Registration of temporal sequences of coronal and sagittal MR images through respiratory patterns

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\textbf{A R T I C L E  I N F O}

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\textbf{A B S T R A C T}

This work discusses the determination of the breathing patterns in time sequence of images obtained from magnetic resonance (MR) and their use in the temporal registration of coronal and sagittal images. The registration is made without the use of any triggering information and any special gas to enhance the contrast. The temporal sequences of images are acquired in free breathing. The real movement of the lung has never been seen directly, as it is totally dependent on its surrounding muscles and collapses without them. The visualization of the lung in motion is an actual topic of research in medicine. The lung movement is not periodic and it is susceptible to variations in the degree of respiration. Compared to computerized tomography (CT), MR imaging involves longer acquisition times and it is preferable because it does not involve radiation. As coronal and sagittal sequences of images are orthogonal to each other, their intersection corresponds to a segment in the three-dimensional space. The registration is based on the analysis of this intersection segment. A time sequence of this intersection segment can be stacked, defining a two-dimension spatio-temporal (2DST) image. The algorithm proposed in this work can detect asynchronous movements of the internal lung structures and lung surrounding organs. It is assumed that the diaphragmatic movement is the principal movement and all the lung structures move almost synchronously. The synchronization is performed through a pattern named respiratory function. This pattern is obtained by processing a 2DST image. An interval Hough transform algorithm searches for synchronized movements with the respiratory function. A greedy active contour algorithm adjusts small discrepancies originated by asynchronous movements in the respiratory patterns. The output is a set of respiratory patterns. Finally, the composition of coronal and sagittal image pairs that are in the same breathing phase is realized by comparing of respiratory patterns originated from diaphragmatic and upper boundary surfaces. When available, the respiratory patterns associated to lung internal structures are also used. The results of the proposed method are compared with the pixel-by-pixel comparison method. The proposed method increases the number of registered pairs representing composed images and allows an easy check of the breathing phase.

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1. Introduction

The lung presents some characteristics that do not allow direct observation, as it collapses if the thoracic cage is opened. The movement of the lung is passive, and it is the result of the movement of other parts of the body, such as the diaphragm and the thoracic cage. The use of internal organ imaging devices is the only way for lung visualization.

Current pulmonary diagnostic methods are lacking in many ways. Spirometry and pulmonary function tests only provide global measures of lung function. High-speed X-ray CT systems are under development and allow the visualization of three-dimensional descriptions of internal structures in time as described by Mori et al. [1]. Currently, various techniques for modeling the lung motion during breathing exclusively based on CT imaging, have been proposed aiming at concentrating a prescribed dose to the tumor and minimizing radiation to surrounding normal tissue [2–5].
field of view (FOV) of the lung, however, makes the repeated use of
those systems prohibitive due to the high radiation exposition.
Independent of the used imaging device, the images obtained
from internal organs suffer from some characteristic imperfections,
as images are generated in an indirect form, pixel intensities derive
from volume averaging, resulting in heterogeneous intensities, low
resolution and low signal to noise ratio (SNR). The direct conse-
quence of this severe imaging limitation is that often the boundaries
of internal organs are not closed, as some parts are not visible,
and therefore disconnected. Mangard and Hammersberg [6] de-
veloped a method to determine the detectability limits for a high-
resolution CT.

Considering the safety of the subjects under observation, MR
devices are preferable. On the other hand, MR imaging is hampered
by several challenges: the low amount of tissue relates to a small
number of protons leading to low signal, countless air–tissue inter-
faces cause substantial susceptibility artifacts, and respiratory and
cardiac motion cause blurred imaging [7,8]. MR signal is generated
from protons within water molecules and organic material. The
lung parenchyma contains only about 800 g of tissue and blood
which is distributed over a volume of 4–6 l. Proton density and
signal intensity are therefore extremely low compared to other
parts of the body. The quick motion of body structures during mea-
surements results in inconsistencies in phase and amplitude of
magnetization, such as the pulsatile movement of fluid inside the
vessels. This magnetization disturbance affects the imaging of those
structures, making them visible only at some time instants (blur-
rning and ghosting). Balanced steady-state free-precession (SSFP)
sequences such as the TrueFISP sequence are particularly suited
for lung MRI because of their high SNR efficiency [8]. SNR effi-
ciency is the ratio of SNR to the square root of total imaging time.
The TrueFISP high SNR efficiency compared to other conventional
sequences such as the TrueFISP sequence are particularly suited
for acquiring artifact-free time sequence images using navigator
echoes that are placed on the dome of the hemidiaphragm, and
the position of the diaphragm is monitored to determine the infla-
tion level. Singh et al. [17] used dynamic MRI sequences to create a
4D representation of the swallowing process, in which sagittal and
coronal slices were registered in time.

