ITERATIVE SORTING FOR 4DCT IMAGES BASED ON INTERNAL ANATOMY MOTION

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ABSTRACT

Geometric uncertainties caused by respiratory motion complicate radiotherapy treatment planning. Therefore 4D CT imaging is important in characterizing anatomy motion during breathing. Current 4D CT imaging techniques using multislice CT scanners involve multiple scans at several axial positions and retrospective sorting processes. Most sorting methods are based on externally monitored signals recorded by external monitoring instruments, which may not always accurately catch the actual breathing status and may lead to severe discontinuity artifacts in the sorted CT volumes. We propose a method to reconstruct time-resolved CT volumes based on internal motion to avoid the inaccuracies caused by external breathing signals. In our method, we iteratively sort the 4D CT slices using internal motion based breathing indices. In each iteration, respiratory motion is estimated by updating a motion model to best match a deformed reference volume to each moving multi-slice sub-volumes. The breathing indices as well as the reference volumes are refined for each iteration based on the currently estimated respiratory motion. An example is presented to illustrate the feasibility of our 4D CT sorting method without using any external motion monitoring systems.

Index Terms— 4D CT, motion estimation, registration, amplitude sorting

1. INTRODUCTION

Computed Tomography (CT) image reconstruction algorithms assume the object is still when being scanned. However, respiration causes anatomy movement, violating the motionless assumption. Ignoring this violation and using inconsistent X-ray projection views will result in severe motion artifacts in the reconstructed images, which are unacceptable for diagnosis and treatment planning. Scans under breathhold conditions reduce the motion effects. However, current multi-slice CT scanners can only image a few centimeters in the axial direction per rotation. Covering a whole thorax requires scans at several table positions. Thus the data acquisition time for the thorax is usually longer than the duration for which patients can comfortably hold their breath. Moreover, one state

is insufficient to characterize the anatomy movement of patients during a whole breathing cycle.

To reconstruct time-resolved CT volumes while patients breath freely during the scan, different scanning protocols are being investigated for 4D CT imaging [1]. Although subtle differences exist among those scanning protocols, the general ideas are the same, which can be described by an over-sampling and sorting process. First, each table position is scanned for one to two breathing cycles with a synchronized breathing signal recorded by an external motion monitoring system. Then multiple slices at each axial position are reconstructed, each associated with a breathing index. The slices are sorted into different breathing state bins according to the external breathing signals, and the slices within the same bins are stacked to form a sequence of approximately temporally consistent CT volumes. The recorded breathing signals may reflect the skin motion the skin tension or the tidal volume through the mouth depending on various systems. Such externally monitored signals may not accurately represent the internal motion. Full reliance on it can lead to severe tissue discontinuity artifacts in the reconstructed 4D CT volumes.

To eliminate the need for the possibly inaccurate external breathing signals, we propose an iterative method to sort the slices based on internal anatomy motion. We estimate an internal motion-based breathing indices for each slice; the estimated breathing signals are then used to sort the CT slices to form 4D CT volumes. Using the newly sorted CT volumes, we can continue another iteration of motion estimation and form a refined set of 4D CT volumes. For motion estimation, a motion model is also updated iteratively to best match a continuously deformed reference volume to each axial moving sub-volumes. The motion model we propose assumes that the displacement of each voxel at any time is proportional to the full movement of that voxel from end-exhalation to end-inhalation. The full movement is obtained by registering two CT volumes at near end-exhalation and end-inhalation states. Detail of this method is described next.

2. METHOD

4D CT data are acquired using a multi-slice CT scanner operated in a cine mode. At each table position the patient is scanned for a few seconds that covers at least one breathing

cycle. We call the slices corresponding to each table position a group of moving sub-volumes. Assume N table positions are scanned, then the whole data set contains N sets of moving sub-volumes. We denote the data set $f_n(\mathbf{x}; k)$, $n = 1, \cdots, N$, $k = 1, \cdots, K$, where K is the number of temporal samples in the scanning period at each table position. The nth group of sub-volumes cover the axial range of $z_n - d/2 \leq z \leq z_n + d/2$, where d is the axial coverage of the multi-slice CT scanner for one rotation. To obtain 4D thorax CT volumes, the sub-volumes need to be synchronized and stacked in the axial order. Different to most of the current methods, we do not use external motion moniterning signals to find the temporal correspondences among the acquired sub-volumes. Instead, we use breathing signals estimated based on internal anatomy motion.

An overview of the method is as follows,

Step 0. Obtain two reference volumes at relatively deep exhale and inhale states, denoted $f_{\text{ex}}(\mathbf{x})$ and $f_{\text{in}}(\mathbf{x})$, $\boldsymbol{x} \in \mathbb{R}^3$, using a simple breathing indices as follows. We find the most posterior coordinate on the anterior side of each slice and average them over the slices of each sub-volume. The averaged coordinate value is treated as a breathing index for that sub-volume. Using these simple breathing indices, we form two reference volumes.

