Coil Array Compression for Tissue Phase Mapping

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Introduction: Coil arrays with many elements are applied to enable higher acceleration factors in parallel imaging. However, the increased amount of data slows down the reconstruction process. Coil array compression [1-7] has been introduced to combine the data into fewer 'virtual coils', thus reducing the amount of data while preserving most of the information. In this contribution, the influence of coil array compression on reconstructed velocities for Tissue Phase Mapping (TPM) is investigated.

Theory: K-space data from all coils is transformed by Principle Component Analysis (PCA) [2]. Measured data can be seen as vectors $k_{1...m} \in \mathbb{C}^n$ where the vector space is spanned by the *n* coil elements. Applying the PCA is equal to a base transformation, so that the base vectors (i.e. virtual coil elements) are ordered by decreasing variance (i.e. information) of k-space data along this axis. Removing virtual coils containing least information before reconstruction reduces the amount of data to be processed while having minimal impact on image quality. Mathematically, this equals to dimension reduction, i.e. k-space data can be seen now as vectors $k'_{1...m} \in \mathbb{C}^{n'}$ with $n' \leq n$ virtual coils.

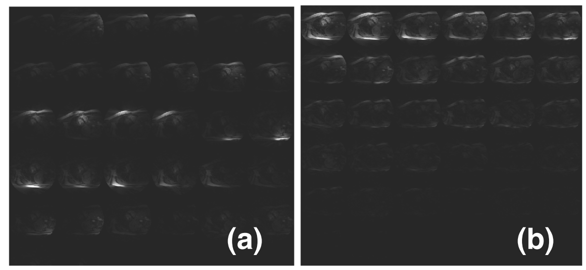

Figure 1: Separate reconstructions for each measured (a) and virtual coil (b).

Methods:

Acquisition: Short axis slices of 6 healthy volunteers were acquired at a Philips 3 T Achieva and a 32-element cardiac coil with a radial segmented, gated and triggered black-blood velocity encoding (TPM) sequence with VENC = 30 cm/s and 6-fold angular undersampling with respect to Nyquist's theorem.

Reconstruction: Eigenvectors and –values were obtained by PCA from a reference scan and then applied to the TPM k-space data. Velocities were reconstructed iteratively [8] in Matlab using data from all $n = 32$ original and $n' \in \{32, 16, 8\}$ virtual coils.

Analysis: Background correction of the reconstructed velocities was performed according to a linear model [9]. The myocardium was divided into 6 circumferential segments. Mean radial (v_r), circumferential (v_c) and longitudinal (v_l) velocities were calculated for each segment over the cardiac cycle, and corrected by their mean velocity over time. Reconstructions from compressed data were compared to full reconstruction by the normalized root-mean-square error $\mathrm{nRMSE}^{\mathrm{d}}_{n'} = \frac{1}{T}\sqrt{\sum_{t=1}^{T}\left(v_{32,\mathrm{d}}(t) - v_{n',\mathrm{d}}(t)\right)^2}$ for each number of virtual coils *n*' and velocity direction $d \in$ {rad., circ., long.}.

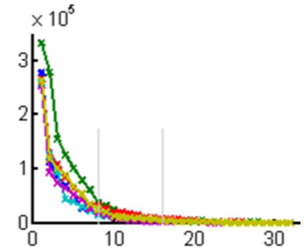

Figure 2: Eigenvalues of coil array compression for all volunteers.

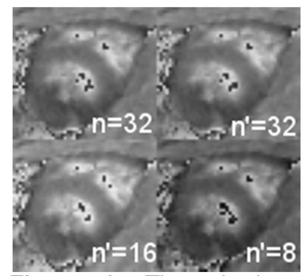

Figure 3: Through-plane velocity images for different coil compressions.

Results: Figure 1 shows the effect of array compression to transform data into virtual coils ordered by decreasing amount of information, which is also indicated by the decrease of eigenvalues (figure 2) from the PCA. Exemplary velocity images (figure 3) and velocity plots (figure 4) exhibit maintained velocity information. Quantitatively, average nRMSE was less than 0.1 cm/s for all investigated *n*' in all velocity directions.

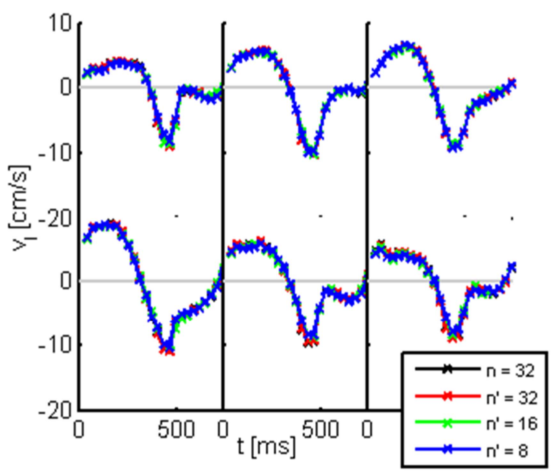

Figure 4: Segmental longitudinal velocities in one volunteer for full and compressed reconstructions.

Conclusion: Coil array compression can be applied to undersampled TPM data for speedup of reconstruction without compromising velocity information.

References: **[1]** Buehrer et al: MRM 2007, 57(6):1131–1139. **[2]** Huang et al.: MRI 2008, 26(1):133–141. **[3]** King et al: MRM 2010, 63(5):1346–1356. **[4]** Feng et al.: MRI 2011, 29(2):209–215. **[5]** Huang et al.: MRM 2012, 67(3):835–843. **[6]** Zhang et al.: MRM 2013, 69(2):571-582. **[7]** Wang et al.: ISMRM 2013, #3832 **[8]** Wundrak et al.: ESMRMB 2012, #691 **[9]** Walker et al.: JMRI 1993, 3:521-530