

# A deep learning network from downsampled diffusion-weighted MRI k-space to image-space

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**Abstract**— Advanced Magnetic Resonance Imaging (MRI) techniques, such as Diffusion Weighted Imaging, usually require long acquisition times and an open challenge is to reduce the acquisition time more and more in order to allow their use in the clinical routine. Downsampling k-space is a way to speed up MRI, but this can generate artefacts in the resulting images when reconstructing them with standard Fourier transform methods.

Here, we used deep learning to perform the inverse Fourier transform from k-space to the Diffusion Weighted (DW) images, and used it to assess the quality of images obtained from significantly reduced k-space acquisition strategies. The hypothesis is that a deep learning algorithm would preserve data quality, learned from the fully sampled k-space association. We tested our deep learning algorithm by reducing the number of acquired k-space rows by 30%, which would correspond to a total acquisition time reduction. We considered different types of k-space downsampling. All the trained networks were able to map the relationship between k-space and DW images, reducing artefacts.

In conclusion, this work paves the way to designing acquisition strategies for fast diffusion imaging.

**Keywords**— k-space, deep learning, reduce time acquisition, diffusion magnetic resonance.

## I. INTRODUCTION

MAGNETIC resonance imaging (MRI) is a very powerful tool used in the clinical field to diagnose, to monitor and to study mechanisms behind human behaviour, function and dysfunction. The great power of MRI depends on the fact that this tool can be exploited to investigate several organ systems and that it can be made sensitive to specific properties of the tissues, such as the diffusion of water molecules to probe tissue microstructure. Diffusion Weighted Imaging (DWI) is sensitive to Brownian motion of water molecules in tissue and, hence, to the microstructure and its alterations in pathological conditions [1][2].

The use of MRI in the clinic is limited to qualitative assessments of brain lesions and morphology due to both high costs and long acquisition times for quantitative MRI.

Furthermore, it is to note that when an MRI acquisition is performed, the signal received with the coil is stored as an image containing the spatial frequency information of the object, called k-space. Importantly, each point of the k-space contains phase and frequency information about the signal coming from the entire sample. For this reason, applying the inverse Fourier transform (FT) to the k-space provides the image in physical space [3] [4].

Moreover, it is known that k-space is highly redundant [5]. It is indeed endowed with Hermitian symmetry [4]. Traditionally, the relationship between k-space data and image data is the Fourier transform (FT) [3].

Here we aimed to shorten the acquisition times of DWI of the brain reducing k-space coverage (i.e. the signal) and substituting the FT operation with a deep learning network, while maintaining image quality. In this way, one of the novelty of our method is that it was possible to downsample the k-space, in order to reduce the acquisition time, obtaining an image that is very similar to the one reconstructed from the entire k-space.

Previous work used a deep learning network to pass from the k-space to the DW physical image of the breast with the main goal of reducing DW-related artifacts [6]. However, in this work the network used as its input the entire acquired k-space, instead of a downsampled version like we did here.

We therefore optimised a network previously proposed [7] for reconstructing T1 and T2 weighted images from their k-space and adapted it to the specific case of DWI data [1]. One of the challenges is that DWI can produce very different contrasts depending on the applied diffusion weighting; mathematical or signal models can then be fitted to DWI data to obtain microstructure parameters maps. The automated transform by manifold approximation (AUTOMAP) [7] network was therefore adapted and optimised here to work with DWI k-space data, independently on the diffusion weighted applied. We gave it as input the k-spaces of the diffusion acquisitions and as output the corresponding magnitude images.

## II. METHODS

### A. Subjects

The database included images of 18 healthy controls (HC, 13 Females, 55.2±9.4 years), 8 primary progressive multiple sclerosis (PPMS, 3 Female, 56.3±9.9 years), 2 relapsing-remitting multiple sclerosis (RRMS; 1 Females, 64±3.6 years), and 31 secondary progressive multiple sclerosis (SPMS; 21 Females, 55.3±7.3 years). 18 subjects were acquired a second time, 18 months after baseline. The total number of datasets was 77.

## B. MRI acquisition

A 3T Philips Ingenia CX scanner was used. The Diffusion Weighted (DW) imaging protocol included a spin-echo EPI with TR = 6287 ms, TE = 96 ms, 76 volumes with b = 1000/2000/2800 s/mm<sup>2</sup> (20/20/36 DW per b-value) and 3 b0 volumes. The spatial resolution was 2x2x2 mm<sup>3</sup> and the matrix size was 112x112x72.

