# Fully automatic 2D segmentation of EPVS on T2 images using max-trees and Random Forest

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## 1. Introduction

Enlarged perivascular spaces (EPVS) are neuroimaging biomarkers that are visible on axial slices of T2 images as bright structures of various areas, mean intensity values, shapes and locations. To detect these numerous bright regions, we propose to first apply a max-tree [1], a hierarchical structure representing the inclusion relationships between all the connected components of binary images obtained by thresholding the input image from its highest to lowest gray level. Adapting the idea from [2], developed to segment lymph nodes on PET/CT images, we then train a Random Forest classifier on features extracted from binary images of T2 max-tree nodes, and designed relying on [3]. As the available training images, coming from 12 patients from 2 different cohorts (SABRE and RSS), have different voxel sizes and dimensions, the chosen features are expressed in mm, mm² or dimensionless. The global framework, illustrated in Figure 1, will now be described more precisely.

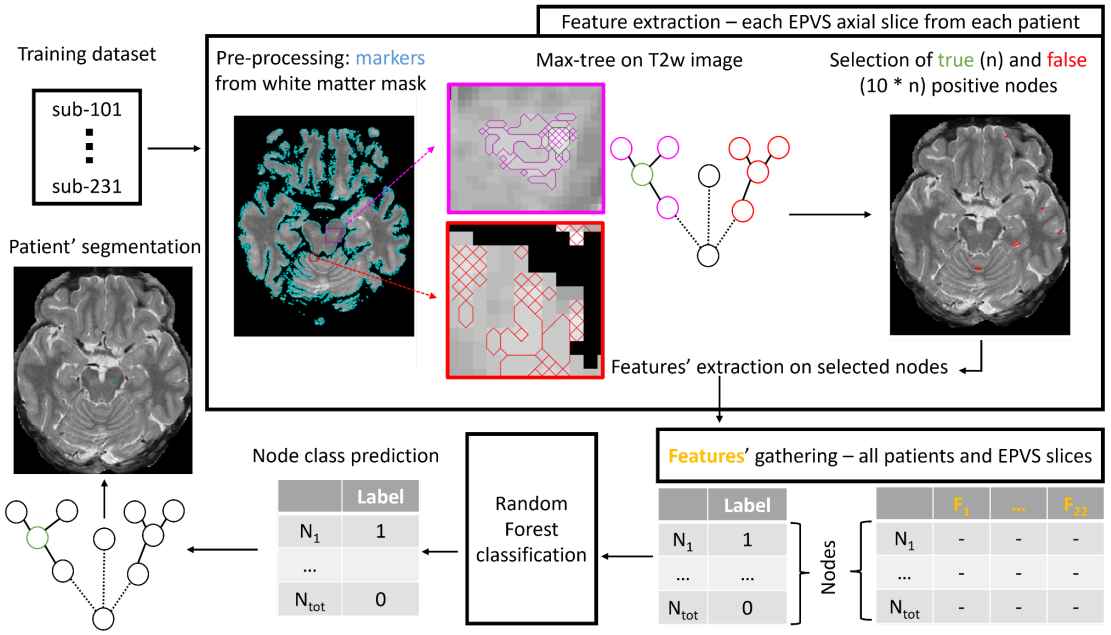


**Figure 1:** global framework of the proposed method.

## 2. Pre-processing

To reduce computation time, a pre-processing step is applied to restrict the region of interest to the white matter, and to compute the max-tree only from specific pixels called the markers. Thus, the tree will only be explored from nodes, namely connected components of the input binary image, including at least one of these markers. The head mask is first obtained by thresholding to 0 the whole T2 image, and then refined using a hole filling operation based on mathematical morphology on each axial slice. More precisely, holes refer to the connected components of the input binary image complement included in connected components of the

input binary image (i.e the background regions included in the foreground regions). Linear intensity normalization is then performed on the whole T2, T1 and FLAIR images, leading to intensity values in [0, 1]. All the images are then cropped to the head mask. The brain mask is segmented by performing an opening with a disk of radius of **10 mm** on each T2 axial slice, and then by applying Otsu's thresholding [4] on the whole T2 volume within the head mask. The brain mask is then refined by hole filling on each axial slice. The white matter mask is obtained by applying Otsu's thresholding [4] on the whole T1 volume within the brain mask. The markers are then created on each axial slice by applying an erosion with a disk of radius of **1 mm** on the binary image of the holes of the white matter. The remaining holes of area less than **100 mm²** are then filled. The markers' connected components having an area less than **100 mm²** are then removed. Finally, the whole T2 image is requantified to **64** gray levels, and then masked on each axial slice by the 2D hole filled binary image of the white matter.

## 3. Method

After pre-processing, a max-tree is performed on each requantified T2 axial slice with markers. For each node of the tree, features belonging to 3 categories were computed :

- shape: area (mm²), diameter (mm), euclidean distance between the node centroid and the closest pixel from the node border (mm), highest Dice value between the node and its fitted ellipse, circle or line,
- intensity: ratio between the mean node intensity value and the mean slice intensity value, ratio between the mean node intensity value and the maximum slice intensity value, ratio between the mean node intensity value and its mean surrounding intensity value ( considering a ring of **1 mm** of diameter),
- location: difference between the number of the node slice and the number of the top of the head slice (mm), mean euclidean distance from the pixel nodes to the vertical line cutting the slice in half (mm), mean euclidean distance from the pixel nodes to the horizontal line cutting the slice in half (mm), percentage of node pixels belonging to each quarter of the slice, percentage of node pixels belonging to the two quarters of the slice at the back of the head, percentage of node pixels belonging to the white matter mask.

As the intensity features are computed on the T1, T2 and FLAIR images, a total of 22 features are computed by node. To reduce the computation time, nodes of area greater than **100** mm² or having a requantified mean intensity value below **15** or above **45** are not considered.

## 4. Training

The nodes used for training are selected among each T2 axial slice where EPVS were manually segmented by at least one expert, and have to belong to a labeled brain region. First, nodes associated with real EPVS are selected, namely nodes that maximize the weighted Dice value (as defined in the challenge's description) between the binary images of this node and the real EPVS. If several nodes get the highest weighted Dice value, the one with the maximal area is selected. However, if the maximal weighted Dice value is less than **0.7**, the node is rejected. Once the nodes associated with real EPVS are selected, on the same axial slice, **10** times as many nodes with no intersection with any real EPVS region are randomly selected. Finally, the training is done on the features of all the selected nodes, performing Random Forest [5] during a 3-cross validation process following the cohorts' distribution: each fold is composed of 2 SABRE and 2 RSS patients. Thus, the features collected from the same patient cannot be used in both training and validation sets. At the end of the 3-cross validation, using the mean weighted Dice value between predicted nodes and associated real EPVS as the cross-validated metric, the classifier is trained again on the whole training set using the

combination of parameter values that achieves the best average performance during the cross-validation process (more precisely a maximum depth of **50** and **200** trees) .

## 5. Implementation and parameter setting

The proposed method was implemented using Python and parallelized using 12 CPUs. The 4-connectivity was used during each connected component labelling step. Other parameter values are indicated in bold.

## 6. Preliminary results

To assess the performances of the proposed algorithm, the nodes were first collected on all the slices with markers. The training dataset was then 5 times randomly divided into training, with 5 SABRE and 5 RSS patients, and test sets, with one SABRE and one RSS patient. The Random Forest classifier was then trained on each training set using 5-cross validation following the cohorts' distribution, and then applied on its associated test set. The average of the mean weighted Dice values over the test patients over the 5 splits was $0.17 \pm 0.07$.

## 7. References


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