Step 1. Find the full deformation for inhalation, $\mathcal{D}_{\text{full}}(\mathbf{x})$, by registering the two reference volumes of the patient, $f_{\text{ex}}(\mathbf{x})$ and $f_{\text{in}}(\mathbf{x})$. The full deformation will be used in the next step for composing a motion model.

Step 2. For each table position, estimate internal motion indices by iteratively updating a motion model to best match the deformed reference volume $f_{\text{ex}}(\mathbf{x})$ to each group of moving sub-volumes, which will be described in more detail later.

Step 3. Sort the slices based on the estimated internal motion indices to form new 4D CT volumes.

Step 4. Select two reference volumes, one at near end of exhale state and one at near end of inhale state to replace the previous $f_{\text{ex}}(\mathbf{x})$ and $f_{\text{in}}(\mathbf{x})$, then go back to Step 1.

In each cycle, refined breathing indices are estimated and are used to sort out reference volumes containing less artifacts. We terminate the iterative sorting process when the estimated breathing indices result in no change in the sorted volumes with respect to those of the previous cycle. Generally three to four cycles are sufficient for convergence.

We now explain each step in more detail.

- Registration

In Step 1 we register the two 3D reference volumes. We use a B-spline based deformation model, i.e.,

$$\mathcal{D}_{\text{full}}(\mathbf{x}) = \sum_i \boldsymbol{\theta}_i \, \beta\left(\frac{\mathbf{x} - \mathbf{x}_i}{\Delta_{\mathbf{x}}}\right), \tag{1}$$

where $\beta(\mathbf{x})$ is the tensor product of cubic B-spline functions, $\mathbf{x}_i$ denotes the spatial control knot locations, and $\Delta_{\mathbf{x}}$ controls

the width of the B-spline functions. A cost function containing a Least-square similarity metric and a Jacobian penalty discouraging irreversible deformations is minimized to find the for deformation parameters.

- Estimation of the internal motion indices

Step 2 is to find a breathing index reflecting the internal anatomy movement for each sub-volume, the key task of this work. In this part we implement N estimations, yielding breathing indices $\{\boldsymbol{\alpha}_n\}_{n=1}^N$ for the all the N scan periods. Each estimator iteratively updates the parameters of a motion model to best match the deformed exhale reference volume, $f_{\text{ex}}(\mathbf{x})$, to a sequence of moving sub-volumes, $f_n(\mathbf{x}; k)$. The motion model we use is based on a motion proportionality assumption. [2]. We assume the displacement of each voxel at any time is proportional to the full movement of that voxel from end-exhalation to end-inhalation. The motion model can be expressed as follows,

$$\mathcal{T}_{\boldsymbol{\rho}}(\boldsymbol{x}; t_n) = \boldsymbol{x} + \rho(t_n)\mathcal{D}_{\text{full}}(\mathbf{x}), \tag{2}$$

where $\rho(t_n)$ denotes the scalar proportionality parameter at time t_n. We allow $\boldsymbol{\rho}$ to be negative or be greater than 1. We solve the parameters by minimizing the following cost function, containing a data fidelity term and a penalty term:

$$\hat{\boldsymbol{\alpha}}_n = \arg\min_{\boldsymbol{\alpha}_n} \quad \bigg(L_n\big(f_n(\mathbf{x}; k), f_{\text{ex}}(\boldsymbol{x} + \mathcal{T}_{\alpha_n}(\boldsymbol{x}; t))\big)$$

$$+ \lambda R(\alpha_n) \bigg), \quad i = 1, \cdots, N, \tag{3}$$

Where $L_n(\cdot)$ is a measure of dissimilarity over the field of view (FOV) of the nth sub-volumes, $R(\cdot)$ is a roughness penalty function, and λ is a scalar controlling the tradeoff between the two terms in the cost function. We used the sum of squared differences for the data fidelity term. The roughness penalty discourages rapidly changing motion estimates. It takes the form of $R(\boldsymbol{\alpha}_n) = ||\boldsymbol{C}\boldsymbol{\alpha}_n||^2$, where $\boldsymbol{C}$ is a differencing matrix. To solve this minimization problem, the Conjugate Gradient Descend method is used. The estimated parameters $\{\hat{\boldsymbol{\alpha}}_n\}$ will serve as the breathing indices for sorting the sub-volumes.

