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gNET: gSlider Self-Supervised Neural Network for Accelerated Reconstruction of Super-resolution Diffusion MRI

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Synopsis

Keywords: Diffusion Reconstruction, Diffusion/other diffusion imaging techniques, gSlider, deep-learning, self-supervised, AI/ML Image Reconstruction

Motivation: gSlider utilizes radio-frequency encoding to acquire high and isotropic resolution brain diffusion-MRI with high SNR. However, this comes at the cost of prolonged acquisition time, which also increases the sensitivity to motion.

Goal(s): This work proposes gSlider Network (gNET) to accelerate gSlider from acquisitions with jointly subsampled RF- and q-space.

Approach: The self-supervised model was trained and tested on a 1mm^3 resolution BUDA-gSlider dataset (T_{acq} = 32 min). FSL and the DIMOND self-supervised were used to estimate the diffusion parameters.

Results: gNET achieved an acceleration factor of R=2 and, when combined with DIMOND, reached a total R=4-fold (T_{acq} = 8 min).

Impact: gNET facilitates super-resolution dMRI by reducing the acquisition time by 4-fold with high fidelity. Its application may propel new discoveries in the neuroscientific field and the clinical translation of the gSlider framework.

INTRODUCTION

Diffusion MRI yields valuable information on the brain's structure and connectivity and finds important applications in the diagnosis and monitoring of neurological disorders and in neuroscientific research [1]. Unfortunately, high-resolution dMRI is hampered by its inherently low SNR. Super-resolution techniques help boost the SNR and have been deployed with single-shot approaches [2,3]. More recently, gSlider-SMS achieved whole-brain in vivo sub-millimeter imaging using a RF-encoding to excite a thick slab, from which thin slice images could be resolved by inverting the RF-encoding basis. The drawback is that gSlider RF-encoding prolongs the acquisition time, which hampers its practical utility [4,5].
gSlider-SR [6] was developed to accelerate the gSlider acquisition by reconstructing RF-encoded data using a basis of spherical ridgelets, exploiting redundancies within RF-encoding basis and q-space. The present work pushes the acceleration further using a deep-learning neural network, which resulted in a final R=4-fold speed-up with high fidelity, thus facilitating the application of this encoding technique.
Code repository: https://anonymous.4open.science/r/gSliderRecon-E592/README.md

METHODS

BUDA-gSlider dataset. Acquired [7] on a Siemens 3T MAGNETOM Prisma, it is composed of whole-brain (FOV = 224 x 224 x 130 mm^3) data, separated into 26 slabs of 5 mm each, which required a 32 minutes scan. It uses MultiBand (MB) = 1, $R_{in-plane}$ = 4, partial Fourier = 6/8, TR/TE = 3000/66 ms, and two BUDA shots to yield 60 diffusion directions (b = 1500 s/mm^2) and four b=0 images. For accelerated acquisition, the subsampling patterns across RF and q-space at R_{gs}=2 and R_{gs}=3 in Figure 2 are employed.
gSlider Network (gNET). The proposed NN transforms real-valued RF-encoded low-resolution gSlider data into high-resolution images, by applying two 3D CNN layers and three fully-connected layers (Figure 1). The outputs are then fed to the gSlider forward model to synthesize the input through

$$\boldsymbol{L} = \mathrm{R}\hat{\boldsymbol{H}} + \lambda_{\mathrm{Laplace}}(\mathrm{F}(\boldsymbol{P}\hat{\boldsymbol{H}}))$$

where $\boldsymbol{L}$ is the low-resolution image, R is the RF-encoding matrix, $\hat{\boldsymbol{H}}$ is the high-resolution image, $\lambda_{\mathrm{Laplace}}$ is the penalty parameter, and $\mathrm{F}(\boldsymbol{P}\hat{\boldsymbol{H}})$ is the Laplace regularizer applied to the phase corrected high-resolution image. Constructing the loss function using the difference between the input and synthesized low-resolution volumes allows the model to operate in a self-supervised manner. The NN was implemented using Pytorch and optimized with Rprop 8 and L2 loss. 1/6 of the data was separated for training due to hardware constraints and 5/6 for validation. Learning rate was 0.001, which was reduced to 0.0001 for fine-tuning.
Parameters estimation and validation. Diffusion parameters were firstly estimated using FSL DTIFIT tool [9]. Afterwards, Fractional Anisotropy (FA), Mean Diffusivity (MD) and colored FA were obtained using the self-supervised parameter estimator model called DIMOND [10] under fully sampled (R_d = 1) and subsampled q-space (R_d > 1). The final results were compared to a ground truth (fully-sampled conventional gSlider reconstruction) using normalized mean squared error (NMSE) and structural similarity index (SSIM).

