

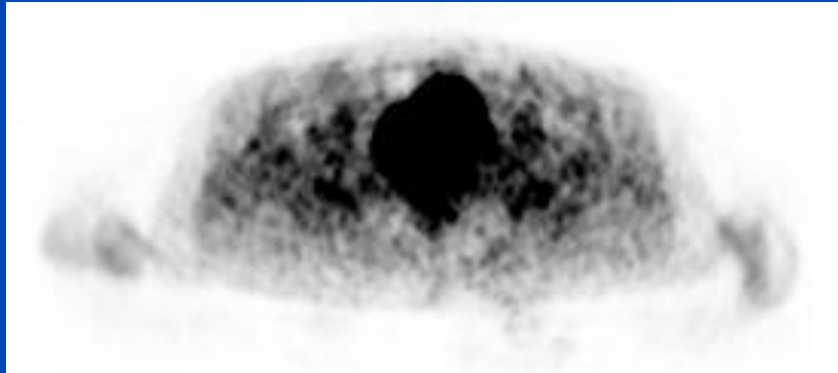
On the Impact of Input Feature Selection in Deep Scatter Estimation for Positron Emission Tomography

Yannick Berker and Marc Kachelrieß

German Cancer Research Center (DKFZ),
Heidelberg, Germany

PET Scatter Correction

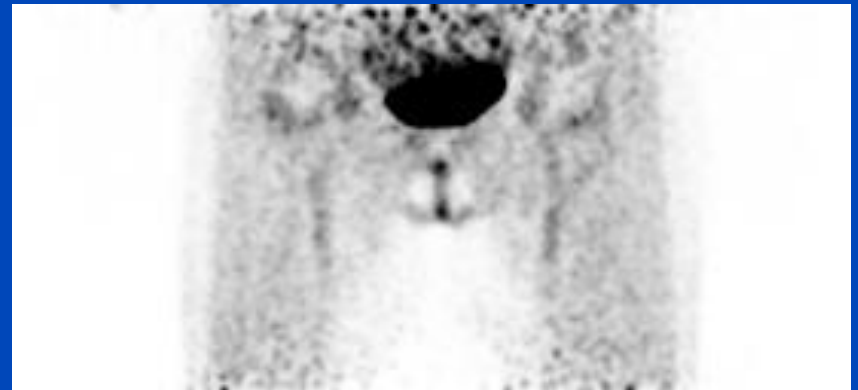
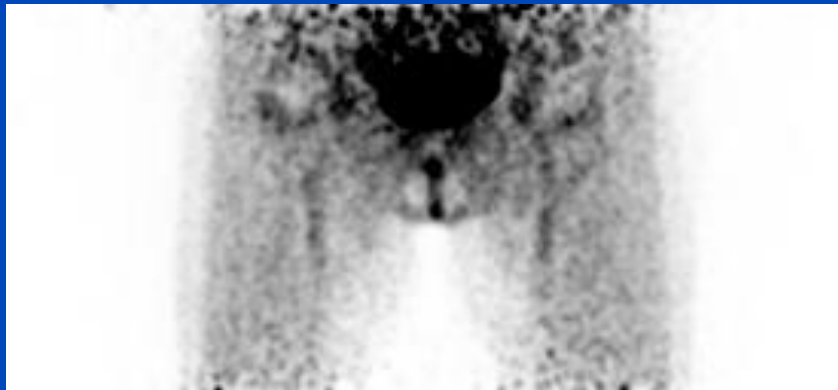
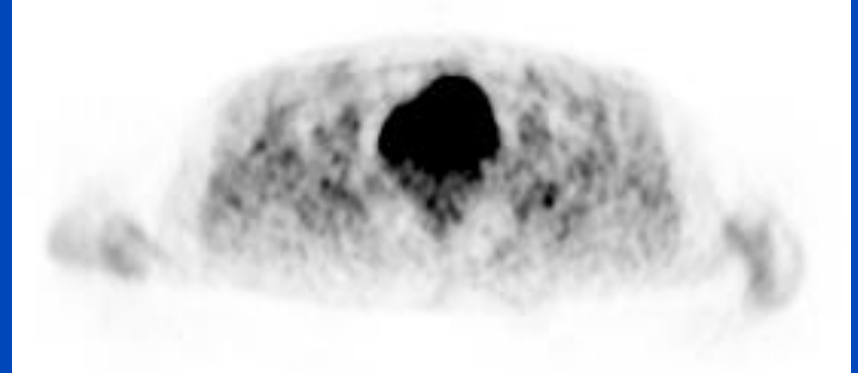
without scatter correction



[kBq/mL]



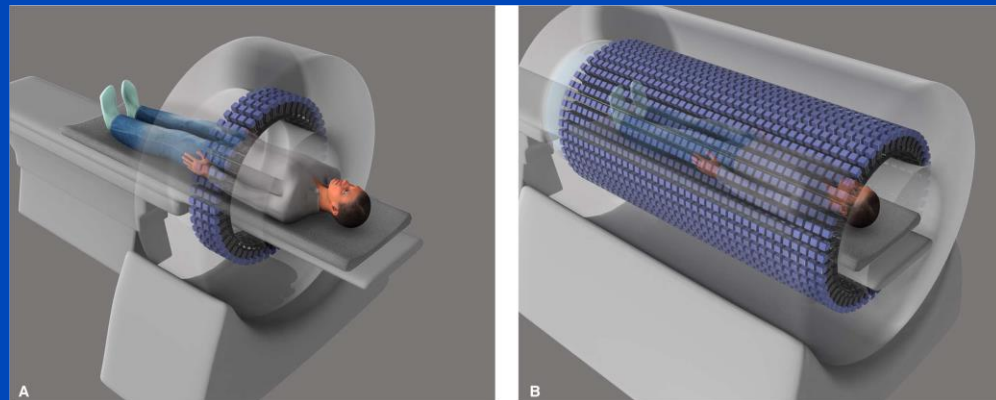
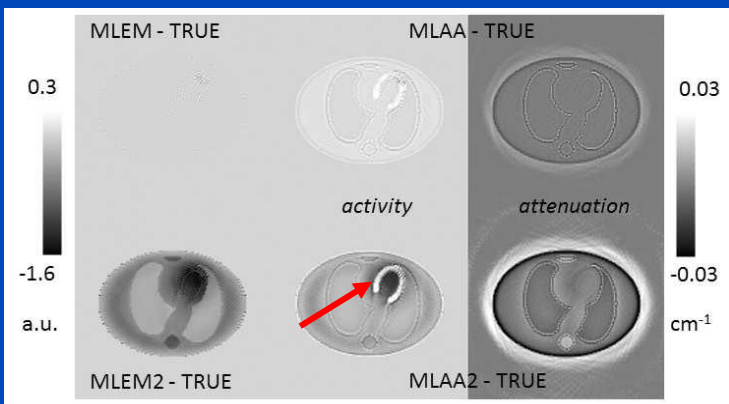
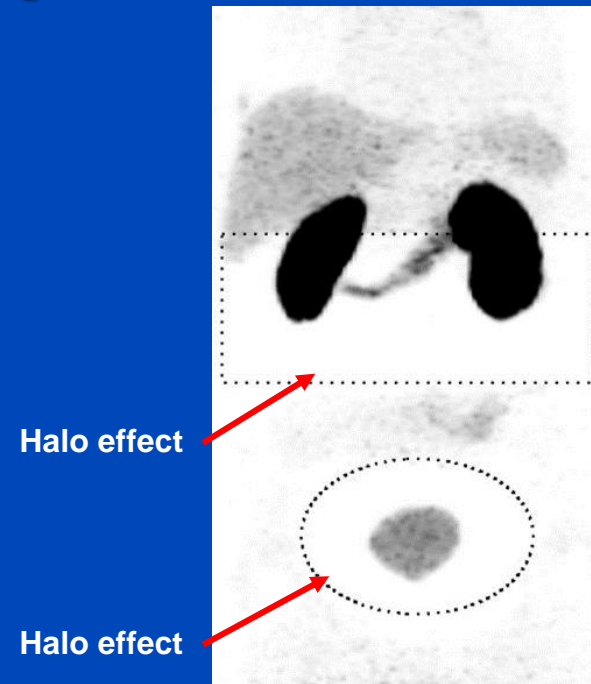
with scatter correction



- improved contrast
- improved lesion detectability
- better quantification

Scatter-Sensitive PET Applications

- Highly-specific PET tracers¹
 - Halo effect with ⁶⁸Ga-PSMA
- Joint estimation^{2,3}
 - Unknown radiotracer and attenuation
- Long-axial-FOV PET scanners⁴
 - Need for fast whole-body scatter simulation



[1] Heußner, Kachelrieß et al. *PLoS ONE*. 2017;12(8):e0183329.

[2] Heußner, Kachelrieß et al. *IEEE Trans Nucl Sci*. 2016;63(5):2443-51.

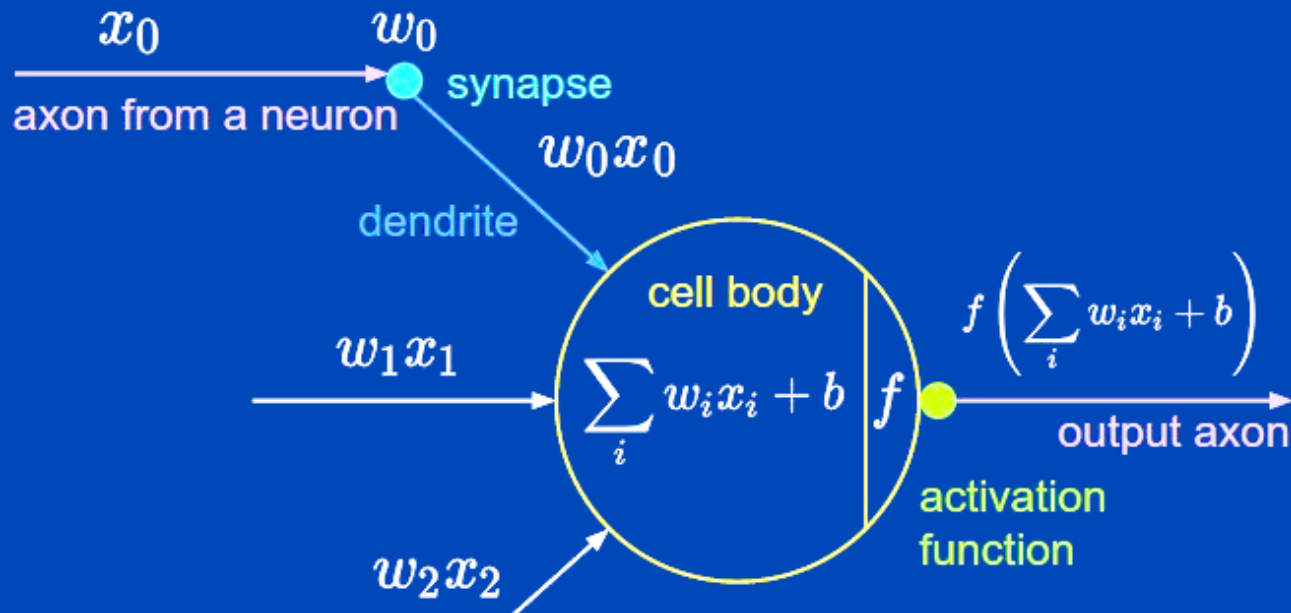
[3] Nuyts et al. *IEEE TRPMS*. 2018;2(4):273-8.

[4] Cherry et al. *Sci Transl Med*. 2017;9(381):eaaf6169.

Motivation

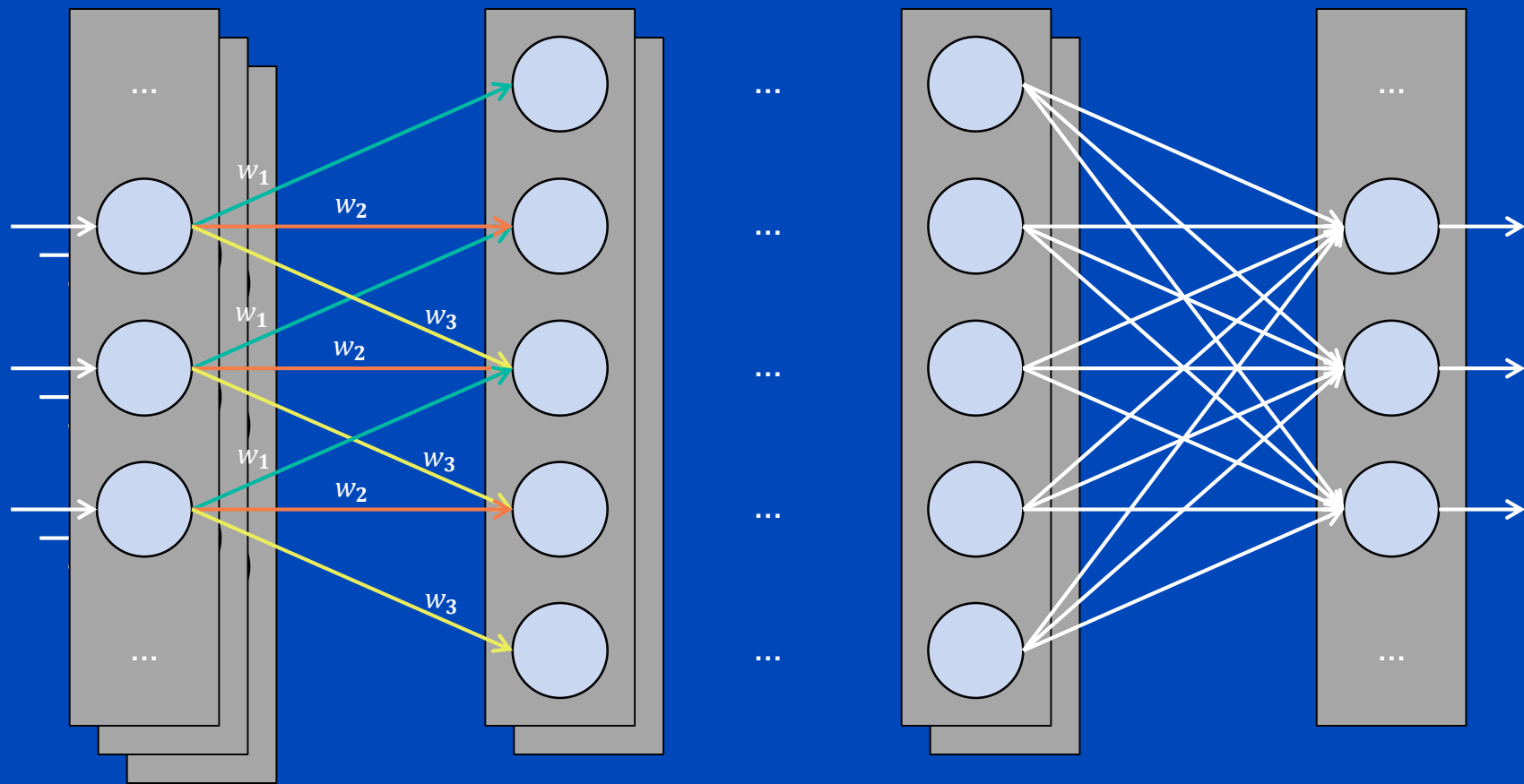
- **Monte Carlo scatter simulation (MCSS)**
 - Highly accurate
 - Slow (computationally expensive)
- **State of the art: Single scatter simulation (SSS)**
 - Relatively fast
 - Inaccurate (tail fitting)
- **Objective** **Fast (and accurate) scatter correction**
- **Approach** **Convolutional Neural Networks (CNNs)**
 - SSS-based: speed-up of (TOF-)SSS still subject of research¹
 - Aim: MC-based deep scatter estimation

