

Deep Learning-Based Detector Row Upsampling for Clinical Spiral CT

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Windmill Artifacts in Multislice Spiral CT

- During backprojection in multislice spiral CT, an interpolation is performed between adjacent detector rows.
- Inadequate longitudinal sampling (not satisfying the Nyquist criterion) leads to so-called windmill artifacts.
- They are characterized by streaks diverging from a focal high-density structure.
- The streaks appear to rotate while scrolling through the affected slices.



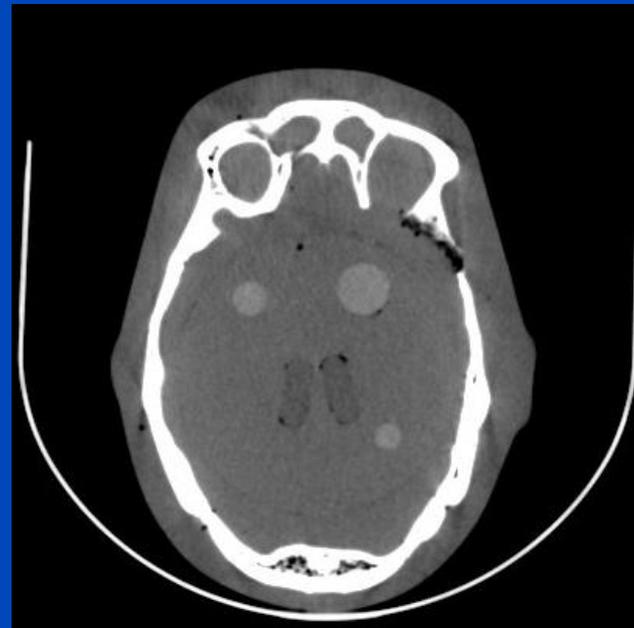
C = 0 HU, W = 200 HU;
collimation: 32×0.6 mm

Windmill Artifact Reduction

- Reducing windmill artifacts by reconstructing thicker slices leads to a reduction of the z-resolution of the reconstructed images.
- Other previous works focus on the reduction of windmill artifacts in image domain¹.
- The state of the art method called z-flying focal spot (zFFS) is hardware-based:



