Optimising Lung Imaging for Cancer Radiation Therapy

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Abstract

Effective radiotherapy is dependent on being able to (i) visualise the tumour clearly, and (ii) deliver the correct dose to the cancerous tissue, whilst sparing the healthy tissue as much as possible. In the presence of tumour motion, both of these tasks become increasingly difficult to perform accurately. This increases the likelihood of an incorrect dose being delivered to cancerous tissue and exposure of healthy tissue to unnecessary radiation. For tumours in the lung and thoracic region subject to respiratory-induced motion, 4D Cone-Beam CT (4D-CBCT) is a novel approach for producing a sequence of 3D images of the patient’s anatomy throughout different phases of the respiratory cycle. However, current implementations involve sub-optimal heuristic approaches to acquire the imaging data required to account for tumour motion. This leads to undersampling of images for particular phases in the respiratory cycle (such as peak inhale and exhale), resulting in noisy or poorly reconstructed 3D images. In this paper we present a novel Mixed Integer Program (MIP) to optimise the timing and angles for the acquisition of imaging data. The results is greatly enhanced image quality for each image across the respiratory cycle, whilst minimising motion blur. Numerical experiments indicate that our approach universally improves over the conventional acquisition process by 93% and simultaneously reduces unnecessary dose to the patient and can be solved in under a minute.

Keywords: OR in Medicine; 4D-Cone Beam CT Imaging.

1 Introduction

Lung cancer remains the leading cause of cancer-related death, with estimates attributing it to around 1.58 million deaths (approximately 19.4%) of the total cancer deaths worldwide (Ferlay et al., 2013). Furthermore, American figures (American Cancer Society (2016)) indicate that the five year survival rate is as low as 17%.

Radiotherapy continues to play a key role in the successful treatment of lung cancer and recent advances with image guidance to localise the tumour have allowed for greater precision in conformal radiation delivery.
This has made it possible to take advantage of dose-escalation techniques (Leng et al. (2008)); enabling enhanced local control and the dose to be delivered across fewer treatments. To ensure this is safe and effective, it is imperative that the tumour target is accurately localised prior to treatment via a high-quality pre-treatment scan, so as to ensure surrounding healthy tissue is spared during delivery. Accurate tumour localisation is significantly more difficult when the tumour and surrounding anatomy are in motion. Tumours located in the lung are often subject to large perturbations (typically 5-10mm of magnitude and up to 50mm) induced by the diaphragm during respiration (Keall et al. (2006)).

Conventional methods for producing a three-dimensional image of the patient’s anatomy such as 3D Cone Beam CT (3D-CBCT), involve positioning a patient on a bench (referred to as a couch) in an axis perpendicular to the rotation of a kilovoltage imager attached to a gantry. As the gantry rotates, a sequence of 2D images known as projections are acquired at specified angles (see Figure 1(a)). These images are used to reconstruct a picture of the 3D anatomy using fit-for-purpose reconstruction algorithms such as the FDK approach developed by Feldkamp et al. (1984).

The 3D-CBCT imaging process however does not account for motion of the patient’s anatomy throughout the image acquisition process. As a CBCT scan requires at least one minute to acquire the projection data, any respiratory-induced motion leads to blurring of the reconstructed 3D images (see Figure 1(b)).

Overcoming this problem has driven the recent development of reconstruction methods that are better equipped to retrospectively account for such motion. One such example is that of 4D-CBCT, which has recently emerged as a clinical guidance strategy; allowing practitioners to mitigate against this motion blur by decomposing the projections acquired throughout the respiratory cycle into different phase bins; producing a movie, or sequence of 3D images depicting the anatomy at each stage of the respiratory cycle. See Figure 2 below.

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1https://www.elekta.com/radiotherapy/treatment-delivery-systems/elekta-synergy/
Figure 2: The 4D-CBCT reconstruction process for 3 respiratory phases: dots represent the time and phase at which 2D images were acquired. Those of the same colour (i.e., in the same respiratory state) are grouped together to produce an image of the anatomy at different respiratory phases and reduce motion-induced blur.

Unfortunately, existing 4D-CBCT approaches utilise a constant gantry rotation speed and imaging pulse rate for acquisition, which leads to poor image quality and high imaging doses. There is therefore significant potential for high-quality images to be produced in close to real-time if the process by which the 2D images are acquired is mathematically optimised. The main contributions in the present paper are:

(i) A novel linear objective cost function capable of reducing large angular gaps between projections. Importantly, it directly allows for optimisation of the selection of projections, without need for an external reference image.

(ii) A Mixed Integer Program (MIP) for optimising the timing and angle of projections in response to a patient’s breathing trace. This MIP is solved exactly and in parallel for each displacement bin.

