KP-GRAPPA: A SELF-CALIBRATED RECONSTRUCTION SCHEME FOR 3D MULTI-PHASE RESPIRATORY CINE

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TARGET AUDIENCE:
Scientists interested in retrospectively reconstructing 3D multi-phase respiratory cine images using free breathing acquisition in order to perform 3D motion field derivation.

PURPOSE:
Simultaneous PET/MR imaging is a promising technique for visualizing and quantifying soft-tissue tumors and metastatic involvement in regions such as the liver. For instance, simultaneously acquired MR images address the problem of respiratory motion blur in the upper abdominal organs. However, the long acquisition time associated with PET imaging, which is on the order of tens of minutes, precludes breath-hold acquisition. Therefore, one key objective for MR/PET motion correction is to obtain 3D MRI images at multiple respiratory phases in order to derive 3D motion fields for PET motion correction. In this respect, the focus of this study is to obtain abdominal MR images at multiple phases of the respiratory cycle while the subjects are breathing freely during acquisition.

METHODS:
All experiments were performed on a Siemens Tim Trio 3T MR scanner (Siemens Healthcare, Erlangen, Germany). A FLASH-based CV sequence with a 1-D pencil beam navigator was used. The navigator was placed along the cranial-caudal axis such that it passed through the lung and the liver. Data was collected from a 30-year-old subject. Written informed consent was obtained. The acquisition was 3D with matrix size = 96x72x112, FOV = 360mm x 270mm x 336 mm, TE = 1.34 ms, TR = 280 ms with 20 repetitions. A navigator was acquired prior to each partition (Kz), while the entire Kx-Ky plane was collected within a single shot. All images were acquired while the subject was breathing freely. As Figure 1 demonstrates, the boundary between the lung and the liver provides an excellent basis for rearranging, or binning, all of the partitions acquired over 20 repetitions into a number of respiratory phases. After the binning process, some respiratory phase bins may contain more than one partition with the same partition index, while some phases may suffer from the lack of certain partitions. The spatiotemporal redundancy in the data can then be used to fill in the missing partitions[1]. Similar to kt-GRAPPA[2], some of the missing partitions are filled out by GRAPPA convolution. The temporal dimension in this study refers to the respiratory phases. Therefore, in order to distinguish our method from kt-GRAPPA, we name the proposed method as kp-GRAPPA where p represents respiratory phases. Furthermore, in kt-GRAPPA, the lines are skipped intentionally and on a regular grid, but in this study, the missing data pattern is of a completely random nature because the respiration pattern is not known a priori.

For each of the equally spaced respiratory phase bins depicted in Figure 1, if multiple partitions with the same index fall into the same bin, only the partition closest to the bin center is used. After the binning is complete, some partitions will probably be missing, especially in the less frequently visited respiratory phases. If the number of missing consecutive partitions is less than 3, and if the neighboring partitions are available along the k and p dimensions, then kp-GRAPPA fills out these partitions. The calibration for deriving the GRAPPA convolution kernel is performed within the central portions of the readout, phase-encode and partition-encode dimensions. Our scheme is self-calibrated in the sense that no additional calibration data needs to be acquired separately. Once kp-GRAPPA convolution is complete, the remaining partitions are filled out using view sharing where any given missing partition is gathered from the closest phase which possesses that partition. If two equally distant phases have the desired partition, then the two partitions are averaged. After the reconstruction of all respiratory phases, the motion fields can be estimated through a 3D nonlinear inter-phase registration.
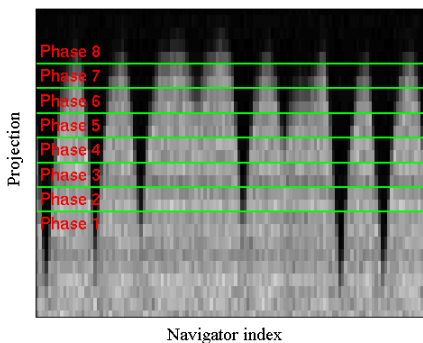

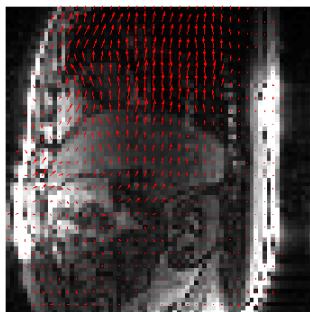Figure 1 - Binning of navigators into respiratory phases
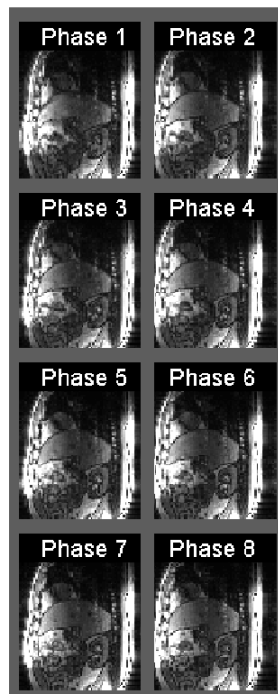

Figure 3 - Motion field [Phase 1 to Phase 8]

Figure 2 - Reconstructed respiratory phases

RESULTS:
Figure 2 shows the reconstructed images using the respiratory phase bins shown in Figure 1 while Figure 3 shows a set of motion field vectors regarding the change of location between two extreme phases. As expected, the dominant type of motion for the upper abdomen is a translation along the cranial-caudal axis.

DISCUSSION:
In this study, we developed a reconstruction method that can reconstruct multiple 3D respiratory phase images during free breathing. This method takes advantage of the redundant information provided by multiple coils and neighboring respiratory phases in order to fill out the missing portion of the data. Unlike kt-GRAPPA, which manipulates the temporal neighborhood, kp-GRAPPA makes use of the neighboring respiratory phases. Since the pieces of data acquired within adjacent time frames do not necessarily come from similar motion states, kp-GRAPPA is expected to be more advantageous within this framework. It is also worth noting that, depending on the motion pattern, the missing partitions for a specific respiratory phase appear in random portions of the k-p space, which makes the reconstruction more challenging. GRAPPA coefficients are derived using a portion of the acquired imaging data without the need of a separate calibration scan. The pencil beam 1D navigators provide a direct measurement of the liver dome position which can provide a reliable means of data binning. The derived 3D motion fields can then be used for PET motion correction.

REFERENCES:
1. Tsao and Kozerke, JMRI 2012; 36(3):543-560 **2.** Huang et al., MRM 2005; 54:1172-1184