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Research report

Distributed performance of white matter properties in chess players: A DWI study using automated fiber quantification

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ABSTRACT

The aim of this study is to verify whether anatomical changes occur in the brains of chess players. Besides, it is a potential attempt to evaluate diffusion properties along the tracts due to the diverse situations at anatomical level in different locations; moreover, conventional voxel-based analysis (VBA) has already been used to calculate the average values within the voxels in the investigated regions as analysis data. In this study, we used automated fiber quantification (AFQ) to automatically identify the major tracts that are related to functional domains of the human brain. AFQ can quantify pointwise white matter (WM) properties to detect specific local differences. We selected chess players with superior logical cognition abilities as the carrier to conduct our AFQ experiments. The diffusion properties of the 20 major tracts of professional chess players ($n = 28$) and matched controls ($n = 29$) were calculated using diffusion weighted imaging (DWI) data. We noted significant differences ($p < 0.05$) in the diffusion properties of some successive locations among 100 equidistant points in several tracts, especially in the left superior longitudinal fasciculus(SLF) and right inferior fronto-occipital fasciculus (IFOF). Professional chess players exhibited increase levels in the studied diffusion metrics with Pearson results paralleled the findings. Afterwards, considering the starting and terminating regions of SLF, IFOF, and thalamic radiation, the connectivity of gray matter (GM) where connections are active in the frontal lobe, temporal lobe, and thalamus was assessed to help with the further experiment. The results confirmed the tendency in which anatomical alterations generated different performances along the tracts; furthermore, long-term cognitive activities, such as chess, may systematically influence the WM properties of early memory, attention, and visual pathways.

1. Introduction

Studies on the structural architecture and function of the brain have been intensively discussed. It is revealed that even with the universality, the anatomical structure of the human brain differs among individuals and may change when function is affected. Researchers have demonstrated the feasibility of structural brain plasticity in WM and indicated the influence of functional integrity or prior experience on structural changes (Lee et al., 2010; Duan et al., 2014). Such changes may occur at the anatomical level under conditions of structural alteration.

Current studies on brain functionality normally use functional magnetic resonance imaging (fMRI) to investigate functional networks (Van Den Heuvel and Hulshoff Pol, 2010). With the power of diffusion magnetic resonance imaging (dMRI), researchers have directly studied WM integrity and connectivity through different modeling methods. Unlike fMRI, which seeks functional systems, dMRI focuses on anatomical level, where WM properties can be applied to quantify the development of major tracts to infer their health status, and hence locates the changes. Conventional methods generally calculate fractional anisotropy (FA) or other diffusion metrics in specific regions of interests (ROIs) to conduct group comparisons, which is the core of VBA. Metrics concluded from the tensor information help quantify the degree of neurodegeneration (Kunimatsu et al., 2004; Farrell et al., 2007). From the precision aspect, VBA does not possess sufficient precision at the individual level for patient populations because the shapes of long-range tracts varies substantially among subjects (Wassermann et al., 2011; Yeatman et al., 2011). To overcome this defect in VBA, Tract-Based Spatial Statistics (TBSS), a voxel skeletons framework, was proposed to achieve improved

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coregistration results (Wassermann et al., 2011; Yeatman et al., 2011). Nevertheless, TBSS still falls to guarantee that any voxel corresponds to the same tract across individuals (Jason Yeatman et al., 2012). As supplementary, in regions with complex fiber architecture, differentiating individual tracts while generating the skeleton and performing projection procedures is difficult or even impossible (Bach et al., 2014). By contrast, the diffusion information in tractography is extracted from specific fiber tracts, thus offering convincing evidence for the detecting disease related abnormalities (Yamasue et al., 2003).

Apart from precision defects, the idea of conventional methods is average-tract which roughly describes properties in investigated regions with one value, from which we fail to obtain more detailed information for correct conclusions. In the human brain, fibers contact with different biological surroundings when they extend, and uncertain interactions may exert different influences and cause lopsided performance towards each part. The major tracts, especially the long association fibers are widely distributed in the human brain (possibly crossing several brain functional regions); thus, the corresponding anatomical changes may vary due to different local positions. Furthermore, research has proven that tissue properties do not remain constant and may vary systematically along each tract; diseases can strike at local positions within the tract and cause significant changes that are not obvious from mean measurements (Jason Yeatman et al., 2012). Consequently, the particularity is equalized because conventional methods rely on mean FA, which weakens the original change in specific sections by dispersing it to the whole bundle.