The imaging of respiratory motion can be classified as two main
approaches: the static approach that uses standard sequence types,
which are applied during repeated breath-holds to gather images in
different respiratory positions; and the fast imaging approach that
captures images during free breathing. The second approach is used
herein. A three-dimensional animated model is created by com-
posing several coronal and sagittal slices. The composition is made
according to some specific rules: the diaphragmatic surface and the
upper boundary must match and both images must be in the same
inhalation/exhalation phase. Whenever possible, the matching of
some internal lung structures are also considered.

2DST images are segmented through respiratory patterns. In
order to be able to determine respiratory patterns in time sequences
of MR images, even in frames where it is not visible, the as-
sumption that the diaphragmatic movement is the principal
movement in the chest was made. Then, all the lung-related struc-
tures do move almost synchronously, and the synchronization is
performed through a pattern named standard respiratory function
[14,18,19]. An interval Hough transform searches for movements
synchronized with the standard respiratory function. The interval
Hough transform propagates the input errors, mainly related to the
discreteness of the image and of the accumulator matrix [20,21]. A
greedy active contour algorithm adjusts small discrepancies in the
tracking. The sagittal and coronal images are three-dimensionally
composed by comparing the respiratory patterns originated from
the diaphragmatic and upper boundary surfaces.

This paper is structured as follows. Section 2 explains back-
ground concepts: the standard respiratory function and the
modified Hough transform. Section 3 explains the developed sys-
tem in which the interval Hough transform and the greedy active

Fig. 1. Samples of MR images: (a) sagittal image and (b) coronal image.
Fig. 2. Two disjoint intersecting images from the same lung. The mismatch is more evident on the contour of the diaphragmatic surface. The intersection between the images is a line segment.

contour algorithm are used. Section 3 also explains the proposed registration algorithm based on respiratory patterns. Section 4 presents some results and the conclusions are in Section 5.

2. Background

Fig. 1(a) shows an example of MR sagittal image and Fig. 1(b) shows a coronal image. These two images were taken at different instants in time. A powerful registration method is necessary, because each image of each slice is taken at a different time instant, with the lung at different stages of the inflating/deflating process. This situation is illustrated in Fig. 2 where two disjointed intersecting images (coronal and sagittal) of the lung are shown. This work is a step towards the development of such a powerful registration algorithm.

2.1. Standard respiratory function

A time sequence of MR images from a slice of the lung can be stacked, defining a spatio-temporal volume (STV) \( I(x, y, t) \) where \( x \) and \( y \) are the coordinates of each pixel of the image and \( t \) is the time. Fig. 3 shows an example of a STV, built from 10 coronal images from the same slice of the lung taken at different time instants. Consider the definition of an arbitrary vertical plane \( Q_s(x_s, y_s) \) that passes on point \( (x_s, y_s) \) and it is parallel to the \( t \) axis. The intersection of the STV \( I(x, y, t) \) with \( Q_s(x_s, y_s) \) defines a 2D spatio-temporal (2DST) image as illustrated in Fig. 4. The 2DST image \( F_s(t, y_s) \) corresponds to the intersection of the STV \( I(x, y, t) \) with \( Q_s(x_s, y_s) \). Fig. 5 shows a vertical 2DST image. It is possible to notice that a motion pattern is present, especially because the moving organs are healthy lungs and the heart. The lung movement has lower frequency and higher amplitude, and the heart movement has higher frequency and lower amplitude.

In the specific case of MR images, the optical flow analysis [22] is not well suited as it is known that the accuracy of the estimation
The lung movement is detected first using an interval Hough transform to determine the presence of motion synchronous with a respiratory pattern up to a scale and an offset. Therefore, each point is supposed to move in time according to this fundamental respiratory pattern of the lung-related structures in the 2DST image. The standard respiratory function is an input to the Hough transform; the 2DST image is on the left and the quantization space is on the right. A respiratory pattern in the 2DST image is mapped as a cell in the quantization space.

2.2. Hough transform as a tool to find respiratory patterns

The Hough transform is a feature extraction technique used in image analysis, computer vision and digital image processing [24]. Usually, it is used for detecting straight lines and curves. The purpose of the technique is to find imperfect instances of patterns within a certain class of shapes through a voting procedure. A modified Hough transform was proposed to determine the presence of respiratory patterns \( f_k(t) \) in 2DST images by Matsushita et al. [19].

