Standardized anatomic space for abdominal fat quantification

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ABSTRACT

The ability to accurately measure subcutaneous adipose tissue (SAT) and visceral adipose tissue (VAT) from images is important for improved assessment and management of patients with various conditions such as obesity, diabetes mellitus, obstructive sleep apnea, cardiovascular disease, kidney disease, and degenerative disease. Although imaging and analysis methods to measure the volume of these tissue components have been developed [1, 2], in clinical practice, an estimate of the amount of fat is obtained from just one transverse abdominal CT slice typically acquired at the level of the L4-L5 vertebrae for various reasons including decreased radiation exposure and cost [3-5]. It is generally assumed that such an estimate reliably depicts the burden of fat in the body. This paper sets out to answer two questions related to this issue which have not been addressed in the literature. How does one ensure that the slices used for correlation calculation from different subjects are at the same anatomic location? At what anatomic location do the volumes of SAT and VAT correlate maximally with the corresponding single-slice area measures? To answer these questions, we propose two approaches for slice localization: *linear mapping* and *non-linear mapping* which is a novel learning based strategy for mapping slice locations to a standardized anatomic space so that same anatomic slice locations are identified in different subjects. We then study the volume-to-area correlations and determine where they become maximal. We demonstrate on 50 abdominal CT data sets that this mapping achieves significantly improved consistency of anatomic localization compared to current practice. Our results also indicate that maximum correlations are achieved at different anatomic locations for SAT and VAT which are both different from the L4-L5 junction commonly utilized.

Keywords: body fat quantification, CT imaging, landmarks, image standardization

1. INTRODUCTION

Obesity and physical inactivity are global epidemics that warrant the immediate attention of the health-care community. An estimated two-thirds of Americans are overweight or obese [1]. The accumulation of abdominal subcutaneous, visceral, and organ fat has adverse effects on health, and increases the risk of heart disease, diabetes mellitus, metabolic disorders, obstructive sleep apnea, and certain cancers. The ability to accurately measure subcutaneous adipose tissue (SAT) and visceral adipose tissue (VAT) becomes more imperative as their contribution to disease pathophysiology becomes clearer [2-5].

In clinical practice, an estimate of the total amount of body fat is typically obtained by the fat area measured from just one transverse abdominal slice (from computed tomography (CT)), commonly acquired at the level of the L4-L5 vertebrae, for various reasons including decreased radiation exposure and cost [6, 7]. It is generally assumed that such an estimate reliably depicts the burden of fat in the body. There are two issues related to this common practice. First, no studies exist that have examined systematically how to specify spatial location for slice(s) in different subjects consistently so that they are in the same homologous anatomic location. Second, by using a facility for consistency of slice localization, such as what we propose, no studies have investigated which single location or multiple locations for the slices yield maximum correlation of the fat areas on the slices with the total fat volume for the SAT and VAT components separately. This paper addresses both these issues. For the purpose of this paper, SAT and VAT volume / area can be quantified from CT or MR images by using the Automatic Anatomy Recognition (AAR) rapid prototyping approach [8].

In this paper, we propose two approaches for slice localization. The first approach is linear mapping, where we linearly map slice locations from all subjects so that the superior-most and inferior-most anatomic slice locations match in the longitudinal direction for all subjects and other locations are linearly interpolated estimations. Although this method is

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similar to the linear interpolation method for the estimation of adipose tissue of different body regions described in [9], where different body regions (referenced to the skeleton), such as trunk, are interpolated to yield 50 slices for every subject, they are used in different ways. After linear interpolation, SAT and VAT volume percentages on every slice are calculated and shown as the distribution of SAT and VAT in the body region. To make interpolation precise, the method requires the patients to be positioned precisely the same way with every patient also marked at the iliac crest during scanning. In this paper, with linear mapping, correlations between SAT (or VAT) area on slices and SAT (or VAT) volume in the body region are calculated to find the site with maximum correlation. For this mapping method, there is no landmark alignment requirement before scanning. In the second approach, slice locations in every subject are mapped non-linearly or deformed so that, in addition to the superior-most and inferior-most locations, several key landmark locations chosen in the longitudinal direction also match for all subjects. To our knowledge, this paper is the first to address the above two issues by exploring anatomic space standardization and correlation calculation for the purpose of fat quantification.

2. METHOD

This paper sets out to answer two questions related to fat quantification which have not been addressed in the literature. How does one ensure that the slices used for correlation calculation from different subjects are at the same anatomic location? At what anatomic location do the volumes of SAT and VAT correlate maximally with the corresponding single-slice area measures?

