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VOMMPI - a tool for merging of MPI multi-patch data

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Abstract

The method of magnetic particle imaging (MPI) is substantially limited by a rather small field of view (FOV) even in preclinical imaging. To cover a bigger FOV, a multi-patch approach – i.e., scanning of a series of small FOVs (patches) shifted in space - is necessary. Here, we present a simple software tool VOMMPI (Volume Merger for MPI) for merging of patches into a final 3D volume data of the scanned object. The software reads reconstructed data produced by a field-free point scanner (MPI 25/20FF, Bruker BioSpin MRI GmbH, Germany), merges them, averages data overlapping in space, and exports them in DICOM format. The software is free for non-commercial use.

I. Introduction

Although MPI scanners have been developed for more than a decade, they still suffer from a row of hardware limitations given by the size of the magnets, strength of the selection and drive fields. Gradient strength of the selection field (absolute values in a Bruker field-free point MPI system are 1.25 T/m in x and y directions, 2.5 T/m in z direction) and the drive field amplitude (14/14/14 mT in $x/y/z$ directions) limit the field of view (FOV) spanned up by the drive field trajectory to $22.4 \times 22.4 \times 11.2$ mm^3, which is insufficient for whole-body scanning of a mouse. Larger FOV can be reached by lowering the gradient of the selection field, which comes however on the expense of a decrease in spatial resolution capability [1], or by increasing the DF amplitude – which is not currently possible on our system. Moreover, a higher DF amplitude may cause peripheral nerve stimulation, thus this possibility is also limited. While the installation of a mouse receive (Rx) coil substantially improves the SNR, it further limits the FOV accessibility, as the small opening of the coil does not permit movement of the calibration sample to the borders of the coil during system function acquisition.

A larger FOV can be acquired either by the "table move" method [2] or by using additional focus field coils [3]. The "table move" method simply moves the sample mechanically through the scanned volume, the images are acquired from different parts of the sample, and then the images are merged into one big volume. This simple and straightforward method is – in a Bruker system with a mouse Rx coil – applicable in x-direction only; there is no space for moving of the animal bed up and down or to the sides inside the Rx coil. Usage of focus field coils enables moving of the small FOV in all three directions, however, may suffer from artifacts caused by different sensitivity of the receive coils in the space and inhomogeneous drive and focus fields. This is very important, as system functions are acquired usually for the middle patch, only.

Both methods require further processing of the processed images – merging of the individual patches into

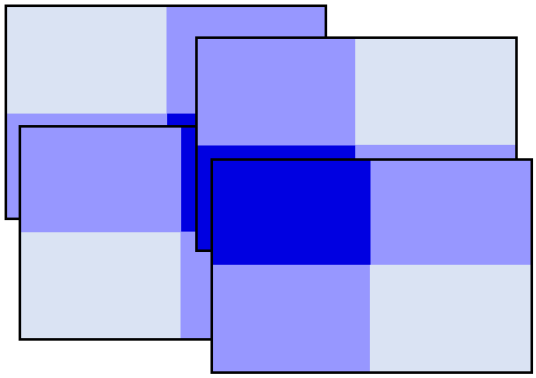

Figure 1: 2D patch overlay. Points falling into the shaded areas are averaged.

one bigger volume. The goal of our work was to develop a simple software tool for processing of the patches and obtaining a final 3D volume image representing the whole scanned object.

II. Material and methods

The program VOMMPI (VOlume Merger for MPI) for merging of patches was written in Python programming language. It loads Bruker data (single files containing a set of patches) and exports processed data in DICOM format. The software is licensed under a Creative Commons Attribution-NonCommercial 4.0 International License (CC BY NC) [4].

Basic functionality enables combination of the patches into the final volume; overlapping areas are simply averaged (Figure 1).

The software was tested on a phantom containing test tubes with various concentrations (24 to 96 mM Fe, sample size was 16 µL) of ferucarbotran (Resovist^{TM}), and *in vivo* on a mouse model, after administration of 100 µL of diluted ferucarbotran (c = 26 mM Fe) via tail vein injection.

