Anatomical characterization of athetotic and spastic cerebral palsy using atlas-based analysis

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Introduction: Cerebral palsy (CP) is a heterogenous group diagnosed based on their clinical condition and includes several subtypes. MRI provides important information about the severity and extent of their multiple structural brain damage and is helpful for understanding of their pathogenesis and planning for clinical intervention [ref1]. However, MRI-based examination remains qualitative and systematic anatomy-function (prognosis) evaluation has been difficult. This difficulty is further augmented by the fact that a specific brain function usually does not have a simple link to a single brain structure (e.g. the motor cortex and the corticospinal tract are not the only structures that determine the motor function) indicating the importance of assessing the anatomical status of the entire brain structures. In this study we analyzed MRI/DTI of two types of CP patients; athetotic-type and spastic-type CP, using an atlas-based whole brain segmentation based on diffeomorphic mapping. Then anatomical correlates of each type of CP were investigated by principal component analysis (PCA).

Methods: We analyzed DTIs of 7 children clinically diagnosed as athetotic CP (age ranged 2-12years, mean 4.14years), 11 children with spastic-type CP (age ranged 2-15years, mean 4.72years), and 20 healthy control children (age ranged 2-13years, mean 4.3years). DTI was obtained with 1.5T scanner, using a 12-different-gradient direction scheme along with 4 reference images (TR / TE = 5700 - 5900 / 102). The maximum *b* value was 500 s/mm^2. The slice thickness was 3 mm with no gap, matrix was 128x128 (interpolated to 256x256), and the FOV was 220 × 220 mm. After tensor calculation, the tensor images were first normalized to the JHU-DTI-MNI "Eve" template [ref2] using a 9-parameter affine transformation of AIR, followed by large deformation diffeomorphic metric mapping (LDDMM) [ref3-4]. The inverse transformation of brain parcellation map [ref1] led to segmentation of the brain into 159 anatomical structures (Fig. 1) [ref2]. For each segmented area, the size, fractional anisotrophy (FA), and mean diffusivity (MD) were measured. We also performed principal component analysis for Z score of these parameters and extracted the principal components which characterized the difference of these three groups.

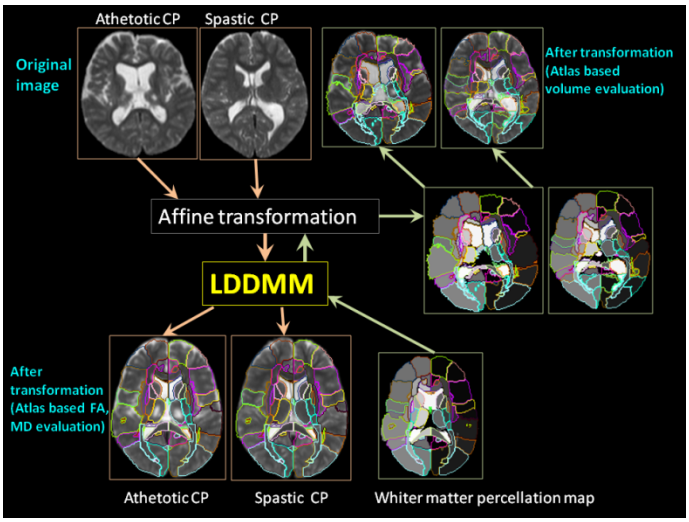


Figure1: Image normalization process. For the "forward" transformation, the subject image was first linearly normalized (affine transformation) followed by nonlinear normalization (LDDMM). For the "backward" transformation, the whiter matter percellation map (WMPM) was transformed to the original MRI.This allows automated segmentation of the original images into 159 subregions (detail in [ref.2-4]).

Result and Discussion: Fig. 2 shows population-averaged Zscore of FA, MD, and normalized volume at representative slices of each groups. In athetotic CP group, diffuse and significant change in FA (decrease), MD (increase), and volume (decrease) were found, while the cerebellum and the temporal lobe were relatively preserved. In spastic CP group, significant changes in all three parameters were concentrated in the periventricular, parietal and occipital white matter, the splenium of the corpus callosum and the thalamus. Notably, posterior thalamocortical pathways and postcentral to occipital area were markedly affected. Principal component analysis could constellate the two types of CP and normal group as partially overlapped groups in 3D scattergram. (Fig. 3). The distribution of parameters in athetotic CP group tended to be away from normal or spastic CP group, and its distribution was more scattered, which could be consistent with their heterogeneity on their clinical pathogenesis. This type of works could build a foundation for accurate functional prognosis based on anatomical features of CP.

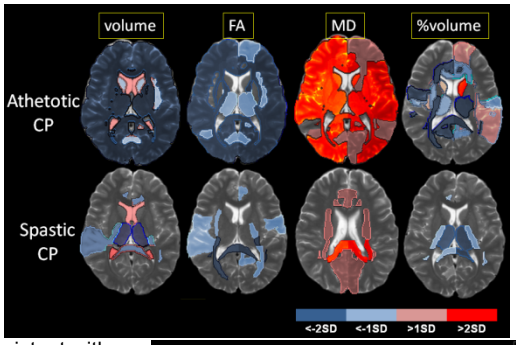
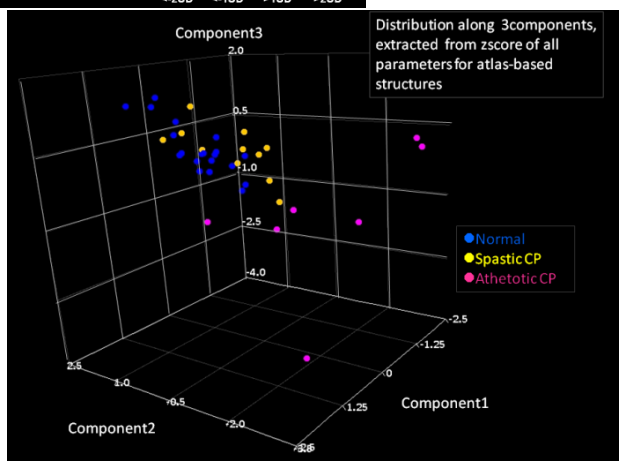


Figure2 (left): Zscore map of spastic CP group (upper row) and athetotic CP group (lower row) for each paremeter.

Figure 3 (bottom): 3D scattergram of each subject, along the principal component extracted from all parameters.



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