(iii) Two greedy heuristics that provide an upper bound for the MIP solution and are solvable in under 10 seconds on average.

(iv) A demonstration that the MIP proposed in (ii) may be solved more quickly by using the greedy heuristics in (iii) as a warm-start for the MIP. In addition, specialised branching rules are utilised to reduce the computation time further.

The rest of this paper is organised as follows: In Section 2, we discuss the occurrence of streak artefacts in image acquisition and recent techniques that have been employed to reduce them. In Section 3 we summarise the acquisition process for 4D-CBCT and the manner in which the two key components of gantry movement and projection acquisition interact to produce 4D-CBCT images. We then outline our proposed MIP model. In Section 4 we propose two greedy heuristics for producing a set of well-spread candidates for acquisition and may be used as a warm-start for the MIP. Our results are outlined in Section 5 and an analysis of these results is provided in Section 6. We discuss some limitations and areas for future research in Section 7.
2 Image Acquisition and Streak Artefacts for 4D-CBCT

The first 4D-CBCT was implemented in 2005 by (Sonke et al., 2005), and was released commercially by Elekta in 2009. Despite being widely used clinically, 4D-CBCT suffers from streak artefacts as a result of projection under sampling (Shieh et al., 2015). This is due to the fact that the gantry rotation speed and projection frequency for 4D-CBCT is constant and in the majority of cases, independent of the patient’s breathing which can lead to projection clustering and large angular gaps between projections, resulting in streak artefacts (O’Brien et al., 2013; Cooper et al., 2015), see Figures 3 and 4.

Figure 3: In the bottom row, the lines indicate the angle at which each projection is acquired. 4D-CBCT Binning provides a sequence of 3D images with less motion blur, but constant pulse rate acquisition may result in clusters of projections that overdose the patient for little improvement in image quality, while large gaps between projections within a bin lead to streak artefacts.

Cooper et al. (2013) investigated the potential improvements of modifying the projection pulse rate and timing to prospectively improve the spread of projections within each phase bin and decrease unnecessary imaging dose. They noted that projections that were too close together contributed little
Figure 4: It may be observed in (a) that using all projections without accounting for motion leads to significant blur. Displacement binning (b) removes motion blur but can lead to projection clustering when a constant-pulse rate acquisition is used. Using an optimised spread of projections within each bin can reduce motion blur and achieve better image quality for less dose, i.e. for less projections (c).

additional visual information, but exposed the patient to increased imaging dose (see Figure 3 and 4). Moreover, the large angular gaps between projection clusters vary with patient breathing rate and lead to poor image quality resulting in streak artefacts (see Figure 5).

A number of attempts to optimise the selection of projections from a set of allowed timings have recently been performed through heuristics. In particular, O’Brien et al. (2013, 2014a) proposed a respiratory-motion-guided approach and optimisation heuristic to regulate the gantry velocity and projection time interval, so as to reduce the prevalence of large angular gaps. The authors also extended this to account for irregular breathing, noting that for the same imaging dose the image quality using the signal-to-noise ratio is improved by 63% on average. This approach achieved the first implementation on a radiotherapy machine O’Brien et al. (2016, 2017).

While these approaches have successfully led to improvement in both image quality and imaging dose reduction, the choice of gantry rotation speed and projection pulse rate is still only determined heuristically, in a sequential manner and using a simple $k$-exchange algorithm. Moreover, the conventional approach for producing 4D-CBCT imaging has traditionally relied heavily on phase binning, which may not always produce the best motion correction as noted in Abdelnour et al. (2007), O’Brien et al. (2014b) and O’Brien et al. (2017). One alternative is that of displacement binning, in which the respiratory trace is divided into 10 displacement bins, for which the first bin corresponds to peak exhale, and the last bin, to peak inhale. These bins are conventionally chosen to be of equal width and provide a partition of the entire respiratory trace. Projections are separated according to the displacement bin to which they belong, rather than being sorted according to their estimated respiratory phase.

In particular, Abdelnour et al. (2007) noted that displacement binning results in correctly grouped images and thus is more sensitive to the actual location of a hysterical tumour, rendering a more accurate recovery of the object size and shape. Thus in the remainder of this work, we will focus our attention on displacement binning.
Figure 5: Examples of streak artefacts caused by projection undersampling and clumped projections. Figure (a) is the 3D image generated using all projections, and (b) is one phase of a 4D image using a subset of projections which has eliminated motion blur through binning, but suffers from streaking artefacts due to projection under sampling.

3 MIP Model for Projection Acquisition Timing

In this section we outline a MIP to determine the optimal timings and angles at which to acquire projections.