RESULTS

As shown in Figure 2, gNET reconstructed accurate BUDA-gSlider DWIs when fully sampled (R_{gs} = 1) and when subsampled with R_{gs} = 2. With NMSE = 5.70% and SSIM = 0.9784, the R_{gs} = 2 images retain high fidelity to the fully sampled case. At the higher acceleration factor of R_{gs} = 3, the image quality is still adequate, yet with lower contrast and some stripe artifacts.
Figure 3 shows the FSL estimation of the reconstructed DWIs for each case. FA from both subsampled cases appear underestimated compared to the fully sampled case, and the R_{gs} = 3 contains subtle stripe artifacts. This FA underestimation leads to higher NMSEs (>10%), which signifies a need for better alternatives to FSL's dtifit.
The results from DIMOND NN demonstrate a denoising effect, leading to higher quality images. MD and FA from R_{gs} x R_d = 2 x 2 are similar to the fully sampled case with NMSE = 8.36% and SSIM = 0.9191. Despite the slight green bias in its colored FA, the regions of the white matter with higher anisotropy are reconstructed adequately.

DISCUSSION AND CONCLUSION

The self-supervised gSlider Network successfully reduced the BUDA-gSlider acquisition time by up to R=4-fold. As shown in Figure 5, gNET achieved R_{gs}=2-fold acceleration during high-resolution gSlider reconstruction and a further R_d=2 acceleration was provided by DIMOND by directly reducing the number of directions, yielding a total R=4 (T_{acq} from 32 minutes to 8 minutes). Future work will explore the creation of a single NN capable of directly estimating the diffusion parameters from the low-resolution data.

Acknowledgements

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References

1. JONES, D. K. Diffusion MRI. Oxford University Press, 2010.

2. PELED, S.; YESHURUN, Y. Superresolution in MRI: application to human white matter fiber tract visualization by diffusion tensor imaging. Magnetic Resonance in Medicine: An Official Journal of the International Society for Magnetic Resonance in Medicine, Wiley Online Library, v. 45, n. 1, p. 29–35, 2001.

3. GREENSPAN, H. et al. MRI inter-slice reconstruction using super-resolution. Magnetic resonance imaging, Elsevier, v. 20, n. 5, p. 437–446, 2002.

4. SETSOMPOP, K. et al. Slice dithered enhanced resolution simultaneous multislice (slider-SMS) for high resolution (700 μm) diffusion imaging of the human brain. In: 23rd Annual Meeting of International Society for Magnetic Resonance in Medicine (ISMRM), Toronto, Canada, p. 339, 2015.

5. HALDAR, J. P.; FAN, Q.; SETSOMPOP, K. Whole-brain quantitative diffusion MRI at 660 μm resolution in 25 minutes using gSlider-SMS and SNR-enhancing joint reconstruction. In: Proceedings of the 24th Annual Meeting of ISMRM, Singapore, p. 102, 2016.

6. RAMOS-LLORDÉN, G. et al. High-fidelity, accelerated whole-brain submillimeter in vivo diffusion MRI using gSlider-spherical ridgelets (gSlider-SR). Magnetic resonance in medicine, Wiley Online Library, v. 84, n. 4, p. 1781–1795, 2020.

7. RAMOS-LLORDEN, G.; BILGIC, B.; HUANG, S. Y. Rapid, high-spatial resolution in vivo diffusion MRI with joint subsampling and reconstruction in k-, q-and RF-space. ISMRM, London, 2022.