- Sorting

After estimating the internal motion indices associated with all the sub-volumes at all table positions, we use a typical binning method in step 3 to divide the sub-volumes into several breathing state bins. Then the sub-volumes located in the same bins can be stacked together in the order of their table positions to form a sequence of temporally consistent CT volumes. We use amplitude based sorting. We first normalize the breathing signals to range $[0, 1]$ and assign each bin with a value of amplitude and a direction of ascending or descending. The value of amplitude represents how deep the breath

is, while the direction indicates whether it is in inhalation or exhalation. The sub-volume whose corresponding breathing index is the closest to the bin value in the bin direction is associated to that state bin.

- Selection of reference volumes

After we obtain sorted 4D CT volumes, we manually select two CT volumes, one at near the end of exhale and one at near the end of inhale states, to be used as the reference volumes in the next round. The reference volumes need not to be at full inhale or exhale state, but should contain minimal discontinuity artifacts. For the results below, we chose the 80% CT volume instead of the 100% as the inhale reference volume since the 100% one presented more discontinuities than the 80% one.

3. EXPERIMENT RESULTS

We applied this method to a set of 4D CT clinical data acquired using a GE 8-slice CT scanner operated in cine mode. The CT images have a resolution of $0.98cm \times 0.98cm$ and a slice thickness of 2.5mm. The patient was scanned at 16 table positions, where position 1 to 16 is numbered in the order from superior to inferior. Each table position was scanned for 5.5 second and 23 sub-volumes were reconstructed in each scanning period, i.e., the sub-volume corresponding to each table position was temporally sampled 23 times in its scanning period. An external breathing signal is recorded using the Real-Time Position Management (RPM) Respiratory Gating System (Varian Medical Systems, Palo Alto, CA [3]). so we can compare it with our estimated internal motion-based breathing signal.
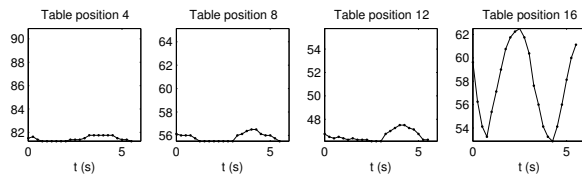

Fig. 1. Extracted simple breathing indices based on the averaged most posterior coordinates of the anterior body surface of the 8 slices of each sub-volume.

We executed three iterations of the 4-step 4D CT reconstruction method. Fig. 1 shows four of the extracted simple breathing indices for position 3 (close to neck), position 7, position 11 and position 15 (close to abdomen) obtained in Step 0. The smallest and the largest values in these breathing signals occur either near deep inhale or exhale state. So we stacked those sub-volumes that corresponded to the extreme breathing states to form an exhale volume and an inhale volume. With the availability of two initial reference volumes, the rest of the procedure can be implemented as explained in Sect 2.

Fig. 2 plots the estimated breathing signals of the final iteration. They were normalized and superimposed with the normalized RPM signals for comparison. These plots show a good correlation between our estimated breathing signals and the recorded external RPM signals, indicating our estimated breathing signals can serve as surrogates of the latter one for sorting the CT images. Since we estimated the breathing indices based on internal anatomy motion, the differences in individual samples from the RPM indices may reflect corrections toward more accurate representation of the respiratory motion. Using the estimated breathing signals, we sorted the sub-volumes into 11-phases. Coronal views of the iteratively sorted 4D CT volumes are shown in Fig. 3. We also sorted the sub-volumes into the same phases using the RPM signals and the coronal views of of the RPM sorted 4D CT volumes are shown in Fig. 4. Due the space limit, we only plotted 6 states. It can be seen that the iteratively sorted ones contain less "flatness" artifacts at the diaphragm dome and less discontinuity artifacts at the edge of heart.

4. CONCLUSION

We proposed a method to obtain iteratively refined breathing signals based on estimated internal anatomy motion, which are used for 4D CT data sorting. An example was presented to illustrate the feasibility of this iterative 4D CT reconstruction method. Advantages of this method include more accurate internal motion based breathing indices for sorting. Although longer computation is required because of registration and motion estimation, this may be acceptable since the 4D CT volumes are used offline.

