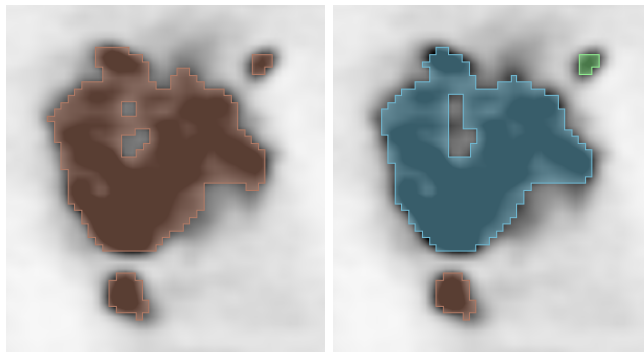


Figure. 2: Ground Truth vs. Prediction

For each lesion :

Approach 1 : $\text{NSD}(\text{prediction}, \text{lesion})$

Approach 2 : $\text{NSD}(\text{predictionS}, \text{lesion})$

For each prediction :

Approach 1 : $\text{NSD}(\text{prediction}, \text{lesion})$

Approach 2 : $\text{NSD}(\text{prediction}, \text{lesionS})$

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For each TMTV-NET prediction, we have this text file :

```
Patient : 11011109131004
Tolerance : 5
Lesionwise threshold : 50.0%

Max SUV = 31.763446807861328
Mean Distance : 5.818 mm
Hausdorff : 160.467 mm
Dice : 0.98
NSD at 5mm : 0.973
BJI at 5mm : 0.973

TMTV calculé par TMTV-NET (Non Thresholded): 258.67ml
TMTV calculé par TMTV-NET (Thresholded): 54.57 ml
TMTV GT (Thresholded): 56.04 ml

TMTV FP Non Thresholded :204.49 ml
TMTV FP Thresholded : 0.39 ml
TMTV FN : 1.86 ml
TMTV TP : 54.18 ml
Precision : 99.29 %
Recall : 96.67999999999999 %

Approach 1 :
Number of Lesions TP : 6 / 16 (37.5%)
Number of Lesions FN : 10 / 16 (62.5%)
Number of Predictions FP : 1 / 5 (20.0%)

Approach 2 :
Number of Lesions TP : 6 / 16 (37.5%)
Number of Lesions FN : 10 / 16 (62.5%)
Number of Predictions FP : 0 / 5 (0.0%)
```

Filtering the results :

By TMTV metrics (tmtv recall and precision)

By Lesionwise metrics (lesionwise recall and precision)

Both

Out of 558 patients :

Lesionwise recall $> 50\%$: 188 patients (33,7%)

Lesionwise precision $> 50\%$: 111 patients (19.9%)

TMTV recall $> 50\%$: 45 patients (8.06%)

TMTV precision $> 50\%$: 124 patients (27,6%)

TMTV&lesionwise recall $>$ than 50 percent : 35 patients (6.27%)

TMTV&lesionwise precision $>$ than 50 percent: 71 patients (12.72%)

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DicomNiftiConversion.py

Most critical problems met :

SimpleITK for PET

Rescale slope multiplication gives wrong suv values

SimpleITK for PET

Example case : patient 11011101021006

When the PET dicom series are turned into a nifti file via sitk : $\text{np.max} = 32745$ and the array is of type int

When it is turned into a nifti file via `dicom2nifti.convert_generic` : $\text{np.max} = 246264.21875$ and when multiplied by the suv factor 0.00049 gives the actual max SUV of the PET scan (given by slicer) : 120.67 instead of 16.04 This obviously affects the prediction process a lot

Rescale Slope multiplication

Example case : patient 11011101061002

Rescale slope = 5.92

Rescale intercept = 0

$Suv_{factor} = 0.00038$

Max raw value = 193791.890625

This means that the raw values should be multiplied by 5.92 then by 0.00038. When we do this with the maximum raw value we obtain a max suv value of 435.95

Merci !