

Super-Resolution for Ultra High-Field MR Images

Qi Wang¹

Julius Steiglechner^{2,1}

Tobias Lindig^{2,1}

Benjamin Bender²

Klaus Scheffler^{3,1}

Gabriele Lohmann^{3,1}

QI.WANG@TUEBINGEN.MPG.DE

JULIUS.STEIGLECHNER@TUEBINGEN.MPG.DE

TOBIAS.LINDIG@MED.UNI-TUEBINGEN.DE

BENJAMIN.BENDER@MED.UNI-TUEBINGEN.DE

KLAUS.SCHEFFLER@TUEBINGEN.MPG.DE

LOHMANN@TUEBINGEN.MPG.DE

¹ *Magnetic Resonance Center, Max Planck Institute for Biological Cybernetics, Tübingen, Germany*

² *Dept. of Diagnostic and Interventional Neuroradiology, University Hospital Tübingen, Germany*

³ *Dept. of Biomedical Magnetic Resonance Imaging, University Hospital Tübingen, Germany*

Editors: Under Review for MIDL 2022

Abstract

Segmenting ultra high-field MR images is an important first step in many applications. Segmentation methods based on machine learning have been shown to be valuable tools for this purpose. However, for ultra high-field MR images (> 7 Tesla), the lack of training data is a problem. Therefore, in this work we propose to use super-resolution for augmenting the training set. Specifically, we describe an efficient super-resolution model based on Generative Adversarial Network(GAN)¹. It produces synthetic images that simulate MR data at ultra high isotropic resolutions of 0.6 mm. We present the first results that show an improvement in segmentation accuracy of imaging data acquired at a 9.4 Tesla MRI scanner.

Keywords: Super-resolution, Ultra high field, Magnetic Resonance Imaging, Generative adversarial network, Data augmentation

1. Introduction

Ultra-high resolution Magnetic Resonance Imaging(MRI) reveals detailed information about brain anatomy and facilitates neuroscience research. However, data acquisition at ultra high-fields is costly and therefore the implementation of deep learning to ultra high-field MRI data suffers from a lack of training data. Here we propose to augment the training set using super-resolution. Specifically, we make use of the fact that MR images at lower resolutions (3 Tesla) are abundant and can be used for as a resource for simulating ultra high-resolution images via super-resolution. It is possible to use super-resolution scheme to produce thousands of high resolution images with realistic perceptual image quality. Our model produces samples at the same resolution as a real 9.4T image, e.g. 0.6 mm isotropic. Subsequently, the generated samples can be fed to the segmentation training set to improve the segmentation accuracy.

1. Our python source code is available at [here](#)

2. Methods

The design of our super-resolution model is close to that of (Wang et al., 2018). The upsampling process was done by a generator network which is made of residual blocks using dense skip connection (Huang et al., 2017). The feature extractor of the network uses a ResNet-10 network, which was pre-trained on a large set of 1.5T and 3T brain MR images (Chen et al., 2019). To stabilize the training process, the discriminator embeds instance normalization layers between each strided convolutional layers and LeakyReLU layers. The loss functions are modifications of the ones described in (Wang et al., 2018).

For training, we used T1w structural MRI data of a healthy subject acquired at 3T, downloaded from Human Connectome Project (Van Essen et al., 2013). The original resolution was 0.8mm isotropic. As pre-processing, we downsampled the image to 1.2mm by linear interpolation. The entire image was patched to size of $64 \times 64 \times 64$, downsampled to resolution of 2.4mm($32 \times 32 \times 32$). Then we pair the corresponding low resolution patches with its reference patches of 1.2mm resolution to train the model. The model was trained for 50 epochs, with 1360 steps per epoch, batch size of 4 and learning rate of 0.0002, using Adam optimizer. The results obtained from super-resolution were then assembled to a new synthetic MRI image.

To compare segmentation results with and without augmentation, we used a T1w structural image acquired at a 9.4T scanner at the Max Planck Institute for Biological Cybernetics, Tübingen. We used the segmentation method described in (Steiglechner et al., 2022) for this purpose. Here, 30 images were extrapolated to ultra-high resolution(0.6mm) via the generator trained on resolution of 1.2mm images. The ground truth labels were produced from Freesurfer (Fischl, 2012), manually corrected, and verified by neuroradiology experts.