Without zFFS
collimation: 96x0.6 mm

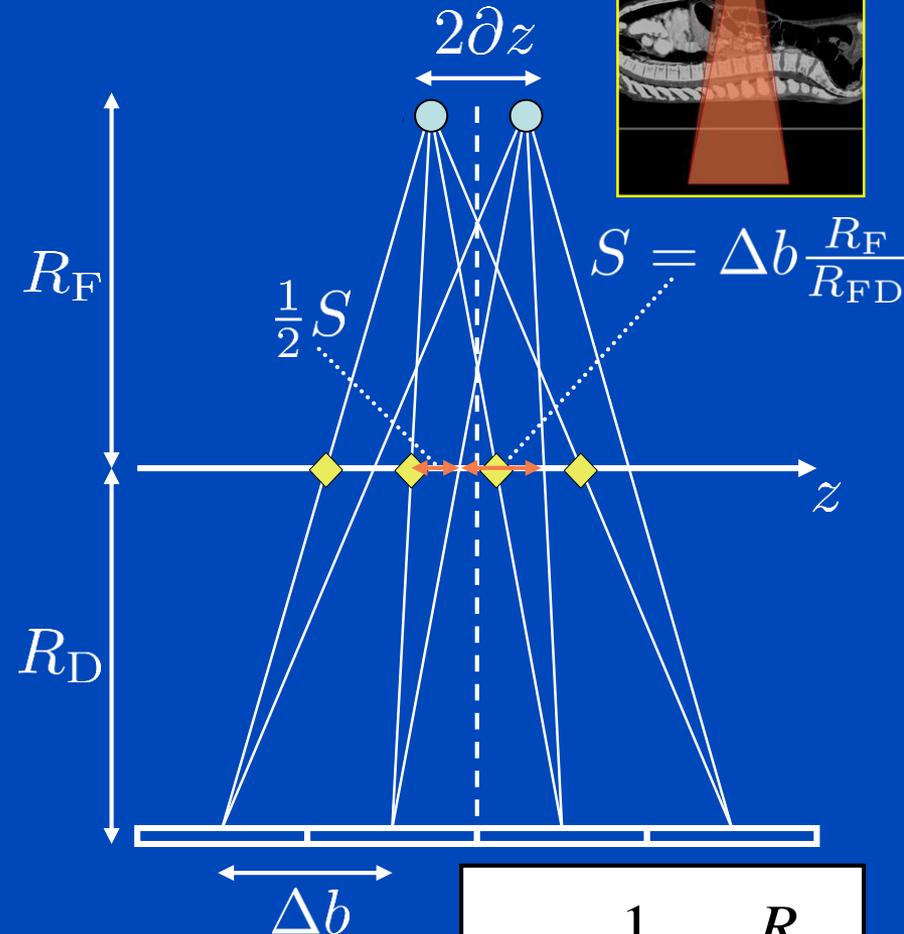


With zFFS
collimation: $2_{zFFS} \cdot 96 \times 0.6$ mm

C = 60 HU, W = 360 HU;
reconstructed
slice width 0.75 mm

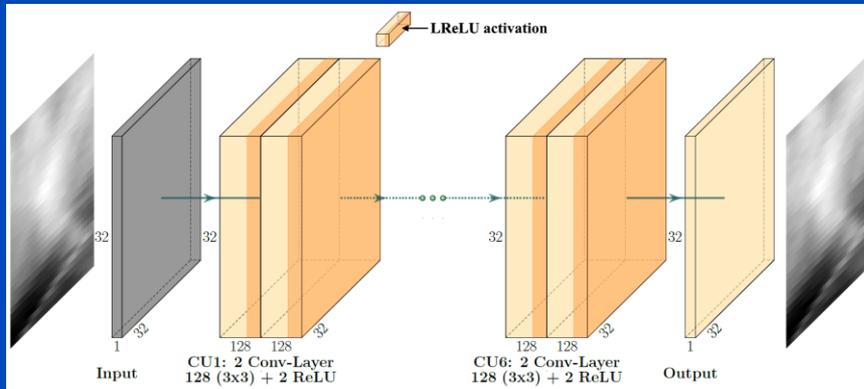
z-Flying Focal Spot (zFFS)

- The zFFS is a periodic motion of the focal spot in longitudinal direction.
- Two subsequent readings are slightly shifted in z-direction to achieve a doubled sampling distance in the isocenter.
- It is only included in high-end CT scanners and may not be available in the fastest scan mode.
- Provide a software-based approach that upsamples the projection data like the zFFS.
- Row interpolation with deep learning (RIDL)

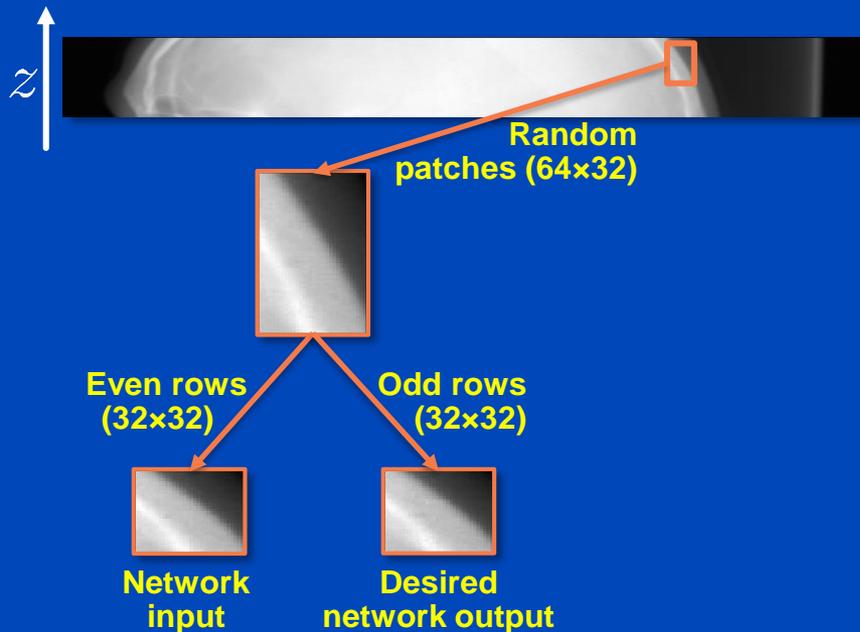


$$\partial z = \frac{1}{4} \Delta b \frac{R_F}{R_D}$$

RIDL-CNN



- Mapping from projection data without zFFS-rows to corresponding zFFS-like rows.
- Network input and output need to be interlaced after prediction to receive upsampled projection.
- Comparable results to RIDL-SRResNet² (presented at Fully3D conference 2021) could be achieved while reducing network complexity.
- Beside a clinical dataset we introduce an experimental synthetic dataset for network training.
- **Advantages of synthetic data:**
 - Any amount of training data with different structures can be simulated.
 - Noise-free simulation possible.
 - No CT scanner with zFFS required for training data acquisition.