3.1 Assumptions

We assume that breathing data from the patient is acquired over a 4-minute time interval, and the binning strategy employed is that of displacement binning. The respiratory trace for each patient is divided into $B = 10$ equally spaced bins. Let $b = 1, \ldots, B$ index the displacement bins, and $t = 1, \ldots, T$ index the discretised time. Denote by $r_t$ and $\theta_t$ the breathing displacement and gantry angle at time $t$ respectively, and associate with each discretised point the triple $(r_t, t, \theta_t)$, which denotes the respiratory displacement, time and gantry angle respectively. In addition, a specified number of projections $P_b$ are acquired for each bin, with the total number of projections $P = \sum_{b=1}^B P_b$. In this paper we will utilise $P = 200$ and $P = 500$ projections, and have the same number of projections in each bin, therefore $P_b = 20$ and $P_b = 50$ for all $b$, in each case, respectively.

We assume a 360° acquisition and that the gantry moves uni-directionally (monotonically increasing in angle $\theta$) at a constant speed or is capable of a stop-start acquisition at different angles. We propose a MIP that can be decomposed by displacement bin $b$, and so the displacement term $r_t$ is dropped once the point has been assigned to a specific bin, see Figure 6. To achieve this, we for each bin $b$ define the ordered set $N_b$,

$$N_b = \{t \in \{1, \ldots, T\} : r_t \in \text{bin } b\}$$

and replace $\bigcup_{t=1,\ldots,T}(r_t, t, \theta_t)$ with the binwise partition $\bigcup_{b=1,\ldots,B} \bigcup_{t \in N_b}(t, \theta_t)$. 

Figure 6: The discretised respiratory trace may be derived from a continuous signal as above. Each candidate point for a projection is denoted by a circle (grey or coloured), and actual projections denoted by the colour of the bin in which they are contained (grey means the projection is not acquired).

We assume that the trace is discretised according to the commonly used 5Hz sample rate and so \( T = 4 \times 60 \times 5 \).

3.2 Decision Variables

Because the spread of projections in a given bin does not affect the spread in another, the MIP can be decomposed according to bin and the solution obtained for each bin separately.

We define the variables:

\[
\Delta_b^t = \begin{cases} 
1, & \text{if a projection occurs at time } t \in N_b; \\
0, & \text{otherwise}.
\end{cases}
\]  

Similarly, we define the variables:

\[
\Delta_{s,t}^b = \begin{cases} 
1, & \text{if projections occur at times } s \text{ and } t \text{ in bin } b; \\
0, & \text{otherwise}.
\end{cases}
\]  

for \( b = 1, \ldots, B \) and \( s, t \in N_b \) with \( s < t \). To ensure that the \( \Delta_{s,t}^b \) variables are consistent with the chosen projections in each bin, we define the constraints below to capture these relationships:

\[
\Delta_{s,t}^b \geq \Delta_s^b + \Delta_t^b - 1 \quad \Delta_t^b \geq \Delta_{s,t}^b \quad \Delta_s^b \geq \Delta_{s,t}^b, \quad s, t \in N_b, \ s < t, \ \text{for } b = 1, \ldots, B
\]
We additionally define the constraint
\[
\sum_{b=1}^{B} \sum_{t \in N_b} \Delta_t^b \geq P
\]
and constraints as follows
\[
\sum_{t \in N_b} \Delta_t^b \geq P_b \quad \text{and} \quad \sum_{s,t \in N_b | s < t} \Delta_s^b \geq P_b (P_b - 1)/2 \quad \text{for } b = 1, \ldots, B.
\]

This ensures the correct number of total projections is achieved. Since we would prefer to have the same number of projections in each bin, we define \( P_b \) to be the number of desired projections in bin \( b \), or \( P_b = P/B \). The first constraint will ensure the number of projections in bin \( b \) is no less than \( P_b \), and it was observed that the second constraint slightly improved runtime.

### 3.3 Objective

An objective measure of image quality typically requires a ground-truth or gold-standard reference image, with which to compare another reconstructed image. Such metrics, e.g. the structural similarity index, provide a metric of the quality of the reconstructed image via an averaged pixel-by-pixel (or voxel-by-voxel) comparison (Wang et al., 2004; Fast et al., 2013; Shieh et al., 2015; Santoso et al., 2016), or via the measurement of a specific attribute (e.g. contrast, luminescence, blur or edge-response width) over a particular subset of the image, such as a tumour or lesion (O’Brien et al., 2017).

Some of the drawbacks of such an approach are that it requires: (i) a previously acquired reference image, which may be difficult to obtain and (ii) a retrospective analysis with a metric different from the one used to reconstruct the CBCT image. This can result in a blind tuning of parameters in the reconstruction process without a guarantee of improved image quality.

