Clinical Implementation of MITS Reconstruction for Linear Tomosynthesis

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Abstract—Tomosynthesis is an X-ray based tomographic modality, which calculates slice images of the examined volume from a set of low dose projection images acquired over a limited scan angle. Due to the limited scan angle, the reconstruction is an extremely ill-posed inverse problem. Therefore, many artefacts degrade the calculated slice images in the case of any reconstruction method. If linear, shift invariant system based algorithm reconstructs these slices, they can be interpreted by utilizing linear systems theory. MITS [1] is one of the most adequate of these methods; although its clinical implementation is not trivial. This paper examines the main difficulties of its clinical implementation from both theoretical and practical viewpoints, proposes modifications to treat these and compensate the possible artifacts (i.e. the intensity oscillation artifact, the partial volume artifact and the effects caused by the low condition of the inverse problem). The proposed modifications preserve the linear, shift invariant nature of the reconstruction, therefore, the reconstruction after applying the proposed modifications, can also be interpreted by analyzing its Transfer Function. The paper also describes the method of this interpretation. A clinical implementation of a linear tomosynthesis system is used for validating the proposed, modified MITS algorithm. The paper concludes that, based on this validation, the proposed modifications significantly decrease the artifacts of the MITS in practical utilization and improve the quality of the reconstructed slice images, while the whole reconstruction remains interpretable (which mean, that we exactly know how any voxel of a reconstruction depend on the internal structure of the examined volume).

Index Terms—tomographic reconstruction, inverse problem, linear tomosynthesis, Matrix Inversion Tomosynthesis

I. INTRODUCTION

DIGITAL tomosynthesis (DTS) is a relatively new X-ray based imaging modality, which can fill the gap between the classical X-ray Radiography (XR) and the Low Dose Computed Tomography (LDCT) modalities. The cost of a DTS examination is app. half, the effective radiation exposure is not more than tenth compared to an LDCT imaging test. The DTS calculates slice images of the examined volume similarly to the LDCT, therefore, its diagnostic value is significantly higher compared to the XR [2]. Although there is no free lunch, the reconstruction problem of the DTS is significantly harder both practically and theoretically compared to the LDCT.

DTS reconstructs coronal slices of the examined volume from a set of low dose X-ray projection images, which are acquired by a flat panel detector over a limited total scan angle (Fig. 1.). Due to the limited angle, the projections do not contain enough information for the reconstruction (the projection images provide measurements from not more than 5% of the spectrum of the sagittal slices of the examined volume, based on the Fourier Slice theorem). Therefore, the whole problem to be solved is an extremely badly conditioned linear MIMO inverse problem:

\[ p = H \cdot r \]  

where \( p \) is the serialized intensities of the acquired projection images, \( H \) is the projection matrix, \( r \) is the serialization of the linear X-ray attenuation coefficient of the examined volume. This model utilizes the Beer-Lambert law, during the reconstruction the value of \( r \) is estimated.

Fig. 1. Geometric arrangement of linear tomosynthesis in chest screening. The detector and the X-ray beam moves continuously in the opposite direction during the image acquisition. A coronal plane is marked by the blue dashed line. The total scan angle cannot be more than 80° in the case of chest imaging.

MITS (Matrix Inversion Tomosynthesis) [1] utilizes the internal structure of \( H \) and in the case of linear tomosynthesis, it reformulates (1) to the MIMO system:

\[ p^{(j)}(\omega) = H(\omega) \cdot r^{(j)}(\omega) \]  

where \( p^{(j)}(\omega) \) is the vector, which stacks the spectral components of the \( j \)-th column of the projection images at \( \omega \) frequency, while \( r^{(j)}(\omega) \) is the similarly defined vector stacked from the \( j \)-th column of the central projection of the coronal slices. The reconstruction calculated by the MITS can be reformulated to the following expression:
\[ \hat{r}^{(i)}(\omega) = \mathbf{H}(\omega)^\dagger \cdot \mathbf{p}^{(i)}(\omega) \]  

where \( \mathbf{A}^\dagger \) is the Moore Penrose pseudo inverse of \( \mathbf{A} \), \( \hat{r} \) is the estimation of \( \mathbf{r} \), therefore, we can conclude that MITS calculates the maximum likelihood estimation of \( \mathbf{r} \) with the assumption of additive i.i.d. Gaussian observation noise.

