Author's response to reviews

Title: Comparison of Human Lung Tissue Mass Measurements from Ex Vivo Lungs and High Resolution CT Software Analysis

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Author's response to reviews: see over
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Dear BioMed Central Editorial Team,

RE: Manuscript ID 6912309105758296, "Comparison of Human Lung Tissue Mass Measurements from Ex Vivo Lungs and High Resolution CT Software Analysis"

Thank you for your email from March 3, 2012 regarding our manuscript. We wish to address the reviewer’s comments in series.

Reviewer: 1

Reviewer’s Report:
This study evaluated the performance of automated CT based lung mass quantification using human lung tissue. The study is well structured and doesn't present any major flaw. As a diagnostic imaging expert I cannot provide any relevant observation regarding the dissection technique adopted; the CT scan technique hereby described is accurate for this kind of study and allows to provide accurate data for automated software evaluation. My suggestion is to accept the paper as is.

Reviewer: 2

Reviewer’s Report:

In this paper, the authors quantified tissue mass of lungs and their different sections with software using 3D CT images. The results are compared to the actual physical measurements of the tissue weight. To accurately weigh the lobar and sublobar, a technique is developed to dissect the lung tissue. The comparison reveals good agreement between the software measurements and actual weight measurements. Despite of that, there are constant biases in both lung dissection measurements and lobar dissection measurements. In the discussion part, the authors explain differences as a result of extraneous tissue. This work is meaningful for developing better “Bronchoscopic Thermal Vapor Ablation (BTVA)” treatments for patients suffering from emphysema, since the dosage of the treatments is depended on the tissue mass of the target. Overall, it is an interesting and well-presented paper.

Questions:

1. It would be beneficial to provide some more details about the algorithm the software is using and how different it is from other software packages, if any.

Information on the current state of lung quantification algorithms and how the studied algorithm compares has been added. Additionally, the description of the studied algorithm has been modified and generalized. Three additional references were added to provide additional background and justification. The revised section is below:

Automatic segmentation and measurement of tissue mass of the lung, lobes, and sublobar segments from CT scans can be computed. Three main algorithmic approaches have been reported in the literature. 1) Approaches based on the explicit segmentation of fissures, 2) Approaches using supervised classification schema, which are particularly sensitive to fissure incompleteness,
nearby tumors, atelectasis or emphysematous changes. 3) Approaches combining multiple sources of information such as bronchi segmentation, vessel segmentation, and absence of larger vessels in proximity to the lobar boundaries to define robust 3D sublobar segments. The lobar algorithm studied in this paper falls in this third category and is, to our knowledge, the only such software commercially available (Pulmonary Workstation 2.0, VIDA Diagnostics, Iowa City, IA). It relies on a validated airway segmentation algorithm and a distinctive processing of the fissure surface at the interface between lobes. Tshcirren et al recommended additional quantitative analysis with in vivo data; however, to date no tissue mass or volume quantification comparative data has been published for lung, lobar, and sublobar dissection.

2. In the page 5, the authors mentioned the tissue density is assumed to be 1.0 g/ml. But some other literatures suggested much smaller density for lungs. For example, “Propagation of stress waves in inflated sheep lungs” by M. Jahed and etc. suggests ~0.2 g/ml. It would be good if the authors could provide an explanation for the discrepancy.

It is true that the density of the entire lung organ is ~0.2 g/ml when inflated with air. The software calculates the volume of the entire lung, the volume associated with air only, and the volume associated with tissue only. When considering only tissue, the density is much higher. The relevant section has been reworded to make this more clear:

“The quantitative analysis report from the software provided segment labeling, airway diameter, total volume, air only volume, and tissue only volume. These values were provided for the lung, lobar, and sublobar segment level. Tissue only volume was converted to tissue mass by multiplying by the density 1.0 g/ml.”

We have submitted a revised version of our manuscript.

Yours sincerely,

Erik Henne, BSME