

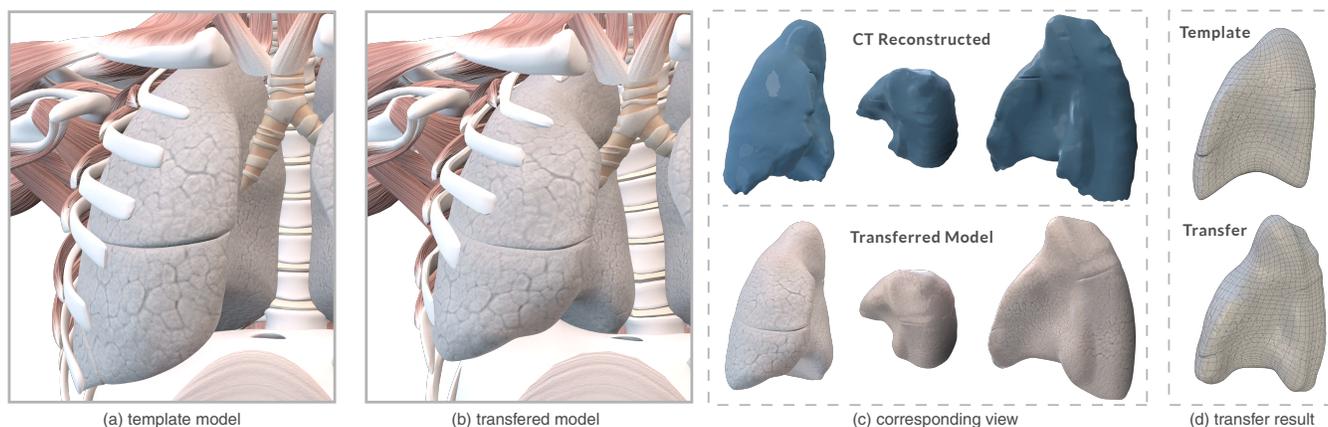
# 利用醫學影像重建精確的完整人體模型

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**Figure 1:** Our method transferred the lung from (a) a template model to (b) a patient’s model with respect to the lung CT scanning. Note that our method not only successfully reconstruct the lung shape (c), but also update the surrounding anatomic structure.

## Abstract

正確的內部組織結構的人體虛擬模型對於醫學應用而言相當重要，例如手術模擬、構造分析等，然而，建構一個三維空間的精準虛擬模型通常需要有經驗的模型師花費大量的時間與精力來完成。我們在本篇論文提出了一套半自動化的方法來更有效率的建構之於特定目標的人體模型，我們不只將人體樣版模型轉換以符合目標外觀，還結合醫學影像使內部器官組織更加準確定位。我們透過求得Laplacian 變形場來變形我們的樣版模型，而整套流程將能處理不同的人體醫學內部結構資料如電腦斷層掃描與核磁共振的切片資料。我們呈現了幾個變形結果，這些結果展示我們的方法在目標區域的準確度不只是在視覺上有效，而在醫學上也兼顧其內容的正確性，而我們也透過兩套不同的Error Metrics 來評估我們的變形結果。

## 1 Introduction

The widespread of the VR/AR devices has ignited the rapid development of high quality virtual content for various applications including entertainment, education, and healthcare. Among them, the development of surgical simulation has drawn a lot of attentions. The major reason is that surgery was traditionally learnt by repeated practice on patients. Trainee surgeons were required to be exposed to innumerable operative cases over many years, with supervision tailored to their needs. However, the recent changed of the development of surgical technique [Kneebone and Aggarwal 2009] has led to the situation where the training opportunities are reduced for young doctors. As a result, in order to provide another ways of accurate training opportunities, they start to use surgical simulations to learn the skills.

