Partial Volume Artifact in MITS Reconstructed Digital Chest Tomosynthesis

Dániel Hadházi, Gábor Horváth
Department of Measurement and Information Systems
Budapest University of Technology and Economics
Budapest, Hungary
Email: {hadhazi, horvath}@mit.bme.hu

***Abstract*—Matrix Inversion Tomosynthesis (MITS) is a linear shift invariant MIMO system that deconvolves the X-ray projections that are acquired in tomosynthesis arrangement. As MITS theoretically models the examined volume by finite, zero thin slices, it has a special effect called partial volume artifact. This paper describes the basics of the MITS reconstruction and the theory of the analyzing of the reconstruction using Modulation Transfer Function (MTF) in detail. The dependency of the partial volume artifact on the number of reconstructed slices is analyzed using MTF and illustrated by slice images. Based on our results reconstructing more than 350 slices is suggested in the case of imaging a 250 mm thick volume.**

Keywords—chest tomosynthesis; MITS; MTF; partial volume artifact

I. Introduction

Digital chest tomosynthesis is a relatively new imaging modality that computes reconstructed slice images from a set of low-dose X-ray projections acquired over a limited angle range by a flat panel detector [1]. Theoretically this modality is equivalent to a limited angle Cone-beam CT. Tomosynthesis was originally developed for breast screening, however nowadays it is starting to be applied in clinical chest screening purposes, too. In this article linear chest tomosynthesis is examined, where the basic arrangement is illustrated by Fig. 1.

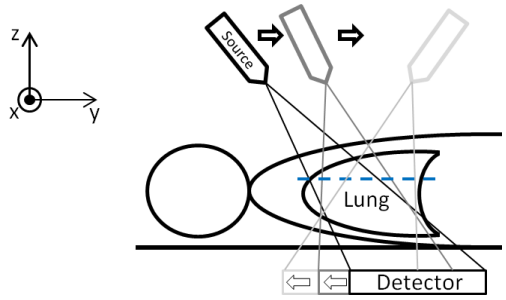

Fig. 1. Schematic arrangement of linear chest tomosynthesis.

In linear chest tomosynthesis arrangement the X-ray source and the flat panel detector move continuously in parallel along the *y* axis in opposite directions. During the motion about 50 projection images are acquired from different positions. According to the figure, the acquired images are located in the *x*-*y* plane, where the rows of the images are parallel with the *x* axis, and the columns of the images are parallel with the *y* axis. From these projections the coronal slices of the 3D examined volume (in our case mainly the lung) are reconstructed (one of them is illustrated by the blue dashed line in the figure). This paper focuses on the partial volume artifact in the case of using Matrix Inversion Tomosynthesis (MITS) algorithm [2] for reconstruction. MITS, which is described in the second section in detail, deconvolves the projections of the coronal slices from the X-ray projections. In the third section the transfer function based analysis of the reconstruction is presented, in section IV the partial volume problem and a possible technique of its treatment is described. Finally in section V conclusions are discussed, and the required number of slices to avoid the artifact caused by the partial volume problem in the case of chest tomosynthesis reconstructed by MITS is determined.

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II. Matrix Inversion Tomosynthesis

In the case of tomosynthesis, the projection images can be modelled as the sum of shifted projections of infinitesimally thin slices of the examined volume [2]. In the special case of linear tomosynthesis arrangement, shifting is always along the *y* axis, and the amount of shifting can be expressed analytically as a function of the geometry of the projections' scanning arrangement (illustrated by Fig. 2.) that is detailed later.

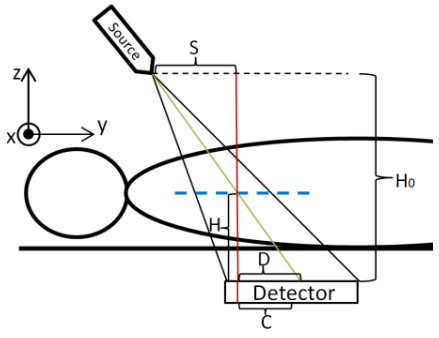

Fig. 2. Projection geometry of linear chest tomosynthesis

In the figure the trajectory of the X-ray beam source is denoted by the black dashed line, and the examined slice is marked by the blue dashed line (*H* denotes its distance from the detector). The red line marks the *x*-*z* plane located at *y*=0, the green