AFQ is a clustering method that automatically identifies major WM tracts with defined waypoint ROIs; achieving automatic reconstruction after deterministic whole-brain tractography and measuring pointwise specific profiles aimed at each tract(Sarica et al., 2017). The tractography contains much useful information and contributes to accurate WM identification. The use of automated fiber quantification is on the rise because it avoids operator-dependent bias in ROI selection (Chen et al., 2016). Distinct anatomical features are involved in the segmentation procedure, and the marked ROIs are equivalent across subjects. Even though the specific cortical locations of a tract typically vary across subjects, the central portion, which is bounded by the manual ROIs, is generally consistent across individuals; thereby avoiding the registration challenge in VBA, which guarantees the consistency among subjects and precision at individual levels. Moreover, different from conventional methods, AFQ resamples 100 points along each tract, thus allowing pointwise assessment that intensively describes trends, and serving as an excellent medium to verify the theses in this study and provide detailed information for impact analysis.

Chess is a highly intelligent activity that requires cognition and logical decisions. Professional chess players with long-term training possess high-level brain functions and cognitive ability which provide a suitable sample for detecting structural and functional alterations. Moreover, the reactions from professional chess players involve both the left and right hemispheres and thus facilitating balance. In this study, chess players were an interesting dataset because we detected difference in healthy populations instead of with disordered people. Chess players as a unique object, have rarely been studied in recent literatures, and previous studies mainly focused on structural connectivity rather than anatomical findings.

Given the complexity of neural activity when engaging in the chess, different functional brain activities are simultaneously recruited into coordination (Hnggi et al., 2014), including several important domains, such as emotional processing (amygdala, subgenual anterior cingulate, and pallidum) (Drevets et al., 2008Grillner et al., 2005), self-referential processes (medial prefrontal cortex, precuneus, and posterior cingulate cortex) (Vogt et al., 1992), cognitive functions related to memory (hippocampus, parahippocampal cortex) (Olton et al., 1979; Tulving and Markowitsch, 1998; Treves and Rolls, 1994), visual processing (fusiform gyrus, lingual gyrus, and lateral temporal cortex) (Cohen et al., 2004), and attention processing (dorsolateral prefrontal cortex, anterior cingulate cortex, thalamus, and insula) (Grossman et al., 1992; Mcalonan et al., 2008; Portas et al., 1998). AFQ involves most tracts and ensures the evaluation of different functional control regions. In this study, we focused on deriving the detailed anatomical differences between professional chess players and normal people, while proving the feasibility and significance of along-tract method in fiber property analysis.

2. Experimental procedure

2.1. Participants

We studied two groups of subjects in this paper. The first group consisted of twenty-eight professional chess players (nine females and nineteen males) with different levels (from grand master to no title). The second group had twenty-nine novice controls (fifteen females and fourteen males) ranging from amateurs to uncomprehending people. The recruited subjects are from the public multimodal MRI dataset provided by Huaxi MR Research Center (HMRRC), West China Hospital of Sichuan University (available at http://fcon_1000.projects.nitrc.org/indi/pro/wchsu_li_index.html). Detailed information about the participants is represented in Table 1.

2.2. Data acquisition

According to the information of the dataset, the data was scanned on a 3T Siemens Trio system (Erlangen, German) at the MR Research Center of West China Hospital of Sichuan University, Chengdu, China. Segmentation was conducted with T1 data (repetition time (TR) = 1900 ms; echo time (TE) = 2.26 ms; TI 900 ms; flip angle (FA) = 9 deg; voxel size: $1.0 \times 1.0 \times 1.0\ \text{mm}^3$; 1.00 mm thickness without gap). And the main DTI parameters were listed as follows: TR = 6800 ms, TE = 93 ms, field of view (FOV) read = 230 mm, voxel size: $1.8 \times 1.8 \times 3\ \text{mm}^3$; slices = 50, slice thickness = 3 mm without gap, the number of gradient directions = 40 (b = 1000). The MRI scans processed all got careful examination to avoid abnormal data.

2.3. AFQ procedure

AFQ method is already developed as a software package (available athttps://github.com/jyeatman/AFQ). In this study, we applied AFQ (version 1.2, on MATLAB R2015a) tool automatically identified 20 major tracts in bilateral hemispheres and calculated the diffusion properties along the fiber tract core. The whole AFQ procedure involved three steps: identification, cleaning and quantification.

The pre-processing procedure was performed using Vistasoft (Stanford University, Stanford, CA,github.com/vistalab/vistasoft/mrDiffusion). Before the eddy-current/motion correction and t1-alignment, a reference image from the dMRI sequence was required. All non-DW images were aligned to the first one to correct for motion, and then averaged. The eddy-current correction combines a rigid-body 3d motion correction (6 parameters) with a constrained non-linear warping (8 parameters) based on a model of the expected eddy-current distortions. The dMRI data (using the mean non-DW image) are then aligned to the t1-weighted high-res volume. The default parameters will be resampled to $2 \times 2 \times 2$ mm voxels with a 7th order b-spline interpolation using interpolation