Each point is supposed to move in time according to this fundamental respiratory pattern up to a scale and an offset. Therefore, the movement in time of each point is described by the following equation:

\[
y = af_k(t) - b \tag{1}
\]

where \( a \) and \( b \) are the scale and the offset of \( f_k(t) \), respectively. The search for respiratory patterns \( f_k(t) \) can be summarized as being the identification of a large set of pairs \((a, b)\) on as many 2DST images as possible from a given STV.

An edge image is determined from the 2DST image using a gradient filter [25]. A respiratory pattern is therefore completely specified by a parameter pair \((a, b)\). For the respiratory pattern detection, the Hough transform maps each edge pixel \((t, y)\) from the 2DST image into the quantized space of \((a, b)\), in which contributions from each feature point to each possible set of \((a, b)\) are evaluated. For this purpose, the quantized space is divided into cells, with each cell corresponding to a pair of quantized \((a, b)\). A multi-dimensional array is used to represent the quantized space.

Every feature point \((t, y)\) in the 2DST edge image represents a line in the quantized space, the corresponding cells of the accumulator are incremented accordingly. This is repeated for all feature points. Every cell in the quantized space maps a respiratory pattern in the 2DST image.

Hence, the intensity of each pixel \((a, b)\) in the parameter space is proportional to the probability to find a scaled and biased respiratory function in the 2DST edge image. Fig. 7 shows two pixels from the 2DST image mapped to two lines in the quantized space. These two lines intersect at a cell in the quantized space, this cell is mapped to a respiratory pattern in the 2DST image. The quantization process determines that the cell with the highest intensity represents a respiratory pattern with most confidence, supposing that such a cell \((a_1, b_1)\) represents the following respiratory pattern:

\[
y = a_1f_k(t) - b_1 \tag{2}
\]

To proceed with the search for other pairs, it is supposed that no intersecting respiratory pattern is allowed. The negatively re-sampling process removes all possible intersecting respiratory patterns with the just found respiratory pattern. The negatively re-sampling process can be defined by noting that \( f_k(t) \) is enclosed by the interval \([0, f_{\text{max}}]\), which defines the angular coefficient limits of the line shown in expression (2). This way, every line crossing \((a_1, b_1)\) in the quantization space with angular coefficient within the interval \([0, f_{\text{max}}]\) must have their pixels intensities set to zero in the quantization space (see Fig. 8). The intensity of every pixel belonging to the region that was just negatively re-sampled, represents a respiratory pattern that intersects the just found respiratory pattern. As all intersecting respiratory patterns have been removed, a new peak can be found in the quantization space and the negatively re-sampling is again executed. This process is repeated as many times as necessary. This algorithm fails in some special situations and detects incoherent respiratory patterns. Considering the following example, the incoherent respiratory pattern pointed by an arrow in Fig. 9(a) was determined by the high intensity cell.
Fig. 8. The region that must be negatively re-sampled is shown in green. This region encloses all lines that go through the cell with highest intensity selected by the algorithm and has angular coefficient inside the interval \([0, f_{\text{max}}]\). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

indicated by an arrow in the quantization space shown in Fig. 9(b).

Appendix A explains the modified Hough transform through some mathematical manipulations.

3. Proposed system

The proposed system searches for an image in a coronal sequence that best registers a given sagittal image, and vice-versa. The proposed system consists of three main modules as shown in Fig. 10. In the first module, the sagittal to coronal mapping is determined. This mapping defines the intersection between the coronal and sagittal images. In the second module, 2DST coronal and sagittal images at the intersection line are obtained and a modified interval Hough transform is applied to determine respiratory patterns. In the third module, the respiratory patterns found are used to register coronal and sagittal images.

3.1. Coronal–sagittal mapping

A pixel in a MR image can be mapped to the three-dimensional space by using the DICOM mapping matrix [14]; however, this matrix is not invertible. Thus, a three-dimensional point in the space cannot be mapped to the MR image. This work solves this problem by defining a pseudo inverse. The pixels contained in a DICOM image can be mapped to the three-dimensional space according to the following:

\[
\begin{bmatrix}
 p_x \\
p_y \\
p_z
\end{bmatrix}
= \begin{bmatrix}
 x_x \cdot \Delta_i & y_x \cdot \Delta_i & 0.0 & s_x \\
x_y \cdot \Delta_i & y_y \cdot \Delta_i & 0.0 & s_y \\
x_z \cdot \Delta_i & y_z \cdot \Delta_i & 0.0 & s_z
\end{bmatrix}
\cdot
\begin{bmatrix}
 i \\
j
\end{bmatrix}
= [M] \cdot \begin{bmatrix}
 i \\
j
\end{bmatrix}
\]  

