Improving High-Resolution Quantitative MRI Maps For In-Vivo Histology MRI Of The Human Brain

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Abstract

To do in-vivo histology MRI of the human brain there is a need to further improve the quality of acquired images using computational methods.

Objectives

- Improve quality of qMRI maps for downstream processing.
- Precise and reliable segmentation of tissue classes and structures in the qMRI maps.

Conclusion

- Deep learning is a flexible tool, that can address all required tasks[**1**].
- The data size is challanging especially for 3D.
- Availability of training data is the problem. Semi-supervised/weakly supervised approaches are needed.

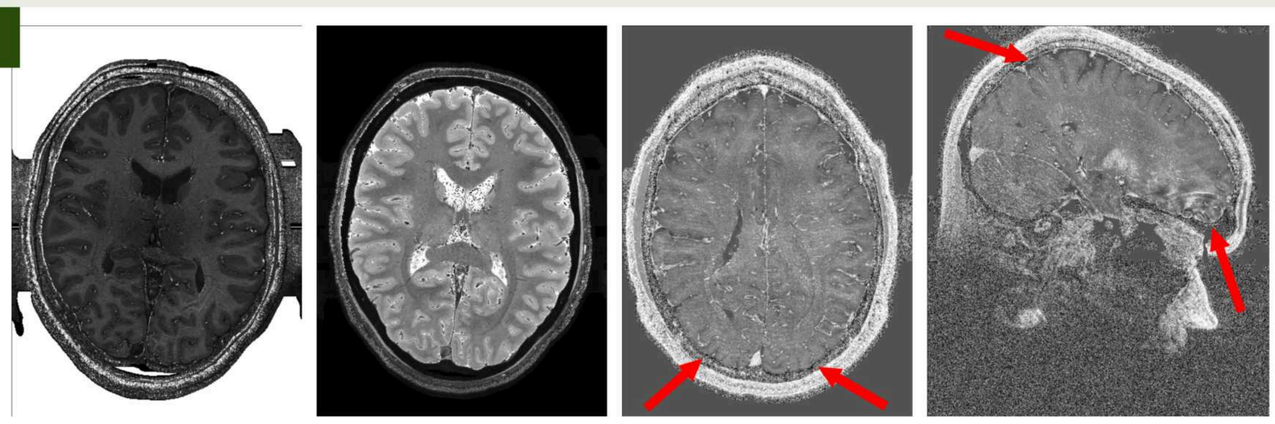
Data Characteristics

- Highly resolved qMRI at the limit of technical possibilities is needed to visualize mesoscopic structures.
- High-res qMRI brings new problems to be addressed.
  - Low signal-to-noise-ratio (SNR).
  - Intensity inhomogeneity related to ultra-high field MRI.
  - qMRI contrasts differ from traditional weighted images.
  - Artifacts from even small-scale motion (e.g. physiological processes like breathing and vascular pulsation).

Challanging Input Data Size

- Image Size: About 500^3 voxels
- Image Data Size: About 2 GB per volume (4x 500 MB)
- Raw Data Size: About 150 GB per volume

