

# Generation of Personalized Computational Phantoms Using Only Patient Metadata

X. Zhong, N. Strobel, J. C. Sanders, M. Kowarschik, R. Fahrig, A. Maier

**Abstract**—The use of personalized computational phantoms (CPs) describing a patient’s anatomy could enable attenuation correction for emission tomography without the need for a separate CT acquisition, thus reducing radiation dose to patients and cost to clinics. We propose a method to estimate such a phantom using only patient entry information (PEI) comprised of gender, height, and weight. The method uses a two-step machine learning-based approach whereby a joint subspace linking PEI to boundaries describing anatomical cavities is learned. Average organs from the training database are then deformed to fit within the cavities and used to populate them. We validate our method against two existing CPs and nine patient CT scans. The results show mean organ center of gravity displacement and volume errors in patients of less than 3 cm and 40%, respectively, in the lungs, liver, spleen, and kidneys. The relatively large volume error was most likely due to large inter-patient variations in organ mass. Nevertheless, our approach represents a step towards personalized CT-less AC and warrants future work to determine clinical relevance.

## I. INTRODUCTION

PATIENT surface and anatomical models – also referred to as computational phantoms (CPs) – have found widespread use for a variety of medical applications. Personalized CPs, have long been used for dosimetry monitoring and optimization of system settings [7], and more recent applications include optimization of acquisition settings and workflow for diagnostic CT [8] and monitoring of skin dose and patient positioning for interventional X-ray scans [6]. This promising technique could also be useful for positron- and single photon- emission tomography (PET and SPECT), which currently relies on CT scans acquired immediately before or after the emission scan to generate a  $\mu$ -map for attenuation correction (AC). The ability to generate a patient-specific model without a full CT could provide a means by which AC could be carried out without an extra transmission scan – reducing radiation dose to patients and cost for clinics.

Existing approaches to generate personalized CPs include deformation of a template using scaling factors derived from anatomical measurements [4], [2], and body mass index (BMI) [3]. Unfortunately, these methods are based on standard measurements taken in a standing pose and do not meet requirements faced in diagnostic scanning, where patients usually lie supine on a table. This change in position may cause inaccuracies as current models have not been designed to adapt their anatomy based on a difference in pose. Moreover, scaling of a template is often insufficient to model deformations of internal organs.

To enable use personalized CPs for AC in the routine clinical setting, any approach must be able to reliably estimate a

sufficiently accurate representation of the patient anatomy in the proper pose. Below, we propose a machine learning-based data-driven method to accomplish this using only metadata from patients.

## II. METHODS

Our approach has two major components: determination of a patient-dependent boundary to guide organ placement, and filling of this volume with models of the organs themselves. We begin by learning a joint subspace linking patient entry information (PEI, comprised of gender, height and weight) to the body surface and internal body cavities under consideration (e.g. thoracic, abdominal). This pipeline is shown in Fig. 1.

We use two separate databases consisting of 1) patient surface meshes (acquired in standing pose) and 2) segmented 3D diagnostic scans (CT, MRI), both with associated PEI, as our training data for the joint subspace learning.

Segmentations of the body surface of each MRI/CT volume, as well as of the internal organs and cavities are available. Database 1 provides a link between the PEI and surface meshes in standing pose. After registration with the surface mesh available from database 2, a further link is then established to the cavity borders contained therein. Database 2 is measured in supine pose, and, as the position of body cavities is pose-related, we account for this difference by calculating a deformation field between the two using non-rigid independent component analysis. We refer to this as the gravity deformation field and map it into the joint subspace. The result is a joint subspace that allows the estimation of organ cavity borders given solely the PEI.

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The workflow for internal organ estimation is shown in Fig. 2. First, we use the PEI and joint subspace from the previous step to estimate each cavity boundary separately. The associated volume in the training set is registered non-rigidly to the estimates using the symmetric image normalization approach [1]. The same deformation field is subsequently applied to internal organs. Subsequently, we average the resulting organ estimates to obtain our final organ estimation. As a last step, the position of the internal organ estimates is fine-tuned based on anatomical prior-knowledge. This ensures that the distance between organs known to be adjacent to each other is minimized.

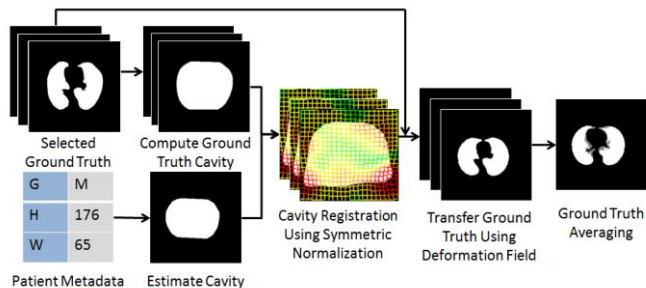


Figure 2. Workflow for internal organ estimation via cavity determination.

