Lung tumour motion models from cone-beam CT

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Abstract. Presented is a method to build a surrogate-driven motion model of a lung tumour from cone-beam CT (CBCT) projection data. The method is markerless and can utilise a standard CBCT scan from radiotherapy treatments. A motion compensated reconstruction of the tumour region also results from calculation of the tumour motion model. It is envisaged that this technique be used to better assess tumour shape and motion prior to dose delivery and over the course of treatment. The method could also be used to guide gated and tracked treatments. The two-step method involves enhancing the tumour region in the projections, and then fitting the surrogate-driven motion model. Preliminary results on a patient dataset using a surrogate extracted directly from the CBCT projections are presented.

1 Introduction

State of the art radiotherapy treatments rely on the accurate identification of cancerous regions and successful exposure of them to lethal doses of radiation [14]. With the advent of stereotactic body radiotherapy (SBRT), involving fewer treatment fractions and higher dose per fraction, it is important that tumour respiratory motion is taken into account. An increasing body of evidence shows that there are indeed changes between planning and treatment fractions [9, 7, 10, 11, 5], which would invalidate motion models built from 4DCT planning data.

4D-CBCT reconstructions [12] are able to provide an indication of tumour motion on the day of treatment, but produces poor quality reconstructions and could underestimate [1] the true extent of

tumour motion. Presented in this work is a method of building a motion model of the tumour, without markers, utilising a standard CBCT scan during treatment. Briefly introduced in [4], preliminary results on clinical patient data are given.

2 Methods and materials

The method involves enhancing the tumour in each projection and then iteratively determining the motion compensated reconstruction (MCR) and surrogate-driven motion model, using an SSD-driven cost function.

2.1 Tumour enhancement

Prior to fitting a motion model to the data, the projections are first pre-processed to enhance the tumour. A standard FDK reconstruction [3] is performed, from which the tumour region is delineated. A simple program to import the target volume from planning was constructed in MatLab (MathWorks, Massachusetts, USA), which also allows the volume to be stretched in superior-inferior (SI), anterior-posterior (AP) and left-right (LR) directions. This target volume should encompass the tumour and the extent of its motion over the entire scan. A mask is created of the tumour region and used to create two volumes. One is of the tumour region with voxels outside set to the intensity of air. The other is of non-tumour region with the tumour region voxels set to the intensity of air. A CBCT is simulated of the non-tumour region volume and the projections subtracted from the original projections. Given a stationary patient, the resulting enhanced projections would be of just the tumour region. In practice these enhanced projections are corrupted with artefacts, of which the effect is minimised by masking the projections according to the projected tumour region volume, giving the tumour region projections. Figure 1 shows an example projection at various stages of the tumour enhancement process.

2.2 Motion models

A motion model is used to constrain the estimated patient motion to physically realistic variation. A realistic parameterisation of the

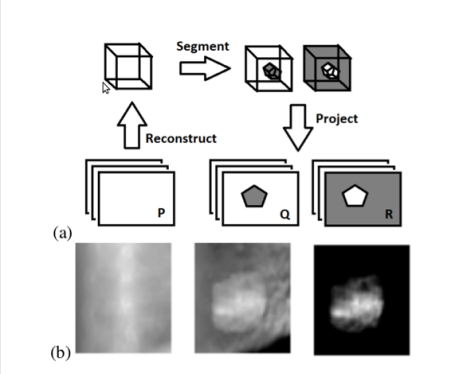

Fig. 1. (a) Illustration of tumour enhancement process. The tumour enhanced projections are the original projections (P) minus non tumour region projections (Q); which are then masked by the tumour region projections (R). (b) Using labels from (a), part of an example projection shown at various stages of tumour enhancement: P, (P-Q) and (P-Q) masked by R, from left to right respectively.

motion of just the tumour region is desired, but one that requires a minimal number of parameters. Assuming that the tumour motion can be approximated as movement of a solid, non-deforming mass, a rigid, translation-only motion model should provide physically realistic motion estimates, whilst providing a low number of parameters to optimise. A simple, linear motion model only requiring the breathing trace current value is used for this work. Surrogate traces were extracted directly from the projections with a method based on [15]. The raw surrogates were then normalised (mean subtracted; divided by standard deviation). The motion model used is:

$$V_{t_n}(\boldsymbol{x}) = V_{t_0}(\boldsymbol{x} + s_{t_n}\boldsymbol{m}), \tag{1}$$

where $\boldsymbol{x}$ is an artibrary point in the patient volume. V_{t_n} is the patient volume at the time t_n of the n^{th} projection, with the first projection taken at time t_0. V_{t_0} is the reference volume. A projection at time t_n has an associated scalar surrogate signal value s_{t_n}. $\boldsymbol{m}$ is a three element vector which determines the SI, AP and LR motion dependence on the current value of the surrogate signal s_{tn}, respectively.

2.3 Iterative approach to calculate motion compensated reconstruction (MCR) and motion model parameters

Using an approach first presented in [4], we attempt to jointly estimate the MCR and motion model parameters iteratively. Beginning with zero motion (i.e. $\boldsymbol{m} = \mathbf{0}$), an MCR is calculated. An open-source, FDK-based reconstruction algorithm was modified for the reconstructions [8]. MCRs werecalculated by back-projecting each projection through the inverse transformation of that that the motion model estimated, given the motion model parameters.

