ANALYSIS OF SEGMENTAL GASTROINTESTINAL MOTION IN AN ANIMAL MODEL USING DYNAMIC MRI AND ACTIVE SHAPE MODELS

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Introduction

The gastrointestinal (GI) tract functions via deformations of the lumen resulting from neurophysiologically induced changes in muscle fiber tone. Peristaltic contractions underlie transport, while segmental contractions facilitate macro mixing in bulk flow. These processes are affected significantly by pathologies of the intestinal tract such as irritable bowel syndrome. The aim of this work is to quantify GI motility in a rat model using dynamic MRI. Although it is known that peristalsis is reduced during anesthesia, segmental contractions still occur. Segmental motions of the rat gut were quantified from dynamically acquired MR images, image segmentation using live-wire [1, 2] and gradient vector flow (GVF) methods [3, 4] and image characterization using active shape models (ASM) [5, 6].

Materials and Methods

Dynamic MRI was performed on rats to quantify the motions of the small intestine. Rats (200-300g) were given an oral gavage of Gd-DPTA (1 ml/kg) approximately 45 minutes before scanning. MRI experiments were performed using a horizontal bore 7 tesla magnet with a 12 cm diameter gradient set and a Varian Direct Drive console. Rats were anesthetized using a mixture of isoflurane and oxygen. Prior to dynamic scanning, a heavily T_1-weighted multi-slice data set covering the whole of the GI tract was acquired to aid localization of the small intestine. For dynamic imaging a respiratory-gated gradient echo pulse sequence (TE 1.6 ms, TR 3.13 ms, 96 × 72 (3/4 partial *k*-space coverage), 1 mm slice thickness, in-plane resolution 312 µm × 416 µm, time resolution 225 ms) was used to acquire sequences of up to 1000 consecutive images to capture the gut motion. Representative images are shown in Figs 1A to 1C. A semi-automated algorithm was developed based on live-wire [1, 2] and GVF [3, 4] algorithms to segment the images. An automated method of labeling landmark points on the aligned images for the ASM was used based on the formulation of Udupa *et al*. [7], and a point distribution model (PDM) was derived. Let x_t be a "vector" of n landmark points on a sample shape at time t. A mean shape of N aligned samples is calculated [5, 6] from N samples. A set of N time samples, with each sample containing $2n$ elements (x and y coordinates), are represented as a "cloud" of N points in $2n$ dimensional space [1, 2]. It is assumed that the spread of N points is correlated and lies in an ellipsoidal region around the mean. Different modes of variation of land-mark points are found by calculating the deviation, dx_t, of each sample from the mean shape, and then calculating a $2n \times 2n$ co-variance matrix [5, 6]:

$$S = \frac{1}{N}\sum_{1}^{N} dx_t dx_t^r \ , \qquad (1)$$

The covariance matrix is used at the kernel to an eigenvalue problem to derive the principle component eigenvectors and eigenmodes. The principal modes are the eigenvectors of S, and the variance of each eigenvector is represented by its corresponding eigenvalue [5, 6]. A $2n$ dimensional ellipsoid can be approximated by the first m eigenvectors which represent a large part (>95%) of the total variance, given by the sum of $2n$ eigenvalues [5, 6]:

$$\lambda_{Total} = \sum_{t=1}^{2n} \lambda_t \ . \qquad (2)$$

Every $2n$ dimensional points lying within an "allowable shape domain" (-3 to +3 standard deviations (SD) around the mean), Figure 1D, within the cloud represents a shape similar to the examples in the training database [5, 6]. The SD for a particular mode m is $\sqrt{\lambda_m}$.

Results and Discussion

Each eigenvector can potentially be associated with a different form of deformation of the gut wall. Analysis of datasets obtained at widely-separated time points during the study of a single animal showed no variation in the number of significant modes and a very small variation (<5%) in the percentage contribution from each mode to the total variance. Two dominant modes were found: mode 1 (26.3% of variance) and mode 2 (24.6% of variance) essentially represents contraction and expansion of the gut, as shown in Figs 1E and 1F. The motions associated with the two modes are out of phase (i.e., during gut contraction in mode 1, mode 2 represents the expansion of the same section). Compared to mode 2, mode 1 had a larger spatial variation in same portion of the gut. The contribution to the total variance of the next five eigenmodes (modes 3-7) was below 6%. These modes represented much smaller spatial variations in the position of the gut wall. The accuracy of the model was verified by overlaying the actual boundary points with the points generated by the sum of the decomposed independent modes. Further analysis showed that the number of modes and contribution of these modes does vary significantly with location within the GI tract, so that the initial collection of high-resolution multi-slice imaging of the entire rat GI tract was important for identifying the location of the small intestine studied.

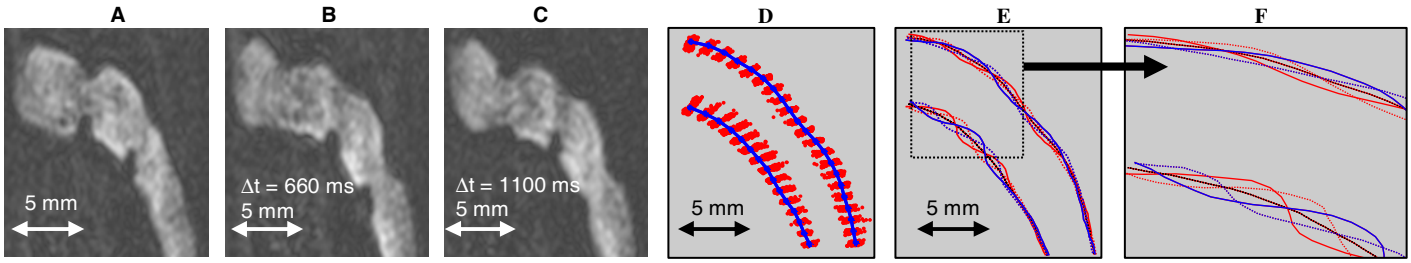

Figure 1: (A-C) Dynamic images (4.5 frames per second) of the gut at times t = 0, 660 ms and 1100 ms. Significant contractile motion can be seen. (D) Time variation of the landmark points (red) with the mean shape (blue) overlaid. (E and F) Variation of mode 1 (solid) and mode 2 (dotted), around the mean shape (black). Mode 1 was scaled from $-3*\sqrt{\lambda_1}$ (solid red) to $3*\sqrt{\lambda_1}$ (solid blue). Mode 2 was scaled from $-3*\sqrt{\lambda_2}$ (dotted red) to $3*\sqrt{\lambda_2}$ (dotted blue).

Conclusion

Quantitative analysis of complex segmental gut motion in the small intestine of anesthetized rats has been performed using dynamic MRI, live-wire and GVF segmentation, and active shape models. Future work will concentrate on analyses of the effects of different types of anesthesia on gut motility, the incorporation of more sophisticated data analysis techniques such as space-time proper orthogonal decomposition, and potential application to different disease models.

References:

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