where \(p_x, p_y, p_z\) are the three-dimensional coordinates associated to pixel \((i, j)\), \(x_x, y_x, x_z\) and \(x_y, y_y, x_y\) are the row \(x\) direction cosine of the image orientation, \(y_x, y_y, y_z\) and \(x_z\) are the column \(y\) direction cosine of the image orientation. \(\Delta_i\) is the column pixel spacing and \(\Delta_j\) is the row pixel spacing. \(s_x, s_y, s_z\) are the start position for the first

Fig. 9. (a) An incoherent respiratory pattern detected by the modified Hough transform is pointed by an arrow. (b) The quantization space is shown and the relevant respiratory pattern \(f_i(t) = (a, b)\) is pointed by an arrow.

Fig. 10. The developed system architecture with the three main modules: extract mapping matrix, determine edges by interval Hough and active contour and temporal registration and three-dimensional visualization.
voxel. Usually, coronal images have a bigger value for $\Delta_i$ and $\Delta_j$ when compared to sagittal images from the same subject. Considering that the number of pixels in the image is constant and equal to $256 \times 256$, the pixel spacing is closely connected to the fov (field of view) parameter.

The sagittal and the coronal images have a common line segment, and the pixels of such a line segment that are in the coronal and sagittal images, respectively $(i_c,j_c)$ and $(i_s,j_s)$, occupy the same three-dimensional space:

$$P_s = [M_s] \cdot \begin{bmatrix} i_s \\ j_s \\ 0 \\ 1 \end{bmatrix} = [M_c] \cdot \begin{bmatrix} i_c \\ j_c \\ 0 \\ 1 \end{bmatrix} = P_c \quad (4)$$

where $[M_s]$ and $[M_c]$ are the sagittal and coronal mapping matrix, respectively. It is possible to isolate one of the pixel coordinates. Given a pixel $(i_c,j_c)$ in the coronal image belonging to the intersection line, the corresponding pixel $(i_s,j_s)$ in the sagittal image is given by

$$\begin{bmatrix} i_s \\ j_s \\ 0 \\ 1 \end{bmatrix} = [M_c]^{-1} \cdot [M_s] \cdot \begin{bmatrix} i_c \\ j_c \\ 0 \\ 1 \end{bmatrix}. \quad (5)$$

---

**Fig. 11.** Edge determination by interval Hough and active contour module. The interval Hough transform corresponds to the following modules: create the edge image, create quantization space, select the brightest pixel and negatively re-sample the respiratory pattern.

**Fig. 12.** The interval Hough transform; the 2DST image is on the left and the quantization space is on the right. A pixel in the 2DST image is mapped as a band line in the quantization space.

**Fig. 13.** (a) The 2DST image and the respiratory pattern found by the modified Hough transform (above), and the respiratory pattern found by the interval method (below). (b) The quantization space and the relevant respiratory pattern for the modified Hough transform. (c) The quantization space and the relevant respiratory pattern for the interval Hough transform.

**Fig. 14.** A respiratory pattern resulting from the interval Hough transform. The active contour algorithm searches in the vertical adjacency of the pixels belonging to the respiratory pattern, for a position with smaller energy.
However, matrix $[M_s]$ has no inverse, as it has a column filled with zeros (the same is true for matrix $[M_c]$). Another information that must be observed is the fact that in the two-dimensional space, coordinate $z$ has no meaning and can be considered as a void. Hence, it is possible to modify the values of the third column of matrixes $[M_s]$ and $[M_c]$, allowing it to have an inverse. Considering that $x_{sc} = x_{sc} = y_{sc} = y_{sc} = 0.0$ for sagittal images and $x_{ic} = x_{ic} = y_{ic} = y_{ic} = 0.0$ for coronal images, a row in matrixes $[M_s]$ and $[M_c]$ can have only zeros, respectively the first and second rows. The following matrixes are defined:

$$[M^*_s] = \begin{bmatrix}
0.0 & 0.0 & 1.0 & s_{xs} \\
x_{ys} \cdot \Delta_{js} & 0.0 & 0.0 & s_{ys} \\
x_{ys} \cdot \Delta_{js} & 0.0 & 0.0 & s_{ys} \\
0.0 & 0.0 & 0.0 & 1.0
\end{bmatrix}$$