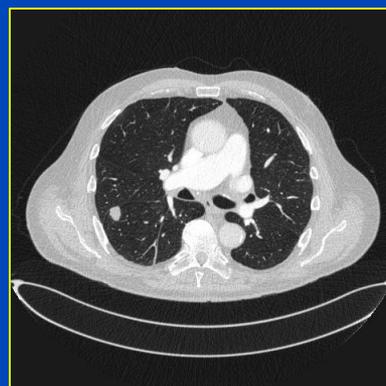
Training and Validation Data

Clinical Dataset

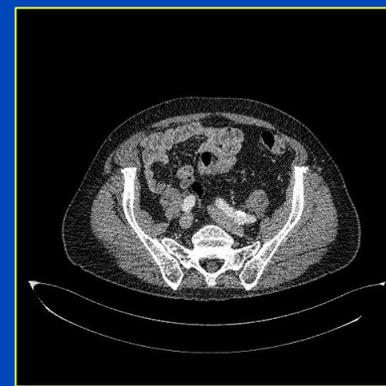
- Clinical dataset with projection data from patient spiral CT scans acquired with zFFS.
- Based on Somatom Definition Flash and Somatom Force scans from 40 patients.
- Projection data acquisition of clinical data after the rebinning.
- 32 scans for training (20 head; 8 thorax; 4 abdomen)
- 8 scans for validation (5 head; 2 thorax; 1 abdomen)



C = 60 HU, W = 360 HU



C = -400 HU, W = 1500 HU



C = 60 HU, W = 400 HU

Training and Validation Data

Synthetic Dataset

- Using the software package CT_Sim based on ray propagation simulation software Deterministic Radiological Simulation (DRASIM).
- Simulating water cylinder (parallel to z-axis) containing 100 randomly arranged spherical shells with varying densities (0.5 – 3.0 g/cm³)
- Water cylinder: length = 10 cm, diameter = 40 cm, density 1.0 g/cm³
- Shell diameter range: 1 – 20 cm; shell width range: 0.3 – 2.0 mm
- Simulated 200,000 noise-free projections (160,000 for training; 40,000 for validation)
- Value range of synthetic projection data was linearly scaled to the value range of the clinical dataset.
- Example projection of a simulated scan with a randomly generated phantom:



80 rows

800 channels

Training Details

- Trained two networks (RIDL CNN) with the clinical and noise-free synthetic dataset separately.
- Training and validation patches for both datasets:
 - 500,000 examples from the corresponding training set
 - 125,000 examples from the corresponding validation set

- Loss function proposed in ¹:

$$L_{\text{comb}}(y, \hat{y}) = \alpha \cdot L_{\text{MS-SSIM}}(y, \hat{y}) + (1 - \alpha) \cdot L_{\text{MAE}}(y, \hat{y})$$

- $\alpha = 0.84$, empirically determined
- Initial learning rate: 1×10^{-5} ; halved once the validation error could not be minimized for 25 epochs; batch size: 256; ADAM optimizer

Evaluation of Windmill Artifact Reduction

- Head phantom scans with real human bones.
- Scanned with Siemens Somatom Force system.
- Head phantom scan 1:
 - Collimation **96×0.6 mm**; acquired with zFFS; pitch = 1.0; 120 kV; reconstructed slice width: 1.0 mm
- Head phantom scan 2:
 - Collimation **48×1.2 mm**; **no zFFS available in this acquisition mode**; pitch = 1.0; 120 kV; reconstructed slice width: 1.5 mm