In contrast, our proposed MIP model seeks to optimise the acquisition process directly, so as to prospectively generate a sequence of projections that provide a reconstructed image with improved image quality. In particular, the choice of objective function in the MIP adopts the approach of O’Brien et al. (2014a, 2016, 2017) by encouraging the optimisation model to select the projection angles and timings to provide a well-spread set of projections for each respiratory bin. This reduces both streak artefacts (resulting from large angular gaps) and unnecessary imaging dose to the patient (from projection clustering).

We require an objective with a unique minimum when the projection angles are equally spaced. The average sum of squared differences between successive projection angles and the ideal projection angle \( 360^\circ/P_b \) was proposed as an objective in O’Brien et al. (2014b) to motivate heuristic methods. Such an objective requires knowledge of the ordering of successive projections, which is not easily encoded in an MIP.

We therefore propose a related objective that does not need to know the ordering of projections:
\[
\min_{\Delta_{s,t}^b} \frac{1}{B} \sum_{b=1}^{B} \frac{1}{P_b (P_b - 1)/2} \sum_{s,t \in N_b | s < t} \Delta_s^b \left( \frac{1}{|\theta_t - \theta_s|} \right), \quad b = 1, \ldots, B.
\]
Testing revealed the parameter $\alpha = 2$ yielded good solution times.

The term
\[
\frac{1}{P_b(P_b - 1)/2} \sum_{s,t \in N_b | s < t} \Delta^b_{s,t} \left( \frac{1}{|\theta_t - \theta_s|^\alpha} \right)
\]
has a lower bound of $(P_b/(360^\circ))^\alpha$ (all angles equally spaced), and an upper bound of $1/\bar{\theta}^\alpha$ (angles spaced at the minimum angle spacing $\bar{\theta}$ as determined by the breathing trace and the time discretisation).

### 3.4 Computational Information

All computational experiments were performed on a 64-bit PC with a 2.6GHz processor, using Matlab R2015a and solved using CPLEX 12.7.0 bundled with the CPLEX Optimization Studio.

#### 3.4.1 Improving Runtime

In order to reduce the solution time of the MIP, we introduced branching priority orders to branch on the $\Delta_t$ variables with higher priority. These were included by using the `Cplex.Order.ind` and `Cplex.Order.pri` commands in CPLEX Optimization Studio. The `Cplex.Order.ind` is used to denote the subset of variables that are to receive branching priority, and the `Cplex.Order.pri` explicitly sets these priorities, with larger numbers indicating to CPLEX that greater priority should be given to branching on these variables than others. We used weights of 10 for each of the $\Delta_t$ variables to indicate that they are are all of greater priority than the other variables (weights set to zero). A third command `Cplex.Order.dir` may be used to specify the precise direction in which CPLEX should branch (i.e. up or down). We did not set this, and instead let CPLEX determine the branching direction.

These orders were written to an .ORD file offline and called at runtime. These priority orders reduced the solution time by approximately 41s per dataset on average (44% reduction).

#### 3.4.2 Reconstructed Figures

The reconstructed figures in Section 7.5.3 and Section 7.5.4 were produced using an *in silico* XCAT (Segars et al. (2008)) phantom with programmable tumour and diaphragm motion. These figures were produced using 3D Slicer (Fedorov et al. (2012)) to obtain the axial and coronal slices from the 3D reconstructed volume, with a windowing level of $[L,W] = [0.0038, 0.038]$.  

9
4 Two Greedy Heuristics

In this section we propose a global greedy heuristic, and a local greedy heuristic for comparison with our proposed MIP model.

4.1 The Global Greedy Heuristic

The objective of the global greedy heuristic is to globally match as many equally spread angles to the available gantry angles within each bin as possible. For angles that cannot be matched with an available angle slot, the algorithm selects the feasible angle closest to the equally spread option.

Algorithm 1 Global Greedy Heuristic

Input: Patient’s breathing trace, the predefined bins, number of projections $P$ and projections per bin $P_b$, for each bin.

For each bin $b$:

1. Create $P_b$ points corresponding to the number of projections in bin $b$ on a unit circle, spaced $360^\circ/P_b$ apart.

2. Rigidly rotate these points so the maximum number of points fall within the angle ranges for each bin.

3. For the rotation in Step 2, fix the points (projection angles) that fall inside the available bin angles.

4. For the points that do not fall inside the available bin angles: push them to the nearest available bin angle.

end

Output: The angle of each projection.

4.2 The Local Greedy Heuristic

The proposed local greedy heuristic sequentially takes equally spread angles where possible, otherwise selects the nearest option to equally spread projections.

Algorithm 2 Local Greedy Heuristic

Input: Patient’s breathing trace, the predefined bins, number of projections $P$ and projections per bin $P_b$, for each bin.

