Noise Bias Reduction and Parallel Imaging for the Measurement of Diffusion Decay

G. Gilbert¹, G. A. Haddad¹, and G. Beaudoin¹

¹Department of Radiology, Centre Hospitalier de l'Université de Montréal, Montreal, QC, Canada

Introduction

The presence of an important magnitude noise bias is known to have very detrimental effects on diffusion measurements in general [1], and in particular on the estimation of diffusion decay. Over the last years, different correction approaches were proposed to reduce or eliminate the influence of the noise bias [2], [3], [4]. A recent signal combination method was shown to significantly improve the accuracy of the estimates of several diffusion tensor imaging (DTI) parameters in the presence of an important noise bias [5]. The present work studies the application of this correction method for the estimation decay parameters. Furthermore, as parallel imaging appears as a very interesting alternative to reduce both scan time and artefacts in diffusion experiments [6], the extension of the method to GRAPPA parallel reconstruction is evaluated. **Methods**

An *in vivo* diffusion data set of a healthy volunteer's brain was acquired for 17 equidistant b values from 0 s/mm² to 4000 s/mm² and 3 orthogonal diffusion directions. The measurements were repeated 25 times for b values lower than 2000 s/mm² and 50 times for b values of 2000 s/mm² and higher. A diffusion-weighted single-shot EPI sequence was used with both a standard (unaccelerated) reconstruction and a GRAPPA reconstruction with an acceleration factor of 2. A commercial 12-channel head coil was used for all measurements.

All images were reconstructed using both a standard sum-ofsquares (SoS) combination and the alternative algorithm (SUPER-D) proposed in [5]. This method makes use of an improved combination of signals from the array coil and complex averaging to reduce the noise bias. To act as a reference, the standard SoS images were also corrected using the statistical method (DHS) proposed in [4], which was extended to take into account the noisy signal distribution of SoS images.

The corrected diffusion decay curves were fitted to a biexponential model. The estimated diffusion parameters were then employed to generate synthetic diffusion images, having the same signal-to-noise ratio as the *in vivo* images, to allow a better estimation of the precision and accuracy of the different noise bias corrections.

Results and Discussion

Fig. 1 presents the *in vivo* diffusion decay curves obtained for both standard and GRAPPA reconstructions, for a region-of-interest in the body of corpus callosum. For the standard reconstruction, the SUPER-D and DHS methods lead to very similar results. However, significant differences appear between the two approaches when a GRAPPA reconstruction is used.

Fig. 2 illustrates the results obtained from the synthetic diffusion data sets. For the standard reconstruction, the SUPER-D and DHS methods allow a correct estimate of the true diffusion decay. In the case of the GRAPPA reconstruction, the SUPER-D method also gives an accurate estimation of the true diffusion signal. However, the accuracy of the DHS method suffers from the fact that the statistical distribution of the signal in GRAPPA images depends on both the coils geometry and the imaged object. Particularly, the DHS approach makes the hypothesis of spatially homogenous noise, which hypothesis does not generally hold for parallel imaging. The accuracy and precision of the two correction methods can be assessed from the simulation results presented in Tab. 1.

Correction	Bi-exponential	Reconstruction	
	parameter	Standard	GRAPPA
DHS [4]	f ₁	0.70 ± 0.09	0.64 ± 0.05
	D ₁ (x10 ⁻³ mm ² /s)	1.2 ± 0.4	1.2 ± 0.2
	D ₂ (x10 ⁻⁴ mm ² /s)	$\textbf{2.8}\pm\textbf{0.9}$	1.7 ± 0.2
SUPER-D	f ₁	0.68 ± 0.02	0.68 ± 0.05
[5]	D ₁ (x10 ⁻³ mm ² /s)	1.30 ± 0.09	1.3 ± 0.2
	$D_2 (x10^{-4} \text{ mm}^2/\text{s})$	2.3 ± 0.2	2.3 ± 0.3

Table 1: Fitted diffusion parameters obtained from numerical simulations. Simulated parameters: $f_1 = 0.69$, $D_1 = 1.28 \times 10^{-3}$ mm²/s, $D_2 = 2.30 \times 10^{-4}$ mm²/s.



Figure 1: In vivo diffusion decay. a) Standard reconstruction b) GRAPPA



Figure 2: Simulated diffusion decay. a) Standard reconstruction b) GRAPPA

As illustrated by the behaviour of the DHS method in the case of the GRAPPA reconstruction, the statistical correction methods developed for standard imaging [2], [3], [4] will generally not work when parallel imaging is employed. Inversely, as the SUPER-D method does not rely on an explicit description of the signal distribution and does not make the hypothesis of spatially homogenous noise, the use of the GRAPPA reconstruction does not appear to affect the accuracy of the method.

However, it is important to place emphasis on the fact that the SUPER-D method is accurate only if a sufficient number of repeated measurements are available. If scan time limitations do not allow the acquisition of a sufficient number of measurements and if parallel imaging is not used, the DHS method generally leads to a more accurate correction.

Conclusion

The presented results illustrate that the SUPER-D combination method can provide accurate estimates of bi-exponential diffusion parameters, for both standard ms were developed for standard imaging, the SUPER-D method appears to provide a

and GRAPPA reconstructions. While other correction algorithms were developed for standard imaging, the SUPER-D method appears to provide a distinctive opportunity when GRAPPA parallel imaging is used. **References**

- 1. Jones, D. K. and Basser, P. J. Magn Reson Med 52, 979-993 (2004).
- 3. Koay, C. G. and Basser, P. J. J Magn Reson 179, 317-322 (2006).
- 5. Gilbert, G. et al. IEEE T Med Imaging 26, 1428-1436 (2007).
- 2. Gudbjartsson, H and Patz, S. Magn Reson Med 34, 910-914 (1996)
- 4. Dietrich, O. et al. Magn Reson Med 45, 448-453 (2001).
- 6. Bhagat, Y. A. et al. Am J Neuroradiol 28, 293-298 (2007).