Capturing breathing motion variability using two signal motion models of the heart

Nicholas McGlashan
nicholas.mcglashan@kcl.ac.uk
Andrew P. King
andrew.king@kcl.ac.uk

Imaging Sciences and Biomed Eng,
King's College London,
St. Thomas' Hospital,
London, SE1 7EH, United Kingdom.

Abstract

Motion models are a potentially promising solution to the problem of respiratory motion in both image acquisition and image-guided interventions. Such models are typically based on a single input signal, such as an MRI navigator on the diaphragm. However, it is possible to form models based on two signals positioned at different anatomical locations. This paper investigates whether this is desirable or not. Cardiac motion models based on single input signals and pairs of input signals were formed from MRI data acquired from 10 volunteers and 1 patient. A measure of the accuracy of these motion models was computed. The results suggest that two signal models are more accurate, but only in the presence of significant cycle to cycle breathing motion variability. Overall the best individual virtual navigator was positioned on the upper chest, and the best pairing consisted of virtual navigators on the upper chest and lower chest. These findings have potential significance for researchers working in the area of motion-corrected image acquisition or motion-corrected image-guided interventions.

1 Introduction

Respiratory motion can cause severe problems in both image acquisition and image-guided interventions. In image acquisition it can cause artefacts that degrade image quality, and in image-guided interventions it can cause registration errors between the guidance information and the real anatomy, making the guidance information less reliable and potentially dangerous. Common solutions to the problem of respiratory motion are breath-holding and gating. However, both have their shortcomings: breath-holding is limited to short periods of time (typically less than 30 seconds), and gating increases scan/procedure time. Motion models offer an alternative strategy in which the motion of the organ(s) is estimated and corrected for whilst allowing the subject to breathe freely.

Motion models typically model a motion field as a function of a 1-D input signal. By acquiring this 1-D signal during image acquisition or an intervention, the function is applied to produce an estimate of the true motion field. For example, in [2] an affine cardiac respiratory motion model was formed by coregistering magnetic resonance imaging (MRI) data. The model estimated an affine transformation as a function of head-foot diaphragm translation, and was used to motion-correct guidance information in image-guided cardiac interventions.

Much previous work on respiratory motion modelling has made the assumption that the motion of organs due to breathing is *cyclic*, i.e. it is the same from cycle to cycle. Such 'average-cycle' models take a single signal as input, such as the diaphragm translation from MRI or X-ray [2]. However, in reality breathing motion is more complex than this, and is rarely the same from cycle to cycle [1].

Motion models based on multiple 1-D signals can potentially predict different types of motion for each cycle if the multiple signals vary in different ways relative to each other. Examples of multiple signals include:

- a signal and a *precursory* signal (i.e. its value at a previous time step) [4],
- a signal and its derivative [6],
- a signal and its amplitude [3], and
- signals at multiple anatomical locations [4, 5].

In this paper we investigate the last option, i.e. motion models based on signals positioned at multiple anatomical locations, specifically with reference to cardiac respiratory motion models. Our hypothesis is that cycle-to-cycle breathing variability can be captured by using multiple signals at different locations, and that consequently such multiple signal models should be more accurate than single signal models in the presence of such variability. We have previously published preliminary results in [5]. Here we include improved validation, two extra datasets and test extra signal placements.

2 Methods and materials

Figure 1 gives an overview of our experimental set-up. Two types of MRI data are required to form the motion models: a single static 3-D high resolution image, and a series of lower resolution 3-D dynamic scans at arbitrary respiratory positions (see Section 2.1). To enable us to test different anatomical locations for our input signals, we compute 'virtual navigators' from the dynamic scans, positioned at a number of different locations (Section 2.2). Motion models are formed from individual and pairs of such navigators using motion estimates computed by image registration between the high resolution and dynamic MRI scans (Section 2.3). Finally, an error measure for each motion model is determined (Section 2.4). We perform *leave-one-out* validation: each dynamic image is left out in turn, and a motion model formed from all remaining dynamics; the motion estimated by this model is compared to the actual motion estimated by registration of the left-out dynamic.

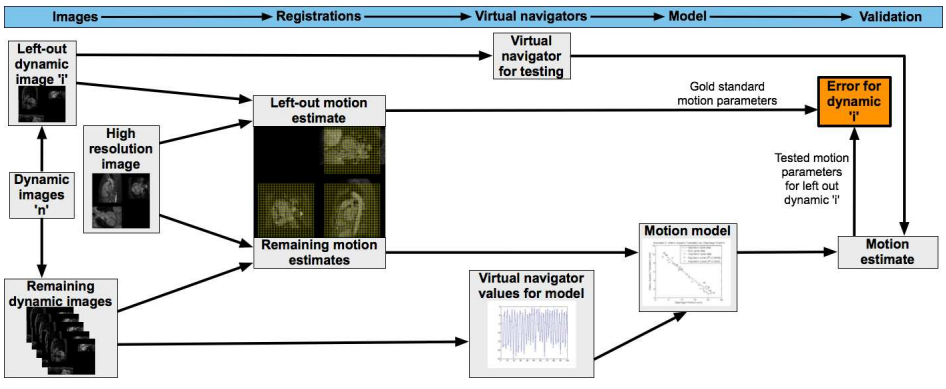

Figure 1: An overview of the motion model accuracy experiments.