To better support the skills translation from the surgical simulation to the real world surgery on patient, it is vital that the simulated environment has to represent the anatomic environment faithfully. Before a surgery procedure is taking place, the doctor must collect the data from the patient, including measuring different body physical data and taking medical images of the affected region. With the

collected patient data, the doctor can start to plan and practice about the surgical procedure using either imagination training or simulation software with reconstructed anatomic environment. However, reconstructing such realistic anatomic environment of the affected region of human body, *i.e.*, the anatomic model for specific patient, requires great amounts of time even for professional 3D artists with anatomy knowledge. Most of the time, the artists use common 3D modeling tools such as Maya, 3D Max, or Blender to create delicate surface model with textures. And then they carefully manipulate the surface model to match the scanned medical images of the patient. This final step is really important for surgical simulation since the it provides the details of the affected region (or affected organs). And the efforts of this step usually takes a great part of the entire workflow.

To address this issue, we propose a framework for reconstructing the accurate anatomic model with provided medical imagings. Our framework takes patient’s medical imagings and body statistics, with a manually built surface-based anatomic model, and generate accurate anatomic model for doctors to practice the surgery in a realistic environment. Our method is based on Anatomy Transfer [Dicko et al. 2013], but focus on accurately reconstructing the affected region instead of an visual pleasing full body anatomy transfer.

Our method start from reconstructing the human shape using the human body statistics, including height, weight, waistline, bust, and so on. We use a deformable shape software [The MakeHuman team ] to generate a human body that fits the body statistics of the patient. In order to search for the right parameters for reconstructing the human body, we use Bayesian Optimization [Brochu et al. 2010] to efficiently search the parameter spaces. Our method then first follow Anatomy Transfer [Dicko et al. 2013] to perform the first step anatomy transfer. However, the transfered anatomy is usually very different from the patient’s situation. The the major challenge of our method, is that how to further improve the accuracy of the reconstructed anatomy model that can faithfully match the patient’s body.

Our framework provides a semi-automatic approach to address this. We first identified the organs in the affected region, and provides a semi-automatic way to find the correspondences between the transferred model of the organ and the reconstructed organ shape from the patient’s scanned data. Once we obtain the correspondences, we can then deform the organ model into the shape to match the patient’s scanned data. As the final step, we reconstruct the entire anatomy models with the affected organs as constraints. The final reconstructed anatomic model is accurate in the affected region, with the other parts are still visually appealing.

## 2 Related works

Ali-Hamadi *et al.* [Dicko et al. 2013] proposed a anatomy transfer method to create a plausible appearance in inner anatomy system using a template model. They consider fat tissue as an outside layer to be shrinking using a fat distribute map. This process can handle irregular skin bumps like a tumor or different shape between the target and source model. However, they only target on the surface information and simple fat distribution during the registering process. This leads to non-medical-correct result that below the integumentary system. The major difference of our method, is that in order to provide accurate anatomic model reconstruction around the affected region, we take the medical imaging reconstructed volume data into consideration. Saito *et al.* [Saito et al. 2015] proposed another method based on biology growing pattern, with growing of skeletal muscles and subcutaneous fat using physics-based models. The method provides the ability to control the desired shape by manipulating the parameter used for growing pattern. This method is suitable for musculoskeletal modeling, however, they cannot growth inner organs due to the high complexity of the physic simulation process. And the subject parameter search is not intuitive and requires a lot of user’s efforts.

Arnold *et al.* [Arnold et al. 2000] creates subject specific biomechanical musculoskeletal models from MR sequences for the precise surface model in muscle motion status. They utilize the accuracy of MRI imaging technology in muscles and bones, the extracted surface then become a physic simulate system for movement determination application.

## 3 Overview

We show the workflow of our framework in Figure 2. Our goal is to reconstruct the internal body anatomic model that accurately matches the patient’s body around the affected region. The affected region is defined by the doctor, and is represented as the available medical scanning region.