Artificial Neuron¹



- **Nonlinear** activation function f
- Multiple inputs, linearly combined
- Trainable **weights** w_i and **bias** b
- **Supervised learning**: adapt parameters to in-/output

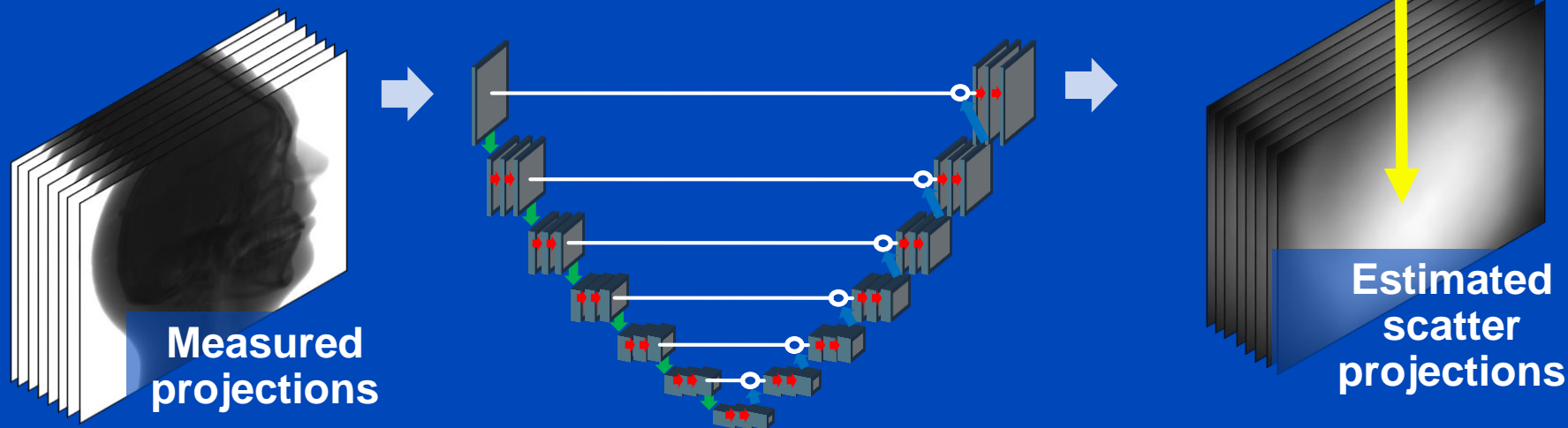
Convolutional Neural Networks



- Fully-connected vs. **convolutional** layers of neurons
- **Vector-valued inputs** (images, channels, features)

Deep Scatter Estimation in CT

- A 2-D CNN to **estimate scatter** from **scatter-contaminated** projections¹⁻³
 - Trained using measurements and reference
 - Applied to individual projections
 - Real-time performance for cone-beam CT



Previous Work in PET

- **Emission and attenuation, detector data¹**
 - **14 phantoms** (13 training, 1 validation)
- **Emission and attenuation, detector data²**
 - **20 whole-body patients** (57/14 bed positions)
 - 3.6% mean absolute error (+ one outlier)
- **Emission only, reconstructed images³**
 - **35 brain patients** (25/10 scans)
 - 1% \pm 5% deviation (+ one outlier)

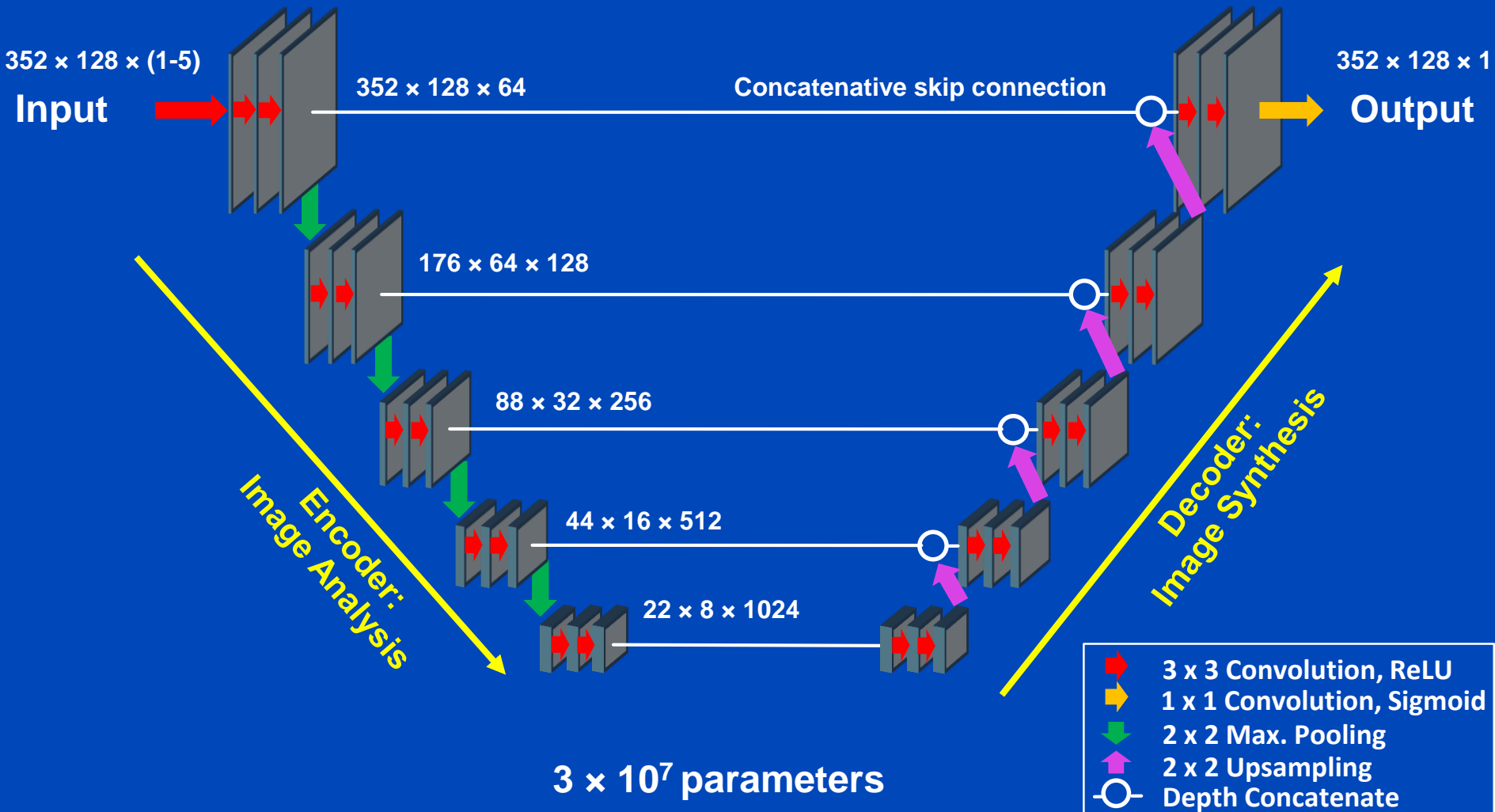
[1] Qian, Rui, De Man. IEEE NSS/MIC 2017;M04-1. [2] Berker, Maier. Kachelrieß. IEEE NSS/MIC 2018;M-17-04.

[3] Yang, Park, Gullberg, Seo. Phys Med Biol. 2019;64(7):075019.

Aim

- Investigate the need to input **emission and/or attenuation data**
- Understand the influence of various other **transformations of the input data**

Network Structure: U-Net¹

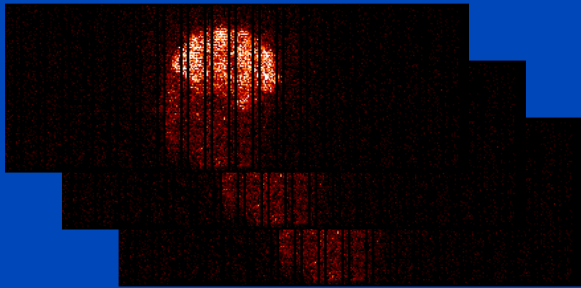


[1] Ronneberger O, Fischer P, Brox T. *MICCAI*. 2015:234-41.

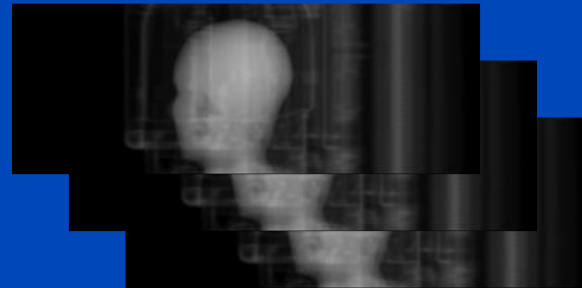
Available Patient Data

- **20 patients:** FDG, Siemens Biograph mMR

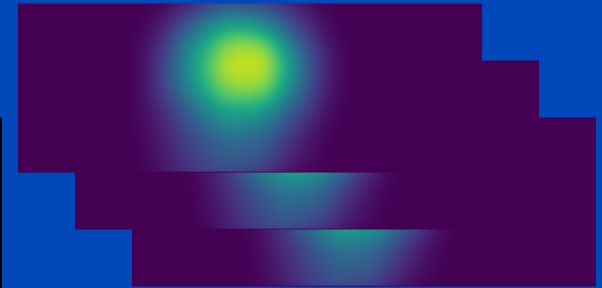
Prompts



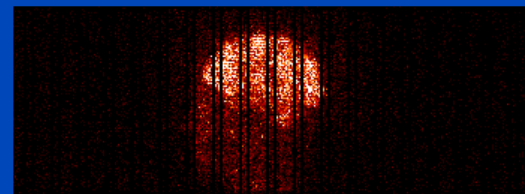
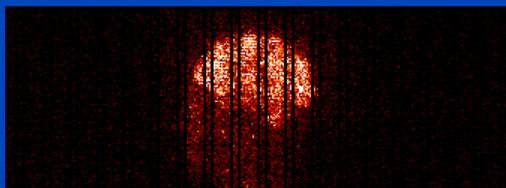
ACFs



Scatter



- **Padding:** $344 \times 127 \rightarrow 352 \times 128$ pixels



Results: Accuracy¹

Normalized Mean Absolute Error: $NMAE = \frac{\sum_i |DSE_i - SSS_i|}{\sum_i |SSS_i|}$

Scatter projections

PET reconstructions

Mean/Std

7.1 ± 1.7 %

3.6 ± 2.2 %

Range

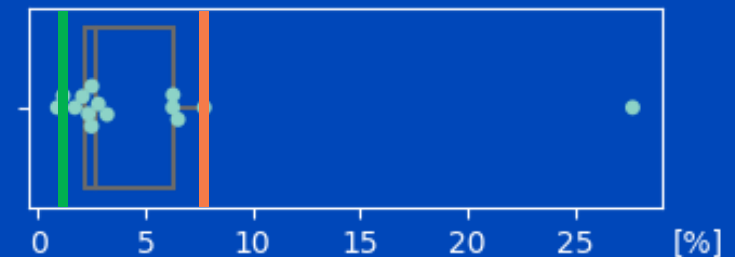
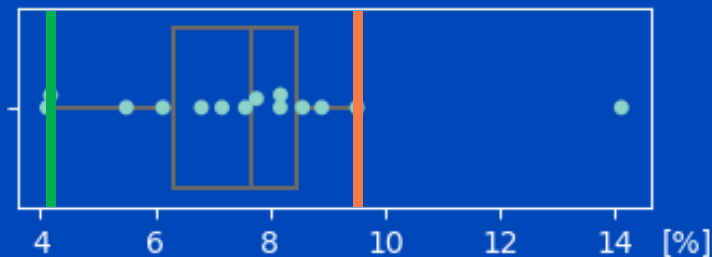
4 – 10 %

