Automated Segmentation of Lesions in Liver using T_1 MR Imaging

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Purpose: Early detection of lesions such as Hepatocellular Carcinoma (HCC) in patients with liver cirrhosis sometime becomes challenging **[1]**. MR imaging could play a critical role in analysis and evaluation of lesions in liver over time. For the same first step is to segment the liver and lesions in it. Manual demarcations on each slice in a 3D stack is practically not feasible and identification of the conditions is further unwieldy. We investigated a semi- automated segmentation methods based on region growing **[2]** using T1 weighted MR imaging that can be used for other sequences as well.

Introduction: Under both research and clinical settings, estimations and quantitative investigation of liver with T1 weighted MRI, it is required to first segment the liver and lesions in it. Radiologist performing manual segmentation on each slice is practical challenging; the procedure is tedious and cumbersome. The motivation behind this study was to implement automated and semi-automated methods such as region-growing algorithm for segmentation, within reasonable accuracy, that can additionally be investigated for clinical decision making in cirrhosis and hepatocellular carcinoma.

Methods: MRI datasets from 28 subjects (5 healthy subjects', 11 patients with cirrhosis and 12 patients with hepatocellular carcinoma) were retrospectively analysed for this study. MRI images dataset was acquired with 1.5T (Siemens, Aera) with a phased-array torso coil, TE=102 msec and TR = 2,700 msec, slice thickness = 6mm and matrix size = 320x170. T1 weighted images with hepatic portal-venous phase were used for segmentation as these has the best contrast resolution required. The region-growing algorithm **[3]** was implemented as a semi-automated method optimising computation time and precision in segmentation. It required user inputs only at the initiation of the process that are the seed points for region growing. The algorithm then initialises seed points automatically in subsequent slices of MRI by calculating centroid from previously slice ROIs and continue liver segmentation for the entire 3D anatomy. At each slice a check is being performed confining the region to grow only in liver, the difference in segmented liver slices between two subsequent slices is greater than 40 % is consider error as a smooth transition is expected. In those cases user might be requested to confirm or correct the ROIs for the slice and proceed for further segmentation.

Liver ROIs were demarcated manually by a radiologist (clinical experience of >10 years in cancer imaging), considered as standard liver mask and used to calculate the error in the semi-automatic liver segmentation methodology. The accuracy measure is used to compare the Dice Coefficient (DC) and Jaccard Index (JI). Where $DC = 2.(|A \cap B|/(|A|+|B|))$ and $JI = (|A \cap B|/|A \cup B|)$, A and B are the areas marked by the expert radiologist and segmentation algorithm respectively. Both DC and JI varies between 0-1, 0 indicating poor performance with 100% error and 1 indicating an ideal scenario with 100% accuracy in segmentation. The segmentation algorithm and analysis were implemented with an in-house built toolbox in MATLAB. Histogram analysis was performed calculating mean, std. dev., skewness and kurtosis finding any discriminating features among liver with cirrhotic and HCC. Histogram analysis was performed after normalising the signal intensity with the paraspinal muscles.

Table 1: Average accuracy measured Dice Coefficient (DC) and Jaccard Index (JI) for different liver conditions.

Subjects	Dice Coeff.	Jaccard Index
Normal(n=5)	0.84 ± 0.05	0.73 ± 0.08
Cirrhosis(n=11)	0.73 ± 0.13	0.61 ± 0.15
HCC (n=12)	0.71 ± 0.12	0.60 ± 0.17

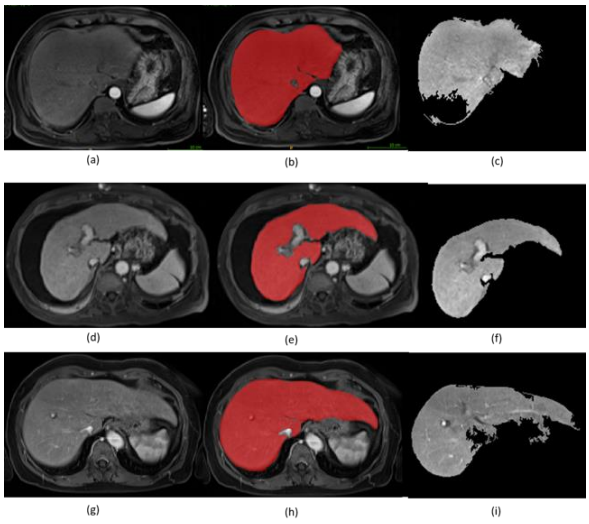

Figure 2:
The figures (a)-(c) are MRI scans of a healthy liver.
The figures (d)-(f) are MRI scans of a liver with cirrhosis.
The figures (g)-(i) are MRI scans of a liver with hepatocellular carcinoma.
The figures (a), (d) and (g) are the T1w MRIs, taken in the HV phase.
The figures (b), (e) and (h) are the MRIs, with a layer marked by a radiologist.
The figures (c), (f) and (i) are livers, segmented by the region-growing algorithm.