Results

Head Phantom Scan 1

Ground truth
with zFFS

Without zFFS

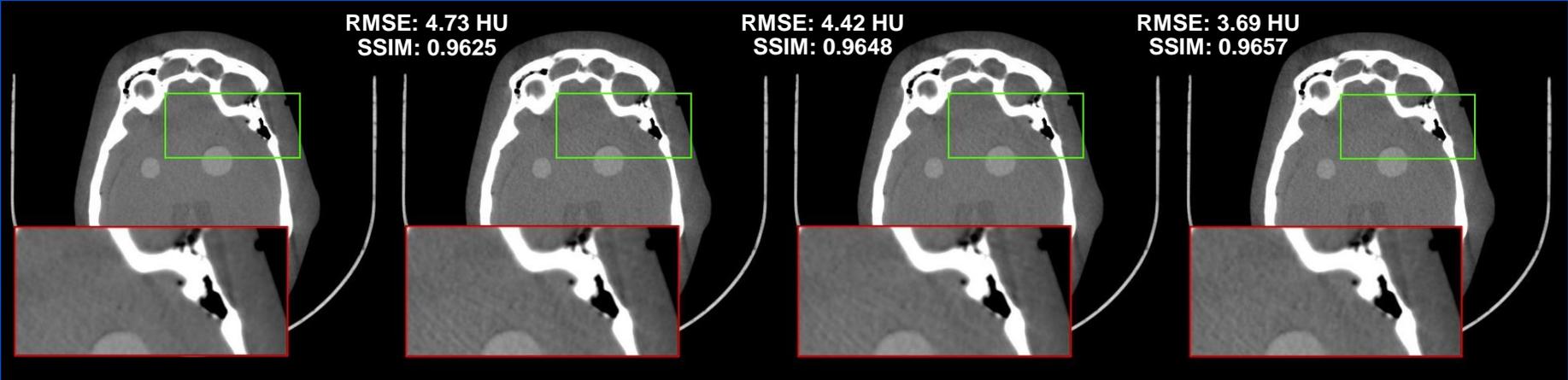
RIDL-CNN trained with
clinical dataset

RIDL-CNN trained with
synthetic dataset

RMSE: 4.73 HU
SSIM: 0.9625

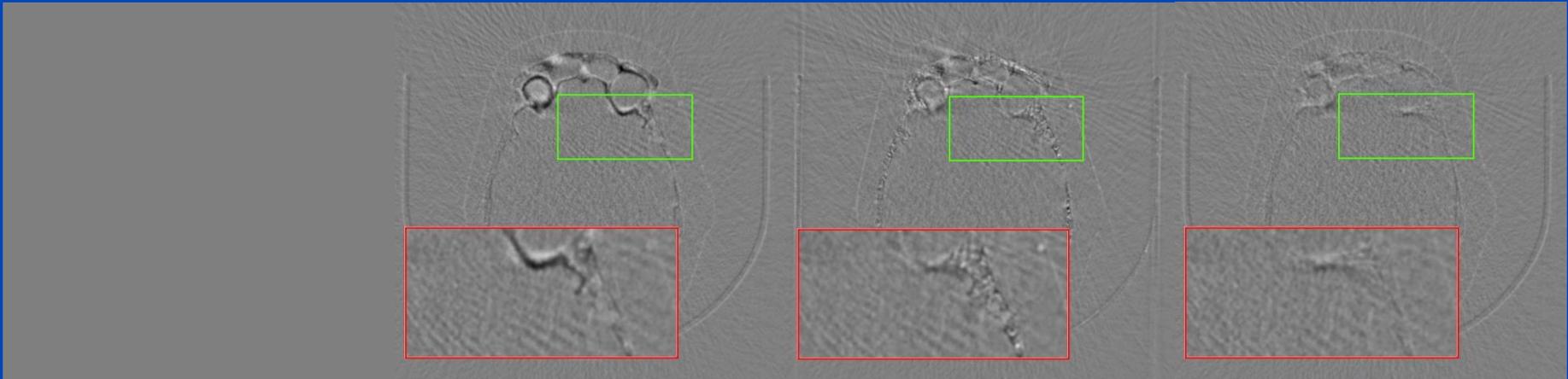
RMSE: 4.42 HU
SSIM: 0.9648

RMSE: 3.69 HU
SSIM: 0.9657



Slice 1

$C = 60$ HU, $W = 360$ HU; collimation: 96×0.6 mm;
reconstructed slice width 1.0 mm



