4. Maravilla JA, Gopalan K, Arias AC, Lustig, M. (2022). Proc. Intl. Soc. Mag. Reson. Med. 30
5. Eggenschwiler, Florent, et al. Magn Reson Med 2012; 67(6): 1609–1619

T11.
Physics-informed conditional autoencoder: A deep learning approach for robust B_1 correction for 7 T CEST MRI

J. R. Rajput[1], T. A. Möhle[2], M. S. Fabian[1], A. Mennecke[1], J. A. Sembill[2], J. B. Kuramatsu[2], M. A. Schmidt[2], A. Dörfler[1], A. Maier[3], M. Zaiss[1]

[1]Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Department of Neuroradiology, Erlangen, Germany;
[2]Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Department of Neurology, Erlangen, Germany;
[3]Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Pattern Recognition Lab, Erlangen, Germany

Introduction Chemical exchange saturation transfer (CEST) is an MRI method that provides insights on the metabolic level [1]. Several metabolite effects appear in the CEST spectrum. These effects are isolated by Lorentzian curve fitting [2]. The separation of CEST effects suffers from the inhomogeneity of the saturation field B_1. This leads to inhomogeneities in the associated metabolic maps. Current B_1 correction methods require at least two sets of CEST-spectra [3]. This at least doubles the acquisition time. In this study, we investigated the use of an unsupervised physics-informed conditional autoencoder (PICAE) to efficiently correct B_1 inhomogeneity and isolate metabolic maps while using a single CEST scan.
Methods The proposed approach uses two neural networks (NNs), the Conditional Autoencoder (CAE) and the Physics-Informed Autoencoder (PIAE). CAE generates B_1-corrected CEST spectra at arbitrary B_1 levels and PIAE isolates CEST maps according to the 5-pool Lorentzian model (water, amide, amine, NOE, MT) [2] from the corrected CEST spectrum. The 5-pool model was described as follows

$$Z(\Delta\omega) = 1 - L_{DS} - L_{ssMT} - L_{Amine} - L_{rNOE} - L_{Amide}, \quad (1)$$

where L denotes the Lorentz function. Both NNs together formed the proposed PICAE method. Both NNs were trained with the mean square error with CEST measurements at 3 B_1 levels from four healthy subjects and tested with two tumor patients and one healthy subject. The acquisition time per B_1 level was 6:42 min. The proposed method was compared with the conventional method, which used interpolation to produce a B_1-corrected CEST spectrum using at least two acquisitions and Lorentzian line fitting to produce CEST maps from the corrected spectrum.
Results Fig. 1 shows Amide metabolic maps isolated from B_1-uncorrected and B_1-corrected CEST Spectra. B_1-correction and fitting was performed using conventional pipeline [2,3]. Red circles indicate the shortcomings of the conventional pipeline, as $B_1 \sim 1$, i.e., uncorrected fit $B_{1nom} = 0.72$, should have higher intensities than corrected fit $B_1 = 0.6$. Moreover, the conventional result for corrected fit $B_1 = 0.8$ completely failed, as most voxels are extrapolated for this value. In contrast, Fig. 2, which shows the result of the PICAE fit, is robust to B_1 inhomogeneities, as the intensities are lower for the 0.6-correction fit and higher for the 0.8-correction fit than for the uncorrected fit of $B_{1nom} = 0.72$.
Discussion In this work, we analyzed the use of deep learning approach to generate B_1-robust CEST contrast maps at arbitrary B_1 levels (cf. Figure 3 a, b, c), which requires multiple acquisitions in conventional methods. This is important because the B_1 dispersion contains information about the exchange rates and concentration of metabolite protons, paving the way for their quantification (cf. Figure 3d). In addition, the optimal B_1 can often only be selected at post-processing during the analysis of the clinical data, as different pools in the CEST spectrum are highlighted at different B_1 levels.
Conclusion The proposed method enables (i) a reduction in scan time of at least 50%, (ii) the generation of reliable CEST contrast maps that are robust to B_1 inhomogeneity at multiple B_1 levels, and (iii) the quantification of CEST contrast maps.