(6)

and

$$[M^*_c] = \begin{bmatrix}
x_{xc} \cdot \Delta_{ic} & 0.0 & 0.0 & s_{xc} \\
0.0 & 0.0 & 1.0 & s_{yc} \\
0.0 & y_{xc} \cdot \Delta_{jc} & 0.0 & s_{xc} \\
0.0 & 0.0 & 0.0 & 1.0
\end{bmatrix}$$

(7)

Matrixes $[M^*_c]$ and $[M^*_s]$ are invertible. The mapping is defined by matrixes $[M^*_c]^{-1} \cdot [M_c]$ and $[M^*_s]^{-1} \cdot [M_s]$. The mapping is used to determine the vertical line in a coronal image that corresponds to a sagittal image and vice-versa.

### 3.2. Edge determination by interval Hough transform and active contour

As shown in Fig. 5, in a chest MR image, the lungs and the heart are moving organs. The movement of the lung has higher amplitude and lower frequency when compared to the movement of the heart.
Initially, the interval Hough transform determines the presence of motion synchronous with breathing. The respiratory pattern found is processed by a greedy active contour algorithm that adjusts asynchronous discrepancies. This algorithm is an improvement of the work proposed by Tavares et al. [26]. The proposed algorithm is shown in Fig. 11. The active contour algorithm is integrated as a step in the interval Hough transform algorithm.

3.2.1. Interval Hough transform

Usually, image processing algorithms assume that a pixel represents an exact location. In practice, discreteness prevails; in the input stage, the data is obtained from a discrete domain (for example, by MR scanners). In the quantization stage, the algorithm is computed using an accumulating matrix that is discrete. However, it is theoretically supposed to be continuous. In this scenario, the algorithm that does not take into account the discreteness of the system often fails with severe consequences. Every pixel ([x], [y]) in the image is represented by an interval pair [27,28]:

$$([x - 0.5, x + 0.5], [y - 0.5, y + 0.5])$$

and its intensity is represented by an interval [I - 0.5, I + 0.5]. Fig. 12 shows that every feature interval ([t], [y]) in the 2DST edge image represents a band line in the quantized space. Consider that the value of the offset interval [b], for a given [a], is determined by the following expression:

$$[b] = ([a][f_k(t)] - [y])$$

where ([t], [y]) is the feature interval. The resulting value of [b] corresponds to an interval. The pair interval ([a], [b]) defines a rectangle representing the area that must be incremented with the pixel ([t], [y]) edge intensity. Usually, this rectangle does not fit the quantization space grid. When a complete cell in the quantization space is internal to the resulting interval [b], then that cell is incremented by the intensity of pixel ([t], [y]). In the case of a partial intersection, the cell is incremented by a value proportional to the intersecting area. This algorithm is very similar to an anti-aliasing algorithm [29]. The resulting quantization space is much smoother than the previous approach. Fig. 13(b) shows the quantized space calculated by the modified Hough transform, and Fig. 13(c) shows the quantized space calculated by the interval Hough transform. Both approaches determine distinct cells with the highest intensity.

The cell with the highest intensity represents a respiratory pattern band. The resulting respiratory function is determined by the following algorithm. In the case in which the band encloses its middle pixel, the middle pixel is selected. Otherwise, the pixel with the largest area intersection is selected. Instead. To proceed with the search for other pairs, the greedy active contour algorithm is applied to the just found respiratory pattern; then, the respiratory pattern resulting from the active contour algorithm is negatively re-sampled and a new peak in the quantization space may be found. It is important to observe that the negatively re-sampling is performed considering the discreteness of the mapping. This process continues until a reasonable number of respiratory patterns have been detected.

3.2.2. Active contour algorithm

Active contour, also called snakes, are splines guided by external and internal forces [23]. The forces attract the spline to pixels with higher gradient and keep the spline continuous until second derivative. An adaptation from a greedy active contour algorithm was used herein [30]. The respiratory pattern that resulted from the interval Hough transform is the initial condition for the greedy active contour algorithm. A respiratory pattern $f_k(t)$ is a set of pixels with only one pixel for every vertical line (see Fig. 14). It is given by

$$f_k(t) = \{y_0, y_1, \ldots , y_n\}$$

where $0 \leq t \leq n$ and $n$ is the number of frames. The energy function to be minimized is defined as

$$E(f_k(t)) = E_{int}(f_k(t)) + E_{image}(f_k(t))$$

![Fig. 17.](image1) ![Fig. 18.](image2)
Fig. 19. (a) and (b) Coronal image has a vertical line showing where a 2DST image was taken. The interval Hough transform found 21 respiratory patterns and only 3 patterns were selected for the temporal registration. (c) and (d) Sagittal image has a vertical line showing where a 2DST image was taken. The interval Hough transform found 21 respiratory patterns and only 4 respiratory patterns were selected for the temporal registration. (e) One example that resulted from the temporal registration.

