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Development of Multi-compartment Model of the Liver Using Image-based Meshing Software

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Abstract— **Computer simulation of biological systems for *in silico* validation has the potential of increasing the efficiency of pharmaceutical research and development by expanding the number of parameters tested virtually. Then only the most interesting subset of these has to be probed *in vivo*. By focusing on variables with the greatest influence on clinical end points, valuable drug targets can be advanced more quickly. A large number of methods have been developed to rebuild a three-dimensional (3D) model of a liver, mostly to prepare a liver surgery. These models are often not accurate and most of the them don't take into account the fluidics inside the vessels.**

The aim of this work is to provide an accurate computational multi-compartement model of the healthy and the pathological liver with their network of blood vessels (vasculature) using a finite-element-modeling software.

Computed tomography (CT) slices, in DICOM format, from two different patients were used to provide the datasets of transverse images for the modeling. Each dataset of images was segmented in order to extract the liver's shape and define the vein and artery networks.

On CT images, the contrast between the liver and the nearby organs (background) is very low because all these structures are a similar density. Thus, we used semi-automatic tools to determine liver contours. Manual segmentation was used as a last resort. Then, strong filtering (bilateral filter) and confidence-connected-region-growing algorithm were applied to rebuild from each - healthy and pathological - liver a multi-compartment model including parenchyma, arteries and veins. The precision of the obtained vasculature model allowed anatomical classification of hepatic segments and the quantification of their volumes.

Although our study demonstrated the difficulties in use of CT images for computational modeling of the liver, it also confirmed that semi-automatic tools can be used to develop anatomically accurate models of hepatic vasculature.

I. Introduction

Recently, liver cancer and metastasis became a major public health issue. Indeed, liver cancer is the seventh most common type of cancer and the forth most common cause of cancer-related death in the world. Risk factors for liver cancer include: alcohol misuse, hepatitis C or B, viral infections, obesity and cirrhosis [1]. And hepatic metastasis occur often in case of the two most frequent cancers in industrial countries, namely lung cancer and colorectal cancer [1].

The main treatments of hepatic lesions are a surgical resection and/or a chemotherapy. A number of experimental treatments are also under development, such as targeted multi-therapy (TMT). This therapy responds to the need of minimally invasive targeted treatments, which are less traumatic and reduce the recovery period for patients. The TMT is based on the destruction of the tumor thanks to thermo-ablation by a super-heated steam; in association with chemical, viral or biologic agents if needed. One of the main advantages of this therapy is that it is not associated with the loss of entire segments or lobes of the liver as it is the case in surgical resection. To perform the computational simulation of this kind of intervention a computational model of the targeted organ is needed.

The advent of image-based finite element modeling and robust segmentation techniques, more advanced computer-aided design (CAD) softwares and meshing tools and the amount of computer power are increasingly easing the pre-clinical simulation of invasive-treatment techniques.

Computer Tomography (CT) data from different patients, if available, can be processed faster and high-quality meshes that can accurately represent the liver geometries can now be generated. As a result, a large number of methods have been developed to rebuild a three-dimensional (3D) model of the liver, mostly to perform liver resection, i.e. the removal of the malignant part of the liver [2],[3].

The aim of our study was to develop an accurate computational multi-compartment geometric model of the healthy and the unhealthy liver with vasculature by converting CT images datasets in meshing models using a finite-element-based software.

II. Materials and Methods

A. CT scan

The images acquisitions were performed in routine using SOMATOM Sensation device (Siemens AG, Germany). Triphasic CT scanning of the liver was performed at 200-250 mAs. Patients were given intravenous contrast of 1.5 ml/Kg with overall dose ranging from 80-100 ml. Patient preparation also included administration of 2000 ml of water/gastrograffin 30-60 minutes prior to the examination used as oral contrast.

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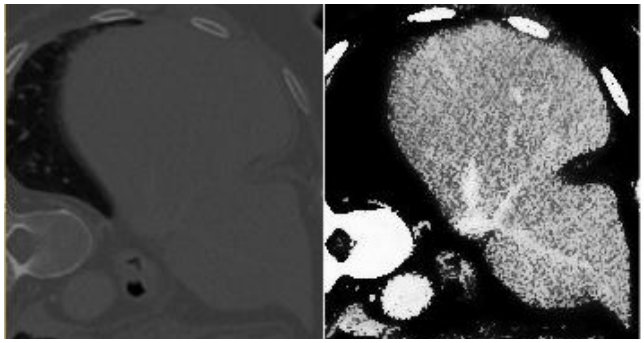

Figure 1. CT slices of the liver before (left) and after (right) filtering

After oral and injection of intravenous contrast material, liver was scanned in arterial (scanning delay, 20-40 seconds), portal (scanning delay, 60-90 seconds), and equilibrium (scanning delay, 2-5 minutes) phases. Enhancement of vessels and lesion(s) in each phase was evaluated, and the lesions were tabulated according to hyper enhancement, hypo enhancement, iso-dense to liver parenchyma and mixed enhancement pattern.