8. RIEDMILLER, Martin; BRAUN, Heinrich. A direct adaptive method for faster backpropagation learning: The RPROP algorithm. In: IEEE international conference on neural networks. IEEE, p. 586-591, 1993.

9. SMITH, Stephen M. et al. Advances in functional and structural MR image analysis and implementation as FSL. Neuroimage, v. 23, p. S208-S219, 2004.

10. ZIHAN, L. et al. Dimond: Diffusion model optimization with deep learning. Magnetic Resonance in Medicine, 2022.

Figures

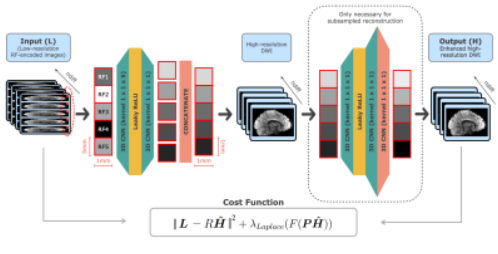

Figure 1: Novel gSlider Network (gNET). One low-resolution (1x1x5 mm) voxel from each of the five acquisitions from the same diffusion direction is inputed into the NN jointly. After the first two 3D CNNs, five 1x1x1 mm voxels are generated, which are concatenated and form a high-resolution part of the DWI. For the accelerated reconstructions, these high-resolution images are inserted into a second part of the model containing 3 extra 3D CNNs in order to enhance their quality.

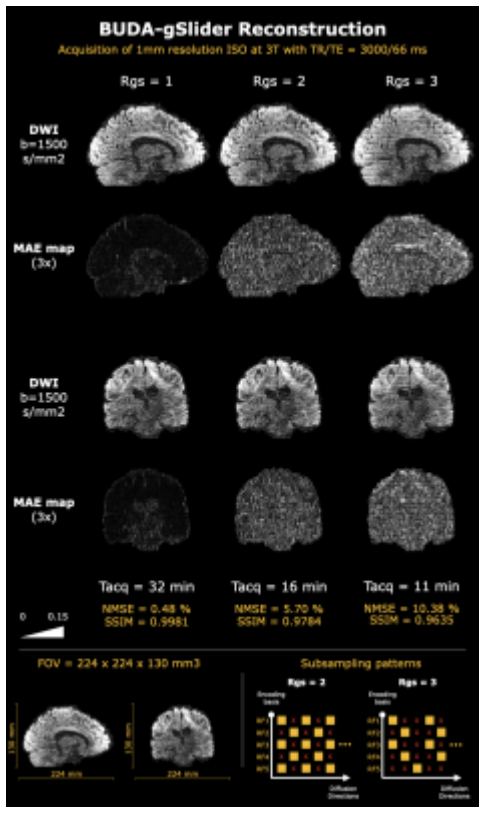

Figure 2: Reconstruction of gSlider DWIs using gNET. The low-resolution images (224 x 224 x 130 mm^3) were acquired using a Siemens 3T MAGNETOM Prisma and then reconstructed using gNET under three different cases: R_{gs} = 1, which is not subsampled in the RF-encoding basis; R_{gs} = 2, which is subsampled and uses half of the original data; and R_{gs} = 3, which uses one third of the original data. The MAE maps and NMSE were calculated comparing the gNET reconstruction to the result from the conventional fully sampled gSlider reconstruction.