## C. Network design

Each DW dataset was used as an independent sample, regardless of whether it belonged to a subject previously acquired. This choice depended by the fact that the problem to be solved was to associate each k-space with its magnitude image. Since the problem could be reduced to assess a regression between datasets, i.e. finding a relationship between input and output, instead of classifying them in different groups, we therefore used the entire dataset regardless the group (i.e., healthy subject or patient), gender (female or male), or any other demographic feature. The 77 acquisition samples were divided as follows: 53 acquisition samples were used for training, 12 for validation and 12 for test. In each set (training, validation and test) there were both healthy and MS subjects.

The magnitude image was calculated for each slide from real (Re(DW)) and imaginary images (Im(DW)):

$$\text{magnitude image} = \sqrt{\text{Re}(DW)^2 + \text{Im}(DW)^2} \quad (1)$$

Using the Fourier transform (FT), the k-space of the magnitude images was calculated:

$$k\text{-space} = FT(\text{magnitude image}) \quad (2)$$

Only DW volumes with a b-value of 0 or 1000 s/mm<sup>2</sup> were considered, so 23 volumes were used for each acquisition dataset. We limited the number of volumes by using the most commonly acquired b-value [8] in order to reduce the amount of data and thus the training time to cope with long calculation times and memory problems. Consequently, for training, the number of input data was 76337 (53 subjects, for each subject 23 volumes, and for each volume about 63 slices), for validation 18699, and for test 18446.

The k-space data had to be normalised before being passed as input: for each batch size, the real and imaginary part was divided by magnitude of the maximum of all values in the entire database.

The 2D k-space matrices in axial planes were then given as input to the network. The real and imaginary parts of the k-space were provided as 2 input channels (m x n x 2).

The output target for the network was the magnitude image corresponding to the DW k-space data.

We adapted the AUTOMAP architecture [7]. The network was developed using TensorFlow (Keras) [9] and each network training was run using an NVIDIA Tesla T4 GPU.

We had a k-space of size m x n: the complex data of the k-space were separated into real and imaginary parts and were given to the network as input to two different channels (m x n x 2). The network architecture is pictured in Fig.1.

This architecture was made of two fully connect layers (FC)

at the beginning, followed by three convolutional layers (Conv). Because of the fully connected layers, the number of network parameters increases noticeably and makes training very slow. For this reason, it was necessary to resize the k-space from a 112x112 matrix to a 64x64 one. The k-space and DW images were resampled using spline interpolation.

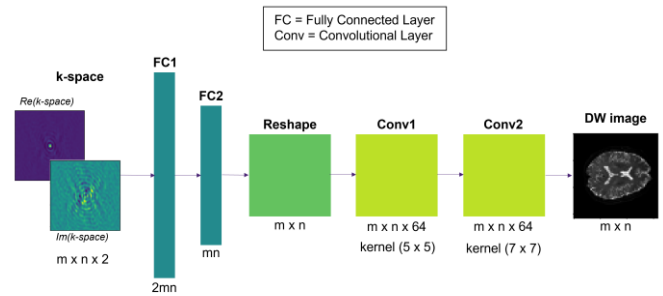


Fig. 1: Architecture of AUTOMAP.

## D. Network training

The tuning of the hyperparameters was conducted by giving as input the k-space and as output the corresponding DW magnitude images, both of reduced size i.e. 64x64; we called this experiment *from 64 to 64*.

We searched manually for the best hyperparameter configuration by training the network several times and changing the loss function, activation functions and optimizer. The best hyperparameters were selected minimizing the Root Mean Square Error (RMSE) on the validation set.

In order to prevent the overfitting we applied data augmentation on the fly [10] using two different ways: images were randomly rotated anti-clockwise by 0, 90, 180 or 270° and images were scaled in intensity by a random value so that they became darker or brighter.

## E. Network applications

Once the hyperparameters of the network were fixed, four experiments were considered to train the network accordingly:

- *from 64 to 112*: from a k-space of size 64x64 to a magnitude image of 112x112, increasing the resolution along each of the 2D dimensions of the image from 64 to 112. The DW magnitude image was therefore in the original space.
- *Zero fill*: from a k-space of size 64x64, with the last 19 rows filled with zeros, to a corresponding magnitude image of size 64x64.
- *Delete rows*: from a k-space of size 45x64, where the last 19 rows were deleted, to a corresponding magnitude image of size 64x64.
- *Mixed downsampling*: from a k-space of size 45x64, where the last 19 rows (top) or the first 19 rows (bottom) were deleted, to a corresponding magnitude image of size 64x64. This last network aims to test whether AUTOMAP can cope with different downsampling or needs retraining every time k-space

is sampled differently.

