5195

Improving the Noise Propagation Behavior of Different Fatty Acid Quantification Techniques using Spectral Denoising

Manuel Schneider[1], Felix Lugauer[1], Dominik Nickel[2], Brian M Dale[3], Berthold Kiefer[2], Andreas Maier[1], and Mustafa R Bashir[4,5]

[1]Pattern Recognition Lab, Department of Computer Science, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany, [2]MR Applications Predevelopment, Siemens Healthcare GmbH, Erlangen, Germany, [3]MR R&D Collaborations, Siemens Healthcare, Cary, NC, United States, [4]Radiology, Duke University Medical Center, Durham, NC, United States, [5]Center for Advanced Magnetic Resonance Development, Duke University Medical Center, Durham, NC, United States

Synopsis

MRI is not only capable of quantifying the fat content, but also the fatty acid composition of human adipose tissue. Especially for low fat fractions, fatty acid quantification is sensitive to image noise. Including prior information or additional parameter approximations into the quantification method helped to improve the noise propagation behavior, but also introduced a systematic bias. Performing spectral denoising in between image reconstruction and fatty acid quantification kept the systematic bias as well as the noise in the parameter maps low, and hence allows for more flexible protocol selection and shorter acquisition times.

Purpose

Recent studies suggest the use of the hepatic fatty acid (FA) composition as a biomarker for distinguishing non-alcoholic steatohepatitis (NASH) and simple steatosis[1,2]. Quantifying the FA composition of adipose tissue using MRI at clinical field strengths is sensitive to image noise, which is usually addressed by long echo trains and signal averaging[3]. Thus, in-vivo validation of those methods is so far limited to protocols achieving sufficient SNR, having acquisition times of up to several minutes[3,4]. The aim of this work was to quantitatively assess three FA quantification methods regarding their systematic bias and noise performance using numerical simulations and in-vivo data. Moreover, we propose to use spectral denoising to improve MR-based fat composition quantification on noisy input images.

Methods

Three FA quantification approaches were considered, which differ in the derivation of the number of double bonds (ndb), number of methylene-interrupted double bonds (nmidb), and the chain length (CL). All of them incorporate a heuristic approximation for the CL[5]. In the first method (termed "Pinv"), water, fat and two additional fat contribution parameter maps are calculated using a linear model as has been previously described[4]. The second technique (termed "IneqConst") additionally adds inequality constraints based on prior FA composition information ($ndb \leq 6; nmidb \leq 3$), and solves the resulting inequality-constrained linear least-squares problem using quadratic programming. The third method (termed "Iter") makes use of an additional approximation for the nmidb and solves two subsequent non-linear least-square fits iteratively[6]. The calculated parameters were used to determine the fractions of unsaturated FAs (UFAs), saturated FAs (SFAs), mono-unsaturated FAs (MUFAs), and poly-unsaturated FAs (PUFAs). Every experiment was conducted twice: once without denoising, and once including a Dixon water-fat spectral denoising method[7] prior to the FA quantification.

FA compositions that span symmetrically over typical adipose human tissue values[8] (UFA = 72.9±15%, PUFA = 23.4±15%) were taken into account when generating the synthetic dataset. Fat fractions (FFs) from 15% to 50% were simulated. For every FA composition and FF combination, a complex-valued signal was synthesized for 8 different echo times (TE1 = 1.35ms, ΔTE = 1.25ms). The mean absolute errors and mean standard deviations of the calculated parameter maps were derived numerically by employing additive Gaussian noise and repeating the simulation 1000 times.

For in-vivo validation, eight echoes of MR data (2D GRE with 16 slices, TE1 = 1.28ms, ΔTE = 1.19ms, TR = 175ms, flip angle = 10°, spatial resolution: 3.75x3.75x10mm^3, bandwidth = 1953Hz/px, bipolar readout) from a clinical trial subject suffering from non-alcoholic fatty liver disease (NAFLD) were acquired on a 3T MR scanner (MAGNETOM Trio, Siemens Healthcare, Erlangen, Germany) under IRB approval. Prior to the FA quantification, complex-valued images were calculated using a prototype, and compensated for field inhomogeneities and eddy current effects. The field map and eddy current-correcting phase were calculated using a variable projection least-squares fit, which employed region growing to enforce spatial smoothness. The phase-corrected complex images were used to estimate T2* relaxation by means of variable projection.