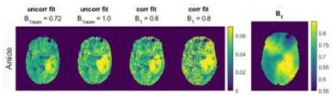

Fig. 1: Amide metabolic maps generated with conventional method and B_1 inhomogeneity map. Red circles indicate the subregion where B_1 is almost equal to the nominal setting.

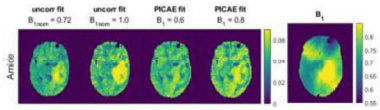

Fig. 2: Amide metabolic maps generated with the proposed PICAE method and B_1 inhomogeneity map

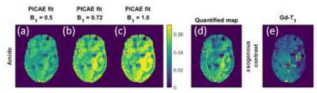

Fig. 3: Amide metabolic maps generated by the proposed PICAE method using a single scan (a, b, c) at arbitrary B_1 levels, (d) showing the quantified amide map, and (e) the exogenous Gadolinium contrast.

References
1- Van Zijl PC et al. Magn Reson Med. 2011;65(4):927–48
2- Mennecke A. NMR Biomed. 2022
3- Windschuh J et al1. NMR Biomed. 2015;28(5):529–3

T12.
On the use of autoencoder to denoise diffusion MRI

S. Soundarresan[1], Z. Tan[1], P. Liebig[2], R. Heidemann[2], F. Laun[1], F. Knoll[1]

[1]Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Erlangen, Germany;
[2]Siemens Healthineers, Erlangen, Germany

Introduction Diffusion MRI (dMRI) is a powerful imaging modality for clinical diagnosis of stroke and tumors, as well as for the investigation of brain microstructures. However, dMRI suffers from long acquisition time, low spatial resolution, and low signal-to-noise ratio (SNR). To improve dMRI, joint k-q-space sampling and reconstruction [1–2] has been proposed to jointly reconstruction all diffusion-weighted images (DWI) by exploiting the complementary sampling pattern. Joint reconstruction, however, requires the knowledge of proper image priors. In this work, we trained a autoencoder neural network to learn the q-space prior and employed it as a denoiser.
Methods A two-shot EPI was used to collect the dMRI data at 7 T (Magnetom Terra, Siemens, Erlangen). The acquisition parameter were: 1.2 mm isotropic resolution, FOV 220 mm, and b-value of 1000 s/mm2. The dataset consisted of 32 diffusion directions with TE = 47 ms and TR 4300 ms. The total acquisition time was 5 min for 94 slices with in-plane acceleration factor of 3 and slice acceleration factor of 2.

The DAE was trained using a dictionary created using the biophysical model. The initial parameters required to create the dictionary were the b and g values that were obtained from the acquisition protocol. The free model parameters are discretized within their biophysical range as D in [0.1, 4] mm2/s. The simulated diffusion signals were modulated with white Gaussian noise at various levels. Both the real and corrupted data (with and without noise) were used for training. The training was performed using about 700,000 instances of the diffusion signals.

The network consisted of four fully connected layers with input size same as the q-space. Three DAEs were trained with data converged to 10, 15 and 5 neurons in the bottleneck layer for testing purposes. Standard DAE training procedures were utilized in Pytorch with stochastic gradient descent (SGD). The atoms were randomized during each epoch to help achieve faster convergence. 100 epochs with batch size of 210 were used with the mean-squared error (MSE) loss function. Once the DAE was trained, the diffusion signals from various recordings were transformed to image space by using SENSE or MUSE. These were then passed through the trained DAE model to generate denoised images. A schematic of this is presented in Fig. 1.

Results The latent space for the DAE is decided based on experimenting. The dataset"s b and g values were used to generate a dictionary. This dictionary was divided into training set, validation set and testing set with a distribution of 70%, 20% and 10%. The latent space of the DAE is varied from 1 to 20 and trained and validated using the training set and validation set. An analysis of the performance of the trained models was made based on MSE on testing set. The MSE vs latent space graph can be seen in Fig. 2.

After a latent of 6, there was extremely little decrease in the MSE. A latent space of 10 was hence chosen. Plus, compared to the MSE of the SVD based denoising method, the DAE method performs much better on the test data.

