Respiratory Gated VIBE Sequence

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Introduction: The spatial resolution in dynamic breath-hold liver imaging using gadolinium-based unspecific extracellular contrast media is limited by the breath-hold capabilities of the patient. Liver imaging during the uptake phase of novel hepatobiliary contrast media allows acquisition windows of several minutes. The aim of this work is to describe a recently developed navigator gated 3D spoiled gradient echo sequence (gated VIBE), which might be used to translate the extended acquisition window into increased spatial resolution and anatomical coverage. See ref. 1-3 for related work.

Methods: Figure 1 shows a schematic plot of the respiratory gated VIBE sequence. Each VIBE module acquires multiple k_y /k_z views. A navigator is inserted in the normal sequence cycle to measure the respiratory motion. If spectral fat suppression is used this navigator is inserted just before the spectral fat suppression module (FS). The diaphragm position measured with the navigator is analyzed by the gating algorithm for a prospective real-time decision, which k_y /k_z views are to be acquired by the next VIBE module (grey box). If FS is used, the processing necessary to make this decision is done during the execution of the FS module and therefore does not cost extra time. If Dixon is used, the processing is done during an extra TR interval without data readout. Specific features of the sequence include:

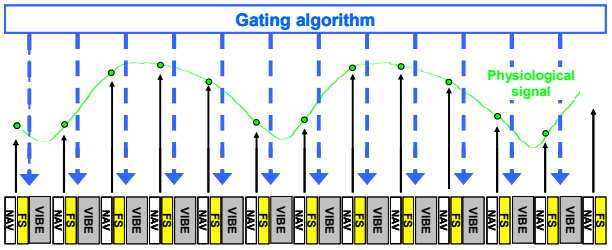

Figure 1: Schematics of the respiratory gated VIBE sequence.

Navigator: Compared to most other navigator approaches signal localisation is done via phase encoding and not by 2D excitation. A navigator is a fast 2D FLASH sequence, which acquires a coronal 2D image with a pixel size of 2mm in HF direction and 16 mm in LR direction. The navigator box, which is positioned by the operator on the liver dome, determines a window within this image used for pattern matching. Compared to the navigator used in the Siemens product for respiratory triggering the duration of the navigator was shortened to 26 ms by a coarser image matrix, shorter RF-pulse and by exploiting the performance of the gradient system. A five degree flip angle avoids saturation of the liver parenchyma.

k_y-k_z-Order: The imaging data acquired in one TR interval after a particular two dimensional phase encoding (k_y and k_z) step are referred to as "view" in the following. The set of all views acquired after a particular navigator/FS pulse is called a shot. Since the magnetization after the navigator/FS pulse is in a transient state, the temporal order of k_y-k_z views determines the modulation of k-space and hence image quality. Figure 2 is a simplified illustration of the radial phase encoding scheme: The k-space views to be acquired are separated in sectors. Views allocated to the same sector are drawn in the same color. The number of different sectors is equal to the number of views acquired per shot and is a user adjustable parameter. The number of views per sector is equal to the number of shots used for final image reconstruction. Views that are allocated to a particular sector have a similar distance from k-space center and are located in the same half-space (in Figure 2 the first half space is characterized by $k_y > 0$ (or $k_y = 0$ and $k_z \geq 0$)).

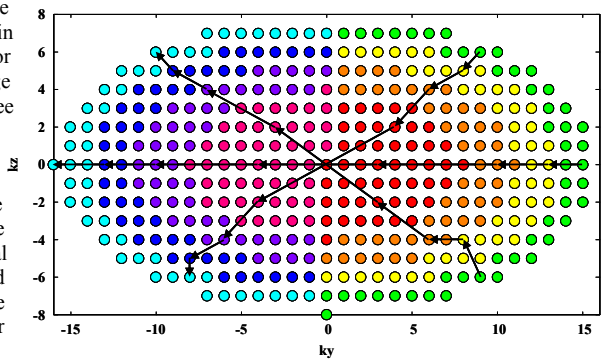

Figure 2: Exemplary k_y-k_z-space consisting of 64 k_y-lines and 32 k_z partitions. Each dot corresponds to an acquired view.

