Computer oriented image acquisition of the liver: Toward a better numerical model for radiofrequency ablation

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Abstract—Simulating physiological interventions for planning purposes requires an accurate virtual liver model as computation input. To best meet the demands the data acquisition has to be oriented on image processing purposes. We provide a CT imaging protocol which makes it possible to extract much more vessels with the same segmentation algorithms than when using them on data sets from the clinical routine.

Medical evaluation of physiological models demand a statistical evaluation in a pre-clinical study, that means in a first step reproducible results for a large number of subjects. So data acquisition should be as automatic as possible without neglecting modeling demands. Image quality should be reproducible to guarantee an ongoing high quality of image processing results.

We evaluate the protocol by comparison of segmentation results with results achieved on standard data sets from clinical routine using the same segmentation methods. Results show that typically up to ten times more vessels can be extracted and the surface accuracy is improved.

I. INTRODUCTION

For interventions where the planning does not only rely on anatomical information but also depends on physiological processes model computations are necessary to predict the intervention result. Where physiology goes hand in hand with anatomy, the computational model relies on anatomical imaging as geometry input. As the acquired images are not processed for visualization but for computation, accuracy and low error rates gain much higher importance.

The paper discusses different requirements for intervention simulations and shows how to adapt standard imaging techniques to computer needs to get the best possible outcome of the image processing. The aim is to generate a model suited for computations for physiological intervention result prediction. As models are intervention specific the image acquisition is too. The presented work focuses on radiofrequency ablation as example.

a) Radiofrequency Ablation as clinical intervention: RFA is a minimally invasive procedure, where a needle electrode is inserted percutaneously into a tumor. The electrode emits electromagnetic waves and the tumor is heated up and

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Philipp B. Stiegler is with the Institute of Transplantation Surgery, Graz University Clinic of Surgery, Auenbruggerplatz 10, 8010 Graz, Austria rupert.portugaller|philipp.stiegler@meduni-graz.at thereby destroyed. A detailed description of the procedure in clinical practice can be found for example in [1] and [2].

The intervention is successful, if the resulting necrosis zone encompasses the whole tumor and a safety margin without damaging too much surrounding healthy organ tissue. Success is claimed if follow up scans do not show a local recurrence of the tumor.

b) Biothermal modeling of the process: From an engineering point of view, the needle electrode sends electromagnetic waves into the tissue. The ions in the tissue start moving and friction generates heat. Tissue coagulates and cell fluid starts boiling. The electro physiological principles are explained in detail by Organ [3].

Different effects determine the shape of the necrosis zone. Most dominant here is the heat sink effect in proximity to larger vessels [4]. Minor effects concern for example tissue properties and inhomogeneities.

Physiologically modeling radiofrequency ablation is done by applying the bioheat-equation including a term for heating by electromagnetic power (compare f.e. [5]).

$$pc\frac{\partial T}{\partial t} = \nabla \cdot (k\nabla T) + \vec{J} \cdot \vec{E} - h_{bl} \left(T - T_{bl}\right) - Q_m \quad (1)$$

Model equations like that are computed applying Finite Element Analysis to solve the partial differential equation in three space dimensions.

II. RELATED WORK

A recent physiologically based model was created by Sheu et al. [5]. The used liver model was strongly reduced in complexity and is not suited for treatment planning purposes. Kroeger et al. developed a physiologically based model [6], applying Finite Element Analysis (FEA) to the bioheatequation on real patient data.

There are various segmentation methods for the liver itself, possible tumors and vascular structures. To present all of them would go beyond the scope of this paper. In this work, the semi-automatic method of Unger et al. [7] is applied for segmentation of the liver itself, and an approach for segmentation and separation of the livers vascular trees that is based on the work of Pock et al. [8].

III. MODEL REQUIREMENTS

A. Anatomy and medical instruments as geometrical input

The liver holds as macroscopic structures the parenchyma, three vessel trees, and bile ducts including the gall bladder. The three vessel trees include, besides the hepatic artery and hepatic vein, the portal vein, which delivers nutrients from the digestive tract for processing in the liver.

Due to the importance of the heat sink effect the most relevant anatomical geometry information concerns location and size of the vessel trees in the liver. Bile ducts carry resting fluid and therefore do not contribute to the heat sink effect. So their location and size is not needed as geometry input.

As the whole process is induced by a radiofrequency generator, the electromagnetic dispersion is computed as reason for tissue changes. It originates in the needle electrode tips which are the relevant geometrical information for the medical instruments used in the procedure.

B. Model quality demands

A geometry used as input for computations has to be oriented on its suitability to deliver optimal simulation results. Every error in input will propagate and diminish the quality of the simulation result. So, a high resolution is most desired. Medical studies show, that venous vessel trees with diameter < 3 mm are damaged in the ablation procedure. Arteries are rarely thicker than 2 mm. So according to the sampling theorem (Nyquist - Shannon) images should be reconstructed with resolution of no more than 1 mm – if possible less.

