Towards a New Automated Segmentation Method for Numerous Tissues In Reference to a Whole-Body 3D Anatomical Template

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INTRODUCTION:

Numerical models of the entire human body, with dozens of tissues, are increasingly important for ensuring RF safety in MRI, but the modeling results depend greatly on the subject-specific body type [1]. This indicates the need for many more anatomical models than exist today; however a major obstacle to their production is the lack of a good automated segmentation method for all tissues in the body. In MRI many algorithms exist for segmentation of gray matter, white matter, and cerebro-spinal fluid based on automatic segmentation of images with good contrast between these tissue types; however, little work has been done on segmenting tissues other than these. We are developing a method to identify the location of specific tissues and organs in diverse body shapes using patient-specific images and with reference to a labeled 3D template of a single "reference" body. While contrast on the patient-specific images allows for simple threshold-based segmentation of some tissues and organs, low contrast between other tissues requires more sophisticated methods with reference to the 3D template. While our initial work is with CT datasets for development of anatomical models for safety assurance in MRI, we believe that the general method will eventually have very wide applicability.

METHOD:

Patient-specific CT images from whole-body PET/CT scans acquired for clinically-indicated diagnostic purposes were used in this study with full IRB approval. A previous manual segmentation [2] of the photographic data from the NLM Visual Human Project [3] into 36 tissues produced the necessary 3D Labeled Template. Segmentation of the Patient-specific images is performed in the following steps: (a) Preprocess images to enhance the image contrast and to reduce noise. (b) Perform active contours and level sets algorithms using ITK-SNAP [4]. (c) Employ the Markov random field algorithm (MRF), optimized by mean-field annealing (MFA) [5] to classify the tissues that cannot be extracted by active contours and level sets algorithms. (d) After MRF-MFA segmentation, correlate slices between the patient-specific images and the labeled template. The correlated slices are identified by looking in both the patient-specific images and the labeled template for the first and last slices where kidneys, spleen, and liver are located. (e) Based on the correlated slices discovered in (d), further interpolate each patient-specific slice and correlate it to one or in between two adjacent labeled template slices. Due to the difference in spatial resolution between the patient-specific images (higher resolution) and the labeled template (lower resolution), not every patient-specific image correlates to a single template slice. In such a case, we assume the patient-specific image slice is located between two adjacent template slices. (f) Perform a 2D-rigid transformation and superpose the template slices onto the corresponding patient-specific slices. If the patient-specific slice lies between two adjacent labeled template slices, we superpose both adjacent template slices. (g) Segment the desired tissue on each patient-specific slice by referring to the superposed template slices and using the information of the desired tissue location as well as the surrounding tissue boundaries estimated by the segmentation algorithm in steps (b) and (c). Figure 1 shows steps (d) to (g) in kidney extraction.

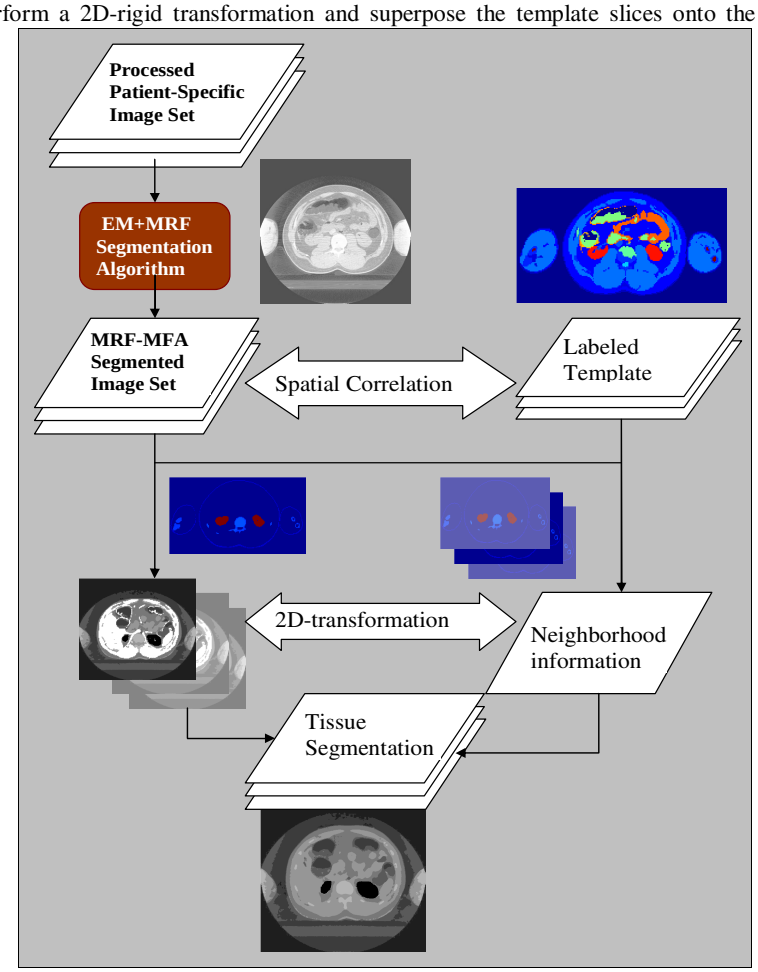

Figure 1. Segmentation steps (d) to (g).

RESULTS:

The tissues/organs in the abdomen that can be successfully extracted by active contours and level sets algorithms are vertebra, colon, ribs, ilium, sacrum, fat, and individual muscles. Using the MRF-MFA segmentation with reference to the labeled template, we are thus far able to also segment kidneys, spleen, and liver on the patient-specific image set.

DISCUSSION:

We developed methodologies to interactively segment patient-specific images. This approach provides satisfactory results when the body shape in patient-specific scans is similar to the labeled template. However, when the body shape in patient-specific scans is significantly different from the template, tissue/organ segmentation is less accurate. Therefore, we are working on 3D segmentation and 3D matching instead of only slice-by-slice correlation and segmentation to derive the optimal location and orientation of individual tissues while superposing the template. A local 3D transformed labeled template that accounts for the diversity of body shapes and changes of tissue location based on the body shapes shows promise in leading to better tissue/organ segmentation.

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