# The EMD-test for shape-based morphometry.

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**Introduction:** Shape-based morphometry is used to analyze shape deformations between aligned and grouped (patient and control) anatomical structures in MRI. We used template-based shape morphometry and an anatomical template, with unit volume normalization, aligned to patient and control subject scans to measure the residual shape variability between groups [1]. Template based shape analyses assume normality and apply an appropriate statistical test correction, however, non-parametric methods such as the KS-test [2] are more suitable when normality is not assured. The Earth Movers Distance test (EMD) is a novel method for statistical comparison in shape analysis that is sensitive to distribution shape. Conceptually, the EMD measures the least amount of work to transform one continuous distribution (pile of earth) into another. A unit of work corresponds to the transporting of a unit of earth by a unit of distance. Computing the EMD is based upon the solution of the transportation problem, a bipartite network flow problem. Our aim was to use non-parametric shape analysis method the EMD-test to investigate shape differences between Huntingtons Disease (HD) patients and controls.

**Methods:** Twenty HD patients and 15 healthy controls and 20 HD patients were examined. For each subject MR scans of the entire brain were obtained with a 3.0T GE system using a T1-weighted spin echo pulse sequence with the following parameters: 2.0 mm sagital slices; echo time = 15 ms; repetition time=500 ms, number of excitations 1; field of view 21x21 cm; and matrix size 256x256. The images were re-sampled and aligned to the MNI standard 1 mm template. For each scan, 17 sub-cortical brain structures were segmented using a Bayesian appearance model [3]. The Bayesian segmentations are in direct correspondence between controls and patients and are used for a shape analysis using the EMD-test in two stages: a learning stage and a classification stage. In the learning stage the distribution of control shapes is modeled as distances between residual vectors using the EMD metric [4]. EMD serves as a method to compare two continuous distributions, approximated using kernel density estimation, as shown in Figure 1. In our method the learning stage computed control EMD values, which describe the variation in the control set using either permutation tests or matched controls. The EMD values were best fit using a Gamma distribution; the distribution shape is shown in Figure 2. In the classification stage the EMD was used to compute the similarity between control and patient shape residual distributions. The previously estimated Gamma distribution was then used to compute a threshold for statistical significance. Any residual has a distance greater than the 95% threshold was considered to constitute a significant variation. The threshold was learnt from the control data and computed by the integration of the inverse gamma cumulative distribution. For comparison significance maps were also generated using a corrected t-test and KS-test.

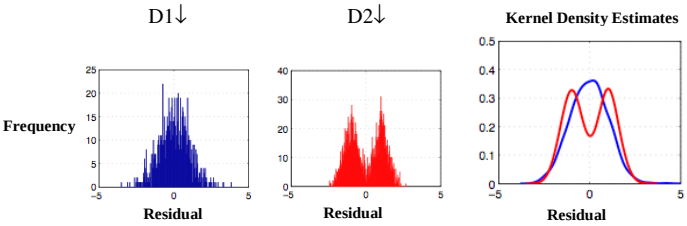
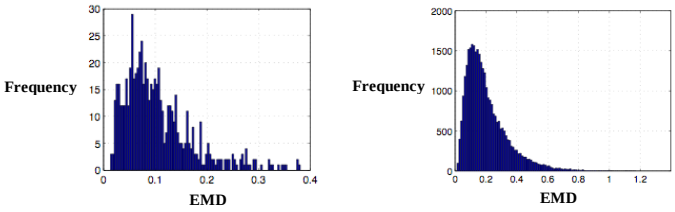


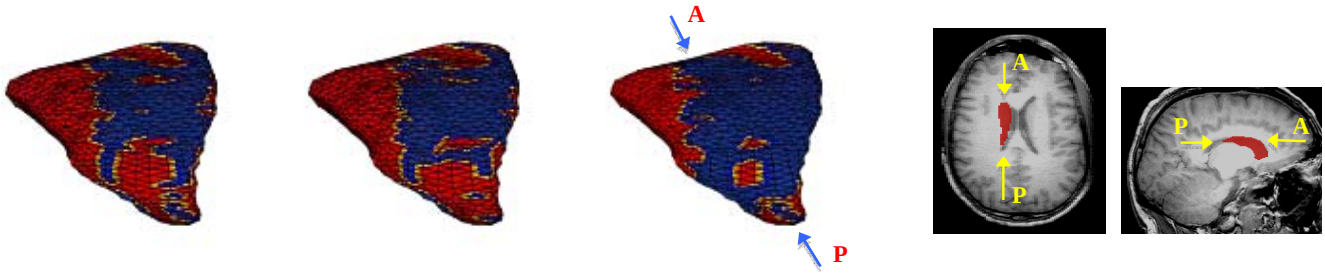

**Figure 1. An overlapping unimodal D1 and bimodal D2 distribution. Kernel Density estimates are used to compute the EMD.**




Matched Controls Permutation tests

**Figure 2. EMD distributions using matched controls or permutation tests.**

**Results:** We believe that since shape deformation is nonlinear, it should also produce non-normal shape residuals and influence statistical tests for a shape analysis. The normality of the data is not assured, and to demonstrate, an analysis of the segmented caudate is shown in Figure 3. There are noticeable differences in the result for this anatomical structure between the parametric and non-parametric methods. If the data were truly normally distributed one would expect the results to be identical across methods. The result also shows in the presence of a global atrophy of the caudate there is a differential shape change detected by all methods and for the EMD-test the relative region of significant change is smaller than the corrected tests. This indicates that the EMD-test threshold learnt from the control set is stricter when defining significant regions than FDR.




t-test (FDR corrected) (red) $p < 0.003$ | KS-test (FDR corrected) (red) $p < 0.003$ | EMD-test (red) (95% threshold)

**Figure 3. Comparing shape analysis of the caudate** (global caudate atrophy, p=0.006)

**Conclusion:** We have introduced a new method for shape analysis that does not make any underlying assumption of the distribution of aligned shape differences. The statistical significance of the data is determined by observing the variation in the control set. Without correction it produces similar results to the corrected t-test and KS-test, which in our data provided different significance maps. This indicated that caudate shape residuals were most likely not normally distributed. The EMD method is more accurate at comparing continuous distributions than the t-test, by design. The EMD-test result should also be more meaningful since the significant EMD distance threshold is empirically derived from the control data, amplifying differences between groups and accounting for inter-control variation.

**References:**

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