We first collect patient information including his/her body statistics and medical scannings (using CT or MRI). We use body statistics to reconstruct patient body model, and use the medical scanning to reconstruct an initial volume data of inner anatomic environment including different organs. Meanwhile, we prepare an template model, including the surface model of body surface, and surface model of the entire inner body anatomic environment, including different organs, blood vessel, muscles, and bones. To faithfully reconstruct the anatomic model of a patient around the affected region (in this work, we focus on the organs), we construct an initial transferred anatomic model based on Anatomy Transfer [Dicko et al. 2013] (see Figure 2(a)(b)).

In the second step, we further refine the anatomic model in the affected region by establishing the correspondences between organ models within the affected region. Here we use a semi-automatic approach, we asked the user to create several landmarks between the surface model in pre-built model and the reconstructed volume

model. With the provided landmarks, we utilize a dense correspondence method based on functional map [Nogneng and Ovsjanikov 2017] to obtain the correspondences. If the user is not satisfied with the result, they can kepp adding new landmarks. Our system will highlight the correspondence errors from fucntional map, to help the user better locate where to put more landmarks to make the entire correspondence field more accurate.

After establishing the correspondence field, we utilize it to deform the organs in the initial patient anatomic model to better match the volume data from medical imaging. Finally, we reconstruct the patient anatomic model by solving the same transfer problem with the deformed organs as additional constraints.

## 4 Method

In our framework, we working on transferring anatomic model between the following two shapes:

- **Template model.** We template model is purchased from *PlasticBoy* and it is created by professional artist. The model is in mesh format, and it contains the outer body shape, bones, muscles, and different organs. We denoted the template model as  $\mathbf{M}_T$ .
- **Patient’s body scanning.** For the patient body shape mesh, we use a depth camera [Tong et al. 2012] to obtain the 3D point cloud. We denoted the template model as  $\mathbf{p}$ . And we will use the obtained point cloud for further parametric body shape reconstruction.

### 4.1 Skin Registration

To facilitate transfer anatomic models, we need to first register the subject body scanning to the template model, and obtain the correspondences between them.

#### 4.1.1 Subject body model preparation

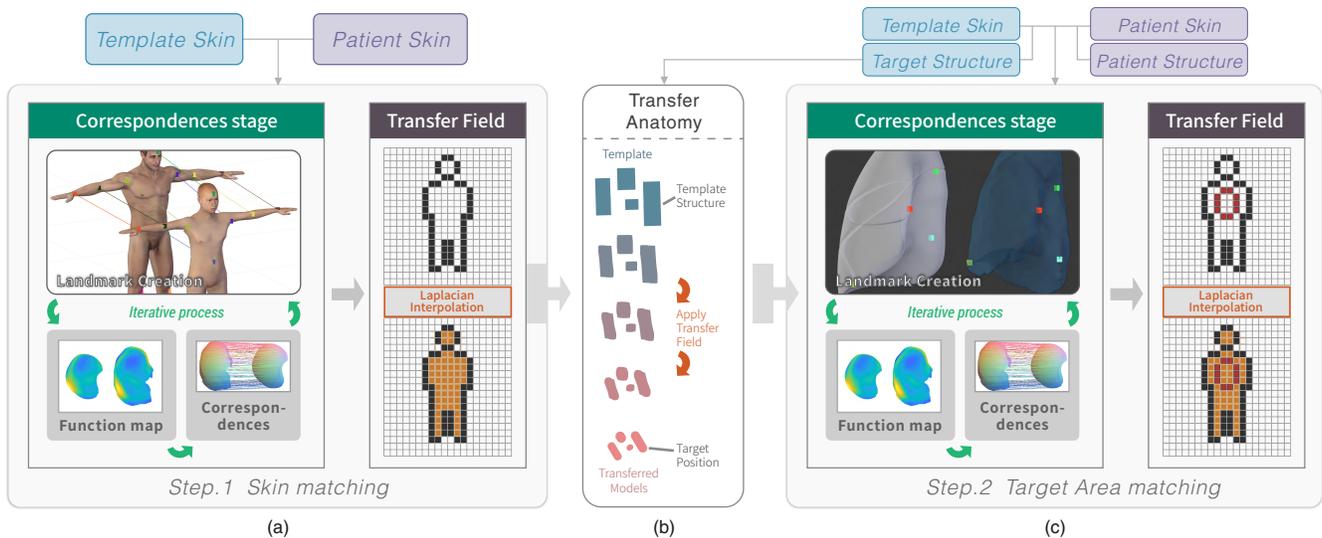
The first material we need, is the registration from the template model to the patient’s scanning data. To achieve better registration result, we tends to perform the registration under the same vertex distribution, since the point cloud in the scanning is quite messy, and the registration algorithm is likely to become unstable under the noisy input. We thus utilize the parametric body model like MakeHuman [The MakeHuman team ] to build the human body model with nice topology. Since there are many parameters in the parametric body model, we thus identify the most relevant 10 parameters, including burst size, hips size, lower leg height, upper leg height. To find the best parameters to match the scanned 3D point cloud, we formulate this problem as follow:

