4669

High-Resolution Simultaneous Mapping of Brain Function and Metabolism

Rong Guo[1,2], Yibo Zhao[1,2], Yudu Li[1,2], Yao Li[3], and Zhi-Pei Liang[1,2]

[1]Electrical and Computer Engineering, University of Illinois at Urbana-Champaign, Urbana, IL, United States, [2]Beckman Institute for Advanced Science and Technology, University of Illinois at Urbana-Champaign, Urbana, IL, United States, [3]Biomedical Engineering, Shanghai Jiao Tong University, Shanghai, China

Synopsis

We present a new method for simultaneous mapping of brain function and metabolism. This method provides an unprecedented capability to simultaneously obtain high-resolution metabolic maps (2.4×2.4×3.0 mm^3) and brain functional maps (3.0×3.0×2.6 mm^3) of the whole brain coverage (230×230×120 mm^3) in 8 minutes. The proposed method extends the subspace-based imaging framework of the SPICE technique with a new data acquisition scheme and exploits the complementary information between MRSI and fMRI signals for high-quality image reconstruction. Brain imaging experiments have been carried out, demonstrating the impressive capability of our method. With further improvement, the method can provide an unprecedented tool for mapping brain function and metabolism simultaneously.

Introduction

Functional MRI (fMRI) has been widely used to map brain function invasively, while MR spectroscopic imaging (MRSI) provides a complementary capability to map the metabolism of brain tissues. Currently, fMRI and MRSI experiments are performed in two separate scans using different data acquisition schemes. Specifically, fMRI acquisitions are based on multislice EPI to avoid long readout and its associated image artifacts due to field inhomogeneity and susceptibility-induced signal loss[1]. MRSI is mostly based on CSI or EPSI trajectory to acquire both spatial and spectral encodings, thereby resulting in lower spatial and temporal resolution[2,3]. Most MRSI techniques in practical use achieve spatial resolution on the order of a centimeter with scan time on the order of 20 minutes[4]. Recently, it has been demonstrated that rapid high-resolution MRSI is possible using a new technique known as SPICE (SPectroscopic Imaging by exploting spatiospecral CorrElation)[5]. In this work, we extend SPICE with a novel data acquisition and processing method that provides an unprecedented capability to achieve simultaneous fMRI and metabolic imaging of the whole brain in high resolution. Our experimental results demonstrate that the proposed method can acquire fMRI images in 3.0×3.0×2.6 mm^3 spatial resolution, 3 seconds temporal resolution and MRSI spatiospectral functions at nominal spatial resolution of 2.4×2.4×3.0 mm^3 in an 8 minutes scan. This capability can significantly enhance the practical utility of MRSI in neuroimaging applications.

Methods

The proposed approach to simultaneous acquisition of fMRI and MRSI signals is shown in Fig.1. This acquisition scheme is distinct from the conventional MRSI and fMRI acquisition methods in several key aspects: (1) acquisition of MRSI and fMRI signals during the same time period in an interleaved fashion; (2) elimination of water and lipid suppression for both MRSI and fMRI data acqusition, which makes simultaneous acquisition of MRSI and fMRI signals possible; (3) use of FID-based acquisition with ultrashort TE (1.6 ms) and short TR (160 ms); (4) large k-space coverage for MRSI using extended EPSI readout with ramp sampling as well as a variable density sampling in the phase encoding direction (Fig. 2a); (5) collection of fMRI signals in EVI-based trajectories with sparse sampling (Fig. 2b), which leads to larger k-space coverage and higher temporal resolution. This acquisition scheme enables simultaneous acquisition of both MRSI and fMRI signals in high spatiospectral/temporal resolution. The dual signals also offer a desired capability for: a) correction of field drifts and head motion artifact in MRSI using the complementary information from fMRI, and b) correction of chemical shift effects, geometric distortion and susceptibility effect using spatiospectral information from the MRSI data. In an 8-minute scan, the proposed method can acquire fMRI images in 3.0×3.0×2.6 mm^3 spatial resolution and 3 second temporal resolution and MRSI spatiospectral functions in 2.4×2.4×3.0 mm^3 nominal spatial resolution with whole brain coverage (230×230×120 mm^3).