II. IMPROVING CLINICAL IMPLEMENTATION OF MITS

The previously described model assumes continuous signals, infinitesimal thin slices and well-conditioned \( \mathbf{H} \) matrices. Because the projection images are digital signals and the limited total scan angle, the first and the third assumptions are never met. The second assumption requires infinite number of modelled slices, which is also impossible.

A. Truncation artifacts

The utilization of DFT for the estimation of (3) causes ringing artifacts in the reconstructed slices. The problem would not occur, if the columns of the projection images (\( \mathbf{p} \)) were circular. This is not true in practice. We proposed a quadratic programming (QP) based method, which extrapolates the projections by minimizing the energy of the derivative of the extrapolated projection images (we adapted [3] to the MIMO system of tomosynthesis). Because the QP contains only equality constraints, the result can be calculated by:

\[ \mathbf{p}'^\dagger = \mathbf{\Gamma} \cdot \mathbf{p} \]  

where \( \mathbf{p}' \) is the extrapolated projections, \( \mathbf{\Gamma} \) is a block matrix. The modification compensates the high frequency artifacts, while it does not degrade \( \mathbf{r} \) in low frequencies.

B. Noise sensitivity

Due to the limited scan angle, the \( \mathbf{H}(\omega) \) matrices are extremely badly conditioned in low frequencies (e.g. at \( \omega = 0 \) its every element is the same). The projections are also noisy. Therefore, we propose the following Tikhonov regularization:

\[ \hat{r}^{(i)}(\omega) = (\mathbf{H}(\omega)^\dagger \mathbf{H}(\omega) + \lambda \mathbf{I})^{-1} \mathbf{H}(\omega)^\dagger \mathbf{p}^{(i)}(\omega) \]  

which is equal to assuming a Gaussian prior on each \( \mathbf{p}(\omega) \).

We used \( \lambda = 1 \) for every \( \omega \). The proposed regularization takes effect only in low frequencies (i.e. \( \leq 0.1 \) cycles / mm). It significantly decreases the low frequency intensity oscillations without increasing the thickness of the reconstructed slices - its extent along the in-depth direction (marked by \( z \) in Fig. 1).

C. Partial volume artifact

By utilizing the Tikhonov regularization, we are able to reconstruct more coronal slices, than the number of input projection images. This is preferred, because (2) assumes infinitesimally thin slices. In order to examine the caused artifacts first examine the transfer function (TF) of the MITS:

\[ \mathbf{S}(\omega) = \mathbf{H}(\omega) \cdot \mathbf{H}'(\omega) \]  

where \( \mathbf{H}'(\omega) \) models significantly more slices compared to \( \mathbf{H}(\omega) \). \( \mathbf{S}(\omega)_{(i,j)} \) is the transfer function between the \( i \)-th reconstructed and \( j \)-th projected coronal slice. Due to the TF of adjacent reconstructed slices, there remain parts of the examined volume (at higher, \( \geq 0.5 \) cycles / mm), which are not reconstructed by the calculated slices, if its number is less than 350. Due to the previously described modifications, we can calculate these slices in less than 1 minute. Based on test scans from physical phantom, this can significantly increase the visibility of small structures, e.g. early stage nodules.

III. DISCUSSION AND CONCLUSIONS

This paper presents the most important difficulties of the MITS algorithm in a clinical DTS system. The proposed modifications (which extend the ones described by [4]) can treat these difficulties without causing any artifacts, while the shift invariant, linear nature of the whole reconstruction is also preserved. Therefore, the TF based analysis (6) of the reconstruction remains utilizable. Due to it; we can exactly know the transfer between tissues located at any height of the examined volume and any reconstructed slice at any spatial frequency. This also implies the robustness and the stability of the proposed reconstruction, which is generally not true for any iterative reconstruction method (e.g. deep learning based ones).

We validated the proposed modifications by qualitative tests. In these tests real tomosynthesis scans are examined from living patients and an anthropomorphic chest phantom. Based on these tests, the previously described artifacts are eliminated, which implies high quality of the reconstruction.

REFERENCES