Images were acquired using a field-free point MPI scanner (Bruker BioSpin MRI GmbH, Ettlingen, Germany) with focus field coils (16 mT) and a mouse Rx coil (Bruker BioSpin MRI GmbH, Ettlingen, Germany). Patch system function measurement was performed using an 8 µL sample (ferucarbotran, 500 mM) with following parameters: DF 14 × 14 × 14 mT, SF 1.25 T/m in x and y directions, 2.5 T/m in z direction, matrix size 24 × 24 × 12, 1 mm spatial resolution. Overscanning was used [5] (drive-field FOV was 22.4 × 22.4 × 11.2 mm^3). An MPI-patch sequence implemented by Bruker measures a sequence of individual patches. Presented data were obtained with 3 patches in x direction, 2 patches in y direction, and 3 patches in z direction with 50% patch overlap. Final FOV covered by the multi-patch sequence was 48 × 36 × 24 mm^3. Total scanning time (with 100 acquisitions) was 39 s. Reconstruction of individual patches was performed using the ParaVision software (Bruker BioSpin MRI GmbH, Ettlingen, Germany) with an implemented joint-reconstruction approach similar to the work of P. Swargulski et al [6]. Reconstruction parameters (regularization 10^{-5}, frequency components 0.06 – 1 MHz, SNR threshold 10, maximum mixing order 24) were the same for both *in vitro* and *in vivo* measurements.

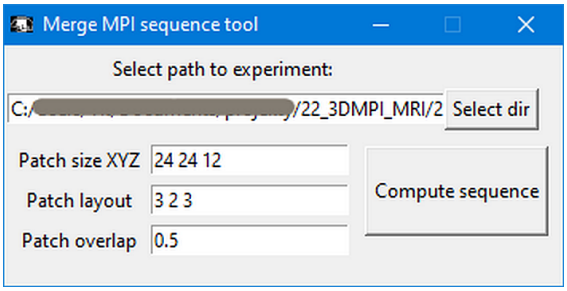

Figure 2: Main software window.

A single file containing a data sequence of individual patches was loaded into the VOMMPI software and processed.

For visualization, the merged *in vivo* MPI data were fused with anatomical MR images obtained by a gradient echo sequence on a 1 T MRI scanner ICON (Bruker BioSpin MRI GmbH, Ettlingen, Germany) using ImageJ software [7]. External markers were used for manual colocalization.

III. Results and discussion

VOMMPI program is made available for download (including its source code) here: https://github.com/martin-soul/VOMMPI

Figure 2 shows the main program window. After specifying the folder containing the data, the software shows imported parameters (such as patch size in voxels, patch layout, patch overlap). The button "Compute sequence" starts the process of calculation, and the result is presented in a new window. Before saving, one can specify data in the DICOM header.

Phantom measurements are illustrated in Figure 3. Moderate melting of the signals obtained at higher concentrations are caused by high concentration differences in the test tubes. Also, regularization parameters chosen for single image reconstruction might contribute to it. Broadening of the strong signal in the middle (a test tube with the highest concentration) might also be caused by the fact, that it lies on the border of two patches, therefore, any artifacts caused by field inhomogeneities are more noticeable.

Figure 4a presents a projection view of the merged 3D data set (a mouse body). Overlapping areas are averaged.

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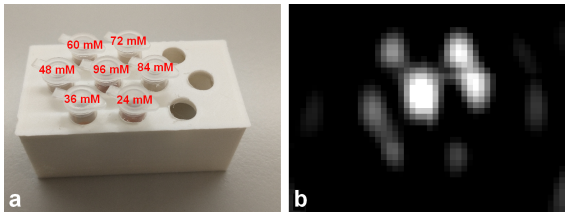

Figure 3: Phantom measurements. (a) A photograph of the phantom with marked concentrations in each test tube. (b) A merged MPI image of the whole phantom.

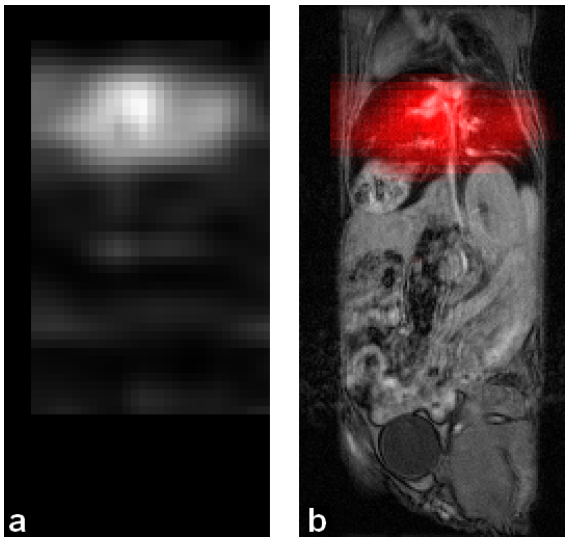

Figure 4: Imaging of a mouse body. (a) A merged MPI image with averaged overlapping areas. (b) Colocalization of the MPI image with an MRI anatomical scan.