Reconstruction of the metabolite spatiospectral functions is done using a union-of-subspaces model[6], which expresses the overall signals as:

$$\rho_{MRSI}(\mathbf{r},t)=\sum_{l_w=1}^{L_w}U_{l_w}(\mathbf{r})V_{l_w}(t)+\sum_{l_f=1}^{L_f}U_{l_f}(\mathbf{r})V_{l_f}(t)+\sum_{l_{MM}=1}^{L_{MM}}U_{l_{MM}}(\mathbf{r})V_{l_{MM}}(t)+\sum_{l_m=1}^{L_m}U_{l_m}(\mathbf{r})V_{l_m}(t)$$

This subspace model not only significantly reduces the number of degrees of freedom for representing the desired spatiospectral function but also enables effective incorporation of spatial and spectral priors to improve SNR.

Reconstruction of the fMRI images from sparsely sampled EVI data is accomplished using a single subspace, exploiting the partial separability[7] of the fMRI images:

$$\rho_{fMRI}(\mathbf{k},T)=\sum_{l_{fMRI}=1}^{L_{fMRI}}U_{l_{fMRI}}(\mathbf{k})V_{l_{fMRI}}(T)$$

This model indicates that the fMRI signals can be expressed by a finite weighted sum of temporal basis functions with a set of spatially dependent coefficients. After the fMRI images are reconstructed, the functional networks are extracted using existing ICA-based method[8].

Results

The proposed method has been evaluated using experimental data obtained from healthy volunteers on a 3T scanner (Siemens Prisma). The data were acquired with the following key parameters: FOV: 230×230×120 mm^3, TR/TE: 160/1.6 ms, readout bandwidth: 100 kHz, echo-space: 1.76 ms, MRSI matrix size: 96×96×72, fMRI matrix size: 76×80×46, total time: 8 minutes. Some representative experimental results are shown in Figs. 3 and 4 to demonstrate the capability of the proposed method. Figure 3 shows some of the extracted resting-state networks including default mode network (DWN), visual cortex network (OVN, DVN), somato-motor network (SMN) and auditory cortex network (ACN). These functional network structures are consistent with previous studies[9]. Figure 4 shows the reconstructed metabolite maps and spatially resolved spectra. As can be seen, the proposed method can simultaneously produce high-resolution high-quality metabolite maps and resting-state networks from an 8 minutes scan.

Conclusion

We have developed a new imaging method for brain mapping applications. This method provides an unprecedented tool for simultaneous mapping of brain function and metabolism in high resolution with the whole brain coverage. This tool may significantly enhance our capability to investigate brain function and metabolism in both scientific and clinical applications.

Acknowledgements

This work was supported in part by the National Institutes of Health (NIH-R21-EB021013, NIH-R21-EB023413, NIH-R01-EB023704, and NIH-P41-EB022544)

References

1. Biswal B, Zerrin F, Haughton VM, et al. Functional connectivity in the motor cortex of resting human brain using echo-planar MRI. Magn Reson Med. 1995;34(4):537-541.

2. Brown TR, Kincaid BM, Ugurbil K. NMR chemical shift imaging in three dimensions. Proc Natl Acad Sci. 1982;79(11):3523-3526.

3. Posse S, Tedeschi G, Risinger R, et al. High speed 1H spectroscopic imaging in human brain by echo planar spatial-spectral encoding. Magn Reson Med. 1995;33(1):34-40.

4. Lam F, Liang ZP. A subspace approach to high-resolution spectroscopic imaging. Magn Reson Med. 2014;71(4):1349-1357.

5. Lecocq A, Le Fur Y, Maudsley AA, et al. Whole-brain quantitative mapping of metabolites using short echo three-dimensional proton MRSI. J Magn Reson Imaging. 2015;42(2):280-289.

6. Ma C, Lam F, Johnson CL, et al. Removal of nuisance signals from limited and sparse 1H MRSI data using a union-of-subspaces model. Magn Reson Med. 2016;75(2):488-497.

