COMPARISON OF DIFFERENT MOTION CORRECTION METHODS FOR PROPELLER MRI

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TARGET AUDIENCE: Researchers and clinicians interested in motion correction

PURPOSE: Proper reference for motion estimation is critical for accurate and robust motion correction in PROPELLER MRI. Traditionally, single blade (SBR) or combined blade (CBR) may be chosen as the reference [1]. However, these methods may be unstable for some motion patterns. Liu, *et al*. has designed an algorithm to classify the blades into groups, and choose the dominant group as the reference (GBR) [2]. Recently, Pipe, *et al*. has proposed a novel idea in which no reference blade (NBR) is needed for motion correction [3]. This work focuses on the comparison of these methods, and aims to provide suggestions for choosing proper methods for motion correction.

METHODS: In this work, simulation and *in vivo* study were performed to evaluate their estimation accuracy and robustness.

Simulation: A phantom image was acquired by a 2D fast spin echo (FSE) sequence on a Philips 3T scanner, with TR/TE = 3000/80 ms, FOV = 250×250 mm^2 and slice thickness of 4 mm. The image was reconstructed with inverse fast Fourier transform (FFT) and then blade data were generated according to PROPELLER trajectories. 15 blades were generated to cover the full k-space for a single slice, with 30 frequency encoding lines in each blade. The matrix size of the reconstructed image was 256×256. Only in-plane random rigid motion was introduced to the blade data. Specifically, rotation within range of [-5°, 5°], and translation within range to be [-5, 5] pixels along x or y direction were added to the data. To evaluate the estimation precision, 100 random cases within the specified motion range were simulated and reconstructed using all the methods mentioned above. To evaluate the results, absolute estimation error, defined as the difference between estimated parameter and true parameter, was calculated.

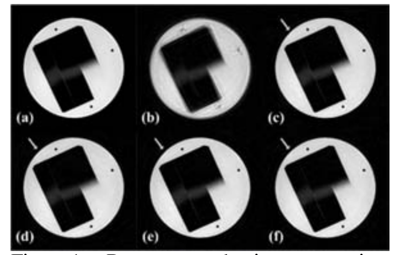

Fig. 1 Reconstructed images using simulation data: (a) reference, images (b) without correction, images reconstructed using (c) NBR, (d) SBR, (e) CBR, (f) GBR.

In vivo study: *In vivo* data were acquired using a TSE based PROPELLER sequence with an 8-channel head coil. The imaging parameters are listed as below, TR/TE = 5000/101 ms, blade number = 20, phase encoding steps in each blade = 30, slice number = 11. The matrix size of the reconstructed image was 300×300. The volunteers were asked to keep still during the first acquisition (reference scan), and move his/her head within a moderate range during the following scans.

Image reconstruction: To study the influence of reference chosen from different methods, all methods above, including SBR, CBR, GBR and NBR, were compared in this work. For the motion estimation, Fourier based image registration algorithm was used for all the implementations [4]. For SBR, CBR and GBR, 5 iterations were performed, and no iteration was performed for NBR. After motion correction, the blade data were weighted and gridded into Cartesian grids, then inverse FFT was used to generate the final images.

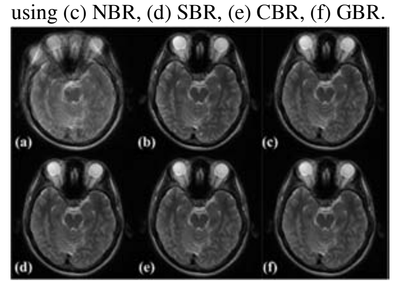

Fig. 2 Reconstructed images using in vivo data: (a) without correction, (b) reference images, images reconstructed using (c) NBR, (d) SBR, (e) CBR, (f) GBR.

RESULTS AND DISCUSSION: Simulation: The estimation errors were calculated and averaged, which was summarized in Table 1. Although NBR method presents superior performance over the others, it is worthwhile to note that the differences in the final images cannot be observed visually, which was shown in Fig. 1. Only some slight streak artifacts appear in the final image (pointed by arrows), which is caused by the under-sampling in k-space from the motion interference, rather than the estimation errors.