For each bin $b$:

1. Take a projection as soon as the bin is entered.

2. While possible take another projection spaced exactly $360^\circ/P_b$ from the previous projection, where $P_b$ is the number of desired projections in bin $b$.

3. If the next equally spaced projection does not lie in the bin. Either:
   
   - Take a projection at the angle at which the trace leaves the bin, or
   
   - Take a projection immediately when the trace re-enters the bin. If it does not re-enter the bin again, take a projection at the last time it left the bin.

   Choose the option that results in an angle closest to the equally-spread separation ($360^\circ/P_b$).

4. If the trace has not ended, go to 2.

end

Output: The angle of each projection.
5 Numerical Experiments

5.1 Datasets

To test the effectiveness of the MIP for projection timing, we tested our approach on 10 different lung-cancer patient breathing traces drawn from the Virginia Commonwealth University (VCU) datasets (described in George et al. (2006)). We use a subset of those acquired in this study, and include patients using free-breathing, audio, and audio-visual biofeedback to guide their breathing (see Table 1 and Figure 7) with an average duration of 4 minutes. We tested the performance of our algorithms for 200 and 500 total projections respectively. For each patient, we determined the boundary of peak inhale and peak exhale by examining the maximum and minimum displacements; dividing these into $B = 10$ displacement bins of equal width.

<table>
<thead>
<tr>
<th>Patient No.</th>
<th>Average Breathing Period (s)</th>
<th>Average Displacement (mm)</th>
<th>Regularity</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2.8</td>
<td>3.9</td>
<td>Baseline Drift</td>
</tr>
<tr>
<td>2</td>
<td>2.7</td>
<td>3.5</td>
<td>Baseline Drift</td>
</tr>
<tr>
<td>3</td>
<td>4.5</td>
<td>5.0</td>
<td>Low</td>
</tr>
<tr>
<td>4</td>
<td>4.1</td>
<td>2.7</td>
<td>Moderate</td>
</tr>
<tr>
<td>5</td>
<td>5.0</td>
<td>5.9</td>
<td>Moderate</td>
</tr>
<tr>
<td>6</td>
<td>13.0</td>
<td>9.3</td>
<td>High</td>
</tr>
<tr>
<td>7</td>
<td>10.0</td>
<td>9.0</td>
<td>High</td>
</tr>
<tr>
<td>8</td>
<td>5.0</td>
<td>4.3</td>
<td>High</td>
</tr>
<tr>
<td>9</td>
<td>5.0</td>
<td>9.4</td>
<td>High</td>
</tr>
<tr>
<td>10</td>
<td>4.6</td>
<td>6.5</td>
<td>High</td>
</tr>
</tbody>
</table>

Table 1: Characteristics of the 10 breathing traces. The degree of regularity denotes the amount by which each breathing trace consistently reach the first and last respiratory bins per cycle. Baseline drift refers to a breathing trace that while remaining regular, trends upwards or downwards with time.

5.2 Metrics

We record the total Root Mean Squared Error (RMSE) and the total time required for solving the MIP. The RMSE is used as a surrogate for image quality (see Shieh et al. (2014)), and is defined as:

$$RMSE^2_b = \frac{1}{P_b} \sum_{i=1}^{P_b-1} [\theta_{b,i+1} - \theta_{b,i} - \theta_{opt}]^2 + [\theta_{b,1} + 360^\circ - \theta_{b,P_b} - \theta_{opt}]^2$$  \hspace{1cm} (7)

$$RMSE^2 = \sum_{b=1}^{B} RMSE^2_b$$  \hspace{1cm} (8)

where $\theta_{b,i}$ denotes the angle of projection $i$ in bin $b$, $P_b$ the number of projections in bin $b$, and $\theta_{opt}$ the optimal spread of projections in each bin for a given number of projections.
Figure 7: Different examples of regularity in a selection of breathing traces

We define $\theta_{opt}$ to be:

$$\theta_{opt} = \frac{360^\circ}{P_b}$$ (9)
5.3 Results for the MIP, Greedy Heuristics and Conventional Base Acquisition

In this section we present our numerical results for the MIP, global greedy heuristic, local greedy heuristic and Base Case for 200 projections and 500 projections respectively. The Base Case involves acquiring projections throughout a 360° rotation with a constant pulse rate.

5.3.1 Using 200 Projections

When requesting 200 projections it may be observed in Table 2 and Figure 14 that our proposed MIP approach provides a significant and universal improvement over the Base Case. In particular, the average RMSE for the MIP is 2.5°, compared with the average of 39.0° for the Base Case; thus the MIP provides a 94% improvement over the Base Case. The MIP also improves over the global heuristics, with an 84% improvement over the local greedy heuristic, and a 58% improvement over the global greedy heuristic.