$C = 0$ HU, $W = 150$ HU

Results

Head Phantom Scan 1

Ground truth
with zFFS

Without zFFS

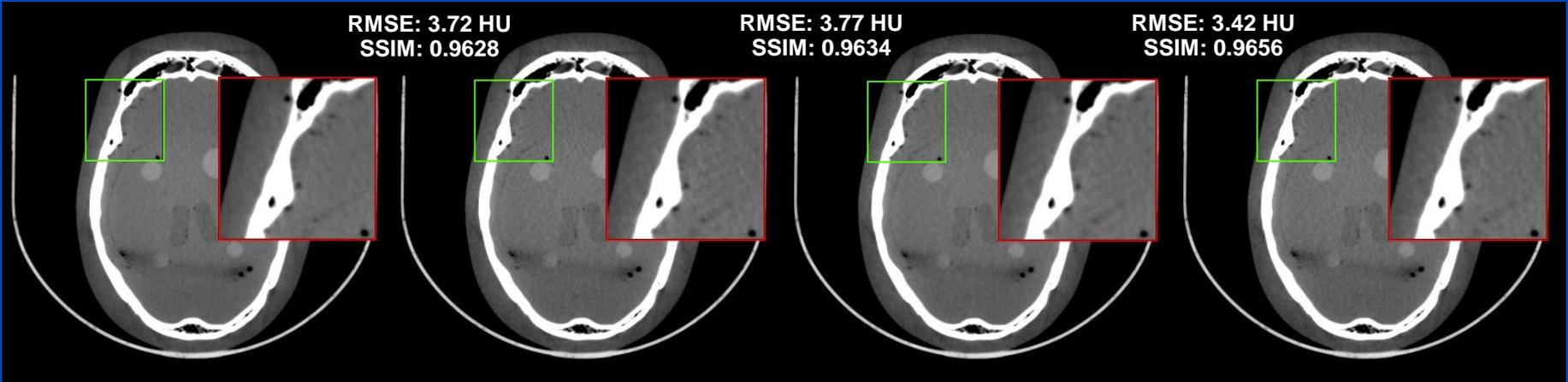
RIDL-CNN trained with
clinical dataset

RIDL-CNN trained with
synthetic dataset

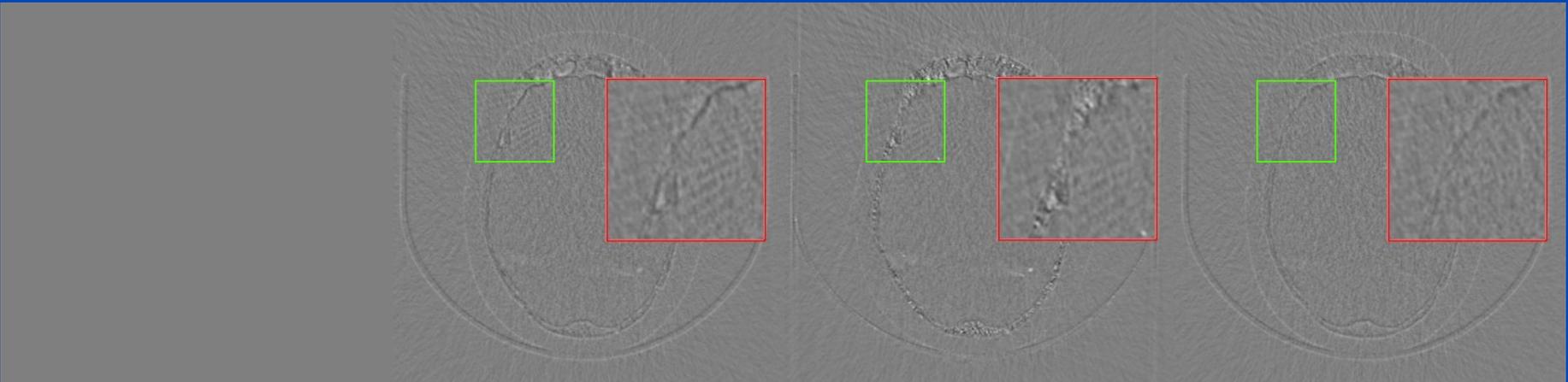
RMSE: 3.72 HU
SSIM: 0.9628

RMSE: 3.77 HU
SSIM: 0.9634

RMSE: 3.42 HU
SSIM: 0.9656



$C = 60$ HU, $W = 360$ HU; collimation: 96×0.6 mm;
reconstructed slice width 1.0 mm