In the last three experiments we reduced the k-space acquisition of 30%, applying some downsampling by deleting k-space rows from different positions. Importantly, k-space was downsampled in ways that could be easily implemented from a pulse sequence design point of view, i.e., directly modifying sequences on an MRI scanner.

#### F. Quantitative evaluation

To compare the DW magnitude images obtained with the traditional FT of k-space and those obtained with the network, it was necessary to normalise the intensity of both images to eliminate simple scale factors. For each acquisition sample, both DW images (GT and network) were divided by the value of the maximum of the respective 4D volume (i.e. including all 23 DW volumes), limiting the calculation to voxels in the brain.

To quantitatively assess how much the two images (DWI GT and DWI network) differed, we calculated the difference image considering the case *from 64 to 64*.

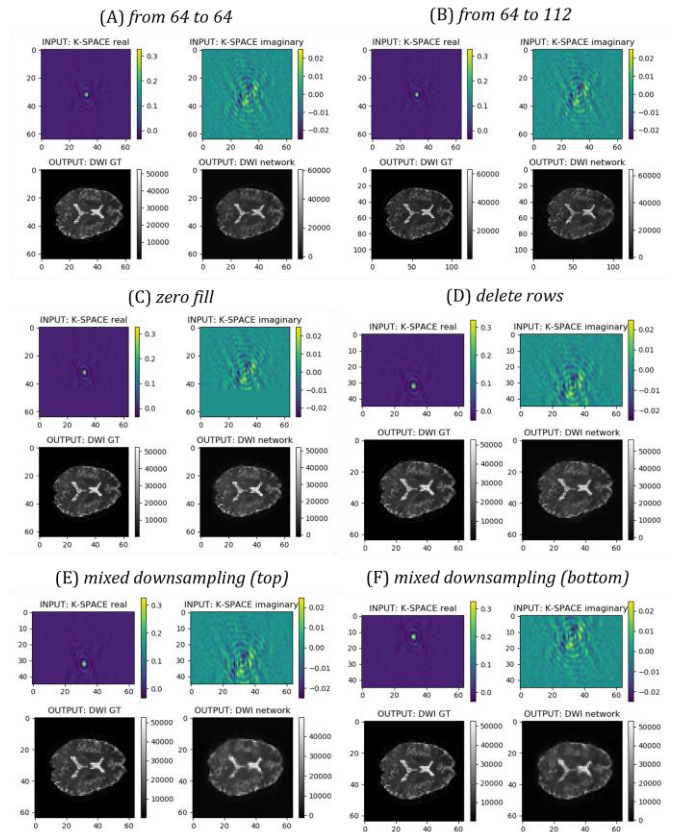
For the experiment with mixed downsampling, we tested the network by giving as input once the first 45 rows (top) and once the last 45 rows (bottom) of k-space.

The Root Mean Square Error (RMSE), Mean Absolute Error (MAE) and Structural Similarity Index (SSIM) [11] calculated between the magnitude DW image and the network output within the brain were chosen as performance metrics.

### III. RESULTS

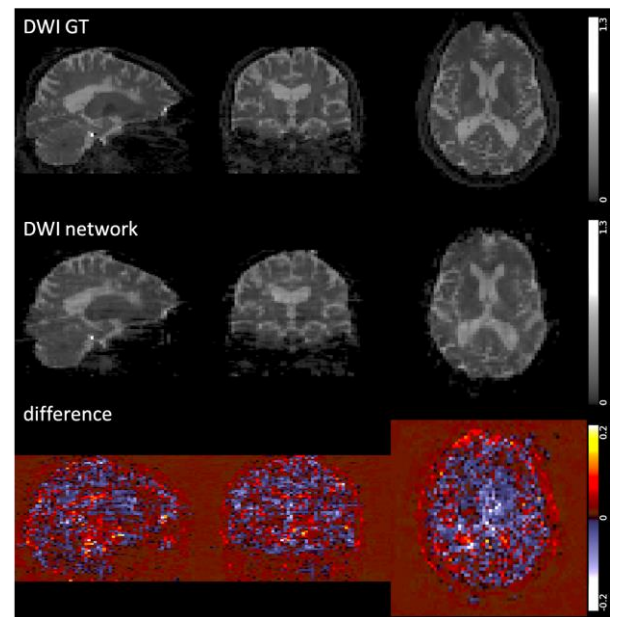
The best hyperparameters were found to be: the sum of RMSE and SSIM as loss function, the hyperbolic tangent for the fully connected layers and the REctified Linear Unit (ReLU) for the convolutional layers using as activation function and the Root Mean Square Propagation (RMS Prop) as optimizer.