There is however an associated increase in time as the RMSE improves. The Base Case has the fastest run time of under 0.1s. The local greedy runs in an average of 2.1s, and the global greedy in 2.5s. This suggests that the global greedy is able to achieve good quality solutions (average RMSE of 5.9°) in under 3s, see Figure 14. Therefore, the Global Greedy Heuristic provides the best trade-off between solution quality and speed in cases for which time is the most important factor. The runtime for the MIP is 55s on average, and under a minute in 6 of the 10 patient instances.

<table>
<thead>
<tr>
<th>Patient Number</th>
<th>MIP 200</th>
<th>Global Greedy</th>
<th>Local Greedy</th>
<th>Base Case</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>RMSE (°)</td>
<td>Time (s)</td>
<td>RMSE (°)</td>
<td>Time (s)</td>
</tr>
<tr>
<td>1</td>
<td>2.8</td>
<td>41.7</td>
<td>10.3</td>
<td>1.9</td>
</tr>
<tr>
<td>2</td>
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<td>35.1</td>
<td>7.5</td>
<td>1.5</td>
</tr>
<tr>
<td>3</td>
<td>3.0</td>
<td>54.5</td>
<td>7.8</td>
<td>2.4</td>
</tr>
<tr>
<td>4</td>
<td>2.5</td>
<td>43.7</td>
<td>8.0</td>
<td>8.6</td>
</tr>
<tr>
<td>5</td>
<td>2.3</td>
<td>64.0</td>
<td>4.1</td>
<td>1.7</td>
</tr>
<tr>
<td>6</td>
<td>2.4</td>
<td>45.8</td>
<td>4.7</td>
<td>1.7</td>
</tr>
<tr>
<td>7</td>
<td>2.5</td>
<td>78.7</td>
<td>4.3</td>
<td>1.8</td>
</tr>
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<td>8</td>
<td>2.4</td>
<td>92.4</td>
<td>6.8</td>
<td>1.8</td>
</tr>
<tr>
<td>9</td>
<td>2.3</td>
<td>45.0</td>
<td>4.7</td>
<td>1.6</td>
</tr>
<tr>
<td>10</td>
<td>2.5</td>
<td>73.3</td>
<td>4.3</td>
<td>1.6</td>
</tr>
<tr>
<td>Average</td>
<td>2.5</td>
<td>54.8</td>
<td>5.9</td>
<td>2.1</td>
</tr>
</tbody>
</table>

Table 2: A comparison of the RMSE and solution times for each of the approaches, for each patient, using 200 projections.
Although we used a surrogate objective measure of the image quality (6), the MIP results perform well on RMSE, a commonly used metric to measure image quality as may be observed in Figure 8. Furthermore, the MIP produces the correct number of projections in each bin, unlike the Base Case.

![Figure 8](image_url)

Figure 8: A comparison of the solution for three bins for Patient 10. The top row denotes the solution using the Base Case (conventional acquisition) and the bottom row the corresponding solution using from the MIP. The MIP solution provides an improved RMSE value for each bin, and the correct number of projections, while the Base Case has higher RMSE and unequal number of projections in each bin.

Figure 9 demonstrates that the MIP solution provides higher quality images in both the axial and coronal reconstructions. The coronal slices divide the body into front and back. The axial slices divide the body into top and bottom.

Images (a), (b) and (c) contain streak and blurring artefacts that are indicated by their respective arrows. These artefacts are not present in the reconstruction of the MIP solution. Moreover, in the axial slices, the image is not clinically useful in any of the images (g), (h) or (i). We are able to replicate current clinical image quality using only 20 projections, with the MIP approach providing sufficient anatomical information not visible in the Base Case for the axial slices. In particular, in Figure 9 (j) improves significantly over (g) for only two thirds of the dose.
Figure 9: A comparison of the axial and coronal reconstructions for Patient 10 using 200 projections. The first row and third rows denote the axial and coronal reconstruction for the Base Case and the second and fourth rows, the corresponding reconstructions using the solution from the MIP. Red arrows correspond to extraneous motion-induced artefacts, and yellow arrows to streak artefacts. For cases in which the reconstruction is not useful clinically, the text “Image not visible” appears on the reconstructed image.
5.3.2 Using 500 projections

When requesting 500 projections Table 3 demonstrates and Figure 15 that our proposed MIP approach provides a significant and universal improvement over the Base Case. In particular, the average RMSE for the MIP is $1.9^\circ$, compared with the average of $24.1^\circ$ for the Base Case; thus the MIP provides a 92% improvement over the Base Case. Moreover the RMSE has decreased for all approaches as the number of projections increased.

