

Abstract: Deep Residual Learning for Limited Angle Artefact Correction

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Using non-conventional scan trajectories for Cone Beam (CB) imaging promise low dose interventions and radiation protection to the personal [1]. The here investigated circular tomosynthesis yields good image quality in two preferred directions, but introduces limited angle artefacts in the third. The artefacts become more severe, the smaller the half tomo angle α gets. Han et al. have previously demonstrated the successful application of deep learning for streaking artefact correction in CT scenarios [2]. We have modified the U-Net to correct artefacts in circular tomosynthesis. 30 CBCTs and circular tomosynthesis scans of the Shepp-Logan phantom with different rotations and scalings were simulated using $\alpha \in \{25^\circ, 35^\circ, 45^\circ\}$. We use 12 scans for training and 18 for validation. The network is trained using reconstructed patches as inputs and the difference between tomosynthesis and CBCT as labels. Training is performed using the Adam optimizer with mini batches. For evaluation we calculate the normalized Root Mean Squared Error ($nRMSE$) of the phantom and the reconstructed data. The CBCT reconstructions achieved a $nRMSE$ of 0.0819 ± 0.0010 , while uncorrected circular tomosynthesis resulted in $nRMSE = 0.1048 \pm 0.0133$. On the training data the presented approach resulted in an average $nRMSE$ of 0.0797 ± 0.0071 which is similar to the value of the CBCTs. On the validation scans we achieved average $nRMSE$ reduction of 28% ($\alpha = 25$), 22% ($\alpha = 35$) and 12% ($\alpha = 45$) compared to the uncorrected circular tomosynthesis data. Conventional approaches such as total variation minimization become more insufficient with decreasing α which we also observed in our simulations. In conclusion our experiments have shown that deep learning can enhance circular tomosynthesis scans to a quality similar to CBCT.

References

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2. Han Y, Yoo JJ, Ye JC. Deep residual learning for compressed sensing CT reconstruction via persistent homology analysis. CoRR. 2016;abs/1611.06391.