B. Meshing software

We used the modeling software provided by Simpleware (Exter, UK). At the first step, CT images were imported in Simpleware paltform and visualized as 2D planes using classical anatomical planes: frontal, transversal and sagittal (ScanIP module). To define these region(s) of interest, the user used one or more processing and segmentation tools.

The thresholding was the main tool, as it is the basis of the creation of structures used in the model conversion. When entering in this tool the pixel intensity boundaries, the user creates a new object corresponding to the range of permitted intensities. Then, several noise reduction filters, corresponding to the most used algorithms, like the Gaussian filter, were used to avoid in the final model errors of structural definition, due to inherent noise when acquiring medical data.

After the segmentation, the images were converted to volumetric and surface meshes. The generated meshes can be directly imported into different finite-element analysis (FEA) and Computational Fluid Dynamics (CFD) software, for example COMSOL Multiphysics.

Segmentation allows us to obtain for each elementary anatomical part a surface defining a volume. A specific algorithm of meshing is used according a relatively conventional idea : a cloud of points is generated within that volume, then the geometry of this volume is reconstructed with tetrahedra. Generally, the obtained tetrahedra have no enough quality to ensure the solving of the numerical problem because some of them have a needle-shaped or have a negative volume. An iterative process allows getting coherent elements.

The counterpart of this precision is the high number of elements so generated which is usually a handicap for the numerical solving. The difficulty can be circumvented because, according to the physical problem studied it is not necessary to take into account all areas (for instance, if the fluid motion in the vessels is studied, it is not necessary to consider the solid part of the liver). It is also possible, when the effect of physics is limited in space, to consider only part of the space and introduce absorbent conditions on the boundary of the studied area.

III. RESULTS

Visualization and segmentation of the liver was difficult because of a low contrast between the liver and the nearby organs. Images histograms were adapted to rearrange the dynamics of greyscale values and to enhance the contrast (Fig. 1).

