

# On the use of autoencoder to denoise diffusion MRI

## Introduction

Diffusion Magnetic Resonance Imaging (dMRI) is a specialization of MRI where the movement of water molecules in biological tissues is studied by measuring the diffusion. One of the main challenges in dMRI reconstruction is that the raw data is often corrupted by noise and artifacts. This can be caused by a variety of circumstances of acquisition settings, such as the limitations of the hardware used to acquire the data, or the presence of metal objects in the body. Other factors that affect the image quality of an dMRI scan are motion, noise, and the specific pulse sequences used. In case of fully sampled data, the challenge is the time of acquisition. Longer acquisition times mean that patients must remain still for a longer period, which can be uncomfortable and even painful for some patients. This can also lead to motion artifacts.

In order to reduce this, undersampling is employed while obtaining the raw data. Even though undersampling reduces acquisition time, risk of motion artifact and improve imaging throughput and patient comfort, it can cause other issues in reconstruction such as reduced spatial resolution and reduced Signal-to-Noise ratio (SNR). In order to remove these artifacts and improve the quality of the images, various reconstruction techniques have been developed.

Although joint k-q acceleration schemes can simultaneously improve k-space and q-space coverage, the reconstruction is challenging. Since each diffusion encoding is highly undersampled, complementary information from k-and q-domains are utilized to design the reconstruction of the individual DWIs. By acquiring data in k-space at a higher resolution than is typically used for MRI, and then applying k-q space reconstruction to the data, researchers can create images with a higher spatial resolution than would be possible with conventional MRI techniques. The disadvantage of this will be the increase in is acquisition time and demands high acceleration for practical imaging.

Some literature [1-4] proposed to jointly reconstruct all DWIs simultaneously by exploiting the complimentary information in both domains. Reconstruction methods that rely on large dictionaries of q-space signals are typically employed to provide high acceleration capabilities.

## Methods

We employ MAGNETOM Terra 7T scanner to obtain brain scans. A single shot EPI acquisition with Stejskal-Tanner diffusion encoding is used to collect the dMRI data.

Dataset is obtained with 2-shot EPI in 7T: 1.2 mm isotropic resolution (FOV: 220 x 220 mm<sup>2</sup>, slice thickness: 1.2 mm) with a b-value of 1000 s/mm<sup>2</sup>. The dataset consists of 32 diffusion directions with TE = 47 ms and partial Fourier (pF) sampling at 75%. The TR

was 4300 ms and the total acquisition time was 5 mins for 94 slices at 7T scanner with in-plane acceleration factor of 3 and slice acceleration factor of 2.

The DAE is trained using a dictionary of dMRI data created using the biophysical model [5]. The initial parameters required to create the dictionary are the b and g values that are obtained from the settings of the measurement. So, the DAE will be retrained every time a different acquisition is used (b-value, sampling points, etc.). The free model parameters are discretized within their biophysical range as D in  $[0.1, 4] \text{ mm}^2/\text{s}$ .

Because the reconstruction involves the recovery of DWIs from noisy k-space data, the phase compensated reconstruction can result in DWIs with small residual noise. 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 7,00,000 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  $2^{10}$  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.