$C = 0$ HU, $W = 150$ HU

Results

Head Phantom Scan 2

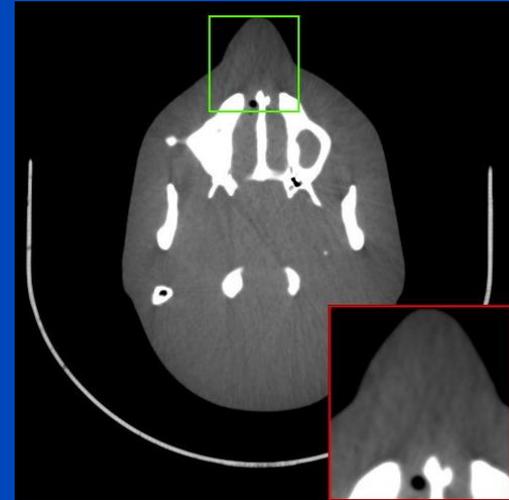
Standard WFBP
no zFFS available



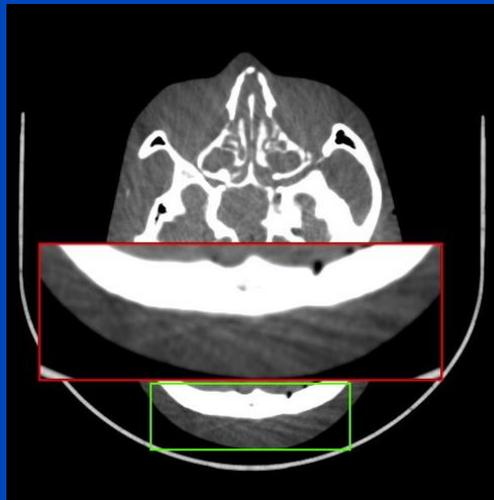
RIDL-CNN trained with
clinical dataset



RIDL-CNN trained with
synthetic dataset



Slice 1



Slice 2

C = 60 HU, W = 360 HU; collimation: 48x1.2 mm;
reconstructed slice width 1.5 mm

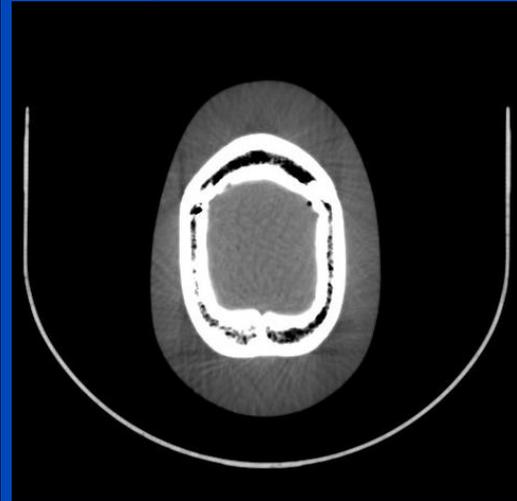
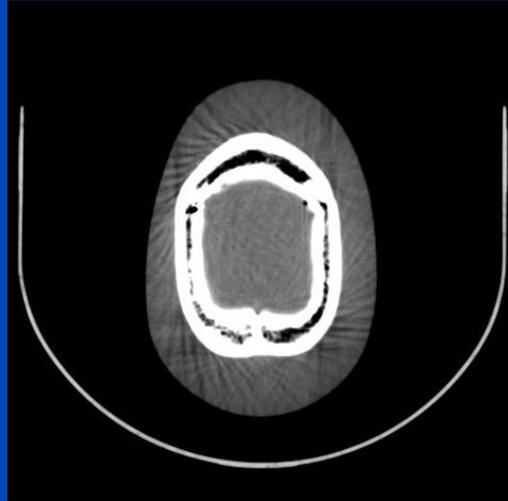
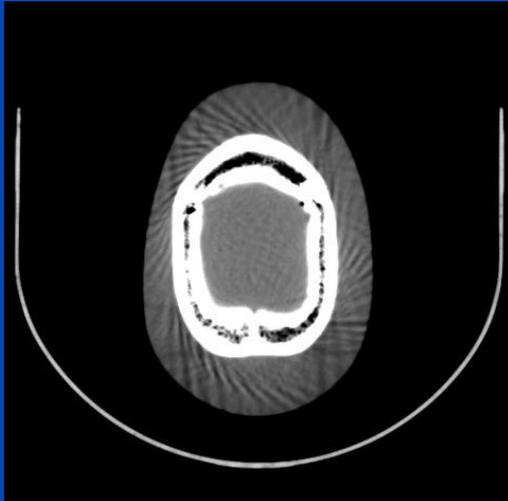
Results

Head Phantom Scan 2

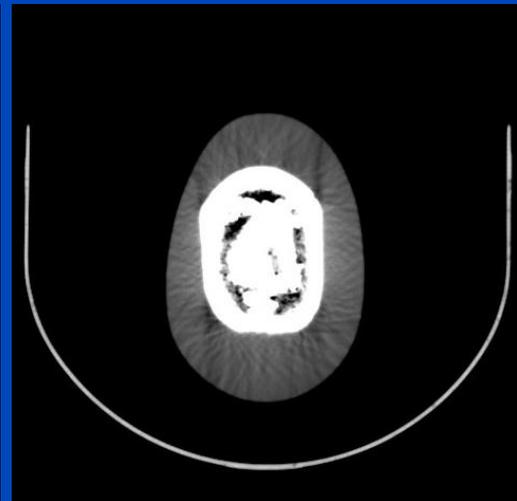
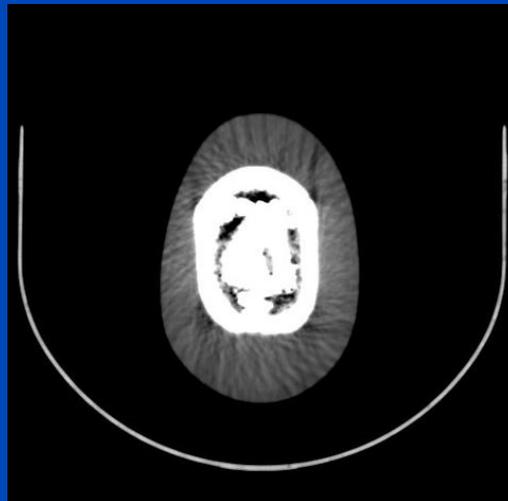
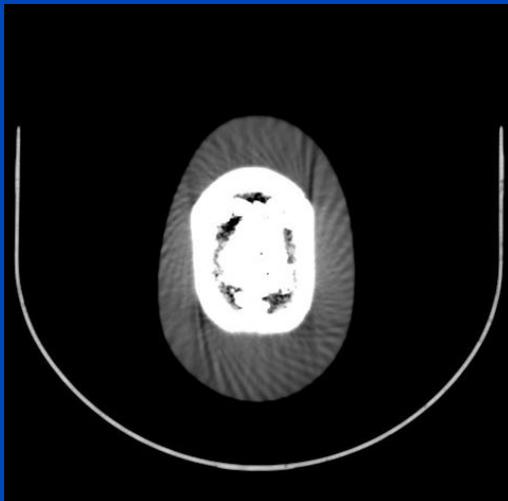
Standard WFBP
no zFFS available