line models the projection beam of the center (x=y=0) of the examined slice (its intersection with the detector's surface is at x=0, y=D). The distance between the detector's surface and the beam's trajectory is denoted by H_0, and the position of the beam source is $(x, y) = (0, S)$, and the center of the detector is at $(x, y) = (0, C)$. The projection of the examined slice is shifted parallel to the y axis, the displacement compared to the situation where the y position of the beam source is 0, and the center of the detector is at $y = 0$, is:

$$D - C = \frac{H \cdot S}{H - H_0} - C \tag{1}$$

Due to the linear tomosynthesis arrangement the shift along the x axis is always zero, so for different x values the intensity profiles can be processed independently of each other as one-dimensional functions of y. Hereafter we will call projections the continuous intensity profiles of the 2D X-ray projection images, that located parallel to the y axis at fixed x positions. These projections are:

$$\begin{aligned} i^{(h)} &= \sum_k \left(r^{(k)} * f_{(k,h)} \right) \\ f_{(k,h)}(x) &= \delta\left(x - D_{(k,h)} \right) \end{aligned} \tag{2}$$

where $i^{(h)}$ denotes the h-th X-ray projection, $r^{(k)}$ denotes the central projection of the k-th modelled slice and $*$ denotes convolution. Central projection means the projection where both the beam source and the detector are at $y = 0$ position, while in modelled slices we mention the non-empty slices (every other slices of the volume presumed empty). $f_{(k,h)}$ is the weight function between the k-th modelled slice and the h-th acquired projection, while the $D_{(k,h)}$ is defined by (1).

The goal of the MITS algorithm [2] is to deblur the conventional Shift And Add (SAA) [3] reconstructed slices. The SAA algorithm is equivalent to the conventional back projection (in the case of linear tomosynthesis), apart from that the outputs of the SAA reconstruction are the projections of the reconstructed slices. The SAA can be modeled as a MIMO linear shift invariant system:

$$\begin{aligned} t^{(h)} &= \sum_h \left(i^{(h)} * f'_{(k,h)} \right) \\ f'_{(k,h)}(x) &= \delta\left(x + D_{(k,h)} \right) \end{aligned} \tag{3}$$

where $t^{(h)}$ denotes the h-th SAA reconstructed slice projection. Based on (2) and (3) the SAA reconstructed slice projections can be expressed as the function of the central projections of the modeled slices:

$$t_j^{(k)} = \sum_h \left(\sum_l r_j^{(l)} * f_{(l,h)} \right) * f'_{(k,h)} \tag{4}$$

The MITS algorithm calculates the estimation of the projections of the modeled slices by deblurring the SAA reconstructed slice projections. As MITS is designed to invert a linear shift invariant MIMO system, it can be derived more easily in spectral domain.

By applying Fourier transform to the second rows of (3) and (2), it is obtained that:

$$FT_\omega\left\{ f_{(k,h)}(x) \right\} = \exp\left(-2\pi j \cdot \omega \cdot D_{(k,h)} \right) = \overline{FT_\omega\left\{ f'_{(k,h)}(x) \right\}} \tag{5}$$

where $\bar{x}$ denotes the complex conjugate of x, and $FT_\omega\{\ \}$ denotes the operator of 1D continuous Fourier transform at ω frequency, j denotes the imaginary unit. Based on this observation (2) and (3) are equivalent to the following:

$$\begin{aligned} \hat{\mathbf{i}}(\omega) &= \mathbf{F}(\omega) \cdot \hat{\mathbf{r}}(\omega) \\ \hat{\mathbf{t}}(\omega) &= \mathbf{F}(\omega)^* \cdot \hat{\mathbf{i}}(\omega) \end{aligned} \tag{6}$$

where $\hat{\mathbf{i}}(\omega)$ denotes a column vector containing the spectral components of the input projections at ω frequency. Similarly $\hat{\mathbf{r}}(\omega)$ is the column vector of the spectrum of the projection of the modeled slices and $\hat{\mathbf{t}}(\omega)$ is the column vector of the spectrum of the SAA reconstructed slice projections at ω frequency. $\mathbf{F}(\omega)$ denotes the projection matrix, where its elements are defined by:

$$\mathbf{F}(\omega)_{(i,j)} = FT_\omega\left\{ f_{(j,i)} \right\} \tag{7}$$

where $\mathbf{A}_{(i,j)}$ denotes the (i, j)-th element of the $\mathbf{A}$ matrix.

