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Structural Connectivity Mapping via the Tensor-Based Morphometry

Abstract No:
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Introduction:

The tensor-based morphometry (TBM) has been widely used in characterizing tissue volume difference between populations at voxel level. So far most TBM studies have performed massive univariate tests in every voxels mainly using the Jacobian determinant. We present a novel structural connectivity analysis framework that can address various brain network hypotheses that massive univariate tests are not able to handle. The main innovation is that the proposed framework does not utilize diffusion tensor images (DTI) but still able to construct the population specific connectivity maps only using T1-weighted magnetic resonance images (MRI). The method is applied in detecting the regions of abnormal corpus callosum connectivity in neglected children (NC) who have been post-institutionalized in Wisconsin.

Methods:

Images:
T1-weighted MRIs were collected using a 3T GE SIGNA scanner for 32 PI and 33 age and sex matched control subjects. Ages range from 9 to 13. The symmetric diffeomorphic image normalization and template construction was performed (Avants et al., 2008). The constructed average template was used to visualize the results in Fig. 1 and 2.

Correlation on Jacobian Fields:
The Jacobian matrix $J = (J_{ij})$ is computed using the deformation field from an individual image to the template. Instead using the Jacobian determinant, we use the dilatation (Chung et al., 2001), which is the linear approximation of the Jacobian determinant, given by

$$\mathrm{tr}\, J = J_{11} + J_{22} + J_{33}.$$

Fig. 1 shows the volume dilation in the cross section taken at the genu of the

corpus callosum. If K is another Jacobian matrix computed at a different voxel position, the correlation ρ between the Jacobian determinants is approximated by

$$\rho(\mathrm{tr}\, J , \mathrm{tr}\, K) = \rho(J11 , K11) + \rho(J22 , K22) + \rho(J33 , K33),$$

the sum of correlations between diagonal terms, under a certain error model.

Connectivity Maps:
By fixing one voxel as a fixed seed, we obtain the map of correlation between the seed and other voxels. The resulting correlation map measures the strength of connection from the seed to other white matter regions. Similar approaches have been proposed in cortical thickness-based connectivity analysis (Lerch et al., 2006). However, this is the first study utilizing the Jacobian determinant in constructing structural connectivity maps. The constructed correlation maps look similar to the probabilistic connectivity maps usually obtained in DTI (Koch et al., 2002).

Statistical Analysis:
Given two connectivity maps ρ1 and ρ2, we constructed the Z-statistic using the Fisher transform:

$$Z = c^*(\operatorname{arctanh} \rho1 - \operatorname{arctanh} \rho2)$$

with some normalizing constant c. By thresholding the Z-statistic map, we can obtain the regions of abnormal connectivity difference as shown in Fig. 2.

Results:
Three seed voxels were chosen at the genu, midbody and splenium of the corpus callosum of the template (Fig. 1 red dots). The connectivity maps were computed for the two groups and shown in Fig. 1 and 2. In Fig. 2, we have overlaid the connectivity maps over the template to show it follows the white matter fiber tracts fairly well. The regions of high connectivity are shown in darker red while the regions of low connectivity is shown in lighter red. Since the seed is taken at the genu, white matter regions near the genu should have higher connectivity as expected.

The regions of the most significant connectivity difference are localized by thresholding the p-values of the Z-statistic (PI- controls) at $p=0.01$ and overlaid on the white matter boundary (Fig. 2). The effected regions are white matter regions connecting the anterior prefrontal cortex for the genu, and right anterior cingulate cortex for the midbody. In all cases, the negative correlation difference (negative Z-statistic) is negligible so we are mainly seeing the highly clustered regions of positive correlation difference only. It should be interpreted as follows. Increase in the white matter volume in the genu and the midbody corresponds to more increase of white matter in NC indicating the abnormal corpus callosum connectivity pattern. This does not imply that the NC group has more white matter volume in these regions.

Conclusions:

We have presented a novel structural connectivity mapping technique that utilizes only T1-weighted MRI. The constructed connectivity maps look like probabilistic connectivity maps often obtained using DTI. One can actually trace the gradient of connectivity maps by solving the streamline equation and obtain tracts that should behave like white matter fiber tracts. This is left as a future study and we have mainly focused on quantifying the connectivity map in a clinical population. We have successfully localized the regions of abnormal corpus callosum connectivity difference in NC.