1 – 8 %

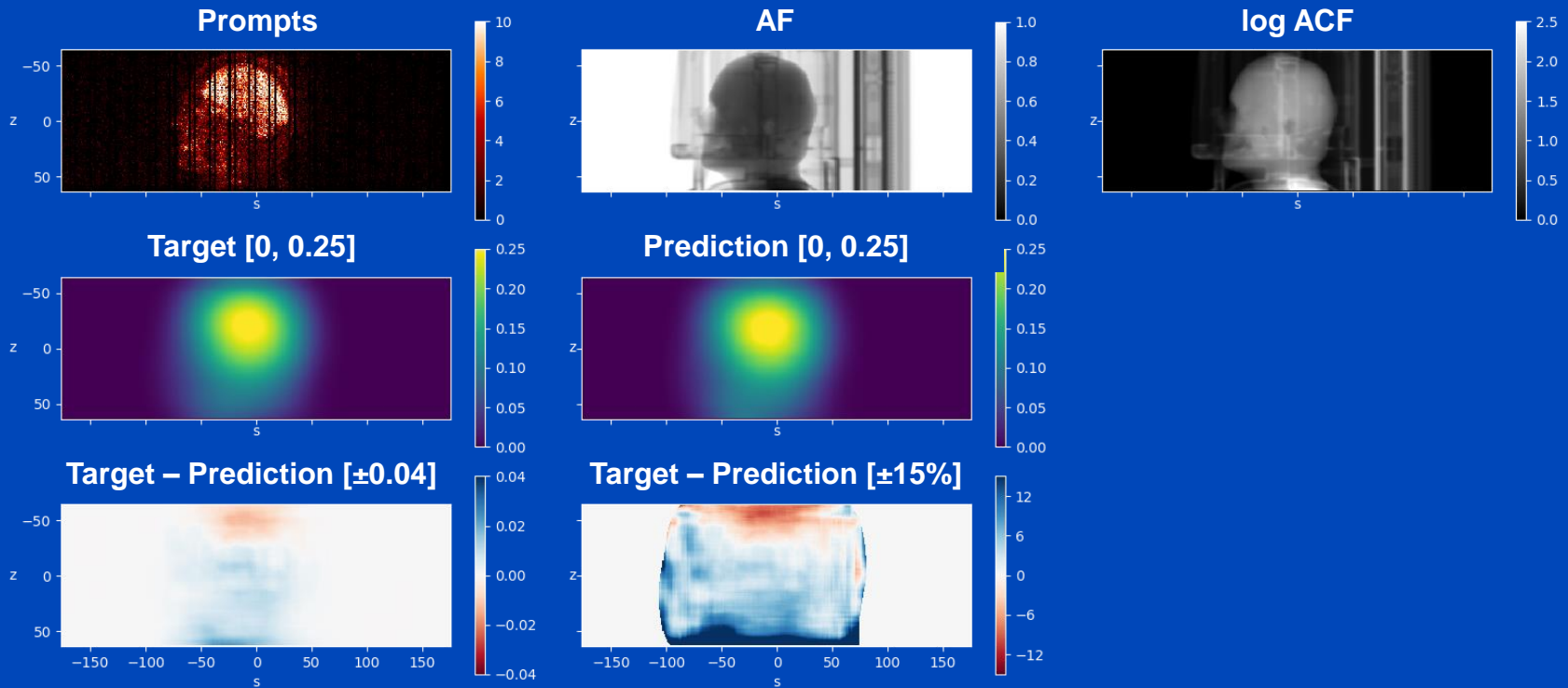
Outlier

14 %

28 %

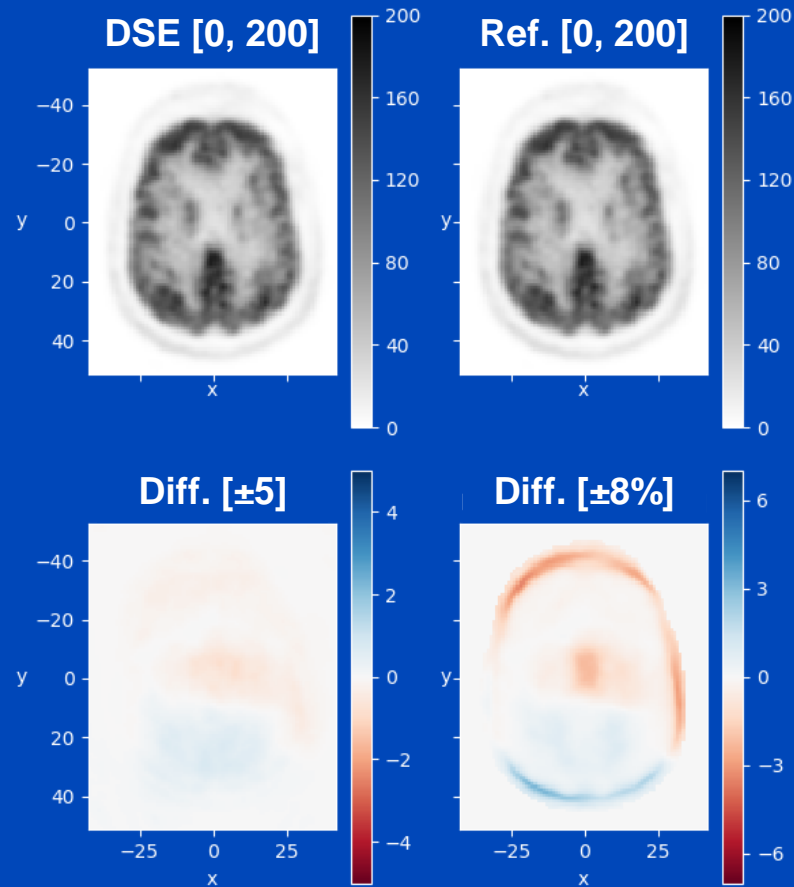


Results: Best Case

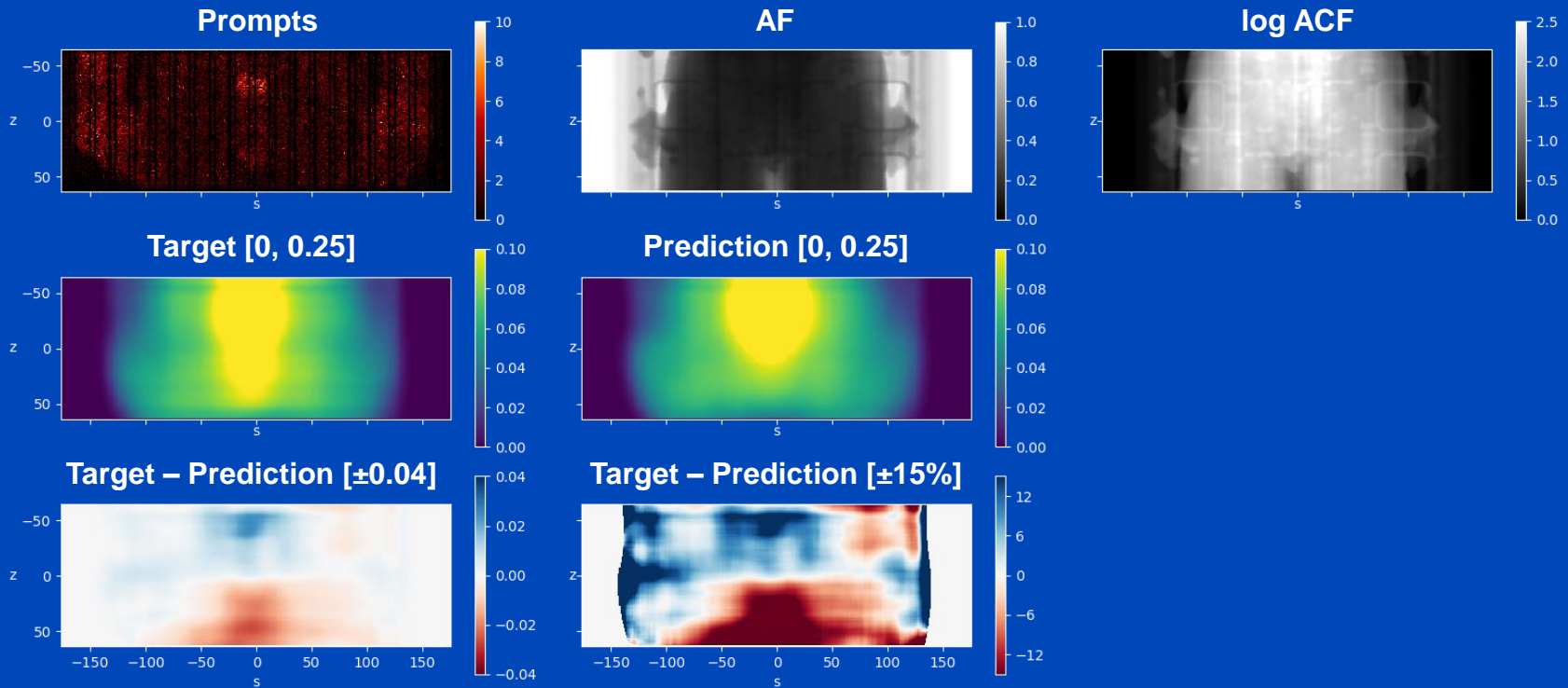


- **Best case: brain bed position**

Results: Best Case

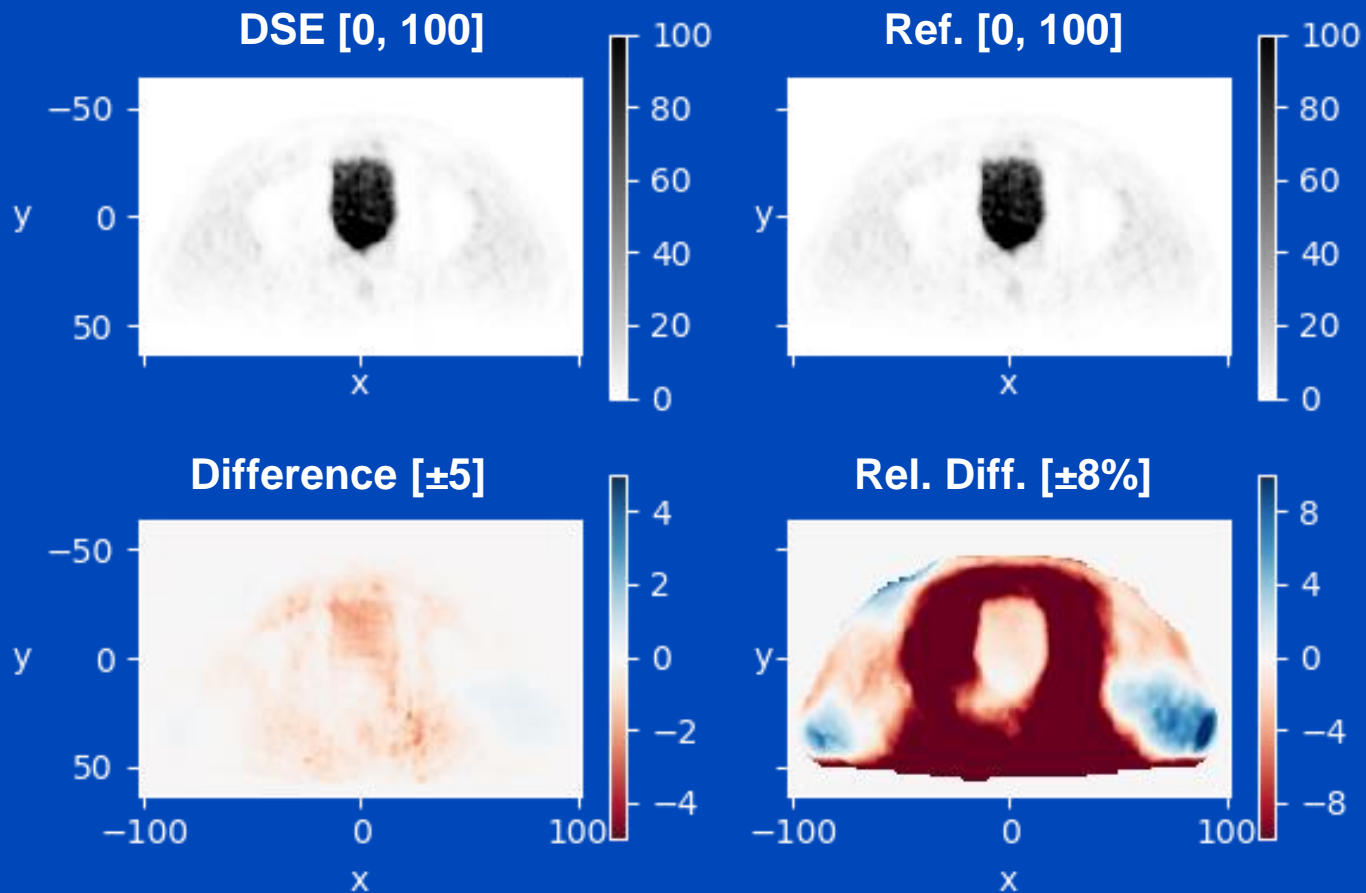


Results: Worst Case



- **Worst case:** filled bladder inside the FOV

Results: Worst Case



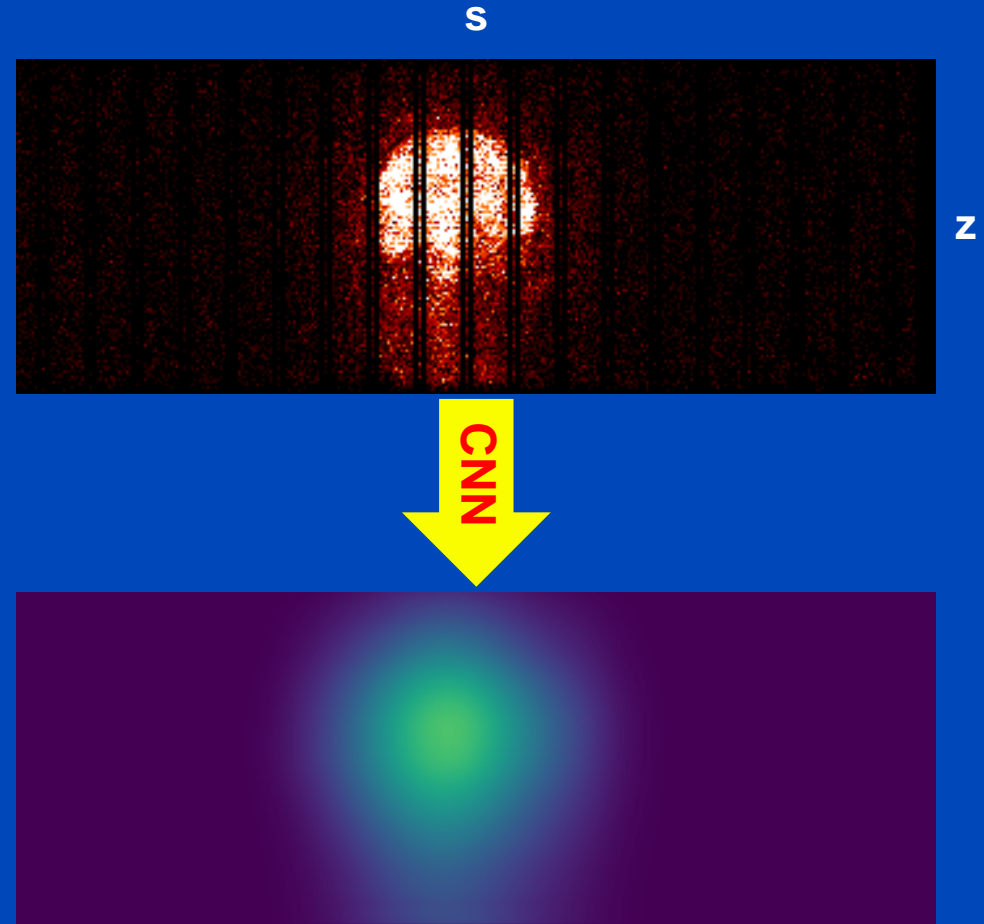
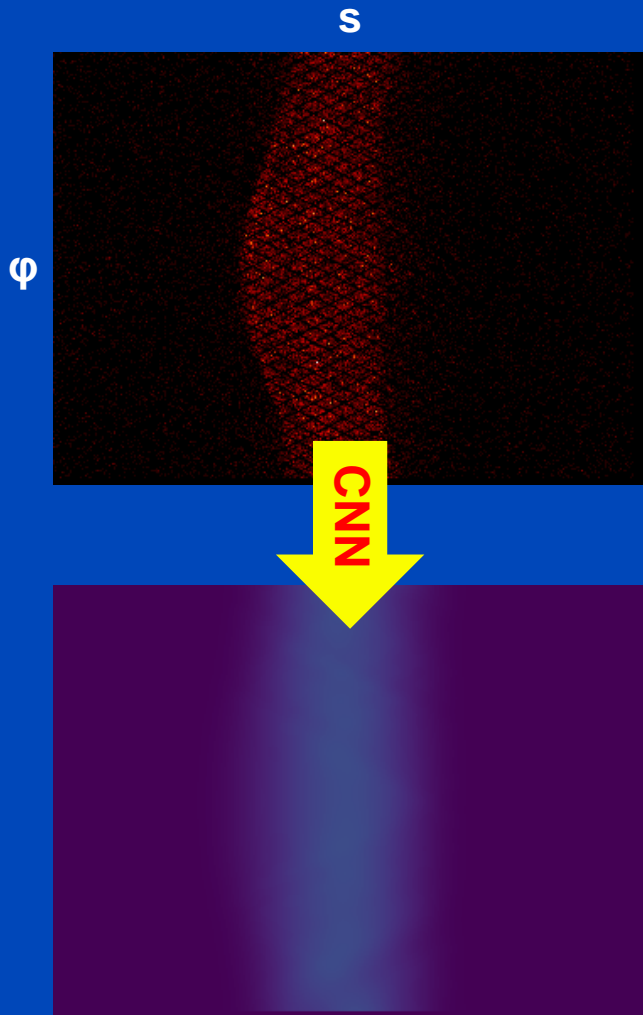
Original vs. Current Parameters

- **Network**
 - Dropout
 - Sigmoid output
 - Poisson loss function
 - **Implementation**
 - TensorFlow-Keras v1.8-v1.12
 - 10 epochs
 - **Adam optimizer**
 - Batch size 4, initial learning rate 10^{-4}
 - **Workstation**
 - Intel Xeon E5-2667 v4 (2 x 8 cores, 256 GB), **NVIDIA Quadro M5000** (2048 cores, 8 GB)
- **Network**
 - No dropout
 - ReLU output
 - Mean absolute error
 - **Implementation**
 - TensorFlow-Keras v1.13.1