7. Liang ZP. Spatiotemporal imaging with partially separable functions. Proc IEEE Int Symp Biomed Imaging. 2007:988–991.

8. McKeown MJ, Makeig S, Brown GG, et al. Analysis of fMRI data by blind separation into independent spatial components. Hum brain mapp. 1998;6(3):160-188.

9. Damoiseaux JS, Rombouts SARB, Barkhof F, et al. Consistent resting-state networks across healthy subjects. Proc Natl Acad Sci. 2006;103(37):13848-13853

Figures

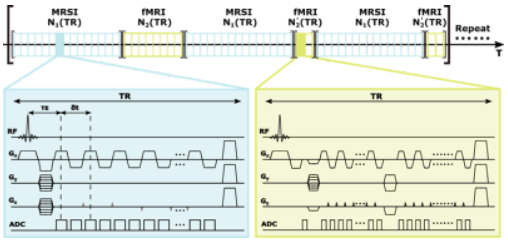

Figure 1. Time diagram of the proposed acquisition sequence. The MRSI and fMRI data are acquired in an interleaved fashion. MRSI is acquired with an EPSI-based sequence, fMRI is acquired with an EVI-based sequence. No water or lipid suppression is applied. TE = 1.6 ms, TR = 160 ms. In the current implementation, N_1 = 15, N_2 = 8, N_2' = 2. This acquisition scheme not only enables high-resolution simultaneous collection of MRSI and fMRI signals, but also make it possible to achieve high quality reconstruction by utilizing the complementary information between MRSI and fMRI.

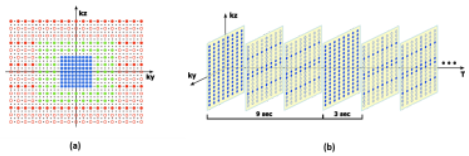

Figure 2. Sampling schemes for both MRSI and fMRI. (a) The phase encoding pattern of MRSI using variable density. The central region (blue) is spatially fully sampled. The outer region 1 (green region) is spatially under-sampled in both ky and kz. The outer region 2 (red region) is spatially under sampled in both ky and kz, as well as temporally under-sampled using blipped gradients. (b) Sparse sampling of (k,T)-space by fMRI signals. A full frame containing 8 TRs is acquired every 3 fMRI frames. The other 2 frames contain only 2 TRs. The resulting temporal resolution for fMRI is 3 seconds.

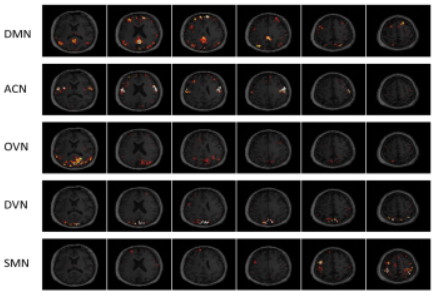

Figure 3. Independent Component (IC) maps representing resting-state networks from an 8-min whole brain simultaneous fMRI-MRSI scan. The IC maps are displayed with threshold |z|>2. From top to bottom: default mode network (DWN), auditory cortex network (ACN), visual cortex network (OVN and DVN) and somato-motor network (SMN). These resting-state network structures are consistent with the literature.

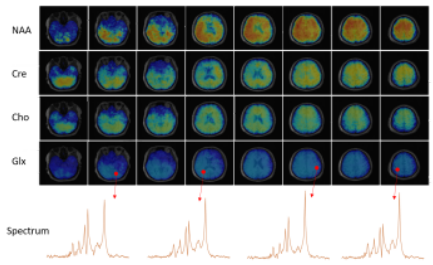

Figure 4. Metabolic maps and localized spectra in the selected spatial locations. The reconstruction results were obtained from the same 8-min simultaneous fMRI-MRSI scan as in Fig. 3. These high-quality metabolite maps cover the whole brain (230×230×120 mm^3) with high spatial resolution (2.4×2.4×3.0 mm^3). The spectra also show high quality in SNR and spectral resolution.