

## Optimized Reconstruction for PROPELLER MRI

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**INTRODUCTION:** The original PROPELLER method (1) estimates bulk motion by reframing rotation estimation as a  $\theta$ -direction shift in polar coordinates, and then using the same shift-detection algorithm for both rotation ( $\theta$ -shift) and x-y translation. For this algorithm, the relative shift  $d = d_g - d_r$  between a reference blade  $g(x-d_g)$  and any other blade  $f(x-d_r)$  is estimated by finding the maximum of

$$p(d) = FT[F(k) G^*(k)], \quad [1]$$

where  $F$  and  $G$  are Fourier pairs of  $f$  and  $g$ . This iterative algorithm relies on finding a "good" reference blade, and the final relative shift ( $d$ ) is chosen with no regard to local curvature of  $p$ , which can affect the robustness of that choice. A new method for shift estimation is proposed that does not require a reference blade, requires no iterations (solves for all shifts together), and considers the curvature of  $p(d)$  for each blade pair.

**THEORY:** Let  $p_{ij}(d)$  be the correlation between any pair of blades  $i$  and  $j$ , where  $p_{ij}$  is calculated as in Eq. [1]. As seen in Fig. 1, an exponential function (yellow) of the  $p_{ij}$  (blue) values, used to increase its dynamic range, is fit locally to a parabola (green), i.e.  $E_{ij} = a_{ij} d^2 + b_{ij} d + c_{ij}$ . The peak of  $E_{ij}$  is found by setting its derivative  $(2 a_{ij} d + b_{ij}) = 0$ , which gives the shift  $d$ . These equations are then written in matrix form as

$$A\Delta = -B, \quad [2]$$

where the matrix  $A$  and vector  $B$  contain the elements  $a_{ij}$  and  $b_{ij}$ , respectively, and the vector  $\Delta$  contains the unknown shifts of each blade. Each equation is weighted by the respective correlation, and the system is solved using the pseudoinverse of  $A$ .

**METHODS:** In a preliminary experiment, using a Philips 3T Ingenia MRI with a PROPELLER-based TSE sequence (23 blades, each 448x30, fov 25cm, 24 slices), 3 volunteers were each scanned 3 times, in which they were asked to create no motion, small motion, and moderate motion. The data were then corrected with the original and proposed method, generating two comparable sets of images.

Two neuroradiologists, blinded to the reconstruction methods (original vs. proposed), compared the resulting (3 volunteers \* 3 motion types \* 24 slices = 216) pairs of images and rated them as "L >> R, L > R, L = R, R > L, and R >> L" with respect to absence of motion artifacts.

**RESULTS:** For most image pairs, the two methods were quite similar, and differences were only seen by switching between them in the same window (this is most of the L<R, L=R, and R>L cases). In the majority of these cases, and in all of the cases where one method was much better than the other (e.g. Fig. 2), the proposed method was judged superior to the original method (see Table 1).

**CONCLUSIONS:** The proposed method for motion estimation has favorable features, and preliminary studies suggest it compares favorably with the original method. A future study will provide a more rigorous comparison of patient data.

**REFERENCES:** 1. Pipe, MRM 42(5), 714-20.

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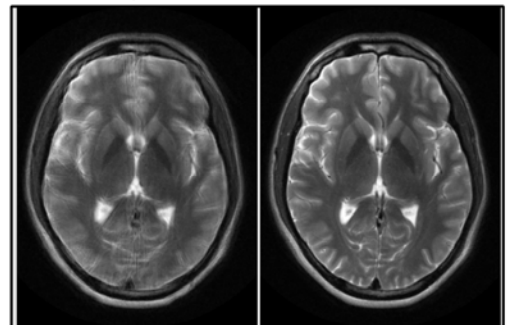
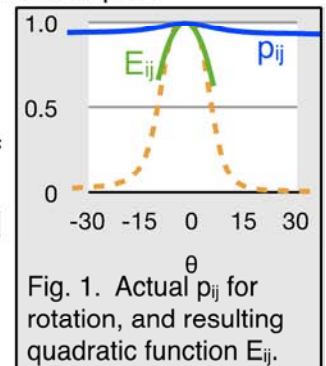


Fig. 2. Example of the proposed method (right) substantially outperforming the original method (left) ( $P \gg O$  in Table 1).

Table 1. Results of Radiologist comparison between original (O) and proposed (P) methods.					
	O>>P	O>P	P=O	P>O	P>>O
Rad 1	0	13	142	59	2
Rad 2	0	40	76	91	9