TBLADE-spatiotemporal PROPELLER MRI

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Introduction: Cartesian segmented cine MRI can be accelerated by a number of methods (e.g. UNFOLD [1], TSENSE [2], kt-BLAST/SENSE [3]). It is well known that radial type k-space trajectories are more robust against motion and undersampling. Reconstruction times reported for generalisations of these methods to a radial k-space trajectory are, however, still beyond clinical accepted values [4]. The PROPELLER trajectory [5] is radial in nature. Here, we show that under certain constraints dynamic PROPELLER MRI can be accelerated by any of these methods and that the reconstruction time is only moderately increased compared to the Cartesian version of the particular method.

Methods: After each R-wave the acquisition of a particular blade is repeated N_P times (where N_P is the number of time frames). Thereby each blade is not sampled fully. Only every A-th line is acquired. Between successive frames the acquired line is shifted, such that the entity of A adjacent frames samples all lines of the blade. The rotation angle of the blade is changed between R-waves (i.e. the repetition loop is within the blade loop). With this sampling pattern the entire data set is split into N_B subsets (N_B is the number of blades). Each subset consists of the N_P incomplete repetitions of a particular blade. The sampling pattern of each subset is identical to the Cartesian sampling pattern used by the methods mentioned in the introduction. Any of these methods can be used to calculate the missing lines and to remove the aliasing that would result otherwise. This step is repeated for the N_B subsets. The remaining reconstruction process for each time frame is identical to the reconstruction process in conventional static PROPELLER MRI.

The method used in this work to complete the subsets is a GRAPPA [6] variant of TSENSE: GRAPPA is applied to each time frame of a particular subset to calculate the missing lines. The linear weights needed for the GRAPPA operation can, for example, be calculated from the time average of all frames of the sub-set. The resulting series is then Fourier transformed along the time dimension t to obtain the temporal frequency spectrum. The frequency terms f_n with $n = j \times N_P/A$ (j integer, $j \neq 0$, n=0 is the DC term) are filtered out to suppress residual artefacts. The resulting series is inverse Fourier transformed along the temporal frequency direction to obtain the final complete sub-set. Figure 1 shows images that were calculated from a single subset of a TrueFISP PROPELLER sequence. The data were collected on a Siemens Magnetom Avanto 1.5 T scanner.
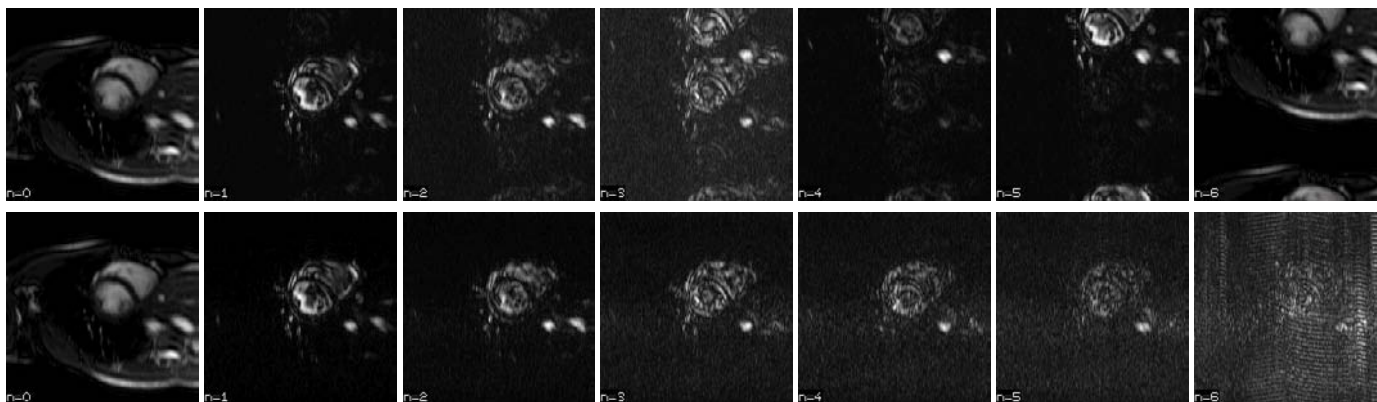

Figure 1: Temporal spectrum of a single subset. Shown are seven frequency terms out of N_P=18 (A=3, 15/45 acquired/total lines per blade). The lower/upper row shows the data before/after the GRAPPA operation, respectively. The term n=6 is removed by filtering. For visualization the data were transformed into image space. The entire processing is done in spatial frequency space.

Discussion and Results: PROPELLER MRI is less sensitive to motion than segmented Cartesian MRI and has capabilities to correct for motion that occurred between the acquisitions of blades. In dynamic PROPELLER MRI of organs which exhibit quasi-periodic motion the repetition loop can be within the blade loop. With this loop structure any method accelerating dynamic Cartesian MRI can be combined with dynamic PROPELLER MRI. The completion of the blades is done before the PROPELLER reconstruction. For most methods the completion of the blades can be done separately for each subset. The reconstruction time is therefore increased by approximately a factor N_B compared to the Cartesian version of the particular method. In our implementation the processing of a particular subset starts as soon as the subset has been acquired. If the processing time per subset is less than the average RR-interval, the parallelization of reconstruction and acquisition process ensures availability of the images immediately after the end of the scan. The acquisition time of a PROPELLER scan is a factor $\pi/2$ longer than the acquisition time of the corresponding Cartesian scan with the same acceleration factor A. To compensate for the additional time, the number of blades can be decreased [7]. A remaining disadvantage of the dynamic PROPELLER method is that the varying phase encoding direction requires a larger FOV or spatial oversampling or some tolerance to fold-in artefacts.

References: [1] Madore B. MRM 42:813-828 (1999) [2] Kellman P. MRM 45:846-852 (2001) [3] Tsao J. MRM 50:1031-1042 (2003) [4] Hansen MS. MRM 55:85-91 (2006) [5] Pipe JG. MRM 42:963-969 (1999) [6] MRM 47:1202-1210 (2002) [7] Arfanakis K. MRM 53:675-683 (2005)