$$\mathbf{x}^* = \operatorname{argmax}_{\mathbf{x} \in \mathcal{P}} f(\mathbf{x}), \quad (1)$$

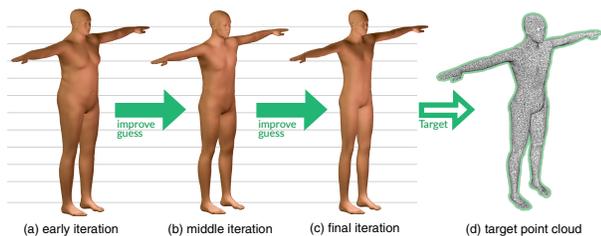
where  $\mathcal{P} \in \mathbb{R}^{10}$  is the 10-dimensional space of the body parameters we want to explore, and  $f(\cdot)$  is a function measuring the difference between scanned 3D point cloud and the generated parametric body model. We define the difference measuring function  $f$  as follow:

$$f(\mathbf{p}, \mathbf{M}^k) = \sum_{p \in \mathbf{P}} \|(\phi(p_i) - p_i)\|_2^2, \quad (2)$$

where  $\mathbf{M}^k$  is the parametric body model at  $k$ -th iteration of Bayesian Optimization, and  $\phi(p_i)$  is the projected point on  $\mathbf{M}$  of point  $p_i$ .



**Figure 2:** The workflow of our two steps anatomic structure transfer framework.

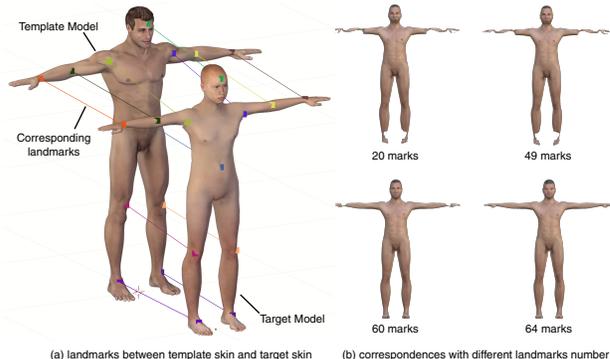


**Figure 3:** We show the Bayesian Optimization process with a sequences from early iteration (1th) to final iteration (50th). The point cloud image in the right hand side is our synthetic data generated with other skin model.

We solve Eq. 1 using Bayesian Optimization, since the MakeHuman [The MakeHuman team] body model generator is hard to evaluate and we don't know its gradients with respect to each of the parameters. We use the expected improvement (EI) as our acquisition function and use Gaussian Process prior to solve the expectation with closed form solution. Please check [Brochu et al. 2010] for details about Bayesian Optimization. In Figure 3, we show that the patient body can be reconstructed faithfully using our Bayesian Optimization and MakeHuman [The MakeHuman team].