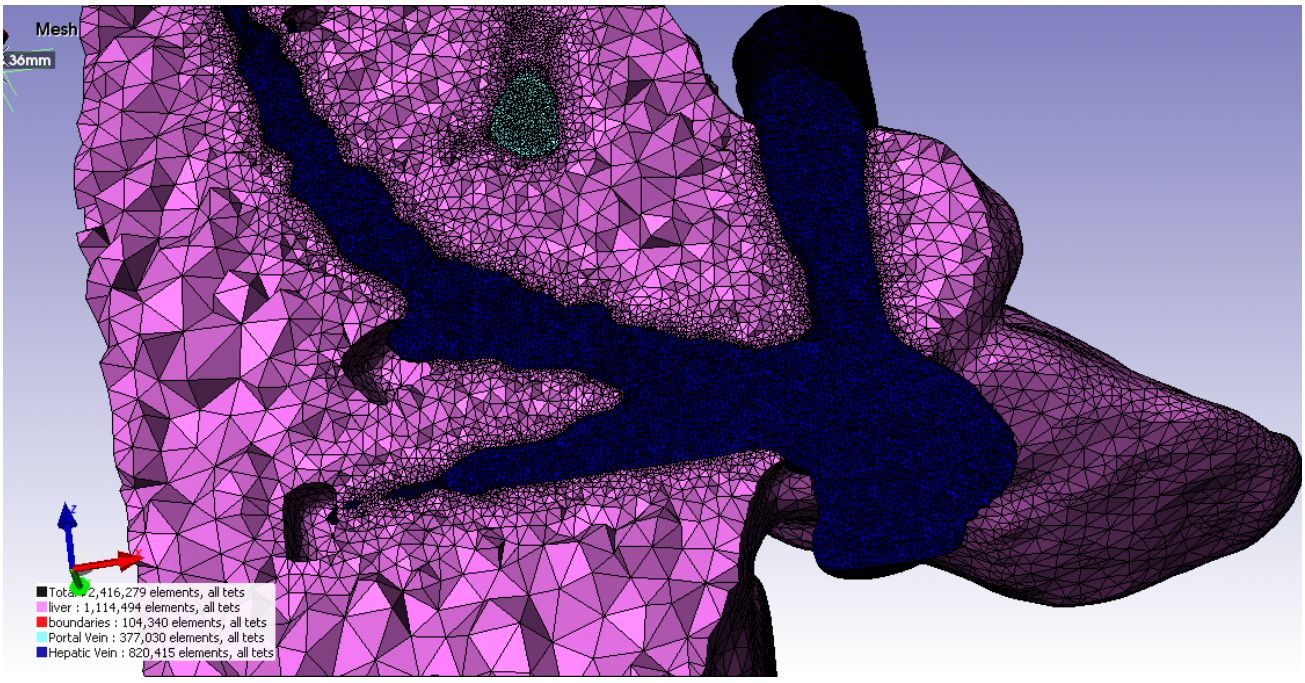

Figure 2. Example of mesh refinement of the liver (pink), arterial (dark blue) and venous (light blue) networks

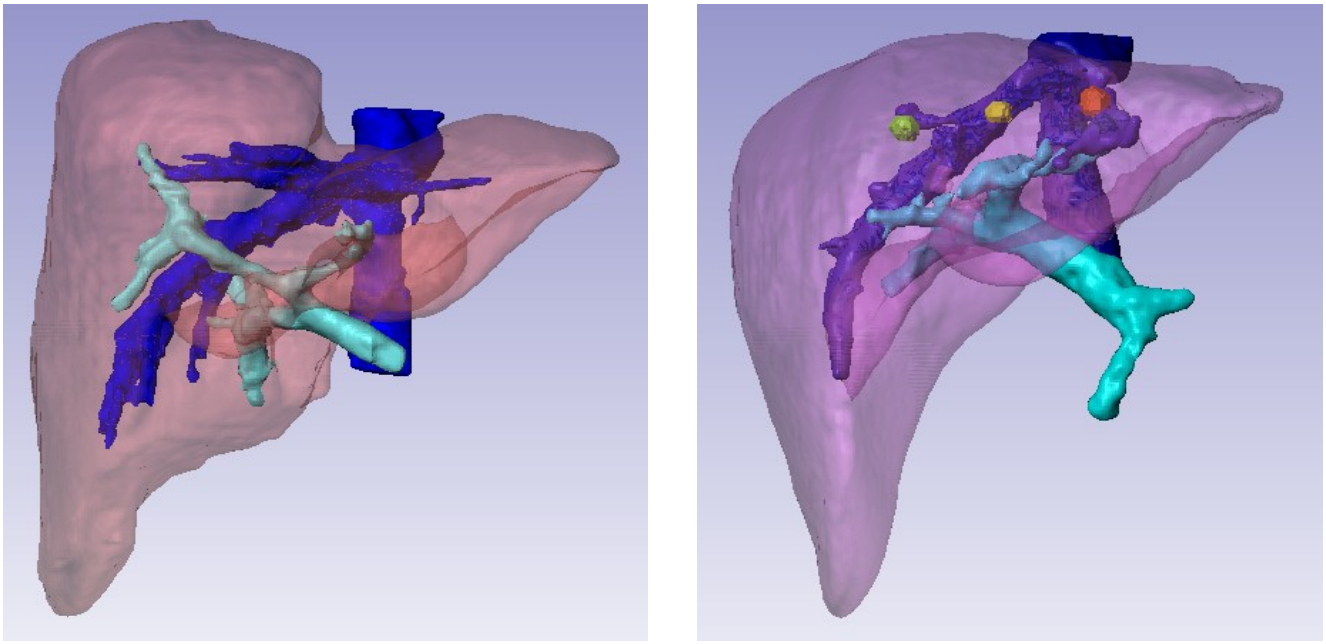

Figure 3. Anterior coronal views of the 3D multi-compartment models of the healthy (left) and the pathological (right) liver

The most reliable automated tool for liver segmentation was "Confidence connected region growing" algorithm. Automated tools were efficient for the extraction of the ROI (liver) from the background. However, in case of other organs pushing up against the liver, such as the gall bladder, no automated tool could determine the boundaries correctly. And manual segmentation was performed as a last resort. The next step was the filtering. The first filter applied to the liver mask was "Morphological filter". Then "Smoothing-recursive Gaussian filter" was used to reduce image noise.

Then "bilateral filter" and "confidence connected region growing" algorithm were applied to determine the masks for arterial and venous networks in the liver. Rectangular solids were drawn at the ends of each vessel in order to create boundaries and to facilitate the import of the model in COMSOL Mutliphysics.

