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CONTEXT

- ¹⁸F-FDG PET is essential in lymphoma imaging for **detecting lesions** and quantifying their metabolic activity.
- Due to the spatial and spectral properties of **PET images**, most **segmentation** methods rely on **intensity-based strategies**, mainly local fixed or adaptive thresholdings, and usually **require user interaction**.
- This process can be **laborious and user-dependent** for lymphomas where lesions are **numerous** and located in **multiple sites** of the body.
- Recent methods also propose to **integrate anatomical priors** to improve the segmentation process.

OBJECTIVE

- In this work, we use **hierarchical approaches** embedding **multi-modality descriptors** for **automated PET lesion segmentation** of the whole body.

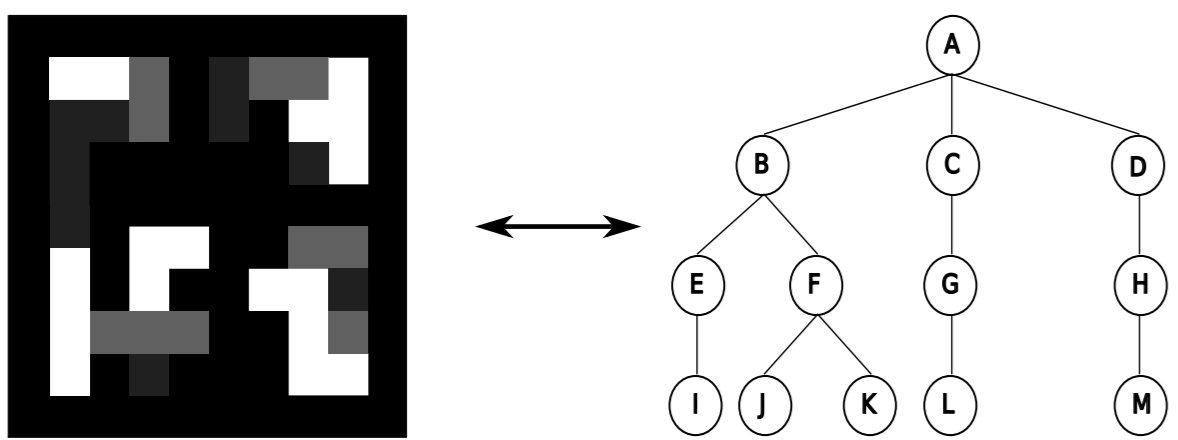
MATERIAL

- 43 multi-centric **PET/CT images** of patients treated for **lymphoma**
- Tumour and Organ segmentations performed on PET by expert (threshold at 41% of SUV_{max} in manually placed VOIs) were considered as **Tumour ground-truth** and **Organ ground-truth**.

METHODS

1. Hierarchical representation : component-tree \mathcal{T}

We use the **component-tree** \mathcal{T} as a relevant data structure to model PET images. This representation models all the connected components (i.e., **maximally connected regions**) of the image I obtained from its successive level sets.