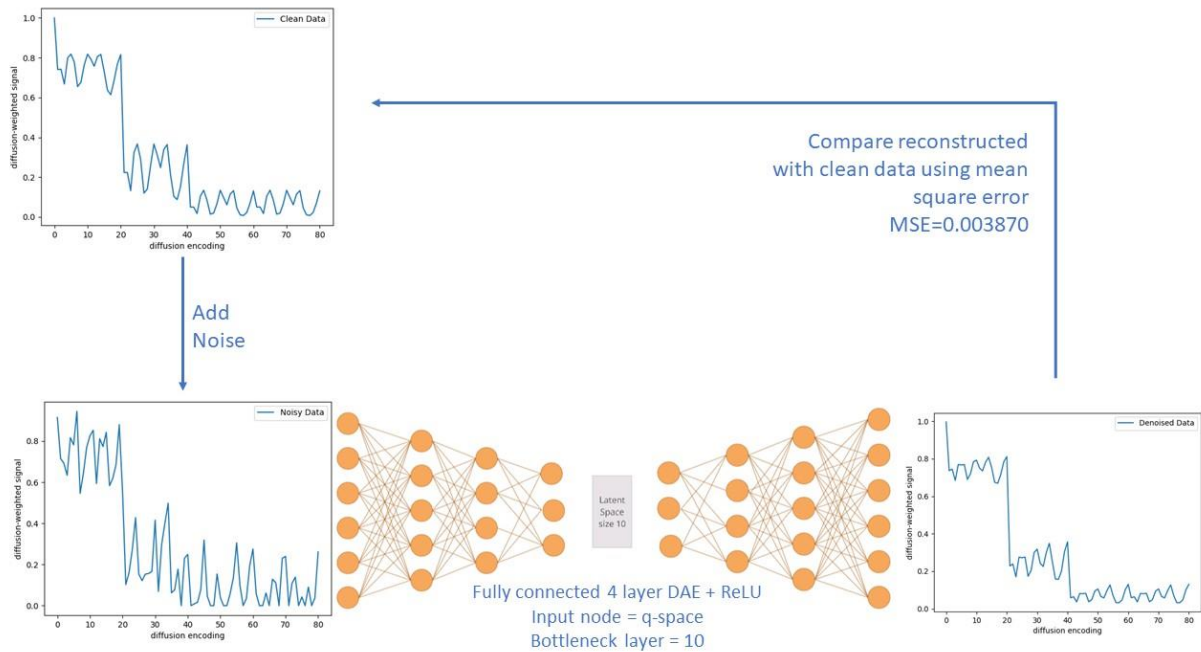


Fig 1 Illustration of the DAE model training procedure for diffusion-weighted signal

## 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.

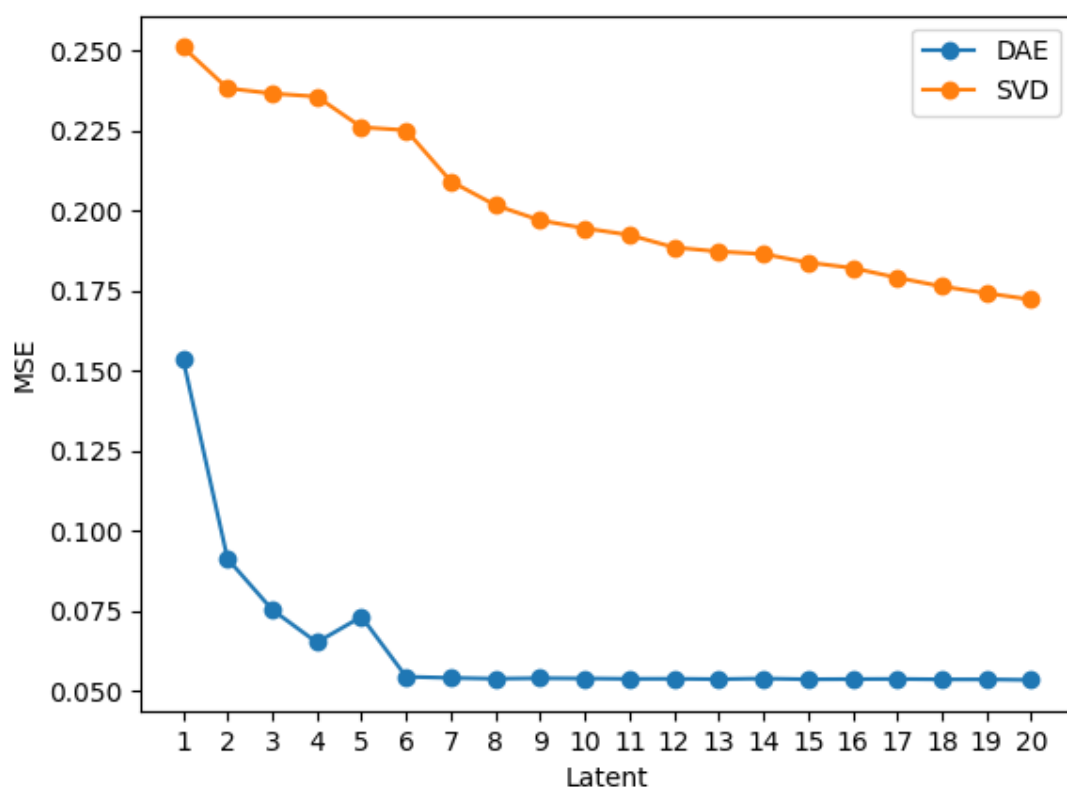


Fig 2 Comparison on the accuracy of the DWI reconstruction between the DAE nonlinear subspace learning and the SVD linear subspace learning.

It can be seen that after a latent of 6, there is extremely little decrease in the MSE. A conservative choice is made and a latent space of 10 is hence chosen to do any further analysis of performance of DAE.

It is also seen that, in comparison of the MSE of the PCA/SVD based denoising method, the DAE method performs much better on the test data.