By substituting the first equation into the second equation of (6), the spectral representation of (4) is derived:

$$\hat{\mathbf{t}}(\omega) = \mathbf{F}(\omega)^* \cdot \mathbf{F}(\omega) \cdot \hat{\mathbf{r}}(\omega) \tag{8}$$

The SAA reconstructed slice projections can be expressed as a function of the slice projections (based on (6)):

$$\mathbf{F}(\omega)^* \cdot \hat{\mathbf{i}}(\omega) = \mathbf{F}(\omega)^* \cdot \mathbf{F}(\omega) \cdot \hat{\mathbf{r}}(\omega) \tag{9}$$

Therefore deblurring the SAA reconstructed slice projections is equivalent to inverting the system described by the first row of (6):

$$\hat{\mathbf{r}}_j(\omega) = \mathbf{F}(\omega)^\dagger \cdot \hat{\mathbf{i}}_j(\omega) \tag{10}$$

where $\mathbf{F}(\omega)^\dagger$ denotes the pseudo inverse of the projection matrix, $\hat{\mathbf{r}}_j(\omega)$ denotes the estimation of $\hat{\mathbf{r}}_j(\omega)$. From this point of view the MITS can be interpreted as a Maximum Likelihood estimation, formally:

$$\hat{\mathbf{r}}_j(\omega) = \arg\max_{\mathbf{x}} \left\{ \Pr\left(\hat{\mathbf{i}}(\omega) \middle| \mathbf{x} \right) \right\} \tag{11}$$

where $\Pr(\mathbf{y}|\mathbf{x})$ is defined by a multivariate Gaussian distribution, with the expected value of $\mathbf{F}(\omega)\cdot\mathbf{x}$, and the covariance matrix of $\sigma^2\cdot\mathbf{I}$, where $\sigma\in\mathbb{R}^+$.

The theory described previously is valid if and only if special conditions are fulfilled. The three most significant conditions are: (*) $FT_\omega\{\cdot\}$ denotes continuous Fourier transform. In digital signal processing the spectrum can be calculated by discrete Fourier transform (DFT). The problem of under-sampling can be avoided by using a detector for image acquisition with sufficiently high resolution. The distortion caused by spectral leakage can be reduced by sufficiently modifying the projections before calculating the reconstruction. The second (**) assumption is that $\mathbf{F}(\omega)$ should be well-, or over-determined, otherwise numerical problems can significantly decrease the quality of the MITS reconstructed slices. As it is shown in [4] - mainly in low frequencies - this condition is always violated and causes numerical sensitivity of the reconstruction. The third (***) assumption is connected to (2) and (4). These equations are adequately modelling the reality if and only if the volume modelled by an infinite number of infinitesimal thin slices ($r^{(k)}$-s). However this can't be realized which causes artifact. As a similar effect in PET and CT modalities is called partial volume effect [7] we will call it as partial volume artifact of tomosynthesis. This paper focuses on this problem, while the other two problems will be examined in forthcoming publications.

III. Transfer Functions of the Reconstruction

As it is given by (10), MITS is considered as a shift invariant linear multiple input–multiple output (MIMO) system. Therefore MITS is characterized in the spatial frequency domain by its transfer function. The transfer function is determined from the reconstruction of the noise-free simulated projections of a so called wire phantom. This phantom contains an infinitesimally thin wire, whose points are defined along a 1D line:

$$\begin{aligned} y &= x\cdot\tan(\theta)\\ z &= x\cdot\tan(\alpha)\cdot\sqrt{\tan^2(\theta)+1}+z0 \end{aligned} \tag{12}$$

where θ denotes the angle between the perpendicular projection of the wire to the $z=0$ plane, and the $z=y=0$ lines. α denotes the angle between the wire and the $z=0$ plane, $z0$ denotes the offset of the wire along the z axis. The value of $z0$, α and θ define the part of the 3D space which reconstruction can be examined by this analysis. The position of the projection of the wire along the x axis is (independently of the positions of the beam source and the center of the detector along the y direction):

$$p(z)=\frac{H_0-z}{H_0}\cdot\frac{z-z0}{\tan(\alpha)\cdot\sqrt{\tan^2(\theta)+1}} \tag{13}$$