Errors in detection of blood vessels as well as errors on their diameter have to be best avoided. Detected structures have to be identified correctly as part of a specific vessel tree, because blood flow differs for the three vessel trees. The dominating effects in modeling rely on proximity to vessels. Hence, information on distance between vessels or else distance from electrode to vessel are very important.

The features of the desired virtual liver can therefore be summarized as follows:

- a full virtual liver model encompassing structures carrying flowing fluids
- a high resolution for the geometry input
- low errors in finding structures or evaluating their size and location
- clear identification of the created substructures

IV. IMAGE ACQUISITION

Imaging opens a wide range of possibilities but medical research and clinical practice when using radiological imaging are oriented on producing images to be interpreted by human experts. Image processing has different necessities and opens new possibilities. For construction of a model for simulation image acquisition should be done oriented on image processing capabilities and necessities to meet the demands defined above.

A. Volumetric image acquisition

CT or MRI are best suited for a reconstruction in 3D. They differ in abilities to image soft tissue, in resolution, slice thickness, and in acquisition time. In both modalities contrast agents (CA) can be used to highlight structures.

Table I compares the image modalities CT and MRI for liver imaging from an image processing point of view. A full virtual liver model encompassing all macroscopic structures that are carrying flowing fluids can be reconstructed from CT as well as MR images. However, segmentation is eased by a high and constant contrast. Consequently, we use mainly CT and a high dose of CA in our experiments.

CA are applied by injection into a peripheral vein. The CA bolus passes the three vessel trees at different times. So which structure is highlighted by the contrast agent depends on the time after injection when the image is taken. For the liver, the CA first reaches the artery, which is visible as one single vessel tree on an image taken in the arterial phase. Next the CA enters through the portal vein and right after that leaving the liver through the hepatic vein. Both venous vessel trees are visible in a short time interval so an image will always show both venous phases. One of them is just less optimal highlighted if the timing is correct.

In clinical practice bolus timing is defined as standard for an average human. With a *sure start* Region of Interest (ROI) detection the delay between arterial and venous phase is typically between 8 s and 20 s depending on the metabolism of the patient. Ideally the last sequence will then show both, the portal veins and the hepatic veins.

B. Subsequent images and registration

While for unprocessed images it is important to have all relevant information in the same image to see their location and distances to each other, a reconstruction from more than one image source is possible applying image processing. Having more than one vessel tree highlighted in the same image makes connecting vessel fragments in post processing difficult in situations where two vessel trees cross or lie close by. Hence, to fulfill the requirement of identifiable imaged structures an acquisition of three separate images in three phases, each one highlighting one single vessel tree would be best suited and most desired. In our case this is limited due to a slightly different pig metabolism.

The main source for deformations of the liver is breathing. Deformations due to heart beat are minor and can be neglected. So as long as image volumes are taken with breath hold no deformations are present in subsequent acquired images and information can be fused directly without nonrigid registrations. This results in a high reliability for location and size of the imaged structures. Acquisition time for one single image volume has to be short to be able to take three images volumes without breathing. A high-end CT scanner can produce images with a high resolution and a small slice distance with a short acquisition time, which fixes the imaging protocol towards CT.

C. Image acquisition protocol to fulfill modeling requirements

We take three volumetric CT images in the same respiration phase. Images are reconstructed as $512 \times 512 \times 320$ matrix with a slice distance of 0.5 mm. *Sure start* ROI detection within the aorta starts five seconds after the image intensity has reached 180 Hu in the aorta. Since we dispose of a 320 lines CT we can take a whole volume within one

TABLE I				
IMAGE MODALITY	FEATURES	IN LIVER	IMAGES	

feature	СТ	MRI
vessel trees bile ducts resolution spatial resolution (slice thickness) acquisition time	imageable using CA, but a maximum of two vessel trees in one image not imageable easily < 1 mm < 1 mm short, ≈ 0.7 s per rotation	all three can be included in one image if not using CA, but three phases are usual imageable better soft tissue distinguishing spatial resolution lower than CT, either thicker slices or very high acquisition time high, difficult to take images with small slice thickness during one breath hold, breathing compensation extends acquisition time

rotation. This also keeps the dose at a lower level. The portal vein scan is performed between 20 and 25 seconds after the arterial scan and another 25 seconds later the hepatic scan is performed. These values also depend on the metabolism of the pigs and is specified when the weight of the pig is known.

V. IMAGE PROCESSING

The applied post processing algorithms and techniques have to be oriented toward avoiding segmentation errors. Semi-automatic methods producing good results are preferred over fully-automatic methods that may produce errors. However, user interaction should be kept as low as possible.