#### 4.1.2 Functional Map Correspondences

After register the template model and the rebuilt model from the patient's scanning, we then further identify the dense correspondences between them. We apply functional map approach [Nogneng and Ovsjanikov 2017] on both polygonal meshes and we choose Laplacian mesh feature as basis, combine with Wave Kernel Signature. We also need to choose some landmarks between two the meshes if they are quite different. In our case, 6 20 landmarks are required user to manually mark. We show the example landmarks in Figure 4, however, it is likely that the initial landmarks can not lead to satisfied correspondences. In our system, we design an iterative process for obtaining the good correspondences. Our system will indicate the bad geometry area with color or displacement as figure 5, and the user can manually put down additional landmarks on these spots. This process iterate until correspondences are satisfied.

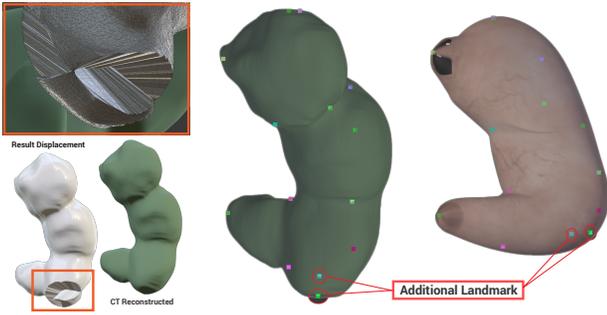


**Figure 4:** (a) Using landmark between template skin and target skin. (b) More landmark will lead to a more stable result. The final correspondences from this topology use 64 landmark for accurate result.

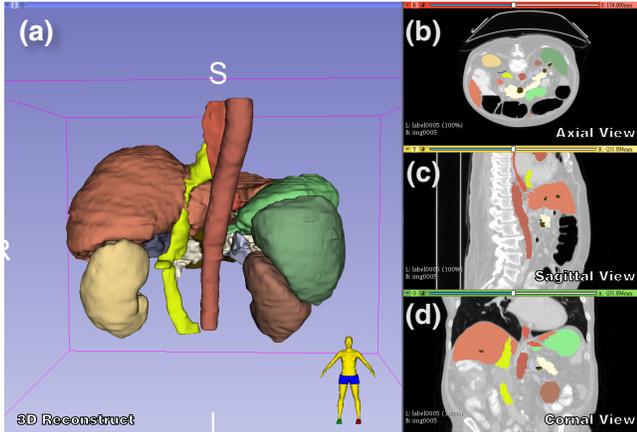
Noted that not every pair of surface shapes can be matched easily using this iterative process. When the two shapes are too different with each other, we can first apply Laplace mesh editing [Sorkine et al. 2004] using small amount of landmark pairs as pivot points, and reduce the shape differences between our subject and target shape. This is more common when dealing with surface shapes of different organs, since the organ in the template model can not match all the possible shapes in real world human organs.

#### 4.1.3 Transfer Displacement Field

After we establish the correspondences between the template model and the patient's skin surface model, we can start to calculate the transfer field between them on the skin surface. The purpose of the transfer field is to facilitate the inner anatomic model transfer. We first build a voxel grid that enclose the surface shape, and uniformly sample many points on the surface. With the established correspondences, we compute the displacement vector of each sample point and its correspondent point. Within each voxel grid, we compute an average displacement vector of all sample point's displacement vectors if the sample point lies inside the voxel grid. We now have



**Figure 5:** The correspondences flow with too few landmarks. The user is able to manually put down additional landmark to improve the result.



**Figure 6:** We show an example abdomen reconstruction using MALBCV [Bennett Landman 2015] dataset. We reconstruct the 3D surface model (a) from the labeled segmentation slices (in three different views (b)(c)(d)) using Marching Cube [Lorensen and Cline 1987] in 3D Slicer [Kikinis et al. 2014].

the displacement of the each outer voxel grid (*i.e.*, the voxel grid that contains surface in it), and we utilize these displacement vectors of voxel grids as Dirichlet boundary constraints and solve the displacement vectors of each inner voxel grids.