 - 5 epochs

Specific Investigations

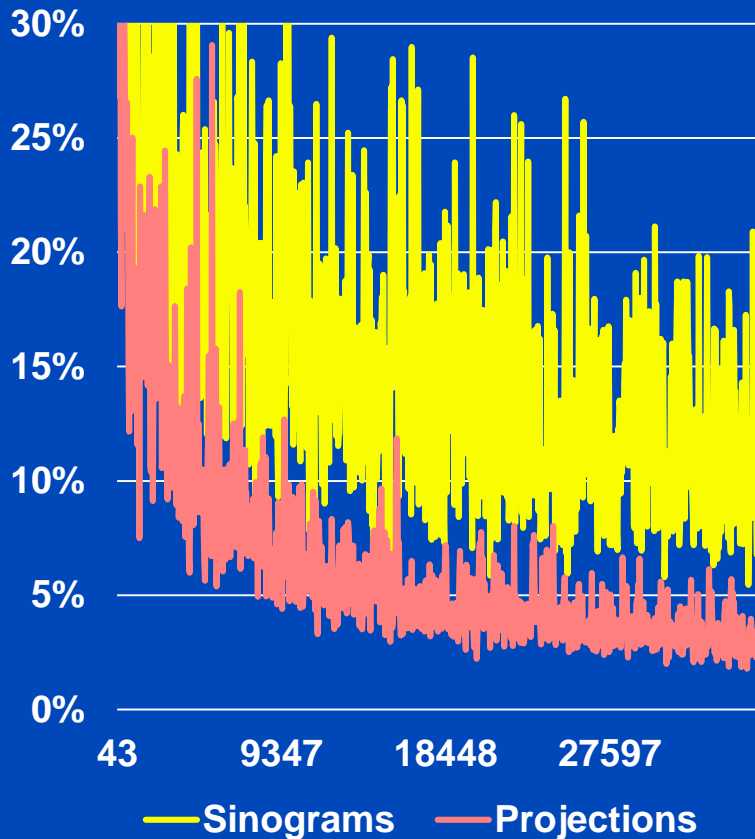
- **Sinograms vs. projections**
- **Choice of input features**
 - Emission *and/or* attenuation
 - Redundant combinations
- **Number of samples**
 - Data augmentation
 - Number of bed positions
- **Transformations**
 - Gap filling of prompts
 - Normalization of inputs
- **Scatter scaling**

Sinograms vs. Projections

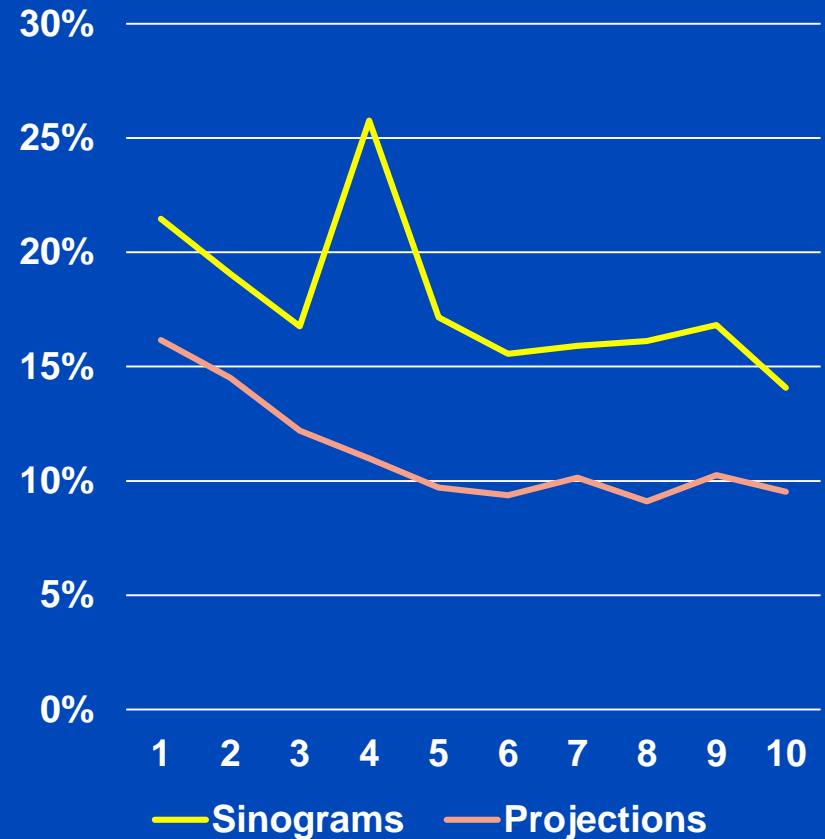


Projections vs. Sinograms

Training NMAE vs. Batches



Validation NMAE vs. Epochs

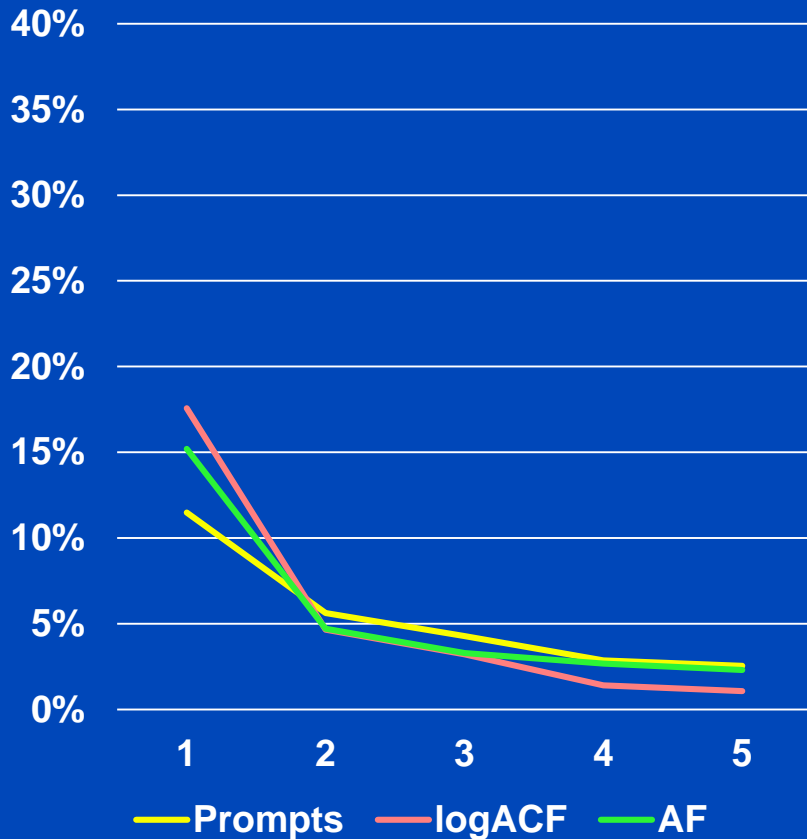


Specific Investigations

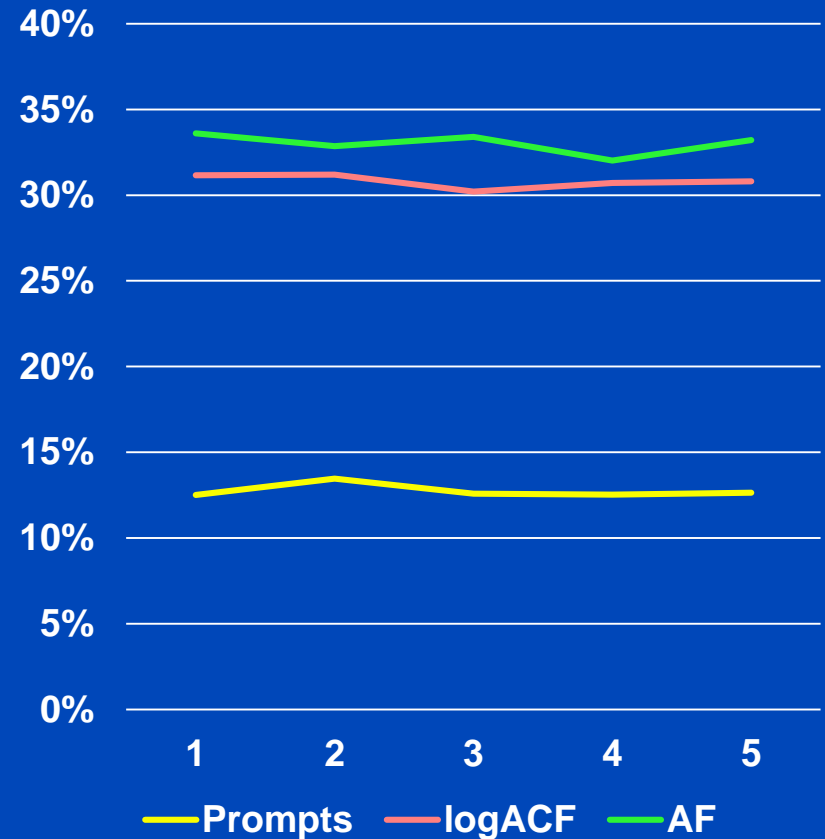
- Sinograms vs. projections
- **Choice of input features**
 - Emission *and/or* attenuation
 - Redundant combinations
- **Number of samples**
 - Data augmentation
 - Number of bed positions
- **Transformations**
 - Gap filling of prompts
 - Normalization of inputs
- **Scatter scaling**

