

# Extraction and Analysis of Patient-specific Hepatic Anatomy from MR Images

## 1 Purpose

The development of a planning tool for liver surgery requires a precise knowledge of the patient-specific intrahepatic structures and their relationship to possible lesions. It is therefore necessary to implement algorithms for the segmentation and analysis of these structures from the input volumetric images and integrate them in an intuitive user-interface that can be used by clinicians to control the output of the process. Here, we describe our HEPAVIRE system for the segmentation and analysis of the liver parenchyma and vessels based on contrast-enhanced Magnetic Resonance (MR) images. These images present a challenge compared to Computerized Tomography (CT) images due to a lower spatial resolution, signal bias and higher image variability. An intuitive user-interface was developed to perform and control the successive steps of the process.

## 2 Method

For the hepatic parenchyma segmentation an interactive approach based on the Watershed algorithm implementation in ITK [3], preceded by an anisotropic filtering to reduce noise. Image edges, that serve as input to the Watersheds module, are obtained by smoothing the image using a Gaussian operator, that acts as a scale selection method, followed by the calculation of the magnitude of the image gradient. This scale selection approach is used also in the further vessel analysis for all derivative calculations. Regarding the Watershed algorithm, we have implemented an interactive approach described first in [1] that allows to interactively select the volumetric regions which form the parenchyma from the Watersheds output. Usually most of the object is extracted in a single region but the approach allows to correct the final segmentation by inclusion or removal of smaller regions. The algorithm itself uses a hierarchical approach that merges the initial catchment basins into larger regions in order to avoid over-segmentations. This process is controlled by a "water level" parameter. The user can also smooth the final segmentation by performing hole and gap filling operations. Finally, a 3D surface representation is generated and the liver volume can be calculated. The segmentation is used as a mask in order to limit the vessel analysis described next to the region inside the parenchyma. Prior to the vessel analysis the MR bias can be eliminated from the original image inside the mask region by applying a median filtering with a large kernel. This allows to apply a global lower threshold to the parenchyma region in order to decrease the number of vessel point candidates and thus speed up the vessel analysis. Next, vessel centerlines are detected by calculating the medialness response as defined by Krissian et al. [4]. Vessels are modeled as tubes with circular cross sections and the medialness response is calculated as the average sum of the gradient

magnitude in the points of a circle that lies in the estimated vessel section. In order to obtain a better response, we use a symmetry factor that penalizes differences in the values of the gradient magnitude along the circle as proposed in [7]. The radius of the circle is defined by the current scale selected in the gradient calculation. If the current point is a vessel center at the appropriate scale, the two eigenvectors corresponding to the two largest eigenvalues of the local Hessian matrix (in absolute value) define a good approximation of the local vessel cross-section [2]. A multiscale approach is used to deal with varying tube radius, where the final response is calculated as the maximum response at multiple scales. Vessel centerlines are obtained from the multiscale medialness response by skeletonization using an iterative thinning algorithm [5]. Here, we also use the medialness response as the distance function for iterative point removal so the centerline is centered where the response is maximum. Further analysis stores the obtained centerlines as connected branches together with the corresponding properties of their points (estimated radius, section, etc.). Small isolated branches are pruned and following the work in [7] vessel branches are reconnected using a minimal path approach. This way a patient-specific vessel model is obtained. After labeling the vessels, this model can be used to approximate the vascular territories that divide the parenchyma in Couinaud segments as in [6]. Developed algorithms have been integrated into a user interface that allow to load and explore the DICOM volumes in 2D and 3D, perform the segmentations in an easy interactive process and save the obtained results.

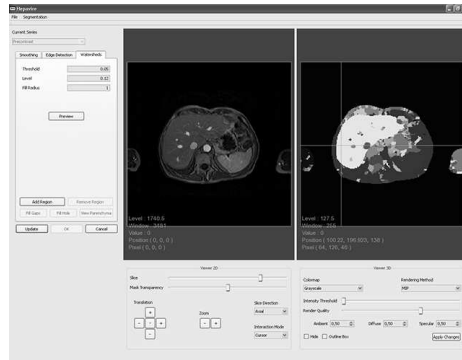
### 3 Results

A preliminary study was conducted using dynamic contrast-enhanced volumetric MR images (VIBE sequence) obtained with a Philips Gyroscan Intera 3T scanner at Cruces Hospital (Barakaldo, Spain). The datasets consisted of 60  $256 \times 256$  slices with in-plane resolution varying from 1.0 – 2.0 mm. and 3.0 mm. thickness. For the segmentation we used the portal venous phase as it shows the best contrast for the vein tree. Figure 1 shows the user interface for the parenchyma segmentation. We can see the output the Watershed algorithm (right) and the segmentation in progress (right). Figure 2 shows the MIP volume rendering of a multiscale medialness response using 10 scales corresponding to tube radius from  $R = 1.25$  mm. to  $R = 4$  mm. Most of the hepatic veins have been detected despite the low resolution of the data. The figure shows also the estimated centerlines (in green) together with estimated section and radius (blue circles) that, in most places, approximate accurately the real vessel section and radius.

### 4 Conclusion

The interactive hierarchical Watersheds method has been proven efficient in order to segment the hepatic parenchyma in MR images, allowing to control the process and increase the overall robustness of the method. Liver volumes can be calculated easily with a few mouse clicks. Regarding the vascular analysis, the multiscale medialness response shows greater robustness than other methods, specially for small vessels with low resolution datasets. However, it requires a posterior analysis to eliminate errors due to noise and false responses and extract relevant information only. In the future we

plan to increase the robustness and global speed of the method and further automate several tasks to make the process as simple as possible for the final user. Finally, the segmentation and analysis algorithms must be evaluated and validated by clinicians.



**Fig. 1.** User interface for the parenchyma segmentation module.

## References

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