## 4.2 Modeling Affected Region

After we reconstruct the initial anatomic model of the patient, we now focus on utilizing the auxiliary patient scanning data to improve the accuracy of the affected region. We achieve this by deform the corresponding organs in the affected region of the initial anatomic model to match the reconstructed models from the segmented scanning organ shapes. We manually assign key points as landmarks between the initial reconstructed models and the scanning models. We then use the models in affected regions as new boundary conditions and solve the entire transfer field again. Finally, we obtain the accurate reconstructed anatomic model.

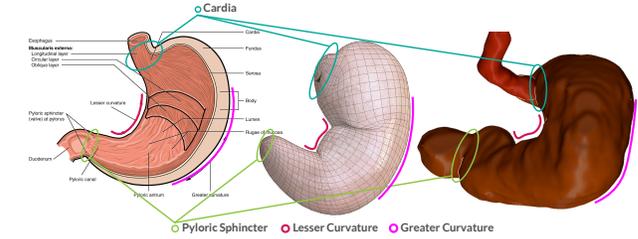
### 4.2.1 Affected Region Organ Modeling

We use an abdomen CT database from Multi-Atlas Labeling Beyond the Cranial Vault [Bennett Landman 2015]. There are in total 50 sequences, and 13 segmentation context ((1) spleen (2) right kidney (3) left kidney (4) gallbladder (5) esophagus (6) liver (7) stomach (8) aorta (9) inferior vena cava (10) portal vein and splenic

vein (11) pancreas (12) right adrenal gland (13) left adrenal gland) are labeled slice by slice (check an example shown in Figure 6). We use *marching cube* [Lorensen and Cline 1987] to reconstruct the 3D surfaces from these labeled slices, and then as target for accurate anatomic model reconstruction.

### 4.2.2 Organ Correspondences

We sample points from the initial reconstructed anatomic model and the reconstructed 3D surfaces and extract their point features using CGF [Khoury et al. 2017]. We perform the registration for each organ separately using FGB [Zhou et al. 2016], and average the obtained transformation matrices to obtain the global transformation matrix.



**Figure 7:** from left to right: stomach illustrate, pre-built stomach, CT reconstruct stomach; The anatomic structure in both pre-built model and CT reconstruct surface share the same feature which can be used as landmark [Gong et al. 1997].

With the aligned organs, we want to establish correspondences of organs-in-interest. Follow the same process of the correspondence establishment of skin model (in Section 4.1.2), we first need to assign some landmarks on the organ models. We assign landmarks in a medical-aware fashion, *i.e.*, for each organ, we first identify several key location using medical-defined structure, *e.g.*, we assign landmarks around Cardia and Pyloric sphincter on stomach model (see Figure 7).

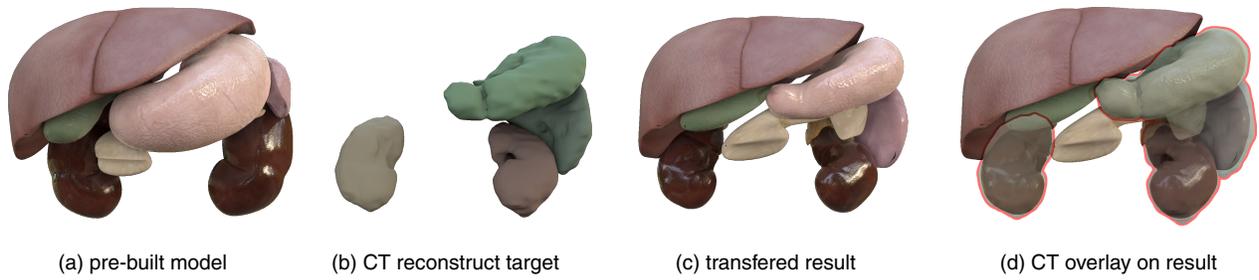
### 4.2.3 Organ Transfer Field

The additional correspondences on organs-in-interest provides additional transfer field. We use these organs' transfer fields as additional boundary condition and perform the transfer again to obtain the final accurate results.

