k-t PCA reconstruction for functional lung MRI by Fourier Decomposition

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Introduction

In view of the limited availability of ³He gas for lung imaging studies, alternative methods for the assessment of pulmonary function have received much attention. A very promising approach utilizes dynamic ultra-short echo time imaging of the native proton signal with subsequent image registration and Fourier decomposition (FD) to construct perfusion and ventilation-weighted images [1,2]. Parallel imaging is used to optimize the signal-to-noise ratio and to achieve sufficiently short acquisition windows to suppress artifacts arising from bulk motion. Beyond parallel imaging and considering that dynamic series of the lung exhibit considerable spatiotemporal correlations, application of k-t undersampling techniques appear promising adjuncts to further accelerate dynamic proton imaging of the lung. It is the objective of the present work to study the feasibility of k-t undersampling in conjunction with the k-t PCA reconstruction framework [3] for accelerating dynamic proton image acquisition of the lung.

Methods

All measurements were performed on a 1.5 T MR scanner (Magnetom Avanto, Siemens Healthcare, Germany) using a combination of a 12-channel body array coil and a 24-channel spine coil. One healthy volunteer (29 y, female) was examined. Time-resolved fully sampled data of 190 coronal lung images were acquired with a 2D balanced steady-state free-precession sequence (bSSFP) in free-breathing. The sequence parameters were: TR/TE/TA = 1.9/0.8/240 ms, 4.1 images/s, FA = 75° , ST = 12 mm, FOV = 425^{2} mm², matrix = 128×128 , bandwidth = 1302 Hz/pixel. The lung images were reconstructed using the fully sampled data for reference purposes. Data undersampling was simulated by applying 5- and 10-fold data decimation according to a variable density sheared grid pattern (Figure 1). Taking into account the densely sampled central region in *k*-space corresponding net reduction factors were 4 and 6.75, respectively. Data reconstruction was performed using *k*-*t* PCA. Therein, the signal ρ is represented by a linear combination of temporal basis functions B(f) with corresponding spatial weightings w(x) whereas the basis set B and signal variance weights w_{train} are determined from low-resolution training data ρ_{train} . Matrix E contains the Fourier encoding coefficients; $\lambda \Psi$ is the weighted noise covariance matrix and vector ρ_{alias} stacks the undersampled data in the spatial-temporal frequency or *x*-*f* domain:



Fig. 1.Variable density sheared grid sampling pattern for dynamic 2D k-t PCA lung imaging. Grey dots indicate sampled positions as a function of phase-encode k_y and time t.

$$\rho(x_i, f_i) = B(f_i) \cdot w(x_i), \quad w_x = \left[\operatorname{diag}\left(\left|w_{\operatorname{train},x}\right|^2\right)\right] E^H \left(E\left[\operatorname{diag}\left(\left|w_{\operatorname{train},x}\right|^2\right)\right] E^H + \lambda \Psi\right)^{\mathsf{T}} \rho_{\operatorname{alias}}$$

To reduce the computational load, array compression was implemented to extract the major modes from the receive array data [4]. Using a single virtual coil composed from twelve physical coil elements as used for data acquisition reconstruction times were 10 min for 190 dynamic frames on standard PC hardware. Subsequently, all images within the coronal slice were corrected for the respiratory motion using a non-rigid registration algorithm [5] implemented on a stand-alone application fMRLung 4.4 (Siemens Corporate Research, Princenton, NJ, USA). For FD, the Fourier transform was applied pixel-wise along the time-axis of the registered data set. Spectral lines representing signal intensity changes in lung parenchyma at respiratory and cardiac frequencies were integrated to calculate ventilation- and perfusion-weighted images. Image reconstruction was implemented in Matlab (Mathworks, Natick, MA, USA). To assess the quality of the images reconstructed from undersampled data with respect to the fully sampled images the mean peak signal-to-noise ratio (PSNR) and root mean square error (RMSE) maps were calculated. The PSNR is given by the formula:

$$PSNR(I,J) = 10 \cdot \log_{10}\left(\frac{k^2}{MSE(I,J)}\right)$$

where I - reference image, J - undersampled image, k - maximal pixel value in an image, MSE - mean square error.

Results

Figure 2 shows example coronal images reconstructed from fully sampled, 5x and 10x undersampled data using the *k-t* PCA method as well as the RMSE maps for a given undersampling factor. The PSNR values calculated for 5x and 10x undersampling factor were 42.12 ± 1.06 and 41.42 ± 1.15 dB, respectively. Perfusion-weighted images obtained using the Fourier decomposition technique in one slice position from the reconstructed data are shown in figure 3.

Fig. 2. Coronal bSSFP image acquired in a healthy volunteer and reconstructed from: fully sampled (a), 5x (b) and 10x undersampled (c) data. RMSE maps calculated for 5x (d) and 10x (e) undersampled data show the spatial distribution of average error.



Discussion

In this work we have presented the *k-t* PCA reconstruction method of dynamically acquired MR data for non-contrast-enhanced functional lung imaging using Fourier decomposition. Here, undersampled data acquisition was simulated to be able to compute error measures. An actual implementation promises considerable advantages as the method potentially permits significant shortening of the total acquisition time per image (from ~240 ms for fully sampled data to ~60 ms and ~35 ms for 5x and 10x undersampling, respectively). As a result, the motion artifacts still present in the fully sampled data will be reduced, and the signal intensity in the lung parenchyma increased by inserting a time interval for partial recovery of the longitudinal magnetization.



Fig. 3. FD perfusion-weighted images acquired at the same slice position and reconstructed from the fully sampled (a), 5x (b) and 10x (c) undersampled data.

References:

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