2.1 Materials

Data were acquired from 10 volunteers and 1 patient. Volunteers A-J consisted of 9 males and 1 female, aged 20-32. Patient A was male, aged 4, and underwent MRI scanning as preparation for a pulmonary vascular resistance study catheterisation. All MRI data were acquired using a 1.5T Philips Achieva MRI scanner. The following sequences were used:

- *High resolution 3-D*: 3D balanced TFE, respiratory gated at end-expiration, cardiac gated at late diastole, typically, 120 sagittal slices, TR=4.4ms, TE=2.2ms, flip angle=90^o, acquired voxel size $2.19 \times 2.19 \times 2.74\text{mm}^3$ (reconstructed $1.37 \times 1.37 \times 1.37\text{mm}^3$), acquisition window $\approx$ 100ms, navigator window 5mm, scan time $\approx$ 5 minutes.
- *Dynamic 3-D*: 3-D TFEPI, cardiac gated at late diastole, typically, 20 slices, TR = 10ms, TE = 4.9ms, flip angle = 20^o, acquired voxel size $2.7 \times 3.6 \times 8.0\text{mm}^3$ (reconstructed $2.22 \times 2.22 \times 4.0\text{mm}^3$), TFE factor 26, EPI factor 13, TFE acq. time 267.9ms.

The dynamic 3-D sequence acquires one 3-D volume every heart beat. A sample scan is shown in Figure 2. These scans were acquired with the subjects breathing in three different breathing patterns: normal breathing (i.e. no breathing instruction given), fast breathing, and deep breathing. This was done to maximise the amount of cycle-to-cycle breathing motion variability. 100 dynamic images (volunteers A-D) or 40 dynamic images (volunteers E-J and patient A) per breathing pattern were acquired.

2.2 Computing virtual navigators

To test different anatomical positionings for the 1-D input signals we produced 'virtual navigator' signals by postprocessing the dynamic 3-D MRI images. The virtual navigators were computed as follows: 3-D rectangular regions of interest were manually defined for each virtual navigator on each subject's dynamic images; one dynamic image was chosen as a reference; for each other 'target' dynamic image, the virtual navigator value was determined as the translation along the long axis of the rectangle that maximised the correlation between the reference image intensities and the translated target image intensities within the rectangle. All virtual navigator signals were manually inspected and modified if they were found to be inaccurate. Virtual navigators positions/orientations are illustrated in Figure 2:

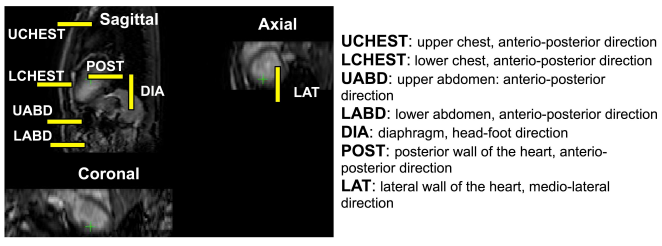

Figure 2: Positioning of virtual navigators on a dynamic MRI scan.

2.3 Registration and motion modelling

The affine motion models were formed using a technique similar to that described in [2]. First, motion estimates were made by registering each 3-D dynamic scan to the 3-D high resolution image. The registrations were performed with an intensity-based affine registration algorithm using normalised mutual information as a similarity measure. An elliptical mask covering the four chambers and major vessels of the heart was used as a region of

interest for computing the similarity measure. Next, 2^{nd} order polynomials were fitted to the variation of each of the 12 affine motion parameters as functions of the input signal(s) used. Univariate polynomials were used for single signal models and bivariate polynomials were used for two signal models. Separate polynomials were used for inspiration and expiration data to capture the hysteresis effect [2]. The motion models formed in this way estimate a set of 12 affine motion parameters given an input signal (or pair of signals) and a breathing direction (inspiration or expiration).

2.4 Error measure

To compare different input signals for motion model formation, we define a motion model error measure: the *root-mean-square error in prediction* (RMSEP) [5]. The RMSEP measures the difference between transforming a set of landmarks by the original registration transformations (see Section 2.3) and the transformations estimated by a motion model. To determine the overall 'leave-one-out' RMSEP for a single subject and input signal(s), we compute the root-mean-square of these errors over a set of landmarks positioned on a Cartesian grid in a region of interest around the heart. Finally, the RMSEP over all subjects for a specific input signal(s) is the root-mean-square of the RMSEP values of all subjects.