We trained our framework using nine male full body CT scans from the Visceral data set and validated results on two voxel models: the Visible Human (VH) and the Golem (G) from the GSF family (PEI is publicly available in both cases). We also tested it on nine manually segmented full-body CTs acquired during a PET/CT protocol. We evaluated errors in the lungs, liver, spleen, and kidneys according to center of gravity (COG) displacement and volume differences.

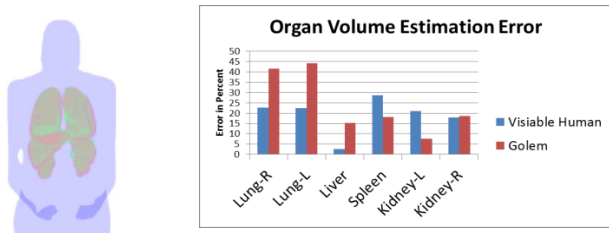


Figure 3. Internal organs of the Visible Human (green) and estimated corresponding models (red) overlaid in AP view (left). Organ volume estimation errors against numerical phantoms (right).

### III. RESULTS

Fig. 3 (left) provides a visual impression of differences between our proposed method and a phantom by superimposing our estimation onto the VH voxel model in anterior-posterior (AP) view. Fig. 3 (right) shows the organ volume estimation error with respect to both phantoms. Largest errors were found in the liver and lungs for VH and G, respectively. The results from the patient validation are summarized in Fig. 4, where the COG error in mm (top) and the volume estimation error (bottom) are shown. Mean COG and volume errors were below 30 mm and 40%, respectively for all organs.

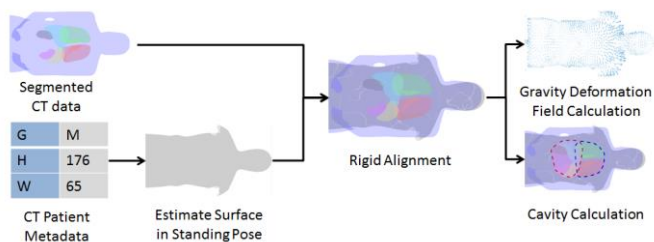


Figure 1. Workflow for estimation of gravity deformation field and cavities.

### IV. DISCUSSION AND CONCLUSION

Our method yielded promising results when estimating the position of the internal organs, but volume errors are relatively large. As organ mass is known to vary widely between individuals, it is somewhat unsurprising that accurate estimation of organ volume is difficult with limited information. Another contributing factor is that our test data were taken from diagnostic scans of patients whose anatomy may be altered by underlying pathology. Although we were not able to account for all inter-patient variations, it is worth noting that existing computational modeling methods [4], [5], [3], [2] rely purely on statistical norms to find target volumes and are therefore even less able to account for individual differences. A limitation of our evaluation is that the number of organs considered is still relatively small. However, this shortcoming is not an inherent restriction of our method, but rather imposed by our training data.

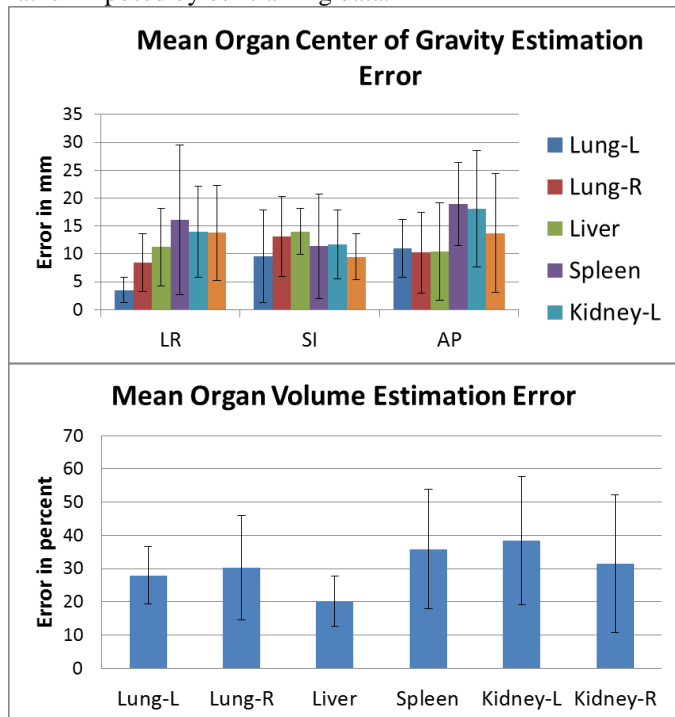


Figure 4. Mean organ COG displacements and volume estimation errors from patient validation.

We proposed a novel personalized anatomical model estimation method. Using only PEI, a personalized patient model can be estimated with mean COG error below 3 cm and volume estimation error below 40%. To determine the ultimate clinical relevance of the method for AC, patient CPs

would need to be converted to  $\mu$ -maps, and the resulting SPECT or PET reconstructions with CT-AC and CP-AC would need to be compared.

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