Novel algorithms to measure complexity in the human brain and to detect statistically significant complexity-differences

e-Poster: 652
Congress: ESMRMB 2006
Type: Scientific Poster
Topic: Imaging: Processing and Quantification
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Keyword: Fractality, fractal dimension, multiple testing

1. Purpose

To measure brain-complexity in segmented MR-images global measures of the fractal dimension (FD), like the density-density correlation or the box-counting method (BCM) are frequently used, where a regression line must be estimated from the data [1]. It was shown by Sandau [2] that FDs based on regression methods are sensitive to rotations and to noise. In addition, the basic maximum property of FDs is violated, FD(Set_1 U Set_2)=max {FD(Set_1), FD(Set_2)}. Therefore, we implemented a more local algorithm reducing the erroneous impact of distortions which is closer to the mathematical concept of a FD [2]. As second, an advanced statistical method [3] with high power was implemented to test differences of FDs.

2. Methods and Materials

The proposed algorithm for calculation of FD proceeds for fractal data on a grid of voxels in R^3 shortly like follows. 1) Define p_1 and p_2; p_1 = -ln(voxelsize), p_2 = -ln(windowsize) for a large observation window. 2) Shift the window within the grid and count for every window position j the number N_j of voxels containing the fractal object. 3) FD is estimated by xdim=$\max_j \{ \ln(N_j)/(p_1 - p_2) \}$.

see: [fig1.jpg]

To detect significant differences of FDs a Monte Carlo procedure was implemented using permutation resampling. Raw and multiplicity adjusted P-values are calculated. This non parametric statistical step-down-method [3] strongly controls the family-wise error, includes all logical restrictions and includes the correlations between the P-values.

3. Results

To demonstrate the advantage of xdim compared to BCM-dim, a plane with blood vessels was analyzed.

see: [fig2.jpg]

In Fig.2 the dimensions for the original, framed, rotated and weakly disturbed data are presented. Evidently, xdim is more robust. An attempt to analyse lobes of a single human cortex malformed by disease is presented in.

see: [fig3.jpg] see: [fig4.jpg]

The cortex was segmented from T1-weighted MR data [1]. The cortex surface between gray and white matter was then extracted by morphological dilation. To produce simple 'lobes', the resulting fractal object was divided into quarters by a central axial and sagittal slice. Xdim was finally calculated for these quarters (2.467, 2.479, 2.418, 2.405) and for four (up-down/left-right) halves (2.479, 2.418, 2.467, 2.479). The raw and adjusted P-values for 8 pairwise FD-differences are shown in Fig. 3. In Fig. 4 for the same 'lobes' the differences of the mean surface densities ($\text{mean}_j \{ \ln(N_j)/(p_1 - p_2) \}$) are compared.

4. Conclusion

Advantages of xdim are exemplified. A preliminary cortex analysis indicates that the detection of statistically significant FD-differences and of mean surface-densities between individual lobes may be feasible. Critical for resampling tests is the correlation within the samples { N_j j }. This effect is 'minimized' by an alternative sampling of local xdim's for disjoint boxes covering a fractal (see fig1.jpg). A spatial autocorrelation analysis to quantify remaining statistical dependences is in progress.

5. References

[1] Kiselev,V.G.,Hahn,K.R.,Auer,D.P.,2003,NeuroImage,20,1765-1774. [2] Sandau,K.,1996,PhysicaA,1-18.
[3] Westfall,P.H.,1997,AmStatAss,51/1,3-8.