Results and Discussion

The numerical simulation results are summarized in Table 1. “Pinv” achieved the lowest mean errors. In comparison, adding inequality constraints (method “IneqConst”) led to slightly lower mean standard deviations, while barely increasing the mean errors. The method “Iter” resulted in the lowest standard deviations (especially for the PUFAs and MUFAs), but also introduced a systematic bias. “Pinv” led to uniform standard deviations for all FA combinations (Fig. 1a), whereas “IneqConst” and “Iter” reduced the noise level for some FA values (Fig. 1b-c). The applied spectral denoising method consistently improved the noise propagation behavior of all analyzed methods four- to five-fold. Particularly for small fat fractions, the methods including spectral denoising performed superiorly compared to the unfiltered cases (Fig. 2).

Representative in-vivo UFA maps are depicted in Fig. 3. For the methods “Pinv” and “IneqConst”, the mean UFA values in the ROI were in compliance with previously published results[3,8]. For these methods the UFA maps from denoised images were more uniform in appearance, and edges were preserved. The method “Iter” (with and without denoising) calculated homogenous UFA values in the subcutaneous tissue (very high FF), but failed to reliably estimate hepatic UFA values.

Conclusion

Including inequality constraints or an approximation of the nmidb parameter in the FA quantification did improve the noise propagation performance, but also increased the mean systematic error. In contrast, applying a spectral denoising algorithm prior to the FA quantification reduced both the systematic error and the noise propagation error. Hence it may be a useful tool to reduce the SNR demand on contrast images and increases the clinical feasibility of MR-based FA quantification.

Acknowledgements

No acknowledgement found.

References

1. van Werven JR, Schreuder TC, Nederveen AJ, et al. Hepatic unsaturated fatty acids in patients with non-alcoholic fatty liver disease assessed by 3.0 T MR spectroscopy. European Journal of Radiology. 2010;75(2):e102–e107.

2. Flintham R, Eddowes P, Semple S, et al. Non-Invasive Quantification and Characterisation of Liver Fat in Non-Alcoholic Fatty Liver Disease (NAFLD) Using Automated Analysis of MRS Correlated with Histology. In: Proceedings of the 24th Annual Meeting of ISMRM; 2016. #0357

3. Berglund J, Ahlström H, Kullberg J. Model-based mapping of fat unsaturation and chain length by chemical shift imaging – phantom validation and in vivo feasibility. Magnetic Resonance in Medicine. 2012;68(6):1815–1827.

4. Peterson P, Månsson S. Simultaneous quantification of fat content and fatty acid composition using MR imaging. Magnetic Resonance in Medicine. 2013;69(3):688–697.

5. Bydder M, Girard O, Hamilton G. Mapping the double bonds in triglycerides. Magnetic Resonance Imaging. 2011;29(8):1041–1046.

6. Leporq B, Lambert SA, Ronot M, et al. Quantification of the triglyceride fatty acid composition with 3.0 T MRI. NMR in Biomedicine. 2014;27(10):1211–1221.

7. Lugauer F, Nickel D, Wetzl J, et al. Robust Spectral Denoising for Water-Fat Separation in Magnetic Resonance Imaging. In: Medical Image Computing and Computer-Assisted Intervention - MICCAI. Springer; 2015. p. 667–674.

8. Ren J, Dimitrov I, Sherry AD, et al. Composition of adipose tissue and marrow fat in humans by 1H NMR at 7 Tesla. Journal of Lipid Research. 2008;49(9):2055–2062.