From the three volumetric dataset the liver itself and the different vessel trees are segmented as outlined in Figure 1. The liver itself is clearly visible in each of the datasets and has to be segmented only in one of the datasets, while the different vessel trees are only imaged optimally in the right phase of the contrast agent distributation and segmented in the according dataset.



Fig. 1. Segmentation pipeline showing data flow and required user input.

For segmentation of the liver the semi-automatic method of Unger et al. [7] is used. The method is based on a 3D global optimal surface finding method embedded as a total variation formulation that allows for an efficient GPU based implementation. The tool requires specification of object and background seeds and adapts the segmentation to boundaries in the image domain separating these seed regions. The method allows for full control over the segmentation result, but typically requires only minimal user interaction. In an evaluation performed by Unger et at. on a publicly available database for segmentation of liver CT datasets with manually generated reference segmentations (http://sliver07.isi.uu.nl) an average rootmean-squared surface distance of 1.93mm was achieved with this method. This value is comparable to the inter-user variance of trained observers and also competitive with other methods specifically developed for liver segmentation [9].

For segmentation of the vessel trees an approach based on previous work of our institute [8] is used. The approach initially identifies all tubular structures in the dataset in a fully automatic fashion. In a subsequent step, a user can select the roots of the different vessel trees and the associated vessel systems are reconstructed based on anatomical knowledge about the structure and the branching pattern of vessel trees. This allows separating multiple interwoven vessel system and generation of completely connected skeletons. In the last step, the derived information is used as a shape prior to constrain in the actual segmentation. The method has been evaluated on clinical datasets based on an assessment by an experienced radiologist who verified the methods ability to successfully identify all visible vessels, to correctly separate and to accurately segment the different vessel trees. Details of the method and the evaluation are to be published.

VI. RESULTS

For evaluation, we present results achieved with these segmentation methods on CT dataset of human livers that were acquired with standard imaging acquisition protocols as used in clinical practice and compare them to results achieved with the proposed imaging acquisition protocol on pig livers, see Figure 2.



Fig. 2. Comparison of extracted portal vein trees from (left) a low contrast and low resolution CT dataset of a human liver and (right) a pig liver imaged with the presented protocol.

During evaluation of our vessel segmentation method on clinical CT datasets of humans and on phantom datasets the use of different imaging protocols already showed a strong influence on the number of identifiable vessels and the achievable surface accuracy. The protocol also allows optimal imaging of all three vessel trees as shown in Figure 3. To account for the different anatomy of humans and pigs we compared the percentage of segmented vascular volume relative to the segmented liver volume. We are able to identify typically up to ten times more vessels with our protocol on pigs compared to a standard protocol applied to patients. The difference can be clearly seen on the portal vein tree example in Figure 2. The segmentation results have been evaluated by physicians who verified that all vessels have been segmented correctly.



Fig. 3. The presented protocol allows optimal imaging of the arteries, portal veins, and hepatic veins such that all tree vessel trees can be reconstructed in detail.

The presented imaging protocol also allows us to generate much smoother and detailed liver surfaces as shown in Figure 4. The accuracy of that surface is a central requirement to guarantee a reasonable simulation within the liver.



Fig. 4. Comparison of segmented livers from (left) a low contrast and low resolution CT dataset of a human and (right) a high contrast and high resolution CT of a pig. In the pig dataset the hole in the liver results from the gall bladder and stomach that were not considered during segmentation. Additionally, a part of an ablation needle and an optical tracking target are visible.

VII. DISCUSSION AND CONCLUSIONS

We created an imaging protocol oriented on needs for the simulation of a physiological intervention (radiofrequency ablation) and on the needs of the applied image processing algorithms. The protocol was applied in the course of an animal study. Most relevant for the geometry information in the simulation is the correct extraction of vascular structures. We show as result of our method that we are able to extract typically up to ten times more vessels as for images acquired during normal patient treatment.

Our method would allow a fully automatic processing if a better control over the bolus timing could be achieved. The aim would be to take really separate images for all three vessel trees which also should be homogeneously highlighted and completely connected. Unfortunately, pig metabolism is too fast to get the images homogeneous in brightness and clearly separated between the portal venous phase and hepatic venous phase.

MRI is often the imaging modality of choice due to its ability for soft tissue resolution. Our demands focus on the location and determination of the real size of vessel trees. These are better achieved using CT as it stands out due to high resolution and low acquisition time, which avoids breathing deformation. MRI can take images with breathing compensation but this extends acquisition time (and therefore time for anesthesia) significantly. Furthermore, MRI introduces the problems of nonlinear gradient decrease with distance from the magnetic iso-center. CT on the other hand images the geometry without implicit distortions.

Due to the high radiation the protocol cannot be applied to patients in clinical practice. However, for evaluation of a model computation in a pre-clinical study, our results offer a great progress. The next efforts go into attaching physiological properties to the virtual liver models and towards computation of simulation results on those.

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