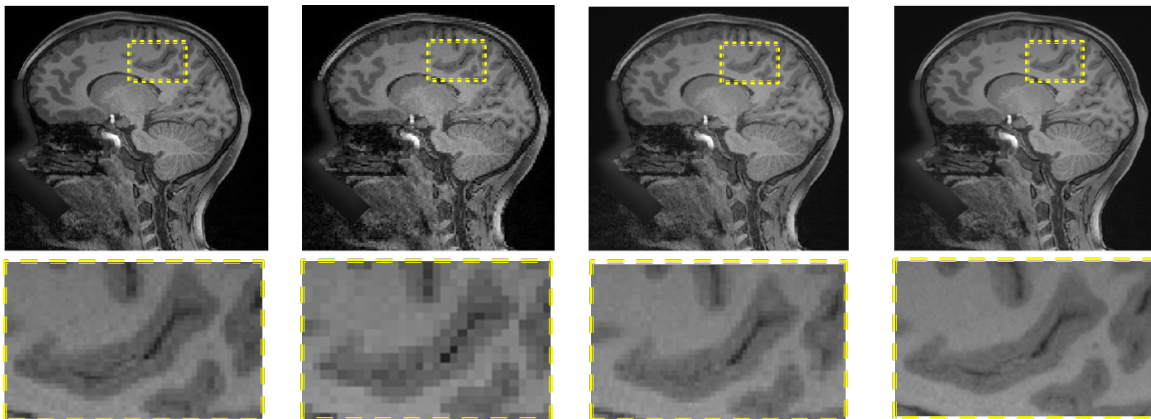


Figure 1: Super-resolution results comparison on a 3T image. From *left to right*: Ground truth, trilinear interpolated data, $\times 2$ super resolved data, $\times 4$ super resolved data.

3. Results

Figure 1 shows that results of the super-resolution applied to a 3T image. We observed that our model is resolution independent. Namely, it is possible to extrapolate the resolution beyond the trained ones preserving meaningful image content. For example, here we trained our model to upscale from 2.4mm to 1.2mm, but used it to obtain resolutions of 0.6mm.

Figure 2 compares segmentation results with and without training data augmentation. Note that the segmentation of frontal cortex clearly benefits from augmentation.

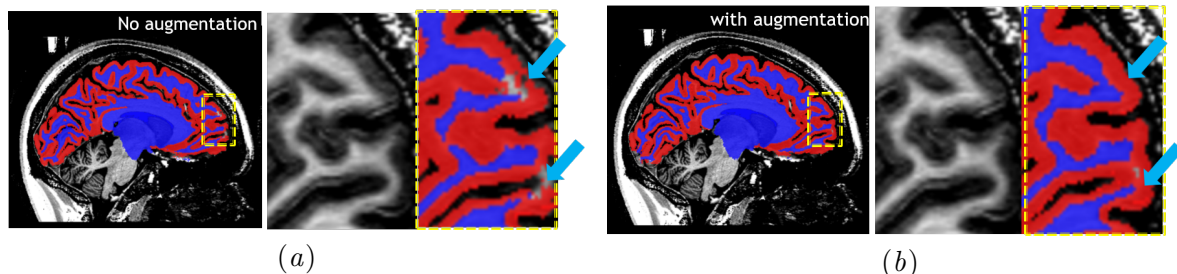


Figure 2: Segmentation results of 9T image before (a) and after (b) augmentation. Cortical grey matter is shown in red, white is in blue.

4. Conclusion

Here we have shown super-resolution can address the lack of training data in ultra high-field segmentation tasks. A novelty in our approach is that our super-resolution model can be used to generate images of higher resolution than the ones used in the training phase.

Acknowledgments

Data were provided in part by the Human Connectome Project, WU-Minn Consortium (Principal Investigators: David Van Essen and Kamil Ugurbil; 1U54MH091657) funded by the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research; and by the McDonnell Center for Systems Neuroscience at Washington University. This project was partially funded by Alzheimer Forschung Initiative e.V. Grant #18052.

References

- S. Chen, K. Ma, and Y. Zheng. Med3D: Transfer Learning for 3D Medical Image Analysis. *arXiv:1904.00625*, 2019.
- B. Fischl. Freesurfer. *NeuroImage*, 62(774-781), 2012.
- G. Huang, Z. Liu, L. van der Maaten, and K.Q. Weinberger. Densely Connected Convolutional Networks. In *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*, July 2017.
- J. Steiglechner, Q. Wang, D. Ramadan, L. Mahler, K. Scheffler, B. Bender, T. Lindig, and G. Lohmann. FLEXseg: Next Generation Brain MRI Segmentation at 9.4 T. In *Medical Imaging with Deep Learning: MIDL 2022(submitted)*, 2022.
- D.C. Van Essen, S.M. Smith, D.M. Barch, T.E.J. Behrens, E. Yacoub, and K. Ugurbil. The WU-Minn Human Connectome Project: An overview. *NeuroImage*, 80(64-79), 2013.
- X. Wang, K. Yu, S. Wu, J. Gu, Y. Liu, C. Dong, Y. Qiao, and C. Loy. ESRGAN: Enhanced super-resolution generative adversarial networks. In *The European Conference on Computer Vision Workshops (ECCVW)*, September 2018.