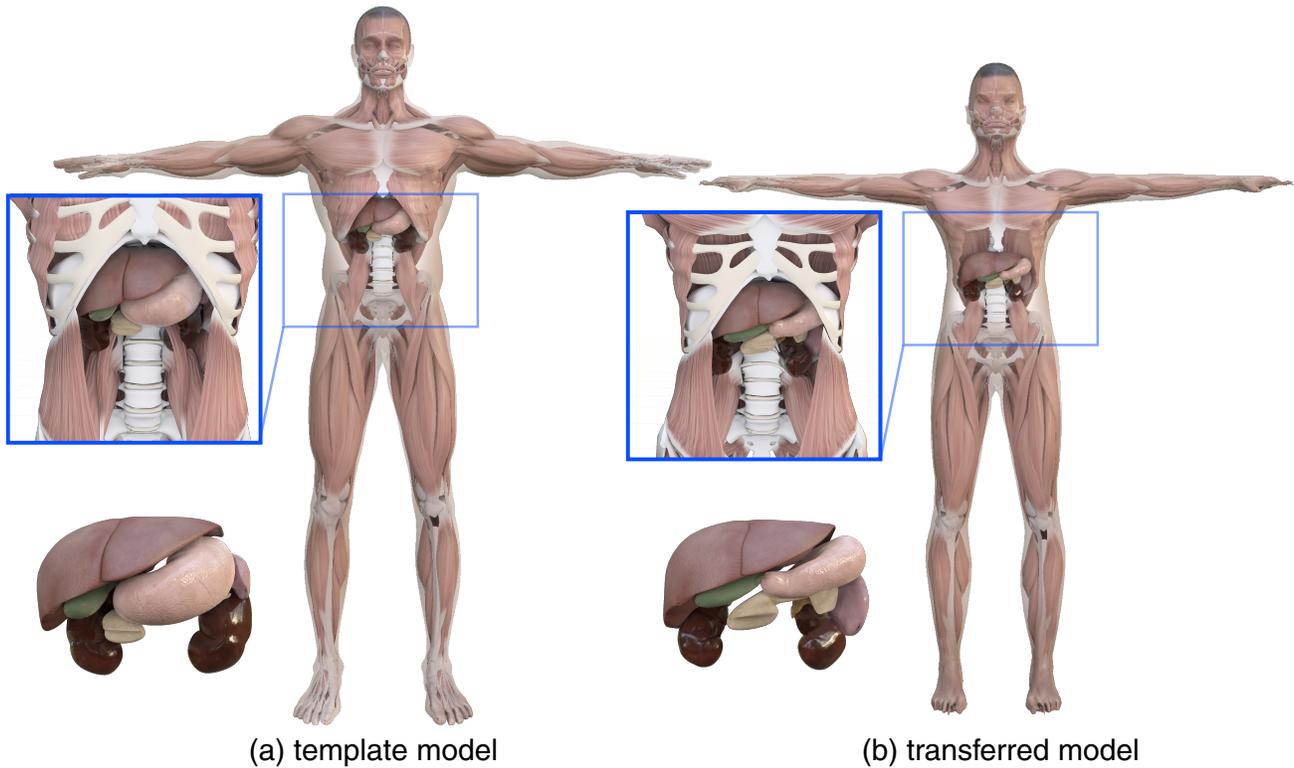
## 5 Result

In this section, we demonstrate our accurate anatomic model transfer with several examples, and evaluate our method using several different error metrics.