Fig. 20. (a) Graphs for all 50 sagittal images and their pixel distance compared to the 7th coronal image. (b) Total distance for all 50 sagittal images when compared to the 7th coronal image. (c) Graphs for all 50 coronal images and their pixel distance compared to the 36th sagittal image. (d) Total distance for all 50 coronal images when compared to the 36th sagittal image. (e) Graph comparing the distance pixel-by-pixel between the 36th sagittal image and the 7th coronal image. (f) Graph comparing the distance pixel-by-pixel between the 36th sagittal image and the 28th coronal image.
where $E_{\text{int}}$ is the internal energy and it is defined by

$$E_{\text{int}}(f_k(t)) = \frac{1}{2} \left( \alpha \left| \frac{\partial f_k(t)}{\partial t} \right|^2 + \beta \left| \frac{\partial^2 f_k(t)}{\partial t^2} \right|^2 \right)$$

(10)

where $\alpha$ and $\beta$ are positive parameters. $E_{\text{image}}$ is the term that pulls the respiratory pattern to the pixels with higher intensity in the edge image. The edge image is obtained by applying a gradient filter to the original image. It is defined by

$$E_{\text{image}}(f_k(t)) = -\frac{\gamma}{\sigma(f_k(t))} |\nabla I(f_k(t))|$$

(11)

where $\gamma$ is a positive parameter, $\sigma(f_k(t))$ is the average of the intensity of pixels composing the respiratory pattern (original image) and $\nabla I(f_k(t))$ is the respiratory pattern edge pixels intensity average (edge image).

The greedy algorithm analyzes the odd verticals in sequence and later the even verticals in sequence. In the search of a respiratory pattern with smaller energy, the vertical adjacency of each pixel of the actual respiratory pattern is analyzed. The process is repeated until no change occurs. Fig. 15 shows the result of the greedy active contour algorithm after the interval Hough transform. It was empirically observed that the contribution of the image component $E_{\text{image}}(f_k(t))$ has a greater influence in the final result than the derivative components. It was chosen to keep the ratio $\gamma/\alpha = \gamma/\beta > 1.0$ constant. The values adopted in this study were $\alpha = 0.7$, $\beta = 0.7$ and $\gamma = 1.2$.

### 3.3. Temporal registration

A lung structure that intersects the coronal and sagittal sequence of images at the intersecting segment can be used in the temporal registration algorithm. The surfaces defined by diaphragm and the upper boundary (apex) are used in this work. The diaphragm has a movement with larger amplitude and a large gradient. The packing and unpacking of the alveoli during inhalation and exhalation causes surface tension to decrease and increase in a way that produces the characteristic hysteresis of the lungs. Hysteresis means that the inflation of the lung follows a different pressure/volume relationship from deflation [31]. Then, respiration has two phases: inspiratory and expiratory.

Consider the example shown in Fig. 16 where the diaphragmatic surface of three lung images (one coronal and two sagittal) have the same level at the intersection segment. However, Fig. 16(a) and (c) are in the exhalation phase, and Fig. 16(d) is in the inhalation phase. The 2DST images shown in Fig. 16(b) and (e) are 2DST images of the intersection line between the coronal and sagittal images. Fig. 17(a) and (b) shows that the diaphragmatic surface contained in coronal and sagittal images have the same level at the intersection segment. A medical expert checked both possibilities and
asserted that Fig. 17(a) is the correct composition without knowing the respiratory phase of the images. Indeed, in the case of Fig. 17(a), both images, coronal and sagittal, are in the same exhalation phase.

The respiratory phase associated to the image can easily be obtained by processing the standard respiratory functions extracted from the sequence of images. The influence of the upper boundary (apex) was observed to be minimal because of the small amplitude of the movement.

The interval Hough transform is an algorithm based on the intensity of the gradient image; the number of respiratory patterns necessary to detect the diaphragmatic movement can vary. The upper boundary of the lung (apex) has a much lower intensity when compared to the diaphragm; consequently, the number of respiratory patterns necessary to be detected, ensuring that the upper boundary is contained in the detected set, is much larger.