As for 200 projections, the MIP improves over the global heuristics, with an 87% improvement over the local greedy heuristic, and a 46% improvement over the global greedy heuristic. The Base Case still has the fastest runtime of under 0.1s. The local greedy runs in an average of 2.2s, and the global greedy has increased to 4s. The runtime for the MIP is 53s on average, and under a minute in 5 of the 10 patient instances.

<table>
<thead>
<tr>
<th>Patient Number</th>
<th>MIP 500 RMSE ($^\circ$)</th>
<th>MIP 500 Time (s)</th>
<th>Global Greedy RMSE ($^\circ$)</th>
<th>Global Greedy Time (s)</th>
<th>Local Greedy RMSE ($^\circ$)</th>
<th>Local Greedy Time (s)</th>
<th>Base Case RMSE ($^\circ$)</th>
<th>Base Case Time (s)</th>
</tr>
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<tr>
<td>1</td>
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<td>83.9</td>
<td>7.0</td>
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<td>14.4</td>
<td>1.9</td>
<td>22.5</td>
<td>&lt;0.1</td>
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<td>2</td>
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<td>4.5</td>
<td>3.5</td>
<td>13.9</td>
<td>2.0</td>
<td>23.9</td>
<td>&lt;0.1</td>
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<td>4.2</td>
<td>3.2</td>
<td>14.2</td>
<td>2.5</td>
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<td>&lt;0.1</td>
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<tr>
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<td>2.1</td>
<td>4.0</td>
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<td>2.4</td>
<td>26.3</td>
<td>&lt;0.1</td>
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<td>3.0</td>
<td>4.6</td>
<td>15.1</td>
<td>2.1</td>
<td>21.5</td>
<td>&lt;0.1</td>
</tr>
<tr>
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<td>18.0</td>
<td>6.6</td>
<td>3.8</td>
<td>15.3</td>
<td>2.4</td>
<td>25.0</td>
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<td>72.4</td>
<td>4.4</td>
<td>3.8</td>
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<td>1.9</td>
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<td>&lt;0.1</td>
</tr>
<tr>
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<td>38.7</td>
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<td>63.3</td>
<td>2.1</td>
<td>3.1</td>
<td>14.4</td>
<td>2.4</td>
<td>24.5</td>
<td>&lt;0.1</td>
</tr>
<tr>
<td>Average</td>
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<td>53.1</td>
<td>3.5</td>
<td>3.9</td>
<td>15.0</td>
<td>2.2</td>
<td>24.0</td>
<td>&lt;0.1</td>
</tr>
</tbody>
</table>

Table 3: A comparison of the RMSE and solution times for each of the approaches, for each patient, using 500 projections.

Moreover, it may be observed in Figures 10 and 11 that as in the case of 200 projections, the Base Case experiences a large spread of projections in any given bin across different datasets. Most notably, in the first (bin 1) and last bin (bin 10), irregular breathing amplitude has an impact on image quality, which results in either too few projections to allow an adequate reconstruction, or unnecessary dose for limited improvement in image quality. Our method ensures the target number of projections that are well-spread to avoid these extremes.

In Figure 12 we observe an even greater improvement in the coronal slices with greater clarity around the diaphragm and ribs. In particular between (f) and (c) and the motion blur is eliminated in (d) in comparison with (a) for 20% less dose; likewise for the corresponding axial slices (j) compared with (g). The streak artefacts in (h) and (i) are eliminated in (k) and (f).
Figure 10: A comparison of the solution for three bins for Patient 10. The top row denotes the solution using the Base Case and the bottom row the corresponding solution using from the MIP.

Figure 11: Box plot of the difference in number of projections between the Base Case and the correct (optimal) number of projections for each bin over the 10 datasets. The zero on the y-axis denotes the correct number of projections. The Base case has the correct number of total projections $P$, but varying values of $P_b$. The height of the blue box depicts this variation.
Figure 12: A comparison of the axial and coronal reconstructions for Patient 10. The first row and third rows denote the axial and coronal reconstruction for the Base Case and the second and fourth rows, the corresponding reconstructions using the solution from the MIP. Red arrows correspond to extraneous motion-induced artefacts, and yellow arrows correspond to streak artefacts.
Figure 13: Plot of the RMSE for each dataset using 200 (blue) and 500 projections (red) with linear fit. The error bars for each dataset depict the standard deviation between each of the bins. It may be observed that higher regularity is correlated with lower RMSE and less variation of RMSE between bins.

Figure 13 depicts the average RMSE for each of the datasets and the error bars correspond to the standard deviation between each of the bins for dataset \( n \). The standard deviation for dataset \( n \) is given by:

\[
\sigma_n = \sqrt{\frac{\sum_{b=1}^{B} (RMSE_b - RMSE_{avg})^2}{B - 1}}
\]

where \( RMSE_b \) and \( RMSE_{avg} \) correspond to those for dataset \( n \).