Table 1 Motion estimation error for SBR, CBR, GBR and NBR

Method	Rotation (degree)	Translation in x direction (pixel)	Translation in y direction (pixel)
SBR	0.0867±0.0575	0.0062±0.0047	0.0063±0.0048
CBR	0.0862±0.0560	0.0053±0.0038	0.0050±0.0036
GBR	0.0847±0.0559	0.0054±0.0040	0.0051±0.0038
NBR	0.0315±0.0234	0.0046±0.0032	0.0048±0.0034

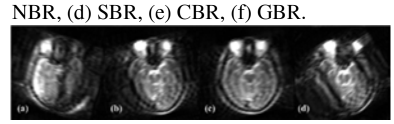

Fig. 4 Images reconstructed from single blades (corrected with NBR), (a) 10th, (b) 11th, (c) 12th, (d) 13th blade.

In vivo study: For most cases, all methods perform well, and a representative slice is shown in Fig. 2. The estimated motion parameters were also calculated and compared, as shown in Fig. 3. For most of blades, motion parameters estimated from different methods are very close to each other. It also should be noticed that the translation estimation of three blades (10th, 11th and 13th blade) don't match well. By observing the images reconstructed from each blade (Fig. 4), we find that the three blades are severely corrupted. Thus it is the corruption that leads to estimation mismatch among different methods. The mismatch doesn't bring much difference among the final images, since the correlation weighting after motion correction can reduce their contribution to the final images.

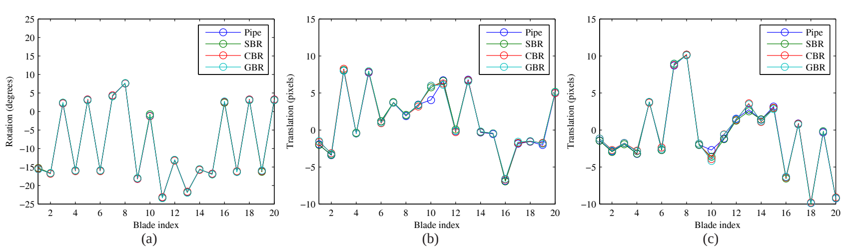

Fig. 3 Motion estimation parameter comparison among SBR, CBR, GBR and NBR (a) Rotation estimation, translation estimation along (b) x and (c) y direction.

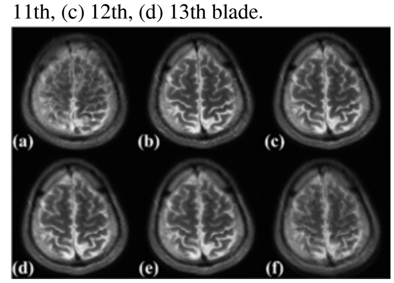

Fig. 5 Reconstructed images using in vivo data: (a) without correction, (b) reference images, images reconstructed using (c) NBR, (d) SBR, (e) CBR, (f) GBR.

In some special cases with severe data corruption (Fig. 5), which is probably caused by through-plane motion [3], SBR, CBR and GBR may fail to converge, but NBR method still maintains relatively good performance. These cases typically appear in slices with less distinguishing features when motion range is substantially big. The reason is still under investigation. This indicates NBR is more robust.

CONCLUSIONS: Simulation results show that all the methods are accurate enough to generate a good image for cases with in-plane rigid motion only. For *in vivo* imaging, SBR, CBR and GBR may fail in some special cases, while NBR still maintains relatively good performance, which indicates NBR is more robust for corrupted data. More cases will be compared in future research.

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REFERENCES: [1] Pipe J.G., MRM 42:963-969, 1999. [2] Liu Z., et al., JMRI, 2013. [3] Pipe J.G., et al., MRM, 2013. [4] Maas L.C., et al, MRM, 37:131-139, 1997.