RIDL-CNN trained with
clinical dataset

RIDL-CNN trained with
synthetic dataset



Slice 3



Slice 4

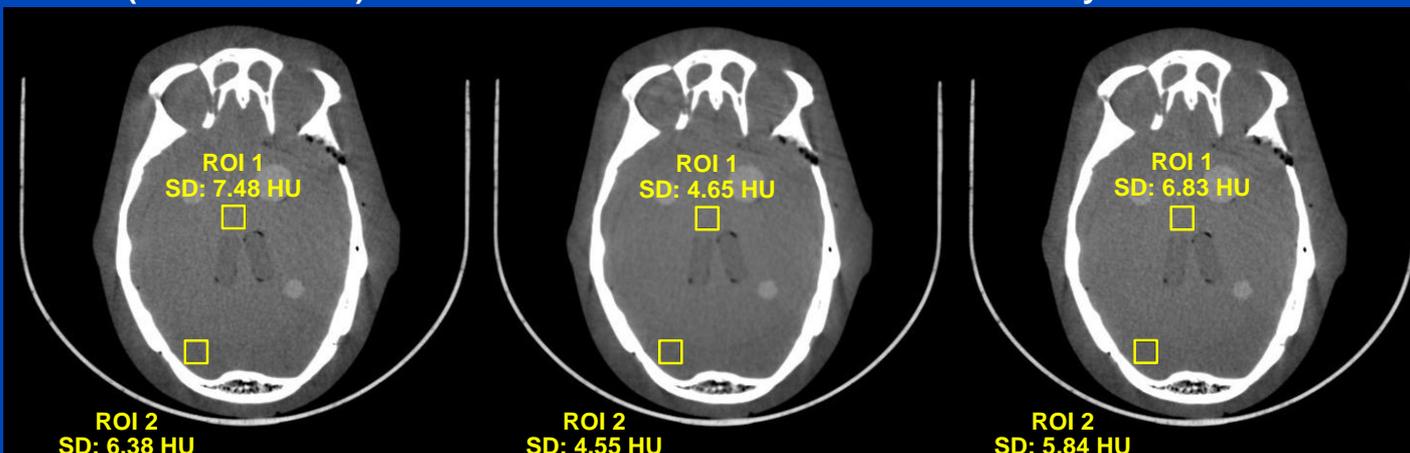
C = 60 HU, W = 360 HU; collimation: 48x1.2 mm;
reconstructed slice width 1.5 mm

Why are Synthetic Data Performing Better?

Ground truth
(removed rows)

RIDL-CNN trained with
clinical dataset

RIDL-CNN trained with
synthetic dataset



C = 60 HU, W = 360 HU;
Reconstructed only network
predicted rows. Removed
every second row from GT
projection data.

- RIDL-CNN trained with real patient data leads to a smoother result (lower SD in ROIs).
- Network seems to also perform a denoising due to different noise distributions present in clinical training data.
- Different structure of projection data in both datasets might have an impact on network training.
- Synthetic projections contain significantly more structures over the whole projection compared to clinical projection data.