Figures

FA Quant. Method	SNR: 50		SNR: 25	
	no denoising	spectral denoising	no denoising	spectral denoising
Pinv:	Mean ± SD (%)	Mean ± SD (%)	Mean ± SD (%)	Mean ± SD (%)
SFA:	0.31 ± 11.2	0.06 ± 2.35	0.81 ± 22.8	0.12 ± 4.68
UFA:	0.31 ± 11.2	0.06 ± 2.35	0.81 ± 22.8	0.12 ± 4.68
PUFA:	0.90 ± 21.5	0.12 ± 4.60	3.36 ± 44.4	0.27 ± 9.21
MUFA:	0.91 ± 28.3	0.16 ± 6.00	2.85 ± 57.8	0.32 ± 12.0
IneqConst:	Mean ± SD (%)	Mean ± SD (%)	Mean ± SD (%)	Mean ± SD (%)
SFA:	0.71 ± 10.9	0.06 ± 2.35	1.98 ± 18.1	0.14 ± 4.63
UFA:	0.71 ± 10.9	0.06 ± 2.35	1.98 ± 18.1	0.14 ± 4.63
PUFA:	1.81 ± 17.8	0.12 ± 4.56	4.27 ± 23.8	0.31 ± 8.72
MUFA:	2.46 ± 24.2	0.16 ± 5.96	6.15 ± 31.0	0.41 ± 11.5
Iter:	Mean ± SD (%)	Mean ± SD (%)	Mean ± SD (%)	Mean ± SD (%)
SFA:	6.07 ± 9.94	5.46 ± 2.37	1.2E5 ± 3.9E6	5.52 ± 4.25
UFA:	6.07 ± 9.94	5.46 ± 2.37	1.2E5 ± 3.9E6	5.52 ± 4.25
PUFA:	5.66 ± 10.2	5.45 ± 2.57	1.2E5 ± 3.9E6	5.49 ± 4.63
MUFA:	11.7 ± 4.78	10.9 ± 1.09	2.5E5 ± 7.8E6	11.0 ± 1.77

Table 1: Quantitative results of the numerical simulation experiment. The given values are the mean errors and mean standard deviations (SDs) over 1000 FA quantification steps on synthesized data with additive, random Gaussian noise. Mean values were calculated considering typical FA combinations in human adipose tissue[8] (see Fig. 1) and FFs from 15% to 50%. "Pinv" achieved the lowest systematic bias, whereas the method "Iter" resulted in the lowest standard deviation. "Iter" got instable for a SNR of 25. Spectral denoising improved the noise propagation behaviour significantly, and did not have a negative effect on the mean error.

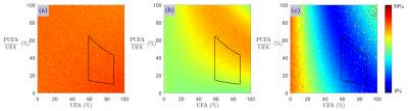

Fig. 1: Exemplary mean standard devations of the MUFA maps of the numerical simulation experiment (SNR = 50, FF = 22%, without spectral denoising) for the methods "Pinv" (a), "IneqConst" (b) and "Iter" (c). The method "Pinv" led to a homogenous FA map, whereas inequality constraints and approximations incorporated into the other two methods reduced the standard deviation for certain FA combinations. The region within the black border characterizes typical FA combinations in adipose tissue[8] (UFA = 72.9±15%, PUFA = 23.4±15%).

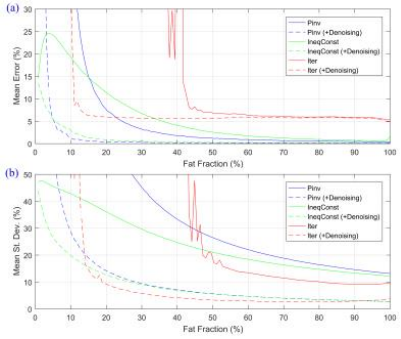

Fig. 2: Results of the numerical simulations for varying FFs. The plots exemplary indicate mean errors (a) and mean standard deviations (b) of the PUFA maps for typical fatty acid combinations in human adipose tissue[8] (see Fig. 1), and for a SNR of 25. The method "Iter" achieved lower standard deviations for high FFs, but did get instable for smaller FFs. Spectral denoising improved the noise propagation behaviour over the whole range of FFs (and for small FFs also the mean error).

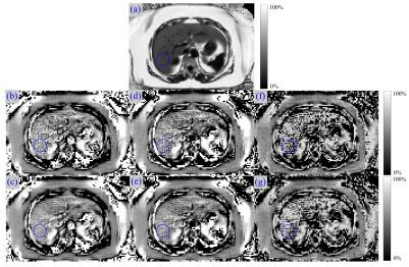

Fig. 3: In-vivo comparison of the three FA quantification methods and visualization of the effect of spectral denoising. (a) fat fraction map (mean ± standard deviation in the ROI: 24.6%±2.2%); (b) "Pinv" UFA map (ROI: 64.8%±15.3%); (c) "Pinv + Denoising" UFA map (ROI: 65.1%±8.8%); (d) "IneqConst" UFA map (ROI: 60.6%±15.5%); (e) "IneqConst + Denoising" UFA map (ROI: 61.5%±10.8%); (f) "Iter" UFA map (ROI: 45.1%±42.3%); (g) "Iter + Denoising" UFA map (ROI: 53.1%±30.7%)