Emission vs. Attenuation

Training NMAE vs. Epochs

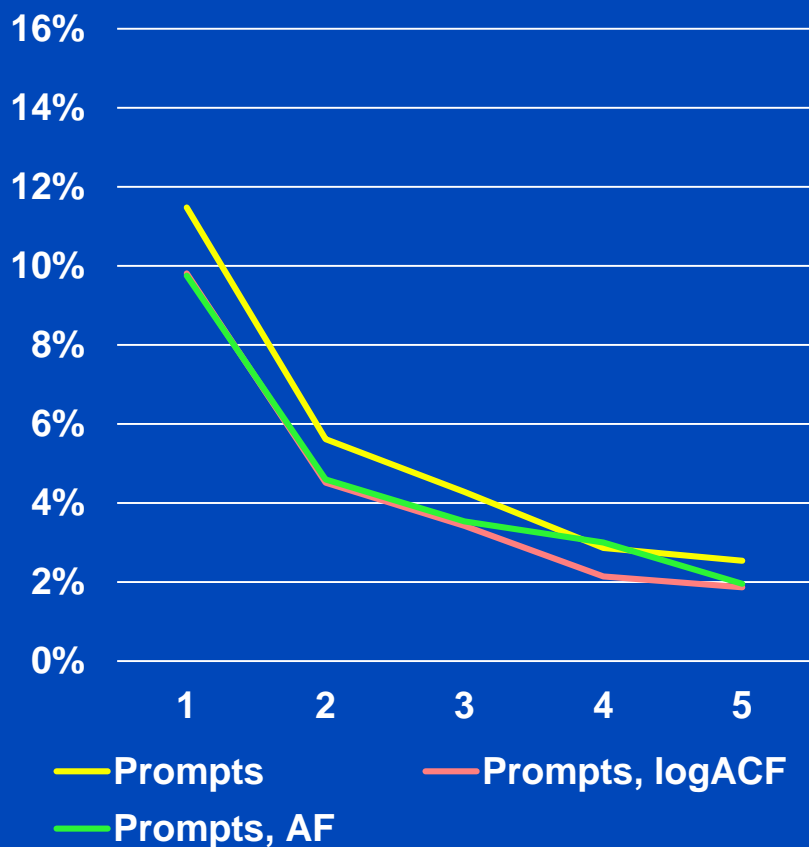


Validation NMAE vs. Epochs

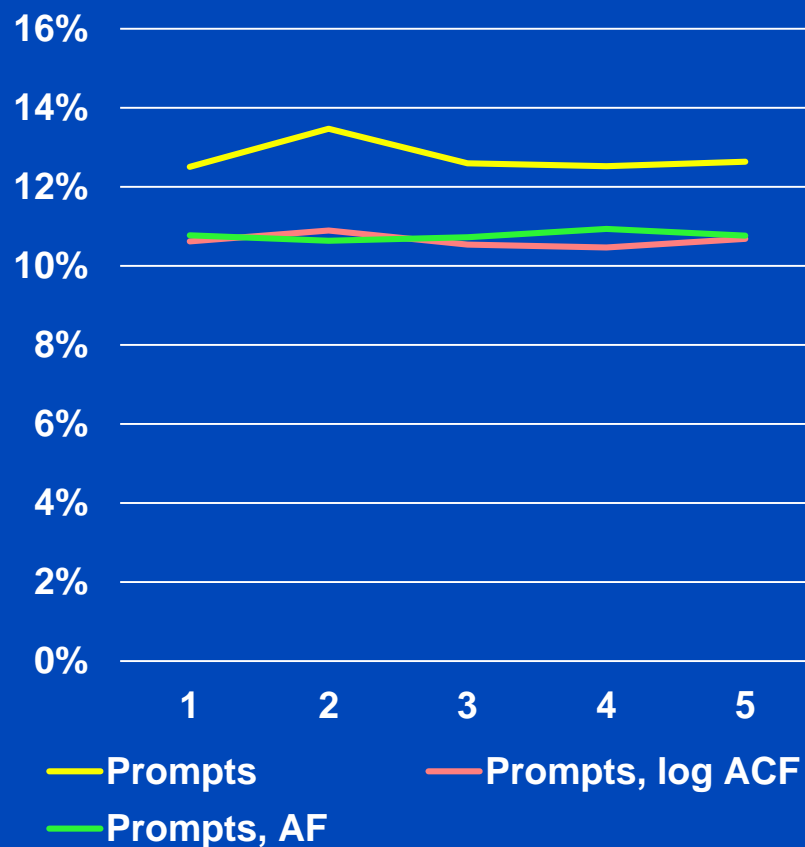


Emission and Attenuation

Training NMAE vs. Epochs

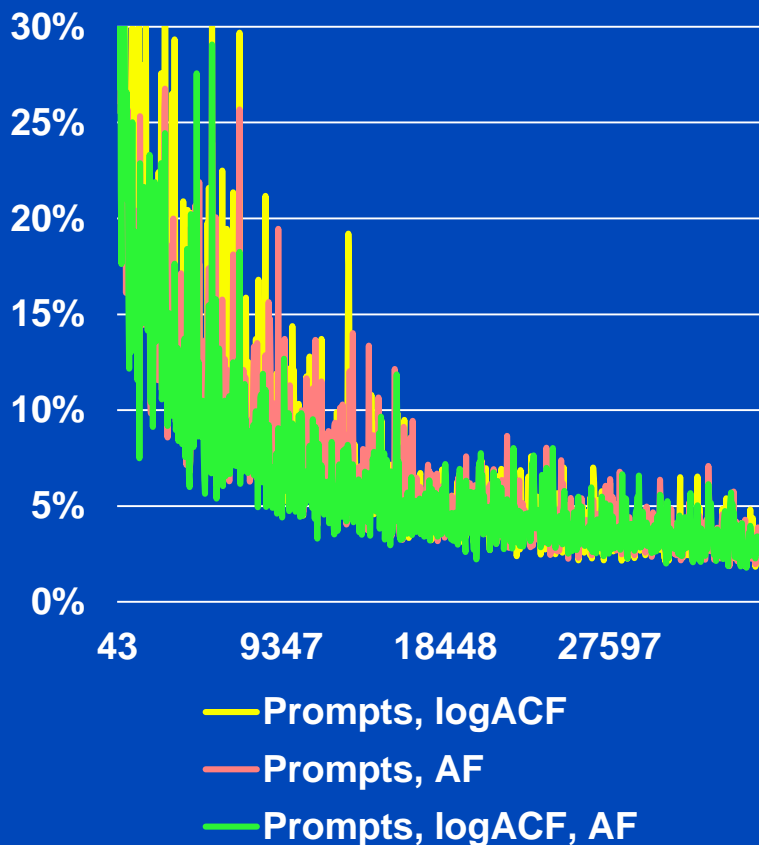


Validation NMAE vs. Epochs

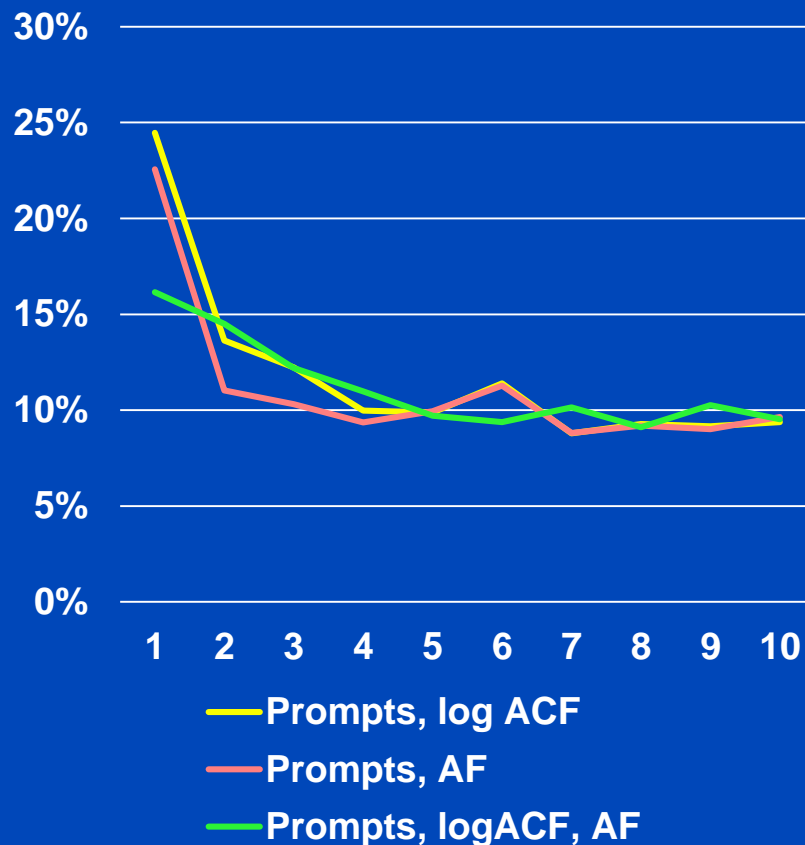


Redundant Features

Training NMAE vs. Epochs



Validation NMAE vs. Epochs

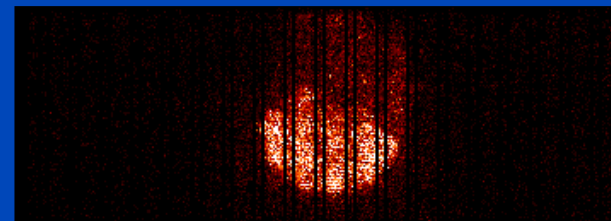
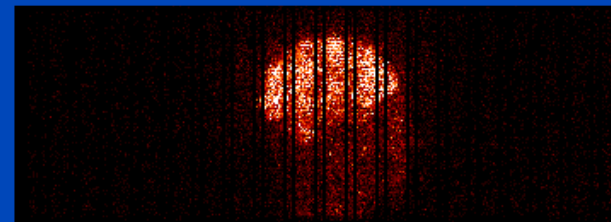
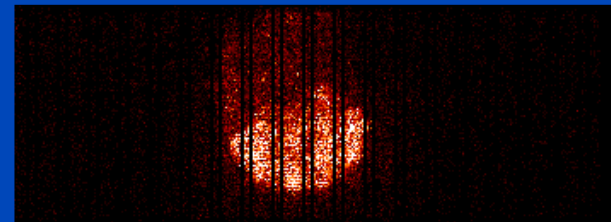
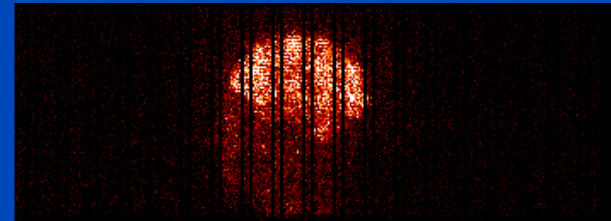


Specific Investigations

- Sinograms vs. projections
- Choice of input features
 - Emission *and/or* attenuation
 - Redundant combinations
- **Number of samples**
 - Data augmentation
 - Number of bed positions
- Transformations
 - Gap filling of prompts
 - Normalization of inputs
- Scatter scaling

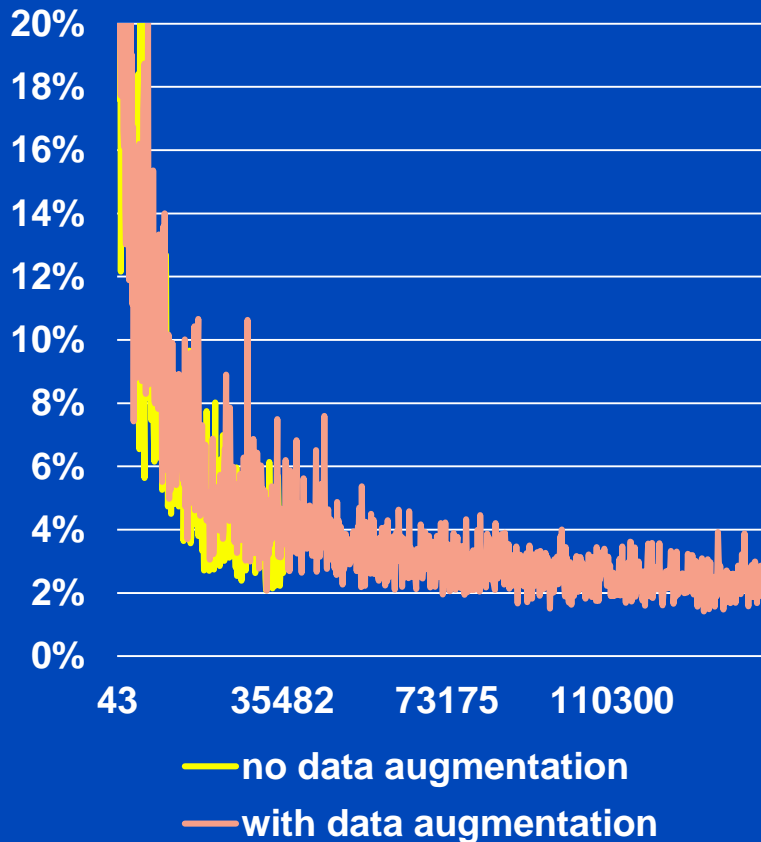
Data Augmentation

- 4 x number of samples
 - Vertical flipping
 - Horizontal flipping
- Expectation
 - Better generalization