The models of the healthy and the pathological liver were meshed using "+FE Free" algorithm with a coarser mesh refinement for the liver (Fig. 2).

To test anatomical accuracy of these models (Fig. 3), we performed manual segmentation of each liver according to Couinaud classification [4] based on the vascular anatomy (Fig. 4).

IV. Discussion

This study is a part of MIOTherIS project (Micro Innovative OncoTherapeutics Injection System) which aims to develop and commercialize an innovative and minimally invasive medical device allowing treatment of the tumourous mass by TMT integrating the most recent progress in the field of oncology. Unrivalled today, this device responds to the need of targeted treatment for cancer, which improves the patient's quality of life, optimizes surgical intervention and decreases the treatment's costs and duration.

Segmentation of the liver and associated structures in medical images is a fundamental task in the development of 3D visualizations. However, this process is very time-consuming task because manual segmentation is often required. The density of the liver tissue is similar to those of

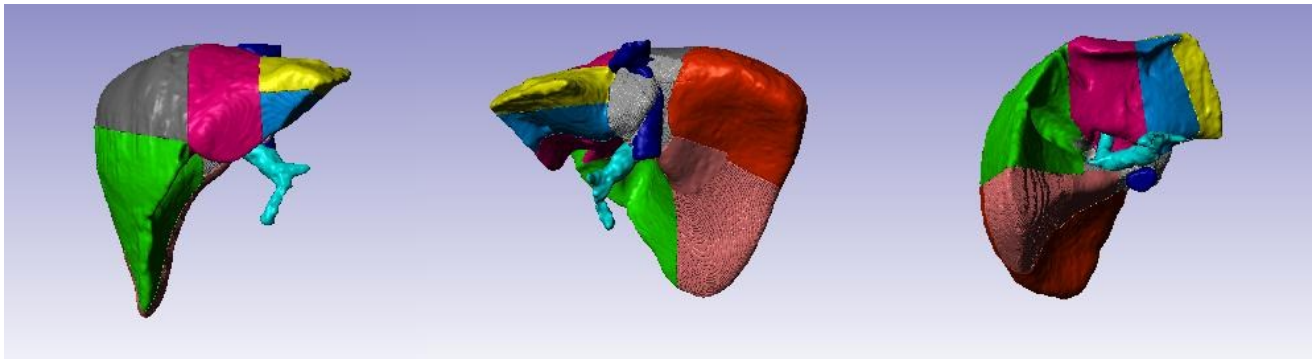

Figure 4. Example of anatomical segmentation of the liver: anterior coronal (left), posterior coronal (middle) and inferior transversal (right) views

some surrounding anatomical structures like the stomach, the pancreas, the kidney, and the muscles. Thus the boundaries between the liver and adjacent organs are often difficult to define making automated tools inefficient.

Several methods incorporating prior knowledge of the liver shape have been developed to fully automate liver segmentation and increase the precision of the model. Even though this method is much faster than manual segmentation, errors still occur in regions where other anatomical structures push up against the liver, such as the lower part of vena cava, the duodenum, the heart, muscles, the stomach and the pancreas [5]. This method is suitable to obtain fast and moderately accurate models of the liver. Segmentation using ScanIP, semi-automated tools and manual segmentation when needed offers to a much more precise model. Indeed, the rapidity is not more the main criterion because of recent increase of computer power, but the accuracy stills really important point.

Thus, FEA models which seemed to be impractical, especially for real-time simulations of complex objects some years ago, are considered now as the more accurate technique for simulating organ deformations. Non linear FEA models can accurately model non-linear elasticity with large deformations in soft tissues [6]. By incorporating non-linear soft tissue properties in 3D models of the liver, it would allow the interaction of the surgeon's instruments and the virtual liver model. According to the movements of the instruments, the liver's deformation can be simulated in a way that resembles a real operation [7],[8].

V. CONCLUSION

Our CT-image-based models were deemed accurate. However, the segmentation process was very much influenced by the quality of the underlying image; therefore better imaging technology is necessary in order to improve the image resolution and contrast. Unfortunately, anatomical structures are even harder to differentiate on MR images - another routinely available medical imaging technique for the liver - compared to CT images. Thus, more work is required in order to develop more accurate mathematical models reflecting in vivo soft tissue biomechanical properties. This would enable operators to construct more realistic simulators and subsequently immerse the user into a realistic virtual environment.

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