Each shot now acquired one view of each sector. Thereby the views of a given sector are always acquired at the same time after the FS pulse. This results in a smooth modulation of k-space and is less prone to ghosting than classical segmentation along one of the Cartesian axis. In the example of Figure 2 eight views are acquired after each FS pulse. The trajectory for three shots is visualized as black arrows pointing from one view of the shot to the next.

Gating algorithm: The gating algorithm is based on the 2bin-PAWS algorithm [4], which is more robust than the classical acceptance/rejection algorithm in the case of a varying breathing pattern. In contrast to the classical PAWS algorithm our variant distinguishes whether a particular diaphragm position (DP) was measured during inspiration or expiration. Real-time scan progress is visualized in a plot below the respiratory curve (Figure 3). Each column of the plot corresponds to a particular shot number. Each horizontal green or yellow box corresponds to a shot cluster. A cluster is characterized by a diaphragm position range (DP) and a respiratory phase (RP- either expiration or inspiration) and comprise all shots already acquired after this particular DP/RP was measured. The DP/RP of a cluster determines its vertical position in Figure 3. If the DP/RP of a particular cluster is measured a missing shot of the cluster is acquired. The seed of a cluster is either at a peripheral shot number or the centre shot. Peripheral and centre clusters alternate. The DP range of a cluster is equal to half the acceptance window (another user adjustable parameter). Adjacent clusters are characterized by the same RP - with one exception: the expiratory cluster with the head most DP and the inspiratory cluster with the head most DP are also treated as neighbours. The scan terminates as soon as two neighbouring clusters span all shots. Only k-space views allotted to the two spanning clusters are used for image reconstruction. The two clusters closest to spanning are drawn in yellow in Figure 3.

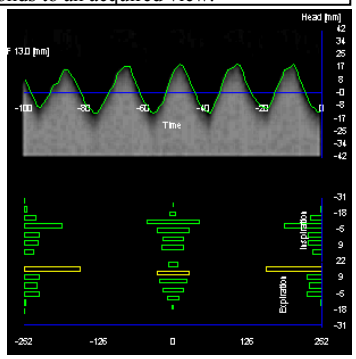

Figure 3: Real time display of respiratory curve and scan progress.

Results & Discussion: Figure 4 shows one axial image acquired in a 29 year old male patient with a Siemens MAGNETOM Tim Trio. Imaging parameters are: Matrix=384; acquired resolution=1×1×2mm^3;TR/TE=4.3/1.5ms; FA=10°; acceptance window=±2mm; 25 views per shot. TA varying; for the case shown in Figure 4 TA was 7:39 min:s, which corresponds to a scan efficiency (accepted scans/total scans) of 38%. Figure 5 shows a coronal reformat using all 104 axial slices of the same scan. We plan to use parallel imaging to decrease the mean TA below five minutes. SNR loss due to parallel imaging may be compensated by flip angle optimization [5]. In PAWS the final accepted DP range is not known before the end of the scan. Hence we store all acquired data till end and our implementation requires up to 5 times more memory than a similar ungated scan. In a next step we will use channel compression [6] to reduce memory demand.

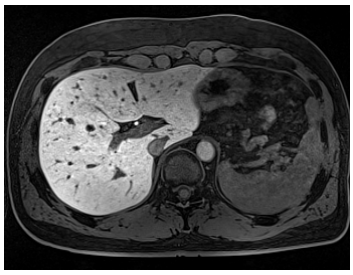

Figure 4: Gated VIBE image acquired in Gd-EOB-DTPA hepatobiliary phase.

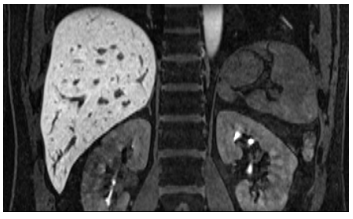

Figure 5: Coronal reformat using all 104 acquired images.

References: [1] Asbach et al. Invest Radiol. 43(11):753-761 (2008); [2] Brau et al. ISMRM 2010, #4443; [3] Xu et al. ISMRM 2011, #3013; [4] Jhooti et al. MRM 43:470-480 (2000); [5] Frydrychowicz et al. JMRI 34:585–594 (2011); [6] Huang et al. IEEE-EMBS 2005, page 1348.