Very few lung internal structures intersect the 2DST image from sagittal images. The vessels and bronchi are mainly perpendicular to the sagittal images [8]. Fig. 18(a) shows a sagittal image with a vertical line where the 2DST image was taken. Several respiratory patterns are external to the lung, and are not used in the temporal registration. The modified Hough transform detects the presence of respiratory patterns in situations defined by the composition of different internal lung structures. Fig. 18(c) has arrows to show some respiratory patterns originating from distinct lung internal structures. Such respiratory patterns must not be used in the temporal registration. In turn, several lung internal structures intersect the 2DST image from coronal images. It was also observed that the upper boundary (apex) and diaphragmatic surface move with a difference in phase of 180°.

The respiratory patterns to be used in the temporal registration are manually selected. The diaphragmatic surface and the upper boundary (apex) create identifiable respiratory patterns in all 2DST images. These two respiratory patterns and the respiratory phase must coincide for a correct registration. Additionally, the respiratory patterns uniquely originated from one internal lung structure can be used in the temporal registration algorithm, even if the structure cannot be identified in the other type of image, coronal or sagittal.

4. Results and discussion

The sequences of MR images used in the experiment were obtained by Symphony (1.5 T) made by Siemens, using the method true Fast Imaging with Steady-State Precession (FISP). The MR images were taken from six healthy non-smoking subjects. Table 1

<table>
<thead>
<tr>
<th>Case</th>
<th>Fov–cor (mm)</th>
<th>Fov–sag (mm)</th>
<th>Total time (s)</th>
<th>Age</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>420 × 420</td>
<td>380 × 380</td>
<td>17</td>
<td>31</td>
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<tr>
<td>C</td>
<td>420 × 420</td>
<td>380 × 380</td>
<td>11</td>
<td>24</td>
</tr>
<tr>
<td>D</td>
<td>450 × 450</td>
<td>450 × 450</td>
<td>27</td>
<td>58</td>
</tr>
<tr>
<td>E</td>
<td>420 × 420</td>
<td>380 × 380</td>
<td>11</td>
<td>50</td>
</tr>
<tr>
<td>F</td>
<td>450 × 450</td>
<td>450 × 450</td>
<td>11</td>
<td>28</td>
</tr>
</tbody>
</table>
shows some characterization of the subjects. The initial images in dynamic data sets were acquired in the transient state of the magnetization; thus they have different signal intensity and contrast. The analysis considered all acquired images, including the initial images. Fig. 19 shows an example of result in which the interval Hough transform found 21 respiratory patterns and only 3 and 4 respiratory patterns were respectively selected in the coronal and sagittal 2DST images.

Stevo et al. [32] compared vertical lines of the 2DST images using two different approaches: pixel-by-pixel and discrete Fourier transform. The same temporal sequences shown in Fig. 16 are used to explain some results obtained by the pixel-by-pixel comparison approach. Fig. 20(a) shows a graph with pixels in the horizontal and pixel intensity in the vertical. There are 50 overlapping graphs and each graph compares the 7th coronal image (represented by the red line in Fig. 16(b)) to one sagittal image contained in its temporal sequence of images. Each graph represents the difference between the pixel intensities in a pixel-by-pixel form. It is possible to observe that all pixels between rows 0–60 show almost no variation in time. The coronal and sagittal sequences present some differences in the pixel intensities as a consequence of their setups.

Fig. 20(b) shows a graph where 50 sagittal images are represented in the horizontal and the vertical has average pixel distance. The graph represents the pixel intensity difference average between the 7th coronal image and all the 50 sagittal images. A 2DST vertical from Fig. 16(e) with similar pixel intensities to the red vertical line represented in Fig. 16(b) is represented with low pixel intensity difference average. In this example, the 36th sagittal image has the smallest average distance in pixel intensity, and no idea about the existence of other possibilities can be retrieved.

Similarly, Fig. 20(c) and (d) shows graphs comparing the 36th sagittal image with all the 50 coronal images in the temporal sequence. Fig. 20(d) shows that the 28th and 45th images have smaller pixel intensity difference average than the 7th image, and the pair with the smallest pixel difference average is the 28th coronal and the 36th sagittal. However, the pair 7th coronal and 36th sagittal, previously obtained from the graph in Fig. 16(b), is also a possibility. Fig. 21(a) and (b) shows the three-dimensional composition of both pairs of images. However, in some specific situations, it is not possible to determine a pair of images with reasonable pixel intensity difference average. Even worse, it is not possible to determine if the desired image is in between two images. The discrete Fourier transform showed similar results.