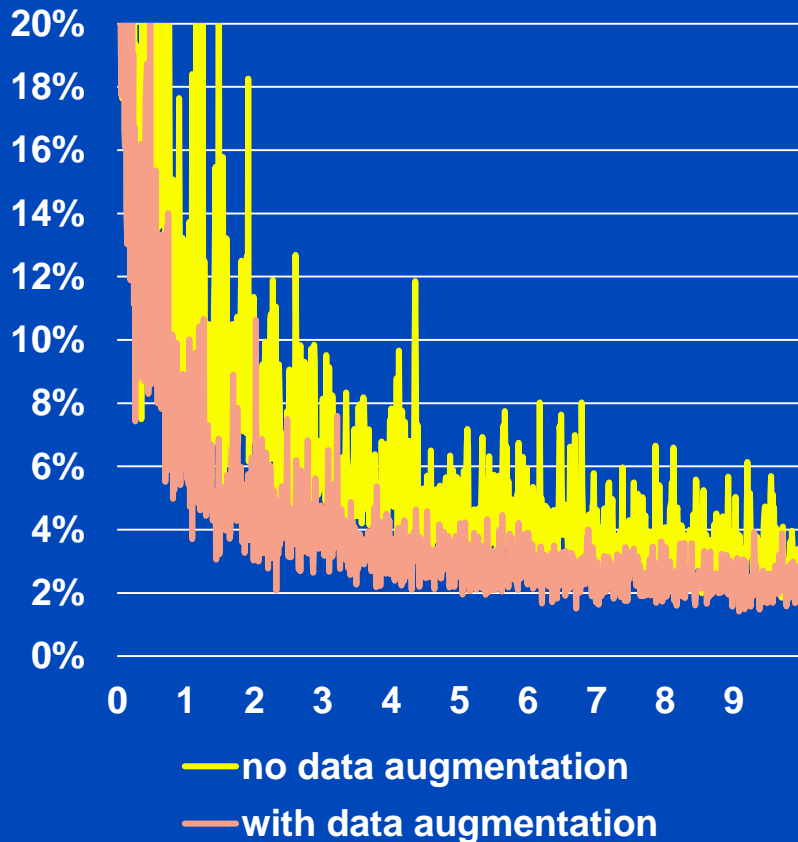
Data Augmentation

Training NMAE vs. Batches

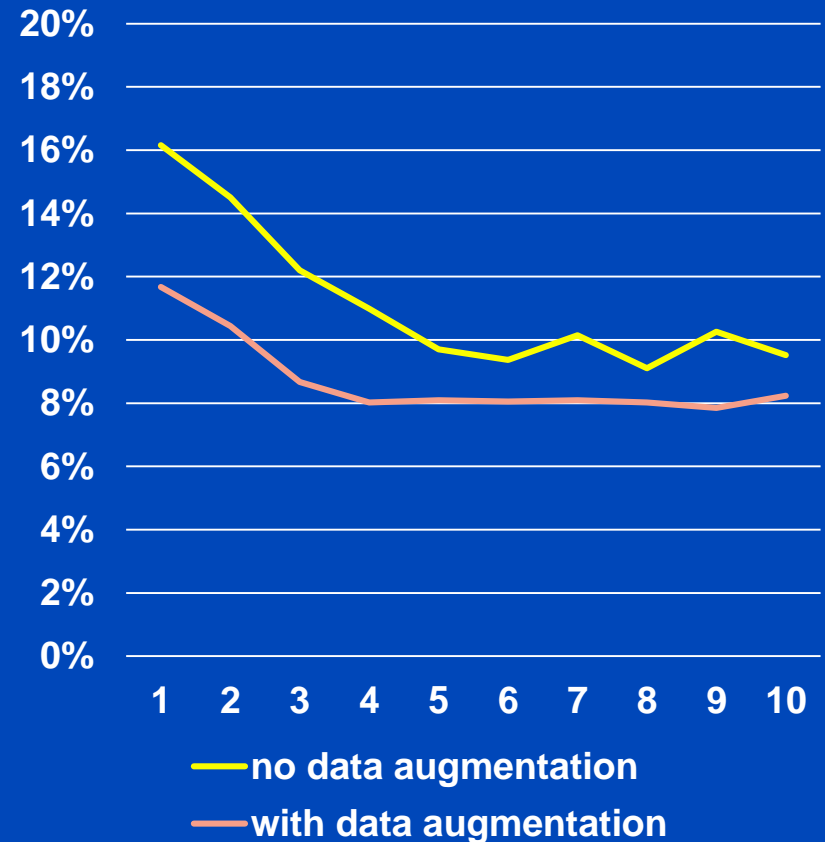


Data Augmentation

Training NMAE vs. Epochs



Validation NMAE vs. Epochs



Number of Bed Positions

Previous study¹

- 2-6 per patient (brain/lungs/pelvis)
- 57/14 bed positions
- 0.8% training NMAE
- 8.3% validation NMAE

Current study

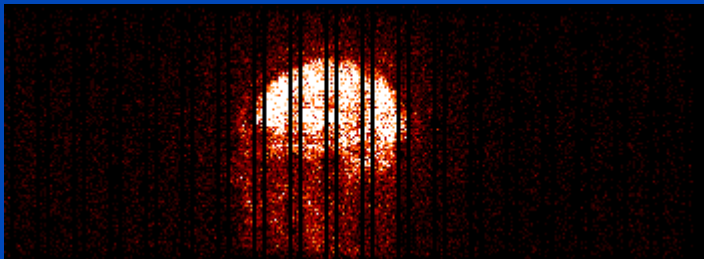
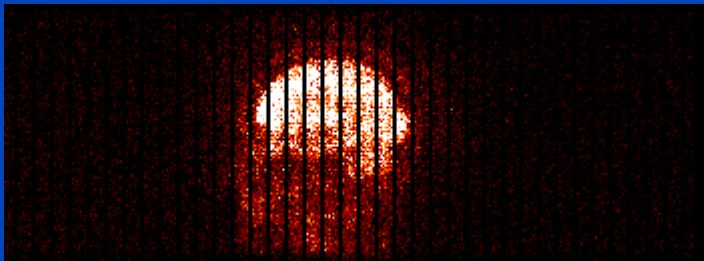
- 5-7 per patient (brain to thighs)
- 88/18 bed positions
- 1.5% training NMAE
- 11.7% validation NMAE

Specific Investigations

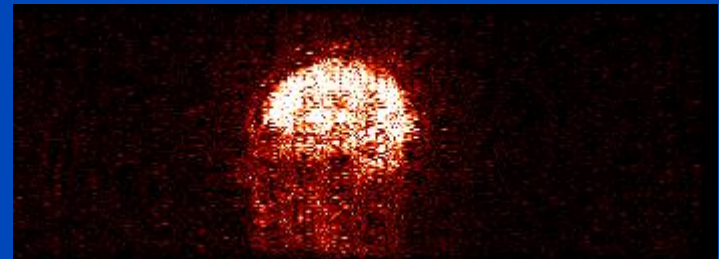
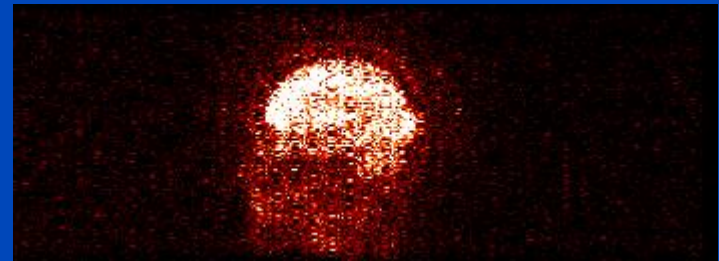
- Sinograms vs. projections
- Choice of input features
 - Emission *and/or* attenuation
 - Redundant combinations
- Number of samples
 - Data augmentation
 - Number of bed positions
- **Transformations**
 - Gap filling of prompts
 - Normalization of inputs
- Scatter scaling

Gap Filling of Prompts

no gap filling

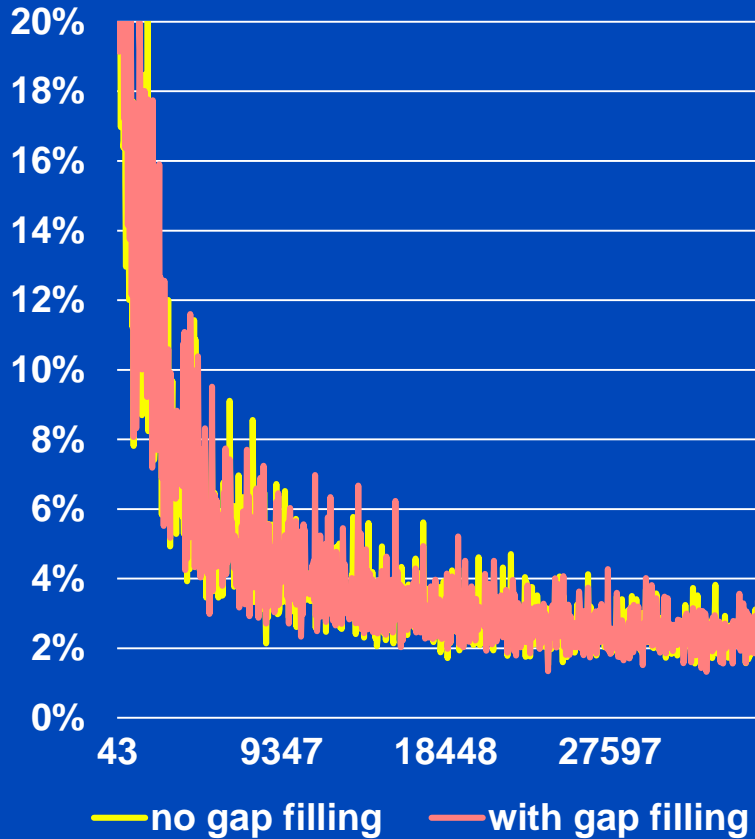


with gap filling

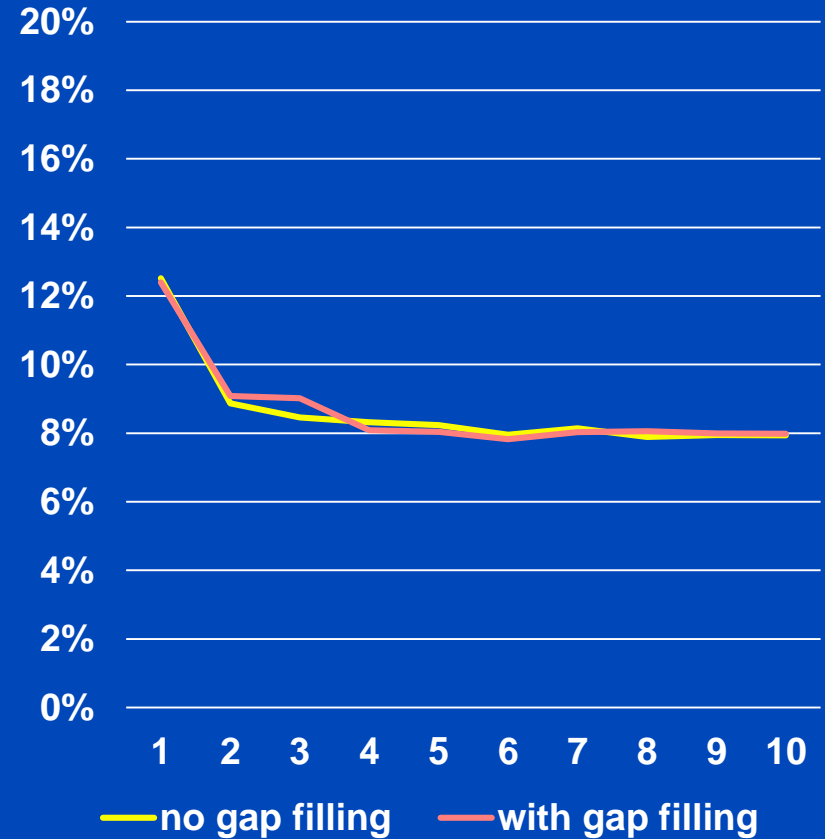


Gap Filling of Prompts

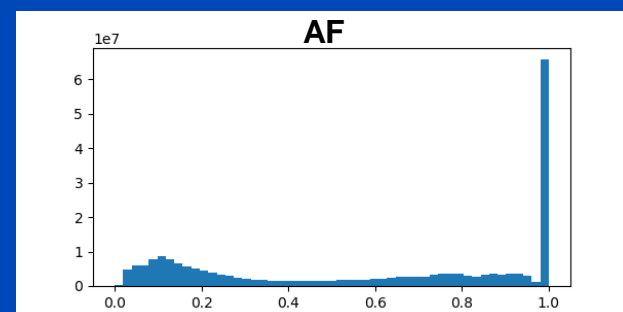
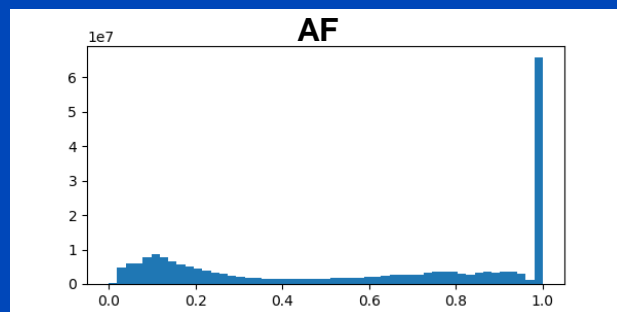
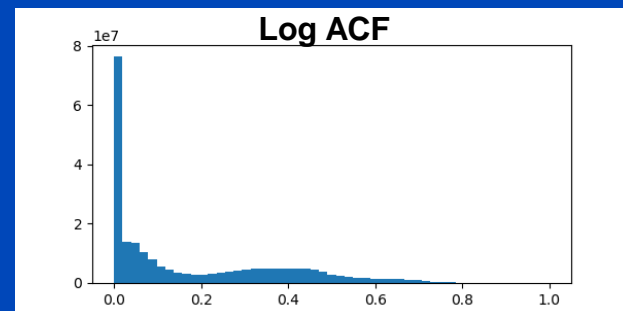
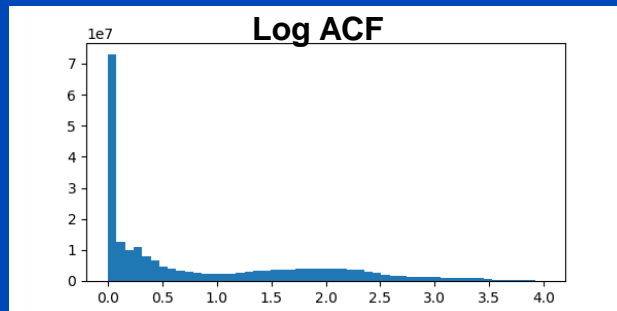
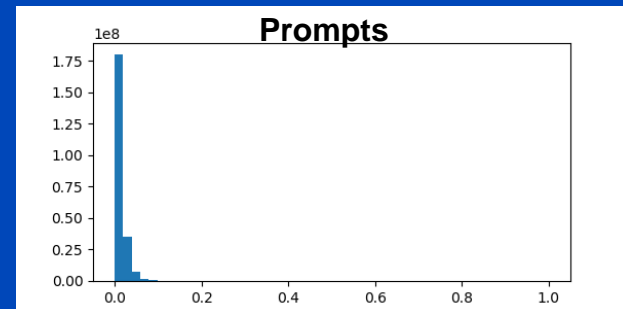
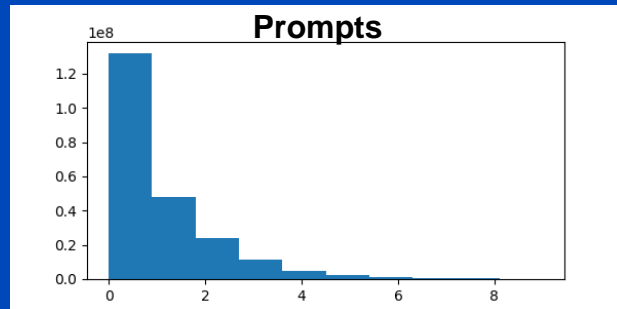
Training NMAE vs. Batches



