

Pixel-based Quantitative Analysis of Dynamic Contrast-enhanced MRI of Lung Tumors

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Introduction

Dynamic contrast-enhanced magnetic resonance image (DCE-MRI) has been known for its efficacy in characterization and treatment monitoring of tumors. Using a pharmacokinetic model, DCE-MRI provides parameters indicating permeability of tumor microvessels which has been shown to be closely related to angiogenesis. Due to heterogeneity of tumor perfusion, a pixel-based quantitative method to analyze tumor perfusion is desirable. To accomplish this, we tried to develop an automatic motion-detection method to co-register the tumors in motion, and tested the pixel-based DCE-MRI technique in lung tumors.

Materials and Methods

Image acquisition

Three patients with lung cancers (2 squamous cell cancers and 1 adenocarcinoma) received DEC-MRI at 1.5-T MRI system (Sonata, Siemens, Erlangen, Germany) with a phased-array torso coil. A saturation-recovery prepared Turbo-FLASH pulse sequence was performed, TR/TE = 200/0.96 ms. Five slices in coronal view covering the targeted tumor were localized. Localization of coronal slices for the tumor was made accurately with the T2WI anatomical images in axial and coronal views. We acquired 5 slices in 1 sec (5 x 200 ms = 1000 ms). By acquiring 100 datasets in 100 sec, temporal resolution of 1 sec for each dataset was achieved. The field of view (FOV) = 302 mm, matrix size = 128 x 128, slice thickness = 8 mm, so the spatial resolution = 2.4 x 2.4 x 8 mm. Water-soluble MR contrast medium (Gd-DTPA) was used with a dose of 0.1 mmole/kg, approximately 10 cc according to the body weight, followed by a saline chase of 15 cc. Bolus injection with an injection rate of 4 cc/ sec was performed through an ante-cubital vein. After the first run of 5 shots, the injection started. Patients breathed calmly throughout the study. Each case had the cinematic images of tumor in five slices and had image acquisition of 100 seconds with temporal resolution of 1 frame per second.

Motion-detection

The motion tracking algorithm entailed determination of the center of mass (COM) of the tumor at each time frame, followed by co-registration of tumor masks based on the location of COM in time. Two different approaches were adopted to determine COM according to the geographic site of the lung tumors. The first approach was used if the tumors were in the lower lung field and close to the diaphragm. The tumors in this region moved in accord with the diaphragm. Based on this relationship, vertical motion of the diaphragm was determined, and COM was shifted with the displacements of the diaphragm. The second approach was used if the tumors were in the upper lung field. The motion of tumors in this region was not related to the movement of the diaphragm. In this case, region growing was applied to binary images converted from images of DCE-MRI with varying thresholds. A statistical algorithm was applied to determine the thresholds of these images so that muscles, lungs, small vessels, and tumors can be separated (Fig. 1). COM at each time frame was determined after region growing in each binary image. After image co-registration, occurrence count over the time domain was performed for each pixel location of the masks. Pixel locations occurred more than 80 out of the 100 time frames were selected to be the mask of the tumor. Time-intensity curve at each pixel of the selected mask was plotted. A pharmacokinetic model proposed by Brix et al. was used to calculate the parameters of k_{out} , A , and k_{el} , reflecting the permeability, micro-vessel density (MVD), and clearance rate of the tumor, respectively. Parameters were rendered in colors and mapped onto original images at reference time frame.

Results

The masks determined by our semi-automatic motion-detection algorithm matched the tumor in all DCE-MR images. After parametric fitting, the parameters of tumor perfusion were displayed in pseudo-colors. Figure 2 shows parametric mapping of A , K_{out} and K_{el} in three patients with lung tumors. Heterogeneous distribution of tumor perfusion can be seen in all cases. Close inspection revealed different patterns of distribution not only in different parameters but also in different patients. The first case showed graded reduction in A , K_{out} and K_{el} from the periphery to the center, whereas the third case exhibited increased perfusion indices in the central portion of the tumor. The second case showed concentric layered pattern in K_{out} mapping.

Conclusions

We have demonstrated the feasibility of pixel-based quantitative analysis of DCE-MRI in lung tumors. Parametric color mapping in three lung cancers showed different patterns of distributions. Further study on histological correlation is required to validate the accuracy of this method.

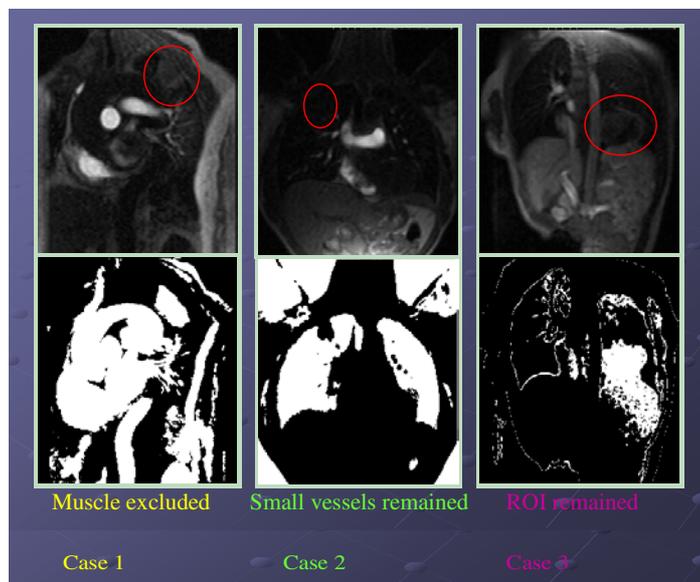


Fig. 1 Segmentation results in three patients using statistical thresholds that separate muscles, lungs, vessels and tumors. The red circles indicate tumor regions.

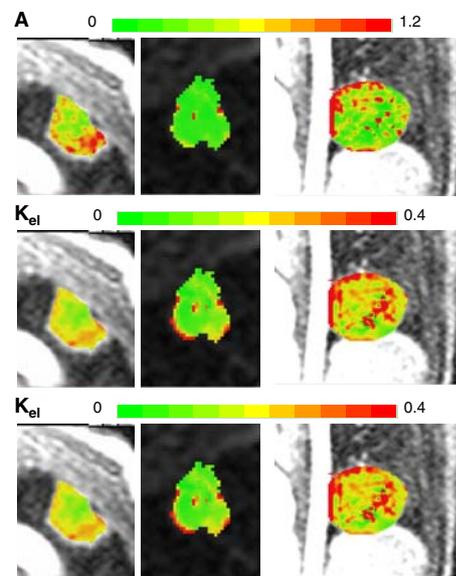


Fig. 2 Parametric color-mapping in three patients.

References

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