

**Purpose:**

Post processing of dynamic ‘cine’ MRI data has been shown to be a powerful technique for quantitatively evaluating small bowel motility in breath-hold acquisitions<sup>1</sup>. Many diseases however affect slow contractions in the small bowel or colon requiring minutes worth of scanning, ill-suited to breath-hold protocols. In this abstract we describe the validation of an additional post-processing step to remove respiratory motion from free breathing motility data while leaving peristalsis un-affected. The respiration corrected data is then processed using an existing optic flow-technique<sup>2</sup> to quantify local deformations caused by peristaltic action in the small bowel.

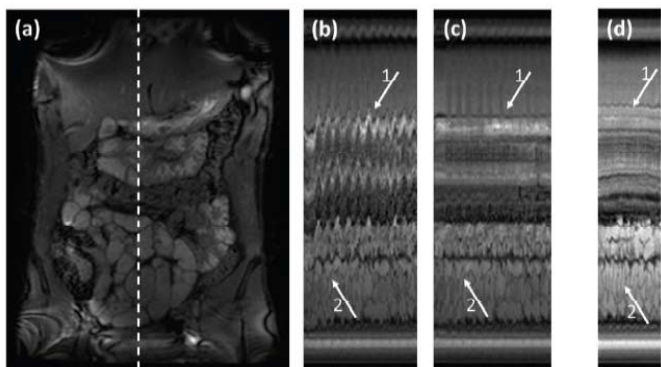


Figure 1. a) Coronal SB with dotted line representing position of temporal profile in free breathing (b), with combined RDDR+OF (c) and using optic flow alone in breath hold (d). Arrows represent motion from a region subject to respiration (arrow 1) and both respiration and peristalsis (arrow 2).

**Methods:**

**Volunteers:** 20 healthy volunteers (13 male, mean age 29 years, range 22-48) were recruited.

**MR Protocol Small bowel:** Volunteers drank 1L of 2% Mannitol solution over the 50 minutes prior to lying prone in a Philips Achieva 3T MRI scanner. Acquisition used a coronal BTFE motility sequence (2.5x2.5x5mm voxel size, FOV 420x420x30mm, FA 20 degrees, TE=1.85ms, TR=3.7ms coronal 2D balanced BTFE) with a 1 second temporal resolution. A 20s breath hold scan was followed immediately by 1 minute free breathing acquisition.

**Motility Analysis:** The optic flow (OF) based registration technique<sup>2</sup> provides deformation fields which may be used to either propagate regions of interest or generate parametric global motility maps. (The map is the average standard deviation of the Jacobian determinant in A.U)<sup>1,2</sup>.

The additional pre-processing proposed here reduces respiratory motion by using the ‘Robust Data Decomposition Registration’ (RDDR)<sup>3</sup> method (the respiration appearing as ‘low rank’ in a robust principal component analysis and removed with an iterative registration).

**Analysis:** (1) A linear ROI was placed across the bowel diameter perpendicular to the central axis. Bland-Altman limits of agreement were used to compare the lengths of lines propagated using registration with and without RDDR processing against lines propagated manually which served as the ground truth. (2) Global ROIs were placed to segment the whole small bowel. Global small bowel motility maps were assessed by comparing motility with and without RDDR pre-processing in free-breathing data series. The ground truth was taken to be breath-hold data (free from respiratory motion) processed with just OF<sup>2</sup>.

**Results**

(1) Mean difference of line length ROIs between OF alone registered data and manual propagation ground truth was -2.5mm (95% LoA ±8.3mm). Mean difference of RDDR pre-processed images to ground truth was -0.49mm (95% LoA ±4.7mm).

(2) Mean global motility score within the global ROIs for the BH data set across the cohort was 0.340AU (range 0.181 to 0.422 AU). Mean global motility score for pre-processed free-breathing data was 0.335AU (range 0.189 to 0.430AU) compared to 0.365 (range 0.268 to 0.458AU) without pre-processing (fig 2).

**Conclusion**

Pre-processing with RDDR makes small bowel motility quantitation robust to the effects of free breathing allowing automated ROI propagation and generation of parametric motility maps in free breathing small bowel data. This advance has direct clinical applicability to dysmotility in diseases as well as serving as a biomarker for drug efficacy studies<sup>1</sup> and having larger applicability to slower contracting regions of the GI tract including the colon.

**References:** [1] Menys et al. Radiol. 2012;22(11):2494-501, [2] Odille et al. MRM 2012;68(3):783-93, [3] Hamy et al. MedIA in press. Funding received by NIHR-BRC.

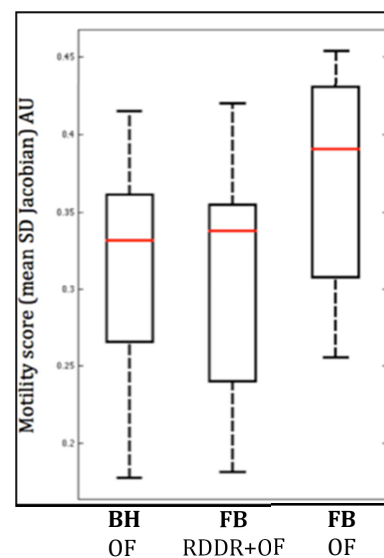


Fig.2 Box plots for 20 subject global motility score. Red line = median, black box = interquartile range and dotted line = data range.