

Quantitative Histology of Contused Lung Tissue with Comparison to Computed Tomography

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ABSTRACT

This study presents an image analysis algorithm for quantifying the volume fraction of pathology in serial histology of the rat lung. The right lung of male Sprague-Dawley rats (n=4) was contused using a controlled insult applied via an instrumented, electronic piston. The right (struck) and left lungs were excised at 48 hours post-insult, fixed in 10% formalin. Serial histology was taken at 1.5 mm intervals on the struck lung and 3 mm intervals on the left lung. Sections were stained with H&E and digitally imaged using a fixed, high-resolution digital camera. Immediately prior to sacrifice, computed tomography images of all subjects were also acquired. An automated image analysis program was applied to each image (8-bit, RGB) using morphological (dilatation and erosion), filtering (circular averaging), and thresholding techniques to sort pixels representing healthy lung tissue, pathologic lung tissue, and blood into separate masks. Blood was determined by multi-channel thresholding in the following inclusive ranges: Red (197-240), Green (0-90) and Blue (115-154). After applying the morphological and filtering operations, lung pathology was identified as all pixels exceeding a grayscale value of 85, with 0 being black and 255 being white. The average normalized volume of pathology across the data set was 12.63 ± 11.40 %. The results showed greater volumes of tissue pathology than blood in all subjects indicating a good model for blunt lung trauma. CT segmentation data from the same four animals was used for a related study but was included for the purposes of comparison. These values were determined through a semi-automated approach and resulted in an average pathology volume of 16.92 ± 9.66 %. Normalized pathology did not differ significantly between histology and CT ($p = 0.18$, paired t-test for sample means, $\alpha = 0.05$). The histology analysis algorithm and CT data resulted in similar trends across the data set. This approach can be used to improve the accuracy of both histology-based and CT-based segmentation processes.