The  $k$ - $q$ -space data obtained for 7T dataset is converted to image space by using MUSE reconstruction algorithm. This image space data is then denoised by mapping it to the learned latent space data using the trained DAE that is trained using the dictionary generated by the  $b$  and  $g$  values of the dataset. It can be seen in figure 3 that the DAE

denoising works visually better when compared to the PCA/SVD method of denoising with the same latent space of 10.

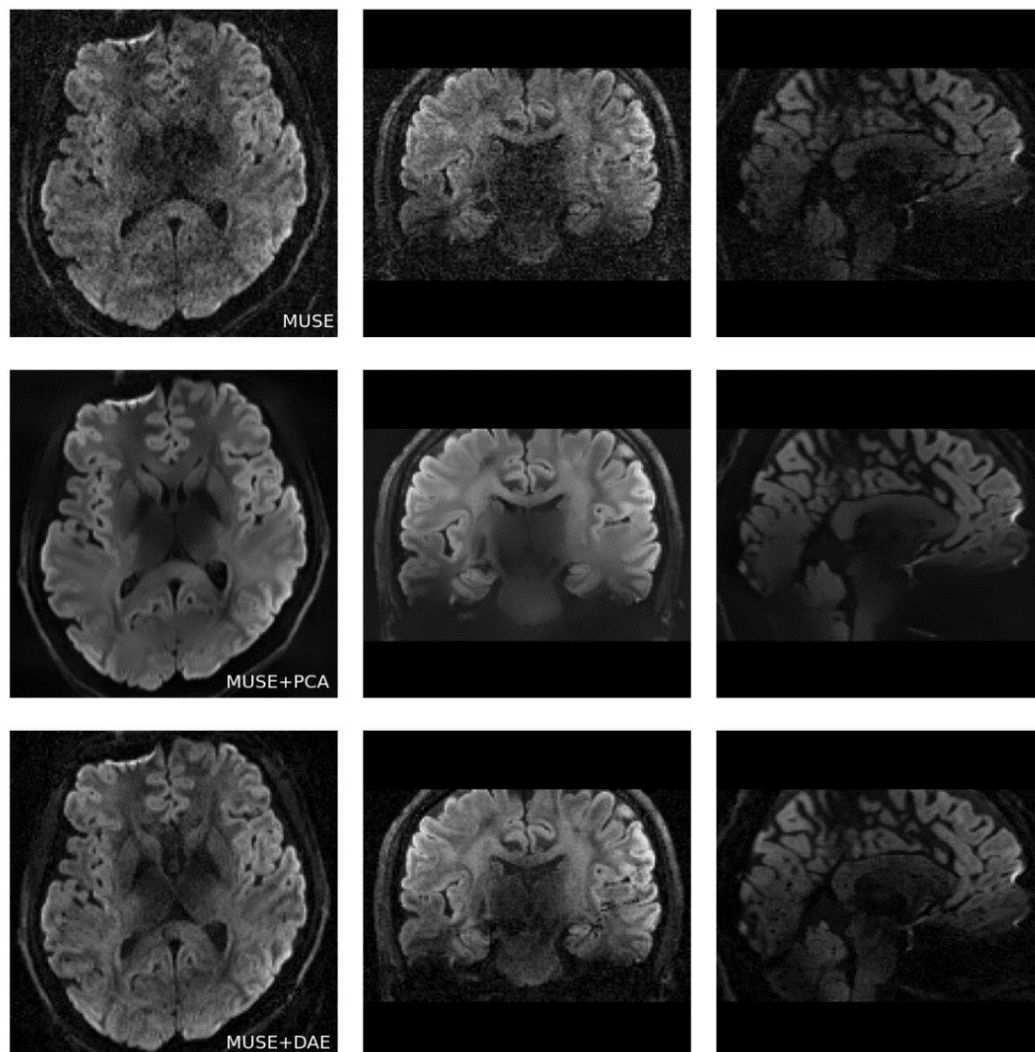


Fig 3 Comparison of denoising with REPCOM (row 2) and DAE (row 3) after MUSE reconstruction (row 1) with each column representing a view from x,y and z axes

## Conclusion

In this paper the use of autoencoder to denoise diffusion MRI is investigated. For this purpose, the denoising autoencoder was trained using a dictionary generated using a biophysical model. The DAE's latent space was tested from 1 through 20 and was concluded that the DAE with latent space 10 outperforms the denoising done using the principal component analysis for 7T datasets.

The DAE is retrained with a biophysical model based dictionary every time a new initial parameter was taken to acquire the scans. This results in eliminating the need for large dictionaries. Since the autoencoder outperforms the principal

component analysis method with a latent space of 10, it gives a better approach into denoising the dMRI signals.

## References

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