The k-q-space data obtained for 7 T dataset was reconstructed via parallel imaging. These DWIs were then denoised by mapping it to the learned latent space data using the trained DAE. As shown in Fig. 3, the DAE denoising on MUSE [3] reconstructed DWIs works visually better when compared to the SVD method with the same latent space of 10.

Discussion and Conclusion Autoencoder is effective in learning the q-space prior for the denoising of diffusion MRI.

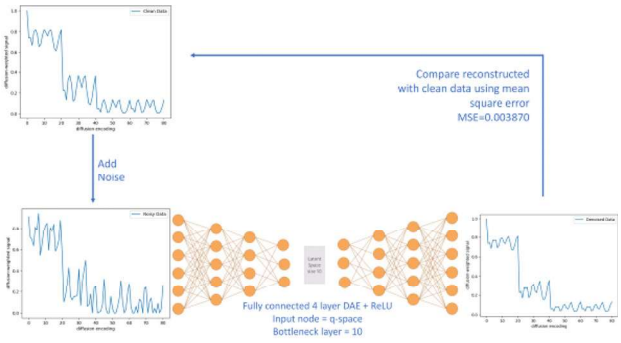

Fig. 1: Illustration of the DAE model training procedure for diffusion-weighted signal

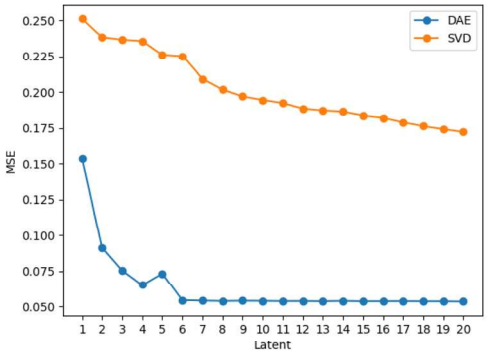

Fig. 2: Comparison on the accuracy of the DWI reconstruction between the DAE nonlinear subspace learning and the SVD linear subspace learning.

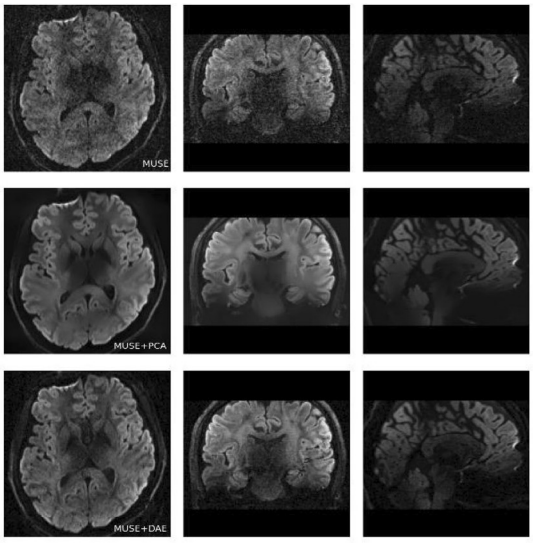

Fig. 3: Comparison of denoising with REPCOM (row 2) and DAE (row 3) anfter MUSE reconstruction (row 1) with each column representing a view from x,y and z axes

References

[1] F Lam, Y Li, X Peng. Constrained Magnetic Resonance Spectroscopic Imaging by Learning Nonlinear Low-Dimensional Models. *IEEE Trans Med Imaging* (2020).

[2] Mani M, Magnotta VA, Jacob M. qModeL: A plug-and-play model-based reconstruction for highly accelerated multi-shot diffusion MRI using learned priors. *Magn Reson Med* (2021).

[3] Chen NK, Guidon A, Chang HC, Song AW. A robust multi-shot scan strategy for high-resolution diffusion weighted MRI enabled by multiplexed sensitivity-encoding (MUSE). *NeuroImage* (2013).

T13.
Simultaneous optimization of MR sequence and reconstruction using MR-zero and variational networks

H. N. Dang[1], J. Endres[1], S. Weinmüller[1], A. Maier[1], F. Knoll[1], M. Zaiss[1,2,3]

[1]*Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Department Artificial Intelligence in Biomedical Engineering, Erlangen, Germany;*