This retrospective study was conducted following approval from the Institutional Review Board at the Hospital of the University of Pennsylvania along with a Health Insurance Portability and Accountability Act (HIPAA) waiver.

We denote by V the set of images available for our study, which is assumed to be a representative subset of $\mathcal{V}$(B, P, G), where $\mathcal{V}$(B, P, G) denotes the set of all possible 3D images of a precisely-defined body region B, taken as per a specified image acquisition protocol P, from a well-defined group of subjects G. Let I^s be an image in V of some subject *s* of his body region B. We view I^s as a set of n_s axial slices $I^s = \{S_1^s, ..., S_{n_s}^s\}$. Since I^s is an image of B, S_1^s and $S_{n_s}^s$ represent anatomic planes bounding B. Our overall approach to seek answers to the three questions posed above consists of the following steps. (1) Segment SAT and VAT in images in V. (2) Map slices in each image I^s to locations $l_1, \ldots, l_L$. (3) For each location l_i, pick corresponding slices in images in V and perform volume-to-area correlation analysis. (4) Find location(s) with maximum correlation for SAT & VAT separately. (5) Output locations for SAT and VAT. These steps are described below.

(1) Segmenting SAT and VAT Regions in Images in V

We modified our AAR system [8] for automatically segmenting these CT images to output 3D SAT and VAT volumes, and utilized the segmented slice areas for SAT and VAT to determine which single slice produced the maximum correlation between area and volume separately for SAT and VAT.

(2) Assigning Landmark Labels $l_1, \ldots, l_L$ to Slices in each Image I^s

Two alternative approaches are explored – *linear* and *non-linear*, and compared to the manual approach. In all approaches, the input is the set V of images and the result is a mapping that indicates the anatomic location (label) associated with each slice of each image of V.

(3) Finding corresponding slices and performing correlation analysis

Linear Approach:

This approach assumes that, once we guarantee that the bounding planes P_S^s and P_I^s, and hence slices S_1^s and $S_{n_s}^s$ of image I^s, correspond to locations l_1^s and l_L^s, respectively, then anatomic locations corresponding to slices S_2^s to $S_{n_s-1}^s$ can be found by linearly mapping the n_s slices from S_1^s to $S_{n_s}^s$ to L slices U_1^s to U_L^s via linear interpolation for any subject *s*. Note that L can be less than, or greater than, or equal to n_s. The only requirement on L is that it should be at least 2. A drawback of the linear approach is that non-linearities in the relationships among anatomic locations in the longitudinal direction cannot be accounted for.

Non-Linear Approach:

In the linear approach, we employed two anatomic landmarks l_1 and l_L to anchor the first and the last slice of B and to predict the anatomic location of all other slices. In the non-linear approach, in addition to l_1 and l_L, other key anatomic landmarks are used to refine mapping. The method consists of two stages – *training* and *transformation*.

The purpose of the *training stage* is to learn any non-linearities that may exist in the relationships among anatomic locations. Typically, we select M = L key anatomic landmarks, denoted by $m_1, \ldots, m_M$, from among $l_1, \ldots, l_L$. In this work, we selected the mid-points (in the vertical direction) of the vertebral bodies from T11 to L4 as key landmarks (so M = 6). Next, these key landmarks are identified manually in a (training) set $U \subset \mathcal{V}(B, P, G)$ of images. For any image I^s in U, we will denote the locations of these key landmarks for subject s by $m_1^s, \ldots, m_M^s$. A standard anatomic scale is then determined to be of length which is the largest of the lengths from P_S^s to P_I^s over all data sets in U. Locations $m_1^s, \ldots, m_M^s$ for every data set in U are then mapped linearly on to the standard scale and the mean positions $\mu_1, \ldots, \mu_M$ of the key points on the standard scale over all mapped data sets of U are computed. The mapping from Scanner Coordinate System (SCS) to Standard Anatomic Space (SAS) where landmarks are defined is subsequently determined to be the piece-wise linear function that maps $m_1^s, \ldots, m_M^s$ to $\mu_1, \ldots, \mu_M$.

In the *transformation stage*, given any image I^s, first the locations of its anatomic landmarks $m_1^s, \ldots, m_M^s$ are identified. Then the mapping function from SCS to SAS determined in the training stage is used to determine the label to be assigned to each slice S_i^s of I^s.

Once the mapping is accomplished, correlation analysis in Step (3) and performing Steps (4) and (5) are straightforward.