5. REFERENCES

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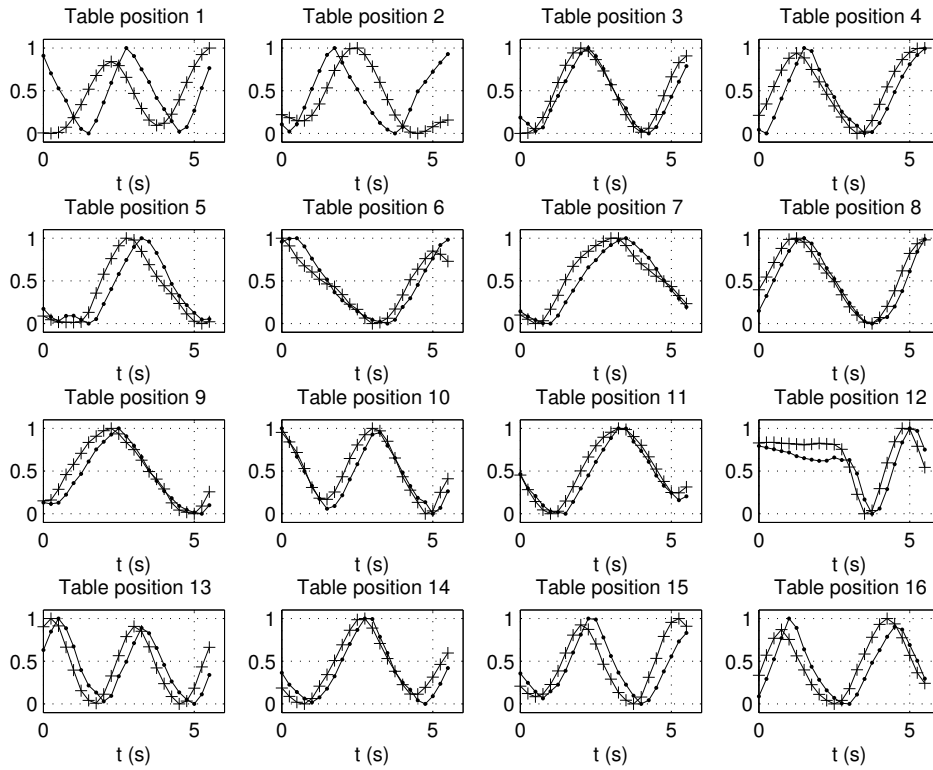
Fig. 2. The estimated breathing signals ('+') and the recorded RPM signals ('·') of the 16 moving sub-volumes.
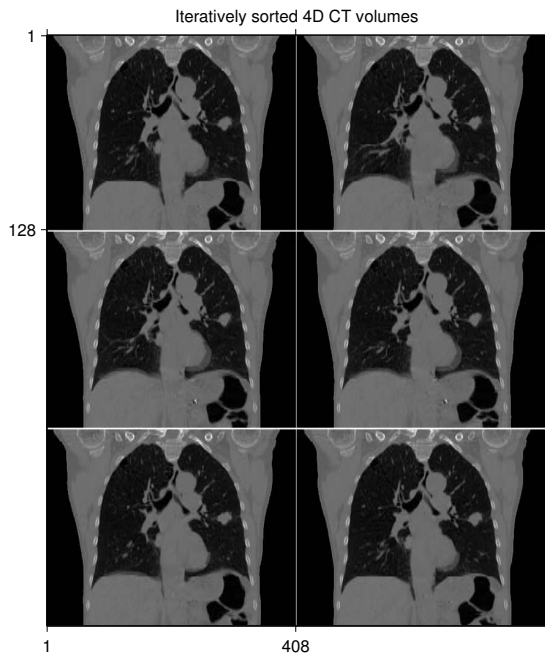

Fig. 3. Coronal views of 6 states of the iteratively sorted 4D CT volumes. In the order of left to right and top to bottom, the breathing state varies from inhale to exhale and back to inhale.
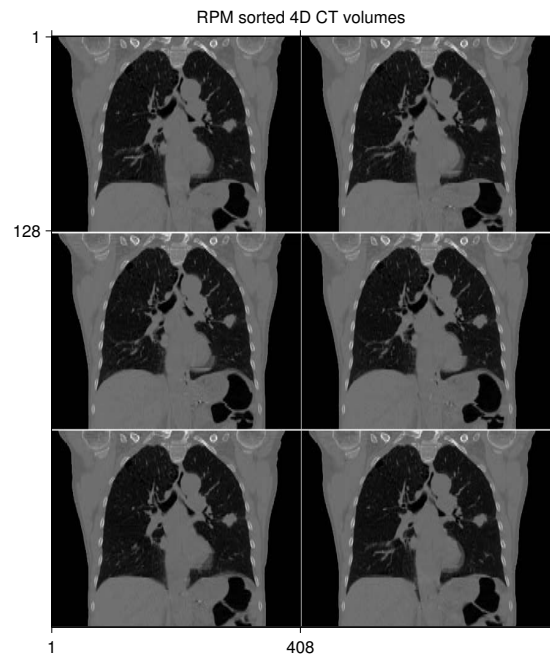

Fig. 4. Coronal views of 6 states of the RPM sorted 4D CT volumes. In the order of left to right and top to bottom, the breathing state varies from inhale to exhale and back to inhale.