6. Mediafiles:

fig1.jpg

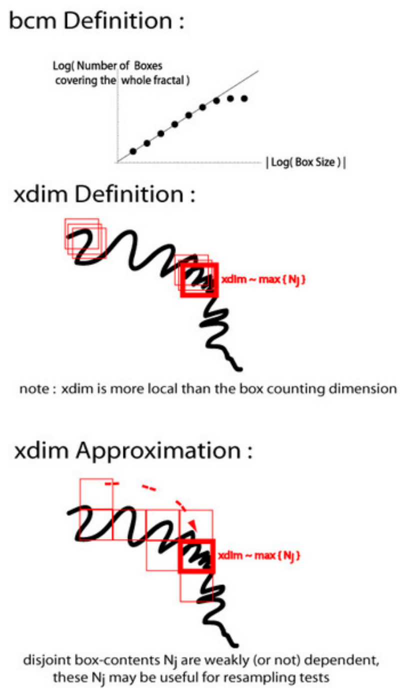


fig2.jpg

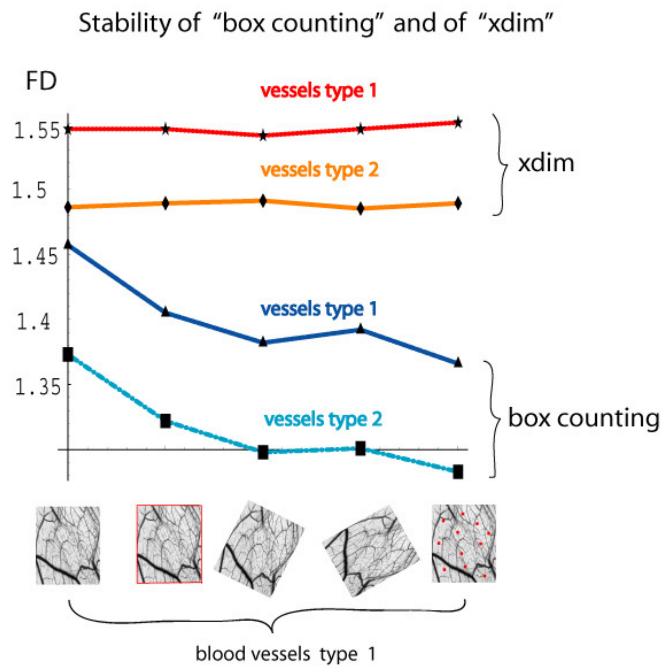


fig3.jpg

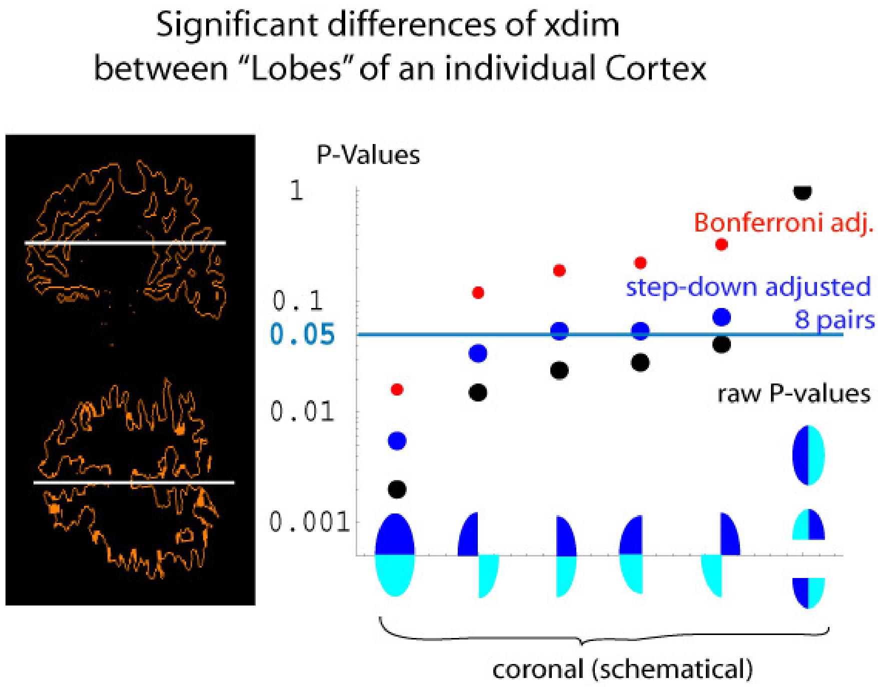
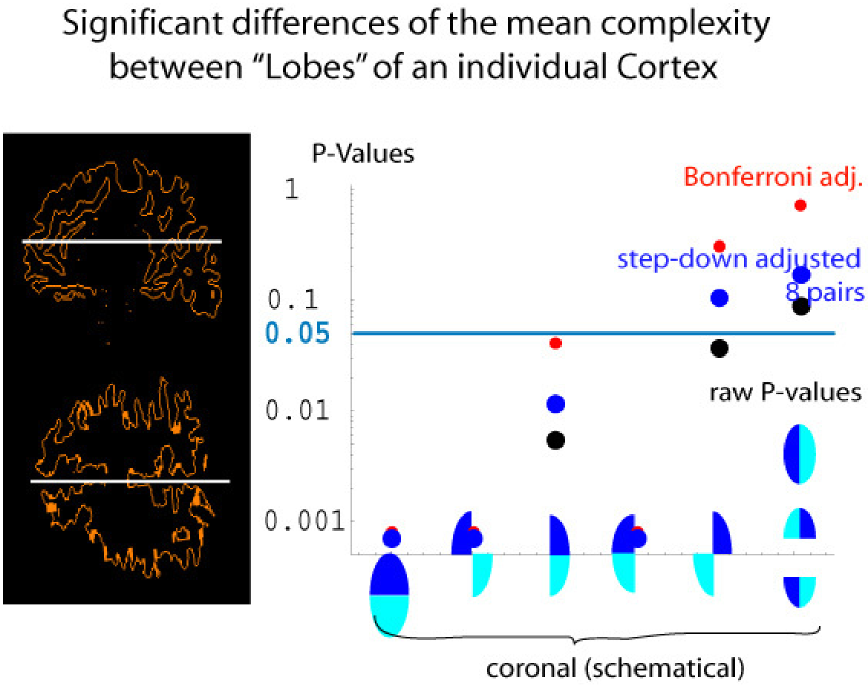


fig4.jpg



Significant differences of the mean complexity
between "Lobes" of an individual Cortex
P-Values
1
0.1
0.05
0.01
0.001
Bonferroni adj.
step-down adjusted
8 pairs
raw P-values
coronal (schematical)