Colocalization of the MPI image with an anatomical MRI (after matching the matrices of the MPI and MRI images; no interpolation was employed to show real image resolution) is shown in Figure 4b. It confirmed accumulation of the tracer in the liver of the animal at 10 minutes post injection.

Visible transitions on the borders of the patches at areas with a low signal were caused by boundary artifacts despite 50 % patch overlap. They can be partially suppressed by weighted averaging, cut off, linear fading in overlapping areas [8] or further data filtering, which is a part of ongoing work on the program. Assuming that data in the middle of the patches are more reliably acquired and processed, the weighted averaging will be justifiable. However, while the so far tested methods based on weighted averaging (with block, Gaussian, truncated Gaussian weight distribution) smoothed the transitions between patches, they often introduced other artifacts. Therefore, their implementation requires further investigation.

Removing – or minimizing – of these artifacts on the level of data acquisition would be more appropriate, however, it is out of the scope of this work.

Possible inhomogeneous sensitivity distribution of the receiver coil may also influence the resulting image; however, it should be noted that the effect of border artifacts (described in [5]) represents the main problem at this moment.

The maximum number of patches we tested (on a phantom, data not shown) was $7 \times 3 \times 6 = 126$ with 80 % overlap, which gave total FOV $49.3 \times 31.4 \times 22.4$ mm^3. High number of the patches and high overlap of course substantially improves the resulting image quality (artifacts are averaged), but also reduces one of the advantages of MPI, i.e., its high temporal resolution.

The multi-patch method can be of course combined with the mechanical table movement (in x direction only with the used scanner) to counteract the impact of the sensitivity profile of the Rx coil.

IV. Conclusions

Multipatch data acquisition seems to be necessary for whole-body imaging (even in small rodents) due to hardware limitations of current field-free point scanners. Although an increase of the drive field amplitude might increase the scanned volume, there are also physiological limitations; alternating field with a high amplitude may cause e.g., peripheral nerve stimulations. The program VOMMPI represents a simple, but useful tool for merging of multi-patch data from an MPI scanner. It enables downloading data in Bruker data format and conveniently exports the results in standard DICOM format, which enables further image processing. Introducing of weighted averaging or further data filtering may help in the future to eliminate some artifacts during image postprocessing.

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Author's statement

Conflict of interest: Authors M.D., L.Š., V.H., state no conflict of interest. J.F. is employee of Bruker BioSpin MRI GmbH. Ethical approval: Animal experiments were approved by the ethics committee of the First Faculty of Medicine, Charles University, and by the Ministry of Education, Youth and Sports of the Czech Republic, and

performed according to Directive 2010/63/EU of the European Parliament and of the Council on the protection of animals used for scientific purposes.

References

[1] J. Rahmer, J. Weizenecker, B. Gleich, and J. Borget. *Signal encoding in magnetic particle imaging: properties of the system function.* BMC Med Imaging vol. 9, article no. 4, 2009.

[2] V. Herynek, P. Francová, L. Šefc, *Sequential scanning of larger objects without focus field.* 9th IWMPI, New York University (NYU), P26, 17-19 March 2019.

[3] J. Rahmer et al., *Results on Rapid 3D Magnetic Particle Imaging with a Large Field of View.* Proc ISMRM, vol. 19, pp. 629, 2011

[4] https://creativecommons.org/licenses/by-nc/4.0/

[5] A. Weber, F. Werner, J. Weizenecker, T. M. Buzug, T. Knopp. *Artifact free reconstruction with the system matrix approach by overscanning the field-free-point trajectory in magnetic particle imaging.* Phys. Med. Biol., vol. 61, pp. 475, 2016

[6] P. Szwargulski, M. Möddel, N. Gdaniec and T. Knopp, *Efficient Joint Image Reconstruction of Multi-Patch Data Reusing a Single System Matrix in Magnetic Particle Imaging. IEEE Trans. Medical Imaging*, vol. 38, no. 4, pp. 932-944, Apr 2019.

[7] W. S. Rasband, *ImageJ*, U. S. National Institutes of Health, Bethesda, Maryland, USA, https://imagej.nih.gov/ij/, 1997-2018.

[8] M. Ahlborg, C. Kaethner, T. Knopp, P. Szwargulski,and T. M. Buzug. *Using data redundancy gained by patch overlaps to reduce truncation artifacts in magnetic particle imaging.* Phys. Med. Biol. Vol. 61, pp. 4583–4598, 2016.

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