We successfully transfer the template model into target shape with affected area information. In Figure 8, we showed the transferred anatomic structures are well aligned with the reconstructed 3D shape from patient's medical scanning data (Figure 8(d)). And the surrounding organs still stay in a relative medical sound positions, which is important because the doctor can obtain accurate affected organ reconstructions, but still retain clear field of vision while operating. Figure 9 shows the transferred result on a CT segmentation set with patient skin surface. In this example, we transfer *integument, muscular, skeleton, respiratory, endocrine, urinary, lymphatic system* models based on the segmentation of corresponding parts in CT scans with medical context landmarks.



**Figure 8:** The transfer result on spleen, kidneys, stomach and skin as target. Note that the CT reconstruct features stay in place in (d) with the overlay view.



**Figure 9:** We transfer the segmentation data label005 in MALBCV. The fully transferred template model, adapt skin, spleen, kidneys, stomach target with 200 vpm (voxel per meter).

### 5.1 Quantitative Error Metric

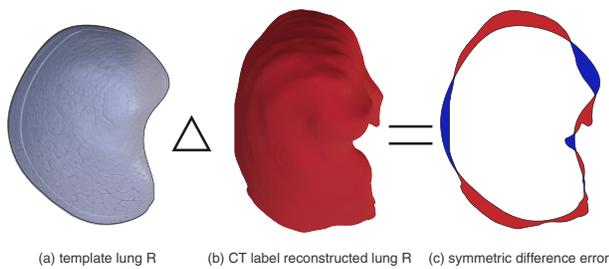
We further evaluate our reconstructed results using two different metrics, *i.e.*, *difference of volume* and *surface correspondence distances*. After each stage of transfer, we can calculate the error between the models of segmented CT regions and the transferred models.

**Difference of Volume.** After the transfer is done, the corresponding anatomic structure should share the same or similar shape and position. We calculate the difference between two meshes by measure the volume of the symmetry difference (XOR) from two shape. Figure 10 illustrates the difference between the lung model in template model and CT reconstructed lung model.

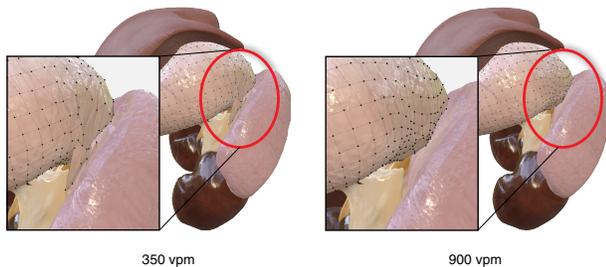
**Correspondences Distances.** Another way to measure the error between the transferred models and the CT reconstructed model is using known correspondences that was solve in section 4.1.2. We measure the Euclidean distances between each correspondences pair. We show the results of two different metrics in Table ??.

## 6 Conclusion and Future works

In this paper, we propose an semi-automatic framework for accurate anatomic model transfer. Unlike previous approaches, we provide effective approach to incorporate auxiliary medical imagings such as CT and MRI to further improve the accuracy of anatomy transfer result. Our method greatly reduce the time and labor efforts for



**Figure 10:** The error metric we use to measure the volume difference between CT reconstructed and our transferred model. It is computed as sum of the blue and red part of the symmetric difference error, denoted as  $A\Delta B$ .



**Figure 11:** The resolution of the enclosed voxel grids introduce intersected transferred results. This problem will be more severe if the position is largely different in pre-built and CT scanned model.

professional artists. The accurate transferred anatomic model can help the applications in surgical simulation using VR or AR.

Although the examples we demonstrated in this paper accurate reconstruct the internal anatomic model, we still discover several directions for improvement. We noticed that the resolution of voxel grid will greatly affect the transferred result around the boundary between each organs, if the neighboring organs are too close to each other and undergo very different deformation behaviors. Figure 11 shows the different vpm (voxel per meter) result for stomach and spleen and kidney registration. This bad topologies will be amplified while the structures relative position is different in template model and the segmentation sequences. We are interested to investigate how multi-resolution voxel grid can help us solve this issue, *i.e.*, we further divide the original voxel grid around the boundary of each organs.

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