# Extraction of abdominal motion for molecular imaging

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## Background

The massive occurrence of colorectal cancer and associated high mortality rate demands early diagnosis. Targeted contrast agents enable the use of magnetic resonance imaging for early detection and selective localization. Yet, MRI of the human bowel is generally complicated due to its motility and due to the intrinsically weak tissue contrast. In the context of molecular imaging, the bowel motion hampers correct signal accumulation and localization of targeted contrast agents. We present a method to extract colon motion without the need for extensive bowel preparation. The method combines the use of chemical-shift induced tissue features with a recursive spatiotemporal method to generate spatially consistent motion patterns without the use of prior tissue-segmentation and -modelling.

### Methods and results

The bowel typically exhibits continuous peristalsis of the small intestine as well as incidental colon contractions. Also, respiratory motion, deteriorates the image quality of the bowel. For high resolution MRI of the colon, all these movements need to be taken into account. Using a gradient echo (TFE) sequence on a 3T whole body scanner (Intera, Philips Medical Systems, Best, The Netherlands), we are able to capture virtually the entire bowel volume  $(400 \times 400 \times 100 \text{ mm})$  fast enough to critically sample also the fastest motion exhibited by the small intestine (sample period 400 ms), which is in line with measurements by Froehlich *et al.* [1].

Motion estimation requires the presence of anatomical contrast. We deliberately used out-of-phase TFE in order to get hypointense contours at the water-fat interface. As such, these contours largely outline the colon and small intestine, providing sufficient detail to perform estimation of the tissue motion. Figure 1 shows a subset of the motion vectors which have been estimated using a three-dimensional recursive search block matching method, which has shown to capture true motion exceedingly better then many other block-matching based motion-estimation methods [3]. Here, the method is used to generate a motion vector for every 2×2 pixels, and at time instances centred between the original sample moments. The sequence of alternating original and synthetic slices in Figure 2 shows that not only the respiratory motion is captured, but also peristals is reproduced correctly.

Our prime application is imaging of targeted contrast agents on the basis of perfluorocarbons [4]. The <sup>19</sup>F-signal is captured at intermediate time instances between <sup>1</sup>H-acquisitions. Using the 3D motion information at these intermediate instances allows various options to combine the <sup>19</sup>F-data along the motion trajectory. The most straightforward case is motion-compensated signal accumulation, which is schematically depicted in Figure 3 using a simulated <sup>19</sup>F-signal.

## Conclusion

The generation of hypointense contours at water-fat transitions allows successful tracking of the bowel motion. The use of a recursive spatiotemporal motion-estimation method results in reliable motion estimates. Simulation of motion-compensated signal reconstruction of  $^{19}$ F-data, at new intermediate temporal instances, shows promising results for the application in molecular imaging of  $^{19}$ F-based targeted contrast agents.

#### References

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Figure 2: Sequence of alternated original and temporally-interpolated slices, in chronologic order, starting with an original at top left. Apart from respiratory motion also subtle peristaltic motion is correctly rendered (circle).

Figure 1: Estimated motion during in- and exhale. Motion vectors (not all depicted) are generated per region of 2×2 pixels (indicated by the dot-pitch).



Figure 3: Simulation setup for motion-compensated signal accumulation of <sup>19</sup>F-based targeted contrast agent, using motion information extracted from the <sup>1</sup>H-acquisitions.