Supplemental online material

Empathizing associates with mean diffusivity

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Supplemental Methods

Additional details of diffusion image acquisition. There are acquisitions for phase

correction and for signal stabilization and these are not used as reconstructed images. MD

and FA maps were calculated from the collected images using a commercially available

diffusion tensor analysis package on the MR consol. This practice has been used in many

of our previous studies [1-5]. Furthermore, the results of analyses using these images were

congruent with those of previous studies in which other methods were used [6, 7], suggesting

the validity of this method. These procedures involved correction for motion and

distortion caused by eddy currents. Calculations were performed according to a

previously proposed method [8]. These descriptions were mostly reproduced from our

previous study using the same method [9].

Preprocessing of imaging data

Preprocessing and analysis of functional activation data were performed using

SPM8 implemented in Matlab. Most of the following descriptions were reproduced

from our previous study using the similar methods [9]. First, the skull in the mean $b = 0$

image of each participant was stripped as described previously [4]; using the resulting

image, diffusion images were linearly aligned to the skull-stripped $b = 0$ image template

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created previously [4] to assist with the following procedures.

Subsequently, using a previously validated two-step new segmentation algorithm of diffusion images and the previously validated diffeomorphic anatomical registration through exponentiated lie algebra (DARTEL)-based registration process that utilized the information of the FA signal distribution within the white matter tissue (for details, see ref [2]), all images, including gray matter segments [regional gray matter density (rGMD) map], white matter segments [regional white matter density (rWMD) map], and cerebrospinal fluid (CSF) segments [regional CSF density (rCSFD) map] of diffusion images, were normalized. The voxel size of these normalized images was 1.5 × 1.5 × 1.5 mm^3. In these processes, we used the template for the DARTEL process that we created in our previous study from subjects that participated in the same project (for details, see ref [2]).

Next, we created average images of normalized rGMD and rWMD images of all subjects whose diffusion imaging data were obtained in the pre-experiment. Subsequently, for the analyses of MD images from the normalized images of the (a) MD, (b) rGMD, and (c) rWMD maps, we created images where areas that were not strongly likely to be gray or white matter in our averaged normalized rGMD and rWMD images (defined by "gray matter tissue probability + white matter tissue probability <

0.99") were removed (to exclude the strong effects of CSF on MD throughout analyses).

These images were then smoothed (8 mm full-width half-maximum) and carried

through to the second-level analyses of MD.

We did not use T1 weighted structural images for normalization and

calculation of GMC and WMC maps for correction. This is because T1 weighted

structural images and EPI images have apparent differences due to the distortion caused

by 3T MRI and simply it is apparently not suited for the accurate and precise

segmentation and normalization images of MD maps.

Supplemental Discussion

Limitations of this study

There was at least one limitation to this study, and this was identical to that of

our previous studies as well as of other studies that use college cohorts [4, 10-13], is that we

used young healthy subjects with a high educational background. Limited sampling of

the full range of intellectual abilities and age is a common hazard when sampling from

college cohorts [10]. Whether the findings from this cohort would also hold across the full

range of population samples and a normal distribution must be determined with larger

and more representative samples.

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