3 Results

We computed overall RMSEP values for motion models based on all single signals and every combination of signal pairings. Figure 3 shows the RMSEP values computed using all dynamic MRI images, i.e. for all 3 breathing patterns combined. Overall the mean RMSEP for single signal models was 5.27mm, and for pairs of signals it was 4.83mm. Using a 2-tailed unpaired student's t-test we found a statistically significant difference between the two sets of RMSEP values ($p < 0.01$).

We also computed the same figures for individual breathing patterns. The mean RMSEP values for single/paired signal models were 2.39/2.53mm for normal breathing, 2.85/2.95mm for fast breathing and 4.23/4.1mm for deep breathing. However, for these experiments we found no statistically significant difference in the RMSEP figures ($p = 0.83$ for normal breathing, $p = 0.53$ for fast breathing, and $p = 0.62$ for deep breathing).

4 Discussion and conclusions

We have presented an analysis of the impact of using motion models with input signals positioned at multiple anatomical locations. Our results show that, compared to the more commonly used single signal models, two signal models perform better when all breathing patterns are combined, but no better for individual breathing patterns. This is an interesting finding, because during a single breathing pattern it is reasonable to expect that breathing motion variability would be less, whereas when combining data from different breathing patterns we would expect the variability to be greater. Therefore these results support our original hypothesis that two signal models perform better in the presence of cycle-to-cycle breathing variability. Overall the best individual virtual navigator was positioned on the upper chest, and the best pairing consisted of navigators on the upper chest and lower chest.

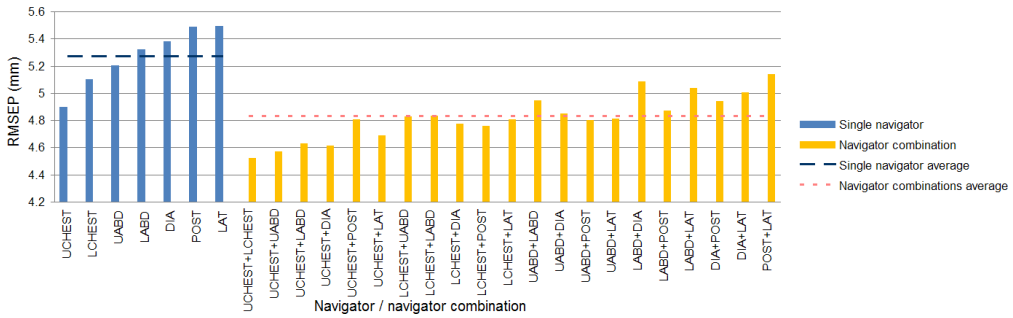

Figure 3: Leave-one-out RMSEP values over all breathing patterns.

These findings will be of interest to researchers working in the area of motion modelling for both image acquisition and image-guided interventions. In many applications there is the possibility to acquire multiple input signals, for example in the MRI scanner using navigator echos or when using an optical tracking system such as the Varian Real-time Position Management (RPM) system. In these cases it would be worth considering including extra input signals if breathing motion variability is anticipated.

Acknowledgments

This work was funded by EPSRC grant EP/H046410/1 and the HYPERimage project which is supported by the European Union under the 7th framework program (201651).

References

[1] J. M. Blackall, S. Ahmad, M. E. Miquel, J. R. McClelland, D. B. Landau, and D. J. Hawkes. MRI-based measurements of respiratory motion variability and assessment of imaging strategies for radiotherapy planning. *Phys Med Biol*, 51:4147–4169, 2006.

[2] A. P. King, R. Boubertakh, K. S. Rhode, Y. L. Ma, P. Chinchapatnam, G. Gao, T. Tangcharoen, M. Ginks, M. Cooklin, J. S. Gill, D. J. Hawkes, R. S. Razavi, and T. Schaeffter. A subject-specific technique for respiratory motion correction in image-guided cardiac catheterisation procedures. *Med Image Anal*, 13(3):419–431, 2009.

[3] A. P. King, K. S. Rhode, R. S. Razavi, and T. R. Schaeffter. An adaptive and predictive respiratory motion model for image-guided interventions: Theory and first clinical application. *IEEE Trans Med Imaging*, 28(12):2020–2032, 2009.

[4] D. Manke, K. Nehrke, and P. Bornert. Novel prospective respiratory motion correction approach for free-breathing coronary MR angiography using a patient-adapted affine motion model. *Magn Reson Med*, 50:122–131, 2003.

[5] F. Savill, T. Schaeffter, and A. P. King. Assessment of input signal positioning for cardiac respiratory motion models during different breathing patterns. In *Proc ISBI*, 2011, in press.

[6] D. Yang, W. Lu, D. A. Low, J. O. Deasy, A. J. Hope, and I. El Naqa. 4D-CT motion estimation using deformable image registration and 5D respiratory motion modeling. *Med Phys*, 35(10):4577–4590, 2008.