The MCR was used as the reference volume and the motion model parameter updates calculated. An SSD-based cost function is combined with an optical flow approach, to re-express the difference between actual and simulated projections (residue) as motion model parameter updates [6]. Because of the form of the motion model, the cost function could be expressed in a manner which reduced the optimisation time.

$$\boldsymbol{\delta m} = \underset{\boldsymbol{\delta m}}{argmin} \left[\sum_{\theta,\phi=0}^{3} \lambda_\theta \lambda_\phi \sum_{t_n} \sum_{pixels} C_\theta C_\phi \right], \tag{2}$$

where

$$\begin{aligned} &\lambda_0 = 1; \quad C_0 = R_{t_n}; \\ &\lambda_1 = \delta m_z; \, C_1 = -s_{t_n} P_{t_n} \left(\partial_z V_{t_n} \right); \\ &\lambda_2 = \delta m_y; \, C_2 = -s_{t_n} P_{t_n} \left(\partial_y V_{t_n} \right); \\ &\lambda_3 = \delta m_x; \, C_3 = -s_{t_n} P_{t_n} \left(\partial_x V_{t_n} \right); \end{aligned} \tag{3}$$

R_{t_n} is the residue for the simulated and actual projections at time t_n, described earlier. P_{t_n} is the forward projection operator. ∂_z, ∂_y and ∂_x are the partial derivatives in SI, AP and LR directions, respectively. The parameter space was searched for the minimum, giving the motion model parameter updates $\boldsymbol{\delta m}$. A BFGS Quasi-Newton method with a cubic line search procedure [2] was used to search the parameter space. The new motion model parameters $\boldsymbol{m}_{new}$ can now be calculated:

$$\boldsymbol{m}_{new} = \boldsymbol{m} + \boldsymbol{\delta m}. \tag{4}$$

After recalculating the MCR with the new motion model parameters, the process is repeated until the convergence. The algorithm was terminated if the motion model updates gave a maximum additional shift of less than one voxel (i.e. the largest additional shift over all seen surrogate values less than one voxel), or if a maximum number of iterations was met (set at 10).

3 Results

Preliminary testing of the algorithm on patient data is given. Two sequential CBCT scans (termed scan A and scan B) during a fraction of SBRT treatment were used. Scans were taken on an Elekta Synergy (Elekta, Crawley, UK) at Guys and St. Thomas Hospital (London, UK). For this dataset, circa 700 projections were taken at an acquisition rate of 5.5Hz. Simulating the 3D trajectory of both scans and motion model parameters, the average maximum variations were 11.9, 2.10 and 0.63mm in the superior-inferior (SI), anterior-posterior (AP) and left-right (LR) directions, respectively. The mean (max) RMS errors of using either extracted motion model parameters were 0.412mm (1.09) for the scan A estimated trajectory, and 0.425mm (1.16) for scan B's. Please see Table 1 for further information. Figure 2 shows the original and motion compensated reconstructions using the original projections of scan B.

Table 1. Maximum tumour motion by surrogate source and extracted motion model parameters.

Trajectory	Motion model parameters	Max. motion (mm) (SI,AP,LR)
Scan A	Scan A	12.5, 1.75, 1.23
Scan A	Scan B	11.0, 2.42, 0.01
Scan B	Scan A	12.7, 1.78, 1.25
Scan B	Scan B	11.2, 2.46, 0.01
Mean		11.9, 2.10, 0.63

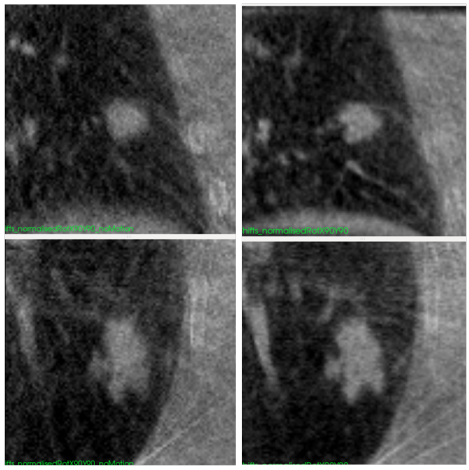

Fig. 2. Slices of scan B reconstructions with (right) and without (left) motion compensation.

4 Discussion

The authors have presented preliminary evidence that tumour motion can be extracted from a CBCT scan and used to build a motion model and MCR. The simple motion model presented here is able to improve the quality of the reconstruction and allow target volume motion to be assessed prior to treatment. There is an improvement in contrast of the surrounding structures, such as airways, which move similarly to the tumour. Structures that do not move as the tumour appear more blurred in the MCR. The method provides encouraging results, even in the presence of scatter and limited field of view (possible missing patient anatomy in the reconstruction) artefacts affecting CBCT scans. By optimising the code and utilising a GPU, the authors are confident convergence could be achieved within a clinical timeframe; minutes as opposed to hours. The authors are currently performing tests on further datasets and with other surrogates. Motion models which can account for hysteresis are also being tested. Work on extending the motion model to include more complex deformations, and modelling motion of the organs at risk are also planned.

Acknowledgments

James Martin gratefully acknowledges the support of the EPSRC funded UCL VEIV EngD programme and Vision RT. Jamie McClelland acknowledges the support of EPSRC project EP/H046410/1.

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