Let $\mathbf{R}^{(i)}$ denote the projection of the i-th reconstructed slice calculated by MITS from the projections of the wire. Due to invertibility of $p(l)$ $\mathbf{R}^{(i)}_{(:,p(l))}$ is the weight function between the projection of the plane of the examined volume located at $z=l$ and the *i*-th reconstructed slice. From this reconstruction the transfer functions of the MITS reconstruction can be calculated:

$$\begin{aligned} \mathbf{O}^{(i)}_{(\omega,l)} &= DFT_\omega\left\{\mathbf{R}^{(i)}_{(:,p(l))}\right\}\\ \mathbf{M}^{(i)}_{(\omega,l)} &= \left|\mathbf{O}^{(i)}_{(\omega,l)}\right| \end{aligned} \tag{14}$$

where $\mathbf{O}^{(i)}_{(:,l)}$ denotes the optical transfer function (OTF) of the reconstruction of the slice located at $z=l$, while $\mathbf{M}$ denotes the modulation transfer function (MTF) of the reconstruction. Fig. 3. illustrates $\mathbf{M}^{(i)}$ as an intensity image.

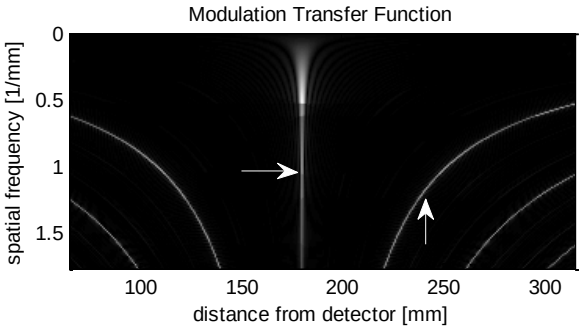

Fig. 3. MTF of a MITS reconstructed slice. The horizontal arrow points to the main lobe, which determine the height of structures reconstructed as in-plane signal. The vertical arrow points to leakage from distant planes.

IV. Partial Volume Artifact

According to [5] the number of the reconstructed slices should not be more than the number of the projections, however our previously published results confirmed that the number of the reconstructed slices can be increased without decreasing the quality of the reconstruction [6]. In the case of chest tomosynthesis typically 40-60 projections are acquired, the angular range of projections is limited to ±20°, and the total thickness (extension along the *z* axis) of the examined volume is not less than 250 mm. If only a few (e.g. 60), evenly spaced slices of the volume are reconstructed there will remain parts of the volume that have not been reconstructed in any slice, mainly in higher frequencies. Fig. 4 illustrates the main lobe of the aggregated MTF of two adjacent slices in the case of 60 (in the upper picture) and in the case of 400 (in the lower picture) reconstructed slices. The aggregated MTF is:

$$\mathbf{M}'^{(i)}=\max\left\{\mathbf{M}^{(i)},\mathbf{M}^{(i+1)}\right\} \tag{15}$$

where $\max\{\cdot,\cdot\}$ denotes the elementwise maximum operator.

From the figure it is clearly visible that if only 60 slices are

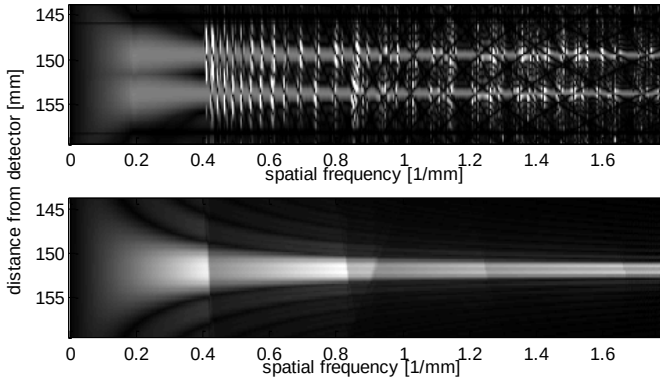

Fig. 4. Central lobe of a typical aggregated MTF of adjacent reconstructed coronal slices. In the case of the upper picture 60 slices are reconstructed, while in the case of the lower 400 slices are reconstructed from the same projections.

mm from the detector are not reconstructed into any of their two enclosing slices at >0.4 1/mm frequencies. In the second case (400 slices are reconstructed) such a problem did not occurred. Fig. 5. shows reconstructions of an ideal spherical artificial chest nodule (with the diameter of 3.5 mm) located at an anthropomorphic phantom. The visibility (therefore the detectability) of the nodule is significantly lower in the case of 60 slices compared to the case of 400 slices. This phenomenon is not the same, but similar to the so called partial volume artifact [7], therefore we use the same term.