Fig. 2 shows the input, the k-space with real and imaginary part, the desired output (GT) and the output of the network of the performed experiments: from 64 to 64 (A), from 64 to 112 (B), zeros fill (C), delete rows (D), mixed downsampling (top) (E) and mixed downsampling (bottom) (F).



**Fig. 2:** Each different experiment is shown in each image from (A) to (F). The first row shows the input to the network: on the left the real part and on the right the imaginary part of the k-space. The second row shows the magnitude Diffusion Weighted (DW) image: on the left the ground truth (GT) (desired output) and on the right the output of the network.

Fig. 3 shows for a random test subject the DW images, i.e., DWI GT and DWI network, after the intensity normalization and their difference image in the case *from 64 to 64*.



**Fig. 3:** The first row shows the DWI GT, the second row the DWI network and the third row the image of the difference between the first two rows for a random test subject.

Table I shows the performance metrics (mean and standard deviation) between the GT DW images and the network DW images, calculated on the 12 test subjects over voxels that belong to the brain mask.

TABLE I: PERFORMANCE METRICS ON THE TEST SUBJECTS FOR EACH NETWORK EXAMPLE.

	RMSE	MAE	SSIM
<i>from 64 to 64</i>	0.035 ± 0.004	0.022 ± 0.004	0.757 ± 0.057
<i>from 64 to 112</i>	0.020 ± 0.007	0.015 ± 0.006	0.734 ± 0.228
<i>zeros fill</i>	0.030 ± 0.012	0.020 ± 0.007	0.660 ± 0.208
<i>delete rows</i>	0.032 ± 0.01	0.021 ± 0.007	0.655 ± 0.206
<i>mixed downsampling (top)</i>	0.034 ± 0.011	0.021 ± 0.007	0.658 ± 0.207
<i>mixed downsampling (bottom)</i>	0.034 ± 0.011	0.022 ± 0.008	0.657 ± 0.207

#### IV. DISCUSSION AND CONCLUSION

We adapted the AUTOMAP network to obtain DW images starting from the relative k-space data.

The network was trained in five different types of experiment. In the simplest case, we started with a k-space of size 64x64 and obtained an image of 64x64. In this case, the best values of the performance metrics were obtained (RMSE = 0.035±0.004; MAE = 0.022±0.004; SSIM = 0.757±0.057).

Notably, the DW images reconstructed with the network showed no region-specific bias with respect to the original ones, as demonstrated with the difference image (Fig. 3). The next four experiments were performed to reconstruct the original DW images from a reduced k-space.

The network is able to capture the relationship between k-space and DW images, even in experiments performed to reconstruct the original DW images from a reduced k-space (Fig. 2; Table I).

In the mixed downsampling case, the network was trained by considering different downsampling of the k-space, i.e. removing rows from above or below the centre of the k-space. In this case, the output obtained on the 12 test subjects achieved similar performance by applying one of the two downsampling strategies.

Furthermore, it is to note that DW images obtained with the network appear to be less noisy. The intrinsic denoising function of the network may be due to the fact that the network learns the relationship between input and output only by structured associations and since noise is random, it is not learned.

To strengthen this work, further analysis will be performed:

in the future, we will apply k-cross validation to better estimate the intrinsic power of the model and to assess it for potential overfitting. Furthermore, to evaluate the sensitivity of our DL reconstructions to the presence of pathology, we will calculate quantitative maps from DW images in both cases (i.e., GT and network) and perform group comparisons between healthy and neurological cohorts. We will therefore determine whether the images reconstructed with the network are able to maintain the details of the original images and are sensitive to pathology (e.g. in lesions of subjects with multiple sclerosis).

Furthermore, it would be useful to check whether it would be possible to further reduce the number of k-space rows without losing the quality of the DW image.

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