3. RESULTS

Image Data

Variables G and P defining $\mathcal{V}(B, P, G)$ for our experiments were as follows. Contrast-enhanced abdominal CT image data sets from fifty 50-60 year-old male subjects with an image voxel size of $0.9 \times 0.9 \times 5$ mm^3 were utilized in our study. The subjects were radiologically normal with exception of minimal incidental focal abnormalities. The abdominal body region B was defined in the same way for the 50 subjects, with P_S located at the superior most aspect of the liver and P_I corresponding to the point of bifurcation of the abdominal aorta into common iliac arteries. Of the 50 data sets, 5 were used for training (constituting U) and the rest (constituting V) were used for testing.

To illustrate the anatomic variability that exists among subjects, in Figure 1 we plot schematically the locations of the mid points of vertebral bodies in the cranio-caudal (vertical) direction for all subjects considered in the study. The top and the bottom of the vertical line drawn for each subject indicate the extent of B in relation to the vertebral bodies. For example, in subject numbered 50 (the right-most location on the abscissa), the abdominal region starts from roughly the T11 vertebra and ends at the L5 vertebra. The locations of both the top-most and bottom-most slices have significant variability in terms of anatomic correspondence as seen in Figure 1.

Correlation analysis

We considered 34 subjects for correlation analysis by selecting those subjects whose body region B covered vertebrae from T8 to L4 among the 50 subjects. For all 34 subjects, six spinal landmarks were selected from T10 to L3 as the mid points of the respective vertebral bodies. Although we illustrate our method by using 6 landmarks here, this number can be set to any value greater than or equal to 2 and any other landmarks can also be used. In order to study how correlation may vary for different anatomic slice locations, in Figure 2, we display the correlation values as a curve for different slice locations for SAT and VAT by using linear and non-linear mappings. Some key landmark positions are indicated along the horizontal axis in the bottom row of the figure.

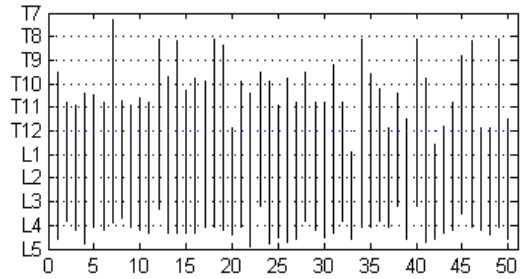

Figure 1. Anatomic locations of slices in B = Abdominal Region for 50 subjects. Abscissa shows subject numbers, and ordinate indicates the extent of B in different subjects in the cranio-caudal direction in terms of the vertebral bodies.

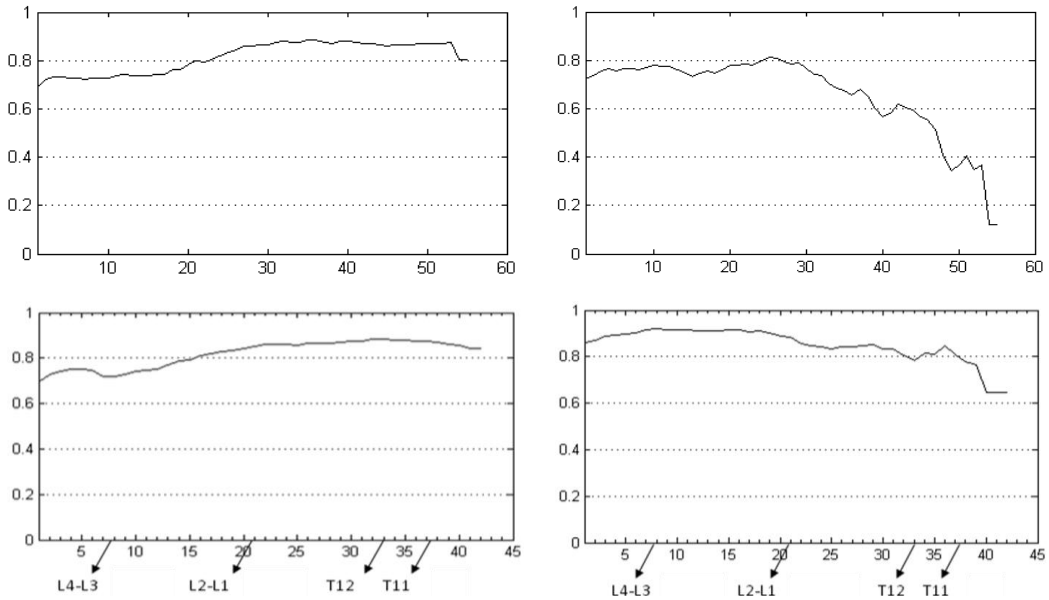

Figure 2. Correlation values from linear mapping (top row) and non-linear mapping (bottom row) for SAT (left) and VAT (right). The horizontal axis shows the location of image slices (Slice 1 is at the inferior most position). Some key landmark positions are indicated along the horizontal axis in the bottom row.