Fig. 22 shows three graphs obtained using the proposed approach. It is represented the difference between the diaphragmatic level of a specific coronal (sagittal) image and the respiratory pattern determined in the sagittal (coronal) temporal sequence of images. The same situations analyzed in Fig. 22(a)–(f) is represented here. When the graph intersects the x-axis, a perfect match of the diaphragmatic surfaces occurs. The respiratory phase is very clear in the resulting graphs. Considering the graph associated with the 7th coronal image, the registration occurs with sagittal images 3 and 36. These two pairs of images register perfectly. Also, a possible registration exists between sagittal images 17 and 18. Fig. 23(a)–(d) shows some additional registration pairs.

The temporal registration algorithm proposed in this work has better results than the algorithms proposed by Stevo et al. [32]. The approaches proposed by Stevo et al. are based on less elaborated processing algorithm solely considering the intensity of the pixels that are strongly affected by the blurring and ghosting. The temporal registration algorithm proposed here uses high level information about the structures of the lung and determines images that exclusively make a perfect composition. The proposed approach detected a larger number of registration pairs and allow the determination of a possible registration pair between two consecutive images in the temporal sequence.

Several authors make strong assumptions about the regularity of the respiratory motion and parameterize this motion with a one-dimensional displacement or phase, very similar to the standard respiratory function proposed here. Although respiration clearly shows a repetitive character, the reduction of the respiratory organ deformation to a single parameter neglects all residual variability and may be a too coarse approximation in some cases. This leads to artifacts in the reconstructed images and considerable uncertainties [33–36].

von Siebenthal [37] tracked liver vascular structures present on sagittal images during complete breathing cycles, and used a navigator slice that contained vessels cross-sections that are distributed over the entire slice of the liver and that are easily trackable. He tracked the motion of the liver vascular structures in the two-dimensional space. Several authors used a similar approach to track lung internal structures in image sequences obtained from CT [5,38–40], and it was not possible to find a similar approach for images of the lung obtained from MR.

The approach proposed here has the confidence that the diaphragmatic and upper boundary can be correctly composed in the correct breathing phase. When available in both images (coronal and sagittal), internal lung structures are also correctly composed. One drawback is the fact the respiratory patterns of interest must be manually selected from the set obtained from the interval Hough transform.

5. Conclusions

A method for three-dimensional animated reconstruction using sagittal and coronal MR images acquired during free breathing is proposed here. Several sagittal and coronal slices are composed. An important requirement for the developed imaging technique was the capability to handle and visualize the variability of organ motion. Whilst most imaging methods were developed for diagnostic purpose and acquire only a few breathing cycles, the MR approach described here is intended to acquire detailed 4D data...
Appendix A. Understanding the modified Hough transform

Considering the following variable substitution \( r = f(t) \), Eq. (1) can be rewritten as follows:

\[
y = ar - b
\]

where \( r \) is an integer and belongs to the interval \([0, f_{\text{max}}]\). This is a typical Hough transform, in which straight lines are detected. Fig. A.24 shows the Hough transform after the variable substitution. However, depending on \( f(t) \), some values between 0 and \( f_{\text{max}} \) may not be present. The variable substitution \( r = f(t) \) corresponds to vertical lines rearrangement. As asserted previously, \( f(t) \) is supposed to correspond to a respiratory pattern with approximately the maximum amplitude (a vertical 2DST is chosen and it is around the middle of the lung).

Supposing that the pair \((a_1, b_1)\) has been selected with the highest intensity cell. The extreme points of the mapped segment is given by

\[
r = 0 \Rightarrow y = -b_1, \quad r = f_{\text{max}} \Rightarrow y = a_1 f_{\text{max}} - b_1
\]

Then the minimum value for \( y \) is given by

\[
y_{\text{min}} = \begin{cases} 
-a_1 & \text{if } a_1 \geq 0 \\
\frac{a_1 f_{\text{max}} - b_1}{f_{\text{max}}} & \text{if } a_1 < 0
\end{cases}
\]

and the maximum value for \( y \) is given by

\[
y_{\text{max}} = \begin{cases} 
-a_1 & \text{if } a_1 \geq 0 \\
\frac{a_1 f_{\text{max}} - b_1}{f_{\text{max}}} & \text{if } a_1 < 0
\end{cases}
\]

The line segment goes through \((a_1, b_1)\) and is enclosed in the interval \([y_{\text{min}}, y_{\text{max}}]\), and the respiratory pattern is also enclosed in such an interval. The negatively re-sampling is shown in Fig. A.25; every line crossing a selected cell \((a_1, b_1)\) in the quantization space with angular coefficient inside the interval \([0, f_{\text{max}}]\) must be negatively re-sampled.

References