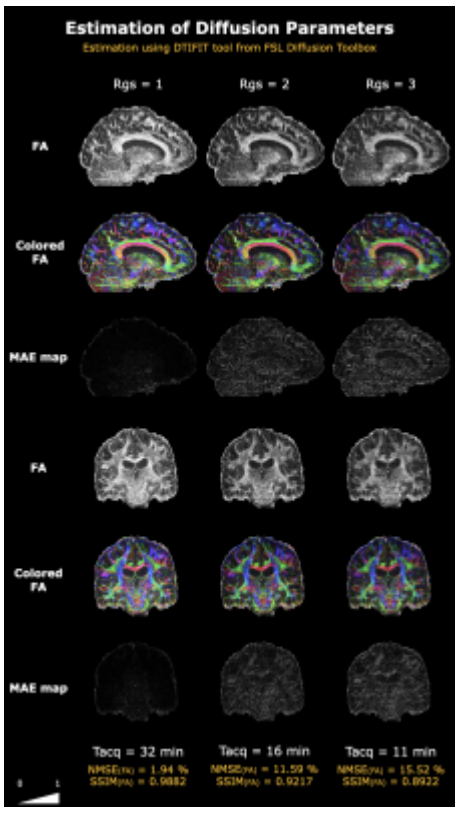

Figure 3: Diffusion parameters after gNET reconstruction. The diffusion parameters estimation was done using the DTIFIT tool from FSL Diffusion Toolbox utilizing all diffusion directions. For each of the three cases, the Fractional Anisotropy (FA) and Colored FA were estimated. The MAE maps and NMSE values show the difference between the FA images estimated after gNET reconstruction and the FA images estimated after conventional fully sampled gSlider reconstruction.

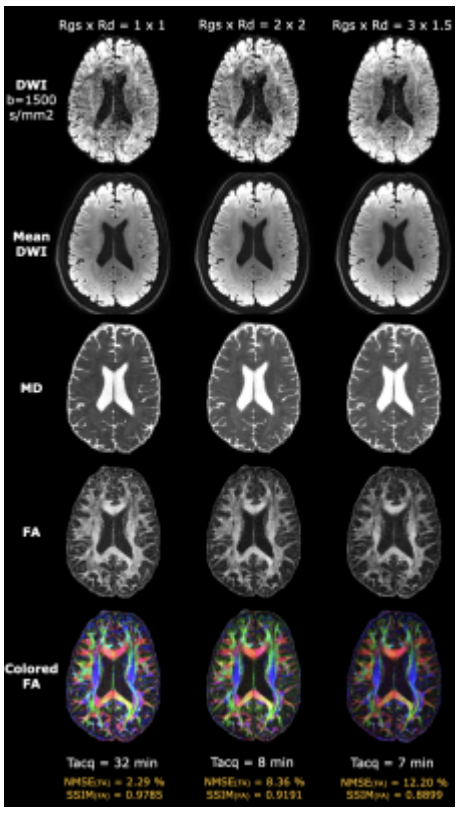

Figure 4: gNET + DIMOND. R_{gs} stands for **gS**lider acceleration and indicates the subsampling factor of the RF-encoding basis applied in gNET reconstruction. R_d stands for **D**IMOND acceleration and indicates the subsampling factor of the q-space applied in DIMOND estimation. Three different cases are presented: R_{gs} x R_d = 1 x 1, R_{gs} x R_d = 2 x 2, and R_{gs} x R_d = 3 x 1.5. The Mean DWI, Mean Diffusivity (MD), Fractional Anisotropy (FA) and Colored FA were estimated, and the NMSE was calculated comparing the FA estimated with DIMOND after gNET and the FA estimated with DIMOND after conventional gSlider.

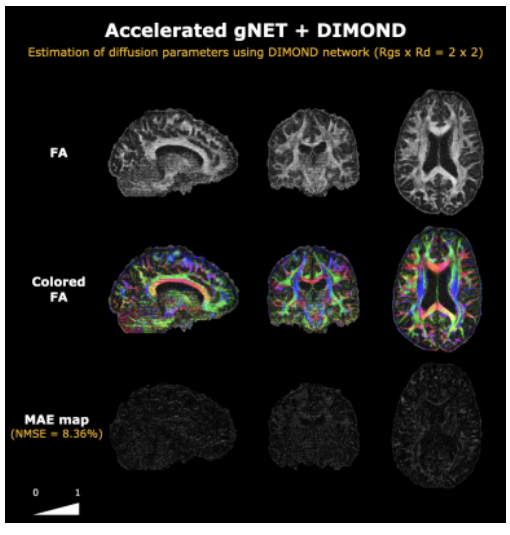

Figure 5: Accelerated gNET + DIMOND (AF = 4.0). All views from the R_{gs} x R_d = 2 x 2 presented in a closer look. MAE map and NMSE calculated comparing the FA estimated with DIMOND after gNET and the FA estimated with DIMOND after conventional gSlider.

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