Results: Table 1 shows mean and standard deviation of DC and JI for the segmentation methodology over subjects. For the healthy liver, the algorithm gives a high accuracy (DC: ~84% & JI: ~73%); cirrhosis have lower values (DC: ~74% & JI: ~64%), due to high inhomogeneity in the liver. Similarly the hepatocellular carcinoma has a comparable accuracy to cirrhosis (DC: ~74% & JI: ~61%), due to larger inhomogeneous and lesions within liver. The segmentation took ~4-6 seconds per slice. Figure 2 shows representative cases with the automated segmentation and manual demarcated liver for the three groups. Figure 3 shows the comparative histogram analysis of liver with cirrhosis and HCC. The mean intensity in HCC liver is same as patients with cirrhosis but with narrow confidence interval. SD is observed to be considerably higher and skewness much lower in patients with HCC compared to cirrhotic liver. Kurtosis shows no appreciable differences except tight confidence interval in patients with HCC.

Discussion: The semi-automated segmentation algorithm showed reasonably good segmentation (>70%) for liver in T1W MR images. The average intra- and inter-rater variability is ~7-15% in manual demarcation of liver and underlying lesion (cysts, HCC etc.). Comparing that >70% accuracy in diseased and >80% accuracy in segmentation of healthy liver is practically good. Further quantitative analysis with histogram, textural analysis can be performed for clinical decision making. Further segmentation within liver for identification of lesions (tumour/cyst/haemangioma etc.) can be performed using the same approach with the segmented liver. The histogram analysis of cirrhosis and patients with HCC revealed general symmetric trends in cirrhotic cases as compared to skewed distributions in HCC. This can be used as distinguish parameters. These parameters can be further fine-tuned to obtain a distinguishing tool, capable of early trends of HCC appearance in cirrhosis.

Conclusion: The semi-automatic region growing segmentation method with a reasonable precision and requires limited manual inputs has been developed. It requires significantly lesser time in liver segmentation and will be helpful in developing a liver diagnosis toolbox.

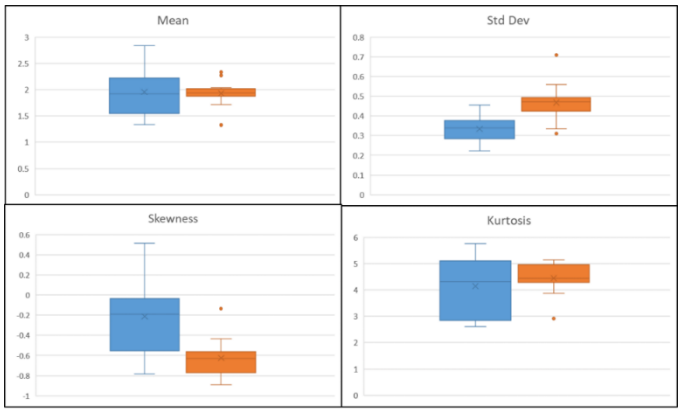

Figure 3: Contrast between cirr (blue) and hcc (orange) on various parameters.

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References: **[1]** Oliva MR, Saini S. Liver cancer imaging role of CT, MRI, US and PET. Cancer Imaging. 2004; 4(Spec No A):S42-S46. doi:10.1102/1470-7330.2004.0011. **[2]** Daniel, University Hospital of Marburg (2011) Region growing (2D/3D grayscale) (https://in.mathworks.com/matlabcentral/fileexchange/32532-region-growing--2d-3d-grayscale-) MATLAB Central File Exchange.**[3]** Y. Chen, Z. Wang, W. Zhao and X. Yang, "Liver Segmentation from CT Images Based on Region Growing Method," 2009 3rd International Conference on Bioinformatics and Biomedical Engineering, Beijing, 2009, pp. 1-4.