Validation NMAE vs. Epochs

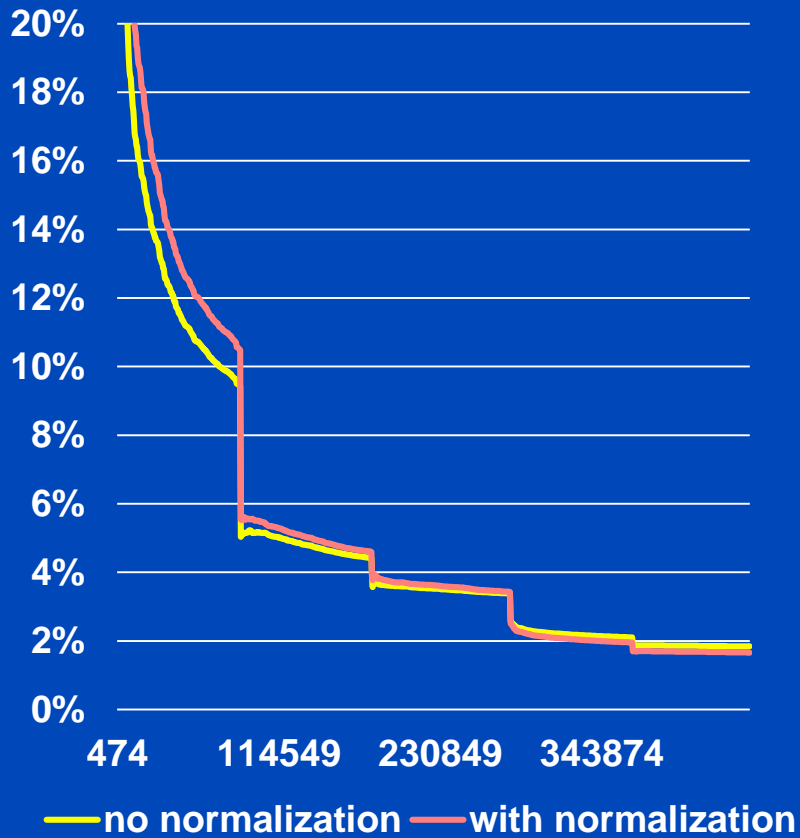


Input Normalization: Range [0, 1]

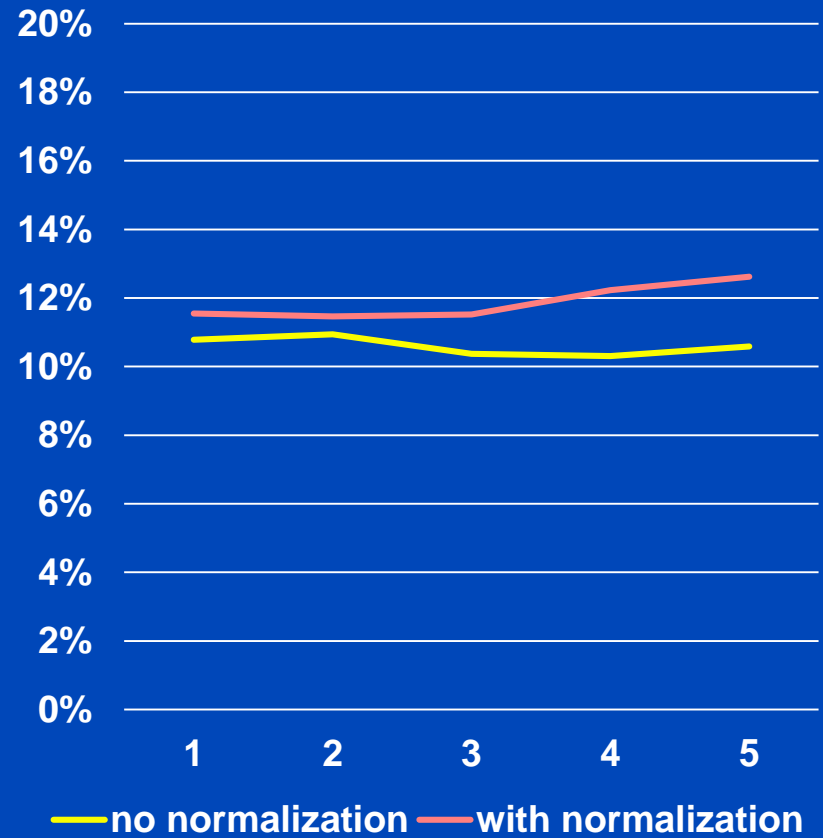


Input Normalization: [0, 1]

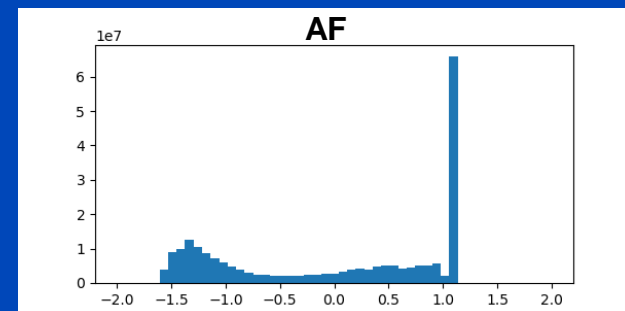
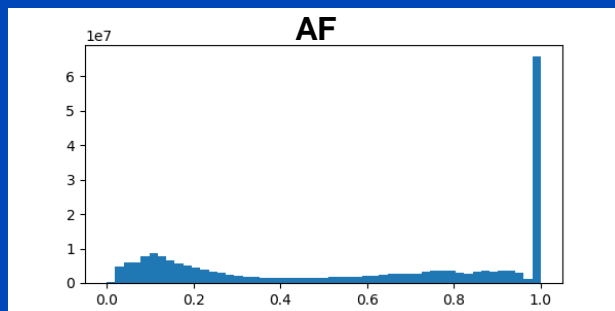
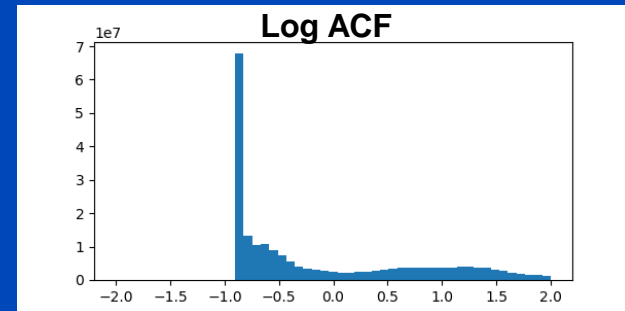
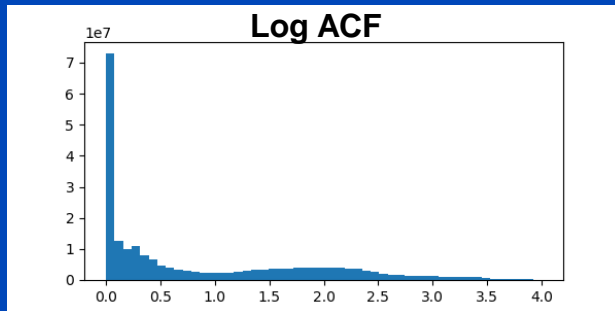
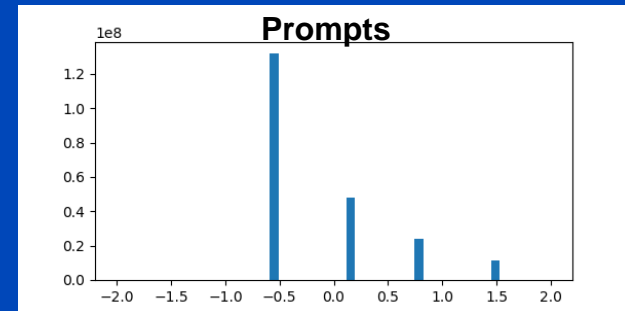
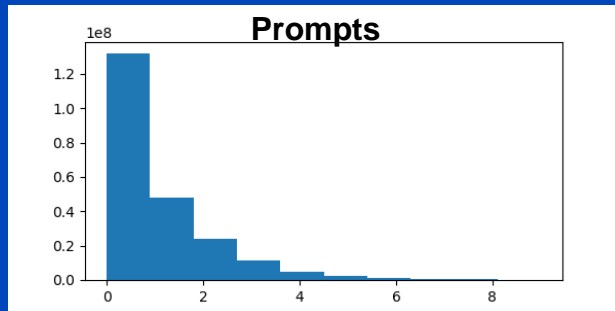
Training NMAE vs. Batches



