

Improved Sampling Density Correction for PROPELLER MRI

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Introduction: Non-uniform data collection for PROPELLER MRI⁽¹⁾ necessitates a sampling density correction step within the data reconstruction algorithm⁽²⁾. Each point is weighted based on the number of sampling points within a specified radial distance. With the previous method for estimating PROPELLER sampling density⁽³⁾, sampling points are first mapped to the nearest Cartesian points via a convolution kernel. The estimated sampling density at these Cartesian points are then re-assigned back to the sampling points; this “double convolution” is computationally efficient, but results in small errors in the estimation of sampling density. The proposed PROPELLER-specific sampling density correction method utilizes the regular geometries associated with the data collection to facilitate searches for neighboring points, resulting in efficient and smooth density correction. The sampling points are assigned weights based on the number of neighboring points before the gridding process. This improves the results noticeably compared to the previous method.

Methods and Results: The new sampling density correction method utilizes the size and rotation angle of the PROPELLER blades to determine where the intersections and places of overlap occur. This mathematical approach capitalizes on the symmetries characteristic of PROPELLER to generate density profiles with a high level of efficiency. The result is a more thorough and accurate density correction without compromising the speed of the reconstruction algorithm overall. To compare the existing methods with the new approach, a real valued signal of uniform intensity was fed into the PROPELLER reconstruction network for each density correction method. The outputs were compared based on smoothness and the presence of extraneous peaks in intensity. In addition, a synthetic, circular data set was transformed, fed through the network, and transformed back to illustrate the removal of image artifacts.

Figure 1: (Middle) The diagram illustrates how the individual blades are rotated to create the circular images seen. **(Right)** The top images show the calculated density correction for a single blade. The blade A utilizes the new method and does not contain the obvious hash marks seen in blade B, reconstructed with the old density correction method. Image A shows the new method's effect on a set of sixteen rotated blades. Just below is the graph of the intensities through the diameter. Image B shows the output of the previous algorithm. Note the relative smoothness of graph A, particularly in contrast to the peak seen in the center and the sharp changes towards the edges of graph B that correspond to the bright center region and depressed outer ring seen in the rotated image.

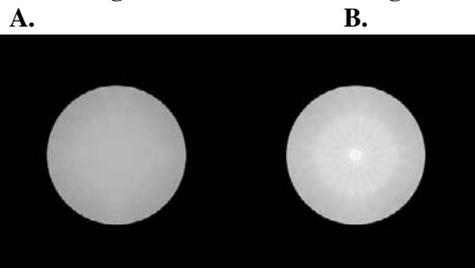
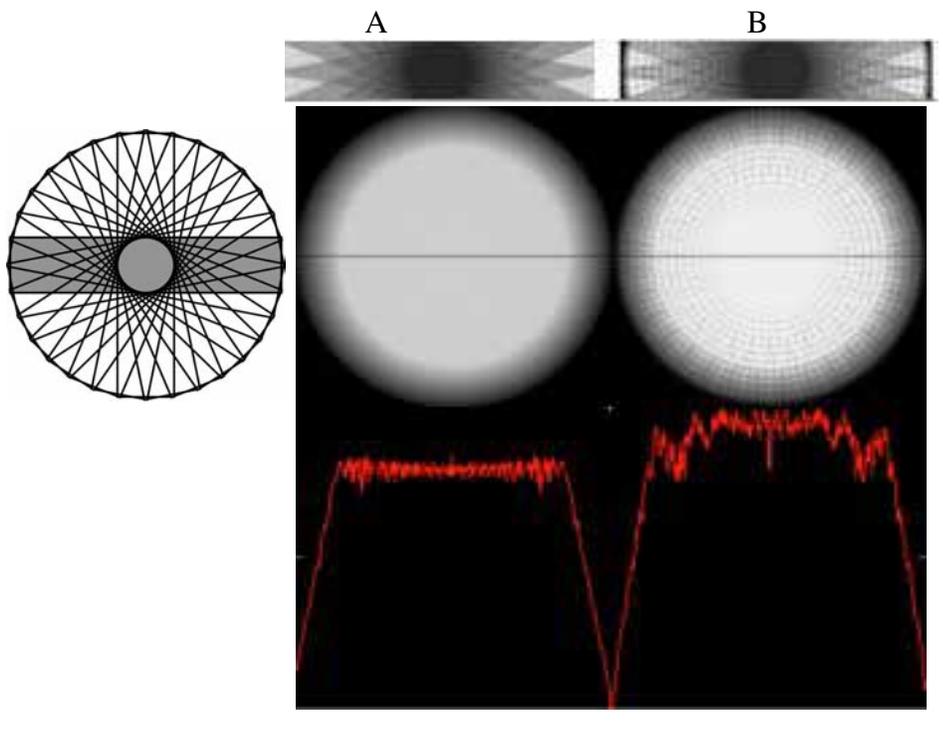


Figure 2. (Left) These images were generated from circularly symmetric data. Perfect sampling density correction should generate a perfectly uniform output. Image A, generated with the new algorithm is noticeably lacking the bright center point and ringing seen with Image B, generated with the old method.

References: 1. Mag Res Med 42: 963. 2. IEEE Trans Med Imag 10: 473. 3. Mag Res Med 41: 179.

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