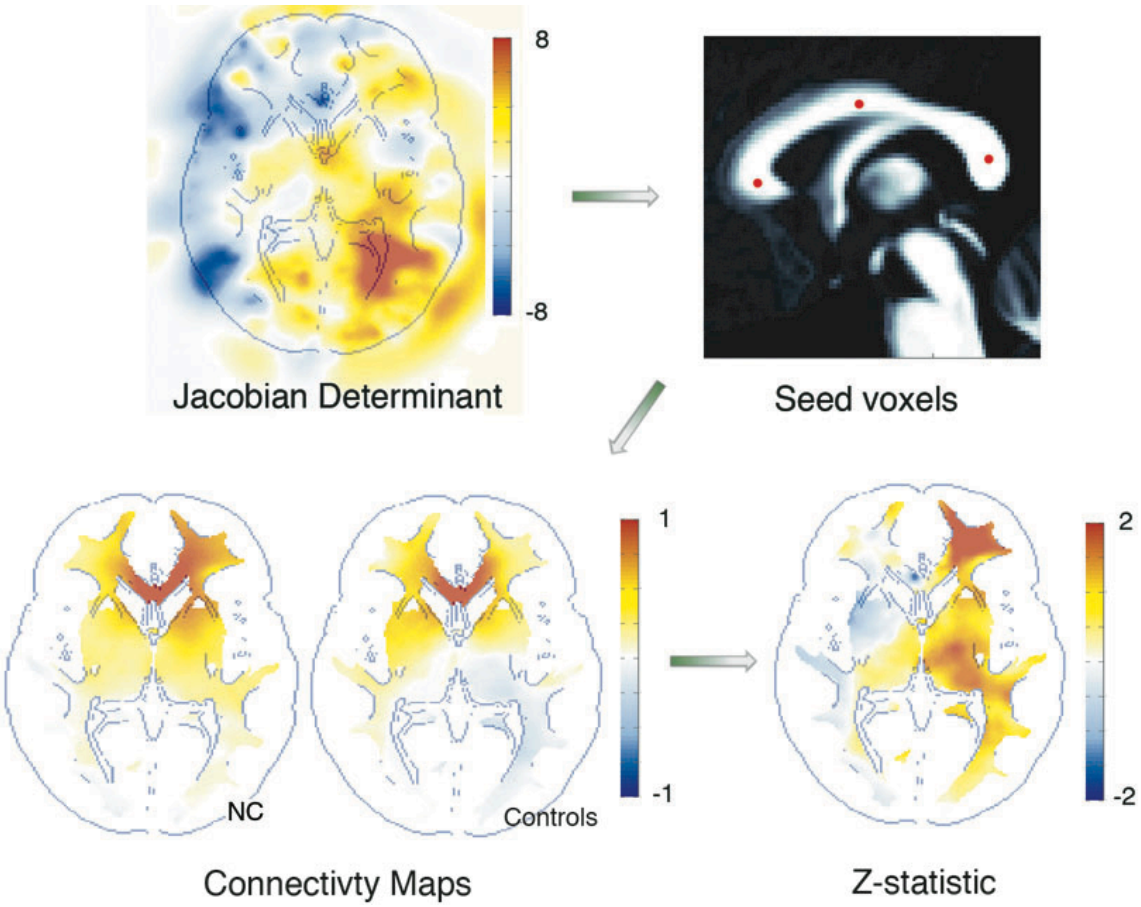

Figure 1.

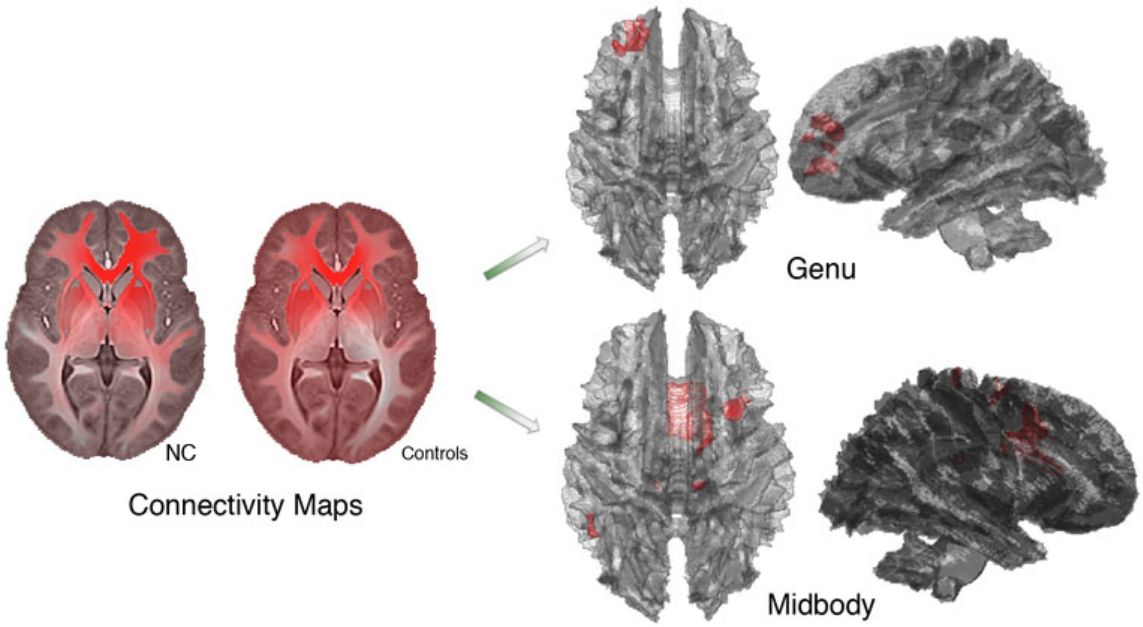

Figure 2.

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Categories

- Anatomical Studies (Neuroanatomy)
- Multivariate Modeling, PCA and ICA (Modeling and Analysis)