Free-breathing dynamic magnetic resonance imaging of the abdomen

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Abdominal magnetic resonance imaging (MRI) is complicated by tissue motion as well as by weak tissue contrast. The major source of motion is respiration, which can be dealt with by breath-hold imaging or by respiratory triggering. Nevertheless, these commonly used methods are known to have their limitations in terms of patient burden as well as in image quality. We propose a method that allows 3-dimensional (3D) motion-compensated imaging of the bowel in the presence of continued respiratory motion and normal bowel peristalsis. The method is based on a computationally efficient spatiotemporal recursive search cube matching algorithm which allows accurate real-time volumetric motion estimation and compensation for the respiratory motion. We are currently evaluating the application to motion-compensated reconstruction of dynamic contrast-enhanced data of the colon.

Background

With various recent developments, MRI becomes a more and more credible candidate for examination of the abdomen, because of its low invasiveness and high analytical potential. In order to capture a large field of view with sufficient spatial resolution and temporal resolution, scan times easily reach 20 seconds or more. Such breath-hold periods may be easy to achieve by a healthy volunteer but often beyond the reach of a patient. The general solution is to confine the acquisition to the relatively motionless periods between respiration cycles. Yet, the exact end of an exhale period is ill defined and the thorax tends to continue settling after exhale, leading to residual motion artifacts.

Although retrospective compensation of global motion is not uncommon to MRI, it is generally confined to relatively rigid tissues such as the brain or the liver. The bowel, on the other hand, exhibits a complex and relatively random peristaltic motion which is incidental along the colon but continuous along the small intestine. From an image-processing point of view, the entire bowel manifests itself as a single enclosed organ with a continuously changing texture, such that traditional, generally correlation-based, methods for motion tracking fail.

Methods and Results

Using a gradient echo (TFE) sequence on a 3T whole-body scanner (Achieva, Philips Healthcare, Best, The Netherlands) the entire bowel volume (400×400×100 mm) is captured at time intervals of 400 ms. At this rate, the peristaltic motion of the small intestinal can be captured unambiguously, as the sample rate fulfills the Nyquist-Shannon criterion [1]. Thus, a time sequence of about 1000 volumes is created and stored with a resolution of generally 320×320×7 voxels. By deliberately applying out-of-phase TFE, hypointense contours appear along each water-fat interface, as depicted in Fig. 1, largely revealing the outline of both the colon and the small intestine, that otherwise would exhibit insufficient contrast for motion estimation [2].

The motion is estimated in three spatial directions between each pair of consecutive volumes using cube-matching, essentially a 3-D version of conventional planar 2-D block matching. The planar components of the motion in the *x*- and *y*-direction are determined for each adjacent block of 8×8 voxels. As spatial resolution in the *z*-direction is relatively small, for each stack of 8×8 blocks, only one single *z*-component is estimated of the motion. For each consecutive volume pair the motion is described as a 2-D field of 3-D motion vectors, with one vector for each cube of 8×8×7 voxels, as indicated in Fig. 2. By using a new 3D implementation of the spatiotemporally recursive search algorithm by De Haan *et al.* [3], each motion vector is based on the evaluation of a relatively small set of about 14 vector candidates, which significantly reduces computational requirements and, more importantly, adds to the consistency of the motion vector with the true tissue motion.

The 3D global motion is extracted from the block-wise motion vector field using an affine motion model with robust parameter estimation [3]. In order to evaluate the accuracy of the global model, synthetic data was created on the basis of real breath-hold data which was subjected to an artificial respiration motion at various speeds. The global translational parameters that were estimated from this data were compared with the imposed breathing motion signal. At various velocities the global motion parameters show to be subpixel accurate in all three spatial directions.

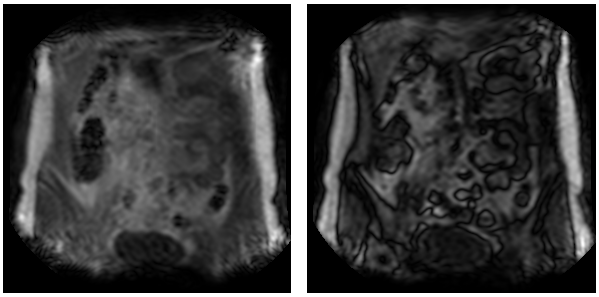

Figure 1: In-phase (left) and out-of-phase TFE data. The hypointense water-fat interfaces in the out-of-phase data largly indicate the shape of the intestines.

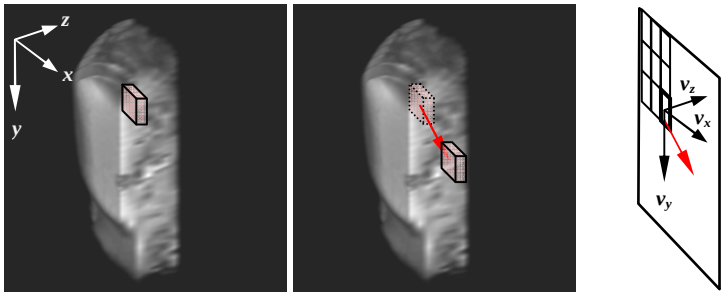

Figure 2: Schematic illustration of the 3D motion-estimation process. Each 3D motion vector results from the best match between a matching sub-volume between two temporally consecutive volumes (left and middle). The found 3D vector is stored as part of a 2D field of 3D vectors (right).

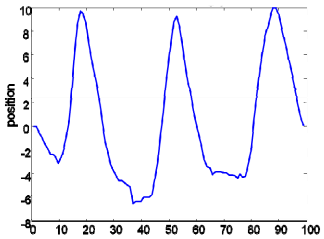

Figure 3: Estimated vertical position as function of time, extracted from a free-breathing subject.

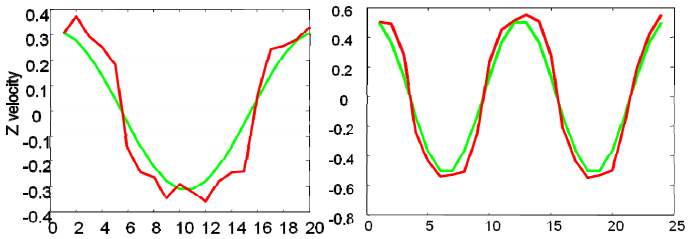

Figure 4: True velocity v_z (light green) and measured velocity (dark red) as a function of time, revealing the sub-pixel accuracy of the global motion estimation. The accuracy is achieved in all three spatial directions in the presence of normal bowel peristalsis.

References

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