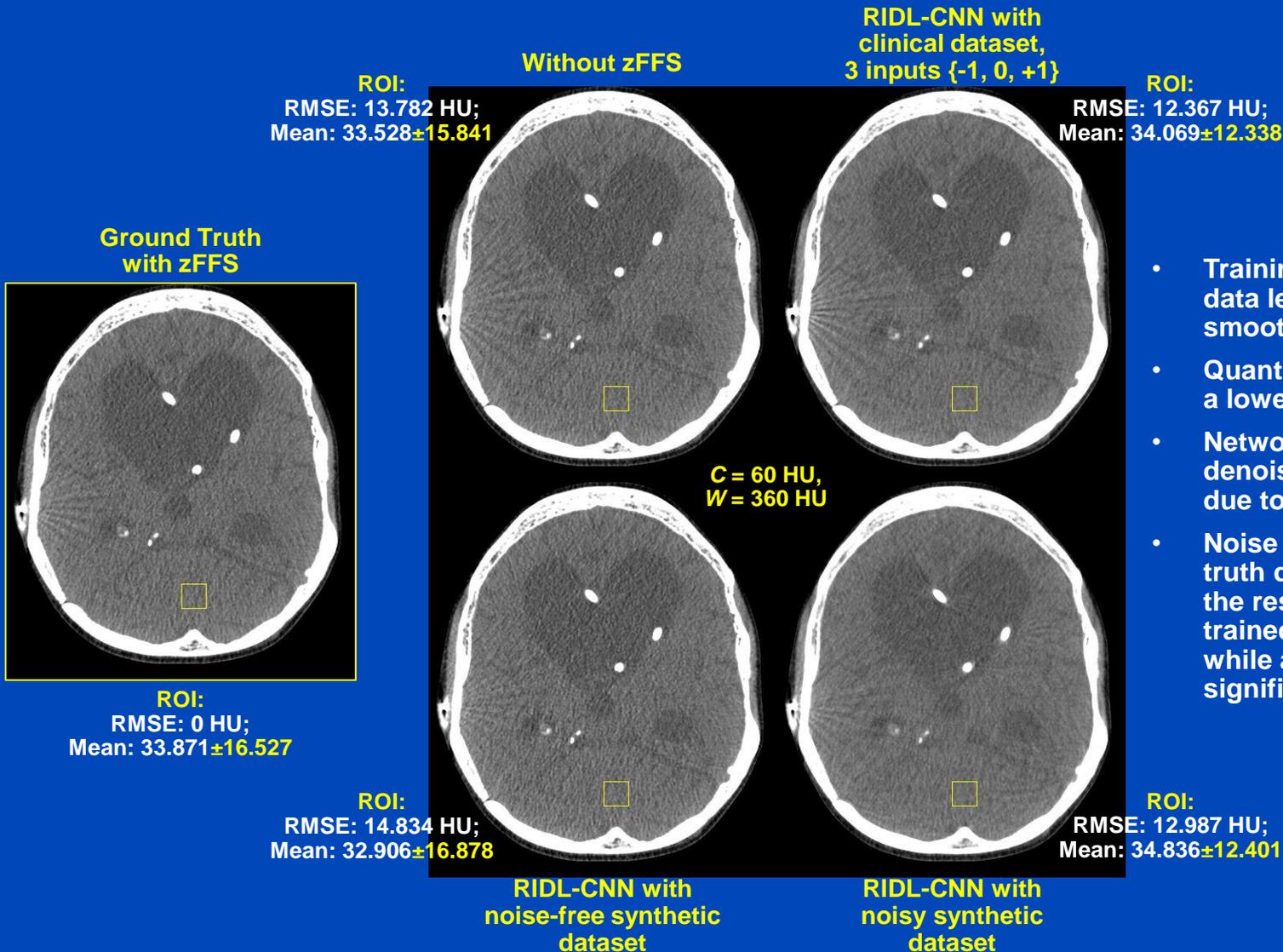
Example projection from the clinical dataset (head scan)



Example projection from the synthetic dataset



Synthetic Data With Noise Do Not Perform as Good as Without Noise.



- Training with noisy clinical data leads objectively to a smoother result.
- Quantitatively represented by a lower standard deviation.
- Network seems to perform a denoising in the prediction due to noise in training data.
- Noise distribution of ground truth data correlates more with the result of the RIDL-CNN trained with synthetic data, while artifacts are also significantly reduced.

Conclusions

- The proposed method can reduce windmill artifacts and does not require additional hardware.
- RIDL-CNN trained with noise-free synthetic data could reduce windmill artifacts more effectively than a corresponding network trained with clinical data.
- Inferior results of the clinical data may be attributed to the quantum noise in the clinical dataset.
- Training with clinical and synthetic dataset still can be optimized.
- **Outlook:**
 - Evaluation of network results on clinical patient scans.
 - Improvement of the synthetic dataset.

Thank You!

This presentation will soon be available at www.dkfz.de/ct

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