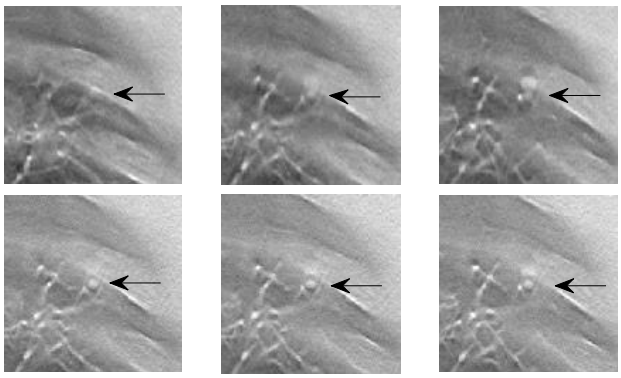

Fig. 5. Adjacent 3 slices of the same reconstructed volume. In the upper row 60 slices, in the lower row 400 slices were reconstructed. The arrows point to the nodule's reconstruction.

V. Results and Discussions

The accumulated extent of the parts of the examined volume which is not reconstructed by any of the slices as in-plane signal (not covered by the union of the main lobes of the reconstructed slices' MTF) at a given spatial frequency is:

$$V_{(\omega)} = \left(H - \sum_i \int f_{(\omega,i)}(l) \cdot g_{(i)}(l)\, dl \right) \Big/ (2H) \qquad (16)$$

where H denotes the thickness (extent along the *z* axis) of the examined volume, $g_{(i)}(l) = ind\left(h(i-1) \le l \le h(i+1)\right)$ and $f_{(\omega,i)}(l)$ is defined by the full width half maximum principle:

$$f_{(\omega,i)}(l) = ind\left(\mathbf{M}^{(i)}_{(\omega,p(l))} \ge \max_{p(h(i-1)) \le v \le p(h(i+1))} \left\{ \mathbf{M}^{(i)}_{(\omega,v)} \right\} \Big/ 2 \right) \qquad (17)$$

$ind(\cdot)$ denotes the logical indicator function. Its value is 1 if and only if its argument is true, else it is zero. Based on our observations $V_{(\omega)}$ significantly depends on the number of reconstructed slices. v as the function of spatial frequency (denoted by ω) and as the function of the number of the reconstructed slices is illustrated by Fig. 6.

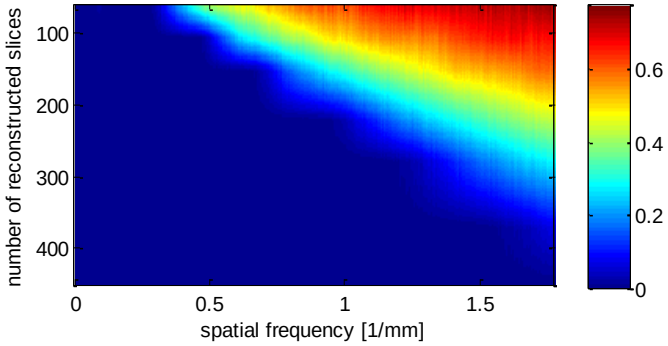

Fig. 6. The relative extent of the volume, which is not reconstructed as in-plane signal by any of the slices as a function of the spatial frequency and the number of reconstructed slices.

From the figure we can conclude that to compute approx. 350-400 slices is necessary in order to completely avoid the problem of partial volume in the case of chest tomosynthesis reconstructed by the MITS algorithm. The recommended minimum number of the slices depends on the thickness of the examined volume and the thickness of the reconstructed slices. This concrete result corresponds to 250 mm thick chests reconstructed by the previously described MITS algorithm. For linear shift invariant reconstruction methods the optimal parameters of the reconstruction in the sense of minimizing the partial volume artifact can be determined by the previously described MTF based method.

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