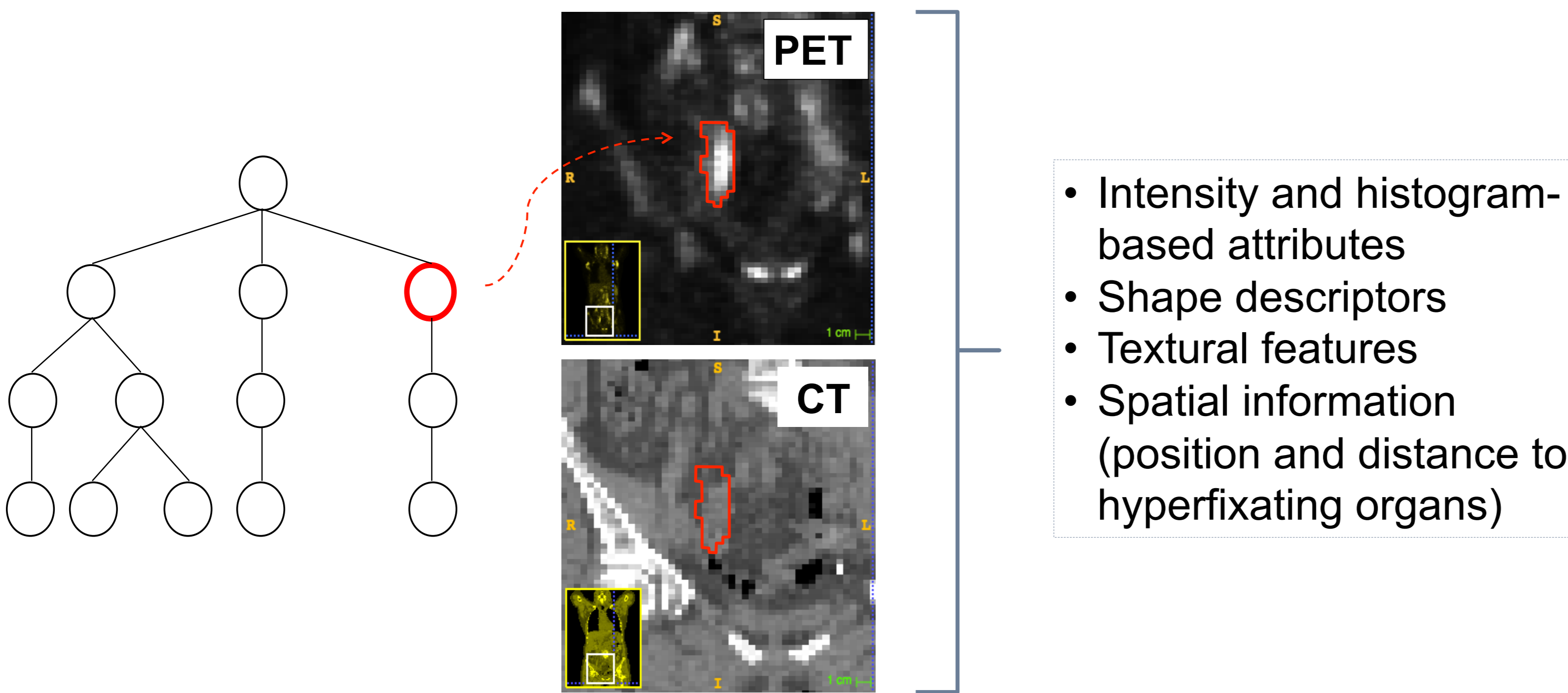


- Each *node* corresponds to a connected PET regions, and each *edge* represent the inclusion relationship between them.

- \mathcal{T} is a *lossless* image representation.
- Processing I via \mathcal{T} is a low-cost operation.