Validation NMAE vs. Epochs

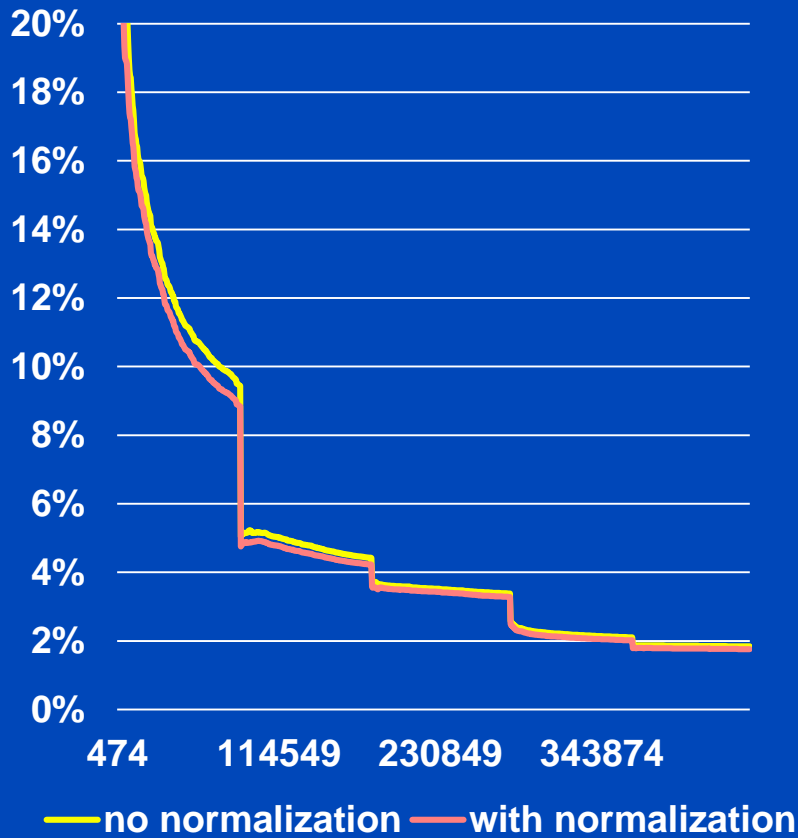


Input Normalization: Zero Mean, Unit Variance

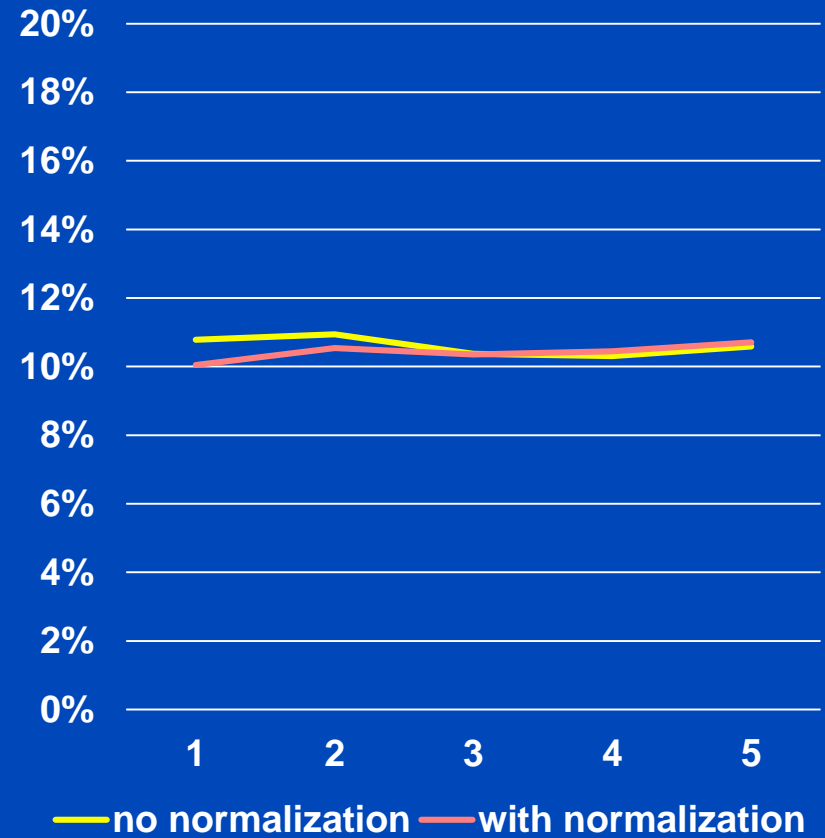


Input Normalization: Zero Mean, Unit Variance

Training NMAE vs. Batches



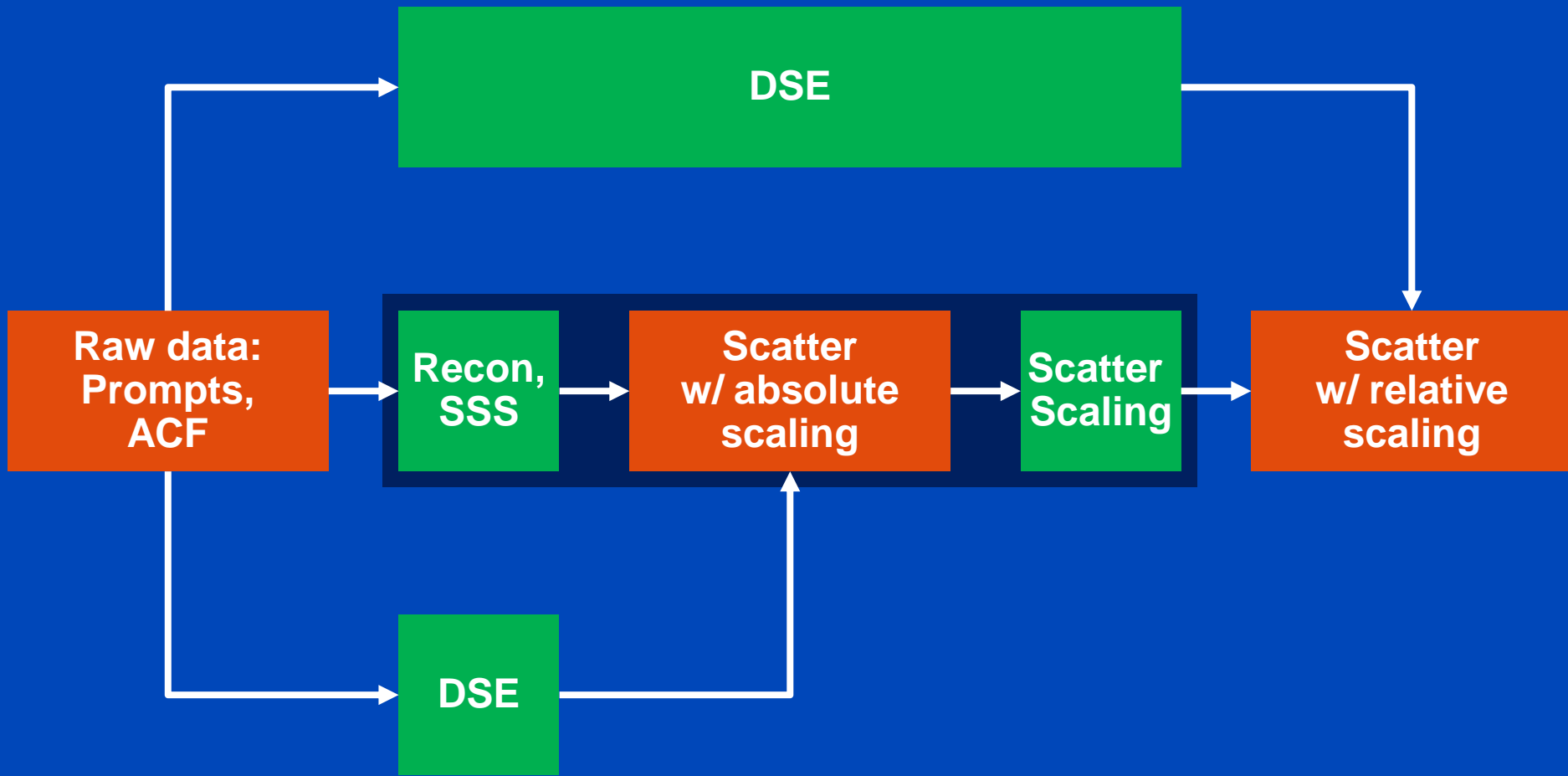
Validation NMAE vs. Epochs



Specific Investigations

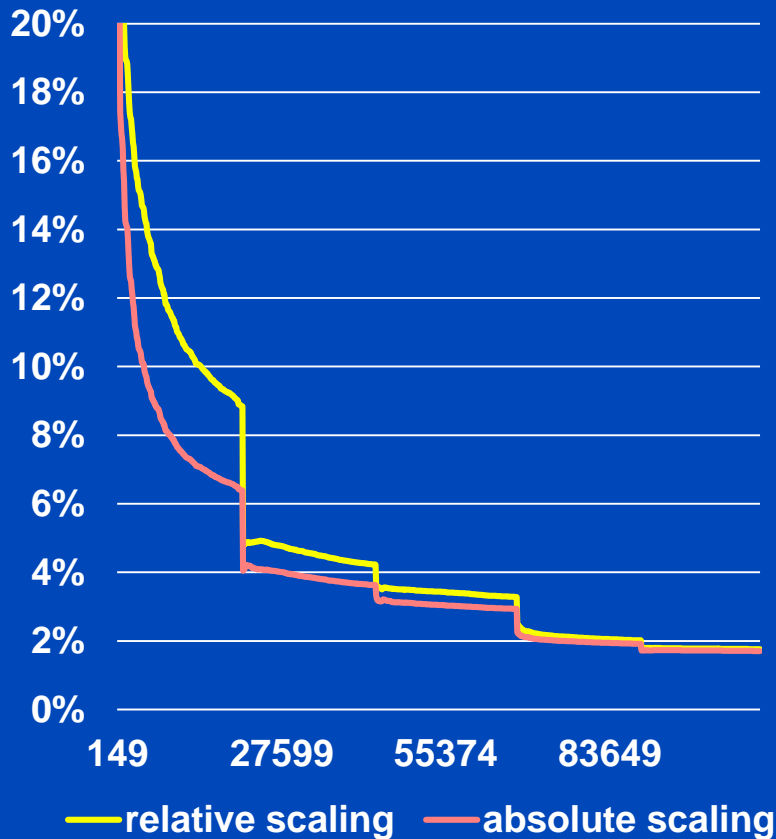
- Sinograms vs. projections
- Choice of input features
 - Emission *and/or* attenuation
 - Redundant combinations
- Number of samples
 - Data augmentation
 - Number of bed positions
- Transformations
 - Gap filling of prompts
 - Normalization of inputs
- Scatter scaling

Scatter Scaling

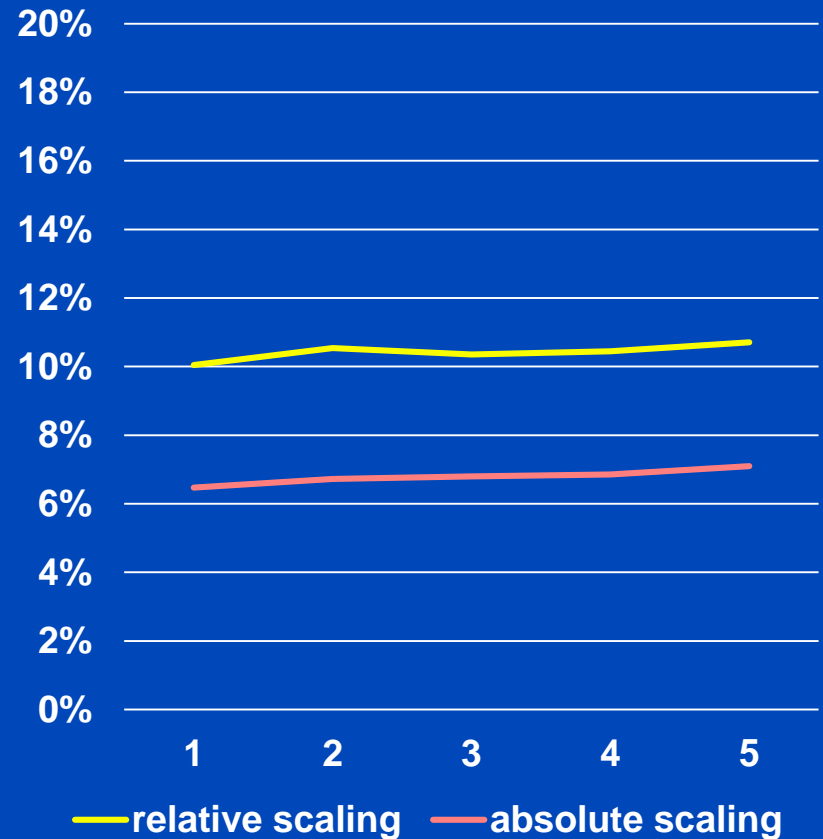


Scatter Scaling

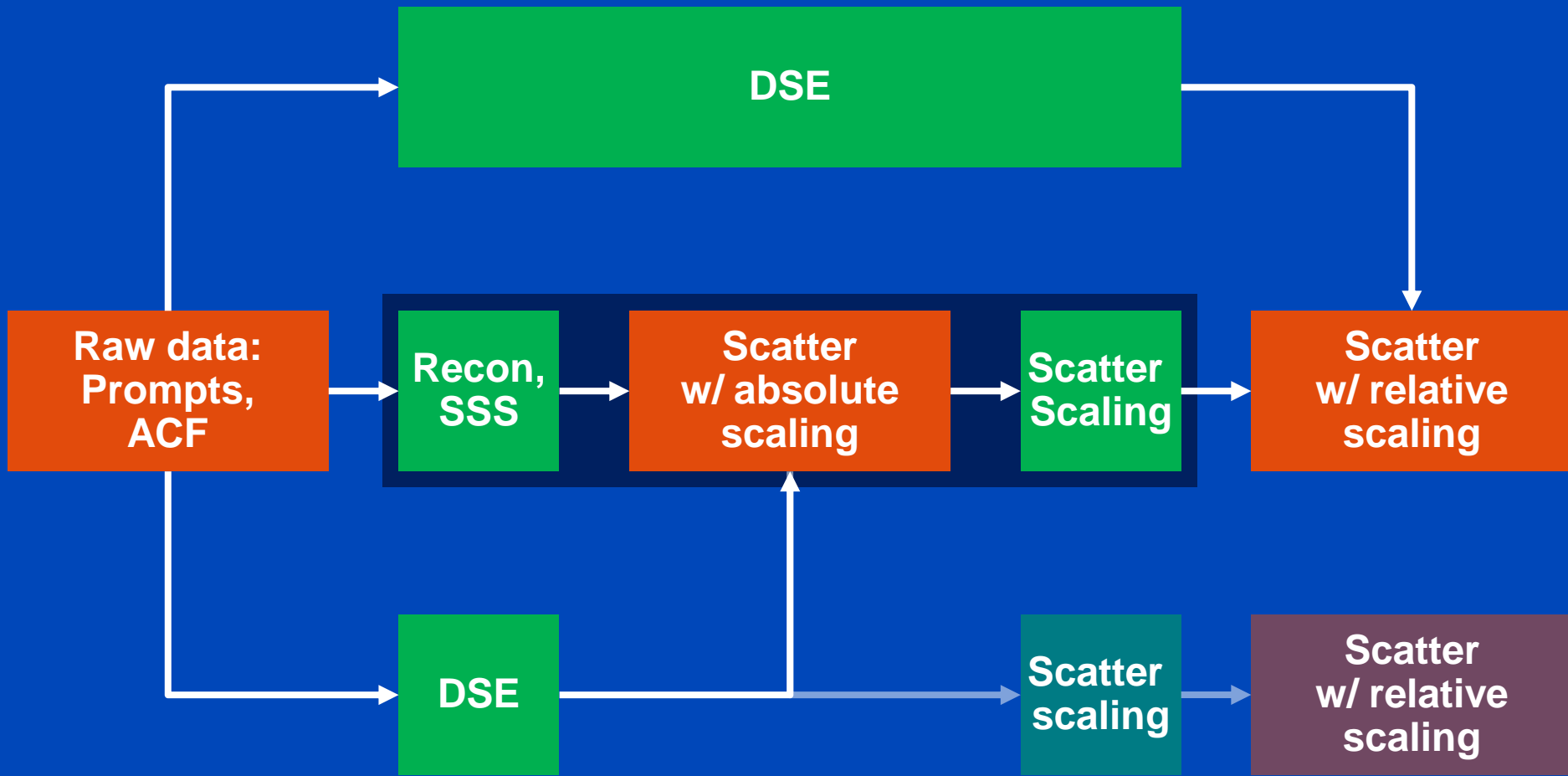
Training NMAE vs. Batches



Validation NMAE vs. Epochs



Scatter Scaling



Conclusion

- A U-Net CNN can reproduce Siemens SSS with $<7\%$ NMAE
- No improvements seen by
 - additional bed positions (less specialized CNN, $+3\%$ NMAE)
 - redundant features (only for smaller dataset)
 - gap filling, input normalization
- Improvements seen by
 - using projections rather than sinograms ($\sim 5\%$ NMAE)
 - data augmentation ($\sim 2\%$ NMAE)
 - using emission *and* attenuation data ($\sim 2\%$ NMAE)
 - training without scatter scaling ($\sim 4\%$ NMAE)
- Aim: **Deep Scatter Estimation** trained with **Monte Carlo** scatter

Thank You!



The 6th International Conference on Image Formation in X-Ray Computed Tomography

August 3 - August 7 • 2020 • Regensburg • Germany • www.ct-meeting.org



© Bild Regensburg Tourismus GmbH

Conference Chair: **Marc Kachelrieß**, German Cancer Research Center (DKFZ), Heidelberg, Germany

This presentation will soon be available at www.dkfz.de/ct.
Supported by a DKFZ Postdoc fellowship – also apply for a DKFZ PhD fellowship.
Parts of the reconstruction software were provided by RayConStruct® GmbH, Nürnberg, Germany.