There appears to be a modest relationship between smaller RMSE and dataset regularity. The standard deviation between bins also appears to decrease as the regularity of the breathing trace increases.

5.4 MIP with a heuristic warm-start

We compare warm-starting the MIP with the solutions from the local greedy and global greedy heuristics with the default MIP initialisation.

Table 4 and Figure 14 demonstrate that the MIP warm-started with the local greedy solution produces a decrease in overall computation time of 28.7s on average, or a 52% improvement in computation time over the MIP. When using the global greedy solution as a warm-start a reduction in overall computation time of 30.4s, or an average improvement of 56% is observed.
<table>
<thead>
<tr>
<th>Patient Number</th>
<th>MIP 200 Total Time (s)</th>
<th>Global Greedy with MIP 200 Total Time (s)</th>
<th>Local Greedy with MIP 200 Total Time (s)</th>
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<td>14.6</td>
<td>42.3</td>
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<tr>
<td>Average</td>
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<td>24.5</td>
<td>26.1</td>
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</tbody>
</table>

Table 4: A comparison of the 200-projection performance of using the MIP with heuristics as a warm-start.

In Table 5 and Figure 15 the MIP warm-started with the local greedy solution produces a decrease in overall computation time of 15.8s on average, or a 30% improvement. When using the global greedy solution as a warm-start a reduction in overall computation time of 13.0s, or an average improvement of 25% is observed.

<table>
<thead>
<tr>
<th>Patient Number</th>
<th>MIP 500 Total Time (s)</th>
<th>Global Greedy with MIP 500 Total Time (s)</th>
<th>Local Greedy with MIP 500 Total Time (s)</th>
</tr>
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<tbody>
<tr>
<td>1</td>
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<tr>
<td>Average</td>
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<td>40.0</td>
<td>36.6</td>
</tr>
</tbody>
</table>

Table 5: A comparison of the 500-projection performance of using the MIP with heuristics as a warm-start.
Figure 14: RMSE vs time for each of the approaches using 200 projections.

Figure 15: RMSE vs time for each of the approaches using 500 projections.
6 Discussion

In this paper we have proposed:-(i) a novel linear objective cost function capable of reducing large angular gaps between projections, without requiring an external reference image; (ii) a MIP for optimising the timing and angle of projections in response to a patient’s breathing trace; (iii) two greedy heuristics that accelerate the MIP solution. Specialised branching rules reduced the computation time further. The results of the numerical experiments in Section 5 highlight a number of key advantages of our models over conventional constant-pulse rate acquisition.

Universal improvement of projection uniformity over conventional acquisition and heuristics

The MIP provides a substantial and universal improvement over the conventional constant pulse rate acquisition, and both of the stand-alone greedy heuristics. This improvement is observed over all datasets and for both 200 and 500 projections. On average the MIP provides an improvement of 52% over the global greedy heuristic, an improvement of 86% over the local greedy heuristic, and a 93% improvement over the Base Case.

MIP speedups from priority branching and heuristic warm-starts

The improvement of the MIP over the Base Case indicates that there is significant value in optimising the timing of projections in response to the patient’s breathing cycle. Although the MIP takes an average of 57s to solve compared with 0.05s for the Base Case, the computational time required for the MIP remains practical in a clinical setting, and the improvement of 93% in image quality (from a maximum possible 100% improvement) more than offsets this increase in time. Furthermore, we have demonstrated that it is possible to further reduce the computational time of the MIP by between 13 and 27s by warm-starting with one of the proposed local greedy or global greedy heuristics. There is also no significant increase in runtime between the 200-projection and 500-projection cases.

Optimal dose per bin

One of the key advantages of the MIP over the conventional constant pulse-rate acquisition is that the MIP guarantees the correct number of projections in each bin. In comparison, it may be observed in Figure 11 that the number of projections in each bin varies considerably in the case of the constant pulse-rate acquisition. In particular, there can be up to twice as many projections in some bins when compared with the MIP solution - resulting in twice the delivered dose to the patient with sometimes poorer image quality. Conversely, some of the bins have too few projections resulting in very poor image quality and unusable images.
7 Limitations and future research

In this work we have focussed on the development of a MIP to optimise the timing and angle of projections in response to a patient breathing trace. We assumed the gantry to have the characteristics of conventional machines, that is, move unidirectionally, and at a constant speed.

Future work will investigate whether this optimisation can be further improved for next-generation gantries able to move multi-directionally and with variable speed. This will also involve optimising the gantry trajectory in order to realise a multi-directional movement and ensure constraints on velocity and acceleration are satisfied. For tumours located in the mediastinum, close to both the diaphragm and heart, optimising image acquisition for dual respiratory and cardiac motion will be developed.

8 Acknowledgements

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References