1

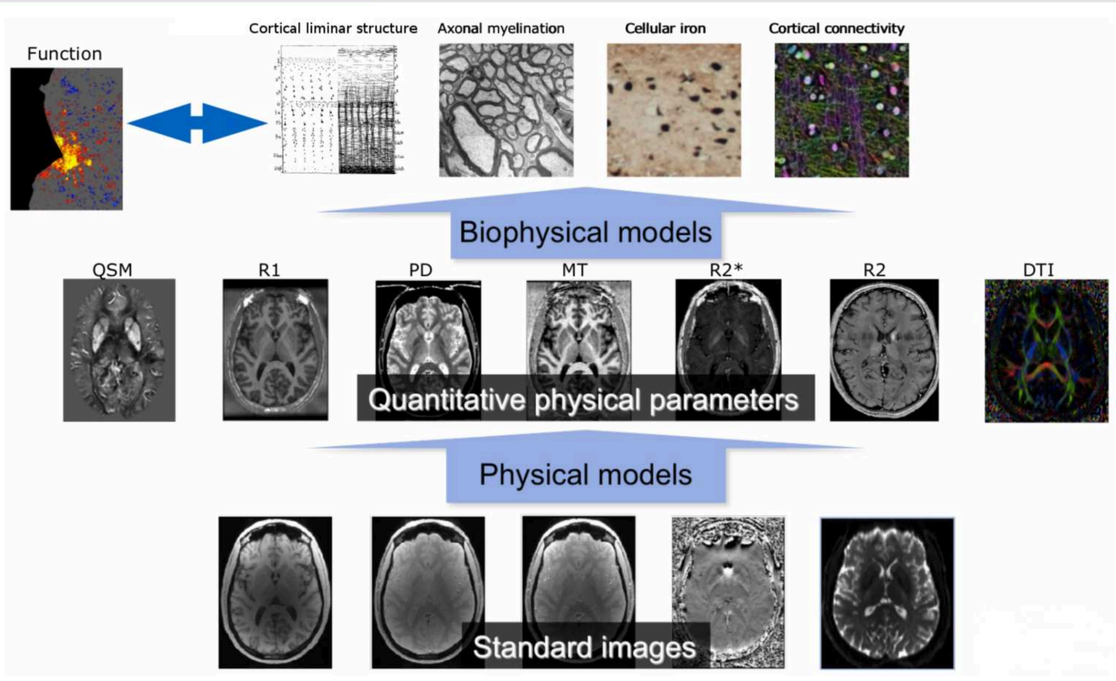


(a) (b) (c) (d)

Exemplary input data: Examples of multi-parametric qMRI maps reconstructed from 3D multi-echo fast low-angle shot (FLASH) with prospective motion correction (PMC) at 0.4 mm^3/voxel isotropic resolution **[2][3]** showing axial slice of (a) R1, (b) PD*, (c) R2* and saggital slice of R2* map. Note the motion artifacts still present (red arrows) and the signal loss towards inferior areas.

Goals & Methods

2



From standard MRI to in-vivo histology. qMRI uses different MRI contrasts are to generate quantitative maps of underlying physical parameters. hMRI uses biophysical models to convert qMRI data to specific biological metrics. Ultimately, hMRI may provide a detailed micro-structural description of the brain. Adapted from **[4]**.

Data Cleaning

- 2D CARE-Net **[7]**: Residual U-Net predicting Laplace probability density function (PDF) $\exp(-|z-\mu|/\sigma)/(2\sigma)$
- Training Loss: Voxelwise logarithm of inverse PDF
- 2.5D input (5 surrounding slices)
- Training Data:
  - Image of one session and average image of 3 sessions
  - Alternative: Original MRI image with added Rician noise
- Metrics: PSNR

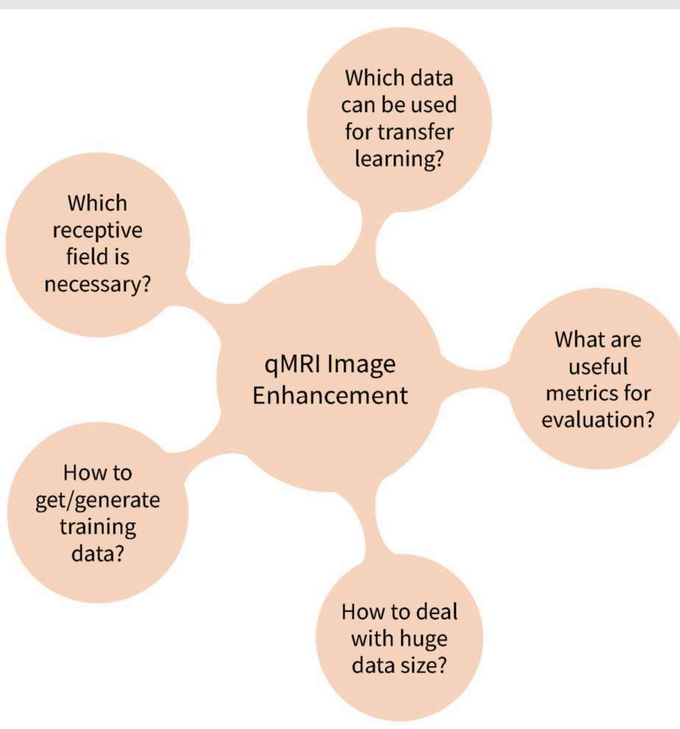
Super Resolution

- Multi-scale dense CNN (MS-D Net)**[5]**
- Input:
  - Bilinear upsampled slices
  - Multiple parameter maps as input channels (R1, R2*, PD*)
- Training Objective: MAE+MS-SSIM
- Training Data: Downsampled Images
- Metrics: PSNR, SSIM and MS-SSIM

Cortex Segmentation

- 3D U-Net **[6]**
- Predict priors for MGDM segmetnation
- Training Data:
  - Upsampled images from MRBrainS Challange
  - Freesurfer/FIRST segmentation from 7T Human Connectome Project data

3



Central questions concerning all of the described methods.

References

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