AN AUTOMATIC PARENCHYMA EXTRACTION METHOD FOR MRI R2* RELAXOEMTRY OF IRON LOADED LIVER

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Target audience: Clinicians and engineers who are interested in the liver R2* relaxometry

Purpose: In the R2* measurement for assessing hepatic iron concentration (HIC), ¹one or multiple regions-of-interest (mROI) manually delineated on the homogenous parenchyma area devoid of visible vessels and artifacts are traditionally used in the clinical practice. However, the mROI method may suffer from sample errors. ^{2,3}The whole liver ROI method for R2* measurement has been shown better reproducibility than the mROI method, but still suffer from noise, partial volume effect and subjective segmentation of tissues. This study aimed to propose and evaluate an automatic parenchyma extraction (APE) method from a whole manual region-of-interest in the liver R2* measurement for assessing HIC.

Methods:

The proposed APE method consisted of five steps: 1) pre-filter the images with the non-local means algorithm, 2) calculate the R2* map by pixel-wise fitting with ⁴a noise-corrected exponential function, 3) extract parenchyma pixels from a manually whole liver ROI by using the fuzzy c-means algorithm on the R2* map, 4) use morphological operator to diminish the partial volume effect, 5) calculate the output R2* value by fitting the average signal of the parenchyma with the noise-corrected exponential function.

The accuracy of R2* measured by using the APE method was evaluated in the simulation. The mathematical simulations were based on liver scan protocols and took into account the impact on R2* relaxometry of partial volume effect, intensity heterogeneity and Rician-distributed noise. The performance of the APE method was evaluated for R2* ranging from 100 to 1000 s⁻¹ and varying signal-noise-ratio (SNR) levels.

In total of 108 transfusion-dependent patients (age 23 ± 10 years old, 56 males) were scanned using a multiple gradient-echo (GRE) sequence on a 1.5T MRI scanner (Siemens Sonata) (flip angle 20° , repetition time 200 ms, 12 echo times from 0.97 to 16 ms, slice thickness 10mm, matrix 64×128). The R2* values measured by using the APE method were compared with that measured by using the mROI method with three small ROIs as shown in Fig. 1. We also adopted the coefficient of variation (CoV) that was defined as the standard deviation of the differences between the two independent measurements divided by their means and expressed as a percentage to assess the variability between methods and inter-observer reproducibility. Correlation analysis was performed using Pearson's test. For all statistical analysis, P < 0.05 was considered statistically significant.

Results: The mean R2* evaluation error percentage of the APE method compared to the true R2* was 0.34% (ranged -0.39 ~1.08%) as shown in Fig. 2. Fig. 3 shows an example of segmentation of liver parenchyma by using the APE method (R2*=367.7 s⁻¹). The Bland–Altman plots of the inter-observer reproducibility for the APE and mROI methods are shown in Fig. 4. The CoV of inter-observer variability for the APE method was 1.39% (r=0.9997, P<0.001), compared with 6.28% (r=0.9940, P<0.001) for the mROI method. The correlation between R2* values measured by using the APE and mROI methods for liver iron quantification was significant (r=0.9960, P<0.001) as shown in Fig. 5.

Discussion: The low R2* evaluation error percentage indicated the APE method provided a reliable and accuracy method for R2* measurement in the simulation. Compared to the higher CoV for the mROI method, which may due to the sampling errors from the placement of ROIs, the APE method provided more robust R2* measurement with lower inter-observer variability and therefore dramatically reduced the operator dependence

Conclusions: The proposed APE method may be important for increasing the diagnostic confidence of R2* measurement and performing effective prognosis of transfused patients



Fig. 1 Three ROIs drawn on parenchyma



Fig. 3 Segmentation result on R2* map

References:

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Fig. 2 Error percentage of R2*meaured by the APE method



Fig. 5 Scatter plot for R2* comparison between the APE and mROI methods