To examine how the location of maximum correlation may vary across subjects, in Figure 3, we display the anatomic landmark locations at which maximum correlation occurred for SAT and VAT for the two methods for different subjects. The site of maximum correlation derived from non-linear mapping has more precision than from simple linear mapping. In the bottom row of Figure 3, there is a small variation of locations over all subjects which is less than 5.0 mm (same as slice spacing), implying that the slice localizations are anatomically very precise in the SAS compared to about 16-18 mm for the linear method. Again, the anatomic location of maximum correlation for SAT is different from that of VAT.

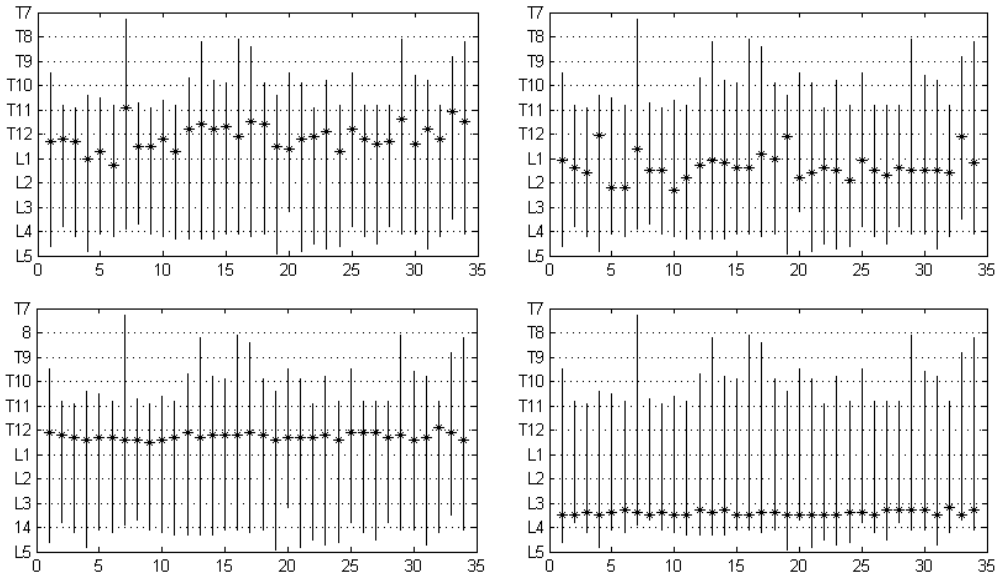

Figure 3. Anatomic locations (marked with '*') of maximum correlation between single slice area and volume (SAT on left, VAT on right, linear method in top row, non-linear method in bottom row). The horizontal axis shows subject numbers, and the vertical axis shows anatomic location from L5 to T7.

4. CONCLUSION

Correlation analysis to determine the optimal anatomic slice locations in the abdomen for estimating body fat has not previously been performed to our knowledge. The optimal anatomic slice locations for single-slice SAT and VAT estimation are not the same, contrary to common assumption. This result is important since these fat components may have different effects upon the pathophysiology of different disease processes. Experimental results on 50 abdominal CT image data sets showed that the standardized anatomic space created through non-linear mapping of slice locations achieves better anatomic localization than linear mapping. The proposed method can be extended with greater or fewer landmarks than those adopted in this paper. Overall, our conclusions are as follows:

1. The maximum area-to-volume correlation achieved is quite high, suggesting that it is reasonable to estimate body fat by measuring the area of fat from a single anatomic slice at the site of maximum correlation.
2. However, the site of maximum correlation is not at L4-L5 as commonly assumed but is more superiorly located at T12-L1 for SAT. The ideal sites for SAT and VAT estimation are not the same, contrary to common assumption. The optimal site for VAT is located at L3-L4.
3. It is important for correlation analysis to make sure that the slices for different subjects are selected at homologous anatomic locations.
4. The proposed standardized space mapping achieves this consistency of location by managing non-linearities in the relationships among landmarks accurately.

The goal of this research is to find optimal location(s) of slices for any given patient group and body region utilizing the data sets under any given image modality. Once the optimal locations are determined in the manner demonstrated in this paper, actual acquisition of images at precisely those locations in clinical practice can be implemented without difficulty by making appropriate changes to the scan protocol, for example by marking off plane locations on scout views. One drawback of the proposed strategy is that it is difficult to implement on MR images since it is quite challenging to segment vertebral bodies in MR images. However, if certain features to tag anatomic locations reliably can be identified on slice images, then the method can be implemented in a straightforward manner.

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