Semi-Automatic Segmentation of Lung Tumors in MRI Images of a Mouse Tumor Model

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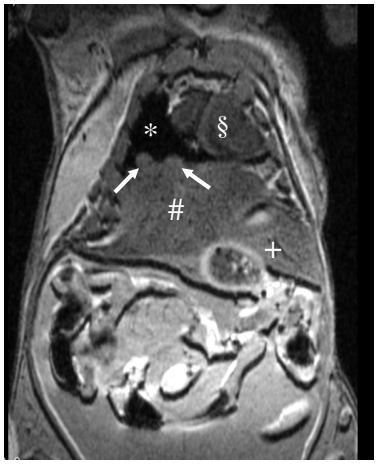

Figure 1: Coronal 3D gradient echo image of a mouse abdomen. The lung (*), liver (#), heart (§), and spleen (+) are visualized. Two lung tumors in contact with the diaphragm are visible (arrows).

Purpose: Currently, the evaluation of lung tumors is carried out according to the RECIST or the WHO criteria [1]. These assessments are based on the measurements of one or two diameters of selected target lesions. This leads to large measurement errors and consequently the changes in tumor size that are accepted to show progress or regress are also large. The more precise volume assessment is time consuming because the tumor has to be outlined in every slice of the volume data set. Therefore, the purpose of this study is to evaluate a semi-automatic tool that measures tumor volume as well as RECIST and WHO assessment criteria after initial seed point placement by an operator.

Material and Methods: Lung tumor bearing female A/J strain mice were imaged in a 4.7T small animal MRI scanner using a RARE sequence (TR: 2500ms, TE: 17ms, echotrain length: 4, signal averages: 4, FoV: 40 x 40mm, Matrix 256 x256, 30 slices, slice thickness 0.5mm, acquisition time 10 minutes) and a 3D gradient echo sequence (TR: 60ms, TE: 3.2ms, flip angle: 30°, signal averages: 1, FoV: 40 x 40mm, Matrix 205 x256, 30 slices, slice thickness 0.3mm, acquisition time: 9 minutes). The images were acquired in the coronal and the axial plane. The animals were anesthetized, but free-breathing. No ECG- or respiratory gating was applied. Following the MRI scans, the animals were sacrificed but the tumors sizes measured histologically.
The tumor segmentation is based on a hybrid method combining region growing adapted to local histograms and morphological image processing [2]. The morphological separation of tumor and neighboring isointense structures is guided by analysis of the geometry of connecting vasculature based on local extrema of the distance map for tumor intense structures in relation to the back-ground. Seed point placement was the only user interaction necessary for tumor segmentation. Semi-automatically segmented volumes were compared those of histological analysis.

Results: All tumors identified on MRI (Figure 1) were confirmed by histology. The algorithm was able to outline the tumors (Figure 2) with minimal user interaction. Even tumors located on the diaphragm in close proximity or with contact to the liver were segmented and their volumes were measured correctly.

Conclusions: This study demonstrated the feasibility of semi-automatic tumor volumetry in MRI data sets of mouse lung tumors. This will enable the evaluation of tumor volumes instead of diameters as used in RECIST and WHO assessment for tumor response to therapy.

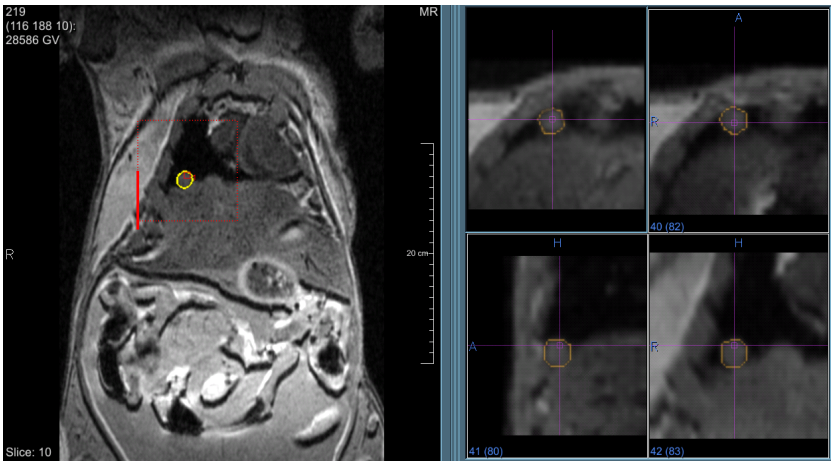

Figure 2: Same animal as in figure 1. After seed point placement, the algorithm segmented and outlined the tumor automatically.
Left side: The tumor is outlined on the original image.
Right side: Cropped images of the tumor region.
Top left: 3D projection of the tumor.
Remaining panels: Axial (top right), sagittal (lower left) and coronal (lower right) reconstructed views of the tumor area.

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References:

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2. Bornemann L, Kuhnigk JM, Dicken V. et al. New tools for computer assistance in thoracic CT - Part II: Therapy monitoring of pulmonary metastases. Radiographics 25(3): 841-848, 2005 May 1