The influence of tissue composition on signal to noise ratio of MR measurements

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Introduction

Contrast in MR imaging arises from spatial variations in NMR properties such as relaxation times, which reflect underlying variations in tissue water and macro-molecular contents. While average macroscopic values of NMR parameters may be ascribed to individual specific tissues, at a more detailed level some degree of spatial variation will inevitably be measurable. We have begun to probe the intrinsic variations in relaxation properties within tissues at a microscopic level in order to relate these fluctuations to underlying variations in proteomic and other properties. All MRI images, even of a uniform sample, contain some spatial variance of signal because of the presence of additive random noise. However, at high spatial resolution some of this variance may reflect not only thermal noise (temporal variance, which averages incoherently as more images are acquired) but also microscopic inhomogeneities in tissue composition (spatial variance), which comes from variations in tissue composition. We have developed methods to quantify and examine the nature of these spatial variances in MR images. The ultimate goal of this research is to determine how these systematic variances correlate with the underlying macro-molecular composition of tissues.

Materials and Methods

We examined the signal to noise (SNR) characteristics of images from a variety of tissues to determine the influence of intrinsic, systematic variance of tissue properties on apparent SNR behavior. Mouse kidney, liver and muscle were freshly excised and used in our imaging study. After excision, each tissue was sealed independently in 10 mm Eppendorf tubes. Each sample was imaged using a 10mm tube coil with a Varian 7T MR scanner. Images were also acquired of simple water samples. Spin echo images from a single slice in each sample were acquired 50 times in single imaging session (TR = 2400, TE = 20ms, 512x256, 25.6x11.2 mm^2 FOV, slice thickness = 1mm). Time averaged images were generated by sampling and averaging these 50 images to generate composite images with different SNR as a function of the number of acquisitions (N_{acq}). SNR for tissue and a pure water sample in each image set were generated by manually selecting ROIs within different regions. Expected SNR values for each tissue and water sample were generated by extrapolating the SNR from a single (randomly selected) image using the following expression:

$$SNR(n) = \sqrt{n} * SNR(1), \quad (1)$$

where n is the number of acquisitions. The observed and expected SNR values for each sample were plotted and examined for qualitative differences between samples. We quantified the deviation of each observed SNR value from the standard model of SNR by non-linearly fitting the collected data to the following expression:

$$SNR(n) = C_1 * \sqrt{n} + C_2, \quad (2)$$

where C_1 characterizes the SNR of a single image, and C_2 accounts for any offset in the collected data. The root-mean-square (RMS) residual for each fit was calculated using the following expression:

$$R = \sqrt{\frac{1}{n}\sum_{i}^{N}(SNR_{fit} - SNR_{obs})^2} \quad (3)$$

where, R is the residual, SNR_{fit} is the fitted SNR measurement and SNR_{obs} is the observed SNR measurement; a low R value indicates a better fit to the model.

	R_{tissue}	R_{water}
Liver	0.2629	0.2261
Kidney	1.0764	0.8884
Muscle	2.3437	1.2773

Table 1.

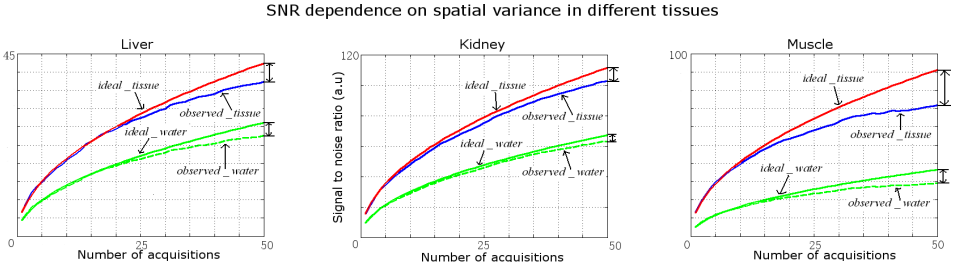

Figure 1

Results

The SNR relationships for each sample vs. N_{acq} are plotted in Fig. 1, with red, blue, solid green, and dashed green, representing an ideal tissue, observed tissue, ideal water, and observed water , respectively. The deviations between the ideal and observed signal are highlighted in each plot and increase going from liver, to kidney, to muscle, and are larger in tissues than in water. The R values for each observed curve fitted against (2) are shown in Table 1. In all cases the R value is greater in tissue than in water, and the deviation across tissues increases from liver to kidney to muscle.

Discussion

These results indicate that at high resolution there are spatial variances in MR properties within single tissues that do not reduce with increased numbers of acquisitions. The spatially-averaged ratio of mean to standard deviation does not reduce with increasing numbers of acquisitions as SNR should, presumably because there are intrinsic variations that add coherently and are not true "noise" (see Tbl. 1, col. 1). We hypothesize that these deviations are the result of spatial variances in the composition for each tissue type. Our results indicate that these variances vary between tissues.

Conclusion

We have demonstrated that MR signals from *ex vivo* tissue demonstrate spatial variations at high resolution. These spatial variances reflect variations in the composition of the tissue. In a related abstract (Sinha et al.) we show how careful coregistration of MR images with mass spectrometry images can be used to relate these intrinsic tissue variations to proteomic content.

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