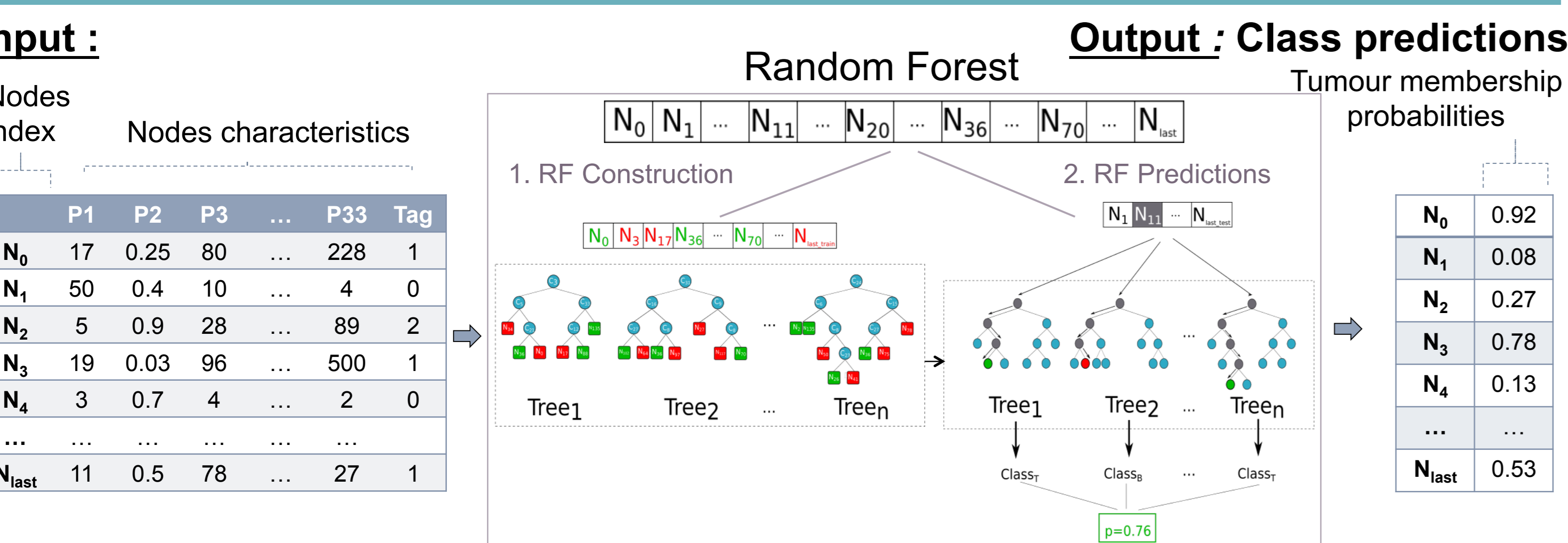
2. PET/CT characterization and tag of regions

1. Each node is characterized with a set of 88 features computed on PET/CT data :



2. Identification of class nodes (0 : Non-relevant / 1: Tumour / 2: Organ), based on *ground-truth* segmentations, and used for the supervised learning step.

3. Machine-learning with Random Forest Classifier



Our segmentation consists of keeping in the model the regions with the **highest tumour membership probabilities**, for each patient.

RESULTS

Given the small size of the considered database, we evaluate the random forest (RF) model using a leave-one patient-out (LOPO) cross-validation strategy. The number of trees to train the RF was set to 10^3 .

We evaluate our methodology by validating

- Node classification results from RF
- Volumic results from the reconstructed tumour regions, compared to ground-truth segmentation

RF validation

Table : Confusion matrix of nodes after RF classification

Actual Class	Predicted Class			
	Class	T	O	NR
T		10 568	1 008	4 754
O		875	12 222	2 435
NR		3 656	1 856	38 840

- Multi-class overall accuracy of 0.81
- Class Tumour vs all:
 - Mean sensitivity and specificity of 0.65 and 0.92 respectively
 - Overall accuracy of 0.85

Tumour Segmentation Results

- Our segmentation method shows promising performances :
 - It locates 92% of all the manually delineated tumours for all the patients.
 - Mean sensitivity and specificity of 0.74 and 0.99 respectively.
- Overall tumoral volume overestimation of 35% in average.
- Few remaining hyperfixating organs.

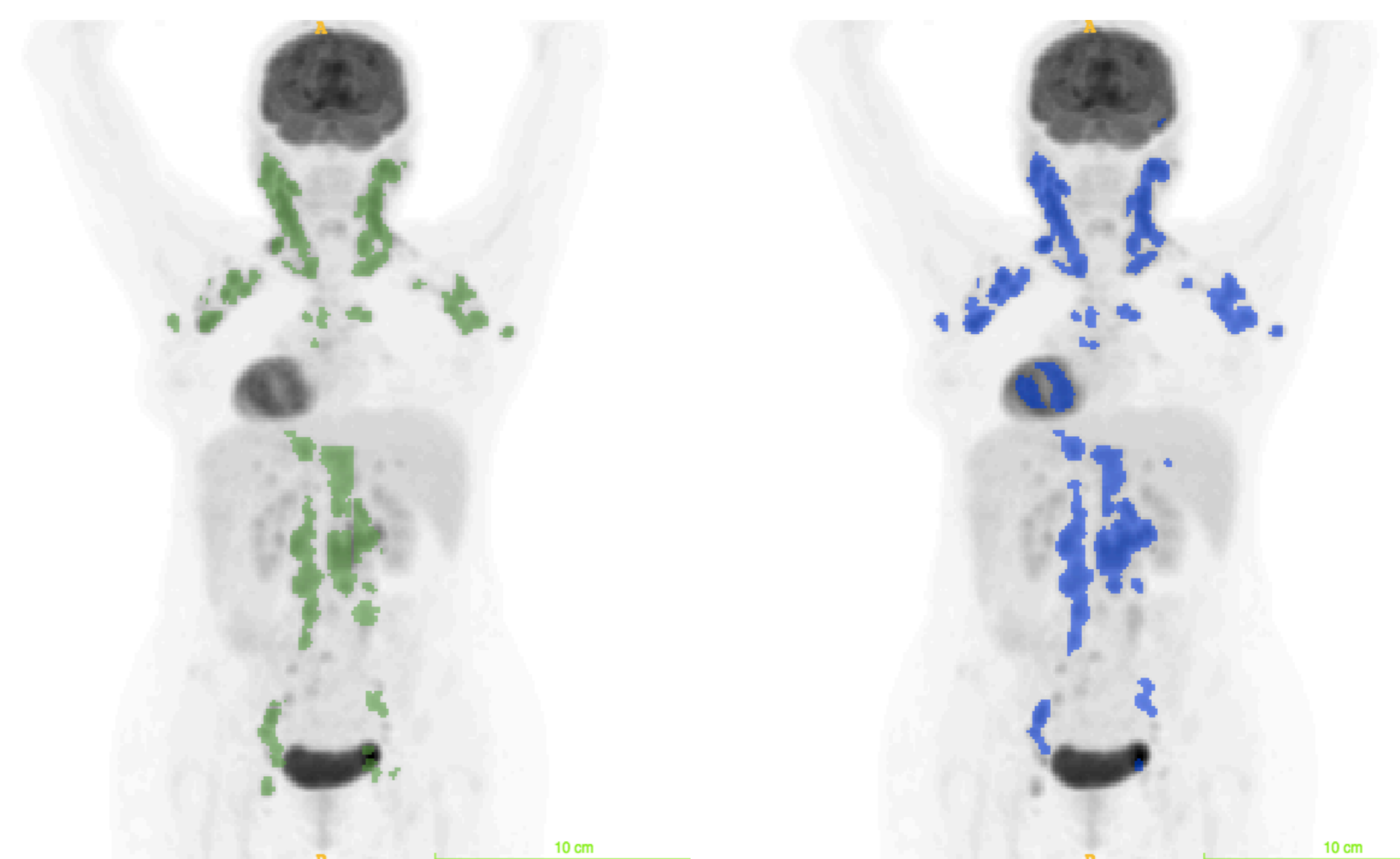


Figure : MIP of PET image (maximum intensity projection) surimposed with ground-truth (in green, on the left) and segmentation result (in blue, on the right).

CONCLUSIONS AND PERSPECTIVES

- Hierarchical approaches involving machine-learning and multi-modality descriptors can automatically and efficiently segment lymphoma lesions in 3D over the whole body : detection of 92% of all lesions.
- Volume overestimation : overestimated tumors + hyperfixating organs.
- The model can be improved considering a learning procedure on a larger database and features selection.
- Beforehand elimination of organs with an anatomical atlas.
- Taking advantage of the hierarchical structure of